

Masaki Yamamoto

List of Publications by Year in descending order

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192
papers

17,506
citations

28190

55
h-index

13727

129
g-index

202
all docs

202
docs citations

202
times ranked

17477
citing authors

#	ARTICLE	IF	CITATIONS
1	The structure of NLRP9 reveals a unique C-terminal region with putative regulatory function. FEBS Letters, 2022, 596, 876-885.	1.3	4
2	A crystal-processing machine using a deep-ultraviolet laser: application to long-wavelength native SAD experiments. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 88-95.	0.4	1
3	Comparison of six antibody assays and two combination assays for COVID-19. Virology Journal, 2022, 19, 24.	1.4	5
4	Structure-based engineering of a short-chain cis-prenyltransferase to biosynthesize nonnatural all-cis polyisoprenoids: molecular mechanisms for primer substrate recognition and ultimate product chain-length determination. FEBS Journal, 2022, 289, 4602-4621.	2.2	4
5	Macromolecular Crystallography at SPring-8. Nihon Kessho Gakkaishi, 2022, 64, 2-9.	0.0	0
6	In situ crystal data-collection and ligand-screening system at SPring-8. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 241-251.	0.4	7
7	Crystal structure of chalcone synthase, a key enzyme for isoflavonoid biosynthesis in soybean. Proteins: Structure, Function and Bioinformatics, 2021, 89, 126-131.	1.5	6
8	Cryo-EM Structure of the Prostaglandin E Receptor EP4 Coupled to G Protein. Structure, 2021, 29, 252-260.e6.	1.6	32
9	An unprecedented insight into the catalytic mechanism of copper nitrite reductase from atomic-resolution and damage-free structures. Science Advances, 2021, 7, .	4.7	25
10	Evaluation of the data-collection strategy for room-temperature micro-crystallography studied by serial synchrotron rotation crystallography combined with the humid air and glue-coating method. Acta Crystallographica Section D: Structural Biology, 2021, 77, 300-312.	1.1	7
11	Comparison of 12 Molecular Detection Assays for Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). Journal of Molecular Diagnostics, 2021, 23, 164-170.	1.2	29
12	Common architectures in cyanobacteria Prochlorococcus cells visualized by X-ray diffraction imaging using X-ray free electron laser. Scientific Reports, 2021, 11, 3877.	1.6	8
13	XFEL Crystal Structures of Peroxidase Compound II. Angewandte Chemie - International Edition, 2021, 60, 14578-14585.	7.2	18
14	XFEL Crystal Structures of Peroxidase Compound II. Angewandte Chemie, 2021, 133, 14699-14706.	1.6	0
15	Short-lived intermediate in N ₂ O generation by P450 NO reductase captured by time-resolved IR spectroscopy and XFEL crystallography. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	21
16	Guidelines for de novo phasing using multiple small-wedge data collection. Journal of Synchrotron Radiation, 2021, 28, 1284-1295.	1.0	7
17	Structural Basis for the Binding Mechanism of Human Serum Albumin Complexed with Cyclic Peptide Dalbavancin. Journal of Medicinal Chemistry, 2020, 63, 14045-14053.	2.9	13
18	Human adiponectin receptor AdipoR1 assumes closed and open structures. Communications Biology, 2020, 3, 446.	2.0	15

