

Nobuhisa Watanabe

List of Publications by Year in descending order

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81
papers

1,800
citations

257450

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h-index

302126

39
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81
all docs

81
docs citations

81
times ranked

2671
citing authors

#	ARTICLE	IF	CITATIONS
1	Similar structural stabilities of 3-isopropylmalate dehydrogenases from the obligatory piezophilic bacterium <i>Shewanella benthica</i> strain DB21MT-2 and its atmospheric congener <i>S. oneidensis</i> strain MR-1. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 680-691.	2.3	3
2	High-pressure protein crystal structure analysis of <i>Escherichia coli</i> dihydrofolate reductase complexed with folate and NADP ⁺ . <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 895-905.	2.3	17
3	Structural basis of chimpanzee APOBEC3H dimerization stabilized by double-stranded RNA. <i>Nucleic Acids Research</i> , 2018, 46, 10368-10379.	14.5	26
4	Mapping Region of Human Restriction Factor APOBEC3H Critical for Interaction with HIV-1 Vif. <i>Journal of Molecular Biology</i> , 2017, 429, 1262-1276.	4.2	18
5	High-Pressure Protein X-Ray Crystallography. Review of High Pressure Science and Technology/ <i>Koatsuryoku No Kagaku To Gijutsu</i> , 2017, 27, 18-25.	0.0	0
6	Protein crystallography beamline BL2S1 at the Aichi synchrotron. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 338-343.	2.4	32
7	Unique Flap Conformation in an HIV-1 Protease with High-Level Darunavir Resistance. <i>Frontiers in Microbiology</i> , 2016, 7, 61.	3.5	15
8	Structural Insights into HIV-1 Vif-APOBEC3F Interaction. <i>Journal of Virology</i> , 2016, 90, 1034-1047.	3.4	53
9	Pressure adaptation of 3-isopropylmalate dehydrogenase from an extremely piezophilic bacterium is attributed to a single amino acid substitution. <i>Extremophiles</i> , 2016, 20, 177-186.	2.3	28
10	Analysis of the HindIII-catalyzed reaction by time-resolved crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 256-265.	2.5	2
11	High-pressure protein crystallography of hen egg-white lysozyme. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 742-753.	2.5	39
12	High Pressure Macromolecular Crystallography. <i>Sub-Cellular Biochemistry</i> , 2015, 72, 677-686.	2.4	2
13	Structural and genomic DNA analysis of the putative TetR transcriptional repressor SCO7518 from <i>Streptomyces coelicolor</i> A3(2). <i>FEBS Letters</i> , 2014, 588, 4311-4318.	2.8	7
14	Structural and genomic DNA analysis of a putative transcription factor SCO5550 from <i>Streptomyces coelicolor</i> A3(2): Regulating the expression of gene <i>sco5551</i> as a transcriptional activator with a novel dimer shape. <i>Biochemical and Biophysical Research Communications</i> , 2013, 435, 28-33.	2.1	3
15	SCO4008, a Putative TetR Transcriptional Repressor from <i>Streptomyces coelicolor</i> A3(2), Regulates Transcription of <i>sco4007</i> by Multidrug Recognition. <i>Journal of Molecular Biology</i> , 2013, 425, 3289-3300.	4.2	14
16	New methodologies at PF AR-NW12A: the implementation of high-pressure macromolecular crystallography. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 838-842.	2.4	4
17	The APOBEC3C crystal structure and the interface for HIV-1 Vif binding. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1005-1010.	8.2	137
18	Mechanistic Insights into the 1,3-Xylanases: Useful Enzymes for Manipulation of Algal Biomass. <i>Journal of the American Chemical Society</i> , 2012, 134, 3895-3902.	13.7	23

