Ulrich Zachariae

List of Publications by Year
in descending order

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64	2,962	201674	182427
papers	citations	27 h-index	51 g-index

77	77	77	4203
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Coexistence of Ammonium Transporter and Channel Mechanisms in Amt-Mep-Rh Twin-His Variants Impairs the Filamentation Signaling Capacity of Fungal Mep2 Transceptors. MBio, 2022, 13, e0291321.	4.1	6
2	Data-Driven Derivation of Molecular Substructures That Enhance Drug Activity in Gram-Negative Bacteria. Journal of Medicinal Chemistry, 2022, 65, 6088-6099.	6.4	8
3	Characterisation of the Rh50 protein from the ammonia-oxidising bacterium Nitrosomonas europaea. Access Microbiology, 2022, 4, .	0.5	0
4	An antibiotic-resistance conferring mutation in a neisserial porin: Structure, ion flux, and ampicillin binding. Biochimica Et Biophysica Acta - Biomembranes, 2021, 1863, 183601.	2.6	9
5	The Persistent Question of Potassium Channel Permeation Mechanisms. Journal of Molecular Biology, 2021, 433, 167002.	4.2	55
6	Disease related single point mutations alter the global dynamics of a tetratricopeptide (TPR) Î±-solenoid domain. Journal of Structural Biology, 2020, 209, 107405.	2.8	7
7	On the ion coupling mechanism of the MATE transporter ClbM. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183137.	2.6	16
8	GPCRmd uncovers the dynamics of the 3D-GPCRome. Nature Methods, 2020, 17, 777-787.	19.0	90
9	Positively selected modifications in the pore of TbAQP2 allow pentamidine to enter Trypanosoma brucei. ELife, 2020, 9, .	6.0	16
10	A two-lane mechanism for selective biological ammonium transport. ELife, 2020, 9, .	6.0	23
11	High-resolution experimental and computational electrophysiology reveals weak Î²-lactam binding events in the porin PorB. Scientific Reports, 2019, 9, 1264.	3.3	12
12	The lipid environment determines the activity of the Escherichia coli ammonium transporter AmtB. FASEB Journal, 2019, 33, 1989-1999.	0.5	28
13	The O-GlcNAc Transferase Intellectual Disability Mutation L254F Distorts the TPR Helix. Cell Chemical Biology, 2018, 25, 513-518.e4.	5.2	30
14	Intracellular Transfer of Na+ in an Active-State G-Protein-Coupled Receptor. Structure, 2018, 26, 171-180.e2.	3.3	77
15	Merging In-Solution X-ray and Neutron Scattering Data Allows Fine Structural Analysis of Membraneâ€“Protein Detergent Complexes. Journal of Physical Chemistry Letters, 2018, 9, 3910-3914.	4.6	14
16	Ten Years of High Resolution Structural Research on the Voltage Dependent Anion Channel (VDAC)â€”Recent Developments and Future Directions. Frontiers in Physiology, 2018, 9, 108.	2.8	32
17	Direct knock-on of desolvated ions governs strict ion selectivity in K+ channels. Nature Chemistry, 2018, 10, 813-820.	13.6	170
18	Insights into the ion-coupling mechanism in the MATE transporter NorM-VC. Physical Biology, 2017, 14, 045009.	1.8	16

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19	Structure of the MacABâ€“TolC ABC-type tripartite multidrug efflux pump. Nature Microbiology, 2017, 2, 17070.	13.3	140
20	Modulation of the Neisseria gonorrhoeae drug efflux conduit MtrE. Scientific Reports, 2017, 7, 17091.	3.3	6
21	A role for loop G in the Î²1 strand in GABA_A receptor activation. Journal of Physiology, 2016, 594, 5555-5571.	2.9	7
22	Insights into the function of ion channels by computational electrophysiology simulations. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 1741-1752.	2.6	60
23	Membrane potentials regulating GPCRs: insights from experiments and molecular dynamics simulations. Current Opinion in Pharmacology, 2016, 30, 44-50.	3.5	32
24	Structural Mechanisms of Voltage Sensing in GÂProtein-Coupled Receptors. Structure, 2016, 24, 997-1007.	3.3	48
25	Direct Contacts of K+ Ions in the Selectivity Filter Enable the High Conductance of K+ Channels. Biophysical Journal, 2015, 108, 129a.	0.5	0
26	Role of Structural Dynamics at the Receptor G Protein Interface for Signal Transduction. PLoS ONE, 2015, 10, e0143399.	2.5	12
27	Mechanisms of Anion Conduction by Coupled Glutamate Transporters. Cell, 2015, 160, 542-553.	28.9	114
28	Molecular Determinants for Nuclear Import of Influenza A PB2 by Importin Î± Isoforms 3 and 7. Structure, 2015, 23, 374-384.	3.3	87
29	Interfacial self-assembly of a bacterial hydrophobin. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5419-5424.	7.1	68
30	The Bacterial Hydrophobin BslA is a Switchable Ellipsoidal Janus Nanocolloid. Langmuir, 2015, 31, 11558-11563.	3.5	28
31	Conserved structure and domain organization among bacterial Slc26 transporters. Biochemical Journal, 2014, 463, 297-307.	3.7	25
32	Crystallographic analysis of Neisseria meningitidis PorB extracellular loops potentially implicated in TLR2 recognition. Journal of Structural Biology, 2014, 185, 440-447.	2.8	32
33	Ion permeation in K ⁺ channels occurs by direct Coulomb knock-on. Science, 2014, 346, 352-355.	12.6	271
34	Position of Transmembrane Helix 6 Determines Receptor G Protein Coupling Specificity. Journal of the American Chemical Society, 2014, 136, 11244-11247.	13.7	105
35	Structural Determinants and Mechanism of Mammalian CRM1 Allostery. Structure, 2013, 21, 1350-1360.	3.3	17
36	Structural Determinants of Conformational Flexibility and Long-Range Allostery of the CRM1 Export Complex. Biophysical Journal, 2013, 104, 68a.	0.5	0

