Surya V S R K Pulavarti

List of Publications by Year
in descending order

21	608	933447 10	839539 18
papers	citations	h-index	g-index

21	21	21	1110
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Accurate de novo design of hyperstable constrained peptides. Nature, 2016, 538, 329-335.	27.8	327
2	Perturbing the energy landscape for improved packing during computational protein design. Proteins: Structure, Function and Bioinformatics, 2021, 89, 436-449.	2.6	85
3	Solution Structure and Dynamics of Peptidyl-tRNA Hydrolase from Mycobacterium tuberculosis H37Rv. Journal of Molecular Biology, 2008, 378, 165-177.	4.2	38
4	Solution structure and dynamics of ADF from Toxoplasma gondii. Journal of Structural Biology, 2011, 176, 97-111.	2.8	28
5	Computational de novo design of a fourâ€helix bundle proteinâ€”<scp>DND</scp>_4<scp>HB</scp>. Protein Science, 2015, 24, 434-445.	7.6	24
6	Folding and Assembly of Short Î±, Î², Î³-Hybrid Peptides: Minor Variations in Sequence and Drastic Differences in Higher-Level Structures. Journal of the American Chemical Society, 2019, 141, 14239-14248.	13.7	18
7	Cytosolic expression, solution structures, and molecular dynamics simulation of genetically encodable disulfideâ€rich de novo designed peptides. Protein Science, 2018, 27, 1611-1623.	7.6	14
8	Solution structure and dynamics of ADF/cofilin from Leishmania donovani. Journal of Structural Biology, 2010, 172, 219-224.	2.8	12
9	Unraveling the stereochemical and dynamic aspects of the catalytic site of bacterial peptidyl-tRNA hydrolase. Rna, 2017, 23, 202-216.	3.5	11
10	Targeted Delivery of Ubiquitin-Conjugated BH3 Peptide-Based Mcl-1 Inhibitors into Cancer Cells. Bioconjugate Chemistry, 2014, 25, 424-432.	3.6	10
11	Solution NMR Experiment for Measurement of ¹⁵Nâ€“¹H Residual Dipolar Couplings in Large Proteins and Supramolecular Complexes. Journal of the American Chemical Society, 2015, 137, 11242-11245.	13.7	10
12	Aromatic oligureas as hosts for anions and cations. Chemical Communications, 2016, 52, 9905-9908.	4.1	10
13	Structural characterization of peptidyl-tRNA hydrolase from Mycobacterium smegmatis by NMR spectroscopy. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 1304-1314.	2.3	9
14	NMR assignment of peptidyl-tRNA hydrolase from Mycobacterium tuberculosis H37Rv. Journal of Biomolecular NMR, 2006, 36, 53-53.	2.8	3
15	NMR assignment of actin depolymerizing and dynamics regulatory protein from Leishmania donovani. Biomolecular NMR Assignments, 2009, 3, 265-267.	0.8	3
16	From Protein Design to the Energy Landscape of a Cold Unfolding Protein. Journal of Physical Chemistry B, 2022, 126, 1212-1231.	2.6	3
17	Solution NMR structure of CD1104B from pathogenic Clostridium difficile reveals a distinct Î±-helical architecture and provides first structural representative of protein domain family PF14203. Journal of Structural and Functional Genomics, 2013, 14, 155-160.	1.2	2
18	Solution NMR structures of homeodomains from human proteins ALX4, ZHX1, and CASP8AP2 contribute to the structural coverage of the Human Cancer Protein Interaction Network. Journal of Structural and Functional Genomics, 2014, 15, 201-207.	1.2	1

#	Article	IF	Citations
19	Solution NMR structures provide first structural coverage of the large protein domain family PF08369 and complementary structural coverage of dark operative protochlorophyllide oxidoreductase complexes. Journal of Structural and Functional Genomics, 2013, 14, 119-126.	1.2	0
20	Solution NMR structures of immunoglobulin-like domains 7 and 12 from obscurin-like protein 1 contribute to the structural coverage of the human cancer protein interaction network. Journal of Structural and Functional Genomics, 2014, 15, 209-214.	1.2	0
21	Polypeptide backbone, Cî² and methyl group resonance assignments of the 24ÂkDa plectin repeat domain 6 from human protein plectin. Biomolecular NMR Assignments, 2015, 9, 135-138.	0.8	0