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	CellRank for directed single-cell fate mapping. Nature Methods, 2022, 19, 159-170.	19.0	286
2	Spatial CRISPR genomics identifies regulators of the tumor microenvironment. Cell, 2022, 185, 1223-1239.e20.	28.9	79
3	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	19.0	37
4	Radiotherapy orchestrates natural killer cell dependent antitumor immune responses through CXCL8. Science Advances, 2022, 8, eabh4050.	10.3	55
5	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
6	Lymphatics act as a signaling hub to regulate intestinal stem cell activity. Cell Stem Cell, 2022, 29, 1067-1082.e18.	11.1	53
7	Frontiers in cancer immunotherapy—a symposium report. Annals of the New York Academy of Sciences, 2021, 1489, 30-47.	3.8	39
8	A gene–environment-induced epigenetic program initiates tumorigenesis. Nature, 2021, 590, 642-648.	27.8	133
9	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
10	A unified atlas of CD8 T cell dysfunctional states in cancer and infection. Molecular Cell, 2021, 81, 2477-2493.e10.	9.7	57
11	Integrated Single-Cell Atlas of Endothelial Cells of the Human Lung. Circulation, 2021, 144, 286-302.	1.6	181
12	A roadmap for the Human Developmental Cell Atlas. Nature, 2021, 597, 196-205.	27.8	114
13	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
14	Mapping the evolution of T cell states during response and resistance to adoptive cellular therapy. Cell Reports, 2021, 37, 109992.	6.4	37
15	Immune profiling of human tumors identifies CD73 as a combinatorial target in glioblastoma. Nature Medicine, 2020, 26, 39-46.	30.7	236
16	Cancer cells deploy lipocalin-2 to collect limiting iron in leptomeningeal metastasis. Science, 2020, 369, 276-282.	12.6	146
17	Single-Cell Transcriptomics Reveals Early Emergence of Liver Parenchymal and Non-parenchymal Cell Lineages. Cell, 2020, 183, 702-716.e14.	28.9	52
18	Notch3 signaling promotes tumor cell adhesion and progression in a murine epithelial ovarian cancer model. PLoS ONE, 2020, 15, e0233962.	2.5	10

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19	Lineage plasticity in cancer: a shared pathway of therapeutic resistance. Nature Reviews Clinical Oncology, 2020, 17, 360-371.	27.6	263
20	Adult Human Glioblastomas Harbor Radial Glia-like Cells. Stem Cell Reports, 2020, 14, 338-350.	4.8	35
21	Regenerative lineages and immune-mediated pruning in lung cancer metastasis. Nature Medicine, 2020, 26, 259-269.	30.7	274
22	L1CAM defines the regenerative origin of metastasis-initiating cells in colorectal cancer. Nature Cancer, 2020, 1, 28-45.	13.2	137
23	Regenerative potential of prostate luminal cells revealed by single-cell analysis. Science, 2020, 368, 497-505.	12.6	165
24	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
25	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
26	Concurrent RB1 and TP53 Alterations Define a Subset of EGFR-Mutant Lung Cancers at risk for Histologic Transformation and Inferior Clinical Outcomes. Journal of Thoracic Oncology, 2019, 14, 1784-1793.	1.1	232
27	Transcriptional Basis of Mouse and Human Dendritic Cell Heterogeneity. Cell, 2019, 179, 846-863.e24.	28.9	359
28	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
29	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
30	Engineering Î³Î´T cells limits tonic signaling associated with chimeric antigen receptors. Science Signaling, 2019, 12, .	3.6	29
31	Natural Genetic Variation Reveals Key Features of Epigenetic and Transcriptional Memory in Virus-Specific CD8 T Cells. Immunity, 2019, 50, 1202-1217.e7.	14.3	51
32	The emergent landscape of the mouse gut endoderm at single-cell resolution. Nature, 2019, 569, 361-367.	27.8	285
33	Characterization of cell fate probabilities in single-cell data with Palantir. Nature Biotechnology, 2019, 37, 451-460.	17.5	393
34	Negative Co-stimulation Constrains T Cell Differentiation by Imposing Boundaries on Possible Cell States. Immunity, 2019, 50, 1084-1098.e10.	14.3	75
35	Stag2 Regulates Hematopoietic Differentiation and Self-Renewal through Alterations in Gene Expression and Topological Control. Blood, 2019, 134, 279-279.	1.4	0
36	Chromosomal instability drives metastasis through a cytosolic DNA response. Nature, 2018, 553, 467-472.	27.8	1,002

