Agnieszka Karczynska

List of Publications by Year
in descending order

14	418	932766 10	1058022 14
papers	citations	h-index	g-index

14	14	14	389
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	Fragments of gD Protein as Inhibitors of BTLA/HVEM Complex Formation - Design, Synthesis, and Cellular Studies. International Journal of Molecular Sciences, 2020, 21, 8876.	1.8	9
3	Truncation of Huia versabilis Bowman-Birk inhibitor increases its selectivity, matriptase-1 inhibitory activity and proteolytic stability. Biochimie, 2020, 171-172, 178-186.	1.3	5
4	Improved Consensus-Fragment Selection in Template-Assisted Prediction of Protein Structures with the UNRES Force Field in CASP13. Journal of Chemical Information and Modeling, 2020, 60, 1844-1864.	2.5	11
5	Scale-consistent approach to the derivation of coarse-grained force fields for simulating structure, dynamics, and thermodynamics of biopolymers. Progress in Molecular Biology and Translational Science, 2020, 170, 73-122.	0.9	20
6	Disulfide-Linked Peptides for Blocking BTLA/HVEM Binding. International Journal of Molecular Sciences, 2020, 21, 636.	1.8	15
7	Blind prediction of homoâ€•and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	1.5	99
8	Evaluation of the scale-consistent UNRES force field in template-free prediction of protein structures in the CASP13 experiment. Journal of Molecular Graphics and Modelling, 2019, 92, 154-166.	1.3	19
9	A structural model of the immune checkpoint CD160-HVEM complex derived from HDX-mass spectrometry and molecular modeling. Oncotarget, 2019, 10, 536-550.	0.8	6
10	UNRES server for physics-based coarse-grained simulations and prediction of protein structure, dynamics and thermodynamics. Nucleic Acids Research, 2018, 46, W304-W309.	6.5	56
11	Use of the UNRES force field in template-assisted prediction of protein structures and the refinement of server models: Test with CASP12 targets. Journal of Molecular Graphics and Modelling, 2018, 83, 92-99.	1.3	19
12	Ergodicity and model quality in templateâ€•restrained canonical and temperature/Hamiltonian replica exchange coarseâ€grained molecular dynamics simulations of proteins. Journal of Computational Chemistry, 2017, 38, 2730-2746.	1.5	8
13	Performance of protein-structure predictions with the physics-based UNRES force field in CASP11. Bioinformatics, 2016, 32, 3270-3278.	1.8	44
14	A Maximum-Likelihood Approach to Force-Field Calibration. Journal of Chemical Information and Modeling, 2015, 55, 2050-2070.	2.5	34