

Ken-ichi Miyazono

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6871330/publications.pdf>

Version: 2024-02-01

118
papers

4,096
citations

201674

27
h-index

123424

61
g-index

119
all docs

119
docs citations

119
times ranked

6053
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular Basis of the Core Regulatory Network in ABA Responses: Sensing, Signaling and Transport. <i>Plant and Cell Physiology</i> , 2010, 51, 1821-1839.	3.1	800
2	Structural basis of abscisic acid signalling. <i>Nature</i> , 2009, 462, 609-614.	27.8	490
3	<i>Arabidopsis</i> DREB2A-Interacting Proteins Function as RING E3 Ligases and Negatively Regulate Plant Drought Stress-Responsive Gene Expression. <i>Plant Cell</i> , 2008, 20, 1693-1707.	6.6	477
4	Single-molecule paleoenzymology probes the chemistry of resurrected enzymes. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 592-596.	8.2	182
5	Structure and function of abscisic acid receptors. <i>Trends in Plant Science</i> , 2013, 18, 259-266.	8.8	164
6	Experimental evidence for the thermophilicity of ancestral life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11067-11072.	7.1	153
7	Coordination to divalent cations by calcium-binding proteins studied by FTIR spectroscopy. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 2319-2327.	2.6	106
8	Infrared studies of interaction between metal ions and Ca ²⁺ -binding proteins Marker bands for identifying the types of coordination of the side-chain COO ⁻ groups to metal ions in pike parvalbumin (pI = 4.10). <i>FEBS Letters</i> , 1994, 349, 84-88.	2.8	95
9	Discovery of a novel restriction endonuclease by genome comparison and application of a wheat-germ-based cell-free translation assay: PabI (5'-GTA/C) from the hyperthermophilic archaeon <i>Pyrococcus abyssi</i> . <i>Nucleic Acids Research</i> , 2005, 33, e112-e112.	14.5	84
10	A Secreted Protein with Plant-Specific Cysteine-Rich Motif Functions as a Mannose-Binding Lectin That Exhibits Antifungal Activity. <i>Plant Physiology</i> , 2014, 166, 766-778.	4.8	83
11	Calaxin drives sperm chemotaxis by Ca ²⁺ -mediated direct modulation of a dynein motor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20497-20502.	7.1	80
12	Three-dimensional Structure of AzoR from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 20567-20576.	3.4	75
13	Purification, characterization, and molecular gene cloning of an antifungal protein from <i>Ginkgo biloba</i> seeds. <i>Biological Chemistry</i> , 2007, 388, 273-80.	2.5	70
14	Infrared spectroscopic study of the metal-coordination structures of calcium-binding proteins. <i>Biochemical and Biophysical Research Communications</i> , 2008, 369, 225-239.	2.1	68
15	Expansion of Substrate Specificity and Catalytic Mechanism of Azoreductase by X-ray Crystallography and Site-directed Mutagenesis. <i>Journal of Biological Chemistry</i> , 2008, 283, 13889-13896.	3.4	58
16	Heat Capacity and Entropy Changes of Calmodulin Induced by Calcium Binding. <i>Journal of Biochemistry</i> , 1984, 95, 643-649.	1.7	52
17	Novel protein fold discovered in the PabI family of restriction enzymes. <i>Nucleic Acids Research</i> , 2007, 35, 1908-1918.	14.5	47
18	Crystal Structure and Desulfurization Mechanism of 2-Hydroxybiphenyl-2-sulfinic Acid Desulfinase. <i>Journal of Biological Chemistry</i> , 2006, 281, 32534-32539.	3.4	44

