Dzmitry Padhorny

List of Publications by Year
in descending order

16 papers	2,709 citations	1040056 9 h-index	996975 15 g-index
17 all docs	17 docs citations	17 times ranked	4942 citing authors

#	Article	IF	Citations
1	The ClusPro web server for proteinâ€“protein docking. Nature Protocols, 2017, 12, 255-278.	12.0	1,959
2	Allostery in Its Many Disguises: From Theory to Applications. Structure, 2019, 27, 566-578.	3.3	285
3	Blind prediction of homoâ€and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99
4	Actionable Cytopathogenic Host Responses of Human Alveolar Type 2 Cells to SARS-CoV-2. Molecular Cell, 2020, 80, 1104-1122.e9.	9.7	94
5	Prediction of protein assemblies, the next frontier: The <scp>CASP14â€CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	2.6	73
6	Proteinâ€“protein docking by fast generalized Fourier transforms on 5D rotational manifolds. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4286-93.	7.1	43
7	ClusPro-DC: Dimer Classification by the Cluspro Server for Proteinâ€“Protein Docking. Journal of Molecular Biology, 2017, 429, 372-381.	4.2	36
8	Templateâ€based modeling by ClusPro in CASP13 and the potential for using coâ€evolutionary information in docking. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1241-1248.	2.6	15
9	Monte Carlo on the manifold and MD refinement for binding pose prediction of proteinâ€“ligand complexes: 2017 D3R Grand Challenge. Journal of Computer-Aided Molecular Design, 2019, 33, 119-127.	2.9	12
10	Assessing the binding properties of <scp>CASP14</scp> targets and models. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1922-1939.	2.6	11
11	Modeling betaâ€sheet peptideâ€protein interactions: Rosetta FlexPepDock in CAPRI rounds 38â€45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1037-1049.	2.6	10
12	Proteinâ€“ligand docking using FFT based sampling: D3R case study. Journal of Computer-Aided Molecular Design, 2018, 32, 225-230.	2.9	9
13	Sampling and refinement protocols for template-based macrocycle docking: 2018 D3R Grand Challenge 4. Journal of Computer-Aided Molecular Design, 2020, 34, 179-189.	2.9	8
14	ClusPro in rounds 38 to 45 of CAPRI: Toward combining templateâ€based methods with free docking. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1082-1090.	2.6	5
15	Elucidation of protein function using computational docking and hotspot analysis by ClusPro and FTMap. Acta Crystallographica Section D: Structural Biology, 2022, 78, 690-697.	2.3	3
16	Side-chain Packing Using SE(3)-Transformer. , 2021, , .		2