

Jani Reddy Bolla

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

2,041
citations

236612

25
h-index

264894

42
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all docs

55
docs citations

55
times ranked

2522
citing authors

#	ARTICLE	IF	CITATIONS
1	Ion currents through Kir potassium channels are gated by anionic lipids. <i>Nature Communications</i> , 2022, 13, 490.	5.8	9
2	Peptidoglycan biosynthesis is driven by lipid transfer along enzyme-substrate affinity gradients. <i>Nature Communications</i> , 2022, 13, 2278.	5.8	20
3	Cryo-EM structures of pentameric autoinducer-2 exporter from <i>Escherichia coli</i> reveal its transport mechanism. <i>EMBO Journal</i> , 2022, 41, .	3.5	8
4	Dynamics of an LPS translocon induced by substrate and an antimicrobial peptide. <i>Nature Chemical Biology</i> , 2021, 17, 187-195.	3.9	41
5	The antibiotic darobactin mimics a β -strand to inhibit outer membrane insertase. <i>Nature</i> , 2021, 593, 125-129.	13.7	112
6	Multiple Roles of SARS-CoV-2 N Protein Facilitated by Proteoform-Specific Interactions with RNA, Host Proteins, and Convalescent Antibodies. <i>Jacs Au</i> , 2021, 1, 1147-1157.	3.6	28
7	Architecture of cell-cell junctions in situ reveals a mechanism for bacterial biofilm inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	22
8	The molecular basis of regulation of bacterial capsule assembly by Wzc. <i>Nature Communications</i> , 2021, 12, 4349.	5.8	25
9	Competitive binding of MatP and topoisomerase IV to the MukB hinge domain. <i>ELife</i> , 2021, 10, .	2.8	8
10	Mass spectrometry informs the structure and dynamics of membrane proteins involved in lipid and drug transport. <i>Current Opinion in Structural Biology</i> , 2021, 70, 53-60.	2.6	12
11	Structural Basis for Silicic Acid Uptake by Higher Plants. <i>Journal of Molecular Biology</i> , 2021, 433, 167226.	2.0	18
12	A "Build and Retrieve" methodology to simultaneously solve cryo-EM structures of membrane proteins. <i>Nature Methods</i> , 2021, 18, 69-75.	9.0	71
13	Mass spectrometry enables the discovery of inhibitors of an LPS transport assembly <i>via</i> disruption of protein-protein interactions. <i>Chemical Communications</i> , 2021, 57, 10747-10750.	2.2	6
14	The structure of nontypeable <i>Haemophilus influenzae</i> SapA in a closed conformation reveals a constricted ligand-binding cavity and a novel RNA binding motif. <i>PLoS ONE</i> , 2021, 16, e0256070.	1.1	3
15	Acyl carrier protein promotes MukBEF action in <i>Escherichia coli</i> chromosome organization-segregation. <i>Nature Communications</i> , 2021, 12, 6721.	5.8	12
16	A Mass Spectrometry-Based Approach to Distinguish Annular and Specific Lipid Binding to Membrane Proteins. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 3523-3528.	7.2	33
17	A Mass Spectrometry-Based Approach to Distinguish Annular and Specific Lipid Binding to Membrane Proteins. <i>Angewandte Chemie</i> , 2020, 132, 3551-3556.	1.6	2
18	Structural Basis of Tail-Anchored Membrane Protein Biogenesis by the GET Insertase Complex. <i>Molecular Cell</i> , 2020, 80, 72-86.e7.	4.5	71