#	ARTICLE	IF	CITATIONS
19	Proteinase Inhibitor from Ginkgo Seeds Is a Member of the Plant Nonspecific Lipid Transfer Protein Gene Family. <i>Plant Physiology</i> , 2008, 146, 1909-1919.	4.8	42
20	Crystal structure of ginkbilobin with homology to the extracellular domain of plant cysteine-rich receptor-like kinases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 247-251.	2.6	41
21	Coordination structures of Ca ²⁺ and Mg ²⁺ in Akazara scallop troponin C in solution. <i>FEBS Journal</i> , 2001, 268, 6284-6290.	0.2	38
22	Cooperative DNA-binding and sequence-recognition mechanism of aristaless and clawless. <i>EMBO Journal</i> , 2010, 29, 1613-1623.	7.8	34
23	Crystal Structures of the Short-Chain Flavin Reductase HpaC from <i>Sulfolobus tokodaii</i> Strain 7 in Its Three States: A NAD(P) ⁺ -Free, NAD ⁺ -Bound, and NADP ⁺ -Bound. <i>Biochemistry</i> , 2006, 45, 5103-5110.	2.5	33
24	Improvement in Quality of Protein Crystals Grown in a High Magnetic Field Gradient. <i>Crystal Growth and Design</i> , 2012, 12, 1141-1150.	3.0	33
25	A sequence-specific DNA glycosylase mediates restriction-modification in <i>Pyrococcus abyssi</i> . <i>Nature Communications</i> , 2014, 5, 3178.	12.8	33
26	Enzymes useful for chiral compound synthesis: structural biology, directed evolution, and protein engineering for industrial use. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 5747-5757.	3.6	30
27	Structural Basis for Cyclization Specificity of Two <i>Azotobacter</i> Type III Polyketide Synthases. <i>Journal of Biological Chemistry</i> , 2013, 288, 34146-34157.	3.4	29
28	Substrate Recognition Mechanism and Substrate-Dependent Conformational Changes of an ROK Family Glucokinase from <i>Streptomyces griseus</i> . <i>Journal of Bacteriology</i> , 2012, 194, 607-616.	2.2	28
29	Structural and Biochemical Elucidation of Mechanism for Decarboxylative Condensation of β^2 -Keto Acid by Curcumin Synthase. <i>Journal of Biological Chemistry</i> , 2011, 286, 6659-6668.	3.4	23
30	Hydrophobic patches on SMAD2 and SMAD3 determine selective binding to cofactors. <i>Science Signaling</i> , 2018, 11, .	3.6	23
31	Cell-Free Protein Synthesis for Structure Determination by X-ray Crystallography. <i>Methods in Molecular Biology</i> , 2010, 607, 149-160.	0.9	23
32	Laminarinase from <i>Flavobacterium</i> sp. reveals the structural basis of thermostability and substrate specificity. <i>Scientific Reports</i> , 2017, 7, 11425.	3.3	22
33	Crystal structure of an archaeal homologue of multidrug resistance repressor protein, EmrR, from hyperthermophilic archaea <i>Sulfolobus tokodaii</i> strain 7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 1138-1146.	2.6	19
34	Different Ca ²⁺ -sensitivities between the EF-hands of T- and L-plastins. <i>Biochemical and Biophysical Research Communications</i> , 2012, 429, 137-141.	2.1	19
35	Complex Structure of the DNA-binding Domain of AdpA, the Global Transcription Factor in <i>Streptomyces griseus</i> , and a Target Duplex DNA Reveals the Structural Basis of Its Tolerant DNA Sequence Specificity. <i>Journal of Biological Chemistry</i> , 2013, 288, 31019-31029.	3.4	19
36	Molecular Mechanism of Distinct Salt-Dependent Enzyme Activity of Two Halophilic Nucleoside Diphosphate Kinases. <i>Biophysical Journal</i> , 2009, 96, 4692-4700.	0.5	18

