

Yoshiki Higuchi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1573650/publications.pdf>

Version: 2024-02-01

124
papers

4,916
citations

126907

33
h-index

98798

67
g-index

127
all docs

127
docs citations

127
times ranked

4184
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and spectroscopic characterization of CO inhibition of [NiFe]-hydrogenase from <i>Citrobacter</i> sp. S-77. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 66-74.	0.8	0
2	The Challenge of Visualizing the Bridging Hydride at the Active Site and Proton Network of [NiFe]-Hydrogenase by Neutron Crystallography. <i>Topics in Catalysis</i> , 2021, 64, 622-630.	2.8	1
3	Rational design of metal-binding sites in domain-swapped myoglobin dimers. <i>Journal of Inorganic Biochemistry</i> , 2021, 217, 111374.	3.5	4
4	Experimental and theoretical study on converting myoglobin into a stable domain-swapped dimer by utilizing a tight hydrogen bond network at the hinge region. <i>RSC Advances</i> , 2021, 11, 37604-37611.	3.6	2
5	3D domain swapping of azurin from <i>Alcaligenes xylosoxidans</i> . <i>Metallomics</i> , 2020, 12, 337-345.	2.4	5
6	Structural Basis of the Function of [NiFe]-hydrogenases. <i>Chemistry Letters</i> , 2020, 49, 164-173.	1.3	11
7	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
8	Towards cryogenic neutron crystallography on the reduced form of [NiFe]-hydrogenase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 946-953.	2.3	2
9	Cysteine SH and Glutamate COOH Contributions to [NiFe] Hydrogenase Proton Transfer Revealed by Highly Sensitive FTIR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 13285-13290.	13.8	31
10	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
11	Cysteine SH and Glutamate COOH Contributions to [NiFe] Hydrogenase Proton Transfer Revealed by Highly Sensitive FTIR Spectroscopy. <i>Angewandte Chemie</i> , 2019, 131, 13419-13424.	2.0	11
12	Structural Changes of the Trinuclear Copper Center in Bilirubin Oxidase upon Reduction. <i>Molecules</i> , 2019, 24, 76.	3.8	3
13	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
14	New assay method based on Raman spectroscopy for enzymes reacting with gaseous substrates. <i>Protein Science</i> , 2019, 28, 663-670.	7.6	5
15	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
16	Head-to-Tail Complex of Dishevelled and Axin-DIX Domains: Expression, Purification, Crystallographic Studies and Packing Analysis. <i>Protein and Peptide Letters</i> , 2019, 26, 792-797.	0.9	0
17	Comprehensive reaction mechanisms at and near the Ni-Fe active sites of [NiFe] hydrogenases. <i>Dalton Transactions</i> , 2018, 47, 4408-4423.	3.3	34
18	Construction of a Triangle-Shaped Trimer and a Tetrahedron Using an α -Helix-Inserted Circular Permutant of Cytochrome <i>c</i> ₅₅₅ . <i>Chemistry - an Asian Journal</i> , 2018, 13, 964-967.	3.3	8

