Leeat Keren

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5649939/publications.pdf

Version: 2024-02-01

26 papers	3,704 citations	394421 19 h-index	526287 27 g-index
32 all docs	32 docs citations	32 times ranked	5085 citing authors

#	Article	IF	Citations
1	High-Dimensional Tissue Profiling by Multiplexed Ion Beam Imaging. Methods in Molecular Biology, 2022, 2386, 147-156.	0.9	2
2	Whole-cell segmentation of tissue images with human-level performance using large-scale data annotation and deep learning. Nature Biotechnology, 2022, 40, 555-565.	17.5	297
3	Transition to invasive breast cancer is associated with progressive changes in the structure and composition of tumor stroma. Cell, 2022, 185, 299-310.e18.	28.9	161
4	The immunoregulatory landscape of human tuberculosis granulomas. Nature Immunology, 2022, 23, 318-329.	14.5	110
5	From genes to modules, from cells toâ€‰ecosystems. Molecular Systems Biology, 2022, 18, e10726.	7.2	4
6	MAUI (MBI Analysis User Interface)â€”An image processing pipeline for Multiplexed Mass Based Imaging. PLoS Computational Biology, 2021, 17, e1008887.	3.2	37
7	Multiplexed imaging analysis of the tumor-immune microenvironment reveals predictors of outcome in triple-negative breast cancer. Communications Biology, 2021, 4, 852.	4.4	25
8	Adjacent Cell Marker Lateral Spillover Compensation and Reinforcement for Multiplexed Images. Frontiers in Immunology, 2021, 12, 652631.	4.8	28
9	Tumor heterogeneity. Cancer Cell, 2021, 39, 1015-1017.	16.8	66
10	Single cell biologyâ€”a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 74-97.	3.8	3
11	Mapping cell phenotypes in breast cancer. Nature Cancer, 2020, 1, 156-157.	13.2	5
12	Modeling Multiplexed Images with Spatial-LDA Reveals Novel Tissue Microenvironments. Journal of Computational Biology, 2020, 27, 1204-1218.	1.6	42
13	MIBI-TOF: A multiplexed imaging platform relates cellular phenotypes and tissue structure. Science Advances, 2019, 5, eaax5851.	10.3	252
14	Central dogma rates and the trade-off between precision and economy in gene expression. Nature Communications, 2019, 10, 68.	12.8	140
15	A Structured Tumor-Immune Microenvironment in Triple Negative Breast Cancer Revealed by Multiplexed Ion Beam Imaging. Cell, 2018, 174, 1373-1387.e19.	28.9	729
16	Massively Parallel Interrogation of the Effects of Gene Expression Levels on Fitness. Cell, 2016, 166, 1282-1294.e18.	28.9	168
17	A Minimalistic Resource Allocation Model to Explain Ubiquitous Increase in Protein Expression with Growth Rate. PLoS ONE, 2016, 11, e0153344.	2.5	18
18	Noise in gene expression is coupled to growth rate. Genome Research, 2015, 25, 1893-1902.	5.5	83

#	Article	IF	Citations
19	Probing the effect of promoters on noise in gene expression using thousands of designed sequences. Genome Research, 2014, 24, 1698-1706.	5.5	118
20	Sequence features of yeast and human core promoters that are predictive of maximal promoter activity. Nucleic Acids Research, 2013, 41, 5569-5581.	14.5	84
21	Promoters maintain their relative activity levels under different growth conditions. Molecular Systems Biology, 2013, 9, 701.	7.2	181
22	Measurements of the Impact of 3â€² End Sequences on Gene Expression Reveal Wide Range and Sequence Dependent Effects. PLoS Computational Biology, 2013, 9, e1002934.	3.2	31
23	Manipulating nucleosome disfavoring sequences allows fine-tune regulation of gene expression in yeast. Nature Genetics, 2012, 44, 743-750.	21.4	185
24	Inferring gene regulatory logic from high-throughput measurements of thousands of systematically designed promoters. Nature Biotechnology, 2012, 30, 521-530.	17.5	439
25	Compensation for differences in gene copy number among yeast ribosomal proteins is encoded within their promoters. Genome Research, 2011, 21, 2114-2128.	5.5	51
26	Self-targeting by CRISPR: gene regulation or autoimmunity?. Trends in Genetics, 2010, 26, 335-340.	6.7	353