

Tomoya Tsukazaki

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5452217/publications.pdf>

Version: 2024-02-01

47
papers

2,412
citations

394421

19
h-index

302126

39
g-index

49
all docs

49
docs citations

49
times ranked

2747
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of the lipid flippase MurJ in a "squeezed" form distinct from its inward- and outward-facing forms. <i>Structure</i> , 2022, , .	3.3	5
2	Crystal structures of a nicotine MATE transporter provide insight into its mechanism of substrate transport. <i>FEBS Letters</i> , 2021, 595, 1902-1913.	2.8	5
3	Preface to the special issue on novel measurement techniques for visualizing "live" protein molecules at work. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129421.	2.4	0
4	Reversible autoinhibitory regulation of <i>Escherichia coli</i> metallopeptidase BepA for selective β -barrel protein degradation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27989-27996.	7.1	4
5	Crystal structure of a YeeE/YedE family protein engaged in thiosulfate uptake. <i>Science Advances</i> , 2020, 6, eaba7637.	10.3	25
6	The bacterial protein YidC accelerates MPlase-dependent integration of membrane proteins. <i>Journal of Biological Chemistry</i> , 2019, 294, 18898-18908.	3.4	15
7	Structural Basis of Sarco/Endoplasmic Reticulum Ca^{2+} -ATPase 2b Regulation via Transmembrane Helix Interplay. <i>Cell Reports</i> , 2019, 27, 1221-1230.e3.	6.4	34
8	Structural Basis of the Sec Translocon and YidC Revealed Through X-ray Crystallography. <i>Protein Journal</i> , 2019, 38, 249-261.	1.6	13
9	A snapshot of membrane protein insertion. <i>EMBO Reports</i> , 2019, 20, e49034.	4.5	1
10	Single-Unit Imaging of Membrane Protein-Embedded Nanodiscs from Two Oriented Sides by High-Speed Atomic Force Microscopy. <i>Structure</i> , 2019, 27, 152-160.e3.	3.3	17
11	Structural Basis for the Function of the β -Barrel Assembly-Enhancing Protease BepA. <i>Journal of Molecular Biology</i> , 2019, 431, 625-635.	4.2	12
12	Structure-based working model of SecDF, a proton-driven bacterial protein translocation factor. <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	41
13	Structural Biology of Sec Translocon. <i>Seibutsu Butsuri</i> , 2018, 58, 078-082.	0.1	0
14	Remote Coupled Drastic β -Barrel to β -Sheet Transition of the Protein Translocation Motor. <i>Structure</i> , 2018, 26, 485-489.e2.	3.3	15
15	2.8-Å... crystal structure of <i>Escherichia coli</i> YidC revealing all core regions, including flexible C2 loop. <i>Biochemical and Biophysical Research Communications</i> , 2018, 505, 141-145.	2.1	18
16	Tunnel Formation Inferred from the I-Form Structures of the Proton-Driven Protein Secretion Motor SecDF. <i>Cell Reports</i> , 2017, 19, 895-901.	6.4	38
17	The TPR domain of BepA is required for productive interaction with substrate proteins and the β -barrel assembly machinery complex. <i>Molecular Microbiology</i> , 2017, 106, 760-776.	2.5	26
18	Crystal Structure of a Plant Multidrug and Toxic Compound Extrusion Family Protein. <i>Structure</i> , 2017, 25, 1455-1460.e2.	3.3	39

