

Surya V S R K Pulavarti

List of Publications by Year in descending order

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21
papers

608
citations

933447

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839539

18
g-index

21
all docs

21
docs citations

21
times ranked

1110
citing authors

#	ARTICLE	IF	CITATIONS
1	From Protein Design to the Energy Landscape of a Cold Unfolding Protein. <i>Journal of Physical Chemistry B</i> , 2022, 126, 1212-1231.	2.6	3
2	Perturbing the energy landscape for improved packing during computational protein design. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 436-449.	2.6	85
3	Folding and Assembly of Short α , β , α -Hybrid Peptides: Minor Variations in Sequence and Drastic Differences in Higher-Level Structures. <i>Journal of the American Chemical Society</i> , 2019, 141, 14239-14248.	13.7	18
4	Cytosolic expression, solution structures, and molecular dynamics simulation of genetically encodable disulfide-rich <i>de novo</i> designed peptides. <i>Protein Science</i> , 2018, 27, 1611-1623.	7.6	14
5	Unraveling the stereochemical and dynamic aspects of the catalytic site of bacterial peptidyl-tRNA hydrolase. <i>Rna</i> , 2017, 23, 202-216.	3.5	11
6	Structural characterization of peptidyl-tRNA hydrolase from <i>Mycobacterium smegmatis</i> by NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1304-1314.	2.3	9
7	Aromatic oligureas as hosts for anions and cations. <i>Chemical Communications</i> , 2016, 52, 9905-9908.	4.1	10
8	Accurate <i>de novo</i> design of hyperstable constrained peptides. <i>Nature</i> , 2016, 538, 329-335.	27.8	327
9	Solution NMR Experiment for Measurement of ^{15}N - ^1H Residual Dipolar Couplings in Large Proteins and Supramolecular Complexes. <i>Journal of the American Chemical Society</i> , 2015, 137, 11242-11245.	13.7	10
10	Computational <i>de novo</i> design of a four-helix bundle protein DND ₄ HB. <i>Protein Science</i> , 2015, 24, 434-445.	7.6	24
11	Polypeptide backbone, $C\alpha$ and methyl group resonance assignments of the 24 kDa plectin repeat domain 6 from human protein plectin. <i>Biomolecular NMR Assignments</i> , 2015, 9, 135-138.	0.8	0
12	Targeted Delivery of Ubiquitin-Conjugated BH3 Peptide-Based Mcl-1 Inhibitors into Cancer Cells. <i>Bioconjugate Chemistry</i> , 2014, 25, 424-432.	3.6	10
13	Solution NMR structures of homeodomains from human proteins ALX4, ZHX1, and CASP8AP2 contribute to the structural coverage of the Human Cancer Protein Interaction Network. <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 201-207.	1.2	1
14	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. <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 209-214.	1.2	0
15	Solution NMR structure of CD1104B from pathogenic <i>Clostridium difficile</i> reveals a distinct α -helical architecture and provides first structural representative of protein domain family PF14203. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 155-160.	1.2	2
16	Solution NMR structures provide first structural coverage of the large protein domain family PF08369 and complementary structural coverage of dark operative protochlorophyllide oxidoreductase complexes. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 119-126.	1.2	0
17	Solution structure and dynamics of ADF from <i>Toxoplasma gondii</i> . <i>Journal of Structural Biology</i> , 2011, 176, 97-111.	2.8	28
18	Solution structure and dynamics of ADF/cofilin from <i>Leishmania donovani</i> . <i>Journal of Structural Biology</i> , 2010, 172, 219-224.	2.8	12

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19	NMR assignment of actin depolymerizing and dynamics regulatory protein from Leishmania donovani. Biomolecular NMR Assignments, 2009, 3, 265-267.	0.8	3
20	Solution Structure and Dynamics of Peptidyl-tRNA Hydrolase from Mycobacterium tuberculosis H37Rv. Journal of Molecular Biology, 2008, 378, 165-177.	4.2	38
21	NMR assignment of peptidyl-tRNA hydrolase from Mycobacterium tuberculosis H37Rv. Journal of Biomolecular NMR, 2006, 36, 53-53.	2.8	3