

Orit Rozenblatt-Rosen

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

30,933
citations

30070

54
h-index

95266

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. <i>Hepatology Communications</i> , 2022, 6, 821-840.	4.3	98
2	Massively parallel phenotyping of coding variants in cancer with Perturb-seq. <i>Nature Biotechnology</i> , 2022, 40, 896-905.	17.5	44
3	SM-Omics is an automated platform for high-throughput spatial multi-omics. <i>Nature Communications</i> , 2022, 13, 795.	12.8	73
4	Tim-3 adapter protein Bat3 acts as an endogenous regulator of tolerogenic dendritic cell function. <i>Science Immunology</i> , 2022, 7, eabm0631.	11.9	22
5	Single-cell RNA-seq reveals cell type-specific molecular and genetic associations to lupus. <i>Science</i> , 2022, 376, eabf1970.	12.6	156
6	Stepwise-edited, human melanoma models reveal mutations' effect on tumor and microenvironment. <i>Science</i> , 2022, 376, eabi8175.	12.6	24
7	Single-nucleus cross-tissue molecular reference maps toward understanding disease gene function. <i>Science</i> , 2022, 376, eabl4290.	12.6	180
8	Tissue-resident memory and circulating T cells are early responders to pre-surgical cancer immunotherapy. <i>Cell</i> , 2022, 185, 2918-2935.e29.	28.9	113
9	Opposing immune and genetic mechanisms shape oncogenic programs in synovial sarcoma. <i>Nature Medicine</i> , 2021, 27, 289-300.	30.7	64
10	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. <i>Science</i> , 2021, 371, .	12.6	197
11	Building a high-quality Human Cell Atlas. <i>Nature Biotechnology</i> , 2021, 39, 149-153.	17.5	48
12	Multimodal pooled Perturb-CITE-seq screens in patient models define mechanisms of cancer immune evasion. <i>Nature Genetics</i> , 2021, 53, 332-341.	21.4	112
13	Transcriptional mediators of treatment resistance in lethal prostate cancer. <i>Nature Medicine</i> , 2021, 27, 426-433.	30.7	90
14	Tim-3 adaptor protein Bat3 is a molecular checkpoint of T cell terminal differentiation and exhaustion. <i>Science Advances</i> , 2021, 7, .	10.3	18
15	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , 2021, 595, 107-113.	27.8	537
16	Tumor and immune reprogramming during immunotherapy in advanced renal cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 649-661.e5.	16.8	263
17	A cellular and spatial map of the choroid plexus across brain ventricles and ages. <i>Cell</i> , 2021, 184, 3056-3074.e21.	28.9	150
18	Interactions between cancer cells and immune cells drive transitions to mesenchymal-like states in glioblastoma. <i>Cancer Cell</i> , 2021, 39, 779-792.e11.	16.8	245

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19	TIM-3 restrains anti-tumour immunity by regulating inflammasome activation. <i>Nature</i> , 2021, 595, 101-106.	27.8	169
20	B cell genomics behind cross-neutralization of SARS-CoV-2 variants and SARS-CoV. <i>Cell</i> , 2021, 184, 3205-3221.e24.	28.9	73
21	Spatially organized multicellular immune hubs in human colorectal cancer. <i>Cell</i> , 2021, 184, 4734-4752.e20.	28.9	256
22	Blood and immune development in human fetal bone marrow and Down syndrome. <i>Nature</i> , 2021, 598, 327-331.	27.8	73
23	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021, 597, 196-205.	27.8	114
24	Epigenetic encoding, heritability and plasticity of glioma transcriptional cell states. <i>Nature Genetics</i> , 2021, 53, 1469-1479.	21.4	100
25	Stem-like intestinal Th17 cells give rise to pathogenic effector T _H 1 cells during autoimmunity. <i>Cell</i> , 2021, 184, 6281-6298.e23.	28.9	99
26	Differential pre-malignant programs and microenvironment chart distinct paths to malignancy in human colorectal polyps. <i>Cell</i> , 2021, 184, 6262-6280.e26.	28.9	125
27	Single-Cell RNA-Seq Reveals Cellular Hierarchies and Impaired Developmental Trajectories in Pediatric Ependymoma. <i>Cancer Cell</i> , 2020, 38, 44-59.e9.	16.8	94
28	An IL-27-Driven Transcriptional Network Identifies Regulators of IL-10 Expression across T Helper Cell Subsets. <i>Cell Reports</i> , 2020, 33, 108433.	6.4	54
29	Cumulus provides cloud-based data analysis for large-scale single-cell and single-nucleus RNA-seq. <i>Nature Methods</i> , 2020, 17, 793-798.	19.0	134
30	Pan-cancer single-cell RNA-seq identifies recurring programs of cellular heterogeneity. <i>Nature Genetics</i> , 2020, 52, 1208-1218.	21.4	226
31	The Human and Mouse Enteric Nervous System at Single-Cell Resolution. <i>Cell</i> , 2020, 182, 1606-1622.e23.	28.9	287
32	Multiplexed single-cell transcriptional response profiling to define cancer vulnerabilities and therapeutic mechanism of action. <i>Nature Communications</i> , 2020, 11, 4296.	12.8	98
33	Endogenous Glucocorticoid Signaling Regulates CD8 ⁺ T Cell Differentiation and Development of Dysfunction in the Tumor Microenvironment. <i>Immunity</i> , 2020, 53, 658-671.e6.	14.3	98
34	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. <i>Nature Medicine</i> , 2020, 26, 792-802.	30.7	381
35	A single-cell landscape of high-grade serous ovarian cancer. <i>Nature Medicine</i> , 2020, 26, 1271-1279.	30.7	267
36	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.	3.7	8

