

Agnieszka Karczynska

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

418
citations

932766

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h-index

1058022

14
g-index

14
all docs

14
docs citations

14
times ranked

389
citing authors

#	ARTICLE	IF	CITATIONS
1	Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1200-1221.	1.5	99
2	Prediction of protein assemblies, the next frontier: The CASP14-CAPRI experiment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1800-1823.	1.5	73
3	UNRES server for physics-based coarse-grained simulations and prediction of protein structure, dynamics and thermodynamics. <i>Nucleic Acids Research</i> , 2018, 46, W304-W309.	6.5	56
4	Performance of protein-structure predictions with the physics-based UNRES force field in CASP11. <i>Bioinformatics</i> , 2016, 32, 3270-3278.	1.8	44
5	A Maximum-Likelihood Approach to Force-Field Calibration. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 2050-2070.	2.5	34
6	Scale-consistent approach to the derivation of coarse-grained force fields for simulating structure, dynamics, and thermodynamics of biopolymers. <i>Progress in Molecular Biology and Translational Science</i> , 2020, 170, 73-122.	0.9	20
7	Use of the UNRES force field in template-assisted prediction of protein structures and the refinement of server models: Test with CASP12 targets. <i>Journal of Molecular Graphics and Modelling</i> , 2018, 83, 92-99.	1.3	19
8	Evaluation of the scale-consistent UNRES force field in template-free prediction of protein structures in the CASP13 experiment. <i>Journal of Molecular Graphics and Modelling</i> , 2019, 92, 154-166.	1.3	19
9	Disulfide-Linked Peptides for Blocking BTLA/HVEM Binding. <i>International Journal of Molecular Sciences</i> , 2020, 21, 636.	1.8	15
10	Improved Consensus-Fragment Selection in Template-Assisted Prediction of Protein Structures with the UNRES Force Field in CASP13. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1844-1864.	2.5	11
11	Fragments of gD Protein as Inhibitors of BTLA/HVEM Complex Formation - Design, Synthesis, and Cellular Studies. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8876.	1.8	9
12	Ergodicity and model quality in template-restrained canonical and temperature/Hamiltonian replica exchange coarse-grained molecular dynamics simulations of proteins. <i>Journal of Computational Chemistry</i> , 2017, 38, 2730-2746.	1.5	8
13	A structural model of the immune checkpoint CD160-HVEM complex derived from HDX-mass spectrometry and molecular modeling. <i>Oncotarget</i> , 2019, 10, 536-550.	0.8	6
14	Truncation of <i>Huia versabilis</i> Bowman-Birk inhibitor increases its selectivity, matriptase-1 inhibitory activity and proteolytic stability. <i>Biochimie</i> , 2020, 171-172, 178-186.	1.3	5