#	ARTICLE	IF	CITATIONS
19	SecY-SecA fusion protein retains the ability to mediate protein transport. PLoS ONE, 2017, 12, e0183434.	2.5	8
20	Crystal Structures of SecYEG in Lipidic Cubic Phase Elucidate a Precise Resting and a Peptide-Bound State. Cell Reports, 2015, 13, 1561-1568.	6.4	58
21	Hydrophilic microenvironment required for the channel-independent insertase function of YidC protein. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5063-5068.	7.1	33
22	Crystallization and preliminary X-ray diffraction analysis of YidC, a membrane-protein chaperone and insertase from <i>Bacillus halodurans</i> . Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1056-1060.	0.8	11
23	Structural basis of Sec-independent membrane protein insertion by YidC. Nature, 2014, 509, 516-520.	27.8	203
24	Conformational variation of the translocon enhancing chaperone SecDF. Journal of Structural and Functional Genomics, 2014, 15, 107-115.	1.2	10
25	Crystal structure of Escherichia coli YidC, a membrane protein chaperone and insertase. Scientific Reports, 2014, 4, 7299.	3.3	109
26	Structural basis for the drug extrusion mechanism by a MATE multidrug transporter. Nature, 2013, 496, 247-251.	27.8	225
27	Structural basis for dynamic mechanism of proton-coupled symport by the peptide transporter POT. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11343-11348.	7.1	197
28	Crystal structure of the channelrhodopsin light-gated cation channel. Nature, 2012, 482, 369-374.	27.8	503
29	Structure and function of a membrane component SecDF that enhances protein export. Nature, 2011, 474, 235-238.	27.8	202
30	Crystallization and preliminary X-ray diffraction of the first periplasmic domain of SecDF, a translocon-associated membrane protein, from <i>Thermus thermophilus</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1367-1370.	0.7	5
31	The mechanism of protein export enhancement by the SecDF membrane component. Biophysics (Nagoya-shi, Japan), 2011, 7, 129-133.	0.4	7
32	Crystal Structure of SecDF, a Sec Translocon-associated Membrane Protein. Seibutsu Butsuri, 2011, 51, 236-237.	0.1	0
33	Molecular Mechanisms Underlying the Early Stage of Protein Translocation through the Sec Translocon. Biochemistry, 2010, 49, 945-950.	2.5	17
34	Mg ²⁺ -dependent gating of bacterial MgtE channel underlies Mg ²⁺ homeostasis. EMBO Journal, 2009, 28, 3602-3612.	7.8	94
35	2SA2-04 Structure and function of bacterial protein translocation machinery(2SA2 Research) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.1	0
36	Conformational Transition of Sec Machinery Inferred from Bacterial SecYE Structures. Seibutsu Butsuri, 2009, 49, 288-289.	0.1	0

#	ARTICLE	IF	CITATIONS
37	Conformational transition of Sec machinery inferred from bacterial SecYE structures. <i>Nature</i> , 2008, 455, 988-991.	27.8	206
38	1P-048 X-ray crystallographic analysis of SecDF periplasmic domain from <i>Thermus thermophilus</i> (The Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.1	0
39	3S2-3 Crystal structure of bacterial Sec translocon(3S2 Structural basis for membrane-mediated) Tj ETQq1 1 0.784314 rgBT /Overlock Seibutsu Butsuri, 2008, 48, S16.	0.1	0
40	1P-041 Crystal structure of bacterial Sec translocon(The 46th Annual Meeting of the Biophysical) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 0	0.1	0
41	Crystal Structure of the Translocation ATPase SecA from <i>Thermus thermophilus</i> Reveals a Parallel, Head-to-Head Dimer. <i>Journal of Molecular Biology</i> , 2006, 364, 248-258.	4.2	84
42	Purification, crystallization and preliminary X-ray diffraction of SecDF, a translocon-associated membrane protein, from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 376-380.	0.7	22
43	Cloning, expression, purification, crystallization and initial crystallographic analysis of the preprotein translocation ATPase SecA from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 909-912.	0.7	2
44	Fluorescence Resonance Energy Transfer Analysis of Protein Translocase. <i>Journal of Biological Chemistry</i> , 2003, 278, 14257-14264.	3.4	50
45	Interactions of Cytochrome c Peroxidase with Lysine Peptides. <i>Biochemical and Biophysical Research Communications</i> , 2000, 268, 395-397.	2.1	6
46	Interactions of Cytochromecand Cytochromefwith Aspartic Acid Peptides. <i>Journal of the American Chemical Society</i> , 1999, 121, 849-855.	13.7	38
47	Effects of charged peptides on electron transfer from [Fe(CN)6]4â€“ to cytochrome c or plastocyanin. <i>Journal of Biological Inorganic Chemistry</i> , 1998, 3, 563-569.	2.6	13