

Kei Wada

List of Publications by Year in descending order

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66
papers

1,328
citations

361413

20
h-index

377865

34
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67
all docs

67
docs citations

67
times ranked

1485
citing authors

#	ARTICLE	IF	CITATIONS
1	Degenerate PCR Targeting the Major Capsid Protein Gene of HcRNAV and Related Viruses. <i>Microbes and Environments</i> , 2022, 37, n/a.	1.6	2
2	Evidence for dynamic in vivo interconversion of the conformational states of IscU during iron-sulfur cluster biosynthesis. <i>Molecular Microbiology</i> , 2021, 115, 807-818.	2.5	6
3	Pathological Features of Ruptured Coronary Plaque and Thrombus Interfaces: Fibrin and von Willebrand Factor as Platelet Scaffolds on Rupture Sites. <i>Thrombosis and Haemostasis</i> , 2021, 121, 234-241.	3.4	5
4	Crystal structures of hydroxymethylbilane synthase complexed with a substrate analog: a single substrate-binding site for four consecutive condensation steps. <i>Biochemical Journal</i> , 2021, 478, 1023-1042.	3.7	9
5	Structural basis of the protochromic green/red photocycle of the chromatic acclimation sensor RcaE. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	11
6	Chronological distribution of dinoflagellate-infecting RNA virus in marine sediment core. <i>Science of the Total Environment</i> , 2021, 770, 145220.	8.0	4
7	Study of Structural Basis for Molecular Mechanisms of Cellular Redox Control. <i>Nihon Kessho Gakkaishi</i> , 2021, 63, 105-112.	0.0	0
8	Super-activator variants of the cyanobacterial transcriptional regulator ChlR essential for tetrapyrrole biosynthesis under low oxygen conditions. <i>Bioscience, Biotechnology and Biochemistry</i> , 2020, 84, 481-490.	1.3	0
9	Recent Advances in the Understanding of the Reaction Chemistries of the Heme Catabolizing Enzymes HO and BVR Based on High Resolution Protein Structures. <i>Current Medicinal Chemistry</i> , 2020, 27, 3499-3518.	2.4	7
10	Crystal structure of phytychromobilin synthase in complex with biliverdin IX β , a key enzyme in the biosynthesis of phytyochrome. <i>Journal of Biological Chemistry</i> , 2020, 295, 771-782.	3.4	2
11	Crystal structure of phytychromobilin synthase in complex with biliverdin IX β , a key enzyme in the biosynthesis of phytyochrome. <i>Journal of Biological Chemistry</i> , 2020, 295, 771-782.	3.4	6
12	Identification of IscU residues critical for de novo iron-sulfur cluster assembly. <i>Molecular Microbiology</i> , 2019, 112, 1769-1783.	2.5	13
13	Crystal structure of a NADPH α -cytochrome P450 oxidoreductase (CYPOR) and heme oxygenase 1 fusion protein implies a conformational change in CYPOR upon NADPH / NADP + binding. <i>FEBS Letters</i> , 2019, 593, 868-875.	2.8	9
14	Bilin-metabolizing enzymes: site-specific reductions catalyzed by two different type of enzymes. <i>Current Opinion in Structural Biology</i> , 2019, 59, 73-80.	5.7	11
15	Crystal Growth of a Bilin Reductase PcyA I86D Mutant-Substrate Complex for Neutron Crystallography. <i>Crystal Growth and Design</i> , 2018, 18, 5174-5181.	3.0	2
16	Structure-Dependent Binding of hnRNPA1 to Telomere RNA. <i>Journal of the American Chemical Society</i> , 2017, 139, 7533-7539.	13.7	48
17	Mapping the key residues of SufB and SufD essential for biosynthesis of iron-sulfur clusters. <i>Scientific Reports</i> , 2017, 7, 9387.	3.3	31
18	Synthesis and evaluation of the inhibitory activity of the four stereoisomers of the potent and selective human β -glutamyl transpeptidase inhibitor GGsTop. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017, 27, 4920-4924.	2.2	4