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19	Crystal sample pins and a storage cassette system compatible with the protein crystallography beamlines at both the Photon Factory and SPring-8. <i>Journal of Applied Crystallography</i> , 2012, 45, 1156-1161.	4.5	0
20	High-pressure-induced water penetration into 3-isopropylmalate dehydrogenase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 300-309.	2.5	40
21	Structural analysis of 3-isopropylmalate dehydrogenase from the obligate piezophile <i>Shewanella benthica</i> DB21MT-2 and the nonpiezophile <i>Shewanella oneidensis</i> MR-1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 265-268.	0.7	19
22	The Structure of <i>Physarum polycephalum</i> Hemagglutinin I Suggests a Minimal Carbohydrate Recognition Domain of Legume Lectin Fold. <i>Journal of Molecular Biology</i> , 2011, 405, 560-569.	4.2	4
23	Semi-automated protein crystal mounting device for the sulfur single-wavelength anomalous diffraction method. <i>Journal of Applied Crystallography</i> , 2010, 43, 341-346.	4.5	17
24	Structure of an archaeal non-discriminating glutamyl-tRNA synthetase: a missing link in the evolution of Gln-tRNA _{Gln} formation. <i>Nucleic Acids Research</i> , 2010, 38, 7286-7297.	14.5	34
25	Crystal Structures of the Multidrug Binding Repressor <i>Corynebacterium glutamicum</i> CgmR in Complex with Inducers and with an Operator. <i>Journal of Molecular Biology</i> , 2010, 403, 174-184.	4.2	58
26	Structural basis of yeast Tim40/Mia40 as an oxidative translocator in the mitochondrial intermembrane space. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14403-14407.	7.1	90
27	Structures of restriction endonuclease <i>Hin</i> III in complex with its cognate DNA and divalent cations. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 1326-1333.	2.5	13
28	Structure of putative 4-amino-4-deoxychorismate lyase from <i>Thermus thermophilus</i> HB8. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1234-1239.	0.7	7
29	X-ray crystallography and structural stability of digestive lysozyme from cow stomach. <i>FEBS Journal</i> , 2009, 276, 2192-2200.	4.7	13
30	3P-O28 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 Tj ETQq0 0 0 0 BT / Overlock 10 Tf 5		
31	Crystal structure of the PH1932 protein, a unique archaeal ArsR type winged HTH transcription factor from <i>Pyrococcus horikoshii</i> OT3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1631-1634.	2.6	4
32	Structural and functional analysis of the TetR-family transcriptional regulator SCO0332 from <i>Streptomyces coelicolor</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 198-205.	2.5	12
33	Structure of mannosyl-3-phosphoglycerate phosphatase from <i>Pyrococcus horikoshii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1267-1276.	2.5	11
34	Spontaneous asparaginyl deamidation of canine milk lysozyme under mild conditions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 313-322.	2.6	8
35	A water molecule identified as a substrate of enzymatic hydrolysis of cellulose: A statistical-mechanics study. <i>Chemical Physics Letters</i> , 2008, 465, 279-284.	2.6	4
36	A Helical String of Alternately Connected Three-Helix Bundles for the Cell Wall-Associated Adhesion Protein Ehb from <i>Staphylococcus aureus</i> . <i>Structure</i> , 2008, 16, 488-496.	3.3	27

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37	SAD phasing by OASIS at different resolutions down to 0.30 nm and below. Chinese Physics B, 2008, 17, 1-9.	1.4	12
38	Structural Basis for Multimeric Heme Complexation through a Specific Protein-Heme Interaction. Journal of Biological Chemistry, 2008, 283, 28649-28659.	3.4	75
39	Structural and Functional Analysis of a Glycoside Hydrolase Family 97 Enzyme from Bacteroides thetaiotaomicron. Journal of Biological Chemistry, 2008, 283, 36328-36337.	3.4	87
40	Structural and functional characterization of the LldR from Corynebacterium glutamicum: a transcriptional repressor involved in L-lactate and sugar utilization. Nucleic Acids Research, 2008, 36, 7110-7123.	14.5	62
41	1P-099 Pepsin Resistance and Conformational Stability of Mammal Digestive Lysozyme(The 46th Annual) Tj ETQq1_1_0.784314 rgBT /Ov	0.1	0
42	Crystal Structure of SCO6571 from Streptomyces coelicolor A3(2). Protein and Peptide Letters, 2008, 15, 709-712.	0.9	1
43	Structural and Mutational Analyses of Drp35 from Staphylococcus aureus. Journal of Biological Chemistry, 2007, 282, 5770-5780.	3.4	39
44	Crystal Structure of Cel44A, a Glycoside Hydrolase Family 44 Endoglucanase from Clostridium thermocellum. Journal of Biological Chemistry, 2007, 282, 35703-35711.	3.4	43
45	Crystallization and Preliminary X-Ray Studies of the Unliganded Wild-Type Bovine Thrombin. Protein and Peptide Letters, 2007, 14, 923-924.	0.9	1
46	Crystal structure analysis reveals a novel forkhead-associated domain of ESAT-6 secretion system C protein in Staphylococcus aureus. Proteins: Structure, Function and Bioinformatics, 2007, 69, 659-664.	2.6	19
47	DNA Recognition Mechanism of the ONECUT Homeodomain of Transcription Factor HNF-6. Structure, 2007, 15, 75-83.	3.3	35
48	Structural basis of CoA recognition by the Pyrococcus single-domain CoA-binding proteins. Journal of Structural and Functional Genomics, 2007, 7, 119-129.	1.2	3
49	Use of Longer Wavelength X-ray in Protein Crystallography. Seibutsu Butsuri, 2007, 47, 174-178.	0.1	0
50	2P034 Crystal structure of Atlantic cod trypsin(29. Protein structure and dynamics (II),Poster) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222	0.1	0
51	Structure of the catalytic nucleotide-binding subunit A of A-type ATP synthase from Pyrococcus horikoshii reveals a novel domain related to the peripheral stalk. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 483-488.	2.5	31
52	SAD phasing by OASIS-2004: case studies of dual-space fragment extension. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 883-890.	2.5	15
53	From phasing to structure refinement in-house: Cr/Cu dual-wavelength system and a loopless free crystal-mounting method. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 891-896.	2.5	16
54	Structural analysis of the transcriptional regulator homolog protein from Pyrococcus horikoshii OT3. Proteins: Structure, Function and Bioinformatics, 2006, 63, 1084-1086.	2.6	7

