

# Takatoshi Arakawa

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

1,911  
citations

394421

19  
h-index

265206

42  
g-index

54  
all docs

54  
docs citations

54  
times ranked

3090  
citing authors

#	ARTICLE	IF	CITATIONS
1	Substrate complex structure, active site labeling and catalytic role of the zinc ion in cysteine glycosidase. <i>Glycobiology</i> , 2022, 32, 171-180.	2.5	6
2	Cysteine Nucleophiles in Glycosidase Catalysis: Application of a Covalent $\beta$ -Arabinofuranosidase Inhibitor. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 5754-5758.	13.8	16
3	Cysteine Nucleophiles in Glycosidase Catalysis: Application of a Covalent $\beta$ -Arabinofuranosidase Inhibitor. <i>Angewandte Chemie</i> , 2021, 133, 5818-5822.	2.0	3
4	Biochemical and structural characterization of a novel $\alpha$ -L-rhamnosyl- $\beta$ -D-glucuronidase from <i>Fusarium oxysporum</i> . <i>FEBS Journal</i> , 2021, 288, 4918-4938.	4.7	9
5	Structural and functional analysis of gum arabic l-rhamnose- $\beta$ -1,4-d-glucuronate lyase establishes a novel polysaccharide lyase family. <i>Journal of Biological Chemistry</i> , 2021, 297, 101001.	3.4	7
6	Identification of difructose dianhydride I synthase/hydrolase from an oral bacterium establishes a novel glycoside hydrolase family. <i>Journal of Biological Chemistry</i> , 2021, 297, 101324.	3.4	13
7	Dissecting the Stereocontrolled Conversion of Short-Lived Sulfenic Acid by Lachrymatory Factor Synthase. <i>ACS Catalysis</i> , 2020, 10, 9-19.	11.2	7
8	Crystallographic and cryogenic electron microscopic structures and enzymatic characterization of sulfur oxygenase reductase from <i>Sulfurisphaera tokodaii</i> . <i>Journal of Structural Biology: X</i> , 2020, 4, 100030.	1.3	3
9	Crystal structure of $\beta$ -L-arabinobiosidase belonging to glycoside hydrolase family 121. <i>PLoS ONE</i> , 2020, 15, e0231513.	2.5	8
10	Structural analysis of $\beta$ -L-arabinobiose-binding protein in the metabolic pathway of hydroxyproline-rich glycoproteins in <i>Bifidobacterium longum</i> . <i>FEBS Journal</i> , 2020, 287, 5114-5129.	4.7	7
11	Molecular analysis of cyclic $\beta$ -maltosyl-(1 $\rightarrow$ 6)-maltose binding protein in the bacterial metabolic pathway. <i>PLoS ONE</i> , 2020, 15, e0241912.	2.5	3
12	Structural basis for broad substrate specificity of UDP-glucose 4-epimerase in the human milk oligosaccharide catabolic pathway of <i>Bifidobacterium longum</i> . <i>Scientific Reports</i> , 2019, 9, 11081.	3.3	17
13	Understanding the Molecular Mechanism Underlying the High Catalytic Activity of <i>p</i> -Hydroxybenzoate Hydroxylase Mutants for Producing Gallic Acid. <i>Biochemistry</i> , 2019, 58, 4543-4558.	2.5	14
14	Structural basis for the specific cleavage of core-fucosylated N-glycans by endo- $\beta$ -N-acetylglucosaminidase from the fungus <i>Cordyceps militaris</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 17143-17154.	3.4	13
15	Structures of the 5-HT <sub>2A</sub> receptor in complex with the antipsychotics risperidone and zotepine. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 121-128.	8.2	133
16	[Review] Structural Features of Cyclic $\beta$ -Maltosyl-(1 $\rightarrow$ 6)-maltose (CMM) Hydrolase from <i>Arthrobacter</i> ; Bacteria Critical for CMM Recognition and Hydrolysis. <i>Bulletin of Applied Glycoscience</i> , 2019, 9, 103-112.	0.0	0
17	Structural and thermodynamic insights into $\beta$ -1,2-glucooligosaccharide capture by a solute-binding protein in <i>Listeria innocua</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 8812-8828.	3.4	19
18	Ligand complex structures of $\alpha$ -amino acid oxidase/monooxygenase from <i>Pseudomonas</i> sp. AU 813 and its conformational change. <i>FEBS Open Bio</i> , 2018, 8, 314-324.	2.3	11