#	ARTICLE	IF	CITATIONS
37	The Crystal Structure of L-Sorbose Reductase from <i>Gluconobacter frateurii</i> Complexed with NADPH and L-Sorbose. <i>Journal of Molecular Biology</i> , 2011, 407, 543-555.	4.2	17
38	Structural basis for α -receptor-regulated SMAD recognition by MAN1. <i>Nucleic Acids Research</i> , 2018, 46, 12139-12153.	14.5	16
39	Hydrolysis of AMPPNP by the motor domain of ncd, a kinesin-related protein. <i>FEBS Letters</i> , 1997, 409, 29-32.	2.8	15
40	Crystal structure and structural stability of acylphosphatase from hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> OT3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 196-205.	2.6	15
41	Fourier transform infrared spectroscopic study on the Ca ²⁺ -bound coordination structures of synthetic peptide analogues of the calcium-binding site III of troponin C. <i>Biopolymers</i> , 2006, 82, 339-343.	2.4	14
42	Crystal structure of KaiC-like protein PH0186 from hyperthermophilic archaea <i>Pyrococcus horikoshii</i> OT3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 1035-1039.	2.6	14
43	Crystal structure of the YjgF/YER057c/UK114 family protein from the hyperthermophilic archaeon <i>Sulfolobus tokodaii</i> strain 7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 557-561.	2.6	13
44	Crystal structure of TTHA1264, a putative M16 family zinc peptidase from <i>Thermus thermophilus</i> HB8 that is homologous to the β^2 subunit of mitochondrial processing peptidase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 774-780.	2.6	13
45	Isolation, cDNA Cloning, and Structure-based Functional Characterization of Oryctin, a Hemolymph Protein from the Coconut Rhinoceros Beetle, <i>Oryctes rhinoceros</i> , as a Novel Serine Protease Inhibitor. <i>Journal of Biological Chemistry</i> , 2010, 285, 30150-30158.	3.4	13
46	Purification and characterization of a novel prolyl endopeptidase from <i>Aspergillus niger</i> . <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 2005, 81, 447-453.	3.8	12
47	Structure of TTHA1623, a novel metallo- β -lactamase superfamily protein from <i>Thermus thermophilus</i> HB8. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 455-459.	0.7	12
48	Structural basis for high substrate-binding affinity and enantioselectivity of 3-quinuclidinone reductase AtQR. <i>Biochemical and Biophysical Research Communications</i> , 2014, 446, 911-915.	2.1	12
49	A novel mode of ferric ion coordination by the periplasmic ferric ion-binding subunit FbpA of an ABC-type iron transporter from <i>Thermus thermophilus</i> HB8. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 196-202.	2.5	12
50	Antifungal and Lipid Transfer Proteins from Ginkgo (<i>Ginkgo biloba</i>) Seeds. , 2011, , 527-534.		11
51	REFOLDdb: a new and sustainable gateway to experimental protocols for protein refolding. <i>BMC Structural Biology</i> , 2018, 17, 4.	2.3	11
52	Crystallization and preliminary X-ray analysis of ginkbilobin-2 from <i>Ginkgo biloba</i> seeds: a novel antifungal protein with homology to the extracellular domain of plant cysteine-rich receptor-like kinases. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 737-739.	0.7	10
53	Expression, high-pressure refolding and purification of human leukocyte cell-derived chemotaxin 2 (LECT2). <i>Protein Expression and Purification</i> , 2013, 88, 221-229.	1.3	10
54	Structural analysis of enzymes used for bioindustry and bioremediation. <i>Bioscience, Biotechnology and Biochemistry</i> , 2015, 79, 1391-1401.	1.3	10