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19	A substrate-bound structure of cyanobacterial biliverdin reductase identifies stacked substrates as critical for activity. <i>Nature Communications</i> , 2017, 8, 14397.	12.8	9
20	Atomic-resolution structure of the phycocyanobilin:ferredoxin oxidoreductase I86D mutant in complex with fully protonated biliverdin. <i>FEBS Letters</i> , 2016, 590, 3425-3434.	2.8	9
21	Phosphonate-based irreversible inhibitors of human $\hat{\Gamma}^3$ -glutamyl transpeptidase (GGT). GGsTop is a non-toxic and highly selective inhibitor with critical electrostatic interaction with an active-site residue Lys562 for enhanced inhibitory activity. <i>Bioorganic and Medicinal Chemistry</i> , 2016, 24, 5340-5352.	3.0	29
22	The crystal structure of isoniazid-bound KatG catalase-peroxidase from <i>Synechococcus elongatus</i> PCC7942. <i>FEBS Journal</i> , 2015, 282, 54-64.	4.7	20
23	Insights into the Proton Transfer Mechanism of a Bilin Reductase PcyA Following Neutron Crystallography. <i>Journal of the American Chemical Society</i> , 2015, 137, 5452-5460.	13.7	42
24	Functional Dynamics Revealed by the Structure of the SufBCD Complex, a Novel ATP-binding Cassette (ABC) Protein That Serves as a Scaffold for Iron-Sulfur Cluster Biogenesis. <i>Journal of Biological Chemistry</i> , 2015, 290, 29717-29731.	3.4	77
25	Crystal structure of the catalase-peroxidase KatG W78F mutant from <i>Synechococcus elongatus</i> PCC7942 in complex with the antitubercular pro-drug isoniazid. <i>FEBS Letters</i> , 2015, 589, 131-137.	2.8	7
26	The 2.2-Å resolution structure of the catalase-peroxidase KatG from <i>Synechococcus elongatus</i> PCC7942. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 288-293.	0.8	10
27	Structure of <i>Bacillus subtilis</i> $\hat{\Gamma}^3$ -glutamyltranspeptidase in complex with acivicin: diversity of the binding mode of a classical and electrophilic active-site-directed glutamate analogue. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 607-614.	2.5	14
28	Structural basis for the electron transfer from an open form of NADPH-cytochrome P450 oxidoreductase to heme oxygenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2524-2529.	7.1	70
29	Glutathione-analogous peptidyl phosphorus esters as mechanism-based inhibitors of $\hat{\Gamma}^3$ -glutamyl transpeptidase for probing cysteinyl-glycine binding site. <i>Bioorganic and Medicinal Chemistry</i> , 2014, 22, 1176-1194.	3.0	20
30	Cysteine 295 indirectly affects Ni coordination of carbon monoxide dehydrogenase-II C-cluster. <i>Biochemical and Biophysical Research Communications</i> , 2013, 441, 13-17.	2.1	23
31	Thermal Denaturation and Renaturation of $\hat{\Gamma}^3$ -Glutamyltranspeptidase of <i>Escherichia coli</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 409-412.	1.3	6
32	$\hat{\Gamma}^3$ -Glutamyl Transpeptidase and its Precursor. , 2013, , 3712-3719.		1
33	Structure and Reaction Mechanism of $\hat{\Gamma}^3$ -Glutamyltranspeptidases. <i>Nihon Kessho Gakkaishi</i> , 2013, 55, 340-344.	0.0	0
34	Establishment of a Bacterial Expression System and Immunoassay Platform for the Major Capsid Protein of HcRNAV, a Dinoflagellate-Infecting RNA Virus. <i>Microbes and Environments</i> , 2012, 27, 483-489.	1.6	3
35	Expression, purification and preliminary X-ray crystallographic analysis of cyanobacterial biliverdin reductase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 313-317.	0.7	4
36	A Simple, Large-Scale Overexpression Method of Deriving Carbon Monoxide Dehydrogenase II from Thermophilic Bacterium <i>Carboxydotherrmus hydrogenoformans</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2011, 75, 1392-1394.	1.3	7

