Sergey Lyskov

List of Publications by Year
in descending order

15 papers	4,263 citations	687363 13 h-index	996975 15 g-index
15 all docs	15 docs citations	15 times ranked	7062 citing authors

#	Article	IF	Citations
1	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. The Biophysicist, 2021, 2, 108-122.	0.3	8
2	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. Nature Communications, 2021, 12, 6947.	12.8	16
3	Better together: Elements of successful scientific software development in a distributed collaborative community. PLoS Computational Biology, 2020, 16, e1007507.	3.2	27
4	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
5	Webâ€accessible molecular modeling with Rosetta: The Rosetta Online Server that Includes Everyone (ROSIE). Protein Science, 2018, 27, 259-268.	7.6	47
6	Modeling and docking of antibody structures with Rosetta. Nature Protocols, 2017, 12, 401-416.	12.0	236
7	Discovery of peptide ligands through docking and virtual screening at nicotinic acetylcholine receptor homology models. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8100-E8109.	7.1	51
8	Computing structure-based lipid accessibility of membrane proteins with mp_lipid_acc in RosettaMP. BMC Bioinformatics, 2017, 18, 115.	2.6	26
9	Improved prediction of antibody V_Lâ€“V_Horientation. Protein Engineering, Design and Selection, 2016, 29, 409-418.	2.1	52
10	DARC 2.0: Improved Docking and Virtual Screening at Protein Interaction Sites. PLoS ONE, 2015, 10, e0131612.	2.5	15
11	Scientific Benchmarks for Guiding Macromolecular Energy Function Improvement. Methods in Enzymology, 2013, 523, 109-143.	1.0	195
12	Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE). PLoS ONE, 2013, 8, e63906.	2.5	348
13	Rosetta3. Methods in Enzymology, 2011, 487, 545-574.	1.0	1,620
14	PyRosetta: a script-based interface for implementing molecular modeling algorithms using Rosetta. Bioinformatics, 2010, 26, 689-691.	4.1	601
15	The RosettaDock server for local protein-protein docking. Nucleic Acids Research, 2008, 36, W233-W238.	14.5	508