

# Po-chia Chen

## List of Publications by Year in descending order

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28  
papers

788  
citations

516710

16  
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docs citations

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times ranked

1098  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular dynamics and functional characterization of I37R-CFTR lasso mutation provide insights into channel gating activity. <i>IScience</i> , 2022, 25, 103710.	4.1	6
2	Molecular Dynamics and Therotyping in Airway and Gut Organoids Reveal R352Q-CFTR Conductance Defect. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2022, 67, 99-111.	2.9	8
3	Integrative Structural Biology of Protein-RNA Complexes. <i>Structure</i> , 2020, 28, 6-28.	3.3	33
4	Structure-based screening of binding affinities via small-angle X-ray scattering. <i>IUCr</i> , 2020, 7, 644-655.	2.2	9
5	Gain-of-Function Variant p.Pro2555Arg of von Willebrand Factor Increases Aggregate Size through Altering Stem Dynamics. <i>Thrombosis and Haemostasis</i> , 2020, , .	3.4	3
6	Combined Small-Angle X-ray and Neutron Scattering Restraints in Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 4687-4698.	5.3	36
7	Structure, dynamics and roX2-lncRNA binding of tandem double-stranded RNA binding domains dsRBD1,2 of <i>Drosophila</i> helicase Maleless. <i>Nucleic Acids Research</i> , 2019, 47, 4319-4333.	14.5	17
8	Structure and dynamics of the platelet integrin-binding C4 domain of von Willebrand factor. <i>Blood</i> , 2019, 133, 366-376.	1.4	22
9	Ab Initio Prediction of NMR Spin Relaxation Parameters from Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 1009-1019.	5.3	23
10	A General Small-Angle X-ray Scattering-Based Screening Protocol Validated for Protein-RNA Interactions. <i>ACS Combinatorial Science</i> , 2018, 20, 197-202.	3.8	18
11	A General SAXS-Based Screening Protocol Validated in RNA-Protein Interactions. <i>Biophysical Journal</i> , 2018, 114, 439a.	0.5	0
12	The role of small-angle scattering in structure-based screening applications. <i>Biophysical Reviews</i> , 2018, 10, 1295-1310.	3.2	10
13	Computing the Rotational Diffusion of Biomolecules via Molecular Dynamics Simulation and Quaternion Orientations. <i>Journal of Physical Chemistry B</i> , 2017, 121, 1812-1823.	2.6	19
14	Disentangling polydispersity in the PCNA-p15PAF complex, a disordered, transient and multivalent macromolecular assembly. <i>Nucleic Acids Research</i> , 2017, 45, 1501-1515.	14.5	33
15	Interpretation of Solution X-Ray Scattering Data by Molecular Dynamics. <i>Biophysical Journal</i> , 2015, 108, 191a.	0.5	1
16	Implementing Solution X-Ray Scattering Data as Active Constraints in MD Simulations. <i>Biophysical Journal</i> , 2015, 108, 183a.	0.5	1
17	Structural Properties of Protein-Detergent Complexes from SAXS and MD Simulations. <i>Journal of Physical Chemistry Letters</i> , 2015, 6, 5116-5121.	4.6	25
18	Interpretation of Solution X-Ray Scattering by Explicit-Solvent Molecular Dynamics. <i>Biophysical Journal</i> , 2015, 108, 2573-2584.	0.5	99

#	ARTICLE	IF	CITATIONS
19	Validating Solution Ensembles from Molecular Dynamics Simulation by Wide-Angle X-ray Scattering Data. <i>Biophysical Journal</i> , 2014, 107, 435-447.	0.5	132
20	Computation of Standard Binding Free Energies of Polar and Charged Ligands to the Glutamate Receptor GluA2. <i>Journal of Physical Chemistry B</i> , 2014, 118, 1813-1824.	2.6	27
21	Developing a Comparative Docking Protocol for the Prediction of Peptide Selectivity Profiles: Investigation of Potassium Channel Toxins. <i>Toxins</i> , 2012, 4, 110-138.	3.4	27
22	A General Prediction Method of Scorpion Toxins' Kv-Channel Selectivity Profiles using Haddock. <i>Biophysical Journal</i> , 2012, 102, 410a.	0.5	0
23	Accurate Determination of the Binding Free Energy for KcsA-Charybdotoxin Complex from the Potential of Mean Force Calculations with Restraints. <i>Biophysical Journal</i> , 2011, 100, 2466-2474.	0.5	62
24	Conformational Docking of Multiple Toxins Against Kv1-Channels Highlight Key Motifs For Selectivity. <i>Biophysical Journal</i> , 2010, 98, 38a.	0.5	0
25	The Pore Domain Outer Helix Contributes to Both Activation and Inactivation of the hERG K <sup>+</sup> Channel. <i>Journal of Biological Chemistry</i> , 2009, 284, 1000-1008.	3.4	43
26	Mechanism and Energetics of Charybdotoxin Unbinding from a Potassium Channel from Molecular Dynamics Simulations. <i>Biophysical Journal</i> , 2009, 96, 2577-2588.	0.5	36
27	Physiologically based calculation of steady-state evoked potentials and cortical wave velocities. <i>Biological Cybernetics</i> , 2008, 98, 1-10.	1.3	19
28	Potential of mean force calculations of ligand binding to ion channels from Jarzynski's equality and umbrella sampling. <i>Journal of Chemical Physics</i> , 2008, 128, 155104.	3.0	79