

Itay Tirosh

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/228137/publications.pdf>

Version: 2024-02-01

70
papers

28,388
citations

57758

44
h-index

98798

67
g-index

78
all docs

78
docs citations

78
times ranked

39655
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide CRISPR screen identifies PRC2 and KMT2D-COMPASS as regulators of distinct EMT trajectories that contribute differentially to metastasis. <i>Nature Cell Biology</i> , 2022, 24, 554-564.	10.3	53
2	An activation to memory differentiation trajectory of tumor-infiltrating lymphocytes informs metastatic melanoma outcomes. <i>Cancer Cell</i> , 2022, 40, 524-544.e5.	16.8	23
3	Tumour inflammation signature and expression of S100A12 and HLA class I improve survival in HPV-negative hypopharyngeal cancer. <i>Scientific Reports</i> , 2021, 11, 1782.	3.3	11
4	A unique subset of glycolytic tumour-propagating cells drives squamous cell carcinoma. <i>Nature Metabolism</i> , 2021, 3, 182-195.	11.9	17
5	Single-Cell Deconvolution of Head and Neck Squamous Cell Carcinoma. <i>Cancers</i> , 2021, 13, 1230.	3.7	26
6	Inhibitory CD161 receptor identified in glioma-infiltrating T cells by single-cell analysis. <i>Cell</i> , 2021, 184, 1281-1298.e26.	28.9	210
7	Glioblastoma cell populations with distinct oncogenic programs release podoplanin as procoagulant extracellular vesicles. <i>Blood Advances</i> , 2021, 5, 1682-1694.	5.2	46
8	Decoding Cancer Biology One Cell at a Time. <i>Cancer Discovery</i> , 2021, 11, 960-970.	9.4	37
9	Decoupling epithelial-mesenchymal transitions from stromal profiles by integrative expression analysis. <i>Nature Communications</i> , 2021, 12, 2592.	12.8	42
10	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
11	OTME-7. Cancer - immune cell interactions drive transitions to mesenchymal-like state in glioblastoma. <i>Neuro-Oncology Advances</i> , 2021, 3, ii14-ii15.	0.7	0
12	Pan-cancer single-cell RNA-seq identifies recurring programs of cellular heterogeneity. <i>Nature Genetics</i> , 2020, 52, 1208-1218.	21.4	226
13	Malignant cell-specific CXCL14 promotes tumor lymphocyte infiltration in oral cavity squamous cell carcinoma. , 2020, 8, e001048.		27
14	Nasopharyngeal carcinoma joins the single-cell party. <i>Cancer Communications</i> , 2020, 40, 453-455.	9.2	3
15	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
16	The Glioma Stem Cell Model in the Era of Single-Cell Genomics. <i>Cancer Cell</i> , 2020, 37, 630-636.	16.8	153
17	A single-cell landscape of high-grade serous ovarian cancer. <i>Nature Medicine</i> , 2020, 26, 1271-1279.	30.7	267
18	Tackling the Many Facets of Glioblastoma Heterogeneity. <i>Cell Stem Cell</i> , 2020, 26, 303-304.	11.1	29

#	ARTICLE	IF	CITATIONS
19	An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. <i>Cell</i> , 2019, 178, 835-849.e21.	28.9	1,408
20	Single-Cell RNA Sequencing in Cancer: Lessons Learned and Emerging Challenges. <i>Molecular Cell</i> , 2019, 75, 7-12.	9.7	319
21	Immunohistochemical quantification of partial-EMT in oral cavity squamous cell carcinoma primary tumors is associated with nodal metastasis. <i>Oral Oncology</i> , 2019, 99, 104458.	1.5	43
22	Single-cell sequencing and its applications in head and neck cancer. <i>Oral Oncology</i> , 2019, 99, 104441.	1.5	65
23	Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. <i>Nature</i> , 2019, 565, 234-239.	27.8	956
24	Deciphering Human Tumor Biology by Single-Cell Expression Profiling. <i>Annual Review of Cancer Biology</i> , 2019, 3, 151-166.	4.5	33
25	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018, 360, 331-335.	12.6	461
26	A Glial Signature and Wnt7 Signaling Regulate Glioma-Vascular Interactions and Tumor Microenvironment. <i>Cancer Cell</i> , 2018, 33, 874-889.e7.	16.8	180
27	Single cell RNA-seq highlights a role for a partial EMT in head and neck cancer. <i>Molecular and Cellular Oncology</i> , 2018, 5, e1448244.	0.7	61
28	Dissecting human gliomas by single-cell RNA sequencing. <i>Neuro-Oncology</i> , 2018, 20, 37-43.	1.2	56
29	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. <i>Cell</i> , 2018, 175, 984-997.e24.	28.9	892
30	T Helper Cell Cytokines Modulate Intestinal Stem Cell Renewal and Differentiation. <i>Cell</i> , 2018, 175, 1307-1320.e22.	28.9	388
31	Combined Analysis of Antigen Presentation and T-cell Recognition Reveals Restricted Immune Responses in Melanoma. <i>Cancer Discovery</i> , 2018, 8, 1366-1375.	9.4	80
32	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. <i>Science</i> , 2017, 355, .	12.6	743
33	Single-Cell Transcriptomic Analysis of Primary and Metastatic Tumor Ecosystems in Head and Neck Cancer. <i>Cell</i> , 2017, 171, 1611-1624.e24.	28.9	1,656
34	A single-cell survey of the small intestinal epithelium. <i>Nature</i> , 2017, 551, 333-339.	27.8	1,197
35	Challenges and emerging directions in single-cell analysis. <i>Genome Biology</i> , 2017, 18, 84.	8.8	258
36	IFN β -Dependent Tissue-Immune Homeostasis Is Co-opted in the Tumor Microenvironment. <i>Cell</i> , 2017, 170, 127-141.e15.	28.9	140

