

Nawsad Alam

List of Publications by Year in descending order

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11
papers

1,079
citations

1040056

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1281871

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docs citations

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times ranked

1426
citing authors

#	ARTICLE	IF	CITATIONS
1	Modeling beta-sheet peptide-protein interactions: Rosetta FlexPepDock in CAPRI rounds 38-45. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1037-1049.	2.6	10
2	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	19.0	513
3	ClusPro in rounds 38 to 45 of CAPRI: Toward combining template-based methods with free docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1082-1090.	2.6	5
4	Novel Structural Mechanism of Allosteric Regulation of Aspartic Peptidases via an Evolutionarily Conserved Exosite. <i>Cell Chemical Biology</i> , 2018, 25, 318-329.e4.	5.2	14
5	Protein-peptide docking: opportunities and challenges. <i>Drug Discovery Today</i> , 2018, 23, 1530-1537.	6.4	212
6	Modeling Peptide-Protein Structure and Binding Using Monte Carlo Sampling Approaches: Rosetta FlexPepDock and FlexPepBind. <i>Methods in Molecular Biology</i> , 2017, 1561, 139-169.	0.9	32
7	ClusPro PeptiDock: efficient global docking of peptide recognition motifs using FFT. <i>Bioinformatics</i> , 2017, 33, 3299-3301.	4.1	102
8	FlexPepDock lessons from CAPRI peptide-protein rounds and suggested new criteria for assessment of model quality and utility. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 445-462.	2.6	19
9	Host FIH-Mediated Asparaginyl Hydroxylation of Translocated <i>Legionella pneumophila</i> Effectors. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 54.	3.9	11
10	High-resolution global peptide-protein docking using fragments-based PIPER-FlexPepDock. <i>PLoS Computational Biology</i> , 2017, 13, e1005905.	3.2	119
11	Structure-Based Identification of HDAC8 Non-histone Substrates. <i>Structure</i> , 2016, 24, 458-468.	3.3	42