

Raimund Dutzler

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3445760/publications.pdf>

Version: 2024-02-01

51
papers

6,905
citations

126907

33
h-index

182427

51
g-index

68
all docs

68
docs citations

68
times ranked

5435
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and functional properties of a magnesium transporter of the SLC11/NRAMP family. <i>ELife</i> , 2022, 11, .	6.0	8
2	Regulators of cell volume: The structural and functional properties of anion channels of the LRRC8 family. <i>Current Opinion in Structural Biology</i> , 2022, 74, 102382.	5.7	8
3	Inhibition mechanism of the chloride channel TMEM16A by the pore blocker 1PBC. <i>Nature Communications</i> , 2022, 13, 2798.	12.8	10
4	Mechanism of pore opening in the calcium-activated chloride channel TMEM16A. <i>Nature Communications</i> , 2021, 12, 786.	12.8	22
5	Gating the pore of the calcium-activated chloride channel TMEM16A. <i>Nature Communications</i> , 2021, 12, 785.	12.8	33
6	Cryo-EM structures of the caspase-activated protein XKR9 involved in apoptotic lipid scrambling. <i>ELife</i> , 2021, 10, .	6.0	22
7	Cryo-EM structures of the TTYH family reveal a novel architecture for lipid interactions. <i>Nature Communications</i> , 2021, 12, 4893.	12.8	11
8	Allosteric modulation of LRRC8 channels by targeting their cytoplasmic domains. <i>Nature Communications</i> , 2021, 12, 5435.	12.8	15
9	Alternative chloride transport pathways as pharmacological targets for the treatment of cystic fibrosis. <i>Journal of Cystic Fibrosis</i> , 2020, 19, S37-S41.	0.7	29
10	Cryo-EM structures and functional properties of CALHM channels of the human placenta. <i>ELife</i> , 2020, 9, .	6.0	26
11	Stepwise activation mechanism of the scramblase nhTMEM16 revealed by cryo-EM. <i>ELife</i> , 2019, 8, .	6.0	82
12	Cryo-EM structures and functional characterization of the murine lipid scramblase TMEM16F. <i>ELife</i> , 2019, 8, .	6.0	105
13	Cryo-EM structures and functional characterization of murine Slc26a9 reveal mechanism of uncoupled chloride transport. <i>ELife</i> , 2019, 8, .	6.0	94
14	Mechanistic basis of the inhibition of SLC11/NRAMP-mediated metal ion transport by bis-isothiourea substituted compounds. <i>ELife</i> , 2019, 8, .	6.0	15
15	Structure of a volume-regulated anion channel of the LRRC8 family. <i>Nature</i> , 2018, 558, 254-259.	27.8	160
16	Calcium-dependent electrostatic control of anion access to the pore of the calcium-activated chloride channel TMEM16A. <i>ELife</i> , 2018, 7, .	6.0	35
17	Structural and mechanistic basis of proton-coupled metal ion transport in the SLC11/NRAMP family. <i>Nature Communications</i> , 2017, 8, 14033.	12.8	68
18	Independent Activation of Ion Conduction Pores in the Double-Barreled Ca ²⁺ -Activated Cl ⁻ Channel TMEM16A. <i>Biophysical Journal</i> , 2017, 112, 421a-422a.	0.5	0

