

# Mamoru Suzuki

## List of Publications by Year in descending order

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97  
papers

5,408  
citations

94269

37  
h-index

82410

72  
g-index

121  
all docs

121  
docs citations

121  
times ranked

5906  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of thaumatin under acidic conditions: Structural insight into the conformations in lysine residues responsible for maintaining the sweetness after heat-treatment. <i>Food Chemistry</i> , 2022, 389, 132996.	4.2	1
2	Capturing structural changes of the S <sub>1</sub> to S <sub>2</sub> transition of photosystem II using time-resolved serial femtosecond crystallography. <i>IUCr</i> , 2021, 8, 431-443.	1.0	24
3	Crystal structure of the C-terminal domain of envelope protein VP37 from white spot syndrome virus reveals sulphate binding sites responsible for heparin binding. <i>Journal of General Virology</i> , 2021, 102, .	1.3	4
4	Microcrystal preparation for serial femtosecond X-ray crystallography of bacterial copper amine oxidase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 356-363.	0.4	2
5	Neutron crystallography of copper amine oxidase reveals keto/enolate interconversion of the quinone cofactor and unusual proton sharing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10818-10824.	3.3	11
6	Viscosity-adjustable grease matrices for serial nanocrystallography. <i>Scientific Reports</i> , 2020, 10, 1371.	1.6	10
7	Subatomic structure of hyper-sweet thaumatin D21N mutant reveals the importance of flexible conformations for enhanced sweetness. <i>Biochimie</i> , 2019, 157, 57-63.	1.3	8
8	X-Ray Crystallographic Structure of <i>Hericium erinaceus</i> Ribonuclease, RNase He1 in Complex with Zinc. <i>Biological and Pharmaceutical Bulletin</i> , 2019, 42, 2054-2061.	0.6	1
9	Positive Charges on the Surface of Thaumatin Are Crucial for the Multi-Point Interaction with the Sweet Receptor. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 10.	1.6	10
10	Immunoglobulin-like domains of the cargo proteins are essential for protein stability during secretion by the type IX secretion system. <i>Molecular Microbiology</i> , 2018, 110, 64-81.	1.2	11
11	Light-induced structural changes and the site of O=O bond formation in PSII caught by XFEL. <i>Nature</i> , 2017, 543, 131-135.	13.7	515
12	Hydroxyethyl cellulose matrix applied to serial crystallography. <i>Scientific Reports</i> , 2017, 7, 703.	1.6	74
13	XFEL structures of the influenza M2 proton channel: Room temperature water networks and insights into proton conduction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13357-13362.	3.3	64
14	Molecular structure of a prostaglandin D synthase requiring glutathione from the brown planthopper, <i>Nilaparvata lugens</i> . <i>Biochemical and Biophysical Research Communications</i> , 2017, 492, 166-171.	1.0	6
15	Atomic resolution structure of serine protease proteinase K at ambient temperature. <i>Scientific Reports</i> , 2017, 7, 45604.	1.6	25
16	Experimental phase determination with selenomethionine or mercury-derivatization in serial femtosecond crystallography. <i>IUCr</i> , 2017, 4, 639-647.	1.0	24
17	XFEL structures of the influenza M2 proton channel at 1.4 Å: room-temperature water networks and insights into proton conduction. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a40-a40.	0.0	0
18	Oil-free hyaluronic acid matrix for serial femtosecond crystallography. <i>Scientific Reports</i> , 2016, 6, 24484.	1.6	46

