Arun Prasad Pandurangan

List of Publications by Year
in descending order

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29 papers	4,100 citations	430874 18 h-index	477307 29 g-index
31 all docs	31 docs citations	31 times ranked	8158 citing authors

#	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	Editorial: Computational Approaches to Study the Impact of Mutations on Disease and Drug Resistance. Frontiers in Molecular Biosciences, 2021, 8, 813552.	3.5	2
3	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
4	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
5	Optopharmacology reveals a differential contribution of native GABAA receptors to dendritic and somatic inhibition using azogabazine. Neuropharmacology, 2020, 176, 108135.	4.1	3
6	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. Methods in Molecular Biology, 2020, 2165, 27-67.	0.9	3
7	Experimental and Computational Approaches to Direct Cell Reprogramming: Recent Advancement and Future Challenges. Cells, 2019, 8, 1189.	4.1	8
8	The SUPERFAMILY 2.0 database: a significant proteome update and a new webserver. Nucleic Acids Research, 2019, 47, D490-D494.	14.5	126
9	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	14.5	1,291
10	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
11	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
12	SDM: a server for predicting effects of mutations on protein stability. Nucleic Acids Research, 2017, 45, W229-W235.	14.5	407
13	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
14	Î³-TEMPy: Simultaneous Fitting of Components in 3D-EM Maps of Their Assembly Using a Genetic Algorithm. Structure, 2015, 23, 2365-2376.	3.3	34
15	TEMPy: a Python library for assessment of three-dimensional electron microscopy density fits. Journal of Applied Crystallography, 2015, 48, 1314-1323.	4.5	75
16	Photo-antagonism of the GABAA receptor. Nature Communications, 2014, 5, 4454.	12.8	22
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	Stepwise visualization of membrane pore formation by suilysin, a bacterial cholesterol-dependent cytolysin. ELife, 2014, 3, e04247.	6.0	145

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19	Conformational States of Macromolecular Assemblies Explored by Integrative Structure Calculation. Structure, 2013, 21, 1500-1508.	3.3	29
20	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
21	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
22	Finding rigid bodies in protein structures: Application to flexible fitting into cryoEM maps. Journal of Structural Biology, 2012, 177, 520-531.	2.8	33
23	Structural Analysis of Coxsackievirus A7 Reveals Conformational Changes Associated with Uncoating. Journal of Virology, 2012, 86, 7207-7215.	3.4	41
24	MOLS sampling and its applications in structural biophysics. Biophysical Reviews, 2010, 2, 169-179.	3.2	1
25	Proteinâ˜Ligand Docking Using Mutually Orthogonal Latin Squares (MOLSDOCK). Journal of Chemical Information and Modeling, 2009, 49, 2687-2694.	5.4	13
26	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
27	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
28	Exploring conformational space using a mean field technique with MOLS sampling. Journal of Biosciences, 2007, 32, 909-920.	1.1	5
29	MOLS--a 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