

Naoki Shibata

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4835484/publications.pdf>

Version: 2024-02-01

87
papers

2,887
citations

218677

26
h-index

175258

52
g-index

87
all docs

87
docs citations

87
times ranked

2755
citing authors

#	ARTICLE	IF	CITATIONS
1	The DIX domain of Dishevelled confers Wnt signaling by dynamic polymerization. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 484-492.	8.2	365
2	Metalation of Expanded Porphyrins: A Chemical Trigger Used To Produce Molecular Twisting and Möbius Aromaticity. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 681-684.	13.8	300
3	Activation Process of [NiFe] Hydrogenase Elucidated by High-Resolution X-Ray Analyses: Conversion of the Ready to the Unready State. <i>Structure</i> , 2005, 13, 1635-1642.	3.3	248
4	A new mode of B12 binding and the direct participation of a potassium ion in enzyme catalysis: X-ray structure of diol dehydratase. <i>Structure</i> , 1999, 7, 997-1008.	3.3	245
5	How a protein generates a catalytic radical from coenzyme B12: X-ray structure of a diol-dehydratase-adeninylpentylcobalamin complex. <i>Structure</i> , 2000, 8, 775-788.	3.3	140
6	High Fidelity Self-Sorting Assembling of meso-Cinchomeronimide Appended meso-meso Linked Zn(II) Diporphyrins. <i>Journal of the American Chemical Society</i> , 2006, 128, 7670-7678.	13.7	111
7	The crystal structure of coenzyme B ₁₂ -dependent glycerol dehydratase in complex with cobalamin and propane-1,2-diol. <i>FEBS Journal</i> , 2002, 269, 4484-4494.	0.2	98
8	Crystal Structures of Ethanolamine Ammonia-lyase Complexed with Coenzyme B12 Analogs and Substrates. <i>Journal of Biological Chemistry</i> , 2010, 285, 26484-26493.	3.4	87
9	Crystal structure of activated ribulose-1,5-bisphosphate carboxylase/oxygenase from green alga <i>Chlamydomonas reinhardtii</i> complexed with 2-carboxyarabinitol-1,5-bisphosphate. <i>Journal of Molecular Biology</i> , 2002, 316, 679-691.	4.2	68
10	Structure of the Cadherin-related Neuronal Receptor/Protocadherin-1 First Extracellular Cadherin Domain Reveals Diversity across Cadherin Families. <i>Journal of Biological Chemistry</i> , 2006, 281, 33650-33663.	3.4	66
11	Substrate-Induced Conformational Change of a Coenzyme B12-Dependent Enzyme: A Crystal Structure of the Substrate-Free Form of Diol Dehydratase. <i>Biochemistry</i> , 2002, 41, 12607-12617.	2.5	64
12	Roles of Functional Loops and the CD-Terminal Segment of a Single-Stranded DNA Binding Protein Elucidated by X-Ray Structure Analysis. <i>Journal of Biochemistry</i> , 2000, 127, 329-335.	1.7	59
13	Crystal Structure of Carboxylase Reaction-oriented Ribulose 1,5-Bisphosphate Carboxylase/Oxygenase from a Thermophilic Red Alga, <i>Galdieria partita</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 15655-15661.	3.4	57
14	Nylon-oligomer Degrading Enzyme/Substrate Complex: Catalytic Mechanism of 6-Aminohexanoate-dimer Hydrolase. <i>Journal of Molecular Biology</i> , 2007, 370, 142-156.	4.2	53
15	Three-dimensional Structure of Nylon Hydrolase and Mechanism of Nylon-6 Hydrolysis. <i>Journal of Biological Chemistry</i> , 2012, 287, 5079-5090.	3.4	48
16	Basis for monomer stabilization in Rhodospseudomonas palustris cytochrome c ₂ derived from the crystal structure. <i>Journal of Molecular Biology</i> , 1998, 284, 751-760.	4.2	47
17	X-ray Crystallographic Analysis of 6-Aminohexanoate-Dimer Hydrolase. <i>Journal of Biological Chemistry</i> , 2005, 280, 39644-39652.	3.4	40
18	Novel Insight into the Copper-Ligand Geometry in the Crystal Structure of <i>Ulva pertusa</i> Plastocyanin at 1.6-Å... Resolution. <i>Journal of Biological Chemistry</i> , 1999, 274, 4225-4230.	3.4	38

