

# Po-Chao Wen

## List of Publications by Year in descending order

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Version: 2024-02-01

27  
papers

1,760  
citations

471509

17  
h-index

552781

26  
g-index

32  
all docs

32  
docs citations

32  
times ranked

2532  
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of internal loop dynamics in antibiotic permeability of outer membrane porins. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	18
2	Structural basis of complex formation between mitochondrial anion channel VDAC1 and Hexokinase-II. Communications Biology, 2021, 4, 667.	4.4	20
3	Rationalizing the generation of broad spectrum antibiotics with the addition of a positive charge. Chemical Science, 2021, 12, 15028-15044.	7.4	16
4	Computational Dissection of Membrane Transport at a Microscopic Level. Trends in Biochemical Sciences, 2020, 45, 202-216.	7.5	21
5	Structural and functional diversity calls for a new classification of ABC transporters. FEBS Letters, 2020, 594, 3767-3775.	2.8	169
6	Structural Insights into the Lipid A Transport Pathway in MsbA. Structure, 2019, 27, 1114-1123.e3.	3.3	41
7	Serotonin transporter-ibogaine complexes illuminate mechanisms of inhibition and transport. Nature, 2019, 569, 141-145.	27.8	187
8	Microscopic view of lipids and their diverse biological functions. Current Opinion in Structural Biology, 2018, 51, 177-186.	5.7	26
9	Probing key elements of teixobactin-lipid II interactions in membranes. Chemical Science, 2018, 9, 6997-7008.	7.4	21
10	Mitochondrial VDAC1: A Key Gatekeeper as Potential Therapeutic Target. Frontiers in Physiology, 2017, 8, 460.	2.8	238
11	The cellular membrane as a mediator for small molecule interaction with membrane proteins. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 2290-2304.	2.6	37
12	Microscopic Characterization of Membrane Transporter Function by In Silico Modeling and Simulation. Methods in Enzymology, 2016, 578, 373-428.	1.0	8
13	Computational characterization of structural dynamics underlying function in active membrane transporters. Current Opinion in Structural Biology, 2015, 31, 96-105.	5.7	49
14	Conformational Dynamics at the Inner Gate of KcsA during Activation. Biochemistry, 2014, 53, 2557-2559.	2.5	16
15	SM proteins Sly1 and Vps33 co-assemble with Sec17 and SNARE complexes to oppose SNARE disassembly by Sec18. ELife, 2014, 3, e02272.	6.0	69
16	Conformational dynamics of the nucleotide binding domains and the power stroke of a heterodimeric ABC transporter. ELife, 2014, 3, e02740.	6.0	114
17	Visualizing Functional Motions of Membrane Transporters with Molecular Dynamics Simulations. Biochemistry, 2013, 52, 569-587.	2.5	46
18	Simulation Studies of the Mechanism of Membrane Transporters. Methods in Molecular Biology, 2013, 924, 361-405.	0.9	7

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19	Transient formation of water-conducting states in membrane transporters. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7696-7701.	7.1	89
20	On the Origin of Large Flexibility of P-glycoprotein in the Inward-facing State. Journal of Biological Chemistry, 2013, 288, 19211-19220.	3.4	120
21	Membrane Transporters: Molecular Machines Coupling Cellular Energy to Vectorial Transport Across the Membrane. , 2011, , 151-181.		0
22	Conformational Coupling of the Nucleotide-Binding and the Transmembrane Domains in ABC Transporters. Biophysical Journal, 2011, 101, 680-690.	0.5	50
23	Detection of focal adhesion kinase activation at membrane microdomains by fluorescence resonance energy transfer. Nature Communications, 2011, 2, 406.	12.8	107
24	Capturing Functional Motions of Membrane Channels and Transporters with Molecular Dynamics Simulation. Journal of Computational and Theoretical Nanoscience, 2010, 7, 2481-2500.	0.4	12
25	Molecular Mechanisms of Active Transport Across the Cellular Membrane. RSC Biomolecular Sciences, 2010, , 248-286.	0.4	2
26	Molecular dynamics simulations of membrane channels and transporters. Current Opinion in Structural Biology, 2009, 19, 128-137.	5.7	201
27	Dimer Opening of the Nucleotide Binding Domains of ABC Transporters after ATP Hydrolysis. Biophysical Journal, 2008, 95, 5100-5110.	0.5	74