

Edward W Yu

List of Publications by Year in descending order

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Version: 2024-02-01

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 | Structural Basis of Multiple Drug-Binding Capacity of the AcrB Multidrug Efflux Pump. <i>Science</i> , 2003, 300, 976-980. | 12.6 | 372 |
| 2 | Crystal structures of the CusA efflux pump suggest methionine-mediated metal transport. <i>Nature</i> , 2010, 467, 484-488. | 27.8 | 223 |
| 3 | A Periplasmic Drug-Binding Site of the AcrB Multidrug Efflux Pump: a Crystallographic and Site-Directed Mutagenesis Study. <i>Journal of Bacteriology</i> , 2005, 187, 6804-6815. | 2.2 | 202 |
| 4 | Crystal structure of the CusBA heavy-metal efflux complex of <i>Escherichia coli</i> . <i>Nature</i> , 2011, 470, 558-562. | 27.8 | 201 |
| 5 | AcrB Multidrug Efflux Pump of <i>Escherichia coli</i> : Composite Substrate-Binding Cavity of Exceptional Flexibility Generates Its Extremely Wide Substrate Specificity. <i>Journal of Bacteriology</i> , 2003, 185, 5657-5664. | 2.2 | 176 |
| 6 | Bacterial Multidrug Efflux Transporters. <i>Annual Review of Biophysics</i> , 2014, 43, 93-117. | 10.0 | 159 |
| 7 | 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 |
| 8 | 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 |
| 9 | 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 |
| 10 | 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 |
| 11 | Functional Cloning and Characterization of the Multidrug Efflux Pumps NorM from <i>Neisseria gonorrhoeae</i> and YdhE from <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 3052-3060. | 3.2 | 76 |
| 12 | Structure and mechanism of the tripartite CusCBA heavy-metal efflux complex. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 1047-1058. | 4.0 | 72 |
| 13 | 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 |
| 14 | Structures and transport dynamics of a <i>Campylobacter jejuni</i> multidrug efflux pump. <i>Nature Communications</i> , 2017, 8, 171. | 12.8 | 69 |
| 15 | Crystal Structure of the <i>Neisseria gonorrhoeae</i> MtrD Inner Membrane Multidrug Efflux Pump. <i>PLoS ONE</i> , 2014, 9, e97903. | 2.5 | 65 |
| 16 | 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 |
| 17 | The Cus efflux system removes toxic ions via a methionine shuttle. <i>Protein Science</i> , 2011, 20, 6-18. | 7.6 | 61 |
| 18 | Cryo-Electron Microscopy Structure of an <i>Acinetobacter baumannii</i> Multidrug Efflux Pump. <i>MBio</i> , 2019, 10, . | 4.1 | 56 |

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|----|---|------|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | Structural and Functional Diversity of Resistance-Modulation Cell Division Transporters. <i>Chemical Reviews</i> , 2021, 121, 5378-5416. | 47.7 | 48 |
| 24 | 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 |
| 25 | Heavy metal transport by the <i>CusCFBA</i> efflux system. <i>Protein Science</i> , 2015, 24, 1720-1736. | 7.6 | 43 |
| 26 | The AbgT family: A novel class of antimetabolite transporters. <i>Protein Science</i> , 2016, 25, 322-337. | 7.6 | 43 |
| 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 | Cryoelectron Microscopy Structures of AdeB Illuminate Mechanisms of Simultaneous Binding and Exporting of Substrates. <i>MBio</i> , 2021, 12, . | 4.1 | 37 |
| 29 | Crystal Structures of CusC Review Conformational Changes Accompanying Folding and Transmembrane Channel Formation. <i>Journal of Molecular Biology</i> , 2014, 426, 403-411. | 4.2 | 36 |
| 30 | Crystal structure of the <i>Alcanivorax borkumensis</i> YdaH transporter reveals an unusual topology. <i>Nature Communications</i> , 2015, 6, 6874. | 12.8 | 35 |
| 31 | A cell-based infection assay identifies efflux pump modulators that reduce bacterial intracellular load. <i>PLoS Pathogens</i> , 2018, 14, e1007115. | 4.7 | 35 |
| 32 | Crystal structure of the <i>Campylobacter jejuni</i> CmeC outer membrane channel. <i>Protein Science</i> , 2014, 23, 954-961. | 7.6 | 30 |
| 33 | 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 |
| 34 | 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 |
| 35 | Structures of the mycobacterial membrane protein MmpL3 reveal its mechanism of lipid transport. <i>PLoS Biology</i> , 2021, 19, e3001370. | 5.6 | 27 |
| 36 | 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 |

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|----|---|-----|-----------|
| 37 | 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 |
| 38 | 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 |
| 39 | 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 |
| 40 | Cryo-EM Structures of CusA Reveal a Mechanism of Metal-Ion Export. <i>MBio</i> , 2021, 12, . | 4.1 | 15 |
| 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 | 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 |
| 45 | Crystal structure of the <i>Mycobacterium tuberculosis</i> transcriptional regulator Rv0302. <i>Protein Science</i> , 2015, 24, 1942-1955. | 7.6 | 11 |
| 46 | Cryo-EM as a tool to study bacterial efflux systems and the membrane proteome. <i>Faculty Reviews</i> , 2021, 10, 24. | 3.9 | 5 |
| 47 | (S)-5-ethynyl-anabasine, a novel compound, is a more potent agonist than other nicotine alkaloids on the nematode <i>Asu</i> -ACR-16 receptor. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2017, 7, 12-22. | 3.4 | 4 |
| 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 | Structural basis of transport and inhibition of the <i>Plasmodium falciparum</i> transporter PfFNT. <i>EMBO Reports</i> , 2021, 22, e53447. | 4.5 | 3 |
| 50 | 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 |
| 51 | 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 |
| 52 | Title is missing!. , 2020, 16, e1009119. | | 0 |
| 53 | Title is missing!. , 2020, 16, e1009119. | | 0 |
| 54 | Title is missing!. , 2020, 16, e1009119. | | 0 |

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| 55 | Title is missing!. , 2020, 16, e1009119. | | 0 |