#	ARTICLE	IF	CITATIONS
19	Structural Rationalization for the Lack of Stereospecificity in Coenzyme B ₁₂ -dependent Diol Dehydratase. <i>Journal of Biological Chemistry</i> , 2003, 278, 22717-22725.	3.4	38
20	X-ray Crystallographic Analysis of the 6-Aminohexanoate Cyclic Dimer Hydrolase. <i>Journal of Biological Chemistry</i> , 2010, 285, 1239-1248.	3.4	38
21	Redesign of coenzyme B ₁₂ dependent diol dehydratase to be resistant to the mechanism-based inactivation by glycerol and act on longer chain 1,2-diols. <i>FEBS Journal</i> , 2012, 279, 793-804.	4.7	35
22	How do the X-ray structure and the NMR structure of FMN-binding protein differ?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 368-371.	2.5	34
23	Release of a Damaged Cofactor from a Coenzyme B ₁₂ -Dependent Enzyme: X-Ray Structures of Diol Dehydratase-Reactivating Factor. <i>Structure</i> , 2005, 13, 1745-1754.	3.3	31
24	Crystal Structures of Hydrogenase Maturation Protein HypE in the Apo and ATP-bound Forms. <i>Journal of Molecular Biology</i> , 2007, 372, 1045-1054.	4.2	30
25	Crystal structure analysis of the translation factor RF3 (release factor 3). <i>FEBS Letters</i> , 2012, 586, 3705-3709.	2.8	30
26	Structural and enzymatic characterization of BacD, an L-α-amino acid dipeptide ligase from <i>Bacillus subtilis</i> . <i>Protein Science</i> , 2012, 21, 707-716.	7.6	30
27	Orderly Disposition of Heterogeneous Small Subunits in D-Ribulose-1,5-bisphosphate Carboxylase/Oxygenase from Spinach. <i>Journal of Biological Chemistry</i> , 1996, 271, 26449-26452.	3.4	25
28	Molecular design of a nylon-6 byproduct-degrading enzyme from a carboxylesterase with a β-lactamase fold. <i>FEBS Journal</i> , 2009, 276, 2547-2556.	4.7	23
29	Two alternative modes for optimizing nylon-6 byproduct hydrolytic activity from a carboxylesterase with a β-lactamase fold: X-ray crystallographic analysis of directly evolved 6-aminohexanoate-dimer hydrolase. <i>Protein Science</i> , 2009, 18, 1662-1673.	7.6	21
30	Molecular basis for specificities of reactivating factors for adenosylcobalamin-dependent diol and glycerol dehydratases. <i>FEBS Journal</i> , 2007, 274, 5556-5566.	4.7	20
31	Molecular architectures and functions of radical enzymes and their (re)activating proteins. <i>Journal of Biochemistry</i> , 2015, 158, 271-292.	1.7	20
32	Direct Participation of a Peripheral Side Chain of a Corrin Ring in Coenzyme B ₁₂ Catalysis. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 7830-7835.	13.8	20
33	Mutational analysis of 6-aminohexanoate-dimer hydrolase: Relationship between nylon oligomer hydrolytic and esterolytic activities. <i>FEBS Letters</i> , 2006, 580, 5054-5058.	2.8	19
34	Zwitterionic Corroles: Regioselective Nucleophilic Pyridination of a Doubly Linked Biscorrole. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 2388-2390.	13.8	16
35	How Coenzyme B ₁₂ -Dependent Ethanolamine Ammonia-Lyase Deals with Both Enantiomers of 2-Amino-1-propanol as Substrates: Structure-Based Rationalization. <i>Biochemistry</i> , 2011, 50, 591-598.	2.5	15
36	A direct heterotypic interaction between the DIX domains of Dishevelled and Axin mediates signaling to β-catenin. <i>Science Signaling</i> , 2019, 12, .	3.6	15