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19	Room-temperature crystallography using a microfluidic protein crystal array device and its application to protein–ligand complex structure analysis. <i>Chemical Science</i> , 2020, 11, 9072-9087.	3.7	18
20	Isoprenoid-chained lipid EROCO17+4: a new matrix for membrane protein crystallization and a crystal delivery medium in serial femtosecond crystallography. <i>Scientific Reports</i> , 2020, 10, 19305.	1.6	16
21	Methods and application of coherent X-ray diffraction imaging of noncrystalline particles. <i>Biophysical Reviews</i> , 2020, 12, 541-567.	1.5	16
22	Crystal structure of pathogenic <i>Staphylococcus aureus</i> lipase complex with the anti-obesity drug orlistat. <i>Scientific Reports</i> , 2020, 10, 5469.	1.6	16
23	Computer-controlled liquid-nitrogen drizzling device for removing frost from cryopreserved crystals. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 616-622.	0.4	5
24	Development of SPACE-II for rapid sample exchange at SPring-8 macromolecular crystallography beamlines. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 155-165.	1.1	12
25	Catalytically important damage-free structures of a copper nitrite reductase obtained by femtosecond X-ray laser and room-temperature neutron crystallography. <i>IUCr</i> , 2019, 6, 761-772.	1.0	24
26	Phagocytosis is mediated by two-dimensional assemblies of the F-BAR protein GAS7. <i>Nature Communications</i> , 2019, 10, 4763.	5.8	31
27	An oxyl/oxo mechanism for oxygen-oxygen coupling in PSII revealed by an x-ray free-electron laser. <i>Science</i> , 2019, 366, 334-338.	6.0	248
28	Upgrade of bending magnet MX beamline BL38B1 at SPring-8. <i>AIP Conference Proceedings</i> , 2019, , .	0.3	0
29	Dimeric structures of quinol-dependent nitric oxide reductases (qNORs) revealed by cryo-electron microscopy. <i>Science Advances</i> , 2019, 5, eaax1803.	4.7	14
30	In crystallo thermodynamic analysis of conformational change of the topaquinone cofactor in bacterial copper amine oxidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 135-140.	3.3	10
31	Ligand binding to human prostaglandin E receptor EP4 at the lipid-bilayer interface. <i>Nature Chemical Biology</i> , 2019, 15, 18-26.	3.9	85
32	Crystal structure of the endogenous agonist-bound prostanoid receptor EP3. <i>Nature Chemical Biology</i> , 2019, 15, 8-10.	3.9	49
33	A temperature-controlled cold-gas humidifier and its application to protein crystals with the humid-air and glue-coating method. <i>Journal of Applied Crystallography</i> , 2019, 52, 699-705.	1.9	9
34	DeepCentering: fully automated crystal centering using deep learning for macromolecular crystallography. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 1361-1366.	1.0	18
35	Low-dose X-ray structure analysis of cytochrome c oxidase utilizing high-energy X-rays. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 912-921.	1.0	16
36	Long-wavelength native-SAD phasing: opportunities and challenges. <i>IUCr</i> , 2019, 6, 373-386.	1.0	22

