

# Edward W Yu

## List of Publications by Year in descending order

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55  
papers

3,141  
citations

159585

30  
h-index

189892

50  
g-index

57  
all docs

57  
docs citations

57  
times ranked

2670  
citing authors

#	ARTICLE	IF	CITATIONS
1	An Analysis of the Novel Fluorocycline TP-6076 Bound to Both the Ribosome and Multidrug Efflux Pump AdeJ from <i>Acinetobacter baumannii</i> . <i>MBio</i> , 2022, 13, e0373221.	4.1	13
2	Structural and Functional Diversity of Resistance-Associated Cell Division Transporters. <i>Chemical Reviews</i> , 2021, 121, 5378-5416.	47.7	48
3	Structural basis of transport and inhibition of the <i>Plasmodium falciparum</i> transporter PffNT. <i>EMBO Reports</i> , 2021, 22, e51628.	4.5	13
4	Cryo-electron Microscopy Structures of AdeB Illuminate Mechanisms of Simultaneous Binding and Exporting of Substrates. <i>MBio</i> , 2021, 12, .	4.1	37
5	Cryo-EM as a tool to study bacterial efflux systems and the membrane proteome. <i>Faculty Reviews</i> , 2021, 10, 24.	3.9	5
6	Cryo-EM Structures of CusA Reveal a Mechanism of Metal-Ion Export. <i>MBio</i> , 2021, 12, .	4.1	15
7	Cryo-EM Determination of Eravacycline-Bound Structures of the Ribosome and the Multidrug Efflux Pump AdeJ of <i>Acinetobacter baumannii</i> . <i>MBio</i> , 2021, 12, e0103121.	4.1	29
8	Structural basis of transport and inhibition of the <i>Plasmodium falciparum</i> transporter PffNT. <i>EMBO Reports</i> , 2021, 22, e53447.	4.5	3
9	Structures of the mycobacterial membrane protein MmpL3 reveal its mechanism of lipid transport. <i>PLoS Biology</i> , 2021, 19, e3001370.	5.6	27
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	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
12	Cryo-electron Microscopy Structure of the <i>Acinetobacter baumannii</i> 70S Ribosome and Implications for New Antibiotic Development. <i>MBio</i> , 2020, 11, .	4.1	25
13	Structure and function of LCI1: a plasma membrane CO <sub>2</sub> channel in the <i>Chlamydomonas</i> CO <sub>2</sub> concentrating mechanism. <i>Plant Journal</i> , 2020, 102, 1107-1126.	5.7	17
14	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
15	Title is missing!. , 2020, 16, e1009119.		0
16	Title is missing!. , 2020, 16, e1009119.		0
17	Title is missing!. , 2020, 16, e1009119.		0
18	Title is missing!. , 2020, 16, e1009119.		0

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19	Cryo-Electron Microscopy Structure of an <i>Acinetobacter baumannii</i> Multidrug Efflux Pump. <i>MBio</i> , 2019, 10, .	4.1	56
20	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
21	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
22	Crystallographic Analysis of the CusBA Heavy-Metal Efflux Complex of <i>Escherichia coli</i> . <i>Methods in Molecular Biology</i> , 2018, 1700, 59-70.	0.9	0
23	A cell-based infection assay identifies efflux pump modulators that reduce bacterial intracellular load. <i>PLoS Pathogens</i> , 2018, 14, e1007115.	4.7	35
24	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
25	(S)-5-ethynyl-anabasine, a novel compound, is a more potent agonist than other nicotine alkaloids on the nematode Asu -ACR-16 receptor. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2017, 7, 12-22.	3.4	4
26	Structures and transport dynamics of a <i>Campylobacter jejuni</i> multidrug efflux pump. <i>Nature Communications</i> , 2017, 8, 171.	12.8	69
27	The AbgT family: A novel class of antimetabolite transporters. <i>Protein Science</i> , 2016, 25, 322-337.	7.6	43
28	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
29	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
30	The <i>Ascaris suum</i> nicotinic receptor, ACR-16, as a drug target: Four novel negative allosteric modulators from virtual screening. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2016, 6, 60-73.	3.4	16
31	Heavy metal transport by the <i>CusCFBA</i> efflux system. <i>Protein Science</i> , 2015, 24, 1720-1736.	7.6	43
32	Crystal structure of the <i>Mycobacterium tuberculosis</i> transcriptional regulator Rv0302. <i>Protein Science</i> , 2015, 24, 1942-1955.	7.6	11
33	Crystal structure of the <i>Alcanivorax borkumensis</i> YdaH transporter reveals an unusual topology. <i>Nature Communications</i> , 2015, 6, 6874.	12.8	35
34	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
35	Crystallization of Membrane Proteins by Vapor Diffusion. <i>Methods in Enzymology</i> , 2015, 557, 363-392.	1.0	14
36	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