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19	Allosteric Inhibition of the SARS-CoV-2 Main Protease: Insights from Mass Spectrometry Based Assays**. <i>Angewandte Chemie</i> , 2020, 132, 23750-23754.	1.6	10
20	Allosteric Inhibition of the SARS-CoV-2 Main Protease: Insights from Mass Spectrometry Based Assays**. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 23544-23548.	7.2	92
21	Combining native and ¹⁵ N mass spectrometry to identify endogenous ligands bound to membrane proteins. <i>Nature Methods</i> , 2020, 17, 505-508.	9.0	111
22	A constricted opening in Kir channels does not impede potassium conduction. <i>Nature Communications</i> , 2020, 11, 3024.	5.8	14
23	The use of sonicated lipid vesicles for mass spectrometry of membrane protein complexes. <i>Nature Protocols</i> , 2020, 15, 1690-1706.	5.5	30
24	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.	2.8	17
25	Assembly and regulation of the chlorhexidine-specific efflux pump Acel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17011-17018.	3.3	33
26	Investigating the Conformational Dynamics of the Outer Membrane LPS Translocon LptDE. <i>Biophysical Journal</i> , 2020, 118, 26a.	0.2	0
27	Modular detergents tailor the purification and structural analysis of membrane proteins including G-protein coupled receptors. <i>Nature Communications</i> , 2020, 11, 564.	5.8	72
28	Targeting MmpL3 for anti-tuberculosis drug development. <i>Biochemical Society Transactions</i> , 2020, 48, 1463-1472.	1.6	24
29	Dynamic architecture of the <i>Escherichia coli</i> structural maintenance of chromosomes (SMC) complex, MukBEF. <i>Nucleic Acids Research</i> , 2019, 47, 9696-9707.	6.5	20
30	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.	3.3	94
31	Membrane Protein-Lipid Interactions Probed Using Mass Spectrometry. <i>Annual Review of Biochemistry</i> , 2019, 88, 85-111.	5.0	121
32	The Different Effects of Substrates and Nucleotides on the Complex Formation of ABC Transporters. <i>Structure</i> , 2019, 27, 651-659.e3.	1.6	19
33	Direct observation of the influence of cardiolipin and antibiotics on lipid II binding to MurJ. <i>Nature Chemistry</i> , 2018, 10, 363-371.	6.6	65
34	Structures and transport dynamics of a <i>Campylobacter jejuni</i> multidrug efflux pump. <i>Nature Communications</i> , 2017, 8, 171.	5.8	69
35	The structural basis for CD36 binding by the malaria parasite. <i>Nature Communications</i> , 2016, 7, 12837.	5.8	160
36	Crystal structure of the <i>Mycobacterium tuberculosis</i> transcriptional regulator Rv0302. <i>Protein Science</i> , 2015, 24, 1942-1955.	3.1	11

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37	Crystal structure of the <i>Alcanivorax borkumensis</i> YdaH transporter reveals an unusual topology. <i>Nature Communications</i> , 2015, 6, 6874.	5.8	35
38	Structure and Function of <i>Neisseria gonorrhoeae</i> MtrF Illuminates a Class of Antimetabolite Efflux Pumps. <i>Cell Reports</i> , 2015, 11, 61-70.	2.9	44
39	Crystallization of Membrane Proteins by Vapor Diffusion. <i>Methods in Enzymology</i> , 2015, 557, 363-392.	0.4	14
40	Structural Basis for the Regulation of the MmpL Transporters of <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 28559-28574.	1.6	29
41	Crystal Structure of the Open State of the <i>Neisseria gonorrhoeae</i> MtrE Outer Membrane Channel. <i>PLoS ONE</i> , 2014, 9, e97475.	1.1	51
42	Crystal Structure of the <i>Neisseria gonorrhoeae</i> MtrD Inner Membrane Multidrug Efflux Pump. <i>PLoS ONE</i> , 2014, 9, e97903.	1.1	65
43	Crystal structure of the transcriptional regulator Rv1219c of <i>Mycobacterium tuberculosis</i> . <i>Protein Science</i> , 2014, 23, 423-432.	3.1	24
44	Crystal structure of the <i>Campylobacter jejuni</i> CmeC outer membrane channel. <i>Protein Science</i> , 2014, 23, 954-961.	3.1	30
45	Crystal Structures of CusC Review Conformational Changes Accompanying Folding and Transmembrane Channel Formation. <i>Journal of Molecular Biology</i> , 2014, 426, 403-411.	2.0	36
46	Crystal Structure of the Transcriptional Regulator Rv0678 of <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 16526-16540.	1.6	65
47	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.	1.8	72
48	Structural and functional analysis of the transcriptional regulator Rv3066 of <i>Mycobacterium tuberculosis</i> . <i>Nucleic Acids Research</i> , 2012, 40, 9340-9355.	6.5	44
49	Biomolecular membrane protein crystallization. <i>Philosophical Magazine</i> , 2012, 92, 2648-2661.	0.7	11
50	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.	2.0	51