Jorge Roel-Touris

List of Publications by Year
in descending order

13	684	759233 12	1125743 13
papers	citations	h-index	g-index

17	17	17	826
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The gutSMASH web server:Âautomated identification of primary metabolic gene clusters from the gut microbiota. Nucleic Acids Research, 2021, 49, W263-W270.	14.5	26
2	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
3	LightDock goes information-driven. Bioinformatics, 2020, 36, 950-952.	4.1	30
4	An overview of dataâ€driven HADDOCK strategies in CAPRI rounds 38â€45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1029-1036.	2.6	11
5	Modeling Antibody-Antigen Complexes by Information-Driven Docking. Structure, 2020, 28, 119-129.e2.	3.3	51
6	Integrative modeling of membrane-associated protein assemblies. Nature Communications, 2020, 11, 6210.	12.8	31
7	Coarse-grained (hybrid) integrative modeling of biomolecular interactions. Computational and Structural Biotechnology Journal, 2020, 18, 1182-1190.	4.1	23
8	Blind prediction of homoâ€and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99
9	MARTINI-Based Protein-DNA Coarse-Grained HADDOCKing. Frontiers in Molecular Biosciences, 2019, 6, 102.	3.5	28
10	Less Is More: Coarse-Grained Integrative Modeling of Large Biomolecular Assemblies with HADDOCK. Journal of Chemical Theory and Computation, 2019, 15, 6358-6367.	5.3	43
11	Finding the Î”Î”G spot: Are predictors of binding affinity changes upon mutations in proteinâ€“protein interactions ready for it?. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2019, 9, e1410.	14.6	86
12	LightDock: a new multi-scale approach to proteinâ€“protein docking. Bioinformatics, 2018, 34, 49-55.	4.1	83
13	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