# Arun Prasad Pandurangan

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1037860/publications.pdf

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|---|---|---|---|
| 29<br>papers | 4,100<br>citations | 430874<br>18<br>h-index | 477307<br>29<br>g-index |
| 31<br>all docs | 31<br>docs citations | 31<br>times ranked | 8158<br>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 | 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 | TEMPy: 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 | 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 |
| 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 |

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|---|---|---|---|
| 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 | 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 |
| 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 |