

Eiki Yamashita

List of Publications by Year in descending order

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136
papers

13,503
citations

61945

43
h-index

21521

114
g-index

154
all docs

154
docs citations

154
times ranked

12492
citing authors

#	ARTICLE	IF	CITATIONS
1	Elucidation of master allostery essential for circadian clock oscillation in cyanobacteria. <i>Science Advances</i> , 2022, 8, eabm8990.	4.7	7
2	Regulation mechanisms of the dual ATPase in KaiC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2119627119.	3.3	5
3	Cooperative regulation of PBI1 and MAPKs controls WRKY45 transcription factor in rice immunity. <i>Nature Communications</i> , 2022, 13, 2397.	5.8	20
4	Theoretical Model of the Far-Red-Light-Adapted Photosystem I Reaction Center of Cyanobacterium <i>Acaryochloris marina</i> Using Chlorophyll <i>d</i> and the Effect of Chlorophyll Exchange. <i>Journal of Physical Chemistry B</i> , 2022, 126, 4009-4021.	1.2	8
5	The 1.3-Å... resolution structure of bovine cytochrome c oxidase suggests a dimerization mechanism. <i>BBA Advances</i> , 2021, 1, 100009.	0.7	9
6	Structure of the far-red light utilizing photosystem I of <i>Acaryochloris marina</i> . <i>Nature Communications</i> , 2021, 12, 2333.	5.8	35
7	Structure and function relationship of OqxB efflux pump from <i>Klebsiella pneumoniae</i> . <i>Nature Communications</i> , 2021, 12, 5400.	5.8	22
8	Critical roles of the CuB site in efficient proton pumping as revealed by crystal structures of mammalian cytochrome c oxidase catalytic intermediates. <i>Journal of Biological Chemistry</i> , 2021, 297, 100967.	1.6	14
9	X-ray structures of catalytic intermediates of cytochrome c oxidase provide insights into its O ₂ activation and unidirectional proton-pump mechanisms. <i>Journal of Biological Chemistry</i> , 2020, 295, 5818-5833.	1.6	21
10	SPring-8 BL44XU, a synchrotron radiation beamline for biological macromolecular assemblies, operated by the Institute for Protein Research, Osaka University. <i>Biophysical Reviews</i> , 2019, 11, 521-523.	1.5	2
11	Observation of unexpected molecular binding activity for Mu phage tail fibre chaperones. <i>Journal of Biochemistry</i> , 2019, 166, 529-535.	0.9	3
12	Phage tail fibre assembly proteins employ a modular structure to drive the correct folding of diverse fibres. <i>Nature Microbiology</i> , 2019, 4, 1645-1653.	5.9	45
13	Structures of the wild-type MexAB-OprM tripartite pump reveal its complex formation and drug efflux mechanism. <i>Nature Communications</i> , 2019, 10, 1520.	5.8	77
14	Monomeric structure of an active form of bovine cytochrome <i>c</i> oxidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19945-19951.	3.3	36
15	Low-dose X-ray structure analysis of cytochrome <i>c</i> oxidase utilizing high-energy X-rays. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 912-921.	1.0	16
16	Cytochrome b6f Complex. , 2019, , 1-9.		0
17	Structure of bovine cytochrome <i>c</i> oxidase in the ligand-free reduced state at neutral pH. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 92-98.	0.4	4
18	Chemo-mechanical Coupling Mechanism of Rotation of Mammalian F1-ATPase by Static and Dynamic X-ray Crystallographic Studies. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, e83.	0.5	0

