## Leeat Keren

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	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
2	Inferring gene regulatory logic from high-throughput measurements of thousands of systematically designed promoters. Nature Biotechnology, 2012, 30, 521-530.	17.5	439
3	Self-targeting by CRISPR: gene regulation or autoimmunity?. Trends in Genetics, 2010, 26, 335-340.	6.7	353
4	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
5	MIBI-TOF: A multiplexed imaging platform relates cellular phenotypes and tissue structure. Science Advances, 2019, 5, eaax5851.	10.3	252
6	Manipulating nucleosome disfavoring sequences allows fine-tune regulation of gene expression in yeast. Nature Genetics, 2012, 44, 743-750.	21.4	185
7	Promoters maintain their relative activity levels under different growth conditions. Molecular Systems Biology, 2013, 9, 701.	7.2	181
8	Massively Parallel Interrogation of the Effects of Gene Expression Levels on Fitness. Cell, 2016, 166, 1282-1294.e18.	28.9	168
9	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
10	Central dogma rates and the trade-off between precision and economy in gene expression. Nature Communications, 2019, 10, 68.	12.8	140
11	Probing the effect of promoters on noise in gene expression using thousands of designed sequences. Genome Research, 2014, 24, 1698-1706.	5.5	118
12	The immunoregulatory landscape of human tuberculosis granulomas. Nature Immunology, 2022, 23, 318-329.	14.5	110
13	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
14	Noise in gene expression is coupled to growth rate. Genome Research, 2015, 25, 1893-1902.	5.5	83
15	Tumor heterogeneity. Cancer Cell, 2021, 39, 1015-1017.	16.8	66
16	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
17	Modeling Multiplexed Images with <i>Spatial-LDA</i> Reveals Novel Tissue Microenvironments. Journal of Computational Biology, 2020, 27, 1204-1218.	1.6	42
18	MAUI (MBI Analysis User Interface)—An image processing pipeline for Multiplexed Mass Based Imaging. PLoS Computational Biology, 2021, 17, e1008887.	3.2	37

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19	Measurements of the Impact of 3′ End Sequences on Gene Expression Reveal Wide Range and Sequence Dependent Effects. PLoS Computational Biology, 2013, 9, e1002934.	3.2	31
20	Adjacent Cell Marker Lateral Spillover Compensation and Reinforcement for Multiplexed Images. Frontiers in Immunology, 2021, 12, 652631.	4.8	28
21	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
22	A Minimalistic Resource Allocation Model to Explain Ubiquitous Increase in Protein Expression with Growth Rate. PLoS ONE, 2016, 11, e0153344.	2.5	18
23	Mapping cell phenotypes in breast cancer. Nature Cancer, 2020, 1, 156-157.	13.2	5
24	From genes to modules, from cells to ecosystems. Molecular Systems Biology, 2022, 18, e10726.	7.2	4
25	Single cell biology—a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 74-97.	3.8	3
26	High-Dimensional Tissue Profiling by Multiplexed Ion Beam Imaging. Methods in Molecular Biology, 2022, 2386, 147-156.	0.9	2