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	Ion permeation in K ⁺ channels occurs by direct Coulomb knock-on. Science, 2014, 346, 352-355.	12.6	271
2	Computational Electrophysiology: The Molecular Dynamics of Ion Channel Permeation and Selectivity in Atomistic Detail. Biophysical Journal, 2011, 101, 809-817.	0.5	214
3	Direct knock-on of desolvated ions governs strict ion selectivity in K+ channels. Nature Chemistry, 2018, 10, 813-820.	13.6	170
4	Structure of the MacABâ€“TolC ABC-type tripartite multidrug efflux pump. Nature Microbiology, 2017, 2, 17070.	13.3	140
5	Mechanisms of Anion Conduction by Coupled Glutamate Transporters. Cell, 2015, 160, 542-553.	28.9	114
6	Position of Transmembrane Helix 6 Determines Receptor G Protein Coupling Specificity. Journal of the American Chemical Society, 2014, 136, 11244-11247.	13.7	105
7	Î²-Barrel Mobility Underlies Closure of the Voltage-Dependent Anion Channel. Structure, 2012, 20, 1540-1549.	3.3	104
8	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
9	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
10	GPCRmd uncovers the dynamics of the 3D-GPCRome. Nature Methods, 2020, 17, 777-787.	19.0	90
11	Quantitative Structural Analysis of Importin-Î² Flexibility: Paradigm for Solenoid Protein Structures. Structure, 2010, 18, 1171-1183.	3.3	89
12	Molecular Determinants for Nuclear Import of Influenza A PB2 by Importin Î± Isoforms 3 and 7. Structure, 2015, 23, 374-384.	3.3	87
13	Intracellular Transfer of Na+ in an Active-State G-Protein-Coupled Receptor. Structure, 2018, 26, 171-180.e2.	3.3	77
14	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
15	Toward a Consensus Model of the hERG Potassium Channel. ChemMedChem, 2010, 5, 455-467.	3.2	66
16	An Unusual Hydrophobic Core Confers Extreme Flexibility to HEAT Repeat Proteins. Biophysical Journal, 2010, 99, 1596-1603.	0.5	66
17	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
18	Insights into the function of ion channels by computational electrophysiology simulations. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 1741-1752.	2.6	60

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19	The Persistent Question of Potassium Channel Permeation Mechanisms. Journal of Molecular Biology, 2021, 433, 167002.	4.2	55
20	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
21	Importin-Î²: Structural and Dynamic Determinants of a Molecular Spring. Structure, 2008, 16, 906-915.	3.3	49
22	Structural Mechanisms of Voltage Sensing in GÂProtein-Coupled Receptors. Structure, 2016, 24, 997-1007.	3.3	48
23	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
24	Vacuolar Protein Sorting: Two Different Functional States of the AAA-ATPase Vps4p. Journal of Molecular Biology, 2008, 377, 352-363.	4.2	41
25	Crystallographic analysis of Neisseria meningitidis PorB extracellular loops potentially implicated in TLR2 recognition. Journal of Structural Biology, 2014, 185, 440-447.	2.8	32
26	Membrane potentials regulating GPCRs: insights from experiments and molecular dynamics simulations. Current Opinion in Pharmacology, 2016, 30, 44-50.	3.5	32
27	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
28	Quantifying Disorder through Conditional Entropy: An Application to Fluid Mixing. PLoS ONE, 2013, 8, e65617.	2.5	32
29	The O-GlcNAc Transferase Intellectual Disability Mutation L254F Distorts the TPR Helix. Cell Chemical Biology, 2018, 25, 513-518.e4.	5.2	30
30	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
31	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
32	Picosecond Time-Resolved FRET in the Fluorescent Protein fromDiscosoma Red (wt-DsRed). ChemPhysChem, 2001, 2, 325-328.	2.1	28
33	The Bacterial Hydrophobin BslA is a Switchable Ellipsoidal Janus Nanocolloid. Langmuir, 2015, 31, 11558-11563.	3.5	28
34	The lipid environment determines the activity of the Escherichia coli ammonium transporter AmtB. FASEB Journal, 2019, 33, 1989-1999.	0.5	28
35	A Highly Strained Nuclear Conformation of the Exportin Cse1p Revealed by Molecular Dynamics Simulations. Structure, 2006, 14, 1469-1478.	3.3	27
36	Multistep Mechanism of Chloride Translocation in a Strongly Anion-Selective Porin Channel. Biophysical Journal, 2003, 85, 954-962.	0.5	26