#	ARTICLE	IF	CITATIONS
19	Redox-dependent conformational changes of a proximal [4Fe-4S] cluster in Hyb-type [NiFe]-hydrogenase to protect the active site from O ₂ . <i>Chemical Communications</i> , 2018, 54, 12385-12388.	4.1	14
20	Complete Genome Sequence of a Moderately Thermophilic Facultative Chemolithoautotrophic Hydrogen-Oxidizing Bacterium, <i>Hydrogenophilus thermoluteolus</i> TH-1. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	8
21	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
22	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
23	Structural basis of the correct subunit assembly, aggregation, and intracellular degradation of nylon hydrolase. <i>Scientific Reports</i> , 2018, 8, 9725.	3.3	7
24	Reactivation of standard [NiFe]-hydrogenase and bioelectrochemical catalysis of proton reduction and hydrogen oxidation in a mediated-electron-transfer system. <i>Bioelectrochemistry</i> , 2018, 123, 156-161.	4.6	22
25	Electrostatic roles in electron transfer from [NiFe] hydrogenase to cytochrome c 3 from <i>Desulfovibrio vulgaris</i> Miyazaki F. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 481-487.	2.3	8
26	Formation and carbon monoxide-dependent dissociation of <i>Allochromatium vinosum</i> cytochrome c ₃ -oligomers using domain-swapped dimers. <i>Protein Science</i> , 2017, 26, 464-474.	7.6	13
27	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
28	Structural basis of the redox switches in the NAD ⁺ -reducing soluble [NiFe]-hydrogenase. <i>Science</i> , 2017, 357, 928-932.	12.6	46
29	Ni-elimination from the active site of the standard [NiFe]-hydrogenase upon oxidation by O ₂ . <i>Journal of Inorganic Biochemistry</i> , 2017, 177, 435-437.	3.5	3
30	Equilibrium between inactive ready Ni-SI _r and active Ni-SI _a states of [NiFe] hydrogenase studied by utilizing Ni-SI _r -to-Ni-SI _a photoactivation. <i>Chemical Communications</i> , 2017, 53, 10444-10447.	4.1	11
31	Rational Design of Domain-Swapping-Based c-Type Cytochrome Heterodimers by Using Chimeric Proteins. <i>ChemBioChem</i> , 2017, 18, 1712-1715.	2.6	11
32	Biochemical, spectroscopic and X-ray structural analysis of deuterated multicopper oxidase CueO prepared from a new expression construct for neutron crystallography. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 788-794.	0.8	2
33	Domain swapping oligomerization of thermostable c-type cytochrome in <i>E. coli</i> cells. <i>Scientific Reports</i> , 2016, 6, 19334.	3.3	13
34	Direct electron transfer-type dual gas diffusion H ₂ /O ₂ biofuel cells. <i>Journal of Materials Chemistry A</i> , 2016, 4, 8742-8749.	10.3	61
35	Photoactivation of the Ni-SI _r state to the Ni-SI _a state in [NiFe] hydrogenase: FT-IR study on the light reactivity of the ready Ni-SI _r state and as-isolated enzyme revisited. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 22025-22030.	2.8	16
36	Exogenous acetate ion reaches the type II copper centre in CueO through the water-excretion channel and potentially affects the enzymatic activity. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 558-563.	0.8	4

#	ARTICLE	IF	CITATIONS
37	Structure and function of [NiFe] hydrogenases. <i>Journal of Biochemistry</i> , 2016, 160, 251-258.	1.7	92
38	Mutations affecting the internal equilibrium of the reaction catalyzed by 6-aminohexanoate dimer hydrolase. <i>FEBS Letters</i> , 2016, 590, 3133-3143.	2.8	1
39	Synthesis and Reactivity of a Water-soluble NiRu Monohydride Complex with a Tethered Pyridine Moiety. <i>Chemistry Letters</i> , 2016, 45, 197-199.	1.3	5
40	Dual gas-diffusion membrane- and mediatorless dihydrogen/air-breathing biofuel cell operating at room temperature. <i>Journal of Power Sources</i> , 2016, 335, 105-112.	7.8	67
41	Bioelectrochemical analysis of thermodynamics of the catalytic cycle and kinetics of the oxidative inactivation of oxygen-tolerant [NiFe]-hydrogenase. <i>Journal of Electroanalytical Chemistry</i> , 2016, 766, 152-161.	3.8	17
42	Improved purification, crystallization and crystallographic study of Hyd-2-type [NiFe]-hydrogenase from <i>Citrobacter</i> sp. S-77. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 53-58.	0.8	6
43	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
44	Rational Design of Heterodimeric Protein using Domain Swapping for Myoglobin. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 511-515.	13.8	31
45	FT-IR Characterization of the Light-Induced Ni-L2 and Ni-L3 States of [NiFe] Hydrogenase from <i>Desulfovibrio vulgaris</i> Miyazaki F. <i>Journal of Physical Chemistry B</i> , 2015, 119, 13668-13674.	2.6	28
46	Domain-Swapped Dimer of <i>Pseudomonas aeruginosa</i> Cytochrome c551: Structural Insights into Domain Swapping of Cytochrome c Family Proteins. <i>PLoS ONE</i> , 2015, 10, e0123653.	2.5	19
47	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
48	Change in structure and ligand binding properties of hyperstable cytochrome <i>c</i> ₅₅₅ from <i>Quifex aeolicus</i> by domain swapping. <i>Protein Science</i> , 2015, 24, 366-375.	7.6	18
49	Structural basis for cargo binding and autoinhibition of Bicaudal-D1 by a parallel coiled-coil with homotypic registry. <i>Biochemical and Biophysical Research Communications</i> , 2015, 460, 451-456.	2.1	43
50	Crystallographic analysis of FAD-dependent glucose dehydrogenase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1017-1019.	0.8	1
51	Domain-swapped cytochrome <i>cb</i> ₅₆₂ dimer and its nanocage encapsulating a Zn ²⁺ SO ₄ cluster in the internal cavity. <i>Chemical Science</i> , 2015, 6, 7336-7342.	7.4	37
52	Oligomerization enhancement and two domain swapping mode detection for thermostable cytochrome <i>c</i> ₅₅₂ via the elongation of the major hinge loop. <i>Molecular BioSystems</i> , 2015, 11, 3218-3221.	2.9	15
53	Nanoscale charge transport in cytochrome <i>c</i> ₃ /DNA network: Comparative studies between redox-active molecules. <i>Japanese Journal of Applied Physics</i> , 2015, 54, 095201.	1.5	2
54	Structural insights into the O ₂ reduction mechanism of multicopper oxidase. <i>Journal of Biochemistry</i> , 2015, 158, 293-298.	1.7	53

