

Chih-Chia Su

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

2,539
citations

147801

31
h-index

206112

48
g-index

54
all docs

54
docs citations

54
times ranked

2509
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structures of the CusA efflux pump suggest methionine-mediated metal transport. <i>Nature</i> , 2010, 467, 484-488.	27.8	223
2	Crystal structure of the CusBA heavy-metal efflux complex of <i>Escherichia coli</i> . <i>Nature</i> , 2011, 470, 558-562.	27.8	201
3	Bacterial Multidrug Efflux Transporters. <i>Annual Review of Biophysics</i> , 2014, 43, 93-117.	10.0	159
4	Conformation of the AcrB Multidrug Efflux Pump in Mutants of the Putative Proton Relay Pathway. <i>Journal of Bacteriology</i> , 2006, 188, 7290-7296.	2.2	117
5	Crystal Structure of the Membrane Fusion Protein CusB from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2009, 393, 342-355.	4.2	111
6	MmpL3 is a lipid transporter that binds trehalose monomycolate and phosphatidylethanolamine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11241-11246.	7.1	94
7	Emergence of a Potent Multidrug Efflux Pump Variant That Enhances <i>Campylobacter</i> Resistance to Multiple Antibiotics. <i>MBio</i> , 2016, 7, .	4.1	91
8	Characterization of the multidrug efflux regulator AcrR from <i>Escherichia coli</i> . <i>Biochemical and Biophysical Research Communications</i> , 2007, 361, 85-90.	2.1	83
9	Crystal Structure of the Transcriptional Regulator AcrR from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2007, 374, 591-603.	4.2	79
10	A "Build and Retrieve" methodology to simultaneously solve cryo-EM structures of membrane proteins. <i>Nature Methods</i> , 2021, 18, 69-75.	19.0	71
11	Structures and transport dynamics of a <i>Campylobacter jejuni</i> multidrug efflux pump. <i>Nature Communications</i> , 2017, 8, 171.	12.8	69
12	Crystal Structure of the <i>Neisseria gonorrhoeae</i> MtrD Inner Membrane Multidrug Efflux Pump. <i>PLoS ONE</i> , 2014, 9, e97903.	2.5	65
13	Crystal Structure of the Transcriptional Regulator Rv0678 of <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 16526-16540.	3.4	65
14	The Cus efflux system removes toxic ions via a methionine shuttle. <i>Protein Science</i> , 2011, 20, 6-18.	7.6	61
15	Cryo-Electron Microscopy Structure of an <i>Acinetobacter baumannii</i> Multidrug Efflux Pump. <i>MBio</i> , 2019, 10, .	4.1	56
16	Ligand-transporter interaction in the AcrB multidrug efflux pump determined by fluorescence polarization assay. <i>FEBS Letters</i> , 2007, 581, 4972-4976.	2.8	54
17	Charged Amino Acids (R83, E567, D617, E625, R669, and K678) of CusA Are Required for Metal Ion Transport in the Cus Efflux System. <i>Journal of Molecular Biology</i> , 2012, 422, 429-441.	4.2	51
18	Crystal Structure of the Open State of the <i>Neisseria gonorrhoeae</i> MtrE Outer Membrane Channel. <i>PLoS ONE</i> , 2014, 9, e97475.	2.5	51

