

Vassiliy N Bavro

List of Publications by Year in descending order

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51
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citations

257101

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docs citations

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times ranked

2308
citing authors

#	ARTICLE	IF	CITATIONS
1	A role for the periplasmic adaptor protein AcrA in vetting substrate access to the RND efflux transporter AcrB. <i>Scientific Reports</i> , 2022, 12, 4752.	1.6	8
2	Cefotaxime Exposure Selects Mutations within the CA-Domain of <i>envZ</i> Which Promote Antibiotic Resistance but Repress Biofilm Formation in <i>Salmonella</i> . <i>Microbiology Spectrum</i> , 2022, 10, e0214521.	1.2	4
3	The role of bacterial transport systems in the removal of host antimicrobial peptides in Gram-negative bacteria. <i>FEMS Microbiology Reviews</i> , 2022, 46, .	3.9	4
4	Structure, Assembly, and Function of Tripartite Efflux and Type 1 Secretion Systems in Gram-Negative Bacteria. <i>Chemical Reviews</i> , 2021, 121, 5479-5596.	23.0	103
5	Quantitative real-time analysis of the efflux by the MacAB-TolC tripartite efflux pump clarifies the role of ATP hydrolysis within mechanotransmission mechanism. <i>Communications Biology</i> , 2021, 4, 493.	2.0	7
6	Interchangeability of periplasmic adaptor proteins AcrA and AcrE in forming functional efflux pumps with AcrD in <i>Salmonella enterica</i> serovar Typhimurium. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 2558-2564.	1.3	11
7	Structure-function analysis of MmpL7-mediated lipid transport in mycobacteria. <i>Cell Surface</i> , 2021, 7, 100062.	1.5	2
8	The mycolic acid reductase Rv2509 has distinct structural motifs and is essential for growth in slow-growing mycobacteria. <i>Molecular Microbiology</i> , 2020, 113, 521-533.	1.2	4
9	Mutations in the TolC Periplasmic Domain Affect Substrate Specificity of the AcrAB-TolC Pump. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 166.	1.6	12
10	Cryo-EM Structure and Molecular Dynamics Analysis of the Fluoroquinolone Resistant Mutant of the AcrB Transporter from <i>Salmonella</i> . <i>Microorganisms</i> , 2020, 8, 943.	1.6	25
11	Outer membrane protein size and LPS O-antigen define protective antibody targeting to the <i>Salmonella</i> surface. <i>Nature Communications</i> , 2020, 11, 851.	5.8	49
12	Structure of dual BON-domain protein DolP identifies phospholipid binding as a new mechanism for protein localisation. <i>ELife</i> , 2020, 9, .	2.8	25
13	Defining the RND-binding residues of AcrA. <i>Access Microbiology</i> , 2020, 2, .	0.2	1
14	Experimental evolution selects clinically relevant antibiotic resistance in biofilms but with collateral tradeoffs. <i>Access Microbiology</i> , 2020, 2, .	0.2	0
15	Editorial: Bacterial Mechanisms of Antibiotic Resistance: A Structural Perspective. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 71.	1.6	6
16	Identification of binding residues between periplasmic adapter protein (PAP) and RND efflux pumps explains PAP-pump promiscuity and roles in antimicrobial resistance. <i>PLoS Pathogens</i> , 2019, 15, e1008101.	2.1	32
17	A cytosolic copper storage protein provides a second level of copper tolerance in <i>Streptomyces lividans</i> . <i>Metallomics</i> , 2018, 10, 180-193.	1.0	23
18	Structure-Guided Identification of a Nonhuman Morbillivirus with Zoonotic Potential. <i>Journal of Virology</i> , 2018, 92, .	1.5	23

