Po-chia Chen

List of Publications by Year
in descending order

Version: 2024-02-01

28 papers	788 citations	516710 16 h-index	580821 25 g-index
28 all docs	28 docs citations	28 times ranked	1098 citing authors

#	Article	IF	Citations
1	Validating Solution Ensembles from Molecular Dynamics Simulation by Wide-Angle X-ray Scattering Data. Biophysical Journal, 2014, 107, 435-447.	0.5	132
2	Interpretation of Solution X-Ray Scattering by Explicit-Solvent Molecular Dynamics. Biophysical Journal, 2015, 108, 2573-2584.	0.5	99
3	Potential of mean force calculations of ligand binding to ion channels from Jarzynskiâ€™s equality and umbrella sampling. Journal of Chemical Physics, 2008, 128, 155104.	3.0	79
4	Accurate Determination of the Binding Free Energy for KcsA-Charybdotoxin Complex from the Potential of Mean Force Calculations with Restraints. Biophysical Journal, 2011, 100, 2466-2474.	0.5	62
5	The Pore Domain Outer Helix Contributes to Both Activation and Inactivation of the hERG K+ Channel. Journal of Biological Chemistry, 2009, 284, 1000-1008.	3.4	43
6	Mechanism and Energetics of Charybdotoxin Unbinding from a Potassium Channel from Molecular Dynamics Simulations. Biophysical Journal, 2009, 96, 2577-2588.	0.5	36
7	Combined Small-Angle X-ray and Neutron Scattering Restraints in Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2019, 15, 4687-4698.	5.3	36
8	Disentangling polydispersity in the PCNAâ^’p15PAF complex, a disordered, transient and multivalent macromolecular assembly. Nucleic Acids Research, 2017, 45, 1501-1515.	14.5	33
9	Integrative Structural Biology of Protein-RNA Complexes. Structure, 2020, 28, 6-28.	3.3	33
10	Developing a Comparative Docking Protocol for the Prediction of Peptide Selectivity Profiles: Investigation of Potassium Channel Toxins. Toxins, 2012, 4, 110-138.	3.4	27
11	Computation of Standard Binding Free Energies of Polar and Charged Ligands to the Glutamate Receptor GluA2. Journal of Physical Chemistry B, 2014, 118, 1813-1824.	2.6	27
12	Structural Properties of Proteinâ€“Detergent Complexes from SAXS and MD Simulations. Journal of Physical Chemistry Letters, 2015, 6, 5116-5121.	4.6	25
13	Ab Initio Prediction of NMR Spin Relaxation Parameters from Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2018, 14, 1009-1019.	5.3	23
14	Structure and dynamics of the platelet integrin-binding C4 domain of von Willebrand factor. Blood, 2019, 133, 366-376.	1.4	22
15	Physiologically based calculation of steady-state evoked potentials and cortical wave velocities. Biological Cybernetics, 2008, 98, 1-10.	1.3	19
16	Computing the Rotational Diffusion of Biomolecules via Molecular Dynamics Simulation and Quaternion Orientations. Journal of Physical Chemistry B, 2017, 121, 1812-1823.	2.6	19
17	A General Small-Angle X-ray Scattering-Based Screening Protocol Validated for Proteinâ€“RNA Interactions. ACS Combinatorial Science, 2018, 20, 197-202.	3.8	18
18	Structure, dynamics and roX2-lncRNA binding of tandem double-stranded RNA binding domains dsRBD1,2 of Drosophila helicase Maleless. Nucleic Acids Research, 2019, 47, 4319-4333.	14.5	17

#	Article	IF	Citations
19	The role of small-angle scattering in structure-based screening applications. Biophysical Reviews, 2018, 10, 1295-1310.	3.2	10
20	Structure-based screening of binding affinities via small-angle X-ray scattering. IUCrJ, 2020, 7, 644-655.	2.2	9
21	Molecular Dynamics and Theratyping in Airway and Gut Organoids Reveal R352Q-CFTR Conductance Defect. American Journal of Respiratory Cell and Molecular Biology, 2022, 67, 99-111.	2.9	8
22	Molecular dynamics and functional characterization of I37R-CFTR lasso mutation provide insights into channel gating activity. IScience, 2022, 25, 103710.	4.1	6
23	Gain-of-Function Variant p.Pro2555Arg of von Willebrand Factor Increases Aggregate Size through Altering Stem Dynamics. Thrombosis and Haemostasis, 2020, , .	3.4	3
24	Interpretation of Solution X-Ray Scattering Data by Molecular Dynamics. Biophysical Journal, 2015, 108, 191a.	0.5	1
25	Implementing Solution X-Ray Scattering Data as Active Constraints in MD Simulations. Biophysical Journal, 2015, 108, 183a.	0.5	1
26	Conformational Docking of Multiple Toxins Against Kv1-Channels Highlight Key Motifs For Selectivity. Biophysical Journal, 2010, 98, 38a.	0.5	0
27	A General Prediction Method of Scorpion Toxins' Kv-Channel Selectivity Profiles using Haddock. Biophysical Journal, 2012, 102, 410a.	0.5	0
28	A General SAXS-Based Screening Protocol Validated in RNA-Protein Interactions. Biophysical Journal, 2018, 114, 439a.	0.5	0