Zixuan Cang

List of Publications by Year
in descending order

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	TopologyNet: Topology based deep convolutional and multi-task neural networks for biomolecular property predictions. PLoS Computational Biology, 2017, 13, e1005690.	3.2	194
2	Inferring spatial and signaling relationships between cells from single cell transcriptomic data. Nature Communications, 2020, 11, 2084.	12.8	184
3	Representability of algebraic topology for biomolecules in machine learning based scoring and virtual screening. PLoS Computational Biology, 2018, 14, e1005929.	3.2	168
4	Defining Epidermal Basal Cell States during Skin Homeostasis and Wound Healing Using Single-Cell Transcriptomics. Cell Reports, 2020, 30, 3932-3947.e6.	6.4	139
5	Integration of element specific persistent homology and machine learning for protein–ligand binding affinity prediction. International Journal for Numerical Methods in Biomedical Engineering, 2018, 34, e2914.	2.1	115
6	A topology-based network tree for the prediction of protein–protein binding affinity changes following mutation. Nature Machine Intelligence, 2020, 2, 116-123.	16.0	112
7	Mathematical deep learning for pose and binding affinity prediction and ranking in D3R Grand Challenges. Journal of Computer-Aided Molecular Design, 2019, 33, 71-82.	2.9	106
8	The landscape of cell–cell communication through single-cell transcriptomics. Current Opinion in Systems Biology, 2021, 26, 12-23.	2.6	97
9	A review of mathematical representations of biomolecular data. Physical Chemistry Chemical Physics, 2020, 22, 4343-4367.	2.8	56
10	Analysis and prediction of protein folding energy changes upon mutation by element specific persistent homology. Bioinformatics, 2017, 33, 3549-3557.	4.1	48
11	Deciphering tissue structure and function using spatial transcriptomics. Communications Biology, 2022, 5, 220.	4.4	43
12	A topological approach for protein classification. Computational and Mathematical Biophysics, 2015, 3, .	1.1	42
13	Identifying multicellular spatiotemporal organization of cells with SpaceFlow. Nature Communications, 2022, 13, .	12.8	30
14	Single-cell transcriptomic analysis of zebrafish cranial neural crest reveals spatiotemporal regulation of lineage decisions during development. Cell Reports, 2021, 37, 110140.	6.4	24
15	Protein pocket detection via convex hull surface evolution and associated Reeb graph. Bioinformatics, 2018, 34, i830-i837.	4.1	23
16	Structural cavities are critical to balancing stability and activity of a membrane-integral enzyme. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22146-22156.	7.1	23
17	DEEPsc: A Deep Learning-Based Map Connecting Single-Cell Transcriptomics and Spatial Imaging Data. Frontiers in Genetics, 2021, 12, 636743.	2.3	22
18	A multiscale model via single-cell transcriptomics reveals robust patterning mechanisms during early mammalian embryo development. PLoS Computational Biology, 2021, 17, e1008571.	3.2	11

#	ARTICLE	IF	CITATIONS
19	Persistent Cohomology for Data With Multicomponent Heterogeneous Information. SIAM Journal on Mathematics of Data Science, 2020, 2, 396-418.	1.8	10
20	Evolutionary homology on coupled dynamical systems with applications to protein flexibility analysis. Journal of Applied and Computational Topology, 2020, 4, 481-507.	2.0	6
21	Charge substitutions at the voltage-sensing module of domain III enhance actions of site-3 and site-4 toxins on an insect sodium channel. Insect Biochemistry and Molecular Biology, 2021, 137, 103625.	2.7	2