

# 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  
g-index

67  
all docs

67  
docs citations

67  
times ranked

1485  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structures of $\hat{\gamma}$ -glutamyltranspeptidase from <i>Escherichia coli</i> , a key enzyme in glutathione metabolism, and its reaction intermediate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6471-6476.	7.1	156
2	The Asymmetric Trimeric Architecture of $[2Fe\hat{\gamma}S]$ IscU: Implications for Its Scaffolding during Iron-Sulfur Cluster Biosynthesis. <i>Journal of Molecular Biology</i> , 2008, 383, 133-143.	4.2	88
3	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
4	Crystal Structure of the $\hat{\gamma}$ -Glutamyltranspeptidase Precursor Protein from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 2433-2439.	3.4	73
5	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
6	Crystal structure of the halotolerant $\hat{\gamma}$ -glutamyltranspeptidase from <i>Bacillus subtilis</i> in complex with glutamate reveals a unique architecture of the solvent-exposed catalytic pocket. <i>FEBS Journal</i> , 2010, 277, 1000-1009.	4.7	53
7	Structure-Dependent Binding of hnRNPA1 to Telomere RNA. <i>Journal of the American Chemical Society</i> , 2017, 139, 7533-7539.	13.7	48
8	Crystal Structures of $\hat{\gamma}$ -Glutamyltranspeptidase in Complex with Azaserine and Acivicin: Novel Mechanistic Implication for Inhibition by Glutamine Antagonists. <i>Journal of Molecular Biology</i> , 2008, 380, 361-372.	4.2	47
9	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
10	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
11	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
12	Crystal structure of <i>Escherichia coli</i> SufC, an ABC-type ATPase component of the SUF iron-sulfur cluster assembly machinery. <i>FEBS Letters</i> , 2006, 580, 137-143.	2.8	39
13	Molecular Dynamism of $Fe\hat{\gamma}S$ Cluster Biosynthesis Implicated by the Structure of the SufC-SufD2 Complex. <i>Journal of Molecular Biology</i> , 2009, 387, 245-258.	4.2	39
14	Crystal Structures of BchU, a Methyltransferase Involved in Bacteriochlorophyll c Biosynthesis, and its Complex with S-adenosylhomocysteine: Implications for Reaction Mechanism. <i>Journal of Molecular Biology</i> , 2006, 360, 839-849.	4.2	34
15	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
16	Structural Basis for Thermostability of Endo-1,5- $\hat{\alpha}$ -L-Arabinanase from <i>Bacillus thermodenitrificans</i> TS-3. <i>Journal of Biochemistry</i> , 2005, 137, 587-592.	1.7	32
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	Phosphonate-based irreversible inhibitors of human $\hat{\gamma}$ -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

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19	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
20	Improvement of the Glutaryl-7-Aminocephalosporanic Acid Acylase Activity of a Bacterial $\hat{\Gamma}$ -Glutamyltranspeptidase. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3400-3409.	3.1	21
21	Glutathione-analogous peptidyl phosphorus esters as mechanism-based inhibitors of $\hat{\Gamma}$ -glutamyl transpeptidase for probing cysteinyl-glycine binding site. <i>Bioorganic and Medicinal Chemistry</i> , 2014, 22, 1176-1194.	3.0	20
22	The crystal structure of isoniazidâ€bound KatG catalaseâ€peroxidase from <i>Synechococcus elongatus</i> PCC 7942. <i>FEBS Journal</i> , 2015, 282, 54-64.	4.7	20
23	Mapping of Protein-Protein Interaction Sites in the Plant-Type [2Fe-2S] Ferredoxin. <i>PLoS ONE</i> , 2011, 6, e21947.	2.5	18
24	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
25	Identification of Variant Molecules of <i>Bacillus thermoproteolyticus</i> Ferredoxin: Crystal Structure Reveals Bound Coenzyme A and an Unexpected [3Fe <sup>2+</sup> 4S] Cluster Associated with a Canonical [4Fe <sup>2+</sup> 4S] Ligand Motif. <i>Biochemistry</i> , 2005, 44, 12402-12410.	2.5	14
26	Structure of <i>Bacillus subtilis</i> $\hat{\Gamma}$ -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
27	Identification of IscU residues critical for de novo iron-sulfur cluster assembly. <i>Molecular Microbiology</i> , 2019, 112, 1769-1783.	2.5	13
28	Structure of NADP-dependent glyceraldehyde-3-phosphate dehydrogenase from <i>Synechococcus</i> PCC7942 complexed with NADP. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 315-319.	0.7	11
29	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
30	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
31	Enhancement of glutaryl-7-aminocephalosporanic acid acylase activity of $\hat{\Gamma}$ -glutamyltranspeptidase of <i>Bacillus subtilis</i> . <i>Biotechnology Journal</i> , 2010, 5, 829-837.	3.5	10
32	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
33	Crystal structures of CbiL, a methyltransferase involved in anaerobic vitamin B12 biosynthesis, and CbiL in complex with S-adenosylhomocysteineâ€f implications for the reaction mechanism. <i>FEBS Journal</i> , 2007, 274, 563-573.	4.7	9
34	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
35	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
36	Crystal structure of a NADPH 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

