RaphaÃ«l A G Chaleil

List of Publications by Year
in descending order

17 papers	1,635 citations	623734 14 h-index	888059 17 g-index
17 all docs	17 docs citations	17 times ranked	2479 citing authors

#	Article	IF	Citations
1	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
2	Enhanced sampling of protein conformational states for dynamic crossâ€docking within the proteinâ€protein docking server SwarmDock. Proteins: Structure, Function and Bioinformatics, 2020, 88, 962-972.	2.6	16
3	Butyrophilin-2A1 Directly Binds Germline-Encoded Regions of the VÎ³9VÎ´2 TCR and Is Essential for Phosphoantigen Sensing. Immunity, 2020, 52, 487-498.e6.	14.3	164
4	A Guide for Proteinâ€“Protein Docking Using SwarmDock. Methods in Molecular Biology, 2020, 2165, 199-216.	0.9	1
5	Blind prediction of homoâ€and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99
6	Flexible Protein-Protein Docking with SwarmDock. Methods in Molecular Biology, 2018, 1764, 413-428.	0.9	20
7	The Î³Î´TCR combines innate immunity with adaptive immunity by utilizing spatially distinct regions for agonist selection and antigen responsiveness. Nature Immunology, 2018, 19, 1352-1365.	14.5	163
8	A machine learning approach for ranking clusters of docked proteinâ€protein complexes by pairwise cluster comparison. Proteins: Structure, Function and Bioinformatics, 2017, 85, 528-543.	2.6	18
9	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	2.6	148
10	Updates to the Integrated Proteinâ€“Protein Interaction Benchmarks: Docking Benchmark Version 5 and Affinity Benchmark Version 2. Journal of Molecular Biology, 2015, 427, 3031-3041.	4.2	348
11	A simple biophysical model emulates budding yeast chromosome condensation. ELife, 2015, 4, e05565.	6.0	87
12	SwarmDock: a server for flexible proteinâ€“protein docking. Bioinformatics, 2013, 29, 807-809.	4.1	259
13	A Markovâ€chain model description of binding funnels to enhance the ranking of docked solutions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2143-2149.	2.6	32
14	Implicit flexibility in protein docking: Crossâ€docking and local refinement. Proteins: Structure, Function and Bioinformatics, 2007, 69, 750-757.	2.6	53
15	Modeling the effects of toxins in metabolic networks. IEEE Engineering in Medicine and Biology Magazine, 2007, 26, 37-46.	0.8	10
16	Application of abductive ILP to learning metabolic network inhibition from temporal data. Machine Learning, 2006, 64, 209-230.	5.4	71
17	Evolution of Enzymes in Metabolism: A Network Perspective. Journal of Molecular Biology, 2002, 320, 751-770.	4.2	73