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19	BpeB, a major resistance-nodulation-cell division transporter from <i>Burkholderia cenocepacia</i> : construct design, crystallization and preliminary structural analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 710-716.	0.4	1
20	Three-dimensional structures of bacteriophage neck subunits are shared in <i>Podoviridae</i> , <i>Siphoviridae</i> and <i>Myoviridae</i> . <i>Genes To Cells</i> , 2018, 23, 528-536.	0.5	15
21	Conformational rearrangements of the C1 ring in KaiC measure the timing of assembly with KaiB. <i>Scientific Reports</i> , 2018, 8, 8803.	1.6	26
22	Structure of the β - μ complex of cyanobacterial F1-ATPase reveals a suppression mechanism of the β subunit on ATP hydrolysis in phototrophs. <i>Biochemical Journal</i> , 2018, 475, 2925-2939.	1.7	13
23	Structural Basis for Selective Binding of Export Cargoes by Exportin-5. <i>Structure</i> , 2018, 26, 1393-1398.e2.	1.6	12
24	X-ray structural analyses of azide-bound cytochrome c oxidases reveal that the H-pathway is critically important for the proton-pumping activity. <i>Journal of Biological Chemistry</i> , 2018, 293, 14868-14879.	1.6	13
25	Complex structure of cytochrome <i>c</i> cytochrome <i>c</i> oxidase reveals a novel protein-protein interaction mode. <i>EMBO Journal</i> , 2017, 36, 291-300.	3.5	107
26	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
27	Structural basis for the assembly of the Ragulator-Rag GTPase complex. <i>Nature Communications</i> , 2017, 8, 1625.	5.8	55
28	Crystal structure of tripartite-type ABC transporter MacB from <i>Acinetobacter baumannii</i> . <i>Nature Communications</i> , 2017, 8, 1336.	5.8	74
29	Structure of bovine cytochrome <i>c</i> oxidase crystallized at a neutral pH using a fluorinated detergent. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 416-422.	0.4	8
30	SPRING-8 BL44XU, beamline designed for structure analysis of large biological macromolecular assemblies. <i>AIP Conference Proceedings</i> , 2016, , .	0.3	6
31	Plant-specific DUF1110 protein from <i>Oryza sativa</i> : expression, purification and crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 480-484.	0.4	6
32	Crystal structures of OprN and OprJ, outer membrane factors of multidrug tripartite efflux pumps of <i>Pseudomonas aeruginosa</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 759-769.	1.5	13
33	Structural basis for the development of SARS 3CL protease inhibitors from a peptide mimic to an azadecaline scaffold. <i>Biopolymers</i> , 2016, 106, 391-403.	1.2	6
34	The Mg ²⁺ -containing Water Cluster of Mammalian Cytochrome c Oxidase Collects Four Pumping Proton Equivalents in Each Catalytic Cycle. <i>Journal of Biological Chemistry</i> , 2016, 291, 23882-23894.	1.6	75
35	A Diffraction-Quality Protein Crystal Processed as an Autophagic Cargo. <i>Molecular Cell</i> , 2015, 58, 186-193.	4.5	43
36	Fused-ring structure of decahydroisoquinolin as a novel scaffold for SARS 3CL protease inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2015, 23, 876-890.	1.4	66

