Nir Yosef

List of Publications by Year
in descending order

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	Slingshot: cell lineage and pseudotime inference for single-cell transcriptomics. BMC Genomics, 2018, 19, 477.	2.8	1,562
2	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
3	Deep generative modeling for single-cell transcriptomics. Nature Methods, 2018, 15, 1053-1058.	19.0	1,227
4	Sodium chloride drives autoimmune disease by the induction of pathogenic TH17 cells. Nature, 2013, 496, 518-522.	27.8	1,136
5	Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells. Nature, 2013, 498, 236-240.	27.8	1,103
6	Induction and molecular signature of pathogenic TH17 cells. Nature Immunology, 2012, 13, 991-999.	14.5	980
7	Single-cell RNA-seq reveals dynamic paracrine control of cellular variation. Nature, 2014, 510, 363-369.	27.8	872
8	Induction of pathogenic TH17 cells by inducible salt-sensing kinase SGK1. Nature, 2013, 496, 513-517.	27.8	851
9	Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis. Cell, 2011, 144, 296-309.	28.9	843
10	The epigenetic landscape of T cell exhaustion. Science, 2016, 354, 1165-1169.	12.6	694
11	Dynamic regulatory network controlling TH17 cell differentiation. Nature, 2013, 496, 461-468.	27.8	608
12	Revealing the vectors of cellular identity with single-cell genomics. Nature Biotechnology, 2016, 34, 1145-1160.	17.5	534
13	Single-Cell Genomics Unveils Critical Regulators of Th17 Cell Pathogenicity. Cell, 2015, 163, 1400-1412.	28.9	504
14	A High-Throughput Chromatin Immunoprecipitation Approach Reveals Principles of Dynamic Gene Regulation in Mammals. Molecular Cell, 2012, 47, 810-822.	9.7	375
15	CD5L/AIM Regulates Lipid Biosynthesis and Restrains Th17 Cell Pathogenicity. Cell, 2015, 163, 1413-1427.	28.9	313
16	Combinatorial Patterning of Chromatin Regulators Uncovered by Genome-wide Location Analysis in Human Cells. Cell, 2011, 147, 1628-1639.	28.9	303
17	The transcription factor BATF operates as an essential differentiation checkpoint in early effector CD8+ T cells. Nature Immunology, 2014, 15, 373-383.	14.5	289
18	The Tabula Sapiens: A multiple-organ, single-cell transcriptomic atlas of humans. Science, 2022, 376, eabl4896.	12.6	289

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19	Cross-tissue immune cell analysis reveals tissue-specific features in humans. Science, 2022, 376, eabl5197.	12.6	265
20	Molecular recording of mammalian embryogenesis. Nature, 2019, 570, 77-82.	27.8	257
21	Small-Molecule RORÎ³t Antagonists Inhibit T Helper 17 Cell Transcriptional Network by Divergent Mechanisms. Immunity, 2014, 40, 477-489.	14.3	253
22	Joint probabilistic modeling of single-cell multi-omic data with totalVI. Nature Methods, 2021, 18, 272-282.	19.0	246
23	Integrated single cell analysis of blood and cerebrospinal fluid leukocytes in multiple sclerosis. Nature Communications, 2020, 11, 247.	12.8	242
24	Mapping single-cell data to reference atlases by transfer learning. Nature Biotechnology, 2022, 40, 121-130.	17.5	236
25	Impulse Control: Temporal Dynamics in Gene Transcription. Cell, 2011, 144, 886-896.	28.9	227
26	A Python library for probabilistic analysis of single-cell omics data. Nature Biotechnology, 2022, 40, 163-166.	17.5	216
27	Probabilistic harmonization and annotation of singleâ€cell transcriptomics data with deep generative models. Molecular Systems Biology, 2021, 17, e9620.	7.2	211
28	Metabolic modeling of single Th17 cells reveals regulators of autoimmunity. Cell, 2021, 184, 4168-4185.e21.	28.9	203
29	MicroRNA-21 promotes Th17 differentiation and mediates experimental autoimmune encephalomyelitis. Journal of Clinical Investigation, 2015, 125, 1069-1080.	8.2	201
30	Medical Sequencing at the Extremes of Human Body Mass. American Journal of Human Genetics, 2007, 80, 779-791.	6.2	199
31	Systematic Discovery of TLR Signaling Components Delineates Viral-Sensing Circuits. Cell, 2011, 147, 853-867.	28.9	177
32	Functional interpretation of single cell similarity maps. Nature Communications, 2019, 10, 4376.	12.8	169
33	Single-cell lineages reveal the rates, routes, and drivers of metastasis in cancer xenografts. Science, 2021, 371, .	12.6	166
34	Deconstructing Olfactory Stem Cell Trajectories at Single-Cell Resolution. Cell Stem Cell, 2017, 20, 817-830.e8.	11.1	164
35	Nanowire-Mediated Delivery Enables Functional Interrogation of Primary Immune Cells: Application to the Analysis of Chronic Lymphocytic Leukemia. Nano Letters, 2012, 12, 6498-6504.	9.1	154
36	The single-cell epigenomic and transcriptional landscape of immunity to influenza vaccination. Cell, 2021, 184, 3915-3935.e21.	28.9	133