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37	<i>ZOO</i> : an automatic data-collection system for high-throughput structure analysis in protein microcrystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 138-150.	1.1	156
38	Data Collection Strategy in Protein Micro-crystallography at Synchrotron Facility. <i>Seibutsu Butsuri</i> , 2019, 59, 215-218.	0.0	0
39	Remodeling of the optics for a micro-focusing protein crystallography beamline at SPring-8. , 2019, , .		0
40	Architecture of the complete oxygen-sensing FixL-FixJ two-component signal transduction system. <i>Science Signaling</i> , 2018, 11, .	1.6	38
41	Shot-by-shot characterization of focused X-ray free electron laser pulses. <i>Scientific Reports</i> , 2018, 8, 831.	1.6	20
42	Blue light-excited LOV1 and LOV2 domains cooperatively regulate the kinase activity of full-length phototropin2 from Arabidopsis. <i>Journal of Biological Chemistry</i> , 2018, 293, 963-972.	1.6	17
43	Na ⁺ -mimicking ligands stabilize the inactive state of leukotriene B4 receptor BLT1. <i>Nature Chemical Biology</i> , 2018, 14, 262-269.	3.9	80
44	Crystal Structures of Human Orexin 2 Receptor Bound to the Subtype-Selective Antagonist EMPA. <i>Structure</i> , 2018, 26, 7-19.e5.	1.6	55
45	Structural insights into the subtype-selective antagonist binding to the M2 muscarinic receptor. <i>Nature Chemical Biology</i> , 2018, 14, 1150-1158.	3.9	59
46	Cryogenic Coherent X-ray Diffraction Imaging Techniques for Structural Analyses of Biological Cells and Cellular Organelles. <i>Microscopy and Microanalysis</i> , 2018, 24, 14-15.	0.2	0
47	Molecular Analysis of a <i>bla</i> _{IMP-1} -Harboring Class 3 Integron in Multidrug-Resistant <i>Pseudomonas fulva</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	5
48	Diffraction apparatus and procedure in tomography X-ray diffraction imaging for biological cells at cryogenic temperature using synchrotron X-ray radiation. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 1803-1818.	1.0	10
49	An unprecedented dioxygen species revealed by serial femtosecond rotation crystallography in copper nitrite reductase. <i>IUCr</i> , 2018, 5, 22-31.	1.0	27
50	<i>KAMO</i> : towards automated data processing for microcrystals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 441-449.	1.1	198
51	Crystal structure of a family 80 chitosanase from <i>Mitsuaria chitosanitabida</i> . <i>FEBS Letters</i> , 2017, 591, 540-547.	1.3	22
52	Light-induced structural changes and the site of O=O bond formation in PSII caught by XFEL. <i>Nature</i> , 2017, 543, 131-135.	18.7	515
53	Structural basis for ligand capture and release by the endocytic receptor Apo ER 2. <i>EMBO Reports</i> , 2017, 18, 982-999.	2.0	26
54	Development of a dose-limiting data collection strategy for serial synchrotron rotation crystallography. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 29-41.	1.0	39

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55	A nanosecond time-resolved XFEL analysis of structural changes associated with CO release from cytochrome c oxidase. <i>Science Advances</i> , 2017, 3, e1603042.	4.7	68
56	Capturing an initial intermediate during the P450nor enzymatic reaction using time-resolved XFEL crystallography and caged-substrate. <i>Nature Communications</i> , 2017, 8, 1585.	5.8	74
57	Common structural features of toxic intermediates from $\hat{\pm}$ -synuclein and GroES fibrillogenesis detected using cryogenic coherent X-ray diffraction imaging. <i>Journal of Biochemistry</i> , 2017, 161, 55-65.	0.9	8
58	Protein microcrystallography using synchrotron radiation. <i>IUCr</i> , 2017, 4, 529-539.	1.0	56
59	Experimental phase determination with selenomethionine or mercury-derivatization in serial femtosecond crystallography. <i>IUCr</i> , 2017, 4, 639-647.	1.0	24
60	Coherent X-ray Diffraction Imaging of <i>Cyanidioschyzon merolae</i> . , 2017, , 153-173.		0
61	A nearly on-axis spectroscopic system for simultaneously measuring UV-visible absorption and X-ray diffraction in the SPring-8 structural genomics beamline. <i>Journal of Synchrotron Radiation</i> , 2016, 23, 334-338.	1.0	4
62	SPring-8 BL44XU, beamline designed for structure analysis of large biological macromolecular assemblies. <i>AIP Conference Proceedings</i> , 2016, , .	0.3	6
63	Remote access and automation of SPring-8 MX beamlines. <i>AIP Conference Proceedings</i> , 2016, , .	0.3	23
64	Interspecies Dissemination of a Mobilizable Plasmid Harboring <i>bla_{IMP-19}</i> and the Possibility of Horizontal Gene Transfer in a Single Patient. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 5412-5419.	1.4	17
65	Molecular Mechanism for Conformational Dynamics of Ras-GTP Elucidated from In-Situ Structural Transition in Crystal. <i>Scientific Reports</i> , 2016, 6, 25931.	1.6	42
66	TAKASAGO-6 apparatus for cryogenic coherent X-ray diffraction imaging of biological non-crystalline particles using X-ray free electron laser at SACLA. <i>Review of Scientific Instruments</i> , 2016, 87, 053109.	0.6	27
67	X-ray Crystallographic Structure of Thermophilic Rhodopsin. <i>Journal of Biological Chemistry</i> , 2016, 291, 12223-12232.	1.6	38
68	Specimen preparation for cryogenic coherent X-ray diffraction imaging of biological cells and cellular organelles by using the X-ray free-electron laser at SACLA. <i>Journal of Synchrotron Radiation</i> , 2016, 23, 975-989.	1.0	38
69	Blue Light-excited Light-Oxygen-Voltage-sensing Domain 2 (LOV2) Triggers a Rearrangement of the Kinase Domain to Induce Phosphorylation Activity in Arabidopsis Phototropin1. <i>Journal of Biological Chemistry</i> , 2016, 291, 19975-19984.	1.6	10
70	Taste substance binding elicits conformational change of taste receptor T1r heterodimer extracellular domains. <i>Scientific Reports</i> , 2016, 6, 25745.	1.6	36
71	Cell-free methods to produce structurally intact mammalian membrane proteins. <i>Scientific Reports</i> , 2016, 6, 30442.	1.6	56
72	Structural basis for disruption of claudin assembly in tight junctions by an enterotoxin. <i>Scientific Reports</i> , 2016, 6, 33632.	1.6	85