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37	Channel Crystal Structure and Antimicrobial Mechanism of Dermcidin from Human Skin. Biophysical Journal, 2013, 104, 241a.	0.5	0
38	Identification of a cation transport pathway in Neisseria meningitidis PorB. Proteins: Structure, Function and Bioinformatics, 2013, 81, 830-840.	2.6	13
39	Effect of Protonation State on the Stability of Amyloid Oligomers Assembled from TTR(105â€“115). Journal of Physical Chemistry Letters, 2013, 4, 1233-1238.	4.6	12
40	Crystal structure and functional mechanism of a human antimicrobial membrane channel. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4586-4591.	7.1	104
41	Structural basis for cooperativity of CRM1 export complex formation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 960-965.	7.1	64
42	Quantifying Disorder through Conditional Entropy: An Application to Fluid Mixing. PLoS ONE, 2013, 8, e65617.	2.5	32
43	A Designed Inhibitor of a CLC Antiporter Blocks Function through a Unique Binding Mode. Chemistry and Biology, 2012, 19, 1460-1470.	6.0	25
44	Universal Relaxation Governs the Nonequilibrium Elasticity of Biomolecules. Physical Review Letters, 2012, 109, 118304.	7.8	12
45	Î²-Barrel Mobility Underlies Closure of the Voltage-Dependent Anion Channel. Structure, 2012, 20, 1540-1549.	3.3	104
46	A Molecular Switch Driving Inactivation in the Cardiac K+ Channel hERG. PLoS ONE, 2012, 7, e41023.	2.5	19
47	Computational Electrophysiology: The Molecular Dynamics of Ion Channel Permeation and Selectivity in Atomistic Detail. Biophysical Journal, 2011, 101, 809-817.	0.5	214
48	Computational Electrophysiology on Vdac-1 reveals Mechanism of Anion Flux. Biophysical Journal, 2011, 100, 267a.	0.5	0
49	Quantitative Structural Analysis of Importin-Î² Flexibility: Paradigm for Solenoid Protein Structures. Structure, 2010, 18, 1171-1183.	3.3	89
50	Toward a Consensus Model of the hERG Potassium Channel. ChemMedChem, 2010, 5, 455-467.	3.2	66
51	Functional dynamics in the voltage-dependent anion channel. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22546-22551.	7.1	97
52	Hydrophilic Linkers and Polar Contacts Affect Aggregation of FG Repeat Peptides. Biophysical Journal, 2010, 98, 2653-2661.	0.5	13
53	An Unusual Hydrophobic Core Confers Extreme Flexibility to HEAT Repeat Proteins. Biophysical Journal, 2010, 99, 1596-1603.	0.5	66
54	Side Chain Flexibilities in the Human Ether-a-go-go Related Gene Potassium Channel (hERG) Together with Matched-Pair Binding Studies Suggest a New Binding Mode for Channel Blockers. Journal of Medicinal Chemistry, 2009, 52, 4266-4276.	6.4	44

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55	The Molecular Mechanism of Toxin-Induced Conformational Changes in a Potassium Channel: Relation to C-Type Inactivation. Structure, 2008, 16, 747-754.	3.3	52
56	Importin-Î²: Structural and Dynamic Determinants of a Molecular Spring. Structure, 2008, 16, 906-915.	3.3	49
57	Vacuolar Protein Sorting: Two Different Functional States of the AAA-ATPase Vps4p. Journal of Molecular Biology, 2008, 377, 352-363.	4.2	41
58	A Highly Strained Nuclear Conformation of the Exportin Cse1p Revealed by Molecular Dynamics Simulations. Structure, 2006, 14, 1469-1478.	3.3	27
59	High Resolution Crystal Structures and Molecular Dynamics Studies Reveal Substrate Binding in the Porin Omp32. Journal of Biological Chemistry, 2006, 281, 7413-7420.	3.4	29
60	Improved 3D continuum calculations of ion flux through membrane channels. European Biophysics Journal, 2003, 32, 689-702.	2.2	16
61	Multistep Mechanism of Chloride Translocation in a Strongly Anion-Selective Porin Channel. Biophysical Journal, 2003, 85, 954-962.	0.5	26
62	Electrostatic properties of the anion selective porin Omp32 fromDelftia acidovoransand of the arginine cluster of bacterial porins. Protein Science, 2002, 11, 1309-1319.	7.6	29
63	Proton uptake associated with the reduction of the primary quinone QA influences the binding site of the secondary quinone QB in Rhodopseudomonas viridis photosynthetic reaction centers. Biochimica Et Biophysica Acta - Bioenergetics, 2001, 1505, 280-290.	1.0	21
64	Picosecond Time-Resolved FRET in the Fluorescent Protein fromDiscosoma Red (wt-DsRed). ChemPhysChem, 2001, 2, 325-328.	2.1	28