Brian Jimenez

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1334372/publications.pdf

Version: 2024-02-01

25 papers	2,056 citations	393982 19 h-index	580395 25 g-index
29 all docs	29 docs citations	29 times ranked	1958 citing authors

#	Article	IF	Citations
1	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.	2.0	348
2	Structural Biology in the Clouds: The WeNMR-EOSC Ecosystem. Frontiers in Molecular Biosciences, 2021, 8, 729513.	1.6	308
3	pyDockWEB: a web server for rigid-body proteinâ€“protein docking using electrostatics and desolvation scoring. Bioinformatics, 2013, 29, 1698-1699.	1.8	214
4	SKEMPI 2.0: an updated benchmark of changes in proteinâ€“protein binding energy, kinetics and thermodynamics upon mutation. Bioinformatics, 2019, 35, 462-469.	1.8	191
5	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.	1.5	148
6	Blind prediction of homoâ€•and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	1.5	99
7	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	1.5	87
8	LightDock: a new multi-scale approach to proteinâ€“protein docking. Bioinformatics, 2018, 34, 49-55.	1.8	83
9	Prediction of protein assemblies, the next frontier: The <scp>CASP14â€CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	1.5	73
10	pyDockSAXS: proteinâ€“protein complex structure by SAXS and computational docking. Nucleic Acids Research, 2015, 43, W356-W361.	6.5	61
11	CCharPPI web server: computational characterization of proteinâ€“protein interactions from structure. Bioinformatics, 2015, 31, 123-125.	1.8	61
12	Modeling Antibody-Antigen Complexes by Information-Driven Docking. Structure, 2020, 28, 119-129.e2.	1.6	51
13	Blind prediction of interfacial water positions in CAPRI. Proteins: Structure, Function and Bioinformatics, 2014, 82, 620-632.	1.5	50
14	A proteinâ€RNA docking benchmark (II): Extended set from experimental and homology modeling data. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1872-1882.	1.5	46
15	IRaPPA: information retrieval based integration of biophysical models for protein assembly selection. Bioinformatics, 2017, 33, 1806-1813.	1.8	36
16	Integrative modeling of membrane-associated protein assemblies. Nature Communications, 2020, 11, 6210.	5.8	31
17	LightDock goes information-driven. Bioinformatics, 2020, 36, 950-952.	1.8	30
18	proABC-2: PRediction of AntiBody contacts v2 and its application to information-driven docking. Bioinformatics, 2020, 36, 5107-5108.	1.8	27

#	Article	IF	Citations
19	PRODIGY-crystal: a web-tool for classification of biological interfaces in protein complexes. Bioinformatics, 2019, 35, 4821-4823.	1.8	26
20	Expanding the frontiers of proteinâ€“protein modeling: From docking and scoring to binding affinity predictions and other challenges. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2192-2200.	1.5	20
21	pyDock scoring for the new modeling challenges in docking: Proteinâ€“peptide, homoâ€multimers, and domainâ€“domain interactions. Proteins: Structure, Function and Bioinformatics, 2017, 85, 487-496.	1.5	19
22	pyDockEneRes: per-residue decomposition of proteinâ€“protein docking energy. Bioinformatics, 2020, 36, 2284-2285.	1.8	15
23	<scp>PDBâ€tools</scp> web: A userâ€friendly interface for the manipulation of <scp>PDB</scp> files. Proteins: Structure, Function and Bioinformatics, 2021, 89, 330-335.	1.5	15
24	Structural Characterization of Proteinâ€“Protein Interactions with pyDockSAXS. Methods in Molecular Biology, 2020, 2112, 131-144.	0.4	7
25	Integrative modeling of proteinâ€protein interactions with pyDock for the new docking challenges. Proteins: Structure, Function and Bioinformatics, 2020, 88, 999-1008.	1.5	6