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37	X-ray structure of cyanide-bound bovine heart cytochrome <i>c</i> oxidase in the fully oxidized state at 2.0 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 726-730.	0.4	12
38	Evaluation of transition-state mimics in a superior BACE1 cleavage sequence as peptide-mimetic BACE1 inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2015, 23, 5626-5640.	1.4	9
39	Utilization of light by fucoxanthin-chlorophyll-binding protein in a marine centric diatom, <i>Chaetoceros gracilis</i> . <i>Photosynthesis Research</i> , 2015, 126, 437-447.	1.6	14
40	Atomic-scale origins of slowness in the cyanobacterial circadian clock. <i>Science</i> , 2015, 349, 312-316.	6.0	103
41	Structural and functional analysis of Hikeshi, a new nuclear transport receptor of Hsp70s. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 473-483.	2.5	9
42	Low pH-driven folding of WW45-SARAH domain leads to stabilization of the WW45-Mst2 complex. <i>Journal of Biochemistry</i> , 2015, 158, 181-188.	0.9	3
43	Structural basis for the selective nuclear import of the C2H2 zinc-finger protein Snail by importin β . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1050-1060.	2.5	27
44	X-ray crystal structure of voltage-gated proton channel. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 352-357.	3.6	170
45	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
46	Traffic within the Cytochrome b6 Lipoprotein Complex: Gating of the Quinone Portal. <i>Biophysical Journal</i> , 2014, 107, 1620-1628.	0.2	20
47	An Anhydrous Proton Transfer Pathway in the Cytochrome B6F Complex. <i>Biophysical Journal</i> , 2013, 104, 488a.	0.2	0
48	Methods for Studying Interactions of Detergents and Lipids with α -Helical and β -Barrel Integral Membrane Proteins. <i>Current Protocols in Protein Science</i> , 2013, 74, 29.7.1-29.7.30.	2.8	3
49	Lipid-Induced Conformational Changes within the Cytochrome <i>b</i> ₆ Complex of Oxygenic Photosynthesis. <i>Biochemistry</i> , 2013, 52, 2649-2654.	1.2	33
50	A new protein complex promoting the assembly of Rad51 filaments. <i>Nature Communications</i> , 2013, 4, 1676.	5.8	91
51	Transmembrane signaling and assembly of the cytochrome b6-lipidic charge transfer complex. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2013, 1827, 1295-1308.	0.5	55
52	Crystal structure of the C-terminal domain of Mu phage central spike and functions of bound calcium ion. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 284-291.	1.1	21
53	Quinone-dependent proton transfer pathways in the photosynthetic cytochrome <i>b</i> ₆ complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4297-4302.	3.3	84
54	Crystallization and preliminary X-ray diffraction analysis of human importin β -Snail zinc finger domain complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1049-1051.	0.7	1

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55	Pathways of colicin import: utilization of BtuB, OmpF porin and the TolC drug-export protein. <i>Biochemical Society Transactions</i> , 2012, 40, 1463-1468.	1.6	14
56	Structural flexibility regulates phosphopeptide-binding activity of the tyrosine kinase binding domain of Cbl-c. <i>Journal of Biochemistry</i> , 2012, 152, 487-495.	0.9	9
57	2PT157 X-ray structural analysis of bovine heart cytochrome c oxidase to clarify redox coupled structural changes at H atom level(The 50th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2012, 52, S132.	0.0	0
58	Lipid Binding Sites in Membrane Proteins: Cytochrome BC Complexes. <i>Biophysical Journal</i> , 2011, 100, 383a.	0.2	0
59	Conservation of Lipid Functions in Cytochrome bc Complexes. <i>Journal of Molecular Biology</i> , 2011, 414, 145-162.	2.0	44
60	Membrane proteins in four acts: Function precedes structure determination. <i>Methods</i> , 2011, 55, 415-420.	1.9	8
61	Selective nuclear export mechanism of small RNAs. <i>Current Opinion in Structural Biology</i> , 2011, 21, 101-108.	2.6	31
62	The Q cycle of cytochrome bc complexes: A structure perspective. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2011, 1807, 788-802.	0.5	144
63	Distinguishing between Cl^{+} and O^{2+} as the bridging element between Fe^{3+} and Cu^{2+} in resting-oxidized cytochrome c oxidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 742-744.	2.5	12
64	The host-binding domain of the P2 phage tail spike reveals a trimeric iron-binding structure. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 837-841.	0.7	21
65	Crystallization and preliminary X-ray crystallographic study of the human MST2 SARAH domain. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1403-1405.	0.7	2
66	Crystal Structure of the Cytoplasmic Phosphatase and Tensin Homolog (PTEN)-like Region of <i>Ciona intestinalis</i> Voltage-sensing Phosphatase Provides Insight into Substrate Specificity and Redox Regulation of the Phosphoinositide Phosphatase Activity. <i>Journal of Biological Chemistry</i> , 2011, 286, 23368-23377.	1.6	44
67	Structural insight into maintenance methylation by mouse DNA methyltransferase 1 (Dnmt1). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9055-9059.	3.3	172
68	Bovine cytochrome c oxidase structures enable O^{2-} reduction with minimization of reactive oxygens and provide a proton-pumping gate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7740-7745.	3.3	146
69	The O_2 reduction and proton pumping gate mechanisms of bovine heart cytochrome c oxidase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2010, 1797, 102-103.	0.5	1
70	X-ray structure of the NO-bound CuBin bovine cytochromecoxidase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 251-253.	0.7	18
71	1SE0940 Reaction mechanism of cytochrome c oxidase based on the O_2 analogues-bound structures(1SE Recent Advances in Structural Analyses of Functional Mechanisms Based on Dynamics) <i>Tj ETQq1 1 0.784314 ggBT /Over</i> 2010. 50. S3.	0.0	0
72	Exciton Interactions Between Hemes bn and bp in the Cytochrome b6f Complex. <i>Biophysical Journal</i> , 2010, 98, 564a.	0.2	1