#	ARTICLE	IF	CITATIONS
55	Crystal structure of monomeric sarcosine oxidase from <i>Bacillus</i> sp. NS-129 reveals multiple conformations at the active-site loop. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 2005, 81, 220-224.	3.8	9
56	Regulatory mechanism of abscisic acid signaling. <i>Biophysics (Nagoya-shi, Japan)</i> , 2011, 7, 123-128.	0.4	9
57	High pressure refolding, purification, and crystallization of flavin reductase from <i>Sulfolobus tokodaii</i> strain 7. <i>Protein Expression and Purification</i> , 2012, 84, 214-218.	1.3	9
58	Expression, purification, refolding, and enzymatic characterization of two secretory phospholipases A2 from <i>Neurospora crassa</i> . <i>Protein Expression and Purification</i> , 2015, 115, 69-75.	1.3	9
59	Crystal structure of the novel lesion-specific endonuclease PfuEndoQ from <i>Pyrococcus furiosus</i> . <i>Nucleic Acids Research</i> , 2018, 46, 4807-4818.	14.5	9
60	Crystal structure of curcuminoid synthase CUS from <i>Oryza sativa</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 669-673.	2.6	8
61	Tetrameric structure of the restriction DNA glycosylase R.PabI in complex with nonspecific double-stranded DNA. <i>Scientific Reports</i> , 2016, 6, 35197.	3.3	8
62	In-situ and real-time growth observation of high-quality protein crystals under quasi-microgravity on earth. <i>Scientific Reports</i> , 2016, 6, 22127.	3.3	8
63	Structural basis of stereospecific reduction by quinuclidinone reductase. <i>AMB Express</i> , 2014, 4, 6.	3.0	7
64	Structural basis for substrate recognition and processive cleavage mechanisms of the trimeric exonuclease PhoExo I. <i>Nucleic Acids Research</i> , 2015, 43, 7122-7136.	14.5	7
65	Insight into the transition between the open and closed conformations of <i>Thermus thermophilus</i> carboxypeptidase. <i>Biochemical and Biophysical Research Communications</i> , 2017, 484, 787-793.	2.1	7
66	Characterization of the Ca ²⁺ -coordination structures of L- and T-plastins in combination with their synthetic peptide analogs by FTIR spectroscopy. <i>Scientific Reports</i> , 2019, 9, 4217.	3.3	7
67	Infrared spectroscopic study on Ca ²⁺ binding to Akazara scallop troponin C in comparison with peptide analogues of its Ca ²⁺ -binding Site IV. <i>Vibrational Spectroscopy</i> , 2006, 42, 188-191.	2.2	6
68	Cloning, expression, purification, crystallization and preliminary crystallographic analysis of selenomethionine-labelled KaiC-like protein PHO186 from <i>Pyrococcus horikoshii</i> OT3. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 327-329.	0.7	6
69	Crystal structure of thioredoxin domain of ST2123 from thermophilic archaea <i>Sulfolobus tokodaii</i> strain 7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 204-208.	2.6	6
70	Crystal structure of TTHA0303 (TT2238), a four- α -helix bundle protein with an exposed histidine triad from <i>Thermus thermophilus</i> HB8 at 2.0 Å. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1103-1107.	2.6	6
71	Structure of flap endonuclease 1 from the hyperthermophilic archaeon <i>Desulfurococcus amylolyticus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 209-213.	0.7	6
72	Expression, purification, crystallization and X-ray analysis of 3-quinuclidinone reductase from <i>Agrobacterium tumefaciens</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1237-1239.	0.7	6