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37	Interpretable factor models of single-cell RNA-seq via variational autoencoders. Bioinformatics, 2020, 36, 3418-3421.	4.1	123
38	Polyamine metabolism is a central determinant of helper TÂcell lineage fidelity. Cell, 2021, 184, 4186-4202.e20.	28.9	121
39	Neurological Manifestations of COVID-19 Feature T Cell Exhaustion and Dedifferentiated Monocytes in Cerebrospinal Fluid. Immunity, 2021, 54, 164-175.e6.	14.3	119
40	Performance Assessment and Selection of Normalization Procedures for Single-Cell RNA-Seq. Cell Systems, 2019, 8, 315-328.e8.	6.2	117
41	Lineage tracing reveals the phylodynamics, plasticity, and paths of tumor evolution. Cell, 2022, 185, 1905-1923.e25.	28.9	108
42	Critical role of IRF1 and BATF in forming chromatin landscape during type 1 regulatory cell differentiation. Nature Immunology, 2017, 18, 412-421.	14.5	103
43	Toward accurate reconstruction of functional protein networks. Molecular Systems Biology, 2009, 5, 248.	7.2	90
44	Simulating multiple faceted variability in single cell RNA sequencing. Nature Communications, 2019, 10, 2611.	12.8	89
45	A genome-wide screen for essential yeast genes that affect telomere length maintenance. Nucleic Acids Research, 2009, 37, 3840-3849.	14.5	83
46	Impulse model-based differential expression analysis of time course sequencing data. Nucleic Acids Research, 2018, 46, e119.	14.5	81
47	ANAT: A Tool for Constructing and Analyzing Functional Protein Networks. Science Signaling, 2011, 4, pl1.	3.6	78
48	Systematic identification of gene annotation errors in the widely used yeast mutation collections. Nature Methods, 2012, 9, 373-378.	19.0	78
49	Hotspot identifies informative gene modules across modalities of single-cell genomics. Cell Systems, 2021, 12, 446-456.e9.	6.2	78
50	Targeted reconstruction of T cell receptor sequence from single cell RNA-seq links CDR3 length to T cell differentiation state. Nucleic Acids Research, 2017, 45, e148-e148.	14.5	77
51	Identification and Massively Parallel Characterization of Regulatory Elements Driving Neural Induction. Cell Stem Cell, 2019, 25, 713-727.e10.	11.1	76
52	DestVI identifies continuums of cell types in spatial transcriptomics data. Nature Biotechnology, 2022, 40, 1360-1369.	17.5	75
53	Use antibiotics in cell culture with caution: genome-wide identification of antibiotic-induced changes in gene expression and regulation. Scientific Reports, 2017, 7, 7533.	3.3	67
54	Injury Activates Transient Olfactory Stem Cell States with Diverse Lineage Capacities. Cell Stem Cell, 2017, 21, 775-790.e9.	11.1	67

