

Kaoru Mitsuoka

List of Publications by Year in descending order

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37
papers

4,679
citations

331670

21
h-index

361022

35
g-index

38
all docs

38
docs citations

38
times ranked

3966
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural determinants of water permeation through aquaporin-1. <i>Nature</i> , 2000, 407, 599-605.	27.8	1,584
2	Surface of bacteriorhodopsin revealed by high-resolution electron crystallography. <i>Nature</i> , 1997, 389, 206-211.	27.8	474
3	The three-dimensional structure of aquaporin-1. <i>Nature</i> , 1997, 387, 624-627.	27.8	441
4	Implications of the Aquaporin-4 Structure on Array Formation and Cell Adhesion. <i>Journal of Molecular Biology</i> , 2006, 355, 628-639.	4.2	363
5	The structure of bacteriorhodopsin at 3.0 Å... resolution based on electron crystallography: implication of the charge distribution 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 286, 861-882.	4.2	263
6	Structure and Function of Water Channels. <i>Current Opinion in Structural Biology</i> , 2002, 12, 509-515.	5.7	246
7	Structural basis for induced formation of the inflammatory mediator prostaglandin E ₂ . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 11110-11115.	7.1	139
8	Aquaporin-11 containing a divergent NPA motif has normal water channel activity. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007, 1768, 688-693.	2.6	131
9	Structural Basis for Detoxification and Oxidative Stress Protection in Membranes. <i>Journal of Molecular Biology</i> , 2006, 360, 934-945.	4.2	129
10	The Structure of Aquaporin-1 at 4.5-Å... Resolution Reveals Short α -Helices in the Center of the Monomer. <i>Journal of Structural Biology</i> , 1999, 128, 34-43.	2.8	122
11	Improved specimen preparation for cryo-electron microscopy using a symmetric carbon sandwich technique. <i>Journal of Structural Biology</i> , 2004, 146, 325-333.	2.8	107
12	Neuromyelitis optica and anti-aquaporin-4 antibodies measured by an enzyme-linked immunosorbent assay. <i>Journal of Neuroimmunology</i> , 2008, 196, 181-187.	2.3	102
13	Two-dimensional crystals: a powerful approach to assess structure, function and dynamics of membrane proteins. <i>FEBS Letters</i> , 2001, 504, 166-172.	2.8	83
14	Dodecamer rotor ring defines H ⁺ /ATP ratio for ATP synthesis of prokaryotic V-ATPase from <i>Thermus thermophilus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20256-20261.	7.1	78
15	Projection map of the reaction center-light harvesting 1 complex from <i>Rhodospseudomonas viridis</i> at 10 Å... resolution. <i>FEBS Letters</i> , 1998, 425, 505-508.	2.8	44
16	Cryo EM structure of intact rotary H ⁺ -ATPase/synthase from <i>Thermus thermophilus</i> . <i>Nature Communications</i> , 2018, 9, 89.	12.8	44
17	The 3.0 Å... projection structure of microsomal glutathione transferase as determined by electron crystallography of p 21212 two-dimensional crystals. <i>Journal of Molecular Biology</i> , 1997, 271, 751-758.	4.2	40
18	Electron and atomic force microscopy of membrane proteins. <i>Current Opinion in Structural Biology</i> , 1997, 7, 543-549.	5.7	37

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19	The projection structure of the membrane protein microsomal glutathione transferase at 3 Å.. resolution as determined from two-dimensional hexagonal crystals. <i>Journal of Molecular Biology</i> , 1999, 288, 243-253.	4.2	34
20	The Fold of Human Aquaporin 1. <i>Journal of Molecular Biology</i> , 2000, 300, 987-994.	4.2	34
21	Crystal Structure of the Homer 1 Family Conserved Region Reveals the Interaction Between the EVH1 Domain and Own Proline-rich Motif. <i>Journal of Molecular Biology</i> , 2002, 318, 1117-1126.	4.2	30
22	Automatic recovery of missing amplitudes and phases in tilt-limited electron crystallography of two-dimensional crystals. <i>Physical Review E</i> , 2011, 84, 011916.	2.1	23
23	Simulation of charge effects on density maps obtained by high-resolution electron crystallography. <i>Journal of Electron Microscopy</i> , 2007, 56, 131-140.	0.9	19
24	Examination of the LeafScan 45, a line-illuminating micro-densitometer, for its use in electron crystallography. <i>Ultramicroscopy</i> , 1997, 68, 109-121.	1.9	16
25	Sequence- and seed-structure-dependent polymorphic fibrils of alpha-synuclein. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019, 1865, 1410-1420.	3.8	16
26	High Resolution Structure of Bacteriorhodopsin Determined by Electron Crystallography. <i>Photochemistry and Photobiology</i> , 1997, 66, 764-767.	2.5	15
27	Biochemical and morphological classification of disease-associated alpha-synuclein mutants aggregates. <i>Biochemical and Biophysical Research Communications</i> , 2019, 508, 729-734.	2.1	14
28	Two-dimensional crystallization and analysis of projection images of intact <i>Thermus thermophilus</i> V-ATPase. <i>Journal of Structural Biology</i> , 2006, 153, 200-206.	2.8	11
29	Visualization of two distinct states of disassembly in the bacterial V-ATPase from <i>Thermus thermophilus</i> . <i>Microscopy (Oxford, England)</i> , 2013, 62, 467-474.	1.5	11
30	Mechanical inhibition of isolated Vo from V/A-ATPase for proton conductance. <i>ELife</i> , 2020, 9, .	6.0	11
31	Cryo-EM studies of the rotary H ⁺ -ATPase/synthase from <i>Thermus thermophilus</i> . <i>Biophysics and Physicobiology</i> , 2019, 16, 140-146.	1.0	8
32	A new technique to co-localise membrane proteins with Homer/vesl. <i>Biochemical and Biophysical Research Communications</i> , 2002, 295, 756-765.	2.1	5
33	Chapter 2 The aquaporin superfamily: Structure and function. <i>Current Topics in Membranes</i> , 2001, 51, 39-119.	0.9	3
34	Molecular basis of water selectivity on aquaporin-1. <i>Kidney International</i> , 2001, 60, 399.	5.2	1
35	Processing of Electron Diffraction Patterns with the XDP Program. <i>Methods in Molecular Biology</i> , 2013, 955, 539-550.	0.9	1
36	Electron Crystallography of a Small Membrane-Bound Enzyme, Microsomal Glutathione Transferase. <i>Microscopy and Microanalysis</i> , 2000, 6, 232-233.	0.4	0

#	ARTICLE	IF	CITATIONS
37	Structure of Bacteriorhodopsin Based on Electron Crystallography at 3.0 .ANGS. Resolution.. Seibutsu Butsuri, 1999, 39, 148-153.	0.1	0