

# Xiao-Kang Lun

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7436565/publications.pdf>

Version: 2024-02-01

10  
papers

470  
citations

1306789

7  
h-index

1473754

9  
g-index

13  
all docs

13  
docs citations

13  
times ranked

1414  
citing authors

#	ARTICLE	IF	CITATIONS
1	Simultaneous Multiplexed Imaging of mRNA and Proteins with Subcellular Resolution in Breast Cancer Tissue Samples by Mass Cytometry. <i>Cell Systems</i> , 2018, 6, 25-36.e5.	2.9	214
2	Single-Cell Analysis Uncovers Clonal Acinar Cell Heterogeneity in the Adult Pancreas. <i>Developmental Cell</i> , 2016, 39, 289-301.	3.1	82
3	Influence of node abundance on signaling network state and dynamics analyzed by mass cytometry. <i>Nature Biotechnology</i> , 2017, 35, 164-172.	9.4	39
4	Profiling Cell Signaling Networks at Single-cell Resolution. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 744-756.	2.5	39
5	CellCycleTRACER accounts for cell cycle and volume in mass cytometry data. <i>Nature Communications</i> , 2018, 9, 632.	5.8	36
6	Analysis of the Human Kinome and Phosphatome by Mass Cytometry Reveals Overexpression-Induced Effects on Cancer-Related Signaling. <i>Molecular Cell</i> , 2019, 74, 1086-1102.e5.	4.5	32
7	A quantitative analysis of the interplay of environment, neighborhood, and cell state in 3D spheroids. <i>Molecular Systems Biology</i> , 2020, 16, e9798.	3.2	17
8	Mechanistic Model of Signaling Dynamics Across an Epithelial Mesenchymal Transition. <i>Frontiers in Physiology</i> , 2020, 11, 579117.	1.3	6
9	Stabilized Reconstruction of Signaling Networks from Single-Cell Cue-Response Data. <i>Scientific Reports</i> , 2020, 10, 1233.	1.6	1
10	Analysis of the Human Kinome and Phosphatome Reveals Diseased Signaling Networks Induced by Overexpression. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0