## Tal Nawy

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8962178/publications.pdf

Version: 2024-02-01

92	2,784	12 h-index	49
papers	citations		g-index
115	115	115	4731 citing authors
all docs	docs citations	times ranked	

#	Article	IF	CITATIONS
1	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	9.0	37
2	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
3	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	13.5	334
4	Tracing cellular descent. Nature Methods, 2018, 15, 32-32.	9.0	1
5	Spatial transcriptomics. Nature Methods, 2018, 15, 30-30.	9.0	8
6	Sequence meets space. Nature Methods, 2018, 15, 1000-1000.	9.0	1
7	Protein-based cell barcodes. Nature Methods, 2018, 15, 1002-1002.	9.0	0
8	Cell portrait of a mouse. Nature Methods, 2018, 15, 1001-1001.	9.0	2
9	A winning single-cell combination. Nature Methods, 2018, 15, 859-859.	9.0	1
10	Mechanistic microbiota models. Nature Methods, 2018, 15, 860-860.	9.0	0
11	Variants from the deep. Nature Methods, 2018, 15, 861-861.	9.0	3
12	Organoid hosts for parasitic infection. Nature Methods, 2018, 15, 652-652.	9.0	0
13	Three tissues to gastrulation. Nature Methods, 2018, 15, 652-652.	9.0	2
14	A pan-cancer atlas. Nature Methods, 2018, 15, 407-407.	9.0	13
15	Tissue-specific oncogene screens. Nature Methods, 2018, 15, 408-408.	9.0	0
16	A home for brain organoids. Nature Methods, 2018, 15, 404-404.	9.0	0
17	Transcripts from a spliceosome. Nature Methods, 2018, 15, 480-480.	9.0	0
18	Metastasis in a dish. Nature Methods, 2018, 15, 482-482.	9.0	0

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19	Tumor genetic analysis from single-cell RNA-seq data. Nature Methods, 2018, 15, 571-571.	9.0	2
20	Contrasting PCA across datasets. Nature Methods, 2018, 15, 572-572.	9.0	4
21	Transcript constellations in a tissue's universe. Nature Methods, 2018, 15, 567-567.	9.0	1
22	Capturing microbial interactions. Nature Methods, 2017, 14, 35-35.	9.0	5
23	How single cells do it. Nature Methods, 2017, 14, 33-33.	9.0	2
24	Reprogrammed cells leave their past lives behind. Nature Methods, 2016, 13, 292-292.	9.0	0
25	Root Regeneration Triggers an Embryo-like Sequence Guided by Hormonal Interactions. Cell, 2016, 165, 1721-1733.	13.5	215
26	Tracking expression through the generations. Nature Methods, 2016, 13, 197-197.	9.0	0
27	Driving out malaria. Nature Methods, 2016, 13, 111-111.	9.0	1
28	Integrated single-cell profiles. Nature Methods, 2016, 13, 36-36.	9.0	2
29	Jedi cells patrol the mouse. Nature Methods, 2016, 13, 12-13.	9.0	11
30	Kindred cells among the crowd. Nature Methods, 2015, 12, 170-171.	9.0	0
31	Splice and sequence. Nature Methods, 2015, 12, 488-488.	9.0	0
32	Bacterial recall. Nature Methods, 2015, 12, 12-13.	9.0	0
33	Nanopores for proteins. Nature Methods, 2015, 12, 38-38.	9.0	2
34	Transdifferentiation from the top. Nature Methods, 2015, 12, 701-701.	9.0	1
35	Catching Pol II in the act. Nature Methods, 2015, 12, 597-597.	9.0	0
36	RNA structure served in vivo. Nature Methods, 2015, 12, 383-383.	9.0	0

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37	Quantification of cell identity from single-cell gene expression profiles. Genome Biology, 2015, 16, 9.	3.8	149
38	Cellular diversity in a snapshot. Nature Methods, 2015, 12, 286-286.	9.0	O
39	Fast track to neurons. Nature Methods, 2015, 12, 915-915.	9.0	3
40	The strain in metagenomics. Nature Methods, 2015, 12, 1005-1005.	9.0	5
41	Where the G-quadruplexes are. Nature Methods, 2015, 12, 807-807.	9.0	2
42	Nanopores and the helicase two-step. Nature Methods, 2015, 12, 1119-1119.	9.0	0
43	Deep mutational scans with targeted editing. Nature Methods, 2014, 11, 994-994.	9.0	O
44	Live reporting of kinase dynamics. Nature Methods, 2014, 11, 789-789.	9.0	0
45	Short reads join hands. Nature Methods, 2014, 11, 1198-1198.	9.0	4
46	Nanopores sense protein modifications. Nature Methods, 2014, 11, 226-227.	9.0	2
47	Single cells make the tissue. Nature Methods, 2014, 11, 371-371.	9.0	0
48	The big RNA picture. Nature Methods, 2014, 11, 471-471.	9.0	0
49	Single-cell sequencing. Nature Methods, 2014, 11, 18-18.	9.0	125
50	Memoirs of a gut bacterium. Nature Methods, 2014, 11, 474-474.	9.0	0
51	Versatile clusters formed by light. Nature Methods, 2014, 11, 1087-1087.	9.0	O
52	Cancer stem cells on demand. Nature Methods, 2014, 11, 715-715.	9.0	0
53	A protein code to target RNA. Nature Methods, 2014, 11, 888-889.	9.0	O
54	In situ sequencing. Nature Methods, 2014, 11, 29-29.	9.0	4