#	ARTICLE	IF	CITATIONS
37	Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. <i>Science</i> , 2016, 352, 189-196.	12.6	3,421
38	High-throughput Phenotyping of Lung Cancer Somatic Mutations. <i>Cancer Cell</i> , 2016, 30, 214-228.	16.8	171
39	Single-cell RNA-seq supports a developmental hierarchy in human oligodendrogloma. <i>Nature</i> , 2016, 539, 309-313.	27.8	875
40	Highly Parallel Genome-wide Expression Profiling of Individual Cells Using Nanoliter Droplets. <i>Cell</i> , 2015, 161, 1202-1214.	28.9	5,908
41	Chromatin Mediation of a Transcriptional Memory Effect in Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 829-838.	1.8	11
42	A Genome-wide CRISPR Screen in Primary Immune Cells to Dissect Regulatory Networks. <i>Cell</i> , 2015, 162, 675-686.	28.9	383
43	Single-cell RNA-seq reveals changes in cell cycle and differentiation programs upon aging of hematopoietic stem cells. <i>Genome Research</i> , 2015, 25, 1860-1872.	5.5	614
44	Reconstructing and Reprogramming the Tumor-Propagating Potential of Glioblastoma Stem-like Cells. <i>Cell</i> , 2014, 157, 580-594.	28.9	751
45	Single-cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma. <i>Science</i> , 2014, 344, 1396-1401.	12.6	3,648
46	miR-142 orchestrates a network of actin cytoskeleton regulators during megakaryopoiesis. <i>ELife</i> , 2014, 3, e01964.	6.0	67
47	Promoter Nucleosome Organization Shapes the Evolution of Gene Expression. <i>PLoS Genetics</i> , 2012, 8, e1002579.	3.5	14
48	Expression Noise and Acetylation Profiles Distinguish HDAC Functions. <i>Molecular Cell</i> , 2012, 47, 193-202.	9.7	112
49	Widespread promoter-mediated coordination of transcription and mRNA degradation. <i>Genome Biology</i> , 2012, 13, R114.	9.6	39
50	Computational Analysis of Nucleosome Positioning. <i>Methods in Molecular Biology</i> , 2012, 833, 443-449.	0.9	9
51	Inferring regulatory mechanisms from patterns of evolutionary divergence. <i>Molecular Systems Biology</i> , 2011, 7, 530.	7.2	40
52	Transcriptional priming of cytoplasmic post-transcriptional regulation. <i>Transcription</i> , 2011, 2, 258-262.	3.1	5
53	Extensive divergence of yeast stress responses through transitions between induced and constitutive activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16693-16698.	7.1	36
54	Evolution of Nucleosome Occupancy: Conservation of Global Properties and Divergence of Gene-Specific Patterns. <i>Molecular and Cellular Biology</i> , 2011, 31, 4348-4355.	2.3	28

#	ARTICLE	IF	CITATIONS
55	Coupled Evolution of Transcription and mRNA Degradation. <i>PLoS Biology</i> , 2011, 9, e1001106.	5.6	86
56	Divergence of nucleosome positioning between two closely related yeast species: genetic basis and functional consequences. <i>Molecular Systems Biology</i> , 2010, 6, 365.	7.2	96
57	Chromatin regulators as capacitors of interspecies variations in gene expression. <i>Molecular Systems Biology</i> , 2010, 6, 435.	7.2	56
58	Widespread remodeling of mid-coding sequence nucleosomes by Isw1. <i>Genome Biology</i> , 2010, 11, R49.	9.6	58
59	A Yeast Hybrid Provides Insight into the Evolution of Gene Expression Regulation. <i>Science</i> , 2009, 324, 659-662.	12.6	388
60	Promoter architecture and the evolvability of gene expression. <i>Journal of Biology</i> , 2009, 8, 95.	2.7	96
61	Evolution of gene sequence and gene expression are not correlated in yeast. <i>Trends in Genetics</i> , 2008, 24, 109-113.	6.7	74
62	On the relation between promoter divergence and gene expression evolution. <i>Molecular Systems Biology</i> , 2008, 4, 159.	7.2	70
63	Two strategies for gene regulation by promoter nucleosomes. <i>Genome Research</i> , 2008, 18, 1084-1091.	5.5	351
64	Comparative analysis indicates regulatory neofunctionalization of yeast duplicates. <i>Genome Biology</i> , 2007, 8, R50.	9.6	83
65	Comparative biology: beyond sequence analysis. <i>Current Opinion in Biotechnology</i> , 2007, 18, 371-377.	6.6	45
66	Autocorrelation analysis reveals widespread spatial biases in microarray experiments. <i>BMC Genomics</i> , 2007, 8, 164.	2.8	23
67	The pattern and evolution of yeast promoter bendability. <i>Trends in Genetics</i> , 2007, 23, 318-321.	6.7	62
68	A genetic signature of interspecies variations in gene expression. <i>Nature Genetics</i> , 2006, 38, 830-834.	21.4	250
69	Computational verification of protein-protein interactions by orthologous co-expression. <i>BMC Bioinformatics</i> , 2005, 6, 40.	2.6	28
70	Stochastic transitions as a major source of cancer heterogeneity. <i>Nature Reviews Genetics</i> , 0, , .	16.3	0