

Shashi Bhushan Pandit

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

26

papers

633

citations

13

h-index

25

g-index

27

ext. papers

688

ext. citations

6.5

avg, IF

3.6

L-index

#	Paper	IF	Citations
26	Fr-TM-align: a new protein structural alignment method based on fragment alignments and the TM-score. <i>BMC Bioinformatics</i> , 2008 , 9, 531	3.6	107
25	XTMS: pathway design in an eXTended metabolic space. <i>Nucleic Acids Research</i> , 2014 , 42, W389-94	20.1	81
24	Analysis of TASSER-based CASP7 protein structure prediction results. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69 Suppl 8, 90-7	4.2	60
23	Enumerating metabolic pathways for the production of heterologous target chemicals in chassis organisms. <i>BMC Systems Biology</i> , 2012 , 6, 10	3.5	49
22	Proteomics analysis of carbon-starved Mycobacterium smegmatis: induction of Dps-like protein. <i>Protein Engineering, Design and Selection</i> , 2002 , 15, 503-12	1.9	49
21	Phosphoprotein and phosphopeptide interactions with the FHA domain from Arabidopsis kinase-associated protein phosphatase. <i>Biochemistry</i> , 2007 , 46, 2684-96	3.2	42
20	TASSER-Lite: an automated tool for protein comparative modeling. <i>Biophysical Journal</i> , 2006 , 91, 4180-90	9.9	38
19	Integration of related sequences with protein three-dimensional structural families in an updated version of PALL database. <i>Nucleic Acids Research</i> , 2003 , 31, 486-8	20.1	33
18	SUPFAM--a database of potential protein superfamily relationships derived by comparing sequence-based and structure-based families: implications for structural genomics and function annotation in genomes. <i>Nucleic Acids Research</i> , 2002 , 30, 289-93	20.1	33
17	Performance of the Pro-sp3-TASSER server in CASP8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 77 Suppl 9, 123-7	4.2	31
16	SUPFAM: a database of sequence superfamilies of protein domains. <i>BMC Bioinformatics</i> , 2004 , 5, 28	3.6	27
15	Survey for g-proteins in the prokaryotic genomes: prediction of functional roles based on classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 52, 585-97	4.2	23
14	PSiFR: an integrated resource for prediction of protein structure and function. <i>Bioinformatics</i> , 2010 , 26, 687-8	7.2	13
13	Disulphide bond restrains the C-terminal region of thermostable direct hemolysin during folding to promote oligomerization. <i>Biochemical Journal</i> , 2017 , 474, 317-331	3.8	9
12	PRODOC: a resource for the comparison of tethered protein domain architectures with in-built information on remotely related domain families. <i>Nucleic Acids Research</i> , 2005 , 33, W126-9	20.1	9
11	CSmetaPred: a consensus method for prediction of catalytic residues. <i>BMC Bioinformatics</i> , 2017 , 18, 583	3.6	6
10	Enhanced functional and structural domain assignments using remote similarity detection procedures for proteins encoded in the genome of Mycobacterium tuberculosis H37Rv. <i>Journal of Biosciences</i> , 2004 , 29, 245-59	2.3	5

9	Structural and functional characterization of gene products encoded in the human genome by homology detection. <i>IUBMB Life</i> , 2004 , 56, 317-31	4-7	4
8	Evolutionarily conserved and conformationally constrained short peptides might serve as DNA recognition elements in intrinsically disordered regions. <i>Molecular BioSystems</i> , 2014 , 10, 1469-80		3
7	TASSER_low-zsc: an approach to improve structure prediction using low z-score-ranked templates. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 2769-80	4-2	3
6	Unraveling the structural landscape of intra-chain domain interfaces: Implication in the evolution of domain-domain interactions. <i>PLoS ONE</i> , 2019 , 14, e0220336	3-7	2
5	Tasser-Based Protein Structure Prediction 2010 , 219-242		2
4	Optimal Protein Sequence Design Mitigates Mechanical Failure in Silk β -Sheet Nanocrystals. <i>ACS Biomaterials Science and Engineering</i> , 2021 , 7, 3156-3165	5-5	2
3	Learning Protein Folding Energy Functions. <i>IEEE International Conference on Data Mining</i> , 2011 , 1062-1067		1
2	Unusual commonality in active site structural features of substrate promiscuous and specialist enzymes.. <i>Journal of Structural Biology</i> , 2022 , 214, 107835	3-4	1
1	Dynamics of Protein-Protein Interaction Network in Plasmodium Falciparum 2009 , 257-284		