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19	Membrane protein structure determination by SAD, SIR, or SIRAS phasing in serial femtosecond crystallography using an iododetergent. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13039-13044.	3.3	43
20	Structural characterization of an aldo-keto reductase (AKR2E5) from the silkworm <i>Bombyx mori</i> . <i>Biochemical and Biophysical Research Communications</i> , 2016, 474, 104-110.	1.0	13
21	Redox-coupled structural changes in nitrite reductase revealed by serial femtosecond and microfocus crystallography. <i>Journal of Biochemistry</i> , 2016, 159, 527-538.	0.9	26
22	Redox-coupled proton transfer mechanism in nitrite reductase revealed by femtosecond crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2928-2933.	3.3	88
23	Crystal structure of afadin PDZ domain-nectin-3 complex shows the structural plasticity of the ligand-binding site. <i>Protein Science</i> , 2015, 24, 376-385.	3.1	14
24	An isomorphous replacement method for efficient de novo phasing for serial femtosecond crystallography. <i>Scientific Reports</i> , 2015, 5, 14017.	1.6	54
25	Native sulfur/chlorine SAD phasing for serial femtosecond crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2519-2525.	2.5	51
26	Diverse application platform for hard X-ray diffraction in SACLA (DAPHNIS): application to serial protein crystallography using an X-ray free-electron laser. <i>Journal of Synchrotron Radiation</i> , 2015, 22, 532-537.	1.0	80
27	Effect of the replacement of aspartic acid/glutamic acid residues with asparagine/glutamine residues in RNase He1 from <i>Hericium erinaceus</i> on inhibition of human leukemia cell line proliferation. <i>Bioscience, Biotechnology and Biochemistry</i> , 2015, 79, 211-217.	0.6	6
28	Grease matrix as a versatile carrier of proteins for serial crystallography. <i>Nature Methods</i> , 2015, 12, 61-63.	9.0	193
29	Radically Different Thioredoxin Domain Arrangement of ERp46, an Efficient Disulfide Bond Introducer of the Mammalian PDI Family. <i>Structure</i> , 2014, 22, 431-443.	1.6	49
30	<i>In vivo</i> crystallography at X-ray free-electron lasers: the next generation of structural biology?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130497.	1.8	39
31	X-Ray Crystallographic Structure of RNase Po1 That Exhibits Anti-tumor Activity. <i>Biological and Pharmaceutical Bulletin</i> , 2014, 37, 968-978.	0.6	6
32	Synergistic cooperation of PDI family members in peroxiredoxin 4-driven oxidative protein folding. <i>Scientific Reports</i> , 2013, 3, 2456.	1.6	118
33	New insights into the catalytic mechanism of <i>Bombyx mori</i> prostaglandin E synthase gained from structure-function analysis. <i>Biochemical and Biophysical Research Communications</i> , 2013, 440, 762-767.	1.0	9
34	Three-dimensional structure of a <i>Bombyx mori</i> Omega-class glutathione transferase. <i>Biochemical and Biophysical Research Communications</i> , 2013, 438, 588-593.	1.0	18
35	Crystal structure of a <i>Bombyx mori</i> sigma-class glutathione transferase exhibiting prostaglandin E synthase activity. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2013, 1830, 3711-3718.	1.1	17
36	A new protein complex promoting the assembly of Rad51 filaments. <i>Nature Communications</i> , 2013, 4, 1676.	5.8	91

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37	High-resolution crystal structure of copper amine oxidase from <i>Arthrobacter globiformis</i> : assignment of bound diatomic molecules as O <sub>2</sub> . Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2483-2494.	2.5	17
38	Crystallographic Analysis Reveals Octamerization of Viroplasm Matrix Protein P9-1 of Rice Black Streaked Dwarf Virus. Journal of Virology, 2012, 86, 746-756.	1.5	43
39	Structural flexibility regulates phosphopeptide-binding activity of the tyrosine kinase binding domain of Cbl-c. Journal of Biochemistry, 2012, 152, 487-495.	0.9	9
40	Structural basis for catalytic activity of a silkworm Delta-class glutathione transferase. Biochimica Et Biophysica Acta - General Subjects, 2012, 1820, 1469-1474.	1.1	23
41	Crystal sample pins and a storage cassette system compatible with the protein crystallography beamlines at both the Photon Factory and SPring-8. Journal of Applied Crystallography, 2012, 45, 1156-1161.	1.9	0
42	Beamline AR-NW12A: high-throughput beamline for macromolecular crystallography at the Photon Factory. Journal of Synchrotron Radiation, 2012, 19, 450-454.	1.0	18
43	Structural Basis of an ERAD Pathway Mediated by the ER-Resident Protein Disulfide Reductase ERdj5. Molecular Cell, 2011, 41, 432-444.	4.5	130
44	Refolding, crystallization and preliminary X-ray crystallographic study of the whole extracellular regions of nectins. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 344-348.	0.7	2
45	Crystal Structure of the cis-Dimer of Nectin-1. Journal of Biological Chemistry, 2011, 286, 12659-12669.	1.6	45
46	Crystal Structure of the Cytoplasmic Phosphatase and Tensin Homolog (PTEN)-like Region of <i>Ciona intestinalis</i> Voltage-sensing Phosphatase Provides Insight into Substrate Specificity and Redox Regulation of the Phosphoinositide Phosphatase Activity. Journal of Biological Chemistry, 2011, 286, 23368-23377.	1.6	44
47	Fully Automated Data Collection Using PAM and the Development of PAM-SPACE Reversible Cassettes. , 2010, , .		2
48	High-resolution X-ray crystal structure of bovine H-protein at 0.88 Å resolution. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 698-708.	2.5	9
49	Crystal structures of human Ero1 $\beta$ reveal the mechanisms of regulated and targeted oxidation of PDI. EMBO Journal, 2010, 29, 3330-3343.	3.5	113
50	Crystal structure and enhanced activity of a cutinase-like enzyme from <i>Cryptococcus</i> sp. strain Sâ€². Proteins: Structure, Function and Bioinformatics, 2009, 77, 710-717.	1.5	40
51	Dynamic nature of disulphide bond formation catalysts revealed by crystal structures of DsbB. EMBO Journal, 2009, 28, 779-791.	3.5	74
52	Crystal Structure and Mutational Analysis of Ca <sup>2+</sup> -Independent Type II Antifreeze Protein from Longsnout Poacher, <i>Brachyopsis rostratus</i> . Journal of Molecular Biology, 2008, 382, 734-746.	2.0	66
53	A Pair of Circularly Permuted PDZ Domains Control RseP, the S2P Family Intramembrane Protease of <i>Escherichia coli</i> . Journal of Biological Chemistry, 2008, 283, 35042-35052.	1.6	50
54	Beamline for Biological Macromolecular Assemblies (BL44XU) at SPring-8. AIP Conference Proceedings, 2007, , .	0.3	4

