Takashi Kumasaka

List of Publications by Year
in descending order

168	12,973	76326 40	22832 112
papers	citations	h-index	g-index

172	172	172	13472
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Crystal Structure of Rhodopsin: A G Protein-Coupled Receptor. Science, 2000, 289, 739-745.	12.6	5,486
2	Structural basis of glutamate recognition by a dimeric metabotropic glutamate receptor. Nature, 2000, 407, 971-977.	27.8	1,185
3	Self-assembly of tetravalent Goldberg polyhedra from 144 small components. Nature, 2016, 540, 563-566.	27.8	489
4	Structure of the bacterial flagellar protofilament and implications for a switch for supercoiling. Nature, 2001, 410, 331-337.	27.8	480
5	Crystal structure of an orthologue of the NaChBac voltage-gated sodium channel. Nature, 2012, 486, 130-134.	27.8	439
6	Structural Analyses of DNA Recognition by the AML1/Runx-1 Runt Domain and Its Allosteric Control by CBFÎ². Cell, 2001, 104, 755-767.	28.9	317
7	In silico discovery of small-molecule Ras inhibitors that display antitumor activity by blocking the Rasâ€“effector interaction. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8182-8187.	7.1	272
8	An oxyl/oxo mechanism for oxygen-oxygen coupling in PSII revealed by an x-ray free-electron laser. Science, 2019, 366, 334-338.	12.6	248
9	Self-Assembly of M 30 L 60 Icosidodecahedron. CheM, 2016, 1, 91-101.	11.7	246
10	Protein encapsulation within synthetic molecular hosts. Nature Communications, 2012, 3, 1093.	12.8	208
11	Small-angle X-ray scattering station at the SPring-8 RIKEN beamline. Journal of Applied Crystallography, 2000, 33, 797-800.	4.5	166
12	ZOO: an automatic data-collection system for high-throughput structure analysis in protein microcrystallography. Acta Crystallographica Section D: Structural Biology, 2019, 75, 138-150.	2.3	156
13	Mechanism of c-Mybâ€“C/EBPÎ² Cooperation from Separated Sites on a Promoter. Cell, 2002, 108, 57-70.	28.9	155
14	X-ray Structure of Î²-Carbonic Anhydrase from the Red Alga,Porphyridium purpureum, Reveals a Novel Catalytic Site for CO2 Hydration. Journal of Biological Chemistry, 2000, 275, 5521-5526.	3.4	151
15	Crystal structure of a repair enzyme of oxidatively damaged DNA, MutM (Fpg), from an extreme thermophile,Thermus thermophilusHB8. EMBO Journal, 2000, 19, 3857-3869.	7.8	141
16	Structural Basis for Conformational Dynamics of GTP-bound Ras Protein. Journal of Biological Chemistry, 2010, 285, 22696-22705.	3.4	126
17	Crystal structure of N-carbamyl-d-amino acid amidohydrolase with a novel catalytic framework common to amidohydrolases. Structure, 2000, 8, 729-738.	3.3	122
18	RIKEN structural genomics beamlines at the SPring-8; high throughput protein crystallography with automated beamline operation. Journal of Structural and Functional Genomics, 2006, 7, 15-22.	1.2	94

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19	Crystal Structures of 4-Î±-Glucanotransferase from Thermococcus litoralis and Its Complex with an Inhibitor. Journal of Biological Chemistry, 2003, 278, 19378-19386.	3.4	82
20	Crystal structure of Hfq from Bacillus subtilis in complex with SELEX-derived RNA aptamer: insight into RNA-binding properties of bacterial Hfq. Nucleic Acids Research, 2012, 40, 1856-1867.	14.5	78
21	High-resolution X-ray analysis reveals binding of arginine to aromatic residues of lysozyme surface: implication of suppression of protein aggregation by arginine. Protein Engineering, Design and Selection, 2011, 24, 269-274.	2.1	75
22	Achievement of protein micro-crystallography at SPring-8 beamline BL32XU. Journal of Physics: Conference Series, 2013, 425, 012002.	0.4	72
23	Crystal structure combined with genetic analysis of the Thermus thermophilus ribosome recycling factor shows that a flexible hinge may act as a functional switch. Rna, 2000, 6, 1432-1444.	3.5	70
