

Anna Pavlova

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

21
papers

390
citations

10
h-index

19
g-index

25
ext. papers

549
ext. citations

5.8
avg, IF

3.7
L-index

#	Paper	IF	Citations
21	Simulation-Based Approaches for Determining Membrane Permeability of Small Compounds. <i>Journal of Chemical Information and Modeling</i> , 2016 , 56, 721-33	6.1	127
20	Understanding the role of water in aqueous ruthenium-catalyzed transfer hydrogenation of ketones. <i>ChemPhysChem</i> , 2012 , 13, 3492-6	3.2	57
19	Accelerating Membrane Simulations with Hydrogen Mass Repartitioning. <i>Journal of Chemical Theory and Computation</i> , 2019 , 15, 4673-4686	6.4	33
18	Inhibitor binding influences the protonation states of histidines in SARS-CoV-2 main protease.. <i>Chemical Science</i> , 2021 , 12, 1513-1527	9.4	29
17	Living on the edge: Simulations of bacterial outer-membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016 , 1858, 1753-9	3.8	25
16	Clarifying the role of sodium in the silica oligomerization reaction. <i>Physical Chemistry Chemical Physics</i> , 2013 , 15, 1123-9	3.6	23
15	Development of CHARMM-Compatible Force-Field Parameters for Cobalamin and Related Cofactors from Quantum Mechanical Calculations. <i>Journal of Chemical Theory and Computation</i> , 2018 , 14, 784-798	6.4	14
14	Machine Learning Reveals the Critical Interactions for SARS-CoV-2 Spike Protein Binding to ACE2. <i>Journal of Physical Chemistry Letters</i> , 2021 , 12, 5494-5502	6.4	14
13	Mechanistic Aspects of Using Formate as a Hydrogen Donor in Aqueous Transfer Hydrogenation. <i>ACS Catalysis</i> , 2016 , 6, 5350-5358	13.1	14
12	Tuning Proton Transfer Thermodynamics in SARS-CoV-2 Main Protease: Implications for Catalysis and Inhibitor Design. <i>Journal of Physical Chemistry Letters</i> , 2021 , 12, 4195-4202	6.4	11
11	Redox-Driven Conformational Dynamics in a Photosystem-II-Inspired Hairpin Maquette Determined through Spectroscopy and Simulation. <i>Journal of Physical Chemistry B</i> , 2017 , 121, 3536-3545 ^{3.4}	3.4	9
10	Parametrization of macrolide antibiotics using the force field toolkit. <i>Journal of Computational Chemistry</i> , 2015 , 36, 2052-63	3.5	9
9	Toward the rational design of macrolide antibiotics to combat resistance. <i>Chemical Biology and Drug Design</i> , 2017 , 90, 641-652	2.9	6
8	ACE2 glycans preferentially interact with SARS-CoV-2 over SARS-CoV. <i>Chemical Communications</i> , 2021 , 57, 5949-5952	5.8	6
7	Accurate determination of protein:ligand standard binding free energies from molecular dynamics simulations.. <i>Nature Protocols</i> , 2022 ,	18.8	5
6	Synergistic Biophysical Techniques Reveal Structural Mechanisms of Engineered Cationic Antimicrobial Peptides in Lipid Model Membranes. <i>Chemistry - A European Journal</i> , 2020 , 26, 6247-6256	4.8	2
5	Mechanism of action of HBV capsid assembly modulators predicted from binding to early assembly intermediates		

4	Tuning Proton Transfer Thermodynamics in SARS-Cov-2 Main Protease: Implications for Catalysis and Inhibitor Design. <i>ChemRxiv</i> , 2020 ,	4.4	2
3	Parameterization of a drug molecule with a halogen π -hole particle using ffTK: Implementation, testing, and comparison. <i>Journal of Chemical Physics</i> , 2020 , 153, 164104	3.9	1
2	Critical interactions for SARS-CoV-2 spike protein binding to ACE2 identified by machine learning		1
1	Diverse Protein-Folding Pathways and Functions of π -Hairpins and π -Sheets 2018 , 1-20		