

Masaki Yamamoto

List of Publications by Year in descending order

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193
papers

17,506
citations

28274

55
h-index

13771

129
g-index

202
all docs

202
docs citations

202
times ranked

17477
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal Structure of Rhodopsin: A G Protein-Coupled Receptor. <i>Science</i> , 2000, 289, 739-745.	12.6	5,486
2	Structural basis of glutamate recognition by a dimeric metabotropic glutamate receptor. <i>Nature</i> , 2000, 407, 971-977.	27.8	1,185
3	Native structure of photosystem II at 1.95Å... resolution viewed by femtosecond X-ray pulses. <i>Nature</i> , 2015, 517, 99-103.	27.8	1,050
4	Light-induced structural changes and the site of O=O bond formation in PSII caught by XFEL. <i>Nature</i> , 2017, 543, 131-135.	27.8	515
5	Structure of the bacterial flagellar protofilament and implications for a switch for supercoiling. <i>Nature</i> , 2001, 410, 331-337.	27.8	480
6	Crystal structure of the RNA-dependent RNA polymerase of hepatitis C virus. <i>Structure</i> , 1999, 7, 1417-1426.	3.3	381
7	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.	28.9	366
8	Structural Analyses of DNA Recognition by the AML1/Runx-1 Runt Domain and Its Allosteric Control by CBF β . <i>Cell</i> , 2001, 104, 755-767.	28.9	317
9	Molecular basis of ligand recognition and transport by glucose transporters. <i>Nature</i> , 2015, 526, 391-396.	27.8	305
10	<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.	7.1	272
11	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.	12.6	248
12	Determination of damage-free crystal structure of an X-ray sensitive protein using an XFEL. <i>Nature Methods</i> , 2014, 11, 734-736.	19.0	237
13	<i>KAMO</i> : towards automated data processing for microcrystals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 441-449.	2.3	198
14	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.	3.4	189
15	Crystal structures of the human adiponectin receptors. <i>Nature</i> , 2015, 520, 312-316.	27.8	176
16	Small-angle X-ray scattering station at the SPring-8 RIKEN beamline. <i>Journal of Applied Crystallography</i> , 2000, 33, 797-800.	4.5	166
17	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.	13.7	165
18	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

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19	<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.	2.3	156
20	Mechanism of c-Myb/C/EBP β Cooperation from Separated Sites on a Promoter. <i>Cell</i> , 2002, 108, 57-70.	28.9	155
21	X-ray Structure of $\hat{1}^2$ -Carbonic Anhydrase from the Red Alga, <i>Porphyridium purpureum</i> , Reveals a Novel Catalytic Site for CO ₂ Hydration. <i>Journal of Biological Chemistry</i> , 2000, 275, 5521-5526.	3.4	151
22	Micro-crystallography comes of age. <i>Current Opinion in Structural Biology</i> , 2012, 22, 602-612.	5.7	144
23	Crystal structure of a repair enzyme of oxidatively damaged DNA, MutM (Fpg), from an extreme thermophile, <i>Thermus thermophilus</i> HB8. <i>EMBO Journal</i> , 2000, 19, 3857-3869.	7.8	141
24	Crystal structure of bacterial RNA polymerase bound with a transcription inhibitor protein. <i>Nature</i> , 2010, 468, 978-982.	27.8	140
25	Structural Basis for Conformational Dynamics of GTP-bound Ras Protein. <i>Journal of Biological Chemistry</i> , 2010, 285, 22696-22705.	3.4	126
26	Crystal structure of N-carbamyl-d-amino acid amidohydrolase with a novel catalytic framework common to amidohydrolases. <i>Structure</i> , 2000, 8, 729-738.	3.3	122
27	Molecular dissection of IZUMO1, a sperm protein essential for sperm-egg fusion. <i>Development (Cambridge)</i> , 2013, 140, 3221-3229.	2.5	102
28	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
29	Single-shot three-dimensional structure determination of nanocrystals with femtosecond X-ray free-electron laser pulses. <i>Nature Communications</i> , 2014, 5, 4061.	12.8	91
30	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.	13.7	88
31	Structural basis for disruption of claudin assembly in tight junctions by an enterotoxin. <i>Scientific Reports</i> , 2016, 6, 33632.	3.3	85
32	Ligand binding to human prostaglandin E receptor EP4 at the lipid-bilayer interface. <i>Nature Chemical Biology</i> , 2019, 15, 18-26.	8.0	85
33	Crystal Structures of 4- $\hat{1}$ -Glucanotransferase from <i>Thermococcus litoralis</i> and Its Complex with an Inhibitor. <i>Journal of Biological Chemistry</i> , 2003, 278, 19378-19386.	3.4	82
34	Na ⁺ -mimicking ligands stabilize the inactive state of leukotriene B ₄ receptor BLT1. <i>Nature Chemical Biology</i> , 2018, 14, 262-269.	8.0	80
35	Structure Basis for Antitumor Effect of Aplyronine A. <i>Journal of Molecular Biology</i> , 2006, 356, 945-954.	4.2	77
36	Capturing an initial intermediate during the P450 _{nor} enzymatic reaction using time-resolved XFEL crystallography and caged-substrate. <i>Nature Communications</i> , 2017, 8, 1585.	12.8	74

