

Raphaël A G Chaleil

List of Publications by Year in descending order

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Version: 2024-02-01

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