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19	Identification, functional characterization, and crystal structure determination of bacterial levoglucosan dehydrogenase. <i>Journal of Biological Chemistry</i> , 2018, 293, 17375-17386.	3.4	16
20	Structural features of a bacterial cyclic 1,6-maltosyl-(1 $\rightarrow$ 6)-maltose (CMM) hydrolase critical for CMM recognition and hydrolysis. <i>Journal of Biological Chemistry</i> , 2018, 293, 16874-16888.	3.4	7
21	Identification and characterization of a novel 1,2-D-galactosidase that releases pyruvylated galactose. <i>Scientific Reports</i> , 2018, 8, 12013.	3.3	9
22	Crystal structure of the central and the C-terminal RNase domains of colicin D implicated its translocation pathway through inner membrane of target cell. <i>Journal of Biochemistry</i> , 2018, 164, 329-339.	1.7	6
23	Biochemical and structural analyses of a bacterial endo-1,2-glucanase reveal a new glycoside hydrolase family. <i>Journal of Biological Chemistry</i> , 2017, 292, 7487-7506.	3.4	42
24	The first crystal structure of a family 129 glycoside hydrolase from a probiotic bacterium reveals critical residues and metal cofactors. <i>Journal of Biological Chemistry</i> , 2017, 292, 12126-12138.	3.4	20
25	Molecular Insight into Evolution of Symbiosis between Breast-Fed Infants and a Member of the Human Gut Microbiome <i>Bifidobacterium longum</i> . <i>Cell Chemical Biology</i> , 2017, 24, 515-524.e5.	5.2	102
26	Discovery of 1,2-L-arabinopyranosidases from human gut microbiome expands the diversity within glycoside hydrolase family 42. <i>Journal of Biological Chemistry</i> , 2017, 292, 21092-21101.	3.4	8
27	Isolation and characterization of a thermostable lipase from <i>Bacillus thermoamylovorans</i> NB501. <i>Journal of General and Applied Microbiology</i> , 2016, 62, 313-319.	0.7	7
28	Crystal structure and identification of a key amino acid for glucose tolerance, substrate specificity, and transglycosylation activity of metagenomic 1,2-glucosidase Td2F2. <i>FEBS Journal</i> , 2016, 283, 2340-2353.	4.7	53
29	Crystal structures of archaeal 2-oxoacid:ferredoxin oxidoreductases from <i>Sulfolobus tokodaii</i> . <i>Scientific Reports</i> , 2016, 6, 33061.	3.3	17
30	Characterization and crystal structure determination of 1,2-mannobiose phosphorylase from <i>Listeria innocua</i> . <i>FEBS Letters</i> , 2015, 589, 3816-3821.	2.8	17
31	Open-close structural change upon ligand binding and two magnesium ions required for the catalysis of N-acetylhexosamine 1-kinase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 333-340.	2.3	13
32	Crystal Structure and Substrate Recognition of Cellobionic Acid Phosphorylase, Which Plays a Key Role in Oxidative Cellulose Degradation by Microbes. <i>Journal of Biological Chemistry</i> , 2015, 290, 18281-18292.	3.4	22
33	Gaining insight into the catalysis by GH20 lacto-N-biosidase using small molecule inhibitors and structural analysis. <i>Chemical Communications</i> , 2015, 51, 15008-15011.	4.1	11
34	Structure and mechanism of the mammalian fructose transporter GLUT5. <i>Nature</i> , 2015, 526, 397-401.	27.8	202
35	Crystal structure of the anion exchanger domain of human erythrocyte band 3. <i>Science</i> , 2015, 350, 680-684.	12.6	210
36	Structural basis for the 4-hydroxylation of diclofenac by a microbial cytochrome P450 monooxygenase. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 3081-3091.	3.6	28

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37	Proteoliposome-based Selection of a Recombinant Antibody Fragment Against the Human M2 Muscarinic Acetylcholine Receptor. <i>Monoclonal Antibodies in Immunodiagnosis and Immunotherapy</i> , 2014, 33, 378-385.	1.6	14
38	Crystal structure of a feruloyl esterase belonging to the tannase family: A disulfide bond near a catalytic triad. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2857-2867.	2.6	68
39	Crystal Structure of a Symmetric Football-Shaped GroEL:GroES2-ATP14 Complex Determined at 3.8 Å... Reveals Rearrangement between Two GroEL Rings. <i>Journal of Molecular Biology</i> , 2014, 426, 3634-3641.	4.2	48
40	Crystal structure of glycoside hydrolase family 127 Î²-l-arabinofuranosidase from <i>Bifidobacterium longum</i> . <i>Biochemical and Biophysical Research Communications</i> , 2014, 447, 32-37.	2.1	35
41	Two arginine residues in the substrate pocket predominantly control the substrate selectivity of thiocyanate hydrolase. <i>Journal of Bioscience and Bioengineering</i> , 2013, 116, 22-27.	2.2	6
42	Liprin-Î± controls stress fiber formation by binding to mDia and regulating its membrane localization. <i>Journal of Cell Science</i> , 2012, 125, 108-120.	2.0	36
43	G-protein-coupled receptor inactivation by an allosteric inverse-agonist antibody. <i>Nature</i> , 2012, 482, 237-240.	27.8	274
44	Rho and Anillin-dependent Control of mDia2 Localization and Function in Cytokinesis. <i>Molecular Biology of the Cell</i> , 2010, 21, 3193-3204.	2.1	92
45	Structural Basis for Catalytic Activation of Thiocyanate Hydrolase Involving Metal-Ligated Cysteine Modification. <i>Journal of the American Chemical Society</i> , 2009, 131, 14838-14843.	13.7	42
46	Structure of aspartate racemase complexed with a dual substrate analogue, citric acid, and implications for the reaction mechanism. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1167-1174.	2.6	23
47	Structure and Molecular Dynamics Simulation of Archaeal Prefoldin: The Molecular Mechanism for Binding and Recognition of Nonnative Substrate Proteins. <i>Journal of Molecular Biology</i> , 2008, 376, 1130-1141.	4.2	51
48	Structure of Thiocyanate Hydrolase: A New Nitrile Hydratase Family Protein with a Novel Five-coordinate Cobalt(III) Center. <i>Journal of Molecular Biology</i> , 2007, 366, 1497-1509.	4.2	75
49	Functional expression of thiocyanate hydrolase is promoted by its activator protein, P15K. <i>FEBS Letters</i> , 2006, 580, 4667-4672.	2.8	14
50	Kinetics and Binding Sites for Interaction of the Prefoldin with a Group II Chaperonin. <i>Journal of Biological Chemistry</i> , 2004, 279, 31788-31795.	3.4	53