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37	Achievement of protein micro-crystallography at SPring-8 beamline BL32XU. <i>Journal of Physics: Conference Series</i> , 2013, 425, 012002.	0.4	72
38	Crystal structure of a bacterial homologue of SWEET transporters. <i>Cell Research</i> , 2014, 24, 1486-1489.	12.0	71
39	Crystal structure combined with genetic analysis of the <i>Thermus thermophilus</i> ribosome recycling factor shows that a flexible hinge may act as a functional switch. <i>Rna</i> , 2000, 6, 1432-1444.	3.5	70
40	Highly polarized electrons from GaAs/GaAsP and InGaAs/AlGaAs strained-layer superlattice photocathodes. <i>Journal of Applied Physics</i> , 2005, 97, 094907.	2.5	70
41	A Norovirus Protease Structure Provides Insights into Active and Substrate Binding Site Integrity. <i>Journal of Virology</i> , 2005, 79, 13685-13693.	3.4	70
42	A nanosecond time-resolved XFEL analysis of structural changes associated with CO release from cytochrome c oxidase. <i>Science Advances</i> , 2017, 3, e1603042.	10.3	68
43	The adoption of a twisted structure of importin- β^2 is essential for the protein-protein interaction required for nuclear transport 1 Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 2000, 302, 251-264.	4.2	66
44	Mapping of the basic amino acid residues responsible for tubulation and cellular protrusion by the EFC/F-actin domain of pacsin2/Syndapin II. <i>FEBS Letters</i> , 2010, 584, 1111-1118.	2.8	66
45	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.	2.8	66
46	Mechanism of metal activation of human hematopoietic prostaglandin D synthase. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 291-296.	8.2	64
47	Dose dependence of radiation damage for protein crystals studied at various X-ray energies. <i>Journal of Synchrotron Radiation</i> , 2007, 14, 4-10.	2.4	64
48	Crystal Structure of M-Ras Reveals a GTP-bound "Off" State Conformation of Ras Family Small GTPases. <i>Journal of Biological Chemistry</i> , 2005, 280, 31267-31275.	3.4	63
49	Crystal Structure of H2-Proteinase from the Venom of <i>Trimeresurus flavoviridis</i> . <i>Journal of Biochemistry</i> , 1996, 119, 49-57.	1.7	62
50	The 1.55 Å resolution structure of <i>Nicotiana glauca</i> SF11-RNase associated with gametophytic self-incompatibility. <i>Journal of Molecular Biology</i> , 2001, 314, 103-112.	4.2	61
51	Sample management system for a vast amount of frozen crystals at SPring-8. <i>Journal of Applied Crystallography</i> , 2004, 37, 867-873.	4.5	61
52	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.	2.4	60
53	Structural insights into the subtype-selective antagonist binding to the M2 muscarinic receptor. <i>Nature Chemical Biology</i> , 2018, 14, 1150-1158.	8.0	59
54	Structural Basis of Leukotriene B4 12-Hydroxydehydrogenase/15-Oxo-prostaglandin 13-Reductase Catalytic Mechanism and a Possible Src Homology 3 Domain Binding Loop. <i>Journal of Biological Chemistry</i> , 2004, 279, 22615-22623.	3.4	58