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37	Crystal Structure of the Open State of the <i>Neisseria gonorrhoeae</i> MtrE Outer Membrane Channel. PLoS ONE, 2014, 9, e97475.	2.5	51
38	Crystal Structure of the <i>Neisseria gonorrhoeae</i> MtrD Inner Membrane Multidrug Efflux Pump. PLoS ONE, 2014, 9, e97903.	2.5	65
39	Crystal structure of the <i>Campylobacter jejuni</i> CmeC outer membrane channel. Protein Science, 2014, 23, 954-961.	7.6	30
40	Bacterial Multidrug Efflux Transporters. Annual Review of Biophysics, 2014, 43, 93-117.	10.0	159
41	Crystal Structures of CusC Review Conformational Changes Accompanying Folding and Transmembrane Channel Formation. Journal of Molecular Biology, 2014, 426, 403-411.	4.2	36
42	Crystal Structure of the Transcriptional Regulator Rv0678 of <i>Mycobacterium tuberculosis</i> . Journal of Biological Chemistry, 2014, 289, 16526-16540.	3.4	65
43	Structure and mechanism of the tripartite CusCBA heavy-metal efflux complex. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 1047-1058.	4.0	72
44	Charged Amino Acids (R83, E567, D617, E625, R669, and K678) of CusA Are Required for Metal Ion Transport in the Cus Efflux System. Journal of Molecular Biology, 2012, 422, 429-441.	4.2	51
45	Crystal structure of the CusBA heavy-metal efflux complex of <i>Escherichia coli</i> . Nature, 2011, 470, 558-562.	27.8	201
46	The Cus efflux system removes toxic ions via a methionine shuttle. Protein Science, 2011, 20, 6-18.	7.6	61
47	Crystal structures of the CusA efflux pump suggest methionine-mediated metal transport. Nature, 2010, 467, 484-488.	27.8	223
48	Crystal Structure of the Membrane Fusion Protein CusB from <i>Escherichia coli</i> . Journal of Molecular Biology, 2009, 393, 342-355.	4.2	111
49	Functional Cloning and Characterization of the Multidrug Efflux Pumps NorM from <i>Neisseria gonorrhoeae</i> and YdhE from <i>Escherichia coli</i> . Antimicrobial Agents and Chemotherapy, 2008, 52, 3052-3060.	3.2	76
50	Ligand-transporter interaction in the AcrB multidrug efflux pump determined by fluorescence polarization assay. FEBS Letters, 2007, 581, 4972-4976.	2.8	54
51	Corrigendum to "Ligand-transporter interaction in the AcrB multidrug efflux pump determined by fluorescence polarization assay" [FEBS Lett. 581 (2007) 4972-4976]. FEBS Letters, 2007, 581, 5548-5548.	2.8	0
52	Conformation of the AcrB Multidrug Efflux Pump in Mutants of the Putative Proton Relay Pathway. Journal of Bacteriology, 2006, 188, 7290-7296.	2.2	117
53	A Periplasmic Drug-Binding Site of the AcrB Multidrug Efflux Pump: a Crystallographic and Site-Directed Mutagenesis Study. Journal of Bacteriology, 2005, 187, 6804-6815.	2.2	202
54	Structural Basis of Multiple Drug-Binding Capacity of the AcrB Multidrug Efflux Pump. Science, 2003, 300, 976-980.	12.6	372

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55	AcrB Multidrug Efflux Pump of <i>Escherichia coli</i> : Composite Substrate-Binding Cavity of Exceptional Flexibility Generates Its Extremely Wide Substrate Specificity. Journal of Bacteriology, 2003, 185, 5657-5664.	2.2	176