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55	The Crystal Structure of a Virus-like Particle from the Hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> Provides Insight into the Evolution of Viruses. <i>Journal of Molecular Biology</i> , 2007, 368, 1469-1483.	2.0	115
56	Crystal Structure of Bovine Lipoyltransferase in Complex with Lipoyl-AMP. <i>Journal of Molecular Biology</i> , 2007, 371, 222-234.	2.0	28
57	High resolution X-ray structure of triclinic hen egg-white lysozyme at 0.83 Å. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2007, 63, s141-s141.	0.3	0
58	Crystal Structure of the DsbB-DsbA Complex Reveals a Mechanism of Disulfide Bond Generation. <i>Cell</i> , 2006, 127, 789-801.	13.5	233
59	Development of an automated large-scale protein-crystallization and monitoring system for high-throughput protein-structure analyses. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1058-1065.	2.5	62
60	Crystallization and preliminary X-ray crystallographic analysis of Ca <sup>2+</sup> -independent and Ca <sup>2+</sup> -dependent species of the type II antifreeze protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 538-541.	0.7	7
61	Thermal Stabilization of <i>Bacillus subtilis</i> Family-11 Xylanase by Directed Evolution. <i>Journal of Biological Chemistry</i> , 2006, 281, 10236-10242.	1.6	106
62	Refinement of Taka-amylase crystallized in microgravity environment at 1.0 Å resolution. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2006, 62, s123-s123.	0.3	1
63	Using cryoloops for X-ray data collection from protein crystals at room temperature: A simple applicable method. <i>Journal of Crystal Growth</i> , 2005, 281, 592-595.	0.7	3
64	Molecular mechanism of ubiquitin recognition by GGA3 GAT domain. <i>Genes To Cells</i> , 2005, 10, 639-654.	0.5	37
65	Functions and Structures of Xyloglucan Hydrolases Belonging to Glycoside Hydrolase Family 74. <i>Journal of Applied Glycoscience</i> (1999), 2005, 52, 169-176.	0.3	3
66	Efficiency of light atoms on the low energy SAD phasing. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2005, 61, c141-c141.	0.3	0
67	X-ray crystallographic structure of virus like particle from hyperthermophilic archaea <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2005, 61, c235-c235.	0.3	0
68	Development of protein crystallography beamlines at the Photon Factory for automated experiment. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2005, 61, c138-c138.	0.3	0
69	SR beamline for macromolecular assembly crystallography operated by IPR at SPring-8. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2005, 61, c238-c238.	0.3	0
70	Integrated Controlling System and Unified Database for High Throughput Protein Crystallography Experiments. <i>AIP Conference Proceedings</i> , 2004, , .	0.3	0
71	Tandem Repeat of a Seven-Bladed Î <sup>2</sup> -Propeller Domain in Oligoxyloglucan Reducing-End-Specific Cellobiohydrolase. <i>Structure</i> , 2004, 12, 1209-1217.	1.6	45
72	Secure UNIX socket-based controlling system for high-throughput protein crystallography experiments. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 17-20.	1.0	8

