

Masayuki Oda

List of Publications by Year in descending order

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100
papers

2,429
citations

279487

23
h-index

223531

46
g-index

101
all docs

101
docs citations

101
times ranked

2165
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Analysis of Hen Egg Lysozyme Refolded after Denaturation at Acidic pH. <i>Protein Journal</i> , 2022, 41, 71.	0.7	0
2	Pivotal role of a conserved histidine in <i>Escherichia coli</i> ribonuclease HI as proposed by X-ray crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 390-398.	1.1	4
3	Interdomain interactions in Grb2 revealed by the conformational stability and CD28 binding analysis. <i>Biophysical Chemistry</i> , 2022, 284, 106792.	1.5	1
4	A Trade-off Between Thermostability and Binding Affinity of Anti-(4-hydroxy-3-nitrophenyl)Acetyl Antibodies During the Course of Affinity Maturation. <i>Protein Journal</i> , 2022, 41, 293-303.	0.7	4
5	Structural basis of mutants of PET-degrading enzyme from <i>Saccharomonospora viridis</i> AHK190 with high activity and thermal stability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 502-511.	1.5	17
6	Multiple structural states of Ca ²⁺ -regulated PET hydrolase, Cut190, and its correlation with activity and stability. <i>Journal of Biochemistry</i> , 2021, 169, 207-213.	0.9	12
7	Cutinases from thermophilic bacteria (actinomycetes): From identification to functional and structural characterization. <i>Methods in Enzymology</i> , 2021, 648, 159-185.	0.4	8
8	Structural basis for Ca ²⁺ -dependent catalysis of a cutinase-like enzyme and its engineering: application to enzymatic PET depolymerization. <i>Biophysics and Physicobiology</i> , 2021, 18, 168-176.	0.5	7
9	Molecular interactions of the CTLA-4 cytoplasmic region with the phosphoinositide 3-kinase SH2 domains. <i>Molecular Immunology</i> , 2021, 131, 51-59.	1.0	8
10	Single-chain Fv antibody covalently linked to antigen peptides and its structural evaluation. <i>Analytical Biochemistry</i> , 2021, 629, 114312.	1.1	1
11	Effects of chain length, temperature, and ionic strength on association and dissociation thermodynamics of DNA. <i>Chemical Thermodynamics and Thermal Analysis</i> , 2021, 3-4, 100015.	0.7	1
12	Conformational changes of α -helical peptides with different hydrophobic residues induced by metal-ion binding. <i>Biophysical Chemistry</i> , 2021, 277, 106661.	1.5	2
13	Structural dynamics of a DNA-binding protein analyzed using diffracted X-ray tracking. <i>Biophysical Chemistry</i> , 2021, 278, 106669.	1.5	2
14	DNA-binding function of c-Myb R2R3 around thermal denaturation temperature. <i>Biophysics and Physicobiology</i> , 2021, 18, 78-84.	0.5	4
15	Varying the Directionality of Protein Catalysts for Aldol and Retroaldol Reactions. <i>ChemBioChem</i> , 2021, , .	1.3	0
16	Thermodynamics of nucleic acids. <i>Drug Delivery System</i> , 2021, 36, 353-359.	0.0	0
17	Structural and functional evaluation of single-chain Fv antibody HyC1 recognizing the residual native structure of hen egg lysozyme. <i>Bioscience, Biotechnology and Biochemistry</i> , 2020, 84, 358-364.	0.6	1
18	Na ⁺ -balance between structural stability and DNA-binding ability of c-Myb R2R3 under physiological ionic conditions. <i>Biophysical Chemistry</i> , 2020, 258, 106319.	1.5	8