#	ARTICLE	IF	CITATIONS
37	Structure of Azurin from <i>Achromobacter xylosoxidans</i> NCIB11015 at 2.5 Å... Resolution1. <i>Journal of Biochemistry</i> , 1994, 116, 1193-1197.	1.7	14
38	Crystallization and preliminary X-ray crystallographic studies of the axin DIX domain. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 529-531.	0.7	14
39	Redox Potential-Dependent Formation of an Unusual His-Trp Bond in Bilirubin Oxidase. <i>Chemistry - A European Journal</i> , 2018, 24, 18052-18058.	3.3	14
40	Crystallization and X-ray diffraction analysis of 6-aminohexanoate-dimer hydrolase from <i>Arthrobacter</i> sp. KI72. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 928-930.	0.7	13
41	Formation and carbon monoxide-dependent dissociation of <i>Allochromatium vinosum</i> cytochrome c_2 oligomers using domain-swapped dimers. <i>Protein Science</i> , 2017, 26, 464-474.	7.6	13
42	X-ray induced reduction of the crystal of high-molecular-weight cytochrome revealed by microspectrophotometry. <i>Journal of Synchrotron Radiation</i> , 2004, 11, 113-116.	2.4	12
43	Molecular dynamics studies on the mutational structures of a nylon-6 byproduct-degrading enzyme. <i>Chemical Physics Letters</i> , 2011, 507, 157-161.	2.6	12
44	Photosensitivity of the Ni-A state of [NiFe] hydrogenase from <i>Desulfovibrio vulgaris</i> Miyazaki F with visible light. <i>Biochemical and Biophysical Research Communications</i> , 2013, 430, 284-288.	2.1	11
45	Rational Design of Domain-swapping-Based <i>c₂</i> Type Cytochrome Heterodimers by Using Chimeric Proteins. <i>ChemBioChem</i> , 2017, 18, 1712-1715.	2.6	11
46	Structure of a conserved hypothetical protein, TTHA0849 from <i>Thermus thermophilus</i> HB8, at 2.4 Å... resolution: a putative member of the StAR-related lipid-transfer (START) domain superfamily. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 1027-1031.	0.7	10
47	Determination of the Role of the Carboxyl-terminal Leucine-122 in FMN-binding Protein by Mutational and Structural Analysis. <i>Journal of Biochemistry</i> , 2007, 141, 459-468.	1.7	10
48	Crystallization and preliminary X-ray study of two crystal forms of <i>Klebsiella oxytoca</i> diol dehydratase-cyanocobalamin complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 907-909.	2.5	9
49	The Role of Structural Intersubunit Microheterogeneity in the Regulation of the Activity in Hysteresis of Ribulose 1,5-Bisphosphate Carboxylase/Oxygenase. <i>Journal of Biochemistry</i> , 2000, 128, 591-599.	1.7	8
50	Radical production simulated by photoirradiation of the diol dehydratase-adeninylpentylcobalamin complex. <i>Journal of Synchrotron Radiation</i> , 2001, 8, 1182-1185.	2.4	8
51	Construction of a Triangle-Shaped Trimer and a Tetrahedron Using an α -Helix-Inserted Circular Permutant of Cytochrome <i>c₂</i> . <i>Chemistry - an Asian Journal</i> , 2018, 13, 964-967.	3.3	8
52	Direct Participation of a Peripheral Side Chain of a Corrin Ring in Coenzyme B ₁₂ Catalysis. <i>Angewandte Chemie</i> , 2018, 130, 7956-7961.	2.0	8
53	Structural and functional characterization of nylon hydrolases. <i>Methods in Enzymology</i> , 2021, 648, 357-389.	1.0	8
54	Spectroscopic characterization and kinetic studies of a novel plastocyanin from the green alga <i>Ulva pertusa</i> . <i>Inorganica Chimica Acta</i> , 1998, 283, 184-192.	2.4	7

#	ARTICLE	IF	CITATIONS
55	Structural basis of the correct subunit assembly, aggregation, and intracellular degradation of nylon hydrolase. <i>Scientific Reports</i> , 2018, 8, 9725.	3.3	7
56	Protein surface charge effect on 3D domain swapping in cells for c-type cytochromes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 140265.	2.3	7
57	Structural basis for Ccd1 auto-inhibition in the Wnt pathway through homomerization of the DIX domain. <i>Scientific Reports</i> , 2017, 7, 7739.	3.3	6
58	High-resolution structure of a Y27W mutant of the Dishevelled2 DIX domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 116-122.	0.8	6
59	Crystallization and Preliminary Crystallographic Studies of Ribulose 1,5-Bisphosphate Carboxylase/Oxygenase from a Red Alga, <i>Galdieria partita</i> , with a High Specificity Factor. <i>Journal of Biochemistry</i> , 1996, 120, 1064-1066.	1.7	5
60	Crystallization and preliminary X-ray analysis of CooA from <i>Carboxydotherrmus hydrogenoformans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 471-473.	0.7	5
61	Crystallization and X-ray diffraction analysis of 6-aminohexanoate-cyclic-dimer hydrolase from <i>Arthrobacter</i> sp. KI72. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1209-1211.	0.7	5
62	3D domain swapping of azurin from <i>Alcaligenes xylosoxidans</i> . <i>Metallomics</i> , 2020, 12, 337-345.	2.4	5
63	Thermodynamic Control of Domain Swapping by Modulating the Helical Propensity in the Hinge Region of Myoglobin. <i>Chemistry - an Asian Journal</i> , 2020, 15, 1743-1749.	3.3	5
64	Crystallization and preliminary crystallographic studies of FMN-binding protein from <i>Desulfovibrio vulgaris</i> Miyazaki F. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1089-1090.	2.5	4
65	Crystallization and preliminary X-ray analysis of two inhibitor complexes of the catalytic domain of death-associated protein kinase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 764-766.	2.5	4
66	Crystallization and preliminary X-ray analysis of molecular chaperone-like diol dehydratase-reactivating factor in ADP-bound and nucleotide-free forms. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 603-605.	0.7	4
67	Crystal structure of a hypothetical protein, TTHA0829 from <i>Thermus thermophilus</i> HB8, composed of cystathionine- β -synthase (CBS) and aspartate-kinase chorismate-mutase tyrA (ACT) domains. <i>Extremophiles</i> , 2016, 20, 275-282.	2.3	4
68	Rational design of metal-binding sites in domain-swapped myoglobin dimers. <i>Journal of Inorganic Biochemistry</i> , 2021, 217, 111374.	3.5	4
69	Enzymatic synthesis of nylon-6 units in organic solvents containing low concentrations of water. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2010, 64, 81-88.	1.8	3
70	Crystallization and X-ray diffraction analysis of nylon-oligomer hydrolase (NylC) from <i>Agromyces</i> sp. KY5R. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 892-895.	0.7	3
71	Crystallization and X-ray diffraction analysis of nylon hydrolase (NylC) from <i>Arthrobacter</i> sp. KI72. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1151-1154.	0.7	3
72	Crystallization and preliminary X-ray analysis of the NAD ⁺ -reducing [NiFe] hydrogenase from <i>Hydrogenophilus thermoluteolus</i> TH-1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 96-99.	0.8	3

