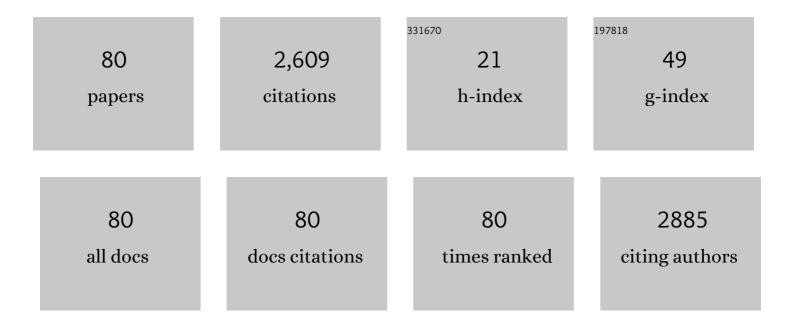
## Yoshito Abe

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Structural Basis of Presequence Recognition by the Mitochondrial Protein Import Receptor Tom20. Cell, 2000, 100, 551-560.	28.9	493
2	Human mitochondrial DNA is packaged with TFAM. Nucleic Acids Research, 2003, 31, 1640-1645.	14.5	321
3	Crystal structure of the anion exchanger domain of human erythrocyte band 3. Science, 2015, 350, 680-684.	12.6	210
4	Regulation of mitochondrial Dâ€loops by transcription factor A and singleâ€stranded DNAâ€binding protein. EMBO Reports, 2002, 3, 451-456.	4.5	190
5	Structure and Function of DnaA N-terminal Domains. Journal of Biological Chemistry, 2007, 282, 17816-17827.	3.4	103
6	NMR identification of the Tom20 binding segment in mitochondrial presequences. Journal of Molecular Biology, 2001, 306, 137-143.	4.2	91
7	Selective and reversible modification of kinase cysteines with chlorofluoroacetamides. Nature Chemical Biology, 2019, 15, 250-258.	8.0	90
8	DiaA Dynamics Are Coupled with Changes in Initial Origin Complexes Leading to Helicase Loading. Journal of Biological Chemistry, 2009, 284, 25038-25050.	3.4	86
9	Disulfide Bond Structure of Human Epidermal Growth Factor Receptor. Journal of Biological Chemistry, 1998, 273, 11150-11157.	3.4	77
10	Characterization of the N-Oligosaccharides Attached to the Atypical Asn-X-Cys Sequence of Recombinant Human Epidermal Growth Factor Receptor. Journal of Biochemistry, 2000, 127, 65-72.	1.7	63
11	Crystal Structure of Tapes japonica Lysozyme with Substrate Analogue. Journal of Biological Chemistry, 2007, 282, 27459-27467.	3.4	57
12	Molecular Basis and Functional Consequences of the Dominant Effects of the Mutant Band 3 on the Structure of Normal Band 3 in Southeast Asian Ovalocytosisâ€. Biochemistry, 2002, 41, 3311-3320.	2.5	44
13	Effect of Salt Concentration on the pKa of Acidic Residues in Lysozyme. Journal of Biochemistry, 1995, 118, 946-952.	1.7	40
14	Structure of the Membrane Domain of Human Erythrocyte Anion Exchanger 1 Revealed by Electron Crystallography. Journal of Molecular Biology, 2010, 397, 179-189.	4.2	40
15	Mechanism for retardation of amyloid fibril formation by sugars in Vλ6 protein. Protein Science, 2013, 22, 467-474.	7.6	39
16	Investigation of the Structural Basis for Thermostability of DNA-binding Protein HU from Bacillus stearothermophilus. Journal of Biological Chemistry, 1998, 273, 19982-19987.	3.4	38
17	Lysozyme requires fluctuation of the active site for the manifestation of activity. Protein Engineering, Design and Selection, 1994, 7, 743-748.	2.1	35
18	Structural and In Vitro Functional Analyses of Novel Plant-Produced Anti-Human PD1 Antibody. Scientific Reports, 2019, 9, 15205.	3.3	34

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19	Histidine-834 of Human Erythrocyte Band 3 Has an Essential Role in the Conformational Changes That Occur during the Band 3-Mediated Anion Exchangeâ€. Biochemistry, 2003, 42, 12927-12932.	2.5	30
20	Crystal structure of a biologically functional form of PriB from Escherichia coli reveals a potential single-stranded DNA-binding site. Biochemical and Biophysical Research Communications, 2005, 326, 766-776.	2.1	28
21	Expression from engineered <i>EscherichiaÂcoli</i> chromosome and crystallographic study of archaeal <i>N</i> , <i>N</i> ′â€diacetylchitobiose deacetylase. FEBS Journal, 2014, 281, 2584-2596.	4.7	22