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19	Current State and Perspectives Related to the Polyethylene Terephthalate Hydrolases Available for Biorecycling. ACS Sustainable Chemistry and Engineering, 2020, 8, 8894-8908.	3.2	181
20	Crystal Structures of Polyethylene Terephthalate-Degrading Enzyme Cut190 in Substrate-Bound States Reveal the Enzymatic Reaction Cycle Accelerated by Calcium Ion. ACS Symposium Series, 2020, , 65-74.	0.5	0
21	Folding thermodynamics of PET-hydrolyzing enzyme Cut190 depending on Ca ²⁺ concentration. Journal of Thermal Analysis and Calorimetry, 2019, 135, 2655-2663.	2.0	31
22	Binding thermodynamics of metal ions to HIV-1 ribonuclease H domain. Journal of Thermal Analysis and Calorimetry, 2019, 135, 2647-2653.	2.0	8
23	Three-dimensional structure of a high affinity anti-(4-hydroxy-3-nitrophenyl)acetyl antibody possessing a glycine residue at position 95 of the heavy chain. Molecular Immunology, 2019, 114, 545-552.	1.0	7
24	Structure and Dynamics of Stacking Interactions in an Antibody Binding Site. Biochemistry, 2019, 58, 2987-2995.	1.2	3
25	Site-specific observation of the conformational change of a protein with ¹⁵ N-labeled Tyr residues using NMR. Analytical Biochemistry, 2019, 574, 34-38.	1.1	0
26	Metal binding to cutinase-like enzyme from <i>Saccharomonospora viridis</i> AHK190 and its effects on enzyme activity and stability. Journal of Biochemistry, 2019, 166, 149-156.	0.9	6
27	Current knowledge on enzymatic PET degradation and its possible application to waste stream management and other fields. Applied Microbiology and Biotechnology, 2019, 103, 4253-4268.	1.7	366
28	Structural and functional properties of Grb2 SH2 dimer in CD28 binding. Biophysics and Physicobiology, 2019, 16, 80-88.	0.5	15
29	Structural and thermodynamic characterization of endo-1,3- β -glucanase: Insights into the substrate recognition mechanism. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 415-425.	1.1	17
30	Effect of a salt-bridge between inter-repeats on the 3D structure of the c-Myb DNA-binding domain revealed by thermodynamic analysis. Journal of Thermal Analysis and Calorimetry, 2018, 131, 335-341.	2.0	8
31	Enzymatic hydrolysis of PET: functional roles of three Ca ²⁺ ions bound to a cutinase-like enzyme, Cut190*, and its engineering for improved activity. Applied Microbiology and Biotechnology, 2018, 102, 10067-10077.	1.7	78
32	DNA-binding induced conformational change of c-Myb R2R3 analyzed using diffracted X-ray tracking. Biochemical and Biophysical Research Communications, 2018, 503, 338-343.	1.0	6
33	Structural Dynamics of the PET-Degrading Cutinase-like Enzyme from <i>Saccharomonospora viridis</i> AHK190 in Substrate-Bound States Elucidates the Ca ²⁺ -Driven Catalytic Cycle. Biochemistry, 2018, 57, 5289-5300.	1.2	59
34	Effects of active site residues of 3β -hydroxysteroid dehydrogenase from <i>Pseudomonas</i> sp. b-0831 on its catalysis and cofactor binding. Bioscience, Biotechnology and Biochemistry, 2018, 82, 1702-1707.	0.6	2
35	Functional characterizations of polyethylene terephthalate-degrading cutinase-like enzyme Cut190 mutants using bis(2-hydroxyethyl) terephthalate as the model substrate. AIMS Biophysics, 2018, 5, 290-302.	0.3	15
36	Mutational analysis of cutinase-like enzyme, Cut190, based on the 3D docking structure with model compounds of polyethylene terephthalate. Journal of Bioscience and Bioengineering, 2017, 124, 28-35.	1.1	51