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73	Structure-Function, Stability, and Chemical Modification of the Cyanobacterial Cytochrome b6f Complex from <i>Nostoc</i> sp. PCC 7120. <i>Journal of Biological Chemistry</i> , 2009, 284, 9861-9869.	1.6	96
74	A peroxide bridge between Fe and Cu ions in the O ₂ reduction site of fully oxidized cytochrome c oxidase could suppress the proton pump. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2165-2169.	3.3	132
75	A description of the structural determination procedures of a gap junction channel at 3.5 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 758-766.	2.5	23
76	Structure of the connexin 26 gap junction channel at 3.5 Å resolution. <i>Nature</i> , 2009, 458, 597-602.	13.7	642
77	A High-Resolution Structure of the Pre-microRNA Nuclear Export Machinery. <i>Science</i> , 2009, 326, 1275-1279.	6.0	367
78	The Structure of Rat Liver Vault at 3.5 Angstrom Resolution. <i>Science</i> , 2009, 323, 384-388.	6.0	135
79	Protein Translocation Across Membranes: Components of Outer Membrane Colicin Translocons. <i>Biophysical Journal</i> , 2009, 96, 211a.	0.2	0
80	1P-083 X-ray structural analysis of cytochrome c oxidase in the resting oxidized state at 1.4 Å resolution (Heme proteins, The 47th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2009, 49, S76.	0.0	0
81	2TP1-02 Cytochrome c oxidase crystal in the F intermediate state produced by reoxidation (The 47th Tj ETQq1 1 0.784314 rgBT /Ove	0.0	0
82	A Description of a Structure Determination Procedure of a Gap Junction Channel at 3.5 Å Resolution.. <i>Nihon Kessho Gakkaishi</i> , 2009, 51, 327-333.	0.0	0
83	A vault ribonucleoprotein particle exhibiting 39-fold dihedral symmetry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 525-531.	2.5	16
84	The structure of melon necrotic spot virus determined at 2.8 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 8-13.	0.7	18
85	Crystal structures of the OmpF porin: function in a colicin translocon. <i>EMBO Journal</i> , 2008, 27, 2171-2180.	3.5	130
86	S11.17 A peroxide bridge between the two metals in the dinuclear center of the fully oxidized cytochrome c oxidase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2008, 1777, S69.	0.5	1
87	On the Structural Role of the Aromatic Residue Environment of the Chlorophyll <i>a</i> in the Cytochrome <i>b₆f</i> Complex. <i>Biochemistry</i> , 2008, 47, 3654-3661.	1.2	21
88	Structural Analysis of Arabidopsis CnfU Protein: An Iron-Sulfur Cluster Biosynthetic Scaffold in Chloroplasts. <i>Journal of Molecular Biology</i> , 2008, 381, 160-173.	2.0	22
89	Structure and Function of the Cytochrome <i>b₆f</i> Complex. <i>Photochemistry and Photobiology</i> , 2008, 84, 1349-1358.	1.3	145
90	Structure of human monoamine oxidase A at 2.2 Å resolution: The control of opening the entry for substrates/inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5739-5744.	3.3	485