22	Flexible Regions within the Membrane-Embedded Portions of Polytopic Membrane Proteins. Biochemistry, 2002, 41, 3852-3854.	2.5	21
23	Identification of Oxidized Methionine Sites in Erythrocyte Membrane Protein by Liquid Chromatography/Electrospray Ionization Mass Spectrometry Peptide Mappingâ€. Biochemistry, 2006, 45, 12117-12124.	2.5	20
24	Solution structure of the rat P2X4 receptor head domain involved in inhibitory metal binding. FEBS Letters, 2015, 589, 680-686.	2.8	20
25	Massspectrometric Analyses of Transmembrane Proteins in Human Erythrocyte Membrane. Journal of Biochemistry, 2004, 136, 97-106.	1.7	18
26	Preparation and characterization of a monoclonal antibody against the refolded and functional extracellular domain of rat P2X4 receptor. Journal of Biochemistry, 2013, 153, 275-282.	1.7	18
27	Functional Characterization of Pembrolizumab Produced in Nicotiana benthamiana Using a Rapid Transient Expression System. Frontiers in Plant Science, 2021, 12, 736299.	3.6	18
28	Analysis of the Stabilization of Hen Lysozyme by Helix Macrodipole and Charged Side Chain Interaction. Journal of Biochemistry, 1997, 121, 1076-1081.	1.7	16
29	Residual Structures in the Acid-Unfolded States of Vλ6 Proteins Affect Amyloid Fibrillation. Journal of Molecular Biology, 2009, 392, 1033-1043.	4.2	16
30	The <scp>DnaA N</scp> â€ŧerminal domain interacts with <scp>Hda</scp> to facilitate replicase clampâ€mediated inactivation of <scp>DnaA</scp> . Environmental Microbiology, 2013, 15, 3183-3195.	3.8	16
31	Structure and mechanism of the primosome protein DnaT– functional structures for homotrimerization, dissociation of ss <scp>DNA</scp> from the PriB·ss <scp>DNA</scp> complex, and formation of the DnaT·ss <scp>DNA</scp> complex. FEBS Journal, 2014, 281, 5356-5370.	4.7	16
32	Preparation and Properties of a Lysozyme Derivative in Which Two Domains Are Cross-Linked Intramolecularly between Trp62 and Asp1011. Journal of Biochemistry, 1991, 110, 719-725.	1.7	15
33	Evidence for detection of rat P2X4 receptor expressed on cells by generating monoclonal antibodies recognizing the native structure. Purinergic Signalling, 2019, 15, 27-35.	2.2	15
34	DnaB helicase is recruited to the replication initiation complex via binding of DnaA domain I to the lateral surface of the DnaB N-terminal domain. Journal of Biological Chemistry, 2020, 295, 11131-11143.	3.4	15
35	The Functional Role of Arginine 901 at the C-Terminus of the Human Anion Transporter Band 3 Protein. Journal of Biochemistry, 2006, 139, 903-912.	1.7	14
36	Helical image reconstruction of the outward-open human erythrocyte band 3 membrane domain in tubular crystals. Journal of Structural Biology, 2010, 169, 406-412.	2.8	14

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37	Role of the osmolyte taurine on the folding of a model protein, hen egg white lysozyme, under a crowding condition. Amino Acids, 2015, 47, 909-915.	2.7	14
38	Situation of Monomethoxypolyethylene Glycol Covalently Attached to Lysozyme. Journal of Biochemistry, 1996, 119, 1086-1093.	1.7	13
39	Evaluation of the conformational equilibrium of reduced hen egg lysozyme by antibodies to the native form. Archives of Biochemistry and Biophysics, 2010, 494, 145-150.	3.0	13
40	Tyrosine Sulfation Restricts the Conformational Ensemble of a Flexible Peptide, Strengthening the Binding Affinity for an Antibody. Biochemistry, 2018, 57, 4177-4185.	2.5	13
41	Domain separation and characterization of <scp>P</scp> ri <scp>C</scp> , a replication restart primosome factor in <i><scp>E</scp>scherichia coli</i> . Genes To Cells, 2013, 18, 723-732.	1.2	12
