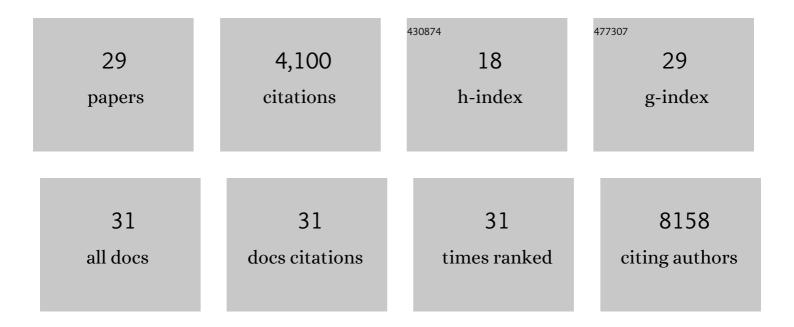
Arun Prasad Pandurangan

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354.	14.5	1,385
2	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	14.5	1,291
3	SDM: a server for predicting effects of mutations on protein stability. Nucleic Acids Research, 2017, 45, W229-W235.	14.5	407
4	Stepwise visualization of membrane pore formation by suilysin, a bacterial cholesterol-dependent cytolysin. ELife, 2014, 3, e04247.	6.0	145
5	Mutations at protein-protein interfaces: Small changes over big surfaces have large impacts on human health. Progress in Biophysics and Molecular Biology, 2017, 128, 3-13.	2.9	129
6	The SUPERFAMILY 2.0 database: a significant proteome update and a new webserver. Nucleic Acids Research, 2019, 47, D490-D494.	14.5	126
7	Two distinct trimeric conformations of natively membrane-anchored full-length herpes simplex virus 1 glycoprotein B. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4176-4181.	7.1	93
8	<i>TEMPy</i> : a Python library for assessment of three-dimensional electron microscopy density fits. Journal of Applied Crystallography, 2015, 48, 1314-1323.	4.5	75
9	Prediction of impacts of mutations on protein structure and interactions: SDM, a statistical approach, and mCSM, using machine learning. Protein Science, 2020, 29, 247-257.	7.6	58
10	The Structure of Herpesvirus Fusion Glycoprotein B-Bilayer Complex Reveals the Protein-Membrane and Lateral Protein-Protein Interaction. Structure, 2013, 21, 1396-1405.	3.3	47
11	Structural Analysis of Coxsackievirus A7 Reveals Conformational Changes Associated with Uncoating. Journal of Virology, 2012, 86, 7207-7215.	3.4	41
12	Genomes, structural biology and drug discovery: combating the impacts of mutations in genetic disease and antibiotic resistance. Biochemical Society Transactions, 2017, 45, 303-311.	3.4	35
13	γ-TEMPy: Simultaneous Fitting of Components in 3D-EM Maps of Their Assembly Using a Genetic Algorithm. Structure, 2015, 23, 2365-2376.	3.3	34
14	Finding rigid bodies in protein structures: Application to flexible fitting into cryoEM maps. Journal of Structural Biology, 2012, 177, 520-531.	2.8	33
15	A new peptide docking strategy using a mean field technique with mutually orthogonal Latin square sampling. Journal of Computer-Aided Molecular Design, 2008, 22, 815-829.	2.9	29
16	Conformational States of Macromolecular Assemblies Explored by Integrative Structure Calculation. Structure, 2013, 21, 1500-1508.	3.3	29
17	Combined approaches to flexible fitting and assessment in virus capsids undergoing conformational change. Journal of Structural Biology, 2014, 185, 427-439.	2.8	23
18	Photo-antagonism of the GABAA receptor. Nature Communications, 2014, 5, 4454.	12.8	22

#	Article	IF	CITATIONS
19	RIBFIND: a web server for identifying rigid bodies in protein structures and to aid flexible fitting into cryo EM maps. Bioinformatics, 2012, 28, 2391-2393.	4.1	19
20	Proteinâ ''Ligand Docking Using Mutually Orthogonal Latin Squares (MOLSDOCK). Journal of Chemical Information and Modeling, 2009, 49, 2687-2694.	5.4	13
21	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. Nucleic Acids Research, 2020, 48, D314-D319.	14.5	13
22	Exploring the conformational space of protein loops using a mean field technique with MOLS sampling. Proteins: Structure, Function and Bioinformatics, 2007, 67, 908-921.	2.6	9
23	Experimental and Computational Approaches to Direct Cell Reprogramming: Recent Advancement and Future Challenges. Cells, 2019, 8, 1189.	4.1	8
24	Exploring conformational space using a mean field technique with MOLS sampling. Journal of Biosciences, 2007, 32, 909-920.	1.1	5
25	Optopharmacology reveals a differential contribution of native GABAA receptors to dendritic and somatic inhibition using azogabazine. Neuropharmacology, 2020, 176, 108135.	4.1	3
26	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. Methods in Molecular Biology, 2020, 2165, 27-67.	0.9	3
27	MOLSa program to explore the potential energy surface of a peptide and locate its low energy conformations. In Silico Biology, 2005, 5, 401-5.	0.9	2
28	Editorial: Computational Approaches to Study the Impact of Mutations on Disease and Drug Resistance. Frontiers in Molecular Biosciences, 2021, 8, 813552.	3.5	2
29	MOLS sampling and its applications in structural biophysics. Biophysical Reviews, 2010, 2, 169-179.	3.2	1