

Vassiliy N Bavro

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

46
papers

1,566
citations

22
h-index

39
g-index

56
ext. papers

1,831
ext. citations

7.5
avg, IF

4.25
L-index

#	Paper	IF	Citations
46	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	4.9	
45	Cefotaxime Exposure Selects Mutations within the CA-Domain of Which Promote Antibiotic Resistance but Repress Biofilm Formation in Salmonella.. <i>Microbiology Spectrum</i> , 2022 , e0214521	8.9	0
44	Structure, Assembly, and Function of Tripartite Efflux and Type 1 Secretion Systems in Gram-Negative Bacteria. <i>Chemical Reviews</i> , 2021 , 121, 5479-5596	68.1	22
43	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	6.7	5
42	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	5.1	3
41	Structure-function analysis of MmpL7-mediated lipid transport in mycobacteria. <i>Cell Surface</i> , 2021 , 7, 100062	4.8	0
40	Cryo-EM Structure and Molecular Dynamics Analysis of the Fluoroquinolone Resistant Mutant of the AcrB Transporter from. <i>Microorganisms</i> , 2020 , 8,	4.9	16
39	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	17.4	23
38	Structure of dual BON-domain protein DolP identifies phospholipid binding as a new mechanism for protein localisation. <i>ELife</i> , 2020 , 9,	8.9	11
37	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	4.1	2
36	Mutations in the TolC Periplasmic Domain Affect Substrate Specificity of the AcrAB-TolC Pump. <i>Frontiers in Molecular Biosciences</i> , 2020 , 7, 166	5.6	6
35	Multidrug Resistance 2019 , 201-237		0
34	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	7.6	17
33	A cytosolic copper storage protein provides a second level of copper tolerance in <i>Streptomyces lividans</i> . <i>Metallomics</i> , 2018 , 10, 180-193	4.5	13
32	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,	6.3	10
31	Structure-Guided Identification of a Nonhuman Morbillivirus with Zoonotic Potential. <i>Journal of Virology</i> , 2018 , 92,	6.6	17
30	Structural and Functional Analysis of the <i>Escherichia coli</i> Acid-Sensing Histidine Kinase EvgS. <i>Journal of Bacteriology</i> , 2017 , 199,	3.5	15

29	Multidrug Efflux in the Context of Two-Membrane Cell Envelopes 2016 , 99-128		
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, 3511-6	11.5	125
27	Cross-species chimeras reveal BamA POTRA and β barrel domains must be fine-tuned for efficient OMP insertion. <i>Molecular Microbiology</i> , 2015 , 97, 646-59	4.1	14
26	Oxidative footprinting in the study of structure and function of membrane proteins: current state and perspectives. <i>Biochemical Society Transactions</i> , 2015 , 43, 983-94	5.1	12
25	Modular Design of the Selectivity Filter Pore Loop in a Novel Family of Prokaryotic Unidirectional Rectifier (NirBac) channels. <i>Scientific Reports</i> , 2015 , 5, 15305	4.9	2
24	Architecture and roles of periplasmic adaptor proteins in tripartite efflux assemblies. <i>Frontiers in Microbiology</i> , 2015 , 6, 513	5.7	41
23	Crystal structure analysis of peroxidase from the palm tree <i>Chamaerops excelsa</i> . <i>Biochimie</i> , 2015 , 111, 58-69	4.6	14
22	Control of KirBac3.1 potassium channel gating at the interface between cytoplasmic domains. <i>Journal of Biological Chemistry</i> , 2014 , 289, 143-51	5.4	17
21	Genetic assessment of the role of AcrB β hairpins in the assembly of the TolC-AcrAB multidrug efflux pump of <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2014 , 91, 965-75	4.1	24
20	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	4.1	32
19	Mutational and topological analysis of the <i>Escherichia coli</i> BamA protein. <i>PLoS ONE</i> , 2013 , 8, e84512	3.7	23
18	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, 158-63	17.6	78
17	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, 26900-12	5.4	41
16	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, 5484-93	5.4	28
15	Functional complementation and genetic deletion studies of KirBac channels: activatory mutations highlight gating-sensitive domains. <i>Journal of Biological Chemistry</i> , 2010 , 285, 40754-61	5.4	22
14	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, 15468-70	16.4	70
13	Conformational changes during the gating of a potassium channel revealed by structural mass spectrometry. <i>Structure</i> , 2010 , 18, 839-46	5.2	66
12	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, 1145-54	5.4	75

11	Mass spectrometry of membrane transporters reveals subunit stoichiometry and interactions. <i>Nature Methods</i> , 2009 , 6, 585-7	21.6	146
10	Assembly and transport mechanism of tripartite drug efflux systems. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009 , 1794, 817-25	4	65
9	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	5.4	2
8	Reconstitution and analysis of the multienzyme Escherichia coli RNA degradosome. <i>Journal of Molecular Biology</i> , 2008 , 382, 870-83	6.5	59
7	Assembly and channel opening in a bacterial drug efflux machine. <i>Molecular Cell</i> , 2008 , 30, 114-21	17.6	140
6	Structure and mechanism of drug efflux machinery in Gram negative bacteria. <i>Current Drug Targets</i> , 2008 , 9, 719-28	3	24
5	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, 760-74	2.8	29
4	Structural basis of dynamic glycine receptor clustering by gephyrin. <i>EMBO Journal</i> , 2004 , 23, 2510-9	13	123
3	A model of a transmembrane drug-efflux pump from Gram-negative bacteria. <i>FEBS Letters</i> , 2004 , 578, 5-9	3.8	69
2	Crystal structure of the GABA(A)-receptor-associated protein, GABARAP. <i>EMBO Reports</i> , 2002 , 3, 183-9	6.5	54
1	Antibiotics select for novel pathways of resistance in biofilms		7