

Takashi Kumasaka

List of Publications by Year in descending order

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168
papers

12,973
citations

76326

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h-index

22832

112
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172
all docs

172
docs citations

172
times ranked

13472
citing authors

#	ARTICLE	IF	CITATIONS
1	Radiation-induced defects in protein crystals observed by X-ray topography. Acta Crystallographica Section D: Structural Biology, 2022, 78, 196-203.	2.3	3
2	Metagenomic mining and structure-function studies of a hyper-thermostable cellobiohydrolase from hot spring sediment. Communications Biology, 2022, 5, 247.	4.4	3
3	<i>In situ</i> crystal data-collection and ligand-screening system at SPring-8. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 241-251.	0.8	7
4	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
5	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
6	Guidelines for <i>de novo</i> phasing using multiple small-wedge data collection. Journal of Synchrotron Radiation, 2021, 28, 1284-1295.	2.4	7
7	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
8	Novel Insights into the Structural Perturbation Induced by the Oncogenic Mutations, Q61L and Q61H, in Ras State 1. Biophysical Journal, 2020, 118, 42a.	0.5	0
9	X-ray dose-dependent structural changes of the [2Fe-2S] ferredoxin from Chlamydomonas reinhardtii. Journal of Biochemistry, 2020, 167, 549-555.	1.7	13
10	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
11	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
12	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
13	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
14	Upgrade of bending magnet MX beamline BL38B1 at SPring-8. AIP Conference Proceedings, 2019, .	0.4	0
15	<i>In crystallo</i> 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
16	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
17	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
18	<i>ZOO</i> : 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

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19	Remodeling of the optics for a micro-focusing protein crystallography beamline at SPring-8. , 2019, , .		0
20	Unpaired Electron Spin Density Distribution across Reduced [2Fe-2S] Cluster Ligands by ^{13}C -Cysteine Labeling. Inorganic Chemistry, 2018, 57, 741-746.	4.0	7
21	Multiple zinc ions maintain the open conformation of the catalytic site in the <i>DNA</i> mismatch repair endonuclease MutL from <i>Aquifex aeolicus</i> . FEBS Letters, 2018, 592, 1611-1619.	2.8	6
22	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
23	Chemo-mechanical Coupling Mechanism of Rotation of Mammalian F1-ATPase by Static and Dynamic X-ray Crystallographic Studies. Biochimica Et Biophysica Acta - Bioenergetics, 2018, 1859, e83.	1.0	0
24	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
25	Fixed-targets serial crystallography at SPring-8 and SACLA. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a337-a337.	0.1	0
26	Present status of SPring-8 macromolecular crystallography beamlines. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e175-e175.	0.1	0
27	Crystal structure of a family 80 chitosanase from <i>Mitsuaria chitosanitabida</i> . FEBS Letters, 2017, 591, 540-547.	2.8	22
28	Development of a dose-limiting data collection strategy for serial synchrotron rotation crystallography. Journal of Synchrotron Radiation, 2017, 24, 29-41.	2.4	39
29	Structural analyses of the nucleosome complexes with human testis-specific histone variants, hTh2a and hTh2b. Biophysical Chemistry, 2017, 221, 41-48.	2.8	12
30	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
31	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
32	Structural basis for intramolecular interaction of post-translationally modified H-Ras-GTP prepared by protein ligation. FEBS Letters, 2017, 591, 2470-2481.	2.8	8
33	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
34	Crystal structure and DNA-binding property of the ATPase domain of bacterial mismatch repair endonuclease MutL from <i>Aquifex aeolicus</i> . Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1178-1187.	2.3	12
35	Crystallization and X-ray analysis of 23-nm virus-like particles from <i>Norovirus</i> Chiba strain. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 568-573.	0.8	5
36	Alteration of the $\beta_1\beta_2$ subunit interface contributes to the increased hemoglobin-oxygen affinity of high-altitude deer mice. PLoS ONE, 2017, 12, e0174921.	2.5	4

