

Mor Nitzan

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

1,612
citations

471509

17
h-index

580821

25
g-index

31
all docs

31
docs citations

31
times ranked

2385
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep learning and alignment of spatially resolved single-cell transcriptomes with Tangram. <i>Nature Methods</i> , 2021, 18, 1352-1362.	19.0	276
2	Gene expression cartography. <i>Nature</i> , 2019, 576, 132-137.	27.8	216
3	Evidence for Functional Networks within the Human Brain's White Matter. <i>Journal of Neuroscience</i> , 2017, 37, 6394-6407.	3.6	176
4	Integration of Bacterial Small RNAs in Regulatory Networks. <i>Annual Review of Biophysics</i> , 2017, 46, 131-148.	10.0	150
5	Single-cell analysis of germinal-center B cells informs on lymphoma cell of origin and outcome. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	117
6	Model-free inference of direct network interactions from nonlinear collective dynamics. <i>Nature Communications</i> , 2017, 8, 2192.	12.8	93
7	ChIP-seq of plasma cell-free nucleosomes identifies gene expression programs of the cells of origin. <i>Nature Biotechnology</i> , 2021, 39, 586-598.	17.5	81
8	NovoSpaRc: flexible spatial reconstruction of single-cell gene expression with optimal transport. <i>Nature Protocols</i> , 2021, 16, 4177-4200.	12.0	55
9	Reversible functional connectivity disturbances during transient global amnesia. <i>Annals of Neurology</i> , 2014, 75, 634-643.	5.3	54
10	Dynamics of the Type III Secretion System Activity of Enteropathogenic <i>Escherichia coli</i> . <i>MBio</i> , 2013, 4, .	4.1	53
11	Revealing physical interaction networks from statistics of collective dynamics. <i>Science Advances</i> , 2017, 3, e1600396.	10.3	52
12	Bundle-forming pilus retraction enhances enteropathogenic <i>Escherichia coli</i> infectivity. <i>Molecular Biology of the Cell</i> , 2011, 22, 2436-2447.	2.1	42
13	Interactions between Distant ceRNAs in Regulatory Networks. <i>Biophysical Journal</i> , 2014, 106, 2254-2266.	0.5	41
14	Analytical results for the distribution of shortest path lengths in random networks. <i>Europhysics Letters</i> , 2015, 111, 26006.	2.0	32
15	Selective flexible packaging pathways of the segmented genome of influenza A virus. <i>Nature Communications</i> , 2020, 11, 4355.	12.8	26
16	Distance distribution in configuration-model networks. <i>Physical Review E</i> , 2016, 93, 062309.	2.1	23
17	A defense-offense multi-layered regulatory switch in a pathogenic bacterium. <i>Nucleic Acids Research</i> , 2015, 43, 1357-1369.	14.5	22
18	Temporal Dissociation of Neocortical and Hippocampal Contributions to Mental Time Travel Using Intracranial Recordings in Humans. <i>Frontiers in Computational Neuroscience</i> , 2018, 12, 11.	2.1	11

#	ARTICLE	IF	CITATIONS
19	Discriminative Learning of Infection Models. , 2016, , .		11
20	Degradation of Ndd1 by APC/CCdh1 generates a feed forward loop that times mitotic protein accumulation. Nature Communications, 2015, 6, 7075.	12.8	10
21	Revealing lineage-related signals in single-cell gene expression using random matrix theory. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	8
22	Stochastic analysis of bistability in coherent mixed feedback loops combining transcriptional and posttranscriptional regulations. Physical Review E, 2015, 91, 052706.	2.1	6
23	Global Regulation of Transcription by a Small RNA: A Quantitative View. Biophysical Journal, 2014, 106, 1205-1214.	0.5	5
24	Programming cell growth into different cluster shapes using diffusible signals. PLoS Computational Biology, 2021, 17, e1009576.	3.2	4
25	Approaches and developments in studying the human microbiome network. Israel Journal of Ecology and Evolution, 2015, 61, 90-94.	0.6	1
26	Flexible level-1 consensus ensuring stable social choice: analysis and algorithms. Social Choice and Welfare, 2018, 50, 457-479.	0.8	0