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37	Tryptophan introduction can change β -glucan binding ability of the carbohydrate-binding module of endo-1,3- β -glucanase. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 951-957.	0.6	2
38	Pronounced effect of hapten binding on thermal stability of an anti-(4-hydroxy-3-nitrophenyl)acetyl antibody possessing a glycine residue at position 95 of the heavy chain. <i>Molecular Immunology</i> , 2017, 85, 130-136.	1.0	6
39	Crystal Structures and Thermodynamic Analysis Reveal Distinct Mechanisms of CD28 Phosphopeptide Binding to the Src Homology 2 (SH2) Domains of Three Adaptor Proteins. <i>Journal of Biological Chemistry</i> , 2017, 292, 1052-1060.	1.6	18
40	First observation of metal ion-induced structural fluctuations of α -helical peptides by using diffracted X-ray tracking. <i>Biophysical Chemistry</i> , 2017, 228, 81-86.	1.5	7
41	A multispecific monoclonal antibody G2 recognizes at least three completely different epitope sequences with high affinity. <i>Protein Science</i> , 2017, 26, 2162-2169.	3.1	8
42	Light-chain residue 95 is critical for antigen binding and multispecificity of monoclonal antibody G2. <i>Biochemical and Biophysical Research Communications</i> , 2017, 490, 1205-1209.	1.0	5
43	Entire-Dataset Analysis of NMR Fast-Exchange Titration Spectra: A Mg ²⁺ Titration Analysis for HIV-1 Ribonuclease H Domain. <i>Journal of Physical Chemistry B</i> , 2016, 120, 12420-12431.	1.2	5
44	Structural and binding properties of laminarin revealed by analytical ultracentrifugation and calorimetric analyses. <i>Carbohydrate Research</i> , 2016, 431, 33-38.	1.1	11
45	Effects of substrate conformational strain on binding kinetics of catalytic antibodies. <i>Biophysics and Physicobiology</i> , 2016, 13, 135-138.	0.5	2
46	Structural dynamics of a single-chain Fv antibody against (4-hydroxy-3-nitrophenyl)acetyl. <i>International Journal of Biological Macromolecules</i> , 2016, 91, 151-157.	3.6	15
47	Molecular dynamics simulations of inclusion complexation of glycyrrhizic acid and cyclodextrins (1:1) in water. <i>Journal of Inclusion Phenomena and Macroscopic Chemistry</i> , 2016, 85, 271-279.	0.9	12
48	Affinity maturation of anti-(4-hydroxy-3-nitrophenyl)acetyl antibodies accompanies a modulation of antigen specificity. <i>Molecular Immunology</i> , 2016, 70, 8-12.	1.0	9
49	Thermodynamic effects of a linker region between two repeats of a protein, c-Myb R2R3, on its stability and structural dynamics. <i>Journal of Thermal Analysis and Calorimetry</i> , 2016, 123, 1763-1767.	2.0	5
50	Folding thermodynamics of c-Myb DNA-binding domain in correlation with its α -helical contents. <i>International Journal of Biological Macromolecules</i> , 2016, 82, 725-732.	3.6	7
51	Functional conformer of c-Myb DNA-binding domain revealed by variable temperature studies. <i>FEBS Journal</i> , 2015, 282, 4497-4514.	2.2	11
52	Structural and physical properties of collagen extracted from moon jellyfish under neutral pH conditions. <i>Bioscience, Biotechnology and Biochemistry</i> , 2015, 79, 1603-1607.	0.6	18
53	Structural basis for the Ca ²⁺ -enhanced thermostability and activity of PET-degrading cutinase-like enzyme from <i>Saccharomonospora viridis</i> AHK190. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 4297-4307.	1.7	95
54	Adaptive Mutations Alter Antibody Structure and Dynamics during Affinity Maturation. <i>Biochemistry</i> , 2015, 54, 2085-2093.	1.2	37