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37	Protein microcrystallography using synchrotron radiation. IUCr, 2017, 4, 529-539.	2.2	56
38	Fixed-target serial crystallography at SACLA. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a341-a341.	0.1	0
39	Automated data-processing system for multiple small-wedge data. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a335-a335.	0.1	2
40	Development of data collections of SPring-8 MX beamlines. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C642-C642.	0.1	0
41	Low-dose X-ray structure analysis of cytochrome oxidase utilizing high-energy X-rays. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C1027-C1027.	0.1	0
42	SPring-8 BL44XU, beamline designed for structure analysis of large biological macromolecular assemblies. AIP Conference Proceedings, 2016, , .	0.4	6
43	Remote access and automation of SPring-8 MX beamlines. AIP Conference Proceedings, 2016, , .	0.4	23
44	Molecular Mechanism for Conformational Dynamics of Ras-GTP Elucidated from In-Situ Structural Transition in Crystal. Scientific Reports, 2016, 6, 25931.	3.3	42
45	Self-assembly of tetravalent Goldberg polyhedra from 144 small components. Nature, 2016, 540, 563-566.	27.8	489
46	Structural Features and Functional Dependency on \hat{I}^2 -Clamp Define Distinct Subfamilies of Bacterial Mismatch Repair Endonuclease MutL. Journal of Biological Chemistry, 2016, 291, 16990-17000.	3.4	17
47	Self-Assembly of M 30 L 60 Icosidodecahedron. Chem, 2016, 1, 91-101.	11.7	246
48	Crystal structures of a subunit of the formylglycinamide ribonucleotide amidotransferase, PurS, from <i>Thermus thermophilus</i> , <i>Sulfolobus tokodaii</i> and <i>Methanocaldococcus jannaschii</i> . Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 627-635.	0.8	1
49	Experimental phasing with serial crystallography at XFEL and synchrotron radiation. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s21-s21.	0.1	0
50	Automated system for data collection and data processing using microcrystals. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s187-s187.	0.1	0
51	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
52	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
53	Structure of the RsbX phosphatase involved in the general stress response of <i>Bacillus subtilis</i> . Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1392-1399.	2.5	8
54	Protein Crystal Mounting Method by Using Humid Air and Hydrophobic Polymer Coating. Nihon Kessho Gakkaishi, 2014, 56, 194-200.	0.0	0

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55	Upgrade of a high flux MX beamline BL41XU at SPring-8. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C331-C331.	0.1	0
56	IPR Beamline for Macromolecular Assemblies at SPring-8 (BL44XU). Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C1684-C1684.	0.1	0
57	Processing of Protein Crystals using by Deep-UV Pulsed Laser. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C334-C334.	0.1	0
58	Current status of protein micro-crystallography at SPring-8. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C333-C333.	0.1	1
59	A new protein crystal mounting method using humid air and glue coating. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C1146-C1146.	0.1	0
60	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
61	Achievement of protein micro-crystallography at SPring-8 beamline BL32XU. Journal of Physics: Conference Series, 2013, 425, 012002.	0.4	72
62	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
63	SPring-8 BL41XU, a high-flux macromolecular crystallography beamline. Journal of Synchrotron Radiation, 2013, 20, 910-913.	2.4	25
64	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
65	Development of an online UV-visible microspectrophotometer for a macromolecular crystallography beamline. Journal of Synchrotron Radiation, 2013, 20, 948-952.	2.4	10
66	<i>In silico</i> discovery of small-molecule Ras inhibitors that display antitumor activity by blocking the Ras-effector interaction. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8182-8187.	7.1	272
67	3D Manipulation of Protein Microcrystals with Optical Tweezers for X-ray Crystallography. Journal of Physics: Conference Series, 2013, 425, 012011.	0.4	2
68	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
69	Dissection of Hydrogen Bond Interaction Network around an Iron-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
70	Protein encapsulation within synthetic molecular hosts. Nature Communications, 2012, 3, 1093.	12.8	208
71	Crystal structure of an orthologue of the NaChBac voltage-gated sodium channel. Nature, 2012, 486, 130-134.	27.8	439
72	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

