Toru Ekimoto

List of Publications by Year in descending order

18 papers	227 citations	1040056 9 h-index	1058476 14 g-index
19 all docs	19 docs citations	19 times ranked	276 citing authors

#	Article	IF	Citations
1	Supramolecular Mechanosensitive Potassium Channel Formed by Fluorinated Amphiphilic Cyclophane. Journal of the American Chemical Society, 2022, 144, 11802-11809.	13.7	17
2	Structural and dynamical insights into the PH domain of p62 in human TFIIH. Nucleic Acids Research, 2021, 49, 2916-2930.	14.5	10
3	Imidazoliumâ€based Multiblock Amphiphile as Transmembrane Anion Transporter. Chemistry - an Asian Journal, 2021, 16, 147-157.	3.3	9
4	Moving toward generalizable NZ-1 labeling for 3D structure determination with optimized epitope-tag insertion. Acta Crystallographica Section D: Structural Biology, 2021, 77, 645-662.	2.3	18
5	Mechanism of Vitamin D Receptor Ligand-Binding Domain Regulation Studied by gREST Simulations. Journal of Chemical Information and Modeling, 2021, 61, 3625-3637.	5.4	3
6	Allosteric Regulation of 3CL Protease of SARS-CoV-2 and SARS-CoV Observed in the Crystal Structure Ensemble. Journal of Molecular Biology, 2021, 433, 167324.	4.2	11
7	Structure-based screening combined with computational and biochemical analyses identified the inhibitor targeting the binding of DNA Ligase 1 to UHRF1. Bioorganic and Medicinal Chemistry, 2021, 52, 116500.	3.0	8
8	Serine 298 Phosphorylation in Linker 2 of UHRF1 Regulates Ligand-Binding Property of Its Tandem Tudor Domain. Journal of Molecular Biology, 2020, 432, 4061-4075.	4.2	8
9	A synthetic ion channel with anisotropic ligand response. Nature Communications, 2020, 11, 2924.	12.8	36
10	An accurate and rapid method for calculating hydration free energies of a variety of solutes including proteins. Journal of Chemical Physics, 2019, 150, 175101.	3.0	20
11	Rotational Mechanism Model of the Bacterial V1 Motor Based on Structural and Computational Analyses. Frontiers in Physiology, 2019, 10, 46.	2.8	7
12	Combination of coarse-grained molecular dynamics simulations and small-angle X-ray scattering experiments. Biophysics and Physicobiology, 2019, 16, 377-390.	1.0	2
13	Multiscale molecular dynamics simulations of rotary motor proteins. Biophysical Reviews, 2018, 10, 605-615.	3.2	19
14	Elimination of Finite-Size Effects on Binding Free Energies via the Warp-Drive Method. Journal of Chemical Theory and Computation, 2018, 14, 6544-6559.	5.3	9
15	Hybrid Methods for Modeling Protein Structures Using Molecular Dynamics Simulations and Small-Angle X-Ray Scattering Data. Advances in Experimental Medicine and Biology, 2018, 1105, 237-258.	1.6	9
16	Rotation Mechanism of Molecular Motor V1-ATPase Studied by Multiscale Molecular Dynamics Simulation. Biophysical Journal, 2017, 112, 911-920.	0.5	10
17	Apo- and Antagonist-Binding Structures of Vitamin D Receptor Ligand-Binding Domain Revealed by Hybrid Approach Combining Small-Angle X-ray Scattering and Molecular Dynamics. Journal of Medicinal Chemistry, 2016, 59, 7888-7900.	6.4	25
18	An accurate and efficient computation method of the hydration free energy of a large, complex molecule. Journal of Chemical Physics, 2015, 142, 175101.	3.0	6