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19	Crystal Structure of the Transcriptional Regulator CmeR from <i>Campylobacter jejuni</i> . <i>Journal of Molecular Biology</i> , 2007, 372, 583-593.	4.2	50
20	Cryo-EM Structures of a Gonococcal Multidrug Efflux Pump Illuminate a Mechanism of Drug Recognition and Resistance. <i>MBio</i> , 2020, 11, .	4.1	50
21	Structural and functional analysis of the transcriptional regulator Rv3066 of <i>Mycobacterium tuberculosis</i> . <i>Nucleic Acids Research</i> , 2012, 40, 9340-9355.	14.5	44
22	Structure and Function of <i>Neisseria gonorrhoeae</i> MtrF Illuminates a Class of Antimetabolite Efflux Pumps. <i>Cell Reports</i> , 2015, 11, 61-70.	6.4	44
23	Heavy metal transport by the <i>CusCFBA</i> efflux system. <i>Protein Science</i> , 2015, 24, 1720-1736.	7.6	43
24	Efflux Pumps of the Resistance-Nodulation-Division Family: A Perspective of their Structure, Function, and Regulation in Gram-Negative Bacteria. <i>Advances in Enzymology and Related Areas of Molecular Biology</i> , 2011, 77, 109-146.	1.3	42
25	Structural mechanisms of heavy-metal extrusion by the <i>Cus</i> efflux system. <i>BioMetals</i> , 2013, 26, 593-607.	4.1	41
26	High-pressure spectroscopic probe of hydrophobic hydration of the methyl groups in dimethyl sulfoxide. <i>Journal of Chemical Physics</i> , 2003, 118, 1802-1807.	3.0	40
27	Crystal structures of the <i>Burkholderia multivorans</i> hopanoid transporter HpnN. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6557-6562.	7.1	40
28	Crystal structures of CmeR-bile acid complexes from <i>Campylobacter jejuni</i> . <i>Protein Science</i> , 2011, 20, 712-723.	7.6	38
29	Cryoelectron Microscopy Structures of AdeB Illuminate Mechanisms of Simultaneous Binding and Exporting of Substrates. <i>MBio</i> , 2021, 12, .	4.1	37
30	Crystal Structures of <i>CusC</i> Review Conformational Changes Accompanying Folding and Transmembrane Channel Formation. <i>Journal of Molecular Biology</i> , 2014, 426, 403-411.	4.2	36
31	Crystal structure of the <i>Alcanivorax borkumensis</i> YdaH transporter reveals an unusual topology. <i>Nature Communications</i> , 2015, 6, 6874.	12.8	35
32	A cell-based infection assay identifies efflux pump modulators that reduce bacterial intracellular load. <i>PLoS Pathogens</i> , 2018, 14, e1007115.	4.7	35
33	Evidence of charge-enhanced C-H...O interactions in aqueous protonated imidazole probed by high pressure infrared spectroscopy. <i>Journal of Chemical Physics</i> , 2003, 119, 10753-10758.	3.0	30
34	Crystal structure of the <i>Campylobacter jejuni</i> CmeC outer membrane channel. <i>Protein Science</i> , 2014, 23, 954-961.	7.6	30
35	Structural Basis for the Regulation of the MmpL Transporters of <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 28559-28574.	3.4	29
36	Structures of the mycobacterial membrane protein MmpL3 reveal its mechanism of lipid transport. <i>PLoS Biology</i> , 2021, 19, e3001370.	5.6	27

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37	Crystal structure of the transcriptional regulator Rv1219c of <i>Mycobacterium tuberculosis</i> . <i>Protein Science</i> , 2014, 23, 423-432.	7.6	24
38	A small molecule that mitigates bacterial infection disrupts Gram-negative cell membranes and is inhibited by cholesterol and neutral lipids. <i>PLoS Pathogens</i> , 2020, 16, e1009119.	4.7	21
39	Structure and function of LCI1: a plasma membrane CO ₂ channel in the <i>Chlamydomonas</i> CO ₂ concentrating mechanism. <i>Plant Journal</i> , 2020, 102, 1107-1126.	5.7	17
40	Pressure-Enhanced Ca ²⁺ Interactions in Aqueous tert-Butyl Alcohol. <i>Journal of Physical Chemistry A</i> , 2004, 108, 11001-11005.	2.5	16
41	Crystallization of Membrane Proteins by Vapor Diffusion. <i>Methods in Enzymology</i> , 2015, 557, 363-392.	1.0	14
42	Structural and functional evidence that lipoprotein LpqN supports cell envelope biogenesis in <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 15711-15723.	3.4	14
43	Structural basis of transport and inhibition of the <i>Plasmodium falciparum</i> transporter PfFNT. <i>EMBO Reports</i> , 2021, 22, e51628.	4.5	13
44	Crystal structure of the <i>Mycobacterium tuberculosis</i> transcriptional regulator Rv0302. <i>Protein Science</i> , 2015, 24, 1942-1955.	7.6	11
45	Intermolecular Interactions in Aqueous Dimethyl Sulphoxide and Acetic Acid Probed by High-Pressure FTIR. <i>Journal of the Chinese Chemical Society</i> , 2002, 49, 663-667.	1.4	5
46	Crystallization and preliminary X-ray diffraction analysis of the multidrug efflux transporter NorM from <i>Neisseria gonorrhoeae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 289-292.	0.7	5
47	Preliminary structural studies of the transcriptional regulator CmeR from <i>Campylobacter jejuni</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 34-36.	0.7	3
48	Crystal structure of a conserved domain in the intermembrane space region of the plastid division protein ARC6. <i>Protein Science</i> , 2016, 25, 523-529.	7.6	3
49	Corrigendum to "Ligand-transporter interaction in the AcrB multidrug efflux pump determined by fluorescence polarization assay" [FEBS Lett. 581 (2007) 4972-4976]. <i>FEBS Letters</i> , 2007, 581, 5548-5548.	2.8	0
50	Title is missing!. , 2020, 16, e1009119.		0
51	Title is missing!. , 2020, 16, e1009119.		0
52	Title is missing!. , 2020, 16, e1009119.		0
53	Title is missing!. , 2020, 16, e1009119.		0