#	ARTICLE	IF	CITATIONS
55	Newton's cradle-proton relay with amide-imidic acid tautomerization in inverting cellulase visualized by neutron crystallography. <i>Science Advances</i> , 2015, 1, e1500263.	10.3	80
56	Refined Regio- and Stereoselective Hydroxylation of <i>L</i> -Pipelicolic Acid by Protein Engineering of <i>L</i> -Proline 4-Hydroxylase Based on the X-ray Crystal Structure. <i>ACS Synthetic Biology</i> , 2015, 4, 383-392.	3.8	30
57	Crystallographic characterization of the C-terminal coiled-coil region of mouse Bicaudal-D1 (BICD1). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1103-1106.	0.8	4
58	Formation of Domain-Swapped Oligomer of Cytochrome <i>c</i> from Its Molten Globule State Oligomer. <i>Biochemistry</i> , 2014, 53, 4696-4703.	2.5	24
59	New insights into the catalytic active-site structure of multicopper oxidases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 772-779.	2.5	23
60	Light-Driven Hydrogen Production by Hydrogenases and a Ru-Complex inside a Nanoporous Glass Plate under Aerobic External Conditions. <i>Journal of Physical Chemistry Letters</i> , 2014, 5, 2402-2407.	4.6	23
61	Catalytic cycle of cytochrome- <i>c</i> 3 hydrogenase, a [NiFe]-enzyme, deduced from the structures of the enzyme and the enzyme mimic. <i>International Journal of Hydrogen Energy</i> , 2014, 39, 18543-18550.	7.1	9
62	Kinetic Analysis of Inactivation and Enzyme Reaction of Oxygen-Tolerant [NiFe]-Hydrogenase at Direct Electron-Transfer Bioanode. <i>Bulletin of the Chemical Society of Japan</i> , 2014, 87, 1177-1185.	3.2	16
63	Gas-diffusion and Direct-electron-transfer-type Bioanode for Hydrogen Oxidation with Oxygen-tolerant [NiFe]-hydrogenase as an Electrocatalyst. <i>Chemistry Letters</i> , 2014, 43, 1575-1577.	1.3	17
64	Control of the Transition between Ni ^{II} and Ni ^{SI} States by the Redox State of the Proximal Fe ₂ S Cluster in the Catalytic Cycle of [NiFe] Hydrogenase. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 13817-13820.	13.8	41
65	Crystal structure of the CueO mutants at Glu506, the key amino acid located in the proton transfer pathway for dioxygen reduction. <i>Biochemical and Biophysical Research Communications</i> , 2013, 438, 686-690.	2.1	10
66	Structural aspects of [NiFe]-hydrogenases. <i>Reviews in Inorganic Chemistry</i> , 2013, 33, 173-192.	4.1	11
67	Formation of Oligomeric Cytochrome <i>c</i> during Folding by Intermolecular Hydrophobic Interaction between N- and C-Terminal α -Helices. <i>Biochemistry</i> , 2013, 52, 8732-8744.	2.5	40
68	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
69	Inhibitory activity of <i>Filipendula ulmaria</i> constituents on recombinant human histidine decarboxylase. <i>Food Chemistry</i> , 2013, 138, 1551-1556.	8.2	23
70	Phase-diagram-guided method for growth of a large crystal of glycoside hydrolase family 45 inverting cellulase suitable for neutron structural analysis. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 859-863.	2.4	14
71	Studies on hydrogenase. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 2013, 89, 16-33.	3.8	43
72	Crystallization and X-ray diffraction analysis of nylon hydrolase (NylC) from <i>Arthrobacter</i> sp. K172. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1151-1154.	0.7	3