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73	Crystallization and preliminary X-ray crystallographic study on a xyloglucan-specific exo- $\beta$ -glucosidase, oligoxyloglucan reducing-end specific cellobiohydrolase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1838-1839.	2.5	6
74	Molecular mechanism of membrane recruitment of GGA by ARF in lysosomal protein transport. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 386-393.	3.6	122
75	Alternate conformations observed in catalytic serine of <i>Bacillus subtilis</i> lipase determined at 1.3 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1168-1174.	2.5	67
76	Structural basis for recognition of acidic-cluster dileucine sequence by GGA1. <i>Nature</i> , 2002, 415, 937-941.	13.7	146
77	Structural basis for the accessory protein recruitment by the $\beta$ -adapin ear domain. <i>Nature Structural Biology</i> , 2002, 9, 527-31.	9.7	34
78	Automatic Weissenberg data collection system for time-resolved protein crystallography. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2001, 467-468, 1367-1371.	0.7	1
79	Rotated-inclined focusing monochromator with simultaneous tuning of asymmetry factor and radius of curvature over a wide wavelength range. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 64-68.	1.0	7
80	Molecular cloning, structural characterization and chromosomal localization of human lipoyltransferase gene. <i>FEBS Journal</i> , 1999, 260, 761-767.	0.2	36
81	Crystal Structure of Human Dopachrome Tautomerase, a Homologue of Macrophage Migration Inhibitory Factor, at 1.54 Å Resolution. <i>Biochemistry</i> , 1999, 38, 3268-3279.	1.2	117
82	High Expression of Macrophage Migration Inhibitory Factor in Human Melanoma Cells and Its Role in Tumor Cell Growth and Angiogenesis. <i>Biochemical and Biophysical Research Communications</i> , 1999, 264, 751-758.	1.0	190
83	Molecular Cloning of Human Dopachrome Tautomerase cDNA: N-terminal Proline Is Essential for Enzyme Activation. <i>Biochemical and Biophysical Research Communications</i> , 1998, 243, 538-544.	1.0	44
84	Crystallization and Preliminary X-Ray Analysis of Human Dopachrome Tautomerase. <i>Journal of Structural Biology</i> , 1997, 120, 105-108.	1.3	16
85	Large-Format Imaging Plate and Weissenberg Camera for Accurate Protein Crystallographic Data Collection Using Synchrotron Radiation. <i>Journal of Synchrotron Radiation</i> , 1997, 4, 136-146.	1.0	14
86	Crystal structure of macrophage migration inhibitory factor from human T lymphocyte at 2.1 Å resolution. <i>FEBS Letters</i> , 1996, 389, 145-148.	1.3	57
87	Identification and immunohistochemical localization of macrophage migration inhibitory factor in human kidney. <i>IUBMB Life</i> , 1996, 40, 1233-1242.	1.5	34
88	Crystal structure of the macrophage migration inhibitory factor from rat liver. <i>Nature Structural Biology</i> , 1996, 3, 259-266.	9.7	173
89	Molecular Structure of Dimeric Magnesium Phenyl Phosphatosulfate. <i>Inorganic Chemistry</i> , 1995, 34, 5388-5389.	1.9	7
90	Crystallization of Rat Liver Macrophage Migration Inhibitory Factor for MAD Analysis. <i>Journal of Structural Biology</i> , 1995, 115, 331-334.	1.3	22

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91	Crystallization and X-ray Studies of the DNA-binding Domain of OmpR Protein, a Positive Regulator Involved in Activation of Osmoregulatory Genes in Escherichia coli. Journal of Molecular Biology, 1994, 235, 780-782.	2.0	12
92	Crystallization and a Preliminary X-ray Diffraction Study of Macrophage Migration Inhibitory Factor from Human Lymphocytes. Journal of Molecular Biology, 1994, 235, 1141-1143.	2.0	19
93	Structure of bis(triethylammonium) phenylphosphonosulfate. Acta Crystallographica Section C: Crystal Structure Communications, 1993, 49, 2119-2121.	0.4	0
94	Crystal structures of ribonuclease HI active site mutants from Escherichia coli.. Journal of Biological Chemistry, 1993, 268, 22092-22099.	1.6	36
95	An automatic diffraction data collection system with an imaging plate. Journal of Applied Crystallography, 1990, 23, 334-339.	1.9	60
96	Peptidyl-prolyl cis-trans isomerase is the cyclosporin A-binding protein cyclophilin. Nature, 1989, 337, 473-475.	13.7	1,098
97	Implementation and evaluation of authorized access LAN sockets using PPPoE. , 0, , .		2