Kathryn A Porter

List of Publications by Year
in descending order

12 papers	2,780 citations	1039406 9 h-index	1199166 12 g-index
13 all docs	13 docs citations	13 times ranked	4504 citing authors

#	Article	IF	Citations
1	The ClusPro web server for proteinâ€“protein docking. Nature Protocols, 2017, 12, 255-278.	5.5	1,959
2	Performance and Its Limits in Rigid Body Protein-Protein Docking. Structure, 2020, 28, 1071-1081.e3.	1.6	306
3	High-resolution global peptide-protein docking using fragments-based PIPER-FlexPepDock. PLoS Computational Biology, 2017, 13, e1005905.	1.5	119
4	ClusPro PeptiDock: efficient global docking of peptide recognition motifs using FFT. Bioinformatics, 2017, 33, 3299-3301.	1.8	102
5	What method to use for proteinâ€“protein docking?. Current Opinion in Structural Biology, 2019, 55, 1-7.	2.6	83
6	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
7	Kinase Atlas: Druggability Analysis of Potential Allosteric Sites in Kinases. Journal of Medicinal Chemistry, 2019, 62, 6512-6524.	2.9	52
8	Proteinâ€“protein docking by fast generalized Fourier transforms on 5D rotational manifolds. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4286-93.	3.3	43
9	Templateâ€based modeling by ClusPro in CASP13 and the potential for using coâ€evolutionary information in docking. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1241-1248.	1.5	15
10	Progress toward improved understanding of antibody maturation. Current Opinion in Structural Biology, 2021, 67, 226-231.	2.6	12
11	ClusPro in rounds 38 to 45 of CAPRI: Toward combining templateâ€based methods with free docking. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1082-1090.	1.5	5
12	Conservation of binding properties in protein models. Computational and Structural Biotechnology Journal, 2021, 19, 2549-2566.	1.9	2