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73	Radiation Damage-Free Structure of Photosystem II Determined by Femtosecond X-Ray Free Electron Laser Pulses. <i>Nihon Kessho Gakkaishi</i> , 2016, 58, 126-132.	0.0	1
74	An isomorphous replacement method for efficient de novo phasing for serial femtosecond crystallography. <i>Scientific Reports</i> , 2015, 5, 14017.	1.6	54
75	Determination of Damage-free Crystal Structure of an X-ray Sensitive Protein Using XFEL. <i>Nihon Kessho Gakkaishi</i> , 2015, 57, 122-128.	0.0	158
76	Crystal Structure of OXA-58 with the Substrate-Binding Cleft in a Closed State: Insights into the Mobility and Stability of the OXA-58 Structure. <i>PLoS ONE</i> , 2015, 10, e0145869.	1.1	7
77	Coherent X-Ray Diffraction Imaging of Chloroplasts from <i>Cyanidioschyzon merolae</i> by Using X-Ray Free Electron Laser. <i>Plant and Cell Physiology</i> , 2015, 56, 1272-1286.	1.5	56
78	Expression, purification, crystallization, and preliminary X-ray crystallographic studies of the human adiponectin receptors, AdipoR1 and AdipoR2. <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 11-23.	1.2	14
79	A Novel Allosteric Mechanism on Protein-DNA Interactions underlying the Phosphorylation-Dependent Regulation of Ets1 Target Gene Expressions. <i>Journal of Molecular Biology</i> , 2015, 427, 1655-1669.	2.0	22
80	Molecular basis of ligand recognition and transport by glucose transporters. <i>Nature</i> , 2015, 526, 391-396.	13.7	305
81	Structure of the RsbX phosphatase involved in the general stress response of <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1392-1399.	2.5	8
82	A magnetic anti-cancer compound for magnet-guided delivery and magnetic resonance imaging. <i>Scientific Reports</i> , 2015, 5, 9194.	1.6	40
83	Small-angle X-ray scattering analysis reveals the ATP-bound monomeric state of the ATPase domain from the homodimeric MutL endonuclease, a GHKL phosphotransferase superfamily protein. <i>Extremophiles</i> , 2015, 19, 643-656.	0.9	6
84	Crystal structures of the human adiponectin receptors. <i>Nature</i> , 2015, 520, 312-316.	13.7	176
85	Cryogenic coherent x-ray diffraction imaging for biological non-crystalline particles using the KOTŌBUKI-1 diffraction apparatus at SACLA. <i>Journal of Physics B: Atomic, Molecular and Optical Physics</i> , 2015, 48, 184003.	0.6	32
86	Native structure of photosystem II at 1.95 Å resolution viewed by femtosecond X-ray pulses. <i>Nature</i> , 2015, 517, 99-103.	13.7	1,050
87	Changes in Surgical Site Infections after Living Donor Liver Transplantation. <i>PLoS ONE</i> , 2015, 10, e0136559.	1.1	17
88	Crystal structure of a bacterial homologue of SWEET transporters. <i>Cell Research</i> , 2014, 24, 1486-1489.	5.7	71
89	Light-induced Conformational Changes of LOV1 (Light Oxygen Voltage-sensing Domain 1) and LOV2 Relative to the Kinase Domain and Regulation of Kinase Activity in <i>Chlamydomonas</i> Phototropin. <i>Journal of Biological Chemistry</i> , 2014, 289, 413-422.	1.6	40
90	Determination of damage-free crystal structure of an X-ray-sensitive protein using an XFEL. <i>Nature Methods</i> , 2014, 11, 734-736.	9.0	237