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55	Combinatorial proteomic analysis of intercellular signaling applied to the CD28 T-cell costimulatory receptor. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1594-603.	7.1	65
56	lentiMPRA and MPRAflow for high-throughput functional characterization of gene regulatory elements. Nature Protocols, 2020, 15, 2387-2412.	12.0	65
57	Inference of single-cell phylogenies from lineage tracing data using Cassiopeia. Genome Biology, 2020, 21, 92.	8.8	61
58	FastProject: a tool for low-dimensional analysis of single-cell RNA-Seq data. BMC Bioinformatics, 2016, 17, 315.	2.6	59
59	Antiviral CD8+ T Cells Restricted by Human Leukocyte Antigen Class II Exist during Natural HIV Infection and Exhibit Clonal Expansion. Immunity, 2016, 45, 917-930.	14.3	59
60	MPRAnalyze: statistical framework for massively parallel reporter assays. Genome Biology, 2019, 20, 183.	8.8	58
61	Oleic acid restores suppressive defects in tissue-resident FOXP3 Tregs from patients with multiple sclerosis. Journal of Clinical Investigation, 2021, 131, .	8.2	56
62	An IL-27-Driven Transcriptional Network Identifies Regulators of IL-10 Expression across T Helper Cell Subsets. Cell Reports, 2020, 33, 108433.	6.4	54
63	CD4+ and CD8+ cytotoxic T lymphocytes may induce mesenchymal cell apoptosis in IgG4-related disease. Journal of Allergy and Clinical Immunology, 2021, 147, 368-382.	2.9	53
64	Oct1 and OCA-B are selectively required for CD4 memory T cell function. Journal of Experimental Medicine, 2015, 212, 2115-2131.	8.5	50
65	Metallothioneins negatively regulate IL-27-induced type 1 regulatory T-cell differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7802-7807.	7.1	48
66	Protein C receptor (PROCR) is a negative regulator of Th17 pathogenicity. Journal of Experimental Medicine, 2016, 213, 2489-2501.	8.5	48
67	Pluripotency Transcription Factor Oct4 Mediates Stepwise Nucleosome Demethylation and Depletion. Molecular and Cellular Biology, 2015, 35, 1014-1025.	2.3	47
68	Writ large: Genomic dissection of the effect of cellular environment on immune response. Science, 2016, 354, 64-68.	12.6	46
69	Integration of multiple epigenomic marks improves prediction of variant impact in saturation mutagenesis reporter assay. Human Mutation, 2019, 40, 1280-1291.	2.5	46
70	Enhancing scientific discoveries in molecular biology with deep generative models. Molecular Systems Biology, 2020, 16, e9198.	7.2	44
71	Protein Sialylation Regulates a Gene Expression Signature that Promotes Breast Cancer Cell Pathogenicity. ACS Chemical Biology, 2016, 11, 2131-2139.	3.4	43
72	Predicting gene expression in massively parallel reporter assays: A comparative study. Human Mutation, 2017, 38, 1240-1250.	2.5	39

