Orit Rozenblatt-Rosen

List of Publications by Year
in descending order

68 papers	30,933 citations	29994 54 h-index	95083 68 g-index
90 all docs	90 docs citations	90 times ranked	41660 citing authors

#	ARTICLE	IF	CITATIONS
1	Single‐Cell, Single‐Nucleus, and Spatial RNA Sequencing of the Human Liver Identifies Cholangiocyte and Mesenchymal Heterogeneity. Hepatology Communications, 2022, 6, 821-840.	2.0	98
2	Massively parallel phenotyping of coding variants in cancer with Perturb-seq. Nature Biotechnology, 2022, 40, 896-905.	9.4	44
3	SM-Omics is an automated platform for high-throughput spatial multi-omics. Nature Communications, 2022, 13, 795.	5.8	73
4	Tim-3 adapter protein Bat3 acts as an endogenous regulator of tolerogenic dendritic cell function. Science Immunology, 2022, 7, eabm0631.	5.6	22
5	Single-cell RNA-seq reveals cell type–specific molecular and genetic associations to lupus. Science, 2022, 376, eabf1970.	6.0	156
6	Stepwise-edited, human melanoma models reveal mutations' effect on tumor and microenvironment. Science, 2022, 376, eabi8175.	6.0	24
7	Single-nucleus cross-tissue molecular reference maps toward understanding disease gene function. Science, 2022, 376, eabl4290.	6.0	180
8	Tissue-resident memory and circulating T cells are early responders to pre-surgical cancer immunotherapy. Cell, 2022, 185, 2918-2935.e29.	13.5	113
9	Opposing immune and genetic mechanisms shape oncogenic programs in synovial sarcoma. Nature Medicine, 2021, 27, 289-300.	15.2	64
10	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. Science, 2021, 371, .	6.0	197
11	Building a high-quality Human Cell Atlas. Nature Biotechnology, 2021, 39, 149-153.	9.4	48
12	Multimodal pooled Perturb-CITE-seq screens in patient models define mechanisms of cancer immune evasion. Nature Genetics, 2021, 53, 332-341.	9.4	112
13	Transcriptional mediators of treatment resistance in lethal prostate cancer. Nature Medicine, 2021, 27, 426-433.	15.2	90
14	Tim-3 adaptor protein Bat3 is a molecular checkpoint of T cell terminal differentiation and exhaustion. Science Advances, 2021, 7, .	4.7	18
15	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. Nature, 2021, 595, 107-113.	13.7	537
16	Tumor and immune reprogramming during immunotherapy in advanced renal cell carcinoma. Cancer Cell, 2021, 39, 649-661.e5.	7.7	263
17	A cellular and spatial map of the choroid plexus across brain ventricles and ages. Cell, 2021, 184, 3056-3074.e21.	13.5	150
18	Interactions between cancer cells and immune cells drive transitions to mesenchymal-like states in glioblastoma. Cancer Cell, 2021, 39, 779-792.e11.	7.7	245

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19	TIM-3 restrains anti-tumour immunity by regulating inflammasome activation. Nature, 2021, 595, 101-106.	13.7	169
20	B cell genomics behind cross-neutralization of SARS-CoV-2 variants and SARS-CoV. Cell, 2021, 184, 3205-3221.e24.	13.5	73
21	Spatially organized multicellular immune hubs in human colorectal cancer. Cell, 2021, 184, 4734-4752.e20.	13.5	256
22	Blood and immune development in human fetal bone marrow and Down syndrome. Nature, 2021, 598, 327-331.	13.7	73
23	A roadmap for the Human Developmental Cell Atlas. Nature, 2021, 597, 196-205.	13.7	114
24	Epigenetic encoding, heritability and plasticity of glioma transcriptional cell states. Nature Genetics, 2021, 53, 1469-1479.	9.4	100
25	Stem-like intestinal Th17 cells give rise to pathogenic effector TÂcells during autoimmunity. Cell, 2021, 184, 6281-6298.e23.	13.5	99
26	Differential pre-malignant programs and microenvironment chart distinct paths to malignancy in human colorectal polyps. Cell, 2021, 184, 6262-6280.e26.	13.5	125
27	Single-Cell RNA-Seq Reveals Cellular Hierarchies and Impaired Developmental Trajectories in Pediatric Ependymoma. Cancer Cell, 2020, 38, 44-59.e9.	7.7	94
28	An IL-27-Driven Transcriptional Network Identifies Regulators of IL-10 Expression across T Helper Cell Subsets. Cell Reports, 2020, 33, 108433.	2.9	54
29	Cumulus provides cloud-based data analysis for large-scale single-cell and single-nucleus RNA-seq. Nature Methods, 2020, 17, 793-798.	9.0	134
30	Pan-cancer single-cell RNA-seq identifies recurring programs of cellular heterogeneity. Nature Genetics, 2020, 52, 1208-1218.	9.4	226
31	The Human and Mouse Enteric Nervous System at Single-Cell Resolution. Cell, 2020, 182, 1606-1622.e23.	13.5	287
32	Multiplexed single-cell transcriptional response profiling to define cancer vulnerabilities and therapeutic mechanism of action. Nature Communications, 2020, 11, 4296.	5.8	98
33	Endogenous Glucocorticoid Signaling Regulates CD8+ T Cell Differentiation and Development of Dysfunction in the Tumor Microenvironment. Immunity, 2020, 53, 658-671.e6.	6.6	98
34	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. Nature Medicine, 2020, 26, 792-802.	15.2	381
35	A single-cell landscape of high-grade serous ovarian cancer. Nature Medicine, 2020, 26, 1271-1279.	15.2	267
36	National Cancer Institute Think-Tank Meeting Report on Proteomic Cartography and Biomarkers at the Single-Cell Level: Interrogation of Premalignant Lesions. Journal of Proteome Research, 2020, 19, 1900-1912.	1.8	8