#	ARTICLE	IF	CITATIONS
19	Generation and Characterization of Anti-VGLUT Nanobodies Acting as Inhibitors of Transport. <i>Biochemistry</i> , 2017, 56, 3962-3971.	2.5	40
20	Activation mechanism of the calcium-activated chloride channel TMEM16A revealed by cryo-EM. <i>Nature</i> , 2017, 552, 421-425.	27.8	231
21	Structural basis for anion conduction in the calcium-activated chloride channel TMEM16A. <i>ELife</i> , 2017, 6, .	6.0	127
22	Independent activation of ion conduction pores in the double-barreled calcium-activated chloride channel TMEM16A. <i>Journal of General Physiology</i> , 2016, 148, 375-392.	1.9	75
23	Structural basis for phospholipid scrambling in the TMEM16 family. <i>Current Opinion in Structural Biology</i> , 2016, 39, 61-70.	5.7	61
24	Signal Transduction at the Domain Interface of Prokaryotic Pentameric Ligand-Gated Ion Channels. <i>PLoS Biology</i> , 2016, 14, e1002393.	5.6	41
25	Structure of a prokaryotic fumarate transporter reveals the architecture of the SLC26 family. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 803-808.	8.2	159
26	Crystal structure of a SLC11 (NRAMP) transporter reveals the basis for transition-metal ion transport. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 990-996.	8.2	171
27	X-ray structure of a calcium-activated TMEM16 lipid scramblase. <i>Nature</i> , 2014, 516, 207-212.	27.8	393
28	Functional characterization of a ClC transporter by solid-supported membrane electrophysiology. <i>Journal of General Physiology</i> , 2013, 141, 479-491.	1.9	19
29	Inhibition of the Prokaryotic Pentameric Ligand-Gated Ion Channel ELIC by Divalent Cations. <i>PLoS Biology</i> , 2012, 10, e1001429.	5.6	44
30	A Versatile and Efficient High-Throughput Cloning Tool for Structural Biology. <i>Biochemistry</i> , 2011, 50, 3272-3278.	2.5	185
31	Ligand Activation of the Prokaryotic Pentameric Ligand-Gated Ion Channel ELIC. <i>PLoS Biology</i> , 2011, 9, e1001101.	5.6	98
32	Structural basis of open channel block in a prokaryotic pentameric ligand-gated ion channel. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1330-1336.	8.2	91
33	Channels and Transporters. <i>Chimia</i> , 2010, 64, 662.	0.6	4
34	A prokaryotic perspective on pentameric ligand-gated ion channel structure. <i>Current Opinion in Structural Biology</i> , 2009, 19, 418-424.	5.7	61
35	X-ray Structure of the C-Terminal Domain of a Prokaryotic Cation-Chloride Cotransporter. <i>Structure</i> , 2009, 17, 538-546.	3.3	49
36	Structure of a potentially open state of a proton-activated pentameric ligand-gated ion channel. <i>Nature</i> , 2009, 457, 115-118.	27.8	504

#	ARTICLE	IF	CITATIONS
37	X-ray structure of a prokaryotic pentameric ligand-gated ion channel. <i>Nature</i> , 2008, 452, 375-379.	27.8	634
38	The Cytoplasmic Domain of the Chloride Channel ClC-0: Structural and Dynamic Characterization of Flexible Regions. <i>Journal of Molecular Biology</i> , 2007, 369, 1163-1169.	4.2	17
39	A structural perspective on ClC channel and transporter function. <i>FEBS Letters</i> , 2007, 581, 2839-2844.	2.8	44
40	Nucleotide recognition by the cytoplasmic domain of the human chloride transporter ClC-5. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 60-67.	8.2	136
41	The Structure of the Cytoplasmic Domain of the Chloride Channel ClC-Ka Reveals a Conserved Interaction Interface. <i>Structure</i> , 2007, 15, 715-725.	3.3	72
42	Synergism Between Halide Binding and Proton Transport in a CLC-type Exchanger. <i>Journal of Molecular Biology</i> , 2006, 362, 691-699.	4.2	103
43	Ion-binding properties of the ClC chloride selectivity filter. <i>EMBO Journal</i> , 2006, 25, 24-33.	7.8	96
44	The ClC family of chloride channels and transporters. <i>Current Opinion in Structural Biology</i> , 2006, 16, 439-446.	5.7	73
45	Crystal Structure of the Cytoplasmic Domain of the Chloride Channel ClC-0. <i>Structure</i> , 2006, 14, 299-307.	3.3	97
46	The structural basis of ClC chloride channel function. <i>Trends in Neurosciences</i> , 2004, 27, 315-320.	8.6	35
47	Structural basis for ion conduction and gating in ClC chloride channels. <i>FEBS Letters</i> , 2004, 564, 229-233.	2.8	54
48	Gating the Selectivity Filter in ClC Chloride Channels. <i>Science</i> , 2003, 300, 108-112.	12.6	747
49	Translocation Mechanism of Long Sugar Chains across the Maltoporin Membrane Channel. <i>Structure</i> , 2002, 10, 1273-1284.	3.3	51
50	X-ray structure of a ClC chloride channel at 3.0 Å... reveals the molecular basis of anion selectivity. <i>Nature</i> , 2002, 415, 287-294.	27.8	1,529
51	Channel specificity: structural basis for sugar discrimination and differential flux rates in maltoporin 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1997, 272, 56-63.	4.2	111