24	A Norovirus Protease Structure Provides Insights into Active and Substrate Binding Site Integrity. Journal of Virology, 2005, 79, 13685-13693.	3.4	70
25	A nanosecond time-resolved XFEL analysis of structural changes associated with CO release from cytochrome c oxidase. Science Advances, 2017, 3, e1603042.	10.3	68
26	The adoption of a twisted structure of importin-Î² is essential for the protein-protein interaction required for nuclear transport 1 1Edited by K. Nagai. Journal of Molecular Biology, 2000, 302, 251-264.	4.2	66
27	Crystal structures of the state 1 conformations of the GTPâ€bound Hâ€Ras protein and its oncogenic G12V and Q61L mutants. FEBS Letters, 2012, 586, 1715-1718.	2.8	66
28	Mechanism of metal activation of human hematopoietic prostaglandin D synthase. Nature Structural and Molecular Biology, 2003, 10, 291-296.	8.2	64
29	The 1.55 Ã… resolution structure of Nicotiana alata SF11-RNase associated with gametophytic self-incompatibility. Journal of Molecular Biology, 2001, 314, 103-112.	4.2	61
30	Sample management system for a vast amount of frozen crystals at SPring-8. Journal of Applied Crystallography, 2004, 37, 867-873.	4.5	61
31	Beamline Scheduling Software: administration software for automatic operation of the RIKEN structural genomics beamlines at SPring-8. Journal of Synchrotron Radiation, 2005, 12, 380-384.	2.4	60
32	Structural basis of the substrate subsite and the highly thermal stability of xylanase 10B from Thermotoga maritima MSB8. Proteins: Structure, Function and Bioinformatics, 2005, 61, 999-1009.	2.6	59
33	Structural Basis of Leukotriene B4 12-Hydroxydehydrogenase/15-Oxo-prostaglandin 13-Reductase Catalytic Mechanism and a Possible Src Homology 3 Domain Binding Loop. Journal of Biological Chemistry, 2004, 279, 22615-22623.	3.4	58
34	Protein microcrystallography using synchrotron radiation. IUCrJ, 2017, 4, 529-539.	2.2	56
35	The 1.3 Ã… crystal structure of a novel endoâ€Î²â€1,3â€glucanase of glycoside hydrolase family 16 from alkaliphilic Nocardiopsis sp. strain F96. Proteins: Structure, Function and Bioinformatics, 2007, 69, 683-690.	2.6	55
36	A rapid and robust method for selective isotope labeling of proteins. Methods, 2011, 55, 370-378.	3.8	55

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37	The 1.48 Ã... Resolution Crystal Structure of the Homotetrameric Cytidine Deaminase from Mouseâ€¡. Biochemistry, 2006, 45, 7825-7833.	2.5	53
38	Crystal structures of RsbQ, a stress-response regulator in Bacillus subtilis. Protein Science, 2005, 14, 558-565.	7.6	49
39	Structural Insight into Modest Binding of a Non-PXXP Ligand to the Signal Transducing Adaptor Molecule-2 Src Homology 3 Domain. Journal of Biological Chemistry, 2003, 278, 48162-48168.	3.4	47
40	Mail-in data collection at SPring-8 protein crystallography beamlines. Journal of Synchrotron Radiation, 2008, 15, 288-291.	2.4	43
41	Molecular Mechanism for Conformational Dynamics of RasÂ·GTP Elucidated from In-Situ Structural Transition in Crystal. Scientific Reports, 2016, 6, 25931.	3.3	42
42	Development of a dose-limiting data collection strategy for serial synchrotron rotation crystallography. Journal of Synchrotron Radiation, 2017, 24, 29-41.	2.4	39
43	Structural Basis of the Catalytic Mechanism Operating in Open-Closed Conformers of Lipocalin Type Prostaglandin D Synthase. Journal of Biological Chemistry, 2009, 284, 22344-22352.	3.4	38
44	Structure of a new `aspzincin' metalloendopeptidase fromGrifola frondosa: implications for the catalytic mechanism and substrate specificity based on several different crystal forms. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 361-368.	2.5	36