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73	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
74	Upgrade of automated sample exchanger SPACE. <i>Journal of Applied Crystallography</i> , 2012, 45, 234-238.	4.5	25
75	Fine-needle capillary mounting for protein microcrystals. <i>Journal of Applied Crystallography</i> , 2012, 45, 785-788.	4.5	3
76	Crystallization and preliminary crystallographic analysis of the complex between triiodothyronine and the ϵ^2 fragment of rat protein disulfide isomerase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 476-478.	0.7	2
77	A Calcium-Dependent Xylan-Binding Domain of Alkaline Xylanase from Alkaliphilic <i>Bacillus</i> sp. Strain 41M-1. <i>Bioscience, Biotechnology and Biochemistry</i> , 2011, 75, 379-381.	1.3	11
78	Crystal Structures and Enzymatic Properties of a Triamine/Agmatine Aminopropyltransferase from <i>Thermus thermophilus</i> . <i>Journal of Molecular Biology</i> , 2011, 408, 971-986.	4.2	26
79	A rapid and robust method for selective isotope labeling of proteins. <i>Methods</i> , 2011, 55, 370-378.	3.8	55
80	Glycine amide shielding on the aromatic surfaces of lysozyme: Implication for suppression of protein aggregation. <i>FEBS Letters</i> , 2011, 585, 555-560.	2.8	15
81	ISC-like [2Fe-2S] ferredoxin (FdxB) dimer from <i>Pseudomonas putida</i> JCM 20004: structural and electron nuclear double resonance characterization. <i>Journal of Biological Inorganic Chemistry</i> , 2011, 16, 923-935.	2.6	12
82	Crystallization and preliminary X-ray analysis of isopentenyl diphosphate isomerase from <i>Methanocaldococcus jannaschii</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 101-103.	0.7	1
83	High-resolution X-ray analysis reveals binding of arginine to aromatic residues of lysozyme surface: implication of suppression of protein aggregation by arginine. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 269-274.	2.1	75
84	Assembly of homogeneous norovirus-like particles accomplished by amino acid substitution. <i>Journal of General Virology</i> , 2011, 92, 2320-2323.	2.9	10
85	Structure of <i>Thermus thermophilus</i> homoisocitrate dehydrogenase in complex with a designed inhibitor. <i>Journal of Biochemistry</i> , 2011, 150, 607-614.	1.7	6
86	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.	3.4	14
87	Present status of SPring-8 macromolecular crystallography beamlines. <i>AIP Conference Proceedings</i> , 2010, , .	0.4	6
88	Improvement in Stability of SPring-8 Standard X-Ray Monochromators with Water-Cooled Crystals. <i>AIP Conference Proceedings</i> , 2010, , .	0.4	3
89	New micro-beam beamline at SPring-8, targeting at protein micro-crystallography. <i>AIP Conference Proceedings</i> , 2010, , .	0.4	18
90	Expression, crystallization and preliminary crystallographic analysis of RNA-binding protein Hfq (YmaH) from <i>Bacillus subtilis</i> in complex with an RNA aptamer. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 563-566.	0.7	9

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91	Crystallization and preliminary X-ray diffraction studies of hyperthermophilic archaeal Rieske-type ferredoxin (ARF) from <i>Sulfolobus solfataricus</i> P1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 842-845.	0.7	4
92	Structural Basis for Conformational Dynamics of GTP-bound Ras Protein. <i>Journal of Biological Chemistry</i> , 2010, 285, 22696-22705.	3.4	126
93	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
94	Expression, crystallization and preliminary crystallographic analysis of the PAS domain of RsbP, a stress-response phosphatase from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 559-561.	0.7	3
95	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
96	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
97	Crystal structure of 3-isopropylmalate dehydrogenase in complex with NAD ⁺ and a designed inhibitor. <i>Bioorganic and Medicinal Chemistry</i> , 2009, 17, 7789-7794.	3.0	10
98	Improvement of Alkaliphily of <i>Bacillus</i> Alkaline Xylanase by Introducing Amino Acid Substitutions Both on Catalytic Cleft and Protein Surface. <i>Bioscience, Biotechnology and Biochemistry</i> , 2009, 73, 965-967.	1.3	36
99	Crystallographic analysis of the PAS domain of RsbP, a stress-response phosphatase in <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2009, 65, s140-s140.	0.3	0
100	Structure of 2-deoxy-2,6-diaminocyclohexane-1,3-diol synthase, a key enzyme in the biosynthesis of 2-deoxystreptomycin-containing aminoglycoside antibiotics, in complex with a mechanism-based inhibitor and NAD ⁺ . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 517-527.	2.6	22
101	Mail-in data collection at SPring-8 protein crystallography beamlines. <i>Journal of Synchrotron Radiation</i> , 2008, 15, 288-291.	2.4	43
102	Crystallization and preliminary X-ray analysis of viceniaminyltransferase VinC. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 558-560.	0.7	4
103	Crystallization and preliminary X-ray diffraction studies of the prototypal homologue of mitoNEET (<i>Tth</i>-NEET0026) from the extreme thermophile <i>Thermus thermophilus</i> HB8. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 1146-1148.	0.7	9
104	Structure of Cu/Zn superoxide dismutase from the heavy-metal-tolerant yeast <i>Cryptococcus liquefaciens</i> strain N6. <i>Biochemical and Biophysical Research Communications</i> , 2008, 374, 475-478.	2.1	10
105	Crystal Structures of Blasticidin S Deaminase (BSD). <i>Journal of Biological Chemistry</i> , 2007, 282, 37103-37111.	3.4	19
106	SPring-8 Structural Biology Beamlines / Automatic Beamline Operation at RIKEN Structural Genomics Beamlines. <i>AIP Conference Proceedings</i> , 2007, , .	0.4	0
107	Characterization of <i>Nocardopsis</i> 1,3-glucanase with additional carbohydrate-binding domains. <i>Nucleic Acids Symposium Series</i> , 2007, 51, 459-460.	0.3	2
108	Contribution of salt bridges to alkaliphily of <i>Bacillus</i> alkaline xylanase. <i>Nucleic Acids Symposium Series</i> , 2007, 51, 461-462.	0.3	6