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91	2P-057 A target recognition mechanism of human Cb1 family ubiquitin E3 ligase(The 46th Annual) Tj ETQq1 1 0.784314 rgBT ₀ /Overlock	0.0	0
92	1P-002 X-ray structure of the vault purified from rat liver(Invited Talk for Early Research in Biophysics) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.0	0
93	1S6-3 Crystal structural analysis using diffraction intensity data collected from many isomorphous protein crystals(1S6 Cutting edge of protein crystallography with synchrotron radiation,The 46th) Tj ETQq1 1 0.784314 rgBTq/Overlock	0.0	0
94	Beamline for Biological Macromolecular Assemblies (BL44XU) at SPring-8. AIP Conference Proceedings, 2007, , .	0.3	4
95	A histidine residue acting as a controlling site for dioxygen reduction and proton pumping by cytochrome c oxidase. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7881-7886.	3.3	109
96	Structure of the Complex of the Colicin E2 R-domain and Its BtuB Receptor. Journal of Biological Chemistry, 2007, 282, 23163-23170.	1.6	54
97	3P105 X-ray structural analysis of catalytic intermediates in bovine heart cytochrome c oxidase(Hemeproteins. Electronic states. Proteins-structure and structure-function) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 497 T	0.0	0
98	The Crystal Structure of a Virus-like Particle from the Hyperthermophilic Archaeon Pyrococcus furiosus Provides Insight into the Evolution of Viruses. Journal of Molecular Biology, 2007, 368, 1469-1483.	2.0	115
99	Structure of the Cytochrome b6f Complex: Quinone Analogue Inhibitors as Ligands of Heme cn. Journal of Molecular Biology, 2007, 370, 39-52.	2.0	130
100	Ultrafast Optical Pump-Probe Studies of the Cytochrome b6f Complex in Solution and Crystalline States. Journal of Physical Chemistry B, 2007, 111, 14405-14410.	1.2	8
101	Structures and physiological roles of 13 integral lipids of bovine heart cytochrome c oxidase. EMBO Journal, 2007, 26, 1713-1725.	3.5	331
102	Crystal Structure of the DsbB-DsbA Complex Reveals a Mechanism of Disulfide Bond Generation. Cell, 2006, 127, 789-801.	13.5	233
103	Crystal structures of the catalytic domain of human stromelysin-1 (MMP-3) and collagenase-3 (MMP-13) with a hydroxamic acid inhibitor SM-25453. Biochemical and Biophysical Research Communications, 2006, 344, 315-322.	1.0	26
104	The Asymmetric IscA Homodimer with an Exposed [2Fe-2S] Cluster Suggests the Structural Basis of the Fe-S Cluster Biosynthetic Scaffold. Journal of Molecular Biology, 2006, 360, 117-132.	2.0	64
105	In Meso Structure of the Cobalamin Transporter, BtuB, at 1.95Å... Resolution. Journal of Molecular Biology, 2006, 364, 716-734.	2.0	94
106	Crystal structures of a multidrug transporter reveal a functionally rotating mechanism. Nature, 2006, 443, 173-179.	13.7	684
107	Absolute configuration of the hydroxyfarnesylethyl group of haem A, determined by X-ray structural analysis of bovine heart cytochrome oxidase using methods applicable at 2.8Å... resolution. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1373-1377.	2.5	7
108	Crystallization and preliminary X-ray analysis of gene product 44 from bacteriophage Mu. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 104-105.	0.7	3

