Dana Pe'er

List of Publications by Year
in descending order

90 papers	30,683 citations	23567 58 h-index	43889 91 g-index
103 all docs	103 docs citations	103 times ranked	40103 citing authors

#	Article	IF	Citations
1	Using Bayesian Networks to Analyze Expression Data. Journal of Computational Biology, 2000, 7, 601-620.	1.6	2,653
2	Single-Cell Mass Cytometry of Differential Immune and Drug Responses Across a Human Hematopoietic Continuum. Science, 2011, 332, 687-696.	12.6	2,097
3	Data-Driven Phenotypic Dissection of AML Reveals Progenitor-like Cells that Correlate with Prognosis. Cell, 2015, 162, 184-197.	28.9	1,791
4	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
5	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. Nature Genetics, 2003, 34, 166-176.	21.4	1,543
6	viSNE enables visualization of high dimensional single-cell data and reveals phenotypic heterogeneity of leukemia. Nature Biotechnology, 2013, 31, 545-552.	17.5	1,481
7	Single-Cell Map of Diverse Immune Phenotypes in the Breast Tumor Microenvironment. Cell, 2018, 174, 1293-1308.e36.	28.9	1,361
8	Causal Protein-Signaling Networks Derived from Multiparameter Single-Cell Data. Science, 2005, 308, 523-529.	12.6	1,267
9	Recovering Gene Interactions from Single-Cell Data Using Data Diffusion. Cell, 2018, 174, 716-729.e27.	28.9	1,197
10	Chromosomal instability drives metastasis through a cytosolic DNA response. Nature, 2018, 553, 467-472.	27.8	1,002
11	Distinct Cellular Mechanisms Underlie Anti-CTLA-4 and Anti-PD-1 Checkpoint Blockade. Cell, 2017, 170, 1120-1133.e17.	28.9	960
12	Innate Immune Landscape in Early Lung Adenocarcinoma by Paired Single-Cell Analyses. Cell, 2017, 169, 750-765.e17.	28.9	937
13	Single-Cell Trajectory Detection Uncovers Progression and Regulatory Coordination in Human B Cell Development. Cell, 2014, 157, 714-725.	28.9	838
14	An Immune Atlas of Clear Cell Renal Cell Carcinoma. Cell, 2017, 169, 736-749.e18.	28.9	751
15	Normalization of mass cytometry data with bead standards. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2013, 83A, 483-494.	1.5	655
16	Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.	30.7	604
17	Wishbone identifies bifurcating developmental trajectories from single-cell data. Nature Biotechnology, 2016, 34, 637-645.	17.5	523
18	Palladium-based mass tag cell barcoding with a doublet-filtering scheme and single-cell deconvolution algorithm. Nature Protocols, 2015, 10, 316-333.	12.0	466

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19	An Integrated Approach to Uncover Drivers of Cancer. Cell, 2010, 143, 1005-1017.	28.9	448
20	Characterization of cell fate probabilities in single-cell data with Palantir. Nature Biotechnology, 2019, 37, 451-460.	17.5	393
21	Transcriptional Basis of Mouse and Human Dendritic Cell Heterogeneity. Cell, 2019, 179, 846-863.e24.	28.9	359
22	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
23	High-resolution analysis of DNA regulatory elements by synthetic saturation mutagenesis. Nature Biotechnology, 2009, 27, 1173-1175.	17.5	322
24	PD-1 Blockade Expands Intratumoral Memory T Cells. Cancer Immunology Research, 2016, 4, 194-203.	3.4	321
25	CellRank for directed single-cell fate mapping. Nature Methods, 2022, 19, 159-170.	19.0	286
26	The emergent landscape of the mouse gut endoderm at single-cell resolution. Nature, 2019, 569, 361-367.	27.8	285
27	Regenerative lineages and immune-mediated pruning in lung cancer metastasis. Nature Medicine, 2020, 26, 259-269.	30.7	274
28	Lineage plasticity in cancer: a shared pathway of therapeutic resistance. Nature Reviews Clinical Oncology, 2020, 17, 360-371.	27.6	263
29	Epigenomic-Guided Mass Cytometry Profiling Reveals Disease-Specific Features of Exhausted CD8ÂT Cells. Immunity, 2018, 48, 1029-1045.e5.	14.3	250
30	Highly multiplexed profiling of single-cell effector functions reveals deep functional heterogeneity in response to pathogenic ligands. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E607-15.	7.1	245
31	Immune profiling of human tumors identifies CD73 as a combinatorial target in glioblastoma. Nature Medicine, 2020, 26, 39-46.	30.7	236
32	Concurrent RB1 and TP53 Alterations Define aÂSubset of EGFR-Mutant Lung Cancers at risk forÂHistologic Transformation and Inferior Clinical Outcomes. Journal of Thoracic Oncology, 2019, 14, 1784-1793.	1.1	232
33	Tumor Analyses Reveal Squamous Transformation and Off-Target Alterations As Early Resistance Mechanisms to First-line Osimertinib in <i>EGFR</i>-Mutant Lung Cancer. Clinical Cancer Research, 2020, 26, 2654-2663.	7.0	230
34	Combination antiâ€"CTLA-4 plus antiâ€"PD-1 checkpoint blockade utilizes cellular mechanisms partially distinct from monotherapies. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22699-22709.	7.1	226
35	Conditional density-based analysis of T cell signaling in single-cell data. Science, 2014, 346, 1250689.	12.6	188
36	Integrated Single-Cell Atlas of Endothelial Cells of the Human Lung. Circulation, 2021, 144, 286-302.	1.6	181