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55	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.	9.1	57
56	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.	3.1	56
57	Cell-free methods to produce structurally intact mammalian membrane proteins. <i>Scientific Reports</i> , 2016, 6, 30442.	3.3	56
58	Protein microcrystallography using synchrotron radiation. <i>IUCr</i> , 2017, 4, 529-539.	2.2	56
59	Crystal Structures of Human Orexin 2 Receptor Bound to the Subtype-Selective Antagonist EMPA. <i>Structure</i> , 2018, 26, 7-19.e5.	3.3	55
60	An isomorphous replacement method for efficient de novo phasing for serial femtosecond crystallography. <i>Scientific Reports</i> , 2015, 5, 14017.	3.3	54
61	The 1.48 Å... Resolution Crystal Structure of the Homotetrameric Cytidine Deaminase from Mouse. <i>Biochemistry</i> , 2006, 45, 7825-7833.	2.5	53
62	KOTOBUKI-1 apparatus for cryogenic coherent X-ray diffraction imaging. <i>Review of Scientific Instruments</i> , 2013, 84, 093705.	1.3	51
63	Crystal structure of the endogenous agonist-bound prostanoid receptor EP3. <i>Nature Chemical Biology</i> , 2019, 15, 8-10.	8.0	49
64	Crystal Structure of the Pyridoxal 5'-phosphate Dependent L-Methionine S-Methyltransferase from <i>Pseudomonas putida</i> . <i>Journal of Biochemistry</i> , 2000, 128, 349-354.	1.7	47
65	Mail-in data collection at SPring-8 protein crystallography beamlines. <i>Journal of Synchrotron Radiation</i> , 2008, 15, 288-291.	2.4	43
66	Molecular Mechanism for Conformational Dynamics of Ras-GTP Elucidated from In-Situ Structural Transition in Crystal. <i>Scientific Reports</i> , 2016, 6, 25931.	3.3	42
67	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.	3.4	40
68	A magnetic anti-cancer compound for magnet-guided delivery and magnetic resonance imaging. <i>Scientific Reports</i> , 2015, 5, 9194.	3.3	40
69	Development of a dose-limiting data collection strategy for serial synchrotron rotation crystallography. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 29-41.	2.4	39
70	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.	3.4	38
71	Interspecies dissemination of a novel class 1 integron carrying bla _{IMP-19} among <i>Acinetobacter</i> species in Japan. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 2480-2483.	3.0	38
72	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.	3.0	38

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73	X-ray Crystallographic Structure of Thermophilic Rhodopsin. <i>Journal of Biological Chemistry</i> , 2016, 291, 12223-12232.	3.4	38
74	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.	2.4	38
75	Architecture of the complete oxygen-sensing FixL-FixJ two-component signal transduction system. <i>Science Signaling</i> , 2018, 11, .	3.6	38
76	Structure of a new 'aspzincin' metalloendopeptidase from <i>Grifola frondosa</i> : implications for the catalytic mechanism and substrate specificity based on several different crystal forms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 361-368.	2.5	36
77	Taste substance binding elicits conformational change of taste receptor T1r heterodimer extracellular domains. <i>Scientific Reports</i> , 2016, 6, 25745.	3.3	36
78	Trichromatic Concept at SPring-8 RIKEN Beamline I. <i>Journal of Synchrotron Radiation</i> , 1998, 5, 222-225.	2.4	35
79	Cryogenic coherent x-ray diffraction imaging for biological non-crystalline particles using the KOTOBUKI-1 diffraction apparatus at SACLA. <i>Journal of Physics B: Atomic, Molecular and Optical Physics</i> , 2015, 48, 184003.	1.5	32
80	Cryo-EM Structure of the Prostaglandin E Receptor EP4 Coupled to G Protein. <i>Structure</i> , 2021, 29, 252-260.e6.	3.3	32
81	Phagocytosis is mediated by two-dimensional assemblies of the F-BAR protein GAS7. <i>Nature Communications</i> , 2019, 10, 4763.	12.8	31
82	The Catalytic Architecture of Leukotriene C4 Synthase with Two Arginine Residues. <i>Journal of Biological Chemistry</i> , 2011, 286, 16392-16401.	3.4	29
83	Comparison of 12 Molecular Detection Assays for Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). <i>Journal of Molecular Diagnostics</i> , 2021, 23, 164-170.	2.8	29
84	Structure and implications for the thermal stability of phosphopantetheine adenylyltransferase from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 97-104.	2.5	28
85	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.	1.3	27
86	An unprecedented dioxygen species revealed by serial femtosecond rotation crystallography in copper nitrite reductase. <i>IUCr</i> , 2018, 5, 22-31.	2.2	27
87	Structural basis for ligand capture and release by the endocytic receptor Apo ER 2. <i>EMBO Reports</i> , 2017, 18, 982-999.	4.5	26
88	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
89	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.	3.4	25
90	Upgrade of automated sample exchanger SPACE. <i>Journal of Applied Crystallography</i> , 2012, 45, 234-238.	4.5	25