42	Factor G Utilizes a Carbohydrate-Binding Cleft That Is Conserved between Horseshoe Crab and Bacteria for the Recognition of β-1,3- <scp>d</scp> -Glucans. Journal of Immunology, 2009, 183, 3810-3818.	0.8	11
43	Kinetically trapped structure in the renaturation of reduced oxindolealanine 62 lysozyme. Biochemistry, 1995, 34, 16178-16185.	2.5	10
44	Functional analysis of CedA based on its structure: residues important in binding of DNA and RNA polymerase and in the cell division regulation. Journal of Biochemistry, 2016, 159, 217-223.	1.7	10
45	Evidence for a novel racemization process of an asparaginyl residue in mouse lysozyme under physiological conditions. Cellular and Molecular Life Sciences, 2005, 62, 199-205.	5.4	9
46	Basic and aromatic residues in the C-terminal domain of PriC are involved in ssDNA and SSB binding. Journal of Biochemistry, 2015, 157, 529-537.	1.7	9
47	Effects of His mutations on the fibrillation of amyloidogenic Vλ6 protein Wil under acidic and physiological conditions. Biochemical and Biophysical Research Communications, 2010, 391, 615-620.	2.1	8
48	The Structure of an Archaeal α-Glucosaminidase Provides Insight into Glycoside Hydrolase Evolution. Journal of Biological Chemistry, 2017, 292, 4996-5006.	3.4	8
49	Crystallization of Human Erythrocyte Band 3, the anion exchanger, at the International Space Station "KIBO― Analytical Biochemistry, 2018, 559, 91-93.	2.4	8
50	Denatured Mammalian Protein Mixtures Exhibit Unusually High Solubility in Nucleic Acid-Free Pure Water. PLoS ONE, 2014, 9, e113295.	2.5	7
51	Inhibition of amyloid fibril formation in the variable domain of λ6 light chain mutant Wil caused by the interaction between its unfolded state and epigallocatechin-3-O-gallate. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 2570-2578.	2.4	7
52	Involvement of histidine in complex formation of PriB and single-stranded DNA. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 299-307.	2.3	6
53	Effect on catalysis by replacement of catalytic residue from hen egg white lysozyme to <i>Venerupis philippinarum</i> lysozyme*. Protein Science, 2016, 25, 1637-1647.	7.6	6
54	Mutation of His 834 in human anion exchanger 1 affects substrate binding. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 903-908.	2.6	5

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55	Solution structure of the Nâ€ŧerminal domain of a replication restart primosome factor, PriC, in <i>Escherichia coli</i> . Protein Science, 2013, 22, 1279-1286.	7.6	5
56	Principal component analysis of data from NMR titration experiment of uniformly 15N labeled amyloid beta (1–42) peptide with osmolytes and phenolic compounds. Archives of Biochemistry and Biophysics, 2020, 690, 108446.	3.0	5
57	Expression and Functional Evaluation of Recombinant Anti-receptor Activator of Nuclear Factor Kappa-B Ligand Monoclonal Antibody Produced in Nicotiana benthamiana. Frontiers in Plant Science, 2021, 12, 683417.	3.6	5
58	Reduction of Disulfide Bonds in Proteins by 2-Aminothiophenol under Weakly Acidic Conditions. Journal of Biochemistry, 1994, 115, 52-67.	1.7	4
59	Assignment of 1H, 13C and 15N resonances of N-terminal domain of DnaA protein. Biomolecular NMR Assignments, 2007, 1, 57-59.	0.8	4
60	Xâ€ <b>ғ</b> ay crystal structure of <i>EscherichiaÂcoli</i> HspQ, a protein involved in the retardation of replication initiation. FEBS Letters, 2017, 591, 3805-3816.	2.8	4