#	ARTICLE	IF	CITATIONS
73	Structural Basis for the Reaction Mechanism of S-Carbamoylation of HypE by HypF in the Maturation of [NiFe]-Hydrogenases. <i>Journal of Biological Chemistry</i> , 2012, 287, 28409-28419.	3.4	40
74	Structural Study Reveals That Ser-354 Determines Substrate Specificity on Human Histidine Decarboxylase. <i>Journal of Biological Chemistry</i> , 2012, 287, 29175-29183.	3.4	65
75	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
76	Crystal structure analysis of the translation factor RF3 (release factor 3). <i>FEBS Letters</i> , 2012, 586, 3705-3709.	2.8	30
77	Structural and oxygen binding properties of dimeric horse myoglobin. <i>Dalton Transactions</i> , 2012, 41, 11378.	3.3	47
78	Domain Swapping of the Heme and N-Terminal $\hat{\pm}$ -Helix in <i>Hydrogenobacter thermophilus</i> Cytochrome c_{552} Dimer. <i>Biochemistry</i> , 2012, 51, 8608-8616.	2.5	41
79	Structural and enzymatic characterization of BacD, an amino acid dipeptide ligase from <i>Bacillus subtilis</i> . <i>Protein Science</i> , 2012, 21, 707-716.	7.6	30
80	Purification, crystallization and preliminary X-ray analysis of human histidine decarboxylase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 675-677.	0.7	9
81	An O $\hat{\pm}$ -Centered Structure of the Trinuclear Copper Center in the Cys500Ser/Glu506Gln Mutant of CueO and Structural Changes in Low to High X $\hat{\pm}$ Ray Dose Conditions. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 1861-1864.	13.8	26
82	Structural basis for a [4Fe-3S] cluster in the oxygen-tolerant membrane-bound [NiFe]-hydrogenase. <i>Nature</i> , 2011, 479, 253-256.	27.8	262
83	Role of $\hat{\pm}$ -Electron Systems in Stabilization of the Oxidized Tetraheme Architecture in Cytochrome c_{13} . <i>Bulletin of the Chemical Society of Japan</i> , 2011, 84, 1096-1101.	3.2	4
84	Positively charged residues located downstream of PIP box, together with TD amino acids within PIP box, are important for CRL4Cdt2-mediated proteolysis. <i>Genes To Cells</i> , 2011, 16, 12-22.	1.2	33
85	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
86	A functional role of the glycosylated N-terminal domain of chondromodulin-I. <i>Journal of Bone and Mineral Metabolism</i> , 2011, 29, 23-30.	2.7	7
87	Crystallographic characterization of the DIX domain of the Wnt signalling positive regulator Ccd1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 758-761.	0.7	1
88	Crystallization and preliminary X-ray diffraction analysis of membrane-bound respiratory [NiFe] hydrogenase from <i>Hydrogenovibrio marinus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 827-829.	0.7	5
89	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
90	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