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55	Quantitative analysis by surface plasmon resonance of CD28 interaction with cytoplasmic adaptor molecules Grb2, Gads and p85 PI3K. <i>Immunological Investigations</i> , 2014, 43, 278-291.	1.0	23
56	Aggregation property of glycyrrhizic acid and its interaction with cyclodextrins analyzed by dynamic light scattering, isothermal titration calorimetry, and NMR. <i>Carbohydrate Research</i> , 2014, 392, 25-30.	1.1	10
57	A novel Ca ²⁺ -activated, thermostabilized polyesterase capable of hydrolyzing polyethylene terephthalate from <i>Saccharomonospora viridis</i> AHK190. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 10053-10064.	1.7	222
58	Identification and characterization of a multispecific monoclonal antibody G2 against chicken prion protein. <i>Protein Science</i> , 2014, 23, 1050-1059.	3.1	13
59	Thermodynamic effects of multiple protein conformations on stability and DNA binding. <i>Archives of Biochemistry and Biophysics</i> , 2013, 537, 225-232.	1.4	32
60	High Resolution Crystal Structure of the Grb2 SH2 Domain with a Phosphopeptide Derived from CD28. <i>PLoS ONE</i> , 2013, 8, e74482.	1.1	17
61	Extensively Hydrated but Folded: A Novel State of Globular Proteins Stabilized at High Pressure and Low Temperature. <i>Biophysical Journal</i> , 2012, 102, L8-L10.	0.2	14
62	Protein Dynamics and the Diversity of an Antibody Response. <i>Journal of Biological Chemistry</i> , 2012, 287, 27139-27147.	1.6	30
63	Critical roles of Asp270 and Trp273 in the $\hat{\pm}$ -repeat of the carbohydrate-binding module of endo-1,3- \hat{I}^2 -glucanase for laminarin-binding avidity. <i>Glycoconjugate Journal</i> , 2012, 29, 77-85.	1.4	7
64	Molecular characterization of endo-1,3- \hat{I}^2 -glucanase from <i>Cellulosimicrobium cellulans</i> : Effects of carbohydrate-binding module on enzymatic function and stability. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 1713-1719.	1.1	20
65	Contribution of the trifluoroacetyl group in the thermodynamics of antigen-antibody binding. <i>Journal of Molecular Recognition</i> , 2010, 23, 263-270.	1.1	6
66	Evaluation of the conformational equilibrium of reduced hen egg lysozyme by antibodies to the native form. <i>Archives of Biochemistry and Biophysics</i> , 2010, 494, 145-150.	1.4	13
67	Creation of a Type 1 Blue Copper Site within a de Novo Coiled-Coil Protein Scaffold. <i>Journal of the American Chemical Society</i> , 2010, 132, 18191-18198.	6.6	33
68	The effect of the side chain length of Asp and Glu on coordination structure of Cu ²⁺ in a <i>de novo</i> designed protein. <i>Biopolymers</i> , 2009, 91, 907-916.	1.2	14
69	Effects of antibody affinity and antigen valence on molecular forms of immune complexes. <i>Molecular Immunology</i> , 2009, 47, 357-364.	1.0	34
70	Exploring the Energy Landscape of Antibody-Antigen Complexes: Protein Dynamics, Flexibility, and Molecular Recognition. <i>Biochemistry</i> , 2008, 47, 7237-7247.	1.2	69
71	1P-067 Roles of the catalytic residues in 3 α -hydroxysteroid dehydrogenase for the cofactor binding and catalytic activity(The 46th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2008, 48, S31.	0.0	0
72	2P-005 Molecular interaction of Grb2 with the cytoplasmic domain of T cell costimulatory receptor CD28(The 46th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2008, 48, S75.	0.0	0