61	Insight into the interaction between PriB and DnaT on bacterial DNA replication restart: Significance of the residues on PriB dimer interface and highly acidic region on DnaT. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 367-375.	2.3	4
62	A Simple Search of TM Segments in Polytopic Membrane Protein Using Matrix - Assisted Laser Desorptionlonization Time - of - Flight Mass Spectrometry. Protein and Peptide Letters, 2006, 13, 761-767.	0.9	3
63	Crystal Structures of K33 Mutant Hen Lysozymes with Enhanced Activities. Journal of Biochemistry, 2008, 144, 619-623.	1.7	3
64	The structure of hyperthermophilic βâ€ <i>N</i> â€acetylglucosaminidase reveals a novel dimer architecture associated with the active site. FEBS Journal, 2014, 281, 5092-5103.	4.7	3
65	Effect of O-glycosylation on amyloid fibril formation of the variable domain in the Vλ6 light chain mutant Wil. International Journal of Biological Macromolecules, 2021, 166, 342-351.	7.5	3
66	Improvement of the affinity of an anti-rat P2X4 receptor antibody by introducing electrostatic interactions. Scientific Reports, 2022, 12, 131.	3.3	3
67	Detection of a Local Interaction of Hen Lysozyme under Highly Denaturing Conditions Using Chemically 13C-Enriched Methionine Resonance. Journal of Biochemistry, 1998, 123, 313-317.	1.7	2
68	Effect of Protein Concentration and pH on the Chitinase Activity of Tapes japonica Lysozyme. Protein and Peptide Letters, 2010, 17, 172-175.	0.9	2
69	A structural model of the PriB–DnaT complex in EscherichiaÂcoli replication restart. FEBS Letters, 2021, 595, 341-350.	2.8	2
70	Detection of Subtle Differences in the Surface Structure of Lysozymes by Use of an Immobilized Fab Fragment. Journal of Biochemistry, 1993, 113, 174-179.	1.7	1
71	An Improved Method for Preparing Lysozyme with Chemically 13C-Enriched Methionine Residues Using 2-Aminothiophenol as a Reagent of Thiolysis. Journal of Biochemistry, 1997, 122, 1153-1159.	1.7	1
72	Arg 901 in the AE1 C-terminal tail is involved in conformational change but not in substrate binding. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 658-665.	2.6	1

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73	Catalytic Mechanism of Lysozyme Based on the Structures of Invertebrate-type Lysozyme and Chicken-type Lysozyme. Seibutsu Butsuri, 2017, 57, 140-143.	0.1	1
74	Analysis of binding residues in monoclonal antibody with high affinity for the head domain of the rat P2X4 receptor. Journal of Biochemistry, 2021, 169, 491-496.	1.7	1
75	A metal binding in the polypeptide chain improves the folding efficiency of a denatured and reduced protein. Biopolymers, 2002, 64, 106-114.	2.4	Ο
76	Evidence for the Binding of Phosphate Ion to the C-Terminus Region in Aβ1-40 Using Heteronuclear NMR Analyses. Protein and Peptide Letters, 2010, 17, 176-180.	0.9	0
77	Helicase and Its Interacting Factors: Regulation Mechanism, Characterization, Structure, and Application for Drug Design. BioMed Research International, 2015, 2015, 1-1.	1.9	Ο
78	Biosynthetic Mechanism of Polytopic Membrane Protein as Deduced by Study of Band 3 Protein. Seibutsu Butsuri, 2006, 46, 4-9.	0.1	0
79	Structural Analysis of Hen Egg Lysozyme Refolded after Denaturation at Acidic pH. Protein Journal, 2022, 41, 71.	1.6	0
80	Compound screening identified gossypetin and isoquercitrin as novel inhibitors for amyloid fibril formations of Vî»6 proteins associated with AL amyloidosis. Biochemical and Biophysical Research	2.1	0

Communications, 2022, 596, 22-28.