45	Improvement of Alkaliphily ofBacillusAlkaline Xylanase by Introducing Amino Acid Substitutions Both on Catalytic Cleft and Protein Surface. Bioscience, Biotechnology and Biochemistry, 2009, 73, 965-967.	1.3	36
46	Trichromatic Concept at SPring-8 RIKEN Beamline I. Journal of Synchrotron Radiation, 1998, 5, 222-225.	2.4	35
47	Humidity control and hydrophilic glue coating applied to mounted protein crystals improves X-ray diffraction experiments. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1839-1849.	2.5	35
48	Structural and functional analyses of nucleosome complexes with mouse histone variants TH2a and TH2b, involved in reprogramming. Biochemical and Biophysical Research Communications, 2015, 464, 929-935.	2.1	31
49	Crystal Structures and Enzymatic Properties of a Triamine/Agmatine Aminopropyltransferase from Thermus thermophilus. Journal of Molecular Biology, 2011, 408, 971-986.	4.2	26
50	Upgrade of automated sample exchanger SPACE. Journal of Applied Crystallography, 2012, 45, 234-238.	4.5	25
51	SPring-8 BL41XU, a high-flux macromolecular crystallography beamline. Journal of Synchrotron Radiation, 2013, 20, 910-913.	2.4	25
52	Remote access and automation of SPring-8 MX beamlines. AIP Conference Proceedings, 2016, , .	0.4	23
53	Trichromatic Concept Optimizes MAD Experiments in Synchrotron X-Ray Crystallography. Structure, 2002, 10, 1205-1210.	3.3	22
54	Structural insight of human DEAD-box protein rck/p54 into its substrate recognition with conformational changes. Genes To Cells, 2006, 11, 439-452.	1.2	22

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55	Structure of 2â€deoxyâ€scylloâ€inosose synthase, a key enzyme in the biosynthesis of 2â€deoxystreptamineâ€containing aminoglycoside antibiotics, in complex with a mechanismâ€based inhibitor and NAD⁺. Proteins: Structure, Function and Bioinformatics, 2008, 70, 517-527.	2.6	22
56	Crystal structure of a family 80 chitosanase from Mitsuaria chitosanitabida. FEBS Letters, 2017, 591, 540-547.	2.8	22
57	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, .	7.1	21
58	Cloning, Expression, Crystallization, and Preliminary X-Ray Analysis of Recombinant Mouse Lipocalin-type Prostaglandin D Synthase, a Somnogen-Producing Enzyme. Journal of Biochemistry, 2003, 133, 29-32.	1.7	20
59	Crystal Structures of Blasticidin S Deaminase (BSD). Journal of Biological Chemistry, 2007, 282, 37103-37111.	3.4	19
60	Development of a shutterless continuous rotation method using an X-ray CMOS detector for protein crystallography. Journal of Applied Crystallography, 2009, 42, 1165-1175.	4.5	19
61	Dissection of Hydrogen Bond Interaction Network around an Ironâ€“Sulfur Cluster by Site-Specific Isotope Labeling of Hyperthermophilic Archaeal Rieske-Type Ferredoxin. Journal of the American Chemical Society, 2012, 134, 19731-19738.	13.7	19
62	New micro-beam beamline at SPring-8, targeting at protein micro-crystallography. AIP Conference Proceedings, 2010, , .	0.4	18
63	Structural Features and Functional Dependency on Î²-Clamp Define Distinct Subfamilies of Bacterial Mismatch Repair Endonuclease MutL. Journal of Biological Chemistry, 2016, 291, 16990-17000.	3.4	17
64	A solute-binding protein in the closed conformation induces ATP hydrolysis in a bacterial ATP-binding cassette transporter involved in the import of alginate. Journal of Biological Chemistry, 2017, 292, 15681-15690.	3.4	16
65	Low-dose X-ray structure analysis of cytochrome c oxidase utilizing high-energy X-rays. Journal of Synchrotron Radiation, 2019, 26, 912-921.	2.4	16
66	Glycine amide shielding on the aromatic surfaces of lysozyme: Implication for suppression of protein aggregation. FEBS Letters, 2011, 585, 555-560.	2.8	15