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91	Single-shot three-dimensional structure determination of nanocrystals with femtosecond X-ray free-electron laser pulses. <i>Nature Communications</i> , 2014, 5, 4061.	5.8	91
92	<i>IDATEN</i> and <i>G-SITENNO</i> : GUI-assisted software for coherent X-ray diffraction imaging experiments and data analyses at SACLA. <i>Journal of Synchrotron Radiation</i> , 2014, 21, 1378-1383.	1.0	18
93	Current status of protein micro-crystallography at SPring-8. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C333-C333.	0.0	1
94	Clinical characteristics and risk factors of non-Candida fungaemia. <i>BMC Infectious Diseases</i> , 2013, 13, 247.	1.3	20
95	Coherent Diffraction Imaging Analysis of Shape-Controlled Nanoparticles with Focused Hard X-ray Free-Electron Laser Pulses. <i>Nano Letters</i> , 2013, 13, 6028-6032.	4.5	57
96	Achievement of protein micro-crystallography at SPring-8 beamline BL32XU. <i>Journal of Physics: Conference Series</i> , 2013, 425, 012002.	0.3	72
97	Molecular dissection of IZUMO1, a sperm protein essential for sperm-egg fusion. <i>Development (Cambridge)</i> , 2013, 140, 3221-3229.	1.2	102
98	Sagittal focusing of synchrotron radiation X-rays using a winged crystal. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 219-225.	1.0	14
99	SPring-8 BL41XU, a high-flux macromolecular crystallography beamline. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 910-913.	1.0	25
100	Development of an online UV-visible microspectrophotometer for a macromolecular crystallography beamline. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 948-952.	1.0	10
101	KOTOBUKI-1 apparatus for cryogenic coherent X-ray diffraction imaging. <i>Review of Scientific Instruments</i> , 2013, 84, 093705.	0.6	51
102	<i>In silico</i> discovery of small-molecule Ras inhibitors that display antitumor activity by blocking the Ras effector interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8182-8187.	3.3	272
103	Tracking X-ray microscopy for alveolar dynamics in live intact mice. <i>Scientific Reports</i> , 2013, 3, 1304.	1.6	12
104	Post-Transcriptional Regulator Hfq Binds Catalase HPII: Crystal Structure of the Complex. <i>PLoS ONE</i> , 2013, 8, e78216.	1.1	8
105	Abstract 5570: Targeted drug delivery system and magnetic resonance imaging with intrinsic ferromagnetic nano-particle compound.., 2013, , .		0
106	Fast microtomography using bright monochromatic x-rays. <i>Review of Scientific Instruments</i> , 2012, 83, 093704.	0.6	13
107	Molecular characterization of IMP-type metallo- β -lactamases among multidrug-resistant <i>Achromobacter xylosoxidans</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 2110-2113.	1.3	38
108	Crystal sample pins and a storage cassette system compatible with the protein crystallography beamlines at both the Photon Factory and SPring-8. <i>Journal of Applied Crystallography</i> , 2012, 45, 1156-1161.	1.9	0

