

Brian Jimenez

List of Publications by Year in descending order

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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	<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
2	Structural Biology in the Clouds: The WeNMR-EOSC Ecosystem. Frontiers in Molecular Biosciences, 2021, 8, 729513.	1.6	308
3	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
4	LightDock goes information-driven. Bioinformatics, 2020, 36, 950-952.	1.8	30
5	Modeling Antibody-Antigen Complexes by Information-Driven Docking. Structure, 2020, 28, 119-129.e2.	1.6	51
6	pyDockEneRes: per-residue decomposition of proteinâ€protein docking energy. Bioinformatics, 2020, 36, 2284-2285.	1.8	15
7	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
8	Integrative modeling of membrane-associated protein assemblies. Nature Communications, 2020, 11, 6210.	5.8	31
9	proABC-2: PRediction of AntiBody contacts v2 and its application to information-driven docking. Bioinformatics, 2020, 36, 5107-5108.	1.8	27
10	Structural Characterization of Proteinâ€Protein Interactions with pyDockSAXS. Methods in Molecular Biology, 2020, 2112, 131-144.	0.4	7
11	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
12	Blind prediction of homoâ€and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	1.5	99
13	PRODIGY-crystal: a web-tool for classification of biological interfaces in protein complexes. Bioinformatics, 2019, 35, 4821-4823.	1.8	26
14	LightDock: a new multi-scale approach to proteinâ€protein docking. Bioinformatics, 2018, 34, 49-55.	1.8	83
15	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
16	IRaPPA: information retrieval based integration of biophysical models for protein assembly selection. Bioinformatics, 2017, 33, 1806-1813.	1.8	36
17	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
18	pyDockSAXS: proteinâ€protein complex structure by SAXS and computational docking. Nucleic Acids Research, 2015, 43, W356-W361.	6.5	61

#	ARTICLE	IF	CITATIONS
19	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
20	CCharPPI web server: computational characterization of protein-protein interactions from structure. <i>Bioinformatics</i> , 2015, 31, 123-125.	1.8	61
21	Blind prediction of interfacial water positions in CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 620-632.	1.5	50
22	Expanding the frontiers of protein-protein modeling: From docking and scoring to binding affinity predictions and other challenges. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2192-2200.	1.5	20
23	pyDockWEB: a web server for rigid-body protein-protein docking using electrostatics and desolvation scoring. <i>Bioinformatics</i> , 2013, 29, 1698-1699.	1.8	214
24	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1980-1987.	1.5	87
25	A protein-RNA docking benchmark (II): Extended set from experimental and homology modeling data. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1872-1882.	1.5	46