#	ARTICLE	IF	CITATIONS
73	Purification, crystallization and preliminary X-ray analysis of OsAREB8 from rice, a member of the AREB/ABF family of bZIP transcription factors, in complex with its cognate DNA. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 491-494.	0.7	6
74	Structural basis for transcriptional coactivator recognition by SMAD2 in TGF- β 2 signaling. <i>Science Signaling</i> , 2020, 13, .	3.6	6
75	A unique catalytic triad revealed by the crystal structure of APE0912, a short-chain dehydrogenase/reductase family protein from <i>Aeropyrum pernix</i> K1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1640-1645.	2.6	5
76	Crystal structure of STS042, a stand-alone RAM module protein, from hyperthermophilic archaeon <i>Sulfolobus tokodaii</i> strain 7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1557-1562.	2.6	5
77	Purification, crystallization and preliminary X-ray analysis of the DNA-binding domain of AdpA, the central transcription factor in the A-factor regulatory cascade in the filamentous bacterium <i>Streptomyces griseus</i> , in complex with a duplex DNA. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 946-949.	0.7	5
78	Infrared study of synthetic peptide analogues of the calcium-binding site III of troponin C: The role of helix F of an EF-hand motif. <i>Biopolymers</i> , 2013, 99, 342-347.	2.4	5
79	Structural basis for the regulation of phytohormone receptors. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 1261-1273.	1.3	5
80	Crystal structure and substrate recognition mechanism of the prolyl endoprotease PEP from <i>Aspergillus niger</i> . <i>Biochemical and Biophysical Research Communications</i> , 2022, 591, 76-81.	2.1	5
81	Cloning, purification, crystallization and preliminary crystallographic analysis of acylphosphatase from <i>Pyrococcus horikoshii</i> OT3. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1135-1136.	2.5	4
82	Crystallization and preliminary X-ray analysis of the YjgF/YER057c/UK114-family protein ST0811 from <i>Sulfolobus tokodaii</i> strain 7. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 828-830.	0.7	4
83	Expression, purification, crystallization and preliminary X-ray analysis of the KaiC-like protein PH0187 from the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> OT3. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 144-146.	0.7	4
84	Crystallization and Preliminary Crystallographic Analysis of the Sarcosine Oxidase from <i>Bacillus</i> sp. NS-129. <i>Journal of Structural Biology</i> , 1997, 120, 109-111.	2.8	3
85	Crystallization and preliminary X-ray analysis of carboxypeptidase 1 from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1445-1446.	2.5	3
86	Crystal structure of the proline iminopeptidase-related protein TTHA1809 from <i>Thermus thermophilus</i> HB8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1646-1649.	2.6	3
87	Crystal structure of hypothetical protein PH0734.1 from hyperthermophilic archaea <i>Pyrococcus horikoshii</i> OT3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 1068-1071.	2.6	3
88	Purification, crystallization and preliminary X-ray analysis of L-sorbose reductase from <i>Gluconobacter frateurii</i> complexed with L-sorbose or NADPH. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 562-564.	0.7	3
89	Crystallization and preliminary X-ray analysis of the NADPH-dependent 3-quinuclidinone reductase from <i>Rhodotorula rubra</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 645-647.	0.7	3
90	A Thermoacidophile-Specific Protein Family, DUF3211, Functions as a Fatty Acid Carrier with Novel Binding Mode. <i>Journal of Bacteriology</i> , 2013, 195, 4005-4012.	2.2	3