67	Critical Roles of Interactions among Switch I-preceding Residues and between Switch II and Its Neighboring Î±-Helix in Conformational Dynamics of the GTP-bound Ras Family Small GTPases. Journal of Biological Chemistry, 2011, 286, 15403-15412.	3.4	14
68	Structural Basis for Polymer Packing and Solvation Properties of the Organogermanium Crystalline Polymer Propagermanium and Its Derivatives. Journal of Pharmaceutical Sciences, 2015, 104, 2482-2488.	3.3	14
69	Analysis of oscillatory rocking curve by dynamical diffraction in protein crystals. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3634-3639.	7.1	13
70	X-ray dose-dependent structural changes of the [2Fe-2S] ferredoxin from Chlamydomonas reinhardtii. Journal of Biochemistry, 2020, 167, 549-555.	1.7	13
71	ISC-like [2Feâ€“2S] ferredoxin (FdxB) dimer from Pseudomonas putida JCM 20004: structural and electronâ€“nuclear double resonance characterization. Journal of Biological Inorganic Chemistry, 2011, 16, 923-935.	2.6	12
72	Structural analyses of the nucleosome complexes with human testis-specific histone variants, hTh2a and hTh2b. Biophysical Chemistry, 2017, 221, 41-48.	2.8	12

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73	Crystal structure and DNA-binding property of the ATPase domain of bacterial mismatch repair endonuclease MutL from Aquifex aeolicus. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1178-1187.	2.3	12
74	Development of SPACE-II for rapid sample exchange at SPring-8 macromolecular crystallography beamlines. Acta Crystallographica Section D: Structural Biology, 2020, 76, 155-165.	2.3	12
75	Resonance Raman characterization of archaeal and bacterial Rieske protein variants with modified hydrogen bond network around the [2Fe-2S] center. Protein Science, 2006, 15, 2019-2024.	7.6	11
76	A Calcium-Dependent Xylan-Binding Domain of Alkaline Xylanase from AlkaliphilicBacillussp. Strain 41M-1. Bioscience, Biotechnology and Biochemistry, 2011, 75, 379-381.	1.3	11
77	Structure of Cu/Zn superoxide dismutase from the heavy-metal-tolerant yeast Cryptococcus liquefaciens strain N6. Biochemical and Biophysical Research Communications, 2008, 374, 475-478.	2.1	10
78	Crystal structure of 3-isopropylmalate dehydrogenase in complex with NAD+ and a designed inhibitor. Bioorganic and Medicinal Chemistry, 2009, 17, 7789-7794.	3.0	10
79	Assembly of homogeneous norovirus-like particles accomplished by amino acid substitution. Journal of General Virology, 2011, 92, 2320-2323.	2.9	10
80	Development of an online UVâ€“visible microspectrophotometer for a macromolecular crystallography beamline. Journal of Synchrotron Radiation, 2013, 20, 948-952.	2.4	10
81	In crystallo thermodynamic analysis of conformational change of the topaquinone cofactor in bacterial copper amine oxidase. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 135-140.	7.1	10
82	A multiple-CCD X-ray detector and its basic characterization. Journal of Synchrotron Radiation, 1999, 6, 6-18.	2.4	9
83	Cloning and functional characterization of the copper/zinc superoxide dismutase gene from the heavy-metal-tolerant yeast Cryptococcus liquefaciens strain N6. Molecular Genetics and Genomics, 2007, 277, 403-412.	2.1	9
84	Crystallization and preliminary X-ray diffraction studies of the prototypal homologue of mitoNEET (Tth-NEET0026) from the extreme thermophileThermus thermophilusHB8. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 1146-1148.	0.7	9
85	Expression, crystallization and preliminary crystallographic analysis of RNA-binding protein Hfq (YmaH) fromBacillus subtilisin complex with an RNA aptamer. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 563-566.	0.7	9
