Motoyuki Hattori

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4946290/publications.pdf

Version: 2024-02-01

39 1,834 18 32 g-index

430874 414414 32 43 43 2348

times ranked

citing authors

docs citations

all docs

#	Article	IF	CITATIONS
1	Recent progress in the structural biology of <scp>P2X</scp> receptors. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1779-1785.	2.6	18
2	P2X3-selective mechanism of Gefapixant, a drug candidate for the treatment of refractory chronic cough. Computational and Structural Biotechnology Journal, 2022, 20, 1642-1653.	4.1	9
3	The long \hat{I}^2 2,3-sheets encoded by redundant sequences play an integral role in the channel function of P2X7 receptors. Journal of Biological Chemistry, 2022, 298, 102002.	3.4	3
4	Mutagenesis Analysis of GMN Motif in <i> Arabidopsis thaliana < /i > Mg2+ Transporter MRS2-1. Bioscience, Biotechnology and Biochemistry, 2022, , .</i>	1.3	1
5	Recent Advances in the Structural Biology of Mg2+ Channels and Transporters. Journal of Molecular Biology, 2022, 434, 167729.	4.2	12
6	Structural basis for the Mg $<$ sup $>$ 2+ $<$ /sup $>$ recognition and regulation of the CorC Mg $<$ sup $>$ 2+ $<$ /sup $>$ transporter. Science Advances, 2021, 7, .	10.3	41
7	Fluorescence-detection size-exclusion chromatography utilizing nanobody technology for expression screening of membrane proteins. Communications Biology, 2021, 4, 366.	4.4	10
8	The structure of MgtE in the absence of magnesium provides new insights into channel gating. PLoS Biology, 2021, 19, e3001231.	5 . 6	8
9	Identification and mechanistic analysis of an inhibitor of the CorC Mg2+ transporter. IScience, 2021, 24, 102370.	4.1	5
10	Functional Analysis of the GPI Transamidase Complex by Screening for Amino Acid Mutations in Each Subunit. Molecules, 2021, 26, 5462.	3.8	5
11	TMC1 and TMC2 Proteins Are Pore-Forming Subunits of Mechanosensitive Ion Channels. Neuron, 2020, 105, 310-321.e3.	8.1	109
12	A FRET-based screening method to detect potential inhibitors of the binding of CNNM3 to PRL2. Scientific Reports, 2020, 10, 12879.	3.3	5
13	Structure-based engineering of anti-GFP nanobody tandems as ultra-high-affinity reagents for purification. Scientific Reports, 2020, 10, 6239.	3.3	25
14	Molecular mechanisms of human P2X3 receptor channel activation and modulation by divalent cation bound ATP. ELife, 2019, 8, .	6.0	30
15	Druggable negative allosteric site of P2X3 receptors. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4939-4944.	7.1	73
16	Functional roles of Mg2+ binding sites in ion-dependent gating of a Mg2+ channel, MgtE, revealed by solution NMR. ELife, 2018, 7, .	6.0	10
17	Cryo-EM structures of the human volume-regulated anion channel LRRC8. Nature Structural and Molecular Biology, 2018, 25, 797-804.	8.2	104
18	Structural insights into the nucleotide base specificity of P2X receptors. Scientific Reports, 2017, 7, 45208.	3.3	41

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19	Structural insights into the competitive inhibition of the ATP-gated P2X receptor channel. Nature Communications, 2017, 8, 876.	12.8	75
20	ATP-dependent modulation of MgtE in Mg2+ homeostasis. Nature Communications, 2017, 8, 148.	12.8	54
21	Starting a Lab in China. Seibutsu Butsuri, 2017, 57, 323-324.	0.1	O
22	Crystal structures of the TRIC trimeric intracellular cation channel orthologues. Cell Research, 2016, 26, 1288-1301.	12.0	21
23	Conductance of P2X ₄ purinergic receptor is determined by conformational equilibrium in the transmembrane region. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4741-4746.	7.1	23
24	Structural Insights into Divalent Cation Modulations of ATP-Gated P2X Receptor Channels. Cell Reports, 2016, 14, 932-944.	6.4	59
25	Structural basis for ion selectivity revealed by high-resolution crystal structure of Mg2+ channel MgtE. Nature Communications, 2014, 5, 5374.	12.8	41
26	A Fluorescence-Detection Size-Exclusion Chromatography-Based Thermostability Assay for Membrane Protein Precrystallization Screening. Structure, 2012, 20, 1293-1299.	3.3	222
27	Spatial distribution of cytoplasmic domains of the Mg2+-transporter MgtE, in a solution lacking Mg2+, revealed by paramagnetic relaxation enhancement. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 1129-1135.	2.3	5
28	Molecular mechanism of ATP binding and ion channel activation in P2X receptors. Nature, 2012, 485, 207-212.	27.8	460
29	Structural Basis of Novel Interactions Between the Small-GTPase and GDI-like Domains in Prokaryotic FeoB Iron Transporter. Structure, 2009, 17, 1345-1355.	3.3	32
30	Mg2+-dependent gating of bacterial MgtE channel underlies Mg2+ homeostasis. EMBO Journal, 2009, 28, 3602-3612.	7.8	94
31	Mg ²⁺ -sensing mechanism of Mg ²⁺ transporter MgtE probed by molecular dynamics study. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15393-15398.	7.1	56
32	3S2-1 Structure and Mechanism of the MgtE Mg^<2+> transporter(3S2 Structural basis for) Tj ETQq0 0 0 rg	gBT /Overlo	ock 10 Tf 50 0
33	1P-042 Structure and Mechanism of the MgtE Mg^<2+> transporter(The 46th Annual Meeting of the) Tj ETQq1 1	0,784314	4 rgBT /Ov <mark>e</mark> r
34	1P-033 Crystal structures of the cytosolic domain of the Mg^<2+> transporter MgtE(The 46th) Tj ETQq0 0 C) rgBT /Ov	erlock 10 Tf
35	1P115 Crystal structure of the MgtE Mg^<2+> transporter(Membrane proteins,Oral) Tj ETQq1 1 0.784314 r	gBT/Over	lock 10 Tf 5
36	Crystallization and preliminary X-ray diffraction analysis of the full-length Mg ²⁺ transporter MgtE. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 682-684.	0.7	9

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37	Crystallization and preliminary X-ray diffraction analysis of the cytosolic domain of a cation diffusion facilitator family protein. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 771-773.	0.7	6
38	Crystal structure of the MgtE Mg2+ transporter. Nature, 2007, 448, 1072-1075.	27.8	166
39	2P151 Crystallization and preliminary X-ray analysis of the bacterial membrane transporters(34.) Tj ETQq1 1 0.7 2006, 46, S333.	84314 rgB ⁻ 0.1	「/Overlock 1 O