

# Orit Rozenblatt-Rosen

## List of Publications by Year in descending order

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Version: 2024-02-01

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 RNA-seq highlights intratumoral heterogeneity in primary glioblastoma. <i>Science</i> , 2014, 344, 1396-1401.	6.0	3,648
2	Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. <i>Science</i> , 2016, 352, 189-196.	6.0	3,421
3	Single-cell RNA-seq reveals new types of human blood dendritic cells, monocytes, and progenitors. <i>Science</i> , 2017, 356, .	6.0	1,846
4	Single-Cell Transcriptomic Analysis of Primary and Metastatic Tumor Ecosystems in Head and Neck Cancer. <i>Cell</i> , 2017, 171, 1611-1624.e24.	13.5	1,656
5	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	2.8	1,547
6	An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. <i>Cell</i> , 2019, 178, 835-849.e21.	13.5	1,408
7	A single-cell survey of the small intestinal epithelium. <i>Nature</i> , 2017, 551, 333-339.	13.7	1,197
8	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. <i>Cell</i> , 2018, 175, 984-997.e24.	13.5	892
9	A revised airway epithelial hierarchy includes CFTR-expressing ionocytes. <i>Nature</i> , 2018, 560, 319-324.	13.7	878
10	Single-cell RNA-seq supports a developmental hierarchy in human oligodendrogloma. <i>Nature</i> , 2016, 539, 309-313.	13.7	875
11	Massively parallel single-nucleus RNA-seq with DroNc-seq. <i>Nature Methods</i> , 2017, 14, 955-958.	9.0	859
12	Intra- and Inter-cellular Rewiring of the Human Colon during Ulcerative Colitis. <i>Cell</i> , 2019, 178, 714-730.e22.	13.5	806
13	Reconstructing and Reprogramming the Tumor-Propagating Potential of Glioblastoma Stem-like Cells. <i>Cell</i> , 2014, 157, 580-594.	13.5	751
14	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. <i>Science</i> , 2017, 355, .	6.0	743
15	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , 2021, 595, 107-113.	13.7	537
16	Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. <i>Nature Biotechnology</i> , 2020, 38, 737-746.	9.4	527
17	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018, 360, 331-335.	6.0	461
18	The neuropeptide NMU amplifies ILC2-driven allergic lung inflammation. <i>Nature</i> , 2017, 549, 351-356.	13.7	460

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19	Single-cell transcriptomics to explore the immune system in health and disease. <i>Science</i> , 2017, 358, 58-63.	6.0	440
20	Checkpoint Blockade Immunotherapy Induces Dynamic Changes in PD-1 <sup>hi</sup> CD8 <sup>+</sup> Tumor-Infiltrating T Cells. <i>Immunity</i> , 2019, 50, 181-194.e6.	6.6	424
21	Decoding human fetal liver haematopoiesis. <i>Nature</i> , 2019, 574, 365-371.	13.7	392
22	T Helper Cell Cytokines Modulate Intestinal Stem Cell Renewal and Differentiation. <i>Cell</i> , 2018, 175, 1307-1320.e22.	13.5	388
23	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. <i>Nature Medicine</i> , 2020, 26, 792-802.	15.2	381
24	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. <i>Cell</i> , 2019, 176, 1325-1339.e22.	13.5	345
25	Induction and transcriptional regulation of the co-inhibitory gene module in T cells. <i>Nature</i> , 2018, 558, 454-459.	13.7	336
26	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	13.5	334
27	A Distinct Gene Module for Dysfunction Uncoupled from Activation in Tumor-Infiltrating T Cells. <i>Cell</i> , 2016, 166, 1500-1511.e9.	13.5	315
28	The Human and Mouse Enteric Nervous System at Single-Cell Resolution. <i>Cell</i> , 2020, 182, 1606-1622.e23.	13.5	287
29	Resolving medulloblastoma cellular architecture by single-cell genomics. <i>Nature</i> , 2019, 572, 74-79.	13.7	273
30	A single-cell landscape of high-grade serous ovarian cancer. <i>Nature Medicine</i> , 2020, 26, 1271-1279.	15.2	267
31	Tumor and immune reprogramming during immunotherapy in advanced renal cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 649-661.e5.	7.7	263
32	Spatially organized multicellular immune hubs in human colorectal cancer. <i>Cell</i> , 2021, 184, 4734-4752.e20.	13.5	256
33	Interactions between cancer cells and immune cells drive transitions to mesenchymal-like states in glioblastoma. <i>Cancer Cell</i> , 2021, 39, 779-792.e11.	7.7	245
34	Pan-cancer single-cell RNA-seq identifies recurring programs of cellular heterogeneity. <i>Nature Genetics</i> , 2020, 52, 1208-1218.	9.4	226
35	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. <i>Science</i> , 2021, 371, .	6.0	197
36	Single-nucleus cross-tissue molecular reference maps toward understanding disease gene function. <i>Science</i> , 2022, 376, eabl4290.	6.0	180