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37	Mapping of Protein-Protein Interaction Sites in the Plant-Type [2Fe-2S] Ferredoxin. PLoS ONE, 2011, 6, e21947.	2.5	18
38	é%o,,ç «é»,,,ã,`ãf ©ã,1ã,¿ãf1/4ç”ÿâ*æ`ãfžã,`ãfŠãf³ãf1/4ã@æ§«éã*ã1/2œã«æ ©ÿæ§«. Kagaku To Seibutsu, 2010, 48, 830-838. 1		
39	Enhancement of glutaryl-7-aminocapthosporanic acid acylase activity of Î³-glutamyltranspeptidase of <i>Bacillus subtilis</i>. Biotechnology Journal, 2010, 5, 829-837.	3.5	10
40	Crystal structure of the halotolerant Î³-glutamyltranspeptidase from <i>Bacillus subtilis</i> in complex with glutamate reveals a unique architecture of the solvent-exposed catalytic pocket. FEBS Journal, 2010, 277, 1000-1009.	4.7	53
41	One residue substitution in PcyA leads to unexpected changes in tetrapyrrole substrate binding. Biochemical and Biophysical Research Communications, 2010, 402, 373-377.	2.1	4
42	Structural and Functional Analyses of the Proteins Involved in the Iron-Sulfur Cluster Biosynthesis. Nihon Kessho Gakkaishi, 2010, 52, 174-183.	0.0	0
43	Molecular Dynamism of Fe-S Cluster Biosynthesis Implicated by the Structure of the SufC2-SufD2 Complex. Journal of Molecular Biology, 2009, 387, 245-258.	4.2	39
44	Crystal Structures of Î³-Glutamyltranspeptidase in Complex with Azaserine and Acivicin: Novel Mechanistic Implication for Inhibition by Glutamine Antagonists. Journal of Molecular Biology, 2008, 380, 361-372.	4.2	47
45	The Asymmetric Trimeric Architecture of [2Fe-S] IscU: Implications for Its Scaffolding during Iron-Sulfur Cluster Biosynthesis. Journal of Molecular Biology, 2008, 383, 133-143.	4.2	88
46	Improvement of the Glutaryl-7-Aminocapthosporanic Acid Acylase Activity of a Bacterial Î³-Glutamyltranspeptidase. Applied and Environmental Microbiology, 2008, 74, 4983-4983.	3.1	2
47	Improvement of the Glutaryl-7-Aminocapthosporanic Acid Acylase Activity of a Bacterial Î³-Glutamyltranspeptidase. Applied and Environmental Microbiology, 2008, 74, 3400-3409.	3.1	21
48	Crystal Structure of the Î³-Glutamyltranspeptidase Precursor Protein from Escherichia coli. Journal of Biological Chemistry, 2007, 282, 2433-2439.	3.4	73
49	Crystal structures of CbiL, a methyltransferase involved in anaerobic vitamin B12 biosynthesis, and CbiL in complex with S-adenosylhomocysteine-implications for the reaction mechanism. FEBS Journal, 2007, 274, 563-573.	4.7	9
50	Crystal structure of Escherichia coli SufC, an ABC-type ATPase component of the SUF iron-sulfur cluster assembly machinery. FEBS Letters, 2006, 580, 137-143.	2.8	39
51	Crystal Structures of BchU, a Methyltransferase Involved in Bacteriochlorophyll c Biosynthesis, and its Complex with S-adenosylhomocysteine: Implications for Reaction Mechanism. Journal of Molecular Biology, 2006, 360, 839-849.	4.2	34
52	Structure of NADP-dependent glyceraldehyde-3-phosphate dehydrogenase from Synechococcus PCC7942 complexed with NADP. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 315-319.	0.7	11
53	Structure of apo-glyceraldehyde-3-phosphate dehydrogenase from Synechococcus PCC7942. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 727-730.	0.7	5
54	Crystal structures of Î³-glutamyltranspeptidase from Escherichia coli, a key enzyme in glutathione metabolism, and its reaction intermediate. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6471-6476.	7.1	156

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55	Crystallization and preliminary X-ray diffraction study of BchU, a methyltransferase from <i>Chlorobium tepidum</i> involved in bacteriochlorophyll biosynthesis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 712-714.	0.7	3
56	Structural Basis for Thermostability of Endo-1,5- α -L-Arabinanase from <i>Bacillus thermodenitrificans</i> TS-3. <i>Journal of Biochemistry</i> , 2005, 137, 587-592.	1.7	32
57	Identification of Variant Molecules of <i>Bacillus thermoproteolyticus</i> Ferredoxin: Crystal Structure Reveals Bound Coenzyme A and an Unexpected [3Fe ²⁺ 4S] Cluster Associated with a Canonical [4Fe ²⁺ 4S] Ligand Motif. <i>Biochemistry</i> , 2005, 44, 12402-12410.	2.5	14
58	Crystal structure of <i>Escherichia coli</i> SufA involved in biosynthesis of iron-sulfur clusters: Implications for a functional dimer. <i>FEBS Letters</i> , 2005, 579, 6543-6548.	2.8	42
59	Crystal Structure of Chloroplastic Ascorbate Peroxidase from Tobacco Plants and Structural Insights into its Instability. <i>Journal of Biochemistry</i> , 2003, 134, 239-244.	1.7	45
60	Crystallization and preliminary X-ray diffraction studies of catalase-peroxidase from <i>Synechococcus</i> PCC 7942. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 157-159.	2.5	33
61	Crystallization and preliminary X-ray diffraction analysis of chloroplastic ascorbate peroxidase of tobacco plants. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 559-561.	2.5	5
62	Characterization of monoclonal antibodies against ascorbate peroxidase isoenzymes: purification and epitope-mapping using immunoaffinity column chromatography. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2001, 1526, 168-174.	2.4	16
63	Crystallization and preliminary X-ray analysis of a novel pectolytic enzyme, polymethoxygalacturonase SX1 from <i>Trichosporon penicillatum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 457-458.	2.5	0
64	Purification, crystallization and preliminary X-ray diffraction analysis of the fructose-1,6-/sedoheptulose-1,7-bisphosphatase of <i>Synechococcus</i> PCC 7942. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 454-456.	2.5	1
65	Crystallization and preliminary X-ray diffraction analysis of NADP-dependent glyceraldehyde-3-phosphate dehydrogenase of <i>Synechococcus</i> PCC 7942. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 879-881.	2.5	3
66	Crystallization and preliminary X-ray analysis of endopolygalacturonase SE1 from <i>Trichosporon penicillatum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1668-1669.	2.5	2