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37	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
38	CD49b defines functionally mature Treg cells that survey skin and vascular tissues. Journal of Experimental Medicine, 2018, 215, 2796-2814.	8.5	37
39	Learning time-varying information flow from single-cell epithelial to mesenchymal transition data. PLoS ONE, 2018, 13, e0203389.	2.5	18
40	Epigenomic-Guided Mass Cytometry Profiling Reveals Disease-Specific Features of Exhausted CD8ÂT Cells. Immunity, 2018, 48, 1029-1045.e5.	14.3	250
41	Single-Cell Map of Diverse Immune Phenotypes in the Breast Tumor Microenvironment. Cell, 2018, 174, 1293-1308.e36.	28.9	1,361
42	Recovering Gene Interactions from Single-Cell Data Using Data Diffusion. Cell, 2018, 174, 716-729.e27.	28.9	1,197
43	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
44	Innate Immune Landscape in Early Lung Adenocarcinoma by Paired Single-Cell Analyses. Cell, 2017, 169, 750-765.e17.	28.9	937
45	An Immune Atlas of Clear Cell Renal Cell Carcinoma. Cell, 2017, 169, 736-749.e18.	28.9	751
46	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
47	Distinct Cellular Mechanisms Underlie Anti-CTLA-4 and Anti-PD-1 Checkpoint Blockade. Cell, 2017, 170, 1120-1133.e17.	28.9	960
48	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
49	Bayesian Inference for Single-cell Clustering and Imputing. Genomics and Computational Biology, 2017, 3, 46.	0.7	41
50	Wishbone identifies bifurcating developmental trajectories from single-cell data. Nature Biotechnology, 2016, 34, 637-645.	17.5	523
51	PD-1 Blockade Expands Intratumoral Memory T Cells. Cancer Immunology Research, 2016, 4, 194-203.	3.4	321
52	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
53	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
54	Scalable microfluidics for single-cell RNA printing and sequencing. Genome Biology, 2015, 16, 120.	9.6	115

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55	Context Sensitive Modeling of Cancer Drug Sensitivity. PLoS ONE, 2015, 10, e0133850.	2.5	13
56	Interferon Î±/Î² Enhances the Cytotoxic Response of MEK Inhibition in Melanoma. Molecular Cell, 2015, 57, 784-796.	9.7	29
57	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
58	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
59	Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.	30.7	604
60	Data-Driven Phenotypic Dissection of AML Reveals Progenitor-like Cells that Correlate with Prognosis. Cell, 2015, 162, 184-197.	28.9	1,791
61	Trajectories of cell-cycle progression from fixed cell populations. Nature Methods, 2015, 12, 951-954.	19.0	97
62	Integration of Genomic Data Enables Selective Discovery of Breast Cancer Drivers. Cell, 2014, 159, 1461-1475.	28.9	77
63	Conditional density-based analysis of T cell signaling in single-cell data. Science, 2014, 346, 1250689.	12.6	188
64	Single-Cell Trajectory Detection Uncovers Progression and Regulatory Coordination in Human B Cell Development. Cell, 2014, 157, 714-725.	28.9	838
65	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
66	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
67	Can CAD cure cancer?. , 2013, , .		1
68	Environmental Stresses Disrupt Telomere Length Homeostasis. PLoS Genetics, 2013, 9, e1003721.	3.5	89
69	Genotype-Environment Interactions Reveal Causal Pathways That Mediate Genetic Effects on Phenotype. PLoS Genetics, 2013, 9, e1003803.	3.5	72
70	Mapping Differentiation under Mixed Culture Conditions Reveals a Tunable Continuum of T Cell Fates. PLoS Biology, 2013, 11, e1001616.	5.6	86
71	<i>RHPN2</i> Drives Mesenchymal Transformation in Malignant Glioma by Triggering RhoA Activation. Cancer Research, 2013, 73, 5140-5150.	0.9	49
72	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

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73	Inference of modules associated to eQTLs. Nucleic Acids Research, 2012, 40, e98-e98.	14.5	12
74	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
75	Principles and Strategies for Developing Network Models in Cancer. Cell, 2011, 144, 864-873.	28.9	167
76	Single-Cell Mass Cytometry of Differential Immune and Drug Responses Across a Human Hematopoietic Continuum. Science, 2011, 332, 687-696.	12.6	2,097
77	JISTIC: Identification of Significant Targets in Cancer. BMC Bioinformatics, 2010, 11, 189.	2.6	41
78	An Integrated Approach to Uncover Drivers of Cancer. Cell, 2010, 143, 1005-1017.	28.9	448
79	Learning Signaling Network Structures with Sparsely Distributed Data. Journal of Computational Biology, 2009, 16, 201-212.	1.6	25
80	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
81	Harnessing gene expression to identify the genetic basis of drug resistance. Molecular Systems Biology, 2009, 5, 310.	7.2	43
82	Learning a Prior on Regulatory Potential from eQTL Data. PLoS Genetics, 2009, 5, e1000358.	3.5	177
83	High-resolution analysis of DNA regulatory elements by synthetic saturation mutagenesis. Nature Biotechnology, 2009, 27, 1173-1175.	17.5	322
84	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
85	Bayesian Network Analysis of Signaling Networks: A Primer. Science Signaling, 2005, 2005, pl4-pl4.	3.6	117
86	Causal Protein-Signaling Networks Derived from Multiparameter Single-Cell Data. Science, 2005, 308, 523-529.	12.6	1,267
87	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. Nature Genetics, 2003, 34, 166-176.	21.4	1,543
88	Minreg: Inferring an active regulator set. Bioinformatics, 2002, 18, S258-S267.	4.1	63
89	Using Bayesian networks to analyze expression data. , 2000, , .		110
90	Using Bayesian Networks to Analyze Expression Data. Journal of Computational Biology, 2000, 7, 601-620.	1.6	2,653