RaphaÃ«l A G Chaleil

List of Publications by Year
in descending order

17 papers	1,635 citations	623188 14 h-index	887659 17 g-index
17 all docs	17 docs citations	17 times ranked	2479 citing authors

#	Article	IF	Citations
1	Updates to the Integrated Protein–Protein Interaction Benchmarks: Docking Benchmark Version 5 and Affinity Benchmark Version 2. Journal of Molecular Biology, 2015, 427, 3031-3041.	2.0	348
2	SwarmDock: a server for flexible protein–protein docking. Bioinformatics, 2013, 29, 807-809.	1.8	259
3	Butyrophilin-2A1 Directly Binds Germline-Encoded Regions of the Vγ9Vδ2 TCR and Is Essential for Phosphoantigen Sensing. Immunity, 2020, 52, 487-498.e6.	6.6	164
4	The γδTCR combines innate immunity with adaptive immunity by utilizing spatially distinct regions for agonist selection and antigen responsiveness. Nature Immunology, 2018, 19, 1352-1365.	7.0	163
5	Prediction of homoprotein and heteroprotein complexes by protein docking and template‐based modeling: A CASP–CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	1.5	148
6	Blind prediction of homo‐and hetero‐protein complexes: The CASP13–CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	1.5	99
7	A simple biophysical model emulates budding yeast chromosome condensation. ELife, 2015, 4, e05565.	2.8	87
8	Evolution of Enzymes in Metabolism: A Network Perspective. Journal of Molecular Biology, 2002, 320, 751-770.	2.0	73
9	Prediction of protein assemblies, the next frontier: The <scp>CASP14–CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	1.5	73
10	Application of abductive ILP to learning metabolic network inhibition from temporal data. Machine Learning, 2006, 64, 209-230.	3.4	71
11	Implicit flexibility in protein docking: Cross‐docking and local refinement. Proteins: Structure, Function and Bioinformatics, 2007, 69, 750-757.	1.5	53
12	A Markov‐chain model description of binding funnels to enhance the ranking of docked solutions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2143-2149.	1.5	32
13	Flexible Protein-Protein Docking with SwarmDock. Methods in Molecular Biology, 2018, 1764, 413-428.	0.4	20
14	A machine learning approach for ranking clusters of docked protein‐protein complexes by pairwise cluster comparison. Proteins: Structure, Function and Bioinformatics, 2017, 85, 528-543.	1.5	18
15	Enhanced sampling of protein conformational states for dynamic cross‐docking within the protein‐protein docking server SwarmDock. Proteins: Structure, Function and Bioinformatics, 2020, 88, 962-972.	1.5	16
16	Modeling the effects of toxins in metabolic networks. IEEE Engineering in Medicine and Biology Magazine, 2007, 26, 37-46.	1.1	10
17	A Guide for Protein–Protein Docking Using SwarmDock. Methods in Molecular Biology, 2020, 2165, 199-216.	0.4	1