#	ARTICLE	IF	CITATIONS
91	Expression, high-pressure refolding, purification, crystallization and preliminary X-ray analysis of a novel single-strand-specific 3'→5' exonuclease PhoExo I from <i>Pyrococcus horikoshii</i> OT3. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1076-1079.	0.8	3
92	Distortion of double-stranded DNA structure by the binding of the restriction DNA glycosylase R.PabI. <i>Nucleic Acids Research</i> , 2020, 48, 5106-5118.	14.5	3
93	Crystal structure of (S)-3-O-geranylgeranyl glycerol phosphate synthase from <i>Thermoplasma acidophilum</i> in complex with the substrate sn-glycerol 1-phosphate. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 470-479.	0.8	3
94	Crystallization and preliminary X-ray analysis of flap endonuclease 1 (FEN1) from <i>Desulfurococcus amolyticus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 923-925.	0.7	2
95	A class-A GPCR solubilized under high hydrostatic pressure retains its ligand binding ability. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 2145-2151.	2.6	2
96	Crystal structure of acylphosphatase from hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> OT3. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 2004, 80, 439-442.	3.8	1
97	Crystallization and preliminary X-ray analysis of PH1010 from <i>Pyrococcus horikoshii</i> OT3, a member of the archaeal DUF54 family of proteins. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 532-534.	0.7	1
98	Crystal structure of the DUF54 family protein PH1010 from hyperthermophilic archaea <i>Pyrococcus horikoshii</i> OT3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 256-260.	2.6	1
99	Crystallization and preliminary X-ray analysis of 5-keto-D-gluconate reductase from <i>Gluconobacter suboxydans</i> IFO12528 complexed with 5-keto-D-gluconate and NADPH. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1680-1682.	0.7	1
100	Purification, crystallization and preliminary X-ray analysis of glucokinase from <i>Streptomyces griseus</i> in complex with glucose. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 914-916.	0.7	1
101	Coordination to Divalent Cations by Calcium-Binding Proteins. <i>Methods in Molecular Biology</i> , 2019, 1929, 127-134.	0.9	1
102	<i>Ginkgo biloba</i> Seeds. , 2020, , 241-254.		1
103	Crystal structure and DNA cleavage mechanism of the restriction DNA glycosylase R.CcoI from <i>Campylobacter coli</i> . <i>Scientific Reports</i> , 2021, 11, 859.	3.3	1
104	Recent Progress and Development of Crystal Structure Analysis of Enzymes and Other Proteins. <i>Nihon Kessho Gakkaishi</i> , 2010, 52, 8-13.	0.0	1
105	Crystal Structure of Nucleotide-free Kinesin-1 Motor Domain Explains Coordinated Walking Mechanism. <i>Biophysical Journal</i> , 2009, 96, 571a.	0.5	0
106	Χϕ-ψμϵ™ϳæš<é€èš£æžæ³. <i>Kagaku To Seibutsu</i> , 2009, 47, 486-492.	0.0	0
107	3P-028 X-ray structural analysis of N-terminal domain of KaiC (KaiCI) for understanding of restrained ATPase activity (Protein: Structure & Function, The 47th Annual Meeting of the Biophysical Society of Japan). <i>Tj ETQq1 1 0.784314 rgbT / Over</i>	0.8	0
108	1P-146 Crystal Structure of Nucleotide-free Kinesin-1 Motor Domain Explains Coordinated Walking Mechanism (Molecular motor, The 47th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuru</i> , 2009, 49, S85.	0.1	0

#	ARTICLE	IF	CITATIONS
109	1TP4-06 Crystal Structure of Nucleotide-free Kinesin-1 Motor Domain Explains Coordinated Walking Mechanism(The 47th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2009, 49, S36.	0.1	0
110	2P030 The crystal structure of L-sorbose reductase from Gluconobacter frateurii complexed with NADPH and L-sorbose(The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S87.	0.1	0
111	1P046 1YA1045 Structural basis of abscisic acid signaling(Protein:Structure & Function,Early) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 457	0.1	0
112	Structural Basis for the Coordinated Processive Movement of Kinesin-1 studied by Structural and Single Molecule Analyses. Biophysical Journal, 2011, 100, 120a-121a.	0.5	0
113	Title is missing!. Kagaku To Seibutsu, 2011, 49, 74-76.	0.0	0
114	Purification, crystallization and preliminary X-ray analysis of SGR6054, aStreptomyceshomologue of the mycobacterial integration host factor mIHf. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1085-1088.	0.7	0
115	1P-151 Unique conformation of kinesin's neck linker in the nucleotide-free state(The 46th Annual) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 457	0.1	0
116	1P190 1B1435 Structural basis for the coordinated processive movement of kinesin-1 studied by structural and single molecule analyses(Molecular motor,Oral Presentations,The 48th Annual) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 457	0.0	0
117	Mechanistic Basis for Plant Responses to Drought Stress: Regulatory Mechanism of Abscisic Acid Signaling. Nihon Kessho Gakkaishi, 2011, 53, 178-185.	0.0	0
118	Recent Progress in Abscisic Acid Receptor Research. Seibutsu Butsuri, 2011, 51, 026-027.	0.1	0