86	A temperature-controlled cold-gas humidifier and its application to protein crystals with the humid-air and glue-coating method. Journal of Applied Crystallography, 2019, 52, 699-705.	4.5	9
87	Crystals of ternary proteinâ€“DNA complexes composed of DNA-binding domains of c-Myb or v-Myb, C/EBPÎ± or C/EBPÎ² andtom-1A promoter fragment. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1655-1658.	2.5	8
88	Structure of the RsbX phosphatase involved in the general stress response of Bacillus subtilis. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1392-1399.	2.5	8
89	Structural basis for intramolecular interaction of postâ€translationally modified Hâ€Rasâ€¢<scp>GTP</scp> prepared by protein ligation. FEBS Letters, 2017, 591, 2470-2481.	2.8	8
90	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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91	Development of high-speed Imaging Plate detector. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 2001, 467-468, 1160-1162.	1.6	7
92	Crystallization and preliminary X-ray analyses of quaternary, ternary and binary proteinâ€“DNA complexes with involvement of AML1/Runx-1/CBFÎ± Runt domain, CBFÎ² and the C/EBPÎ² bZip region. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 850-853.	2.5	7
93	Crystallization and X-ray analysis of 2-deoxy-scyllo-inososе synthase, the key enzyme in the biosynthesis of 2-deoxystreptamine-containing aminoglycoside antibiotics. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 709-711.	0.7	7
94	Unpaired Electron Spin Density Distribution across Reduced [2Fe-2S] Cluster Ligands by ¹³C_{Î²}-Cysteine Labeling. Inorganic Chemistry, 2018, 57, 741-746.	4.0	7
95	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.	2.3	7
96	Guidelines for de novo phasing using multiple small-wedge data collection. Journal of Synchrotron Radiation, 2021, 28, 1284-1295.	2.4	7
97	Reaction Mechanism and Crystal Structure of 4-.ALPHA.-Glucanotransferase from a Hyperthermophilic Archaeon, Thermococcus litoralis.. Journal of Applied Glycoscience (1999), 2001, 48, 171-175.	0.7	7
98	In situ crystal data-collection and ligand-screening system at SPring-8. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 241-251.	0.8	7
99	Crystallization and preliminary crystallographic analysis of endo-1,3-Î²-glucanase from alkaliphilicNocardiopsisÂsp. strain F96. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 20-22.	0.7	6
100	Contribution of salt bridges to alkaliphily of Bacillusalkaline xylanase. Nucleic Acids Symposium Series, 2007, 51, 461-462.	0.3	6
101	Present status of SPring-8 macromolecular crystallography beamlines. AIP Conference Proceedings, 2010, , .	0.4	6
102	Structure of Thermus thermophilus homoisocitrate dehydrogenase in complex with a designed inhibitor. Journal of Biochemistry, 2011, 150, 607-614.	1.7	6
103	SPring-8 BL44XU, beamline designed for structure analysis of large biological macromolecular assemblies. AIP Conference Proceedings, 2016, , .	0.4	6
104	Structural transition of solvated H-Ras/GTP revealed by molecular dynamics simulation and local network entropy. Journal of Molecular Graphics and Modelling, 2017, 77, 51-63.	2.4	6
105	Multiple zinc ions maintain the open conformation of the catalytic site in the <scp>DNA</scp> mismatch repair endonuclease MutL from Aquifex aeolicus. FEBS Letters, 2018, 592, 1611-1619.	2.8	6
106	Synthetic Diamond Monochromator at SPring-8.. Review of High Pressure Science and Technology/Koatsuryoku No Kagaku To Gijutsu, 2000, 10, 56-61.	0.0	5
107	Structural Analyses of DNA Recognition by the AML1/Runx-1 Runt Domain and Its Allosteric Control by CBFÎ². Cell, 2001, 105, 291.	28.9	5
108	Crystallization and preliminary X-ray studies of xylanase 10B fromThermotoga maritima. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1659-1661.	2.5	5

