Dana Pe'er

List of Publications by Year
in descending order

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		27035	49824
90	30,683	58	91
papers	citations	h-index	g-index
103	103	103	44189
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	CellRank for directed single-cell fate mapping. Nature Methods, 2022, 19, 159-170.	9.0	286
2	Spatial CRISPR genomics identifies regulators of the tumor microenvironment. Cell, 2022, 185, 1223-1239.e20.	13.5	79
3	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	9.0	37
4	Radiotherapy orchestrates natural killer cell dependent antitumor immune responses through CXCL8. Science Advances, 2022, 8, eabh4050.	4.7	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.	5.7	119
6	Lymphatics act as a signaling hub to regulate intestinal stem cell activity. Cell Stem Cell, 2022, 29, 1067-1082.e18.	5.2	53
7	Frontiers in cancer immunotherapyâ€”a symposium report. Annals of the New York Academy of Sciences, 2021, 1489, 30-47.	1.8	39
8	A geneâ€“environment-induced epigenetic program initiates tumorigenesis. Nature, 2021, 590, 642-648.	13.7	133
9	Fully defined human pluripotent stem cell-derived microglia and tri-culture system model C3 production in Alzheimerâ€™s disease. Nature Neuroscience, 2021, 24, 343-354.	7.1	118
10	A unified atlas of CD8 TÂcell dysfunctional states in cancer and infection. Molecular Cell, 2021, 81, 2477-2493.e10.	4.5	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.	13.7	114
13	Signatures of plasticity, metastasis, and immunosuppression in an atlas of human small cell lung cancer. Cancer Cell, 2021, 39, 1479-1496.e18.	7.7	155
14	Mapping the evolution of TÂcell states during response and resistance to adoptive cellular therapy. Cell Reports, 2021, 37, 109992.	2.9	37
15	Immune profiling of human tumors identifies CD73 as a combinatorial target in glioblastoma. Nature Medicine, 2020, 26, 39-46.	15.2	236
16	Cancer cells deploy lipocalin-2 to collect limiting iron in leptomeningeal metastasis. Science, 2020, 369, 276-282.	6.0	146
17	Single-Cell Transcriptomics Reveals Early Emergence of Liver Parenchymal and Non-parenchymal Cell Lineages. Cell, 2020, 183, 702-716.e14.	13.5	52
18	Notch3 signaling promotes tumor cell adhesion and progression in a murine epithelial ovarian cancer model. PLoS ONE, 2020, 15, e0233962.	1.1	10

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19	Lineage plasticity in cancer: a shared pathway of therapeutic resistance. Nature Reviews Clinical Oncology, 2020, 17, 360-371.	12.5	263
20	Adult Human Glioblastomas Harbor Radial Glia-like Cells. Stem Cell Reports, 2020, 14, 338-350.	2.3	35
21	Regenerative lineages and immune-mediated pruning in lung cancer metastasis. Nature Medicine, 2020, 26, 259-269.	15.2	274
22	L1CAM defines the regenerative origin of metastasis-initiating cells in colorectal cancer. Nature Cancer, 2020, 1, 28-45.	5.7	137
23	Regenerative potential of prostate luminal cells revealed by single-cell analysis. Science, 2020, 368, 497-505.	6.0	165
24	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	13.5	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.	3.2	230
26	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.	0.5	232
27	Transcriptional Basis of Mouse and Human Dendritic Cell Heterogeneity. Cell, 2019, 179, 846-863.e24.	13.5	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.	3.3	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.	5.2	106
30	Engineering Î³ÎT cells limits tonic signaling associated with chimeric antigen receptors. Science Signaling, 2019, 12, .	1.6	29
31	Natural Genetic Variation Reveals Key Features of Epigenetic and Transcriptional Memory in Virus-Specific CD8ÂT Cells. Immunity, 2019, 50, 1202-1217.e7.	6.6	51
32	The emergent landscape of the mouse gut endoderm at single-cell resolution. Nature, 2019, 569, 361-367.	13.7	285
33	Characterization of cell fate probabilities in single-cell data with Palantir. Nature Biotechnology, 2019, 37, 451-460.	9.4	393
34	Negative Co-stimulation Constrains T Cell Differentiation by Imposing Boundaries on Possible Cell States. Immunity, 2019, 50, 1084-1098.e10.	6.6	75
35	Stag2 Regulates Hematopoietic Differentiation and Self-Renewal through Alterations in Gene Expression and Topological Control. Blood, 2019, 134, 279-279.	0.6	0
36	Chromosomal instability drives metastasis through a cytosolic DNA response. Nature, 2018, 553, 467-472.	13.7	1,002

