Sikander Hayat

List of Publications by Year
in descending order

22 papers	2,249 citations	933447 10 h-index	839539 18 g-index
24 all docs	24 docs citations	24 times ranked	5780 citing authors

#	Article	IF	Citations
1	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	28.9	1,485
2	Molecular architecture of the active mitochondrial protein gate. Science, 2015, 349, 1544-1548.	12.6	169
3	PconsFold: improved contact predictions improve protein models. Bioinformatics, 2014, 30, i482-i488.	4.1	92
4	Integrative Analysis Reveals a Molecular Stratification of Systemic Autoimmune Diseases. Arthritis and Rheumatology, 2021, 73, 1073-1085.	5.6	81
5	Inclusion of dyad-repeat pattern improves topology prediction of transmembrane Î²-barrel proteins. Bioinformatics, 2016, 32, 1571-1573.	4.1	75
6	Myocyte Specific Upregulation of ACE2 in Cardiovascular Disease: Implications for SARS-CoV-2 Mediated Myocarditis. Circulation, 2020, 142, 708-710.	1.6	73
7	BOCTOPUS: improved topology prediction of transmembrane Î² barrel proteins. Bioinformatics, 2012, 28, 516-522.	4.1	71
8	All-atom 3D structure prediction of transmembrane Î²-barrel proteins from sequences. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5413-5418.	7.1	53
9	Prediction of the burial status of transmembrane residues of helical membrane proteins. BMC Bioinformatics, 2007, 8, 302.	2.6	35
10	TMBHMM: A frequency profile based HMM for predicting the topology of transmembrane beta barrel proteins and the exposure status of transmembrane residues. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 664-670.	2.3	27
11	Ranking models of transmembrane <i>Î²</i>-barrel proteins using Z-coordinate predictions. Bioinformatics, 2012, 28, i90-i96.	4.1	15
12	MACA: marker-based automatic cell-type annotation for single-cell expression data. Bioinformatics, 2022, 38, 1756-1760.	4.1	14
13	Mechanistic insights into cancer cell killing through interaction of phosphodiesterase 3A and schlafen family member 12. Journal of Biological Chemistry, 2020, 295, 3431-3446.	3.4	12
14	Multiscale interactome analysis coupled with off-target drug predictions reveals drug repurposing candidates for human coronavirus disease. Scientific Reports, 2021, 11, 23315.	3.3	10
15	PREDICTION OF THE EXPOSURE STATUS OF TRANSMEMBRANE BETA BARREL RESIDUES FROM PROTEIN SEQUENCE. Journal of Bioinformatics and Computational Biology, 2011, 09, 43-65.	0.8	9
16	Hill Kinetics Meets P Systems: A Case Study on Gene Regulatory Networks as Computing Agents in silico and in vivo. , 2007, , 320-335.		7
17	Towards in vivo computing. , 2006, , .		6
18	Statistical analysis and exposure status classification of transmembrane beta barrel residues. Computational Biology and Chemistry, 2011, 35, 96-107.	2.3	6

#	ARTICLE	IF	CITATIONS
19	Localization Prediction and Structure-Based In Silico Analysis of Bacterial Proteins: With Emphasis on Outer Membrane Proteins. Methods in Molecular Biology, 2013, 939, 115-140.	0.9	3
20	Advances in Computational Methods for Transmembrane Protein Structure Prediction. , 2017, , 135-165.		2
21	Predicting Structural and Functional Properties of Membrane Proteins from Protein Sequence. Annual Reports in Computational Chemistry, 2011, , 39-64.	1.7	1
22	Predicting the burial/exposure status of transmembrane residues in helical membrane proteins. , 2010, , 151-164.		1