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	MACA: marker-based automatic cell-type annotation for single-cell expression data. Bioinformatics, 2022, 38, 1756-1760.	4.1	14
2	Integrative Analysis Reveals a Molecular Stratification of Systemic Autoimmune Diseases. Arthritis and Rheumatology, 2021, 73, 1073-1085.	5.6	81
3	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
4	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
5	Myocyte Specific Upregulation of ACE2 in Cardiovascular Disease: Implications for SARS-CoV-2 Mediated Myocarditis. Circulation, 2020, 142, 708-710.	1.6	73
6	Advances in Computational Methods for Transmembrane Protein Structure Prediction. , 2017, , 135-165.		2
7	Inclusion of dyad-repeat pattern improves topology prediction of transmembrane Î²-barrel proteins. Bioinformatics, 2016, 32, 1571-1573.	4.1	75
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	Molecular architecture of the active mitochondrial protein gate. Science, 2015, 349, 1544-1548.	12.6	169
10	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	28.9	1,485
11	PconsFold: improved contact predictions improve protein models. Bioinformatics, 2014, 30, i482-i488.	4.1	92
12	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
13	Ranking models of transmembrane <i>Î²</i>-barrel proteins using Z-coordinate predictions. Bioinformatics, 2012, 28, i90-i96.	4.1	15
14	BOCTOPUS: improved topology prediction of transmembrane Î² barrel proteins. Bioinformatics, 2012, 28, 516-522.	4.1	71
15	Statistical analysis and exposure status classification of transmembrane beta barrel residues. Computational Biology and Chemistry, 2011, 35, 96-107.	2.3	6
16	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
17	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
18	Predicting Structural and Functional Properties of Membrane Proteins from Protein Sequence. Annual Reports in Computational Chemistry, 2011, , 39-64.	1.7	1

#	ARTICLE	IF	CITATIONS
19	Predicting the burial/exposure status of transmembrane residues in helical membrane proteins. , 2010, , 151-164.		1
20	Hill Kinetics Meets P Systems: A Case Study on Gene Regulatory Networks as Computing Agents in silico and in vivo. , 2007, , 320-335.		7
21	Prediction of the burial status of transmembrane residues of helical membrane proteins. BMC Bioinformatics, 2007, 8, 302.	2.6	35
22	Towards in vivo computing. , 2006, , .		6