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91	SPring-8 BL41XU, a high-flux macromolecular crystallography beamline. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 910-913.	2.4	25
92	An unprecedented insight into the catalytic mechanism of copper nitrite reductase from atomic-resolution and damage-free structures. <i>Science Advances</i> , 2021, 7, .	10.3	25
93	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.	2.2	24
94	Experimental phase determination with selenomethionine or mercury-derivatization in serial femtosecond crystallography. <i>IUCr</i> , 2017, 4, 639-647.	2.2	24
95	Remote access and automation of SPring-8 MX beamlines. <i>AIP Conference Proceedings</i> , 2016, , .	0.4	23
96	Trichromatic Concept Optimizes MAD Experiments in Synchrotron X-Ray Crystallography. <i>Structure</i> , 2002, 10, 1205-1210.	3.3	22
97	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.	4.2	22
98	Crystal structure of a family 80 chitosanase from <i>Mitsuaria chitosanitabida</i> . <i>FEBS Letters</i> , 2017, 591, 540-547.	2.8	22
99	Long-wavelength native-SAD phasing: opportunities and challenges. <i>IUCr</i> , 2019, 6, 373-386.	2.2	22
100	A large-area CMOS imager as an X-ray detector for synchrotron radiation experiments. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 347-352.	2.4	21
101	Short-lived intermediate in N ₂ O generation by P450 NO reductase captured by time-resolved IR spectroscopy and XFEL crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	21
102	Fundamental design of the high energy undulator pilot beamline for macromolecular crystallography at the SPring-8. <i>Review of Scientific Instruments</i> , 1995, 66, 1703-1705.	1.3	20
103	Cloning, Expression, Crystallization, and Preliminary X-Ray Analysis of Recombinant Mouse Lipocalin-type Prostaglandin D Synthase, a Somnogen-Producing Enzyme. <i>Journal of Biochemistry</i> , 2003, 133, 29-32.	1.7	20
104	Clinical characteristics and risk factors of non-Candida fungaemia. <i>BMC Infectious Diseases</i> , 2013, 13, 247.	2.9	20
105	Shot-by-shot characterization of focused X-ray free electron laser pulses. <i>Scientific Reports</i> , 2018, 8, 831.	3.3	20
106	Crystal Structures of Blastocidin S Deaminase (BSD). <i>Journal of Biological Chemistry</i> , 2007, 282, 37103-37111.	3.4	19
107	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.	4.5	19
108	Conceptual design of SPring-8 contract beamline for structural biology. <i>Review of Scientific Instruments</i> , 1995, 66, 1833-1835.	1.3	18