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37	A Designed Inhibitor of a CLC Antiporter Blocks Function through a Unique Binding Mode. Chemistry and Biology, 2012, 19, 1460-1470.	6.0	25
38	Conserved structure and domain organization among bacterial Slc26 transporters. Biochemical Journal, 2014, 463, 297-307.	3.7	25
39	A two-lane mechanism for selective biological ammonium transport. ELife, 2020, 9, .	6.0	23
40	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
41	A Molecular Switch Driving Inactivation in the Cardiac K+ Channel hERG. PLoS ONE, 2012, 7, e41023.	2.5	19
42	Structural Determinants and Mechanism of Mammalian CRM1 Allostery. Structure, 2013, 21, 1350-1360.	3.3	17
43	Improved 3D continuum calculations of ion flux through membrane channels. European Biophysics Journal, 2003, 32, 689-702.	2.2	16
44	Insights into the ion-coupling mechanism in the MATE transporter NorM-VC. Physical Biology, 2017, 14, 045009.	1.8	16
45	On the ion coupling mechanism of the MATE transporter ClbM. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183137.	2.6	16
46	Positively selected modifications in the pore of TbAQP2 allow pentamidine to enter Trypanosoma brucei. ELife, 2020, 9, .	6.0	16
47	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
48	Hydrophilic Linkers and Polar Contacts Affect Aggregation of FG Repeat Peptides. Biophysical Journal, 2010, 98, 2653-2661.	0.5	13
49	Identification of a cation transport pathway in Neisseria meningitidis PorB. Proteins: Structure, Function and Bioinformatics, 2013, 81, 830-840.	2.6	13
50	Universal Relaxation Governs the Nonequilibrium Elasticity of Biomolecules. Physical Review Letters, 2012, 109, 118304.	7.8	12
51	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
52	Role of Structural Dynamics at the Receptor G Protein Interface for Signal Transduction. PLoS ONE, 2015, 10, e0143399.	2.5	12
53	High-resolution experimental and computational electrophysiology reveals weak Î²-lactam binding events in the porin PorB. Scientific Reports, 2019, 9, 1264.	3.3	12
54	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

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55	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
56	A role for loop G in the Î²1 strand in GABA_A receptor activation. Journal of Physiology, 2016, 594, 5555-5571.	2.9	7
57	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
58	Modulation of the Neisseria gonorrhoeae drug efflux conduit MtrE. Scientific Reports, 2017, 7, 17091.	3.3	6
59	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
60	Computational Electrophysiology on Vdac-1 reveals Mechanism of Anion Flux. Biophysical Journal, 2011, 100, 267a.	0.5	0
61	Structural Determinants of Conformational Flexibility and Long-Range Allostery of the CRM1 Export Complex. Biophysical Journal, 2013, 104, 68a.	0.5	0
62	Channel Crystal Structure and Antimicrobial Mechanism of Dermcidin from Human Skin. Biophysical Journal, 2013, 104, 241a.	0.5	0
63	Direct Contacts of K+ Ions in the Selectivity Filter Enable the High Conductance of K+ Channels. Biophysical Journal, 2015, 108, 129a.	0.5	0
64	Characterisation of the Rh50 protein from the ammonia-oxidising bacterium Nitrosomonas europaea. Access Microbiology, 2022, 4, .	0.5	0