Mikael E Trellet

List of Publications by Year
in descending order

23 papers	3,367 citations	516710 16 h-index	677142 22 g-index
25 all docs	25 docs citations	25 times ranked	6259 citing authors

#	Article	IF	Citations
1	The HADDOCK2.2 Web Server: User-Friendly Integrative Modeling of Biomolecular Complexes. Journal of Molecular Biology, 2016, 428, 720-725.	4.2	2,071
2	A Unified Conformational Selection and Induced Fit Approach to Protein-Peptide Docking. PLoS ONE, 2013, 8, e58769.	2.5	163
3	Posttranslational Modification of Pili upon Cell Contact Triggers N. meningitidis Dissemination. Science, 2011, 331, 778-782.	12.6	162
4	Large-scale prediction of binding affinity in proteinâ€“small ligand complexes: the PRODIGY-LIG web server. Bioinformatics, 2019, 35, 1585-1587.	4.1	130
5	Clustering biomolecular complexes by residue contacts similarity. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1810-1817.	2.6	103
6	Blind prediction of homoâ€•and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99
7	pdb-tools: a swiss army knife for molecular structures. F1000Research, 2018, 7, 1961.	1.6	99
8	Performance of HADDOCK and a simple contact-based proteinâ€“ligand binding affinity predictor in the D3R Grand Challenge 2. Journal of Computer-Aided Molecular Design, 2018, 32, 175-185.	2.9	97
9	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	2.6	87
10	SpotOn: High Accuracy Identification of Protein-Protein Interface Hot-Spots. Scientific Reports, 2017, 7, 8007.	3.3	77
11	Defining the limits of homology modeling in informationâ€driven protein docking. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2119-2128.	2.6	63
12	Sense and simplicity in <scp>HADDOCK</scp> scoring: Lessons from <scp>CASPâ€CAPRI</scp> round 1. Proteins: Structure, Function and Bioinformatics, 2017, 85, 417-423.	2.6	44
13	Inhibition of the integrated stress response by viral proteins that block p-eIF2â€“eIF2B association. Nature Microbiology, 2020, 5, 1361-1373.	13.3	39
14	Sharing Data from Molecular Simulations. Journal of Chemical Information and Modeling, 2019, 59, 4093-4099.	5.4	26
15	Information-Driven Modeling of Protein-Peptide Complexes. Methods in Molecular Biology, 2015, 1268, 221-239.	0.9	24
16	Semantics for an Integrative and Immersive Pipeline Combining Visualization and Analysis of Molecular Data. Journal of Integrative Bioinformatics, 2018, 15, .	1.5	20
17	Folding Then Binding vs Folding Through Binding in Macrocyclic Peptide Inhibitors of Human Pancreatic Î±-Amylase. ACS Chemical Biology, 2019, 14, 1751-1759.	3.4	16
18	<scp>PDBâ€tools</scp> web: A userâ€friendly interface for the manipulation of <scp>PDB</scp> files. Proteins: Structure, Function and Bioinformatics, 2021, 89, 330-335.	2.6	15

#	Article	IF	Citations
19	ExaViz: a flexible framework to analyse, steer and interact with molecular dynamics simulations. Faraday Discussions, 2014, 169, 119-142.	3.2	11
20	An overview of dataâ€driven HADDOCK strategies in CAPRI rounds 38â€45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1029-1036.	2.6	11
21	Content and task based navigation for structural biology in 3D environments. , 2015, , .		4
22	Proteinâ€“Protein Modeling Using Cryo-EM Restraints. Methods in Molecular Biology, 2020, 2112, 145-162.	0.9	3
23	West-Life: A Virtual Research Environment for structural biology. Journal of Structural Biology: X, 2019, 1, 100006.	1.3	2