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55	Bacterial genomes by the droplet. Nature Methods, 2013, 10, 386-386.	9.0	1
56	Microbial planet. Nature Methods, 2013, 10, 826-826.	9.0	1
57	Single-cell epigenetics. Nature Methods, 2013, 10, 1060-1060.	9.0	8
58	Embryos under the X-ray. Nature Methods, 2013, 10, 603-603.	9.0	0
59	A tool belt for GFP. Nature Methods, 2013, 10, 930-930.	9.0	1
60	Cancer cells report. Nature Methods, 2013, 10, 195-195.	9.0	0
61	Probing microbiome function. Nature Methods, 2013, 10, 35-35.	9.0	0
62	Dynamics of DNA demethylation. Nature Methods, 2013, 10, 466-466.	9.0	7
63	A map of cell typeâ€specific auxin responses. Molecular Systems Biology, 2013, 9, 688.	3.2	150
64	Engineering off the beaten pathway. Nature Methods, 2013, 10, 938-938.	9.0	0
65	Receptive cells feel the squeeze. Nature Methods, 2013, 10, 198-198.	9.0	5
66	Sequencing down the line. Nature Methods, 2013, 10, 15-15.	9.0	4
67	Partners in time, partners in crime. Nature Methods, 2013, 10, 108-108.	9.0	0
68	The pull of a cell. Nature Methods, 2013, 10, 696-696.	9.0	0
69	A genetically encoded probe for EM. Nature Methods, 2012, 9, 1140-1141.	9.0	1
70	Cancer gene discovery goes viral. Nature Methods, 2012, 9, 868-868.	9.0	2
71	In-depth functional dissection of enhancers. Nature Methods, 2012, 9, 323-323.	9.0	O
72	Probing epigenetic cross-talk. Nature Methods, 2012, 9, 538-538.	9.0	0

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73	Non–model organisms. Nature Methods, 2012, 9, 37-37.	9.0	6
74	Sorting out epigenetic states. Nature Methods, 2012, 9, 641-641.	9.0	0
75	Leaner, meaner siRNAs. Nature Methods, 2012, 9, 1050-1050.	9.0	0
76	Rare variants and the power of association. Nature Methods, 2012, 9, 324-324.	9.0	3
77	The age of yeast. Nature Methods, 2012, 9, 438-438.	9.0	0
78	Ribosomes, start your engines. Nature Methods, 2012, 9, 780-780.	9.0	1
79	Peering deeper into the transcriptome. Nature Methods, 2012, 9, 15-15.	9.0	2
80	High-resolution chromatin immunoprecipitation. Nature Methods, 2012, 9, 130-130.	9.0	1
81	Capturing sequences for bioprospecting. Nature Methods, 2012, 9, 532-532.	9.0	1
82	Turning the lights on a few molecules at a time. Nature Methods, 2011, 8, 538-538.	9.0	0
83	Noncoding RNA's genomic hangouts. Nature Methods, 2011, 8, 1000-1000.	9.0	0
84	Yeast 2.0. Nature Methods, 2011, 8, 895-895.	9.0	5
85	Speed-reading DNA in the dark. Nature Methods, 2011, 8, 708-709.	9.0	2
86	How to spot a cheetah. Nature Methods, 2011, 8, 791-791.	9.0	0
87	The GATA Factor HANABA TARANU Is Required to Position the Proembryo Boundary in the Early Arabidopsis Embryo. Developmental Cell, 2010, 19, 103-113.	3.1	64
88	Paternal Control of Embryonic Patterning in <i>Arabidopsis thaliana</i> . Science, 2009, 323, 1485-1488.	6.0	298
89	Talk global, act localâ€"patterning the Arabidopsis embryo. Current Opinion in Plant Biology, 2008, 11, 28-33.	3.5	36
90	Transcriptional Profile of the Arabidopsis Root Quiescent Center. Plant Cell, 2005, 17, 1908-1925.	3.1	288

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91	Intercellular movement of the putative transcription factor SHR in root patterning. Nature, 2001, 413, 307-311.	13.7	766
92	Signaling the tips: Regulation of stem cell function in plants. Differentiation, 2001, 68, 155-158.	1.0	0