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109	New micro-beam beamline at SPring-8, targeting at protein micro-crystallography. AIP Conference Proceedings, 2010, , .	0.4	18
110	<i>IDATEN</i> and <i>G-SITENNO</i> : GUI-assisted software for coherent X-ray diffraction imaging experiments and data analyses at SACLA. Journal of Synchrotron Radiation, 2014, 21, 1378-1383.	2.4	18
111	Room-temperature crystallography using a microfluidic protein crystal array device and its application to protein-ligand complex structure analysis. Chemical Science, 2020, 11, 9072-9087.	7.4	18
112	XFEL Crystal Structures of Peroxidase Compound II. Angewandte Chemie - International Edition, 2021, 60, 14578-14585.	13.8	18
113	DeepCentering: fully automated crystal centering using deep learning for macromolecular crystallography. Journal of Synchrotron Radiation, 2019, 26, 1361-1366.	2.4	18
114	Interspecies Dissemination of a Mobilizable Plasmid Harboring <i>bla</i> _{IMP-19} and the Possibility of Horizontal Gene Transfer in a Single Patient. Antimicrobial Agents and Chemotherapy, 2016, 60, 5412-5419.	3.2	17
115	Blue light-excited LOV1 and LOV2 domains cooperatively regulate the kinase activity of full-length phototropin2 from Arabidopsis. Journal of Biological Chemistry, 2018, 293, 963-972.	3.4	17
116	Changes in Surgical Site Infections after Living Donor Liver Transplantation. PLoS ONE, 2015, 10, e0136559.	2.5	17
117	Standard Transport Channels of X-ray Beamlines at SPring-8. Journal of Synchrotron Radiation, 1998, 5, 1202-1205.	2.4	16
118	Purification, crystallization and preliminary X-ray diffraction analysis of the Kelch-like motif region of mouse Keap1. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 153-155.	0.7	16
119	Isoprenoid-chained lipid EROCO17+4: a new matrix for membrane protein crystallization and a crystal delivery medium in serial femtosecond crystallography. Scientific Reports, 2020, 10, 19305.	3.3	16
120	Methods and application of coherent X-ray diffraction imaging of noncrystalline particles. Biophysical Reviews, 2020, 12, 541-567.	3.2	16
121	Crystal structure of pathogenic Staphylococcus aureus lipase complex with the anti-obesity drug orlistat. Scientific Reports, 2020, 10, 5469.	3.3	16
122	Low-dose X-ray structure analysis of cytochrome <i>c</i> oxidase utilizing high-energy X-rays. Journal of Synchrotron Radiation, 2019, 26, 912-921.	2.4	16
123	Channeling and conformational changes in the heterotetrameric sarcosine oxidase from Corynebacterium sp. U-96. Journal of Biochemistry, 2010, 148, 491-505.	1.7	15
124	Human adiponectin receptor AdipoR1 assumes closed and open structures. Communications Biology, 2020, 3, 446.	4.4	15
125	Critical Roles of Interactions among Switch I-preceding Residues and between Switch II and Its Neighboring I±-Helix in Conformational Dynamics of the GTP-bound Ras Family Small GTPases. Journal of Biological Chemistry, 2011, 286, 15403-15412.	3.4	14
126	Sagittal focusing of synchrotron radiation X-rays using a winged crystal. Journal of Synchrotron Radiation, 2013, 20, 219-225.	2.4	14

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127	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
128	Dimeric structures of quinol-dependent nitric oxide reductases (qNORs) revealed by cryo-electron microscopy. <i>Science Advances</i> , 2019, 5, eaax1803.	10.3	14
129	Fast microtomography using bright monochromatic x-rays. <i>Review of Scientific Instruments</i> , 2012, 83, 093704.	1.3	13
130	Structural Basis for the Binding Mechanism of Human Serum Albumin Complexed with Cyclic Peptide Dalbavancin. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 14045-14053.	6.4	13
131	Cryocrystallography of 3-Isopropylmalate Dehydrogenase from <i>Thermus thermophilus</i> and its Chimeric Enzyme. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 623-630.	2.5	12
132	Tracking X-ray microscopy for alveolar dynamics in live intact mice. <i>Scientific Reports</i> , 2013, 3, 1304.	3.3	12
133	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.	2.3	12
134	Development of an online UV-visible microspectrophotometer for a macromolecular crystallography beamline. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 948-952.	2.4	10
135	Blue Light-excited Light-Oxygen-Voltage-sensing Domain 2 (LOV2) Triggers a Rearrangement of the Kinase Domain to Induce Phosphorylation Activity in <i>Arabidopsis</i> Phototropin1. <i>Journal of Biological Chemistry</i> , 2016, 291, 19975-19984.	3.4	10
136	<i>In crystallo</i> 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.	7.1	10
137	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.	2.4	10
138	A multiple-CCD X-ray detector and its basic characterization. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 6-18.	2.4	9
139	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.	4.5	9
140	Crystals of ternary protein-DNA complexes composed of DNA-binding domains of c-Myb or v-Myb, C/EBP1 \pm or C/EBP1 2 and tom-1A promoter fragment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1655-1658.	2.5	8
141	Post-Transcriptional Regulator Hfq Binds Catalase HPII: Crystal Structure of the Complex. <i>PLoS ONE</i> , 2013, 8, e78216.	2.5	8
142	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
143	Common structural features of toxic intermediates from I \pm -synuclein and GroES fibrillogenesis detected using cryogenic coherent X-ray diffraction imaging. <i>Journal of Biochemistry</i> , 2017, 161, 55-65.	1.7	8
144	Common architectures in cyanobacteria <i>Prochlorococcus</i> cells visualized by X-ray diffraction imaging using X-ray free electron laser. <i>Scientific Reports</i> , 2021, 11, 3877.	3.3	8

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145	Evaluation of high spatial resolution imaging plate. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 1998, 416, 314-318.	1.6	7
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