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37	PhenoGraph and viSNE facilitate the identification of abnormal Tâ€cell populations in routine clinical flow cytometric data. Cytometry Part B - Clinical Cytometry, 2018, 94, 744-757.	0.7	22
38	CD49b defines functionally mature Treg cells that survey skin and vascular tissues. Journal of Experimental Medicine, 2018, 215, 2796-2814.	4.2	37
39	Learning time-varying information flow from single-cell epithelial to mesenchymal transition data. PLoS ONE, 2018, 13, e0203389.	1.1	18
40	Epigenomic-Guided Mass Cytometry Profiling Reveals Disease-Specific Features of Exhausted CD8ÂT Cells. Immunity, 2018, 48, 1029-1045.e5.	6.6	250
41	Single-Cell Map of Diverse Immune Phenotypes in the Breast Tumor Microenvironment. Cell, 2018, 174, 1293-1308.e36.	13.5	1,361
42	Recovering Gene Interactions from Single-Cell Data Using Data Diffusion. Cell, 2018, 174, 716-729.e27.	13.5	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.	0.6	1
44	Innate Immune Landscape in Early Lung Adenocarcinoma by Paired Single-Cell Analyses. Cell, 2017, 169, 750-765.e17.	13.5	937
45	An Immune Atlas of Clear Cell Renal Cell Carcinoma. Cell, 2017, 169, 736-749.e18.	13.5	751
46	Measuring Signaling and RNA-Seq in the Same Cell Links Gene Expression to Dynamic Patterns of NF-ÎºB Activation. Cell Systems, 2017, 4, 458-469.e5.	2.9	141
47	Distinct Cellular Mechanisms Underlie Anti-CTLA-4 and Anti-PD-1 Checkpoint Blockade. Cell, 2017, 170, 1120-1133.e17.	13.5	960
48	The Human Cell Atlas. ELife, 2017, 6, .	2.8	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.	9.4	523
51	PD-1 Blockade Expands Intratumoral Memory T Cells. Cancer Immunology Research, 2016, 4, 194-203.	1.6	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.	0.7	39
54	Scalable microfluidics for single-cell RNA printing and sequencing. Genome Biology, 2015, 16, 120.	13.9	115

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55	Context Sensitive Modeling of Cancer Drug Sensitivity. PLoS ONE, 2015, 10, e0133850.	1.1	13
56	Interferon Î±/Î² Enhances the Cytotoxic Response of MEK Inhibition in Melanoma. Molecular Cell, 2015, 57, 784-796.	4.5	29
57	Palladium-based mass tag cell barcoding with a doublet-filtering scheme and single-cell deconvolution algorithm. Nature Protocols, 2015, 10, 316-333.	5.5	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.	3.3	245
59	Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.	15.2	604
60	Data-Driven Phenotypic Dissection of AML Reveals Progenitor-like Cells that Correlate with Prognosis. Cell, 2015, 162, 184-197.	13.5	1,791
61	Trajectories of cell-cycle progression from fixed cell populations. Nature Methods, 2015, 12, 951-954.	9.0	97
62	Integration of Genomic Data Enables Selective Discovery of Breast Cancer Drivers. Cell, 2014, 159, 1461-1475.	13.5	77
63	Conditional density-based analysis of T cell signaling in single-cell data. Science, 2014, 346, 1250689.	6.0	188
64	Single-Cell Trajectory Detection Uncovers Progression and Regulatory Coordination in Human B Cell Development. Cell, 2014, 157, 714-725.	13.5	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.	3.3	50
66	viSNE enables visualization of high dimensional single-cell data and reveals phenotypic heterogeneity of leukemia. Nature Biotechnology, 2013, 31, 545-552.	9.4	1,481
67	Can CAD cure cancer?. , 2013, , .		1
68	Environmental Stresses Disrupt Telomere Length Homeostasis. PLoS Genetics, 2013, 9, e1003721.	1.5	89
69	Genotype-Environment Interactions Reveal Causal Pathways That Mediate Genetic Effects on Phenotype. PLoS Genetics, 2013, 9, e1003803.	1.5	72
70	Mapping Differentiation under Mixed Culture Conditions Reveals a Tunable Continuum of T Cell Fates. PLoS Biology, 2013, 11, e1001616.	2.6	86
71	<i>RHPN2</i> Drives Mesenchymal Transformation in Malignant Glioma by Triggering RhoA Activation. Cancer Research, 2013, 73, 5140-5150.	0.4	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.	1.1	655

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73	Inference of modules associated to eQTLs. Nucleic Acids Research, 2012, 40, e98-e98.	6.5	12
74	Using systems and structure biology tools to dissect cellular phenotypes. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 171-175.	2.2	6
75	Principles and Strategies for Developing Network Models in Cancer. Cell, 2011, 144, 864-873.	13.5	167
76	Single-Cell Mass Cytometry of Differential Immune and Drug Responses Across a Human Hematopoietic Continuum. Science, 2011, 332, 687-696.	6.0	2,097
77	JISTIC: Identification of Significant Targets in Cancer. BMC Bioinformatics, 2010, 11, 189.	1.2	41
78	An Integrated Approach to Uncover Drivers of Cancer. Cell, 2010, 143, 1005-1017.	13.5	448
79	Learning Signaling Network Structures with Sparsely Distributed Data. Journal of Computational Biology, 2009, 16, 201-212.	0.8	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.	3.3	53
81	Harnessing gene expression to identify the genetic basis of drug resistance. Molecular Systems Biology, 2009, 5, 310.	3.2	43
82	Learning a Prior on Regulatory Potential from eQTL Data. PLoS Genetics, 2009, 5, e1000358.	1.5	177
83	High-resolution analysis of DNA regulatory elements by synthetic saturation mutagenesis. Nature Biotechnology, 2009, 27, 1173-1175.	9.4	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.	3.3	126
85	Bayesian Network Analysis of Signaling Networks: A Primer. Science Signaling, 2005, 2005, pl4-pl4.	1.6	117
86	Causal Protein-Signaling Networks Derived from Multiparameter Single-Cell Data. Science, 2005, 308, 523-529.	6.0	1,267
87	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. Nature Genetics, 2003, 34, 166-176.	9.4	1,543
88	Minreg: Inferring an active regulator set. Bioinformatics, 2002, 18, S258-S267.	1.8	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.	0.8	2,653