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37	Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. <i>Nature Biotechnology</i> , 2020, 38, 737-746.	17.5	527
38	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	28.9	334
39	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.	0.9	3
40	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.	0.7	0
41	Mitogenic and progenitor gene programmes in single pilocytic astrocytoma cells. <i>Nature Communications</i> , 2019, 10, 3731.	12.8	45
42	An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. <i>Cell</i> , 2019, 178, 835-849.e21.	28.9	1,408
43	Resolving medulloblastoma cellular architecture by single-cell genomics. <i>Nature</i> , 2019, 572, 74-79.	27.8	273
44	Intra- and Inter-cellular Rewiring of the Human Colon during Ulcerative Colitis. <i>Cell</i> , 2019, 178, 714-730.e22.	28.9	806
45	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. <i>Nature Communications</i> , 2019, 10, 2907.	12.8	117
46	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.	14.3	154
47	Decoding human fetal liver haematopoiesis. <i>Nature</i> , 2019, 574, 365-371.	27.8	392
48	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019, 49, 10-29.	7.0	57
49	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. <i>Cell</i> , 2019, 176, 1325-1339.e22.	28.9	345
50	Checkpoint Blockade Immunotherapy Induces Dynamic Changes in PD-1 ^{hi} CD8 ⁺ Tumor-Infiltrating T Cells. <i>Immunity</i> , 2019, 50, 181-194.e6.	14.3	424
51	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018, 360, 331-335.	12.6	461
52	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. <i>Cell</i> , 2018, 175, 984-997.e24.	28.9	892
53	T Helper Cell Cytokines Modulate Intestinal Stem Cell Renewal and Differentiation. <i>Cell</i> , 2018, 175, 1307-1320.e22.	28.9	388
54	A revised airway epithelial hierarchy includes CFTR-expressing ionocytes. <i>Nature</i> , 2018, 560, 319-324.	27.8	878

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55	Induction and transcriptional regulation of the co-inhibitory gene module in T cells. Nature, 2018, 558, 454-459.	27.8	336
56	Single-cell RNA-seq reveals new types of human blood dendritic cells, monocytes, and progenitors. Science, 2017, 356, .	12.6	1,846
57	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science, 2017, 355, .	12.6	743
58	Single-cell transcriptomics to explore the immune system in health and disease. Science, 2017, 358, 58-63.	12.6	440
59	The neuropeptide NMU amplifies ILC2-driven allergic lung inflammation. Nature, 2017, 549, 351-356.	27.8	460
60	Single-Cell Transcriptomic Analysis of Primary and Metastatic Tumor Ecosystems in Head and Neck Cancer. Cell, 2017, 171, 1611-1624.e24.	28.9	1,656
61	A single-cell survey of the small intestinal epithelium. Nature, 2017, 551, 333-339.	27.8	1,197
62	Massively parallel single-nucleus RNA-seq with DroNc-seq. Nature Methods, 2017, 14, 955-958.	19.0	859
63	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
64	Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. Science, 2016, 352, 189-196.	12.6	3,421
65	A Distinct Gene Module for Dysfunction Uncoupled from Activation in Tumor-Infiltrating T Cells. Cell, 2016, 166, 1500-1511.e9.	28.9	315
66	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. Nature, 2016, 539, 309-313.	27.8	875
67	Reconstructing and Reprogramming the Tumor-Propagating Potential of Glioblastoma Stem-like Cells. Cell, 2014, 157, 580-594.	28.9	751
68	Single-cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma. Science, 2014, 344, 1396-1401.	12.6	3,648