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37	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
38	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
39	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
40	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
41	Thermal Denaturation and Renaturation of $\hat{I}^3$ -Glutamyltranspeptidase of <i>Escherichia coli</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 409-412.	1.3	6
42	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
43	Crystal structure of phytychromobilin synthase in complex with biliverdin IX $\hat{I}$ , a key enzyme in the biosynthesis of phytyochrome. <i>Journal of Biological Chemistry</i> , 2020, 295, 771-782.	3.4	6
44	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
45	Structure of apo-glyceraldehyde-3-phosphate dehydrogenase from <i>Synechococcus</i> PCC7942. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 727-730.	0.7	5
46	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
47	One residue substitution in PcyA leads to unexpected changes in tetrapyrrole substrate binding. <i>Biochemical and Biophysical Research Communications</i> , 2010, 402, 373-377.	2.1	4
48	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
49	Synthesis and evaluation of the inhibitory activity of the four stereoisomers of the potent and selective human $\hat{I}^3$ -glutamyl transpeptidase inhibitor GGsTop. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017, 27, 4920-4924.	2.2	4
50	Chronological distribution of dinoflagellate-infecting RNA virus in marine sediment core. <i>Science of the Total Environment</i> , 2021, 770, 145220.	8.0	4
51	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
52	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
53	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
54	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

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55	Improvement of the Glutaryl-7-Aminocephalosporanic Acid Acylase Activity of a Bacterial $\hat{\Gamma}^3$ -Glutamyltranspeptidase. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4983-4983.	3.1	2
56	Crystal Growth of a Bilin Reductase PcyA I86D Mutant's Substrate Complex for Neutron Crystallography. <i>Crystal Growth and Design</i> , 2018, 18, 5174-5181.	3.0	2
57	Crystal structure of phytochromobilin synthase in complex with biliverdin IX $\hat{\Gamma}$ , a key enzyme in the biosynthesis of phytochrome. <i>Journal of Biological Chemistry</i> , 2020, 295, 771-782.	3.4	2
58	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
59	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
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61	$\hat{\Gamma}^3$ -Glutamyl Transpeptidase and its Precursor. , 2013, , 3712-3719.		1
62	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
63	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
64	Study of Structural Basis for Molecular Mechanisms of Cellular Redox Control. <i>Nihon Kessho Gakkaishi</i> , 2021, 63, 105-112.	0.0	0
65	Structural and Functional Analyses of the Proteins Involved in the Iron-Sulfur Cluster Biosynthesis. <i>Nihon Kessho Gakkaishi</i> , 2010, 52, 174-183.	0.0	0
66	Structure and Reaction Mechanism of $\hat{\Gamma}^3$ -Glutamyltranspeptidases. <i>Nihon Kessho Gakkaishi</i> , 2013, 55, 340-344.	0.0	0