Sutanu Bhattacharya

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4205887/publications.pdf

Version: 2024-02-01

12	83	1684188 5	1872680 6
papers	citations	h-index	g-index

16	16	16	57
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	QDeep: distance-based protein model quality estimation by residue-level ensemble error classifications using stacked deep residual neural networks. Bioinformatics, 2020, 36, i285-i291.	4.1	34
2	Does inclusion of residueâ€•residue contact information boost protein threading?. Proteins: Structure, Function and Bioinformatics, 2019, 87, 596-606.	2.6	11
3	Evaluating the significance of contact maps in low-homology protein modeling using contact-assisted threading. Scientific Reports, 2020, 10, 2908.	3.3	11
4	Recent Advances in Protein Homology Detection Propelled by Inter-Residue Interaction Map Threading. Frontiers in Molecular Biosciences, 2021, 8, 643752.	3.5	8
5	Hybridized distance- and contact-based hierarchical structure modeling for folding soluble and membrane proteins. PLoS Computational Biology, 2021, 17, e1008753.	3.2	7
6	<scp>DisCovER</scp>: distanceâ€•and orientationâ€based covariational threading for weakly homologous proteins. Proteins: Structure, Function and Bioinformatics, 2022, 90, 579-588.	2.6	7
7	Contact-assisted Protein Threading. , 2019, , .		1
8	PolyFold: An interactive visual simulator for distance-based protein folding. PLoS ONE, 2020, 15, e0243331.	2.5	1
9	Cover Image, Volume 87, Issue 7. Proteins: Structure, Function and Bioinformatics, 2019, 87, C1-C1.	2.6	0
10	Hybridized distance- and contact- based hierarchical protein structure modeling using DConStruct. , 2021, , .		0
11	How Effective is Contact-assisted Protein Threading?. , 2019, , .		0
12	<scp>rrQNet</scp>: Protein contact map quality estimation by deep evolutionary reconciliation. Proteins: Structure, Function and Bioinformatics, 2022, 90, 2023-2034.	2.6	0