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109	Crystallization and X-ray analysis of the N-terminal core domain of a tumour-associated human DEAD-box RNA helicase, rck/p54. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 156-159.	2.5	5
110	Crystallization and preliminary X-ray diffraction studies of the hyperthermophilic archaeal sulredoxin having the unique Rieske [2Feâ€“2S] cluster environment. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1487-1489.	2.5	5
111	Expression, purification, crystallization and preliminary X-ray analysis of the Met244Ala variant of catalaseâ€“peroxidase (KatG) from the haloarchaeonHaloarcula marismortui. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 940-943.	0.7	5
112	Crystallization and X-ray analysis of 23â€...nm virus-like particles fromNorovirusChiba strain. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 568-573.	0.8	5
113	Computer-controlled liquid-nitrogen drizzling device for removing frost from cryopreserved crystals. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 616-622.	0.8	5
114	A multiple CCD X-ray detector and its first operation with synchrotron radiation X-ray beam. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 1999, 436, 174-181.	1.6	4
115	The Flexible C-Terminal Region of Aspergillus terreus Blasticidin S Deaminase: Identification of Its Functional Roles with Deletion Enzymes. Biochemical and Biophysical Research Communications, 2002, 290, 421-426.	2.1	4
116	Crystallization and preliminary X-ray diffraction studies of the ISC-like [2Feâ€“2S] ferredoxin (FdxB) fromPseudomonas putidaJCM 20004. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 1014-1016.	0.7	4
117	Crystallization and preliminary X-ray analysis of vicenisaminyltransferase VinC. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 558-560.	0.7	4
118	Crystallization and preliminary X-ray diffraction studies of hyperthermophilic archaeal Rieske-type ferredoxin (ARF) fromSulfolobus solfataricusP1. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 842-845.	0.7	4
119	Glutathione Ethylester, a Novel Protein Refolding Reagent, Enhances both the Efficiency of Refolding and Correct Disulfide Formation. Protein Journal, 2012, 31, 499-503.	1.6	4
120	Alteration of the Î±1Î²2/Î±2Î²1 subunit interface contributes to the increased hemoglobin-oxygen affinity of high-altitude deer mice. PLoS ONE, 2017, 12, e0174921.	2.5	4
121	Crystallization and preliminary X-ray crystallographic analysis of chitinase F1 (ChiF1) from the alkaliphilicNocardiopsissp. strain F96. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2016-2018.	2.5	3
122	Crystallization and preliminary X-ray studies on the reaction centerâ€“light-harvesting 1 core complex fromRhodopseudomonas viridis. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 83-86.	0.7	3
123	Expression, crystallization and preliminary crystallographic analysis of the PAS domain of RsbP, a stress-response phosphatase fromBacillus subtilis. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 559-561.	0.7	3
124	Improvement in Stability of SPring-8 Standard X-Ray Monochromators with Water-Cooled Crystals. AIP Conference Proceedings, 2010, , .	0.4	3
125	Fine-needle capillary mounting for protein microcrystals. Journal of Applied Crystallography, 2012, 45, 785-788.	4.5	3
126	Oncogenic mutations Q61L and Q61H confer active form-like structural features to the inactive state (state 1) conformation of H-Ras protein. Biochemical and Biophysical Research Communications, 2021, 565, 85-90.	2.1	3

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127	Radiation-induced defects in protein crystals observed by X-ray topography. Acta Crystallographica Section D: Structural Biology, 2022, 78, 196-203.	2.3	3
