Jorge Roel-Touris

List of Publications by Year
in descending order

13 papers	684 citations	759233 12 h-index	1125743 13 g-index
17 all docs	17 docs citations	17 times ranked	826 citing authors

#	Article	IF	Citations
1	Blind prediction of homo–and hetero–protein complexes: The CASP13–CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99
2	Performance of HADDOCK and a simple contact-based protein–ligand binding affinity predictor in the D3R Grand Challenge 2. Journal of Computer-Aided Molecular Design, 2018, 32, 175-185.	2.9	97
3	Finding the Î"Î"$<i>G</i>$ spot: Are predictors of binding affinity changes upon mutations in protein–protein interactions ready for it?. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2019, 9, e1410.	14.6	86
4	LightDock: a new multi-scale approach to protein–protein docking. Bioinformatics, 2018, 34, 49-55.	4.1	83
5	Prediction of protein assemblies, the next frontier: The <scp>CASP14–CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	2.6	73
6	Modeling Antibody-Antigen Complexes by Information-Driven Docking. Structure, 2020, 28, 119-129.e2.	3.3	51
7	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
8	Integrative modeling of membrane-associated protein assemblies. Nature Communications, 2020, 11, 6210.	12.8	31
9	LightDock goes information-driven. Bioinformatics, 2020, 36, 950-952.	4.1	30
10	MARTINI-Based Protein-DNA Coarse-Grained HADDOCKing. Frontiers in Molecular Biosciences, 2019, 6, 102.	3.5	28
11	The gutSMASH web server: automated identification of primary metabolic gene clusters from the gut microbiota. Nucleic Acids Research, 2021, 49, W263-W270.	14.5	26
12	Coarse-grained (hybrid) integrative modeling of biomolecular interactions. Computational and Structural Biotechnology Journal, 2020, 18, 1182-1190.	4.1	23
13	An overview of data–driven HADDOCK strategies in CAPRI rounds 38–45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1029-1036.	2.6	11