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109	Micro-crystallography comes of age. <i>Current Opinion in Structural Biology</i> , 2012, 22, 602-612.	2.6	144
110	Crystal structures of the state 1 conformations of the GTP-bound H-Ras protein and its oncogenic G12V and Q61L mutants. <i>FEBS Letters</i> , 2012, 586, 1715-1718.	1.3	66
111	Upgrade of automated sample exchanger SPACE. <i>Journal of Applied Crystallography</i> , 2012, 45, 234-238.	1.9	25
112	Fine-needle capillary mounting for protein microcrystals. <i>Journal of Applied Crystallography</i> , 2012, 45, 785-788.	1.9	3
113	Expression, purification and preliminary X-ray crystallographic analysis of cyanobacterial biliverdin reductase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 313-317.	0.7	4
114	Interspecies dissemination of a novel class 1 integron carrying bla _{MP-19} among <i>Acinetobacter</i> species in Japan. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 2480-2483.	1.3	38
115	Critical Roles of Interactions among Switch I-preceding Residues and between Switch II and Its Neighboring α -Helix in Conformational Dynamics of the GTP-bound Ras Family Small GTPases. <i>Journal of Biological Chemistry</i> , 2011, 286, 15403-15412.	1.6	14
116	The Catalytic Architecture of Leukotriene C4 Synthase with Two Arginine Residues. <i>Journal of Biological Chemistry</i> , 2011, 286, 16392-16401.	1.6	29
117	Present status of SPring-8 macromolecular crystallography beamlines. <i>AIP Conference Proceedings</i> , 2010, , .	0.3	6
118	Improvement in Stability of SPring-8 Standard X-Ray Monochromators with Water-Cooled Crystals. <i>AIP Conference Proceedings</i> , 2010, , .	0.3	3
119	New micro-beam beamline at SPring-8, targeting at protein micro-crystallography. <i>AIP Conference Proceedings</i> , 2010, , .	0.3	18
120	Fully Automated Data Collection Using PAM and the Development of PAM-SPACE Reversible Cassettes. , 2010, , .		2
121	Mapping of the basic amino-acid residues responsible for tubulation and cellular protrusion by the EFC/FBAR domain of pacsin2/Syndapin II. <i>FEBS Letters</i> , 2010, 584, 1111-1118.	1.3	66
122	Crystallization and preliminary X-ray crystallographic analysis of <i>Thermus thermophilus</i> transcription elongation complex bound to Gfh1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 64-68.	0.7	4
123	Crystal structure of bacterial RNA polymerase bound with a transcription inhibitor protein. <i>Nature</i> , 2010, 468, 978-982.	13.7	140
124	Channeling and conformational changes in the heterotetrameric sarcosine oxidase from <i>Corynebacterium</i> sp. U-96. <i>Journal of Biochemistry</i> , 2010, 148, 491-505.	0.9	15
125	Structural Basis for Conformational Dynamics of GTP-bound Ras Protein. <i>Journal of Biological Chemistry</i> , 2010, 285, 22696-22705.	1.6	126
126	Structural Basis of the Catalytic Mechanism Operating in Open-Closed Conformers of Lipocalin Type Prostaglandin D Synthase. <i>Journal of Biological Chemistry</i> , 2009, 284, 22344-22352.	1.6	38