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37	Learning a Prior on Regulatory Potential from eQTL Data. PLoS Genetics, 2009, 5, e1000358.	3.5	177
38	Principles and Strategies for Developing Network Models in Cancer. Cell, 2011, 144, 864-873.	28.9	167
39	Regenerative potential of prostate luminal cells revealed by single-cell analysis. Science, 2020, 368, 497-505.	12.6	165
40	Signatures of plasticity, metastasis, and immunosuppression in an atlas of human small cell lung cancer. Cancer Cell, 2021, 39, 1479-1496.e18.	16.8	155
41	Cancer cells deploy lipocalin-2 to collect limiting iron in leptomeningeal metastasis. Science, 2020, 369, 276-282.	12.6	146
42	Measuring Signaling and RNA-Seq in the Same Cell Links Gene Expression to Dynamic Patterns of NF-κB Activation. Cell Systems, 2017, 4, 458-469.e5.	6.2	141
43	L1CAM defines the regenerative origin of metastasis-initiating cells in colorectal cancer. Nature Cancer, 2020, 1, 28-45.	13.2	137
44	A gene–environment-induced epigenetic program initiates tumorigenesis. Nature, 2021, 590, 642-648.	27.8	133
45	Identifying regulatory mechanisms using individual variation reveals key role for chromatin modification. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14062-14067.	7.1	126
46	Cell type and gene expression deconvolution with BayesPrism enables Bayesian integrative analysis across bulk and single-cell RNA sequencing in oncology. Nature Cancer, 2022, 3, 505-517.	13.2	119
47	Fully defined human pluripotent stem cell-derived microglia and tri-culture system model C3 production in Alzheimer's disease. Nature Neuroscience, 2021, 24, 343-354.	14.8	118
48	Bayesian Network Analysis of Signaling Networks: A Primer. Science Signaling, 2005, 2005, pl4-pl4.	3.6	117
49	Scalable microfluidics for single-cell RNA printing and sequencing. Genome Biology, 2015, 16, 120.	9.6	115
50	A roadmap for the Human Developmental Cell Atlas. Nature, 2021, 597, 196-205.	27.8	114
51	Using Bayesian networks to analyze expression data. , 2000, , .		110
52	Cohesin Members Stag1 and Stag2 Display Distinct Roles in Chromatin Accessibility and Topological Control of HSC Self-Renewal and Differentiation. Cell Stem Cell, 2019, 25, 682-696.e8.	11.1	106
53	Trajectories of cell-cycle progression from fixed cell populations. Nature Methods, 2015, 12, 951-954.	19.0	97
54	Environmental Stresses Disrupt Telomere Length Homeostasis. PLoS Genetics, 2013, 9, e1003721.	3.5	89