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55	Crystallization and Preliminary X-Ray Studies of the DNA-Binding Domain of Hepatocyte Nuclear Factor-6α Complexed with DNA. <i>Protein and Peptide Letters</i> , 2006, 13, 531-533.	0.9	2
56	Structure determination of a novel protein by sulfur SAD using chromium radiation in combination with a new crystal-mounting method. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1013-1021.	2.5	37
57	Comparison of phasing methods for sulfur-SAD using in-house chromium radiation: case studies for standard proteins and a 69â€...kDa protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1533-1540.	2.5	22
58	Modified Nextal crystallization device for in situ inspection of protein crystal quality. <i>Journal of Applied Crystallography</i> , 2005, 38, 396-397.	4.5	1
59	The CGL2612 Protein from <i>Corynebacterium glutamicum</i> Is a Drug Resistance-related Transcriptional Repressor. <i>Journal of Biological Chemistry</i> , 2005, 280, 38711-38719.	3.4	33
60	Crystal structure of the ATP-binding cassette of multisugar transporter from <i>Pyrococcus horikoshii</i> OT3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 635-638.	2.6	15
61	Crystal structure of hypothetical protein PH0828 from <i>Pyrococcus horikoshii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 862-865.	2.6	8
62	Crystal structure of hypothetical protein PH0642 from <i>Pyrococcus horikoshii</i> at 1.6Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 869-873.	2.6	38
63	Crystal structure of PH0010 from <i>Pyrococcus horikoshii</i> , which is highly homologous to human AMMECR 1C-terminal region. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 501-503.	2.6	4
64	Crystal structure of conserved protein PH1136 from <i>Pyrococcus horikoshii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 210-213.	2.6	5
65	Crystal structure of human p120 homologue protein PH1374 from <i>Pyrococcus horikoshii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 54, 814-816.	2.6	10
66	Structure analysis of PH1161 protein, a transcriptional activator TenA homologue from the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1094-1100.	2.5	12
67	Preparation and preliminary X-ray analysis of the catalytic module of Î²-1,3-xylanase from the marine bacterium <i>Vibrio</i> sp. AX-4. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1470-1472.	2.5	10
68	Crystallization and preliminary X-ray diffraction study of the catalytic subunit of archaeal H ⁺ -transporting ATP synthase from <i>Pyrococcus horikoshii</i> OT3. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1484-1486.	2.5	7
69	Structural and Enzymatic Properties of 1-Aminocyclopropane-1-carboxylate Deaminase Homologue from <i>Pyrococcus horikoshii</i> . <i>Journal of Molecular Biology</i> , 2004, 341, 999-1013.	4.2	37
70	Reaction Intermediate Structures of 1-Aminocyclopropane-1-carboxylate Deaminase. <i>Journal of Biological Chemistry</i> , 2003, 278, 41069-41076.	3.4	31
71	The crystal structure of human MRP14 (S100A9), a Ca ²⁺ -dependent regulator protein in inflammatory process. <i>Journal of Molecular Biology</i> , 2002, 316, 265-276.	4.2	96
72	Semi-automatic protein crystallization system that allows in situ observation of X-ray diffraction from crystals in the drop. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1527-1530.	2.5	21

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73	The X-ray crystal structure of pyrrolidone-carboxylate peptidase from hyperthermophilic archaea <i>Pyrococcus horikoshii</i> . <i>Journal of Structural and Functional Genomics</i> , 2002, 2, 145-154.	1.2	18
74	Automatic Weissenberg data collection system for time-resolved protein crystallography. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2001, 467-468, 1367-1371.	1.6	1
75	A very simple and cheap greasing device for crystallization plates. <i>Journal of Applied Crystallography</i> , 2001, 34, 224-224.	4.5	0
76	The MinD protein from the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> : crystallization and preliminary X-ray analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 896-897.	2.5	2
77	Expression, purification, crystallization and preliminary X-ray diffraction analysis of the human calcium-binding protein MRP14 (S100A9). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1174-1176.	2.5	6
78	The Three-Dimensional Structure of Septum Site-Determining Protein MinD from <i>Pyrococcus horikoshii</i> OT3 in Complex with Mg-ADP. <i>Structure</i> , 2001, 9, 817-826.	3.3	58
79	Rotated-inclined focusing monochromator with simultaneous tuning of asymmetry factor and radius of curvature over a wide wavelength range. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 64-68.	2.4	7
80	Crystal Structure Analysis of L-Amino Acid: Pyruvate Aminotransferase with a Newly Developed Weissenberg Camera and an Imaging Plate Using Synchrotron Radiation ¹ . <i>Journal of Biochemistry</i> , 1989, 105, 1-3.	1.7	72
81	Application of transform theory to resonance Raman excitation profiles of a cyanine dye. <i>Journal of Raman Spectroscopy</i> , 1987, 18, 381-385.	2.5	17