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127	Crystallization and preliminary X-ray analysis of the stress-response PPM phosphatase RsbX from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1128-1130.	0.7	1
128	Development of a shutterless continuous rotation method using an X-ray CMOS detector for protein crystallography. <i>Journal of Applied Crystallography</i> , 2009, 42, 1165-1175.	1.9	19
129	Process of Accumulation of Metal Ions on the Interior Surface of apo-Ferritin: Crystal Structures of a Series of apo-Ferritins Containing Variable Quantities of Pd(II) Ions. <i>Journal of the American Chemical Society</i> , 2009, 131, 5094-5100.	6.6	88
130	Polymerization of Phenylacetylene by Rhodium Complexes within a Discrete Space of apo-Ferritin. <i>Journal of the American Chemical Society</i> , 2009, 131, 6958-6960.	6.6	165
131	High-throughput crystallization-to-structure pipeline at RIKEN SPring-8 Center. <i>Journal of Structural and Functional Genomics</i> , 2008, 9, 21-28.	1.2	25
132	Mail-in data collection at SPring-8 protein crystallography beamlines. <i>Journal of Synchrotron Radiation</i> , 2008, 15, 288-291.	1.0	43
133	Crystallization and preliminary X-ray diffraction analysis of the LOV1 domains of phototropin 1 and 2 from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 617-621.	0.7	3
134	Interaction and Stoichiometry of the Peripheral Stalk Subunits NtpE and NtpF and the N-terminal Hydrophilic Domain of NtpI of <i>Enterococcus hirae</i> V-ATPase. <i>Journal of Biological Chemistry</i> , 2008, 283, 19422-19431.	1.6	25
135	Crystal Structures of Blasticidin S Deaminase (BSD). <i>Journal of Biological Chemistry</i> , 2007, 282, 37103-37111.	1.6	19
136	Beamline for Biological Macromolecular Assemblies (BL44XU) at SPring-8. <i>AIP Conference Proceedings</i> , 2007, , .	0.3	4
137	Curved EFC/F-BAR-Domain Dimers Are Joined End to End into a Filament for Membrane Invagination in Endocytosis. <i>Cell</i> , 2007, 129, 761-772.	13.5	366
138	Dose dependence of radiation damage for protein crystals studied at various X-ray energies. <i>Journal of Synchrotron Radiation</i> , 2007, 14, 4-10.	1.0	64
139	Preliminary X-ray crystallographic study of glucose dehydrogenase from <i>Thermus thermophilus</i> HB8. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 446-448.	0.7	1
140	The 1.48 Å... Resolution Crystal Structure of the Homotetrameric Cytidine Deaminase from Mouse. <i>Biochemistry</i> , 2006, 45, 7825-7833.	1.2	53
141	Structure Basis for Antitumor Effect of Aplyronine A. <i>Journal of Molecular Biology</i> , 2006, 356, 945-954.	2.0	77
142	RIKEN structural genomics beamlines at the SPring-8; high throughput protein crystallography with automated beamline operation. <i>Journal of Structural and Functional Genomics</i> , 2006, 7, 15-22.	1.2	94
143	Beamline Scheduling Software: administration software for automatic operation of the RIKEN structural genomics beamlines at SPring-8. <i>Journal of Synchrotron Radiation</i> , 2005, 12, 380-384.	1.0	60
144	Purification, crystallization and preliminary X-ray diffraction analysis of the Kelch-like motif region of mouse Keap1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 153-155.	0.7	16

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145	Highly polarized electrons from GaAs/GaAsP and InGaAs/AlGaAs strained-layer superlattice photocathodes. <i>Journal of Applied Physics</i> , 2005, 97, 094907.	1.1	70
146	Crystal Structure of M-Ras Reveals a GTP-bound α -State Conformation of Ras Family Small GTPases. <i>Journal of Biological Chemistry</i> , 2005, 280, 31267-31275.	1.6	63
147	A Norovirus Protease Structure Provides Insights into Active and Substrate Binding Site Integrity. <i>Journal of Virology</i> , 2005, 79, 13685-13693.	1.5	70
148	Structural Basis of the Substrate-specific Two-step Catalysis of Long Chain Fatty Acyl-CoA Synthetase Dimer. <i>Journal of Biological Chemistry</i> , 2004, 279, 31717-31726.	1.6	189
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