#	ARTICLE	IF	CITATIONS
73	Ni-elimination from the active site of the standard [NiFe]â€‘hydrogenase upon oxidation by O ₂ . Journal of Inorganic Biochemistry, 2017, 177, 435-437.	3.5	3
74	Structural Changes of the Trinuclear Copper Center in Bilirubin Oxidase upon Reduction. Molecules, 2019, 24, 76.	3.8	3
75	Crystallization and preliminary crystallographic studies of pink color chromoprotein from <i>Pleurotus salmoneostramineus</i> L. Vass.. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 335-336.	2.5	2
76	Biochemical, spectroscopic and X-ray structural analysis of deuterated multicopper oxidase CueO prepared from a new expression construct for neutron crystallography. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 788-794.	0.8	2
77	Experimental and theoretical study on converting myoglobin into a stable domain-swapped dimer by utilizing a tight hydrogen bond network at the hinge region. RSC Advances, 2021, 11, 37604-37611.	3.6	2
78	Crystallization And Mad Data Collection Of High-Molecular Weight Cytochrome C From <i>Desulfovibrio Vulgaris</i> Miyazaki F. Protein and Peptide Letters, 2004, 11, 93-96.	0.9	1
79	Crystallization and preliminary X-ray analysis of a class II release factor RF3 from a sulfate-reducing bacterium. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 622-624.	0.7	1
80	Crystallization and preliminary X-ray crystallographic study of flavodoxin from <i>Desulfovibrio vulgaris</i> Miyazaki F. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 851-853.	0.7	1
81	Structure analysis of the flavodoxin from <i>Desulfovibrio vulgare</i> Miyazaki F reveals key residues that discriminate the functions and properties of the flavin reductase family. FEBS Journal, 2009, 276, 4840-4853.	4.7	1
82	Expression, crystallization and preliminary X-ray crystallographic study of ethanolamine ammonia-lyase from <i>Escherichia coli</i> . Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 709-711.	0.7	1
83	Crystallographic characterization of the DIX domain of the Wnt signalling positive regulator Ccd1. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 758-761.	0.7	1
84	Mutations affecting the internal equilibrium of the reaction catalyzed by 6â€‘aminohexanoateâ€‘dimer hydrolase. FEBS Letters, 2016, 590, 3133-3143.	2.8	1
85	Coenzyme B12-dependent eliminases: Diol and glycerol dehydratases and ethanolamine ammonia-lyase. Methods in Enzymology, 2022, 668, 181-242.	1.0	1
86	Head-to-Tail Complex of Dishevelled and Axin-DIX Domains: Expression, Purification, Crystallographic Studies and Packing Analysis. Protein and Peptide Letters, 2019, 26, 792-797.	0.9	0
87	Reactivating chaperones for coenzyme B12-dependent diol and glycerol dehydratases and ethanolamine ammonia-lyase. Methods in Enzymology, 2022, 668, 243-284.	1.0	0