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109	Expression and Molecular Characterization of Spherical Particles Derived from the Genome of the Hyperthermophilic Euryarchaeote <i>Pyrococcus furiosus</i> . <i>Journal of Biochemistry</i> , 2005, 138, 193-199.	0.9	14
110	Crystal Structure of Human T-protein of Glycine Cleavage System at 2.0Å... Resolution and its Implication for Understanding Non-ketotic Hyperglycinemia. <i>Journal of Molecular Biology</i> , 2005, 351, 1146-1159.	2.0	30
111	Structure of the Central Hub of Bacteriophage Mu Baseplate Determined by X-ray Crystallography of gp44. <i>Journal of Molecular Biology</i> , 2005, 352, 976-985.	2.0	29
112	Crystallization and preliminary crystallographic analysis of rat monoamine oxidase A complexed with clorgyline. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 317-319.	2.5	10
113	Scaling of one-shot oscillation images with a reference data set. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 60-63.	1.0	2
114	Structure of Rat Monoamine Oxidase A and Its Specific Recognitions for Substrates and Inhibitors. <i>Journal of Molecular Biology</i> , 2004, 338, 103-114.	2.0	198
115	Crystallization and preliminary crystallographic analysis of the importin-Î²-SREBP-2 complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1866-1868.	2.5	3
116	The Structure of Importin-Î± Bound to SREBP-2: Nuclear Import of a Transcription Factor. <i>Science</i> , 2003, 302, 1571-1575.	6.0	188
117	The low-spin heme of cytochrome c oxidase as the driving element of the proton-pumping process. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15304-15309.	3.3	414
118	Crystal Structure of Bacterial Multi-Drug Efflux Transporter AcrB. <i>Nihon Kessho Gakkaishi</i> , 2003, 45, 256-261.	0.0	2
119	Trichromatic Concept Optimizes MAD Experiments in Synchrotron X-Ray Crystallography. <i>Structure</i> , 2002, 10, 1205-1210.	1.6	22
120	Crystal structure of bacterial multidrug efflux transporter AcrB. <i>Nature</i> , 2002, 419, 587-593.	13.7	893
121	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.	2.0	61
122	Optimization of the energy constant of the methionine S-CâŠbond for X-PLOR refinement of protein structure. <i>Journal of Applied Crystallography</i> , 2001, 34, 80-81.	1.9	2
123	Intermonomer interactions in dimer of bovine heart cytochromecoxidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 941-947.	2.5	18
124	Prospects for X-ray Crystal Structure Analysis of Selenoproteins with SPring-8 Synchrotron Radiation.. <i>Journal of Health Science</i> , 2000, 46, 426-429.	0.9	0
125	X-ray Structure of Î²-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.	1.6	151
126	X-ray structure of azide-bound fully oxidized cytochromecoxidase from bovine heart at 2.9Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 529-535.	2.5	36

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127	Crystallization and preliminary X-ray diffraction studies of a $\hat{1}^2$ -carbonic anhydrase from the red alga <i>Porphyridium purpureum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 210-211.	2.5	4
128	Crystal structure of N-carbamyl-D-amino acid amidohydrolase with a novel catalytic framework common to amidohydrolases. <i>Structure</i> , 2000, 8, 729-738.	1.6	122
129	X-ray Crystal Structure of Bovine Heart Cytochrome c Oxidase.. <i>Seibutsu Butsuri</i> , 2000, 40, 5-12.	0.0	0
130	Structure analysis of bovine heart cytochromecoxidase at 2.8Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 31-45.	2.5	14
131	Redox-Coupled Crystal Structural Changes in Bovine Heart Cytochrome c Oxidase. <i>Science</i> , 1998, 280, 1723-1729.	6.0	1,081
132	The Whole Structure of the 13-Subunit Oxidized Cytochrome c Oxidase at 2.8 Å. <i>Science</i> , 1996, 272, 1136-1144.	6.0	2,143
133	Structures of metal sites of oxidized bovine heart cytochrome c oxidase at 2.8 Å. <i>Science</i> , 1995, 269, 1069-1074.	6.0	1,458
134	Effects of ethyleneglycol chain length of dodecyl polyethyleneglycol monoether on the crystallization of bovine heart cytochrome c oxidase. <i>Journal of Molecular Biology</i> , 1995, 246, 572-575.	2.0	6
135	Biological Supramolecular Crystallography.. <i>Nihon Kessho Gakkaishi</i> , 1994, 36, 294-296.	0.0	0
136	Cytochrome b ₆ f Complex, Core Structure, Spectroscopy, and Function of Heme c _n : n-Side Electron and Proton Transfer Reactions. , 0, , 155-179.		12