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