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37	TIM-3 restrains anti-tumour immunity by regulating inflammasome activation. <i>Nature</i> , 2021, 595, 101-106.	13.7	169
38	Single-cell RNA-seq reveals cell type-specific molecular and genetic associations to lupus. <i>Science</i> , 2022, 376, eabf1970.	6.0	156
39	Transcriptional Atlas of Intestinal Immune Cells Reveals that Neuropeptide $\hat{\pm}$ -CGRP Modulates Group 2 Innate Lymphoid Cell Responses. <i>Immunity</i> , 2019, 51, 696-708.e9.	6.6	154
40	A cellular and spatial map of the choroid plexus across brain ventricles and ages. <i>Cell</i> , 2021, 184, 3056-3074.e21.	13.5	150
41	Cumulus provides cloud-based data analysis for large-scale single-cell and single-nucleus RNA-seq. <i>Nature Methods</i> , 2020, 17, 793-798.	9.0	134
42	Differential pre-malignant programs and microenvironment chart distinct paths to malignancy in human colorectal polyps. <i>Cell</i> , 2021, 184, 6262-6280.e26.	13.5	125
43	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. <i>Nature Communications</i> , 2019, 10, 2907.	5.8	117
44	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021, 597, 196-205.	13.7	114
45	Tissue-resident memory and circulating T cells are early responders to pre-surgical cancer immunotherapy. <i>Cell</i> , 2022, 185, 2918-2935.e29.	13.5	113
46	Multimodal pooled Perturb-CITE-seq screens in patient models define mechanisms of cancer immune evasion. <i>Nature Genetics</i> , 2021, 53, 332-341.	9.4	112
47	Epigenetic encoding, heritability and plasticity of glioma transcriptional cell states. <i>Nature Genetics</i> , 2021, 53, 1469-1479.	9.4	100
48	Stem-like intestinal Th17 cells give rise to pathogenic effector T cells during autoimmunity. <i>Cell</i> , 2021, 184, 6281-6298.e23.	13.5	99
49	Multiplexed single-cell transcriptional response profiling to define cancer vulnerabilities and therapeutic mechanism of action. <i>Nature Communications</i> , 2020, 11, 4296.	5.8	98
50	Endogenous Glucocorticoid Signaling Regulates CD8+ T Cell Differentiation and Development of Dysfunction in the Tumor Microenvironment. <i>Immunity</i> , 2020, 53, 658-671.e6.	6.6	98
51	Single-Cell, Single-Nucleus, and Spatial RNA Sequencing of the Human Liver Identifies Cholangiocyte and Mesenchymal Heterogeneity. <i>Hepatology Communications</i> , 2022, 6, 821-840.	2.0	98
52	Single-Cell RNA-Seq Reveals Cellular Hierarchies and Impaired Developmental Trajectories in Pediatric Ependymoma. <i>Cancer Cell</i> , 2020, 38, 44-59.e9.	7.7	94
53	Transcriptional mediators of treatment resistance in lethal prostate cancer. <i>Nature Medicine</i> , 2021, 27, 426-433.	15.2	90
54	B cell genomics behind cross-neutralization of SARS-CoV-2 variants and SARS-CoV. <i>Cell</i> , 2021, 184, 3205-3221.e24.	13.5	73

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55	Blood and immune development in human fetal bone marrow and Down syndrome. <i>Nature</i> , 2021, 598, 327-331.	13.7	73
56	SM-Omics is an automated platform for high-throughput spatial multi-omics. <i>Nature Communications</i> , 2022, 13, 795.	5.8	73
57	Opposing immune and genetic mechanisms shape oncogenic programs in synovial sarcoma. <i>Nature Medicine</i> , 2021, 27, 289-300.	15.2	64
58	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019, 49, 10-29.	3.1	57
59	An IL-27-Driven Transcriptional Network Identifies Regulators of IL-10 Expression across T Helper Cell Subsets. <i>Cell Reports</i> , 2020, 33, 108433.	2.9	54
60	Building a high-quality Human Cell Atlas. <i>Nature Biotechnology</i> , 2021, 39, 149-153.	9.4	48
61	Mitogenic and progenitor gene programmes in single pilocytic astrocytoma cells. <i>Nature Communications</i> , 2019, 10, 3731.	5.8	45
62	Massively parallel phenotyping of coding variants in cancer with Perturb-seq. <i>Nature Biotechnology</i> , 2022, 40, 896-905.	9.4	44
63	Stepwise-edited, human melanoma models reveal mutations' effect on tumor and microenvironment. <i>Science</i> , 2022, 376, eabi8175.	6.0	24
64	Tim-3 adapter protein Bat3 acts as an endogenous regulator of tolerogenic dendritic cell function. <i>Science Immunology</i> , 2022, 7, eabm0631.	5.6	22
65	Tim-3 adaptor protein Bat3 is a molecular checkpoint of T cell terminal differentiation and exhaustion. <i>Science Advances</i> , 2021, 7, .	4.7	18
66	National Cancer Institute Think-Tank Meeting Report on Proteomic Cartography and Biomarkers at the Single-Cell Level: Interrogation of Premalignant Lesions. <i>Journal of Proteome Research</i> , 2020, 19, 1900-1912.	1.8	8
67	Abstract PR-007: Single-nucleus and spatial transcriptomics of archival pancreatic ductal adenocarcinoma reveals multi-compartment reprogramming after neoadjuvant treatment. <i>Cancer Research</i> , 2020, 80, PR-007-PR-007.	0.4	3
68	Anti-Tumor TCF1+ CD8 T Cells are Functionally Diverse and Evolve During Tumorigenesis and Progression. <i>American Journal of Clinical Pathology</i> , 2020, 154, S5-S6.	0.4	0