#	ARTICLE	IF	CITATIONS
91	Concerto catalysis—harmonising [NiFe]hydrogenase and NiRu model catalysts. Dalton Transactions, 2010, 39, 2993.	3.3	16
92	Enzymatic synthesis of nylon-6 units in organic solvents containing low concentrations of water. Journal of Molecular Catalysis B: Enzymatic, 2010, 64, 81-88.	1.8	3
93	Crystallization and preliminary X-ray analysis of NADH:rubredoxin oxidoreductase from <i>Clostridium acetobutylicum</i> . Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 23-25.	0.7	2
94	Crystallization and preliminary X-ray studies of ferredoxin-NADP ⁺ oxidoreductase encoded by <i>Bacillus subtilis</i> yumC. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 301-303.	0.7	3
95	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
96	Purification, crystallization and preliminary X-ray analysis of the dissimilatory sulfite reductase from <i>Desulfovibrio vulgaris</i> Miyazaki F. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1470-1472.	0.7	0
97	Crystallization and preliminary X-ray analysis of dimeric and trimeric cytochromes from horse heart. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1477-1479.	0.7	0
98	Crystal structure analysis of <i>Bacillus subtilis</i> ferredoxin-NADP ⁺ oxidoreductase and the structural basis for its substrate selectivity. Protein Science, 2010, 19, 2279-2290.	7.6	25
99	Crystal structure of NADH:rubredoxin oxidoreductase from <i>Clostridium acetobutylicum</i> : A key component of the dioxygen scavenging system in obligatory anaerobes. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1066-1070.	2.6	6
100	The PHCCE domain of Tiam1/2 is a novel protein- and membrane-binding module. EMBO Journal, 2010, 29, 236-250.	7.8	31
101	Cytochrome <i>c</i> polymerization by successive domain swapping at the C-terminal helix. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12854-12859.	7.1	148
102	Crystal Structures of Ethanolamine Ammonia-lyase Complexed with Coenzyme B12 Analogs and Substrates. Journal of Biological Chemistry, 2010, 285, 26484-26493.	3.4	87
103	Structure and molecular evolution of multicopper blue proteins. Biomolecular Concepts, 2010, 1, 31-40.	2.2	15
104	X-ray Crystallographic Analysis of the 6-Aminohexanoate Cyclic Dimer Hydrolase. Journal of Biological Chemistry, 2010, 285, 1239-1248.	3.4	38
105	X-ray structure of a two-domain type laccase: A missing link in the evolution of multicopper proteins. FEBS Letters, 2009, 583, 1189-1195.	2.8	53
106	Two alternative modes for optimizing nylon byproduct hydrolytic activity from a carboxylesterase with a β -lactamase fold: X-ray crystallographic analysis of directly evolved 6-aminohexanoate dimer hydrolase. Protein Science, 2009, 18, 1662-1673.	7.6	21
107	[NiFe] hydrogenases: structural and spectroscopic studies of the reaction mechanism. Dalton Transactions, 2009, , 7577.	3.3	179
108	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

#	ARTICLE	IF	CITATIONS
109	Crystal Structure of CO-sensing Transcription Activator CooA Bound to Exogenous Ligand Imidazole. <i>Journal of Molecular Biology</i> , 2007, 367, 864-871.	4.2	35
110	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
111	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
112	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
113	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
114	A single-crystal ENDOR and density functional theory study of the oxidized states of the [NiFe] hydrogenase from <i>Desulfovibrio vulgaris</i> Miyazaki F. <i>Journal of Biological Inorganic Chemistry</i> , 2006, 11, 41-51.	2.6	103
115	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
116	Single Crystal EPR Studies of the Reduced Active Site of [NiFe] Hydrogenase from <i>Desulfovibrio vulgaris</i> Miyazaki F. <i>Journal of the American Chemical Society</i> , 2003, 125, 83-93.	13.7	196
117	Structural Studies of the Carbon Monoxide Complex of [NiFe]hydrogenase from <i>Desulfovibrio vulgaris</i> Miyazaki F: Suggestion for the Initial Activation Site for Dihydrogen. <i>Journal of the American Chemical Society</i> , 2002, 124, 11628-11635.	13.7	235
118	The presence of a SO molecule in [NiFe] hydrogenase from <i>Desulfovibrio vulgaris</i> Miyazaki as detected by mass spectrometry. <i>Journal of Inorganic Biochemistry</i> , 2000, 80, 205-211.	3.5	33
119	Structure and Function of [NiFe] Hydrogenase.. <i>Seibutsu Butsuri</i> , 2000, 40, 249-253.	0.1	0
120	Removal of the bridging ligand atom at the Ni-Fe active site of [NiFe] hydrogenase upon reduction with H ₂ , as revealed by X-ray structure analysis at 1.4 Å... resolution. <i>Structure</i> , 1999, 7, 549-556.	3.3	333
121	Crystal structure of DMA photolyase from <i>Anacystis nidulans</i> . <i>Nature Structural and Molecular Biology</i> , 1997, 4, 887-891.	8.2	196
122	Unusual ligand structure in Ni-Fe active center and an additional Mg site in hydrogenase revealed by high resolution X-ray structure analysis. <i>Structure</i> , 1997, 5, 1671-1680.	3.3	374
123	Single crystal EPR study of the Ni center of NiFe hydrogenase. <i>Chemical Physics Letters</i> , 1996, 256, 518-524.	2.6	48
124	Single crystals of hydrogenase from <i>Desulfovibrio vulgaris</i> Miyazaki F. <i>Journal of Biological Chemistry</i> , 1987, 262, 2823-5.	3.4	44