

Bert van den Berg

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

3,544
citations

201674

27
h-index

289244

40
g-index

43
all docs

43
docs citations

43
times ranked

3831
citing authors

#	ARTICLE	IF	CITATIONS
1	A comprehensive structural analysis of the ATPase domain of human DNA topoisomerase II beta bound to AMPPNP, ADP, and the bisdioxopiperazine, ICRF193. <i>Structure</i> , 2022, 30, 1129-1145.e3.	3.3	6
2	Insights into SusCD-mediated glycan import by a prominent gut symbiont. <i>Nature Communications</i> , 2021, 12, 44.	12.8	42
3	Structural Basis for Silicic Acid Uptake by Higher Plants. <i>Journal of Molecular Biology</i> , 2021, 433, 167226.	4.2	18
4	Acquisition of ionic copper by the bacterial outer membrane protein OprC through a novel binding site. <i>PLoS Biology</i> , 2021, 19, e3001446.	5.6	14
5	Porins and small-molecule translocation across the outer membrane of Gram-negative bacteria. <i>Nature Reviews Microbiology</i> , 2020, 18, 164-176.	28.6	225
6	Chitoporin from <i>Serratia marcescens</i> : recombinant expression, purification and crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 536-543.	0.8	3
7	Uptake of monoaromatic hydrocarbons during biodegradation by FadL channel-mediated lateral diffusion. <i>Nature Communications</i> , 2020, 11, 6331.	12.8	10
8	Structural and functional insights into oligopeptide acquisition by the RagAB transporter from <i>Porphyromonas gingivalis</i> . <i>Nature Microbiology</i> , 2020, 5, 1016-1025.	13.3	46
9	Ammonium transceptors: Novel regulators of fungal development. <i>PLoS Pathogens</i> , 2019, 15, e1008059.	4.7	12
10	Modeling of Specific Lipopolysaccharide Binding Sites on a Gram-Negative Porin. <i>Journal of Physical Chemistry B</i> , 2019, 123, 5700-5708.	2.6	11
11	A Multidisciplinary Approach toward Identification of Antibiotic Scaffolds for <i>Acinetobacter baumannii</i> . <i>Structure</i> , 2019, 27, 268-280.e6.	3.3	41
12	Unusual Constriction Zones in the Major Porins OmpU and OmpT from <i>Vibrio cholerae</i> . <i>Structure</i> , 2018, 26, 708-721.e4.	3.3	22
13	Structure and function of a novel periplasmic chitooligosaccharide-binding protein from marine <i>Vibrio</i> bacteria. <i>Journal of Biological Chemistry</i> , 2018, 293, 5150-5159.	3.4	12
14	Structural basis for chitin acquisition by marine <i>Vibrio</i> species. <i>Nature Communications</i> , 2018, 9, 220.	12.8	37
15	TonB-dependent transport by the gut microbiota: novel aspects of an old problem. <i>Current Opinion in Structural Biology</i> , 2018, 51, 35-43.	5.7	49
16	Crystal structure of the <i>Acinetobacter baumannii</i> outer membrane protein Omp33. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 852-860.	2.3	8
17	Getting Drugs into Gram-Negative Bacteria: Rational Rules for Permeation through General Porins. <i>ACS Infectious Diseases</i> , 2018, 4, 1487-1498.	3.8	117
18	Getting Drugs through Small Pores: Exploiting the Porins Pathway in <i>Pseudomonas aeruginosa</i> . <i>ACS Infectious Diseases</i> , 2018, 4, 1519-1528.	3.8	25

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19	Structural basis for nutrient acquisition by dominant members of the human gut microbiota. <i>Nature</i> , 2017, 541, 407-411.	27.8	188
20	Structural basis for maintenance of bacterial outer membrane lipid asymmetry. <i>Nature Microbiology</i> , 2017, 2, 1616-1623.	13.3	118
21	Gram-negative trimeric porins have specific LPS binding sites that are essential for porin biogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5034-43.	7.1	103
22	Structural basis for Mep2 ammonium transceptor activation by phosphorylation. <i>Nature Communications</i> , 2016, 7, 11337.	12.8	52
23	Structural Insights into Outer Membrane Permeability of <i>Acinetobacter baumannii</i> . <i>Structure</i> , 2016, 24, 221-231.	3.3	49
24	Role of Electroosmosis in the Permeation of Neutral Molecules: CymA and Cyclodextrin as an Example. <i>Biophysical Journal</i> , 2016, 110, 600-611.	0.5	55
25	Crystal structure of a COG4313 outer membrane channel. <i>Scientific Reports</i> , 2015, 5, 11927.	3.3	19
26	Outer-membrane translocation of bulky small molecules by passive diffusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2991-9.	7.1	70
27	Small-Molecule Transport by CarO, an Abundant Eight-Stranded β^2 -Barrel Outer Membrane Protein from <i>Acinetobacter baumannii</i> . <i>Journal of Molecular Biology</i> , 2015, 427, 2329-2339.	4.2	54
28	Structure, Dynamics, and Substrate Specificity of the OprO Porin from <i>Pseudomonas aeruginosa</i> . <i>Biophysical Journal</i> , 2015, 109, 1429-1438.	0.5	39
29	Lateral gates: β^2 -barrels get in on the act. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1237-1239.	8.2	11
30	Structural Basis for Outer Membrane Sugar Uptake in Pseudomonads. <i>Journal of Biological Chemistry</i> , 2012, 287, 41044-41052.	3.4	39
31	Crystal Structure of <i>Escherichia coli</i> CusC, the Outer Membrane Component of a Heavy Metal Efflux Pump. <i>PLoS ONE</i> , 2011, 6, e15610.	2.5	91
32	Ligand-gated diffusion across the bacterial outer membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10121-10126.	7.1	66
33	Going Forward Laterally: Transmembrane Passage of Hydrophobic Molecules through Protein Channel Walls. <i>ChemBioChem</i> , 2010, 11, 1339-1343.	2.6	51
34	Crystal Structure of a Full-Length Autotransporter. <i>Journal of Molecular Biology</i> , 2010, 396, 627-633.	4.2	140
35	The Crystal Structure of OprG from <i>Pseudomonas aeruginosa</i> , a Potential Channel for Transport of Hydrophobic Molecules across the Outer Membrane. <i>PLoS ONE</i> , 2010, 5, e15016.	2.5	56
36	Transmembrane passage of hydrophobic compounds through a protein channel wall. <i>Nature</i> , 2009, 458, 367-370.	27.8	134

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37	Outer-membrane transport of aromatic hydrocarbons as a first step in biodegradation. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8601-8606.	7.1	85
38	The FadL family: unusual transporters for unusual substrates. Current Opinion in Structural Biology, 2005, 15, 401-407.	5.7	92
39	Crystal Structure of the Long-Chain Fatty Acid Transporter FadL. Science, 2004, 304, 1506-1509.	12.6	200
40	X-ray structure of a protein-conducting channel. Nature, 2004, 427, 36-44.	27.8	1,134