128	Metagenomic mining and structure-function studies of a hyper-thermostable cellobiohydrolase from hot spring sediment. Communications Biology, 2022, 5, 247.	4.4	3
129	Crystal structure of lipocalin-type prostaglandin D synthase. International Congress Series, 2002, 1233, 453-459.	0.2	2
130	Characterization of Nocardiopsis Â-1,3-glucanase with additional carbohydrate-binding domains. Nucleic Acids Symposium Series, 2007, 51, 459-460.	0.3	2
131	Crystallization and preliminary crystallographic analysis of the complex between triiodothyronine and thebbâ€² fragment of rat protein disulfide isomerase. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 476-478.	0.7	2
132	A convenient tool for gas derivatization using fine-needle capillary mounting for protein crystals. Journal of Synchrotron Radiation, 2013, 20, 999-1002.	2.4	2
133	3D Manipulation of Protein Microcrystals with Optical Tweezers for X-ray Crystallography. Journal of Physics: Conference Series, 2013, 425, 012011.	0.4	2
134	A Lynch syndrome-associated mutation at a Bergerat ATP-binding fold destabilizes the structure of the DNA mismatch repair endonuclease MutL. Journal of Biological Chemistry, 2020, 295, 11643-11655.	3.4	2
135	Automated data-processing system for multiple small-wedge data. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a335-a335.	0.1	2
136	Crystallization and Preliminary X-Ray Study of H2-Proteinase from the Venom of Trimeresurus flavoviridis. Journal of Biochemistry, 1995, 117, 929-930.	1.7	1
137	High Throughput Protein Crystallography at RIKEN Structural Genomic Beamlines. AIP Conference Proceedings, 2004, , .	0.4	1
138	Crystallization and preliminary X-ray analysis of the stress-response PPM phosphatase RsbX fromBacillus subtilis. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1128-1130.	0.7	1
139	Crystallization and preliminary X-ray analysis of isopentenyl diphosphate isomerase fromMethanocaldococcus jannaschii. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 101-103.	0.7	1
140	Crystal structures of a subunit of the formylglycinamide ribonucleotide amidotransferase, PurS, fromThermus thermophilus,Sulfolobus tokodaiiandMethanocaldococcus jannaschii. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 627-635.	0.8	1
141	Construction of a supramolecule comprising [2,3,9,10,16,17,23,24-octakis(2,6-dimethylphenoxy)phthalocyaninato]zinc(II) and (5,10,15,20-tetraphenylporphyrinato)zinc(II). IUCrData, 2018, 3, .	0.3	1
142	Trichromatic Concept for Rapid Protein Crystallographic Analysis. Seibutsu Butsuri, 2001, 41, 156-159.	0.1	1
143	Current status of protein micro-crystallography at SPring-8. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C333-C333.	0.1	1
144	SHIKA: a fast and accurate spot finder for raster scan on microfocus beamlines. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C352-C352.	0.1	1

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145	<title>Performance of multiple-CCD x-ray detector system at SPring-8 for protein crystallography</title>. , 1999, , .		0
146	Prospects for X-ray Crystal Structure Analysis of Selenoproteins with SPring-8 Synchrotron Radiation.. Journal of Health Science, 2000, 46, 426-429.	0.9	0
147	An unexpected gift from fungicide metabolism studies: blasticidin S deaminase (BSD) from Aspergillus terreus. Progress in Biotechnology, 2002, , 55-60.	0.2	0
148	Crystallization and preliminary X-ray diffraction studies of a hyperthermophilic Rieske protein variant (SDX-triple) with an engineered rubredoxin-like mononuclear iron site. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 993-995.	0.7	0
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