

# Zixuan Cang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7157991/publications.pdf>

Version: 2024-02-01

21  
papers

1,455  
citations

516710

16  
h-index

713466

21  
g-index

21  
all docs

21  
docs citations

21  
times ranked

1222  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deciphering tissue structure and function using spatial transcriptomics. <i>Communications Biology</i> , 2022, 5, 220.	4.4	43
2	Identifying multicellular spatiotemporal organization of cells with SpaceFlow. <i>Nature Communications</i> , 2022, 13, .	12.8	30
3	DEEPsc: A Deep Learning-Based Map Connecting Single-Cell Transcriptomics and Spatial Imaging Data. <i>Frontiers in Genetics</i> , 2021, 12, 636743.	2.3	22
4	A multiscale model via single-cell transcriptomics reveals robust patterning mechanisms during early mammalian embryo development. <i>PLoS Computational Biology</i> , 2021, 17, e1008571.	3.2	11
5	The landscape of cell-cell communication through single-cell transcriptomics. <i>Current Opinion in Systems Biology</i> , 2021, 26, 12-23.	2.6	97
6	Charge substitutions at the voltage-sensing module of domain III enhance actions of site-3 and site-4 toxins on an insect sodium channel. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 137, 103625.	2.7	2
7	Single-cell transcriptomic analysis of zebrafish cranial neural crest reveals spatiotemporal regulation of lineage decisions during development. <i>Cell Reports</i> , 2021, 37, 110140.	6.4	24
8	Evolutionary homology on coupled dynamical systems with applications to protein flexibility analysis. <i>Journal of Applied and Computational Topology</i> , 2020, 4, 481-507.	2.0	6
9	Structural cavities are critical to balancing stability and activity of a membrane-integral enzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22146-22156.	7.1	23
10	Defining Epidermal Basal Cell States during Skin Homeostasis and Wound Healing Using Single-Cell Transcriptomics. <i>Cell Reports</i> , 2020, 30, 3932-3947.e6.	6.4	139
11	A review of mathematical representations of biomolecular data. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 4343-4367.	2.8	56
12	A topology-based network tree for the prediction of protein-protein binding affinity changes following mutation. <i>Nature Machine Intelligence</i> , 2020, 2, 116-123.	16.0	112
13	Inferring spatial and signaling relationships between cells from single cell transcriptomic data. <i>Nature Communications</i> , 2020, 11, 2084.	12.8	184
14	Persistent Cohomology for Data With Multicomponent Heterogeneous Information. <i>SIAM Journal on Mathematics of Data Science</i> , 2020, 2, 396-418.	1.8	10
15	Mathematical deep learning for pose and binding affinity prediction and ranking in D3R Grand Challenges. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 71-82.	2.9	106
16	Integration of element specific persistent homology and machine learning for protein-ligand binding affinity prediction. <i>International Journal for Numerical Methods in Biomedical Engineering</i> , 2018, 34, e2914.	2.1	115
17	Protein pocket detection via convex hull surface evolution and associated Reeb graph. <i>Bioinformatics</i> , 2018, 34, i830-i837.	4.1	23
18	Representability of algebraic topology for biomolecules in machine learning based scoring and virtual screening. <i>PLoS Computational Biology</i> , 2018, 14, e1005929.	3.2	168

#	ARTICLE	IF	CITATIONS
19	Analysis and prediction of protein folding energy changes upon mutation by element specific persistent homology. <i>Bioinformatics</i> , 2017, 33, 3549-3557.	4.1	48
20	TopologyNet: Topology based deep convolutional and multi-task neural networks for biomolecular property predictions. <i>PLoS Computational Biology</i> , 2017, 13, e1005690.	3.2	194
21	A topological approach for protein classification. <i>Computational and Mathematical Biophysics</i> , 2015, 3, .	1.1	42