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19	ATP-Binding Cassette Transporter VcaM from <i>Vibrio cholerae</i> is Dependent on the Outer Membrane Factor Family for Its Function. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1000.	1.8	18
20	Structural and Functional Analysis of the <i>Escherichia coli</i> Acid-Sensing Histidine Kinase EvgS. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	31
21	What Keeps TolC Closed? Insights from Molecular Dynamics Simulations. <i>Biophysical Journal</i> , 2016, 110, 625a.	0.2	0
22	Multidrug Efflux in the Context of Two-Membrane Cell Envelopes. , 2016, , 99-128.		0
23	Cross-species chimeras reveal <sc>BamA POTRA</sc> and <sc> β^2 </sc> β -barrel domains must be fine-tuned for efficient <sc>OMP</sc> insertion. <i>Molecular Microbiology</i> , 2015, 97, 646-659.	1.2	17
24	Oxidative footprinting in the study of structure and function of membrane proteins: current state and perspectives. <i>Biochemical Society Transactions</i> , 2015, 43, 983-994.	1.6	15
25	Modular Design of the Selectivity Filter Pore Loop in a Novel Family of Prokaryotic K^+ Inward Rectifier TM (NirBac) channels. <i>Scientific Reports</i> , 2015, 5, 15305.	1.6	2
26	Architecture and roles of periplasmic adaptor proteins in tripartite $e\text{A}^{\sim}\text{A}$ - β assemblies. <i>Frontiers in Microbiology</i> , 2015, 6, 513.	1.5	54
27	Crystal structure analysis of peroxidase from the palm tree <i>Chamaerops excelsa</i> . <i>Biochimie</i> , 2015, 111, 58-69.	1.3	20
28	AcrB drug-binding pocket substitution confers clinically relevant resistance and altered substrate specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3511-3516.	3.3	165
29	Control of KirBac3.1 Potassium Channel Gating at the Interface between Cytoplasmic Domains. <i>Journal of Biological Chemistry</i> , 2014, 289, 143-151.	1.6	20
30	Genetic assessment of the role of <sc>AcrB</sc> β^2 chairpins in the assembly of the <sc>TolC</sc> β <sc>AcrAB</sc> multidrug efflux pump of <sc> <i>E. coli</i> </sc>. <i>Molecular Microbiology</i> , 2014, 91, 965-975.	1.2	25
31	Tripartite efflux pumps: energy is required for dissociation, but not assembly or opening of the outer membrane channel of the pump. <i>Molecular Microbiology</i> , 2013, 88, 590-602.	1.2	37
32	Mutational and Topological Analysis of the <i>Escherichia coli</i> BamA Protein. <i>PLoS ONE</i> , 2013, 8, e84512.	1.1	29
33	Structure of a KirBac potassium channel with an open bundle crossing indicates a mechanism of channel gating. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 158-163.	3.6	92
34	Crystal Structure of a Prokaryotic Kir Channel in an Open Conformation. <i>Biophysical Journal</i> , 2012, 102, 536a.	0.2	0
35	Evidence for the Assembly of a Bacterial Tripartite Multidrug Pump with a Stoichiometry of 3:6:3. <i>Journal of Biological Chemistry</i> , 2011, 286, 26900-26912.	1.6	49
36	Opening of the Outer Membrane Protein Channel in Tripartite Efflux Pumps Is Induced by Interaction with the Membrane Fusion Partner. <i>Journal of Biological Chemistry</i> , 2011, 286, 5484-5493.	1.6	31

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37	Conformational Changes During the Gating of a Potassium Channel Revealed by Structural Mass Spectrometry. <i>Structure</i> , 2010, 18, 839-846.	1.6	76
38	Functional Complementation and Genetic Deletion Studies of KirBac Channels. <i>Journal of Biological Chemistry</i> , 2010, 285, 40754-40761.	1.6	22
39	Radiolytic Footprinting Reveals Conformational Changes During Potassium Channel Gating. <i>Biophysical Journal</i> , 2010, 98, 696a.	0.2	0
40	Ion Mobility Mass Spectrometry of Two Tetrameric Membrane Protein Complexes Reveals Compact Structures and Differences in Stability and Packing. <i>Journal of the American Chemical Society</i> , 2010, 132, 15468-15470.	6.6	77
41	MacB ABC Transporter Is a Dimer Whose ATPase Activity and Macrolide-binding Capacity Are Regulated by the Membrane Fusion Protein MacA. <i>Journal of Biological Chemistry</i> , 2009, 284, 1145-1154.	1.6	88
42	Mass spectrometry of membrane transporters reveals subunit stoichiometry and interactions. <i>Nature Methods</i> , 2009, 6, 585-587.	9.0	164
43	Assembly and transport mechanism of tripartite drug efflux systems. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 817-825.	1.1	74
44	MacB ABC transporter is a dimer whose ATPase activity and macrolide-binding capacity are regulated by the membrane fusion protein MacA. VOLUME 284 (2009) PAGES 1145-1154. <i>Journal of Biological Chemistry</i> , 2009, 284, 8995.	1.6	2
45	Reconstitution and Analysis of the Multienzyme Escherichia coli RNA Degradosome. <i>Journal of Molecular Biology</i> , 2008, 382, 870-883.	2.0	69
46	Assembly and Channel Opening in a Bacterial Drug Efflux Machine. <i>Molecular Cell</i> , 2008, 30, 114-121.	4.5	155
47	Structure and Mechanism of Drug Efflux Machinery in Gram Negative Bacteria. <i>Current Drug Targets</i> , 2008, 9, 719-728.	1.0	28
48	Exploring ligand recognition and ion flow in comparative models of the human GABA type A receptor. <i>Journal of Molecular Graphics and Modelling</i> , 2007, 26, 760-774.	1.3	30
49	Structural basis of dynamic glycine receptor clustering by gephyrin. <i>EMBO Journal</i> , 2004, 23, 2510-2519.	3.5	147
50	A model of a transmembrane drug-efflux pump from Gram-negative bacteria. <i>FEBS Letters</i> , 2004, 578, 5-9.	1.3	71
51	Crystal structure of the GABA A receptor-associated protein, GABARAP. <i>EMBO Reports</i> , 2002, 3, 183-189.	2.0	65