

Somnath Tagore

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2204486/publications.pdf>

Version: 2024-02-01

13
papers

846
citations

1163117

8
h-index

1199594

12
g-index

20
all docs

20
docs citations

20
times ranked

1225
citing authors

#	ARTICLE	IF	CITATIONS
1	A molecular single-cell lung atlas of lethal COVID-19. <i>Nature</i> , 2021, 595, 114-119.	27.8	411
2	A multi-organ chip with matured tissue niches linked by vascular flow. <i>Nature Biomedical Engineering</i> , 2022, 6, 351-371.	22.5	162
3	A modular master regulator landscape controls cancer transcriptional identity. <i>Cell</i> , 2021, 184, 334-351.e20.	28.9	78
4	Dissecting the treatment-naive ecosystem of human melanoma brain metastasis. <i>Cell</i> , 2022, 185, 2591-2608.e30.	28.9	62
5	ChiTaRS-3.1—the enhanced chimeric transcripts and RNA-seq database matched with protein–protein interactions. <i>Nucleic Acids Research</i> , 2017, 45, D790-D795.	14.5	44
6	ChiPPI: a novel method for mapping chimeric protein–protein interactions uncovers selection principles of protein fusion events in cancer. <i>Nucleic Acids Research</i> , 2017, 45, 7094-7105.	14.5	33
7	Oncoprotein-specific molecular interaction maps (SigMaps) for cancer network analyses. <i>Nature Biotechnology</i> , 2021, 39, 215-224.	17.5	21
8	Adaptive Transcriptome Profiling of Subterranean Zokor, <i>Myospalax baileyi</i> , to High-Altitude Stresses in Tibet. <i>Scientific Reports</i> , 2018, 8, 4671.	3.3	10
9	ProtFus: A Comprehensive Method Characterizing Protein-Protein Interactions of Fusion Proteins. <i>PLoS Computational Biology</i> , 2019, 15, e1007239.	3.2	10
10	Cluster Quality based Non-Reductional (CQNR) oversampling technique and effector protein predictor based on 3D structure (EPP3D) of proteins. <i>Computers in Biology and Medicine</i> , 2019, 112, 103374.	7.0	1
11	Design principles of gene evolution for niche adaptation through changes in protein–protein interaction networks. <i>Scientific Reports</i> , 2020, 10, 15628.	3.3	1
12	ASAPP: Architectural Similarity-based Automated Pathway Prediction System and its Application in Host-Pathogen Interactions. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	3.0	0
13	Multi-modal single-cell profiling of sarcomas from archival tissue reveals mechanisms of resistance to immune checkpoint inhibitors. <i>Journal of Clinical Oncology</i> , 2022, 40, e23518-e23518.	1.6	0