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73	Single-cell transcriptomics of the Drosophila wing disc reveals instructive epithelium-to-myoblast interactions. ELife, 2021, 10, .	6.0	39
74	Characterization of transcript enrichment and detection bias in single-nucleus RNA-seq for mapping of distinct human adipocyte lineages. Genome Research, 2022, 32, 242-257.	5.5	39
75	ImpulseDE: detection of differentially expressed genes in time series data using impulse models. Bioinformatics, 2017, 33, 757-759.	4.1	38
76	A Reproducibility-Based Computational Framework Identifies an Inducible, Enhanced Antiviral State in Dendritic Cells from HIV-1 Elite Controllers. Genome Biology, 2018, 19, 10.	8.8	37
77	Benchmarked approaches for reconstruction of inÂvitro cell lineages and in silico models of C. elegans and M. musculus developmental trees. Cell Systems, 2021, 12, 810-826.e4.	6.2	36
78	Coverage-dependent bias creates the appearance of binary splicing in single cells. ELife, 2020, 9, .	6.0	35
79	PeakVI: A deep generative model for single-cell chromatin accessibility analysis. Cell Reports Methods, 2022, 2, 100182.	2.9	34
80	Transcriptional Regulation by CHIP/LDB Complexes. PLoS Genetics, 2010, 6, e1001063.	3.5	28
81	Self-guarding of MORC3 enables virulence factor-triggered immunity. Nature, 2021, 600, 138-142.	27.8	27
82	An Integrative Framework Reveals Signaling-to-Transcription Events in Toll-like Receptor Signaling. Cell Reports, 2017, 19, 2853-2866.	6.4	26
83	The yeast exoribonuclease Xrn1 and associated factors modulate RNA polymerase II processivity in 5â€˜ and 3â€˜ gene regions. Journal of Biological Chemistry, 2020, 295, 11435-11454.	3.4	25
84	Systems-based approaches to study immunometabolism. Cellular and Molecular Immunology, 2022, 19, 409-420.	10.5	25
85	A complex-centric view of protein network evolution. Nucleic Acids Research, 2009, 37, e88-e88.	14.5	24
86	Comparative Analysis of Immune Cells Reveals a Conserved Regulatory Lexicon. Cell Systems, 2018, 6, 381-394.e7.	6.2	19
87	Batf-mediated epigenetic control of effector CD8 + T cell differentiation. Science Immunology, 2022, 7, eabi4919.	11.9	19
88	Understanding Th17 cells through systematic genomic analyses. Current Opinion in Immunology, 2014, 28, 42-48.	5.5	18
89	T cell self-reactivity during thymic development dictates the timing of positive selection. ELife, 2021, 10, .	6.0	17
90	Ets21C sustains a pro-regenerative transcriptional program in blastema cells of Drosophila imaginal discs. Current Biology, 2022, 32, 3350-3364.e6.	3.9	17

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91	Massively parallel reporter perturbation assays uncover temporal regulatory architecture during neural differentiation. Nature Communications, 2022, 13, 1504.	12.8	16
92	Meta‐analysis of massively parallel reporter assays enables prediction of regulatory function across cell types. Human Mutation, 2019, 40, 1299-1313.	2.5	15
93	CXCR3 regulates stem and proliferative CD8+ T cells during chronic infection by promoting interactions with DCs in splenic bridging channels. Cell Reports, 2022, 38, 110266.	6.4	14
94	T Follicular Regulatory Cell–Derived Fibrinogen-like Protein 2 Regulates Production of Autoantibodies and Induction of Systemic Autoimmunity. Journal of Immunology, 2020, 205, 3247-3262.	0.8	13
95	Network-Free Inference of Knockout Effects in Yeast. PLoS Computational Biology, 2010, 6, e1000635.	3.2	11
96	Reconstructing B-cell receptor sequences from short-read single-cell RNA sequencing with BRAPeS. Life Science Alliance, 2019, 2, e201900371.	2.8	9
97	Prediction of Phenotype Information from Genotype Data. Communications in Information and Systems, 2010, 10, 99-114.	0.5	7
98	Mucosal Vaccination with Cyclic Dinucleotide Adjuvants Induces Effective T Cell Homing and IL-17–Dependent Protection against <i>Mycobacterium tuberculosis</i> Infection. Journal of Immunology, 2022, 208, 407-419.	0.8	5
99	Interactive, integrated analysis of single-cell transcriptomic and phylogenetic data with PhyloVision. Cell Reports Methods, 2022, 2, 100200.	2.9	5
100	Mango: Exploratory Data Analysis for Large-Scale Sequencing Datasets. Cell Systems, 2019, 9, 609-613.e3.	6.2	4
101	Connectivity problems on heterogeneous graphs. Algorithms for Molecular Biology, 2019, 14, 5.	1.2	3
102	A new way to build cell lineages. ELife, 2017, 6, .	6.0	2
103	Epitome: predicting epigenetic events in novel cell types with multi-cell deep ensemble learning. Nucleic Acids Research, 2021, 49, e110-e110.	14.5	1
104	Computation Resources for Molecular Biology: Special Issue 2018. Journal of Molecular Biology, 2018, 430, 2181-2183.	4.2	0
105	Evaluation of Davis et Âal.: Exploring Sequence of Determinants of Transcriptional Regulation–The Case of c-AMP Response Element. Cell Systems, 2020, 11, 2-4.	6.2	0