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109	Crystallization and preliminary X-ray diffraction studies of the ISC-like [2Fe-2S] ferredoxin (FdxB) from <i>Pseudomonas putida</i> JCM 20004. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 1014-1016.	0.7	4
110	Expression, purification, crystallization and preliminary X-ray analysis of the Met244Ala variant of catalase-peroxidase (KatG) from the haloarchaeon <i>Haloarcula marismortui</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 940-943.	0.7	5
111	The 1.3 Å... crystal structure of a novel endo-1,3- β -glucanase of glycoside hydrolase family 16 from alkaliphilic <i>Nocardioopsis</i> sp. strain F96. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 683-690.	2.6	55
112	Cloning and functional characterization of the copper/zinc superoxide dismutase gene from the heavy-metal-tolerant yeast <i>Cryptococcus liquefaciens</i> strain N6. <i>Molecular Genetics and Genomics</i> , 2007, 277, 403-412.	2.1	9
113	The 1.48 Å... Resolution Crystal Structure of the Homotetrameric Cytidine Deaminase from Mouse.	2.5	53
114	Crystallization and preliminary crystallographic analysis of endo-1,3- β -glucanase from alkaliphilic <i>Nocardioopsis</i> sp. strain F96. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 20-22.	0.7	6
115	Crystallization and preliminary X-ray diffraction studies of a hyperthermophilic Rieske protein variant (SDX-triple) with an engineered rubredoxin-like mononuclear iron site. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 993-995.	0.7	0
116	Structural insight of human DEAD-box protein rck/p54 into its substrate recognition with conformational changes. <i>Genes To Cells</i> , 2006, 11, 439-452.	1.2	22
117	Resonance Raman characterization of archaeal and bacterial Rieske protein variants with modified hydrogen bond network around the [2Fe-2S] center. <i>Protein Science</i> , 2006, 15, 2019-2024.	7.6	11
118	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
119	Crystal structures of RsbQ, a stress-response regulator in <i>Bacillus subtilis</i> . <i>Protein Science</i> , 2005, 14, 558-565.	7.6	49
120	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
121	Crystallization and preliminary X-ray studies on the reaction center-light-harvesting 1 core complex from <i>Rhodospseudomonas viridis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 83-86.	0.7	3
122	Crystallization and X-ray analysis of 2-deoxy-scyllo-inosose synthase, the key enzyme in the biosynthesis of 2-deoxystreptamine-containing aminoglycoside antibiotics. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 709-711.	0.7	7
123	Structural basis of the substrate subsite and the highly thermal stability of xylanase 10B from <i>Thermotoga maritima</i> MSB8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 999-1009.	2.6	59
124	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
125	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
126	High Throughput Protein Crystallography at RIKEN Structural Genomic Beamlines. <i>AIP Conference Proceedings</i> , 2004, , .	0.4	1

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127	Crystallization and X-ray analysis of the N-terminal core domain of a tumour-associated human DEAD-box RNA helicase, rck/p54. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 156-159.	2.5	5
128	Crystallization and preliminary X-ray diffraction studies of the hyperthermophilic archaeal sulredoxin having the unique Rieske [2Fe ²⁺ 2S] cluster environment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1487-1489.	2.5	5
129	Crystallization and preliminary X-ray crystallographic analysis of chitinase F1 (ChiF1) from the alkaliphilic <i>Nocardia</i> sp. strain F96. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2016-2018.	2.5	3
130	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
131	Crystallization and preliminary X-ray studies of xylanase 10B from <i>Thermotoga maritima</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1659-1661.	2.5	5
132	Mechanism of metal activation of human hematopoietic prostaglandin D synthase. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 291-296.	8.2	64
133	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
134	Structural Insight into Modest Binding of a Non-PXXP Ligand to the Signal Transducing Adaptor Molecule-2 Src Homology 3 Domain. <i>Journal of Biological Chemistry</i> , 2003, 278, 48162-48168.	3.4	47
135	Crystal Structures of 4- β -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
136	Development of Structure Analysis by MAD Method.. <i>Nihon Kessho Gakkaishi</i> , 2003, 45, 14-18.	0.0	0
137	An unexpected gift from fungicide metabolism studies: blasticidin S deaminase (BSD) from <i>Aspergillus terreus</i> . <i>Progress in Biotechnology</i> , 2002, , 55-60.	0.2	0
138	The Flexible C-Terminal Region of <i>Aspergillus terreus</i> Blasticidin S Deaminase: Identification of Its Functional Roles with Deletion Enzymes. <i>Biochemical and Biophysical Research Communications</i> , 2002, 290, 421-426.	2.1	4
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