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37	Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. Nature Biotechnology, 2020, 38, 737-746.	9.4	527
38	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	13.5	334
39	Abstract PR-007: Single-nucleus and spatial transcriptomics of archival pancreatic ductal adenocarcinoma reveals multi-compartment reprogramming after neoadjuvant treatment. Cancer Research, 2020, 80, PR-007-PR-007.	0.4	3
40	Anti-Tumor TCF1+ CD8 T Cells are Functionally Diverse and Evolve During Tumorigenesis and Progression. American Journal of Clinical Pathology, 2020, 154, S5-S6.	0.4	0
41	Mitogenic and progenitor gene programmes in single pilocytic astrocytoma cells. Nature Communications, 2019, 10, 3731.	5.8	45
42	An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. Cell, 2019, 178, 835-849.e21.	13.5	1,408
43	Resolving medulloblastoma cellular architecture by single-cell genomics. Nature, 2019, 572, 74-79.	13.7	273
44	Intra- and Inter-cellular Rewiring of the Human Colon during Ulcerative Colitis. Cell, 2019, 178, 714-730.e22.	13.5	806
45	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. Nature Communications, 2019, 10, 2907.	5.8	117
46	Transcriptional Atlas of Intestinal Immune Cells Reveals that Neuropeptide Î±-CGRP Modulates Group 2 Innate Lymphoid Cell Responses. Immunity, 2019, 51, 696-708.e9.	6.6	154
47	Decoding human fetal liver haematopoiesis. Nature, 2019, 574, 365-371.	13.7	392
48	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	3.1	57
49	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. Cell, 2019, 176, 1325-1339.e22.	13.5	345
50	Checkpoint Blockade Immunotherapy Induces Dynamic Changes in PD-1â¯CD8+ Tumor-Infiltrating T Cells. Immunity, 2019, 50, 181-194.e6.	6.6	424
51	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. Science, 2018, 360, 331-335.	6.0	461
52	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. Cell, 2018, 175, 984-997.e24.	13.5	892
53	T Helper Cell Cytokines Modulate Intestinal Stem Cell Renewal and Differentiation. Cell, 2018, 175, 1307-1320.e22.	13.5	388
54	A revised airway epithelial hierarchy includes CFTR-expressing ionocytes. Nature, 2018, 560, 319-324.	13.7	878

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55	Induction and transcriptional regulation of the co-inhibitory gene module in T cells. Nature, 2018, 558, 454-459.	13.7	336
56	Single-cell RNA-seq reveals new types of human blood dendritic cells, monocytes, and progenitors. Science, 2017, 356, .	6.0	1,846
57	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science, 2017, 355, .	6.0	743
58	Single-cell transcriptomics to explore the immune system in health and disease. Science, 2017, 358, 58-63.	6.0	440
59	The neuropeptide NMU amplifies ILC2-driven allergic lung inflammation. Nature, 2017, 549, 351-356.	13.7	460
60	Single-Cell Transcriptomic Analysis of Primary and Metastatic Tumor Ecosystems in Head and Neck Cancer. Cell, 2017, 171, 1611-1624.e24.	13.5	1,656
61	A single-cell survey of the small intestinal epithelium. Nature, 2017, 551, 333-339.	13.7	1,197
62	Massively parallel single-nucleus RNA-seq with DroNc-seq. Nature Methods, 2017, 14, 955-958.	9.0	859
63	The Human Cell Atlas. ELife, 2017, 6, .	2.8	1,547
64	Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. Science, 2016, 352, 189-196.	6.0	3,421
65	A Distinct Gene Module for Dysfunction Uncoupled from Activation in Tumor-Infiltrating T Cells. Cell, 2016, 166, 1500-1511.e9.	13.5	315
66	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. Nature, 2016, 539, 309-313.	13.7	875
67	Reconstructing and Reprogramming the Tumor-Propagating Potential of Glioblastoma Stem-like Cells. Cell, 2014, 157, 580-594.	13.5	751
68	Single-cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma. Science, 2014, 344, 1396-1401.	6.0	3,648