M S Madhusudhan

List of Publications by Year
in descending order

25	1,099	516710 16	580821 25
papers	citations	h-index	g-index

25	25	25	1952
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Peptide bond planarity constrains hydrogen bond geometry and influences secondary structure conformations. Current Research in Structural Biology, 2021, 3, 1-8.	2.2	18
2	Observation of an Unusually Large IR Red-Shift in an Unconventional Sâ€“HÂ·Â·Â·S Hydrogen-Bond. Journal of Physical Chemistry Letters, 2021, 12, 1228-1235.	4.6	25
3	On and off controls within dyneinâ€“dynactin on native cargoes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	14
4	Methods for Molecular Modelling of Protein Complexes. Methods in Molecular Biology, 2021, 2305, 53-80.	0.9	7
5	PDBe-KB: a community-driven resource for structural and functional annotations. Nucleic Acids Research, 2020, 48, D344-D353.	14.5	87
6	Protein Interaction Z Score Assessment (PIZSA): an empirical scoring scheme for evaluation of proteinâ€“protein interactions. Nucleic Acids Research, 2019, 47, W331-W337.	14.5	20
7	Water-Mediated Selenium Hydrogen-Bonding in Proteins: PDB Analysis and Gas-Phase Spectroscopy of Model Complexes. Journal of Physical Chemistry A, 2019, 123, 5995-6002.	2.5	26
8	Structural insights of a cellobiose dehydrogenase enzyme from the basidiomycetes fungus Termitomyces clypeatus. Computational Biology and Chemistry, 2019, 82, 65-73.	2.3	9
9	Discovering Putative Protein Targets of Small Molecules: A Study of the p53 Activator Nutlin. Journal of Chemical Information and Modeling, 2019, 59, 1529-1546.	5.4	15
10	Predicting and designing therapeutics against the Nipah virus. PLoS Neglected Tropical Diseases, 2019, 13, e0007419.	3.0	24
11	Depth dependent amino acid substitution matrices and their use in predicting deleterious mutations. Progress in Biophysics and Molecular Biology, 2017, 128, 14-23.	2.9	13
12	Computational modeling of protein assemblies. Current Opinion in Structural Biology, 2017, 44, 179-189.	5.7	47
13	In silico methods for design of biological therapeutics. Methods, 2017, 131, 33-65.	3.8	49
14	Topology independent comparison of RNA 3D structures using the CLICK algorithm. Nucleic Acids Research, 2017, 45, e5-e5.	14.5	17
15	Molecular Mechanism Underlying ATP-Induced Conformational Changes in the Nucleoprotein Filament of Mycobacterium smegmatis RecA. Biochemistry, 2016, 55, 1850-1862.	2.5	9
16	Phosphoregulatory protein 14-3-3 facilitates SAC1 transport from the endoplasmic reticulum. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3199-206.	7.1	46
17	Biophysical Properties of Intrinsically Disordered p130Cas Substrate Domain â€” Implication in Mechanosensing. PLoS Computational Biology, 2014, 10, e1003532.	3.2	24
18	Depth: a web server to compute depth, cavity sizes, detect potential small-molecule ligand-binding cavities and predict the pKa of ionizable residues in proteins. Nucleic Acids Research, 2013, 41, W314-W321.	14.5	171

#	Article	IF	Citations
19	SALIGN: a web server for alignment of multiple protein sequences and structures. Bioinformatics, 2012, 28, 2072-2073.	4.1	72
20	CLICKâ€"topology-independent comparison of biomolecular 3D structures. Nucleic Acids Research, 2011, 39, W24-W28.	14.5	112
21	Biological insights from topology independent comparison of protein 3D structures. Nucleic Acids Research, 2011, 39, e94-e94.	14.5	43
22	DEPTH: a web server to compute depth and predict small-molecule binding cavities in proteins. Nucleic Acids Research, 2011, 39, W242-W248.	14.5	88
23	Alignment of multiple protein structures based on sequence and structure features. Protein Engineering, Design and Selection, 2009, 22, 569-574.	2.1	82
24	DBAli tools: mining the protein structure space. Nucleic Acids Research, 2007, 35, W393-W397.	14.5	25
25	Protein complex compositions predicted by structural similarity. Nucleic Acids Research, 2006, 34, 2943-2952.	14.5	56