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55	Mapping Differentiation under Mixed Culture Conditions Reveals a Tunable Continuum of T Cell Fates. PLoS Biology, 2013, 11, e1001616.	5.6	86
56	Spatial CRISPR genomics identifies regulators of the tumor microenvironment. Cell, 2022, 185, 1223-1239.e20.	28.9	79
57	Integration of Genomic Data Enables Selective Discovery of Breast Cancer Drivers. Cell, 2014, 159, 1461-1475.	28.9	77
58	Negative Co-stimulation Constrains T Cell Differentiation by Imposing Boundaries on Possible Cell States. Immunity, 2019, 50, 1084-1098.e10.	14.3	75
59	Genotype-Environment Interactions Reveal Causal Pathways That Mediate Genetic Effects on Phenotype. PLoS Genetics, 2013, 9, e1003803.	3.5	72
60	Minreg: Inferring an active regulator set. Bioinformatics, 2002, 18, S258-S267.	4.1	63
61	A unified atlas of CD8 TÂcell dysfunctional states in cancer and infection. Molecular Cell, 2021, 81, 2477-2493.e10.	9.7	57
62	Radiotherapy orchestrates natural killer cell dependent antitumor immune responses through CXCL8. Science Advances, 2022, 8, eabh4050.	10.3	55
63	Modularity and interactions in the genetics of gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6441-6446.	7.1	53
64	Lymphatics act as a signaling hub to regulate intestinal stem cell activity. Cell Stem Cell, 2022, 29, 1067-1082.e18.	11.1	53
65	Single-Cell Transcriptomics Reveals Early Emergence of Liver Parenchymal and Non-parenchymal Cell Lineages. Cell, 2020, 183, 702-716.e14.	28.9	52
66	Natural Genetic Variation Reveals Key Features of Epigenetic and Transcriptional Memory in Virus-Specific CD8ÂT Cells. Immunity, 2019, 50, 1202-1217.e7.	14.3	51
67	Single-cell mass cytometry of TCR signaling: Amplification of small initial differences results in low ERK activation in NOD mice. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16466-16471.	7.1	50
68	<i>RHPN2</i> Drives Mesenchymal Transformation in Malignant Glioma by Triggering RhoA Activation. Cancer Research, 2013, 73, 5140-5150.	0.9	49
69	Harnessing gene expression to identify the genetic basis of drug resistance. Molecular Systems Biology, 2009, 5, 310.	7.2	43
70	JISTIC: Identification of Significant Targets in Cancer. BMC Bioinformatics, 2010, 11, 189.	2.6	41
71	Bayesian Inference for Single-cell Clustering and Imputing. Genomics and Computational Biology, 2017, 3, 46.	0.7	41
72	Detection of minimal residual disease in <scp>B</scp> lymphoblastic leukemia using vi<scp>SNE</scp>. Cytometry Part B - Clinical Cytometry, 2015, 88, 294-304.	1.5	39

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73	Frontiers in cancer immunotherapy—a symposium report. Annals of the New York Academy of Sciences, 2021, 1489, 30-47.	3.8	39
74	Dirichlet Process Mixture Model for Correcting Technical Variation in Single-Cell Gene Expression Data. JMLR Workshop and Conference Proceedings, 2016, 48, 1070-1079.	1.4	39
75	CD49b defines functionally mature Treg cells that survey skin and vascular tissues. Journal of Experimental Medicine, 2018, 215, 2796-2814.	8.5	37
76	Mapping the evolution of T cell states during response and resistance to adoptive cellular therapy. Cell Reports, 2021, 37, 109992.	6.4	37
77	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	19.0	37
78	Adult Human Glioblastomas Harbor Radial Glia-like Cells. Stem Cell Reports, 2020, 14, 338-350.	4.8	35
79	Interferon α/β Enhances the Cytotoxic Response of MEK Inhibition in Melanoma. Molecular Cell, 2015, 57, 784-796.	9.7	29
80	Engineering $\gamma\delta$T cells limits tonic signaling associated with chimeric antigen receptors. Science Signaling, 2019, 12, .	3.6	29
81	Learning Signaling Network Structures with Sparsely Distributed Data. Journal of Computational Biology, 2009, 16, 201-212.	1.6	25
82	PhenoGraph and viSNE facilitate the identification of abnormal T cell populations in routine clinical flow cytometric data. Cytometry Part B - Clinical Cytometry, 2018, 94, 744-757.	1.5	22
83	Learning time-varying information flow from single-cell epithelial to mesenchymal transition data. PLoS ONE, 2018, 13, e0203389.	2.5	18
84	Context Sensitive Modeling of Cancer Drug Sensitivity. PLoS ONE, 2015, 10, e0133850.	2.5	13
85	Inference of modules associated to eQTLs. Nucleic Acids Research, 2012, 40, e98-e98.	14.5	12
86	Notch3 signaling promotes tumor cell adhesion and progression in a murine epithelial ovarian cancer model. PLoS ONE, 2020, 15, e0233962.	2.5	10
87	Using systems and structure biology tools to dissect cellular phenotypes. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 171-175.	4.4	6
88	Can CAD cure cancer?. , 2013, , .		1
89	Comprehensive Single-Cell RNA-Sequencing Mapping of Primary Acute Myeloid Leukemias and Profiling of NPM1-Mutated Cells. Blood, 2018, 132, 995-995.	1.4	1
90	Stag2 Regulates Hematopoietic Differentiation and Self-Renewal through Alterations in Gene Expression and Topological Control. Blood, 2019, 134, 279-279.	1.4	0