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73	2P-037 Structural and biochemical analysis for the cofactor-induced conformational change of 3 α -hydroxysteroid dehydrogenase(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S80-S81.	0.0	0
74	2P-024 Analysis of conformational change of 3 α -hydroxysteroid dehydrogenase using single-molecule detection system with X-rays(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S82-S83.	0.0	0
75	1P006 Molecular dynamics simulation of 3 α -hydroxysteroid dehydrogenase with NADH : Structural changes in the substrate-binding loop(Proteins-structure and structure-function relationship,Oral Presentations). Seibutsu Butsuri, 2007, 47, S30.	0.78	4
76	3P352 Inclusion complexation of gymnemic acid by β -cyclodextrin(Bioimaging. Behavior. Development and Evolution). Seibutsu Butsuri, 2007, 47, S6.	0.0	0
77	1P026 Interactions of recombinant Gads, Grb2, p85 subunit of PI3K, and their SH2 domains with CD28 cytoplasmic domains(Proteins-structure and structure-function relationship,Oral Presentations). Seibutsu Butsuri, 2007, 47, S30.	0.0	0
78	S04H6 Antigen recognition and hydrolytic mechanism of catalytic antibody(Thermodynamic and Structural Basis for Transition-State Stabilization in Antibody-Catalyzed Hydrolysis. Journal of Molecular Biology, 2007, 369, 198-209.	0.0	0
79	Thermodynamic and Structural Basis for Transition-State Stabilization in Antibody-Catalyzed Hydrolysis. Journal of Molecular Biology, 2007, 369, 198-209.	2.0	12
80	Metal-ion-dependent GFP Emission in Vivo by Combining a Circularly Permutated Green Fluorescent Protein with an Engineered Metal-Ion-Binding Coiled-coil. Journal of the American Chemical Society, 2007, 129, 11378-11383.	6.6	53
81	2P028 Direct observation of antigen-antibody complex : Effects of antigen size, valence, and binding affinity of antibody(Proteins-structure and structure-function relationship,Oral Presentations). Seibutsu Butsuri, 2007, 47, S120.	0.0	0
82	Crystallization and preliminary X-ray analysis of the complex of NADH and 3 α -hydroxysteroid dehydrogenase from <i>Pseudomonas</i> sp. B-0831. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 569-571.	0.7	7
83	Regional and segmental flexibility of antibodies in interaction with antigens of different size. FEBS Journal, 2006, 273, 1476-1487.	2.2	42
84	Apo- and Holo-structures of 3 α -Hydroxysteroid Dehydrogenase from <i>Pseudomonas</i> sp. B-0831. Journal of Biological Chemistry, 2006, 281, 31876-31884.	1.6	16
85	Interaction of gymnemic acid with cyclodextrins analyzed by isothermal titration calorimetry, NMR and dynamic light scattering. FEBS Journal, 2005, 272, 6154-6160.	2.2	16
86	A free energy calculation study of the effect of H ⁺ /F substitution on binding affinity in ligand-antibody interactions. Journal of Computational Chemistry, 2005, 26, 272-282.	1.5	3
87	Structure of β -Glucan Oligomer from Laminarin and Its Effect on Human Monocytes to Inhibit the Proliferation of U937 Cells. Bioscience, Biotechnology and Biochemistry, 2005, 69, 553-558.	0.6	80
88	Transient-phase kinetic studies on the nucleotide binding to 3 α -hydroxysteroid dehydrogenase from <i>Pseudomonas</i> sp. B-0831 using fluorescence stopped-flow procedures. FEBS Journal, 2004, 271, 1774-1780.	0.2	14
89	Kinetic study of the enzymatic cycling reaction conducted with 3 α -hydroxysteroid dehydrogenase in the presence of excessive thio-NAD ⁺ and NADH. Analytical Biochemistry, 2004, 332, 84-89.	1.1	19
90	Molecular characterization of monovalent and multivalent haptens-protein conjugates for analysis of the antigen-antibody interaction. Analytical Biochemistry, 2004, 333, 365-371.	1.1	19

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91	Segmental flexibility and avidity of IgM in the interaction of polyvalent antigens. <i>Molecular Immunology</i> , 2004, 40, 803-811.	1.0	29
92	A role for the P1 anchor residue in the thermal stability of MHC class II molecule I-Ab. <i>Immunology Letters</i> , 2003, 85, 47-52.	1.1	25
93	Thermodynamic and kinetic aspects of antibody evolution during the immune response to hapten. <i>Molecular Immunology</i> , 2003, 39, 801-808.	1.0	55
94	Thermodynamic Analysis of the Increased Stability of Major Histocompatibility Complex Class II Molecule I-Ek Complexed with an Antigenic Peptide at an Acidic pH. <i>Journal of Biological Chemistry</i> , 2003, 278, 14732-14738.	1.6	14
95	Functional Tolerance of <i>Streptomyces Subtilisin</i> Inhibitor toward Conformational and Stability Changes Caused by Single-Point Mutations in the Hydrophobic Core. <i>Journal of Biochemistry</i> , 2002, 132, 991-995.	0.9	4
96	Thermodynamic and kinetic analyses for understanding sequence-specific DNA recognition. <i>Genes To Cells</i> , 2000, 5, 319-326.	0.5	67
97	Reevaluation of stoichiometry and affinity/avidity in interactions between anti-hapten antibodies and mono- or multi-valent antigens. <i>Molecular Immunology</i> , 2000, 37, 1111-1122.	1.0	59
98	Construction of an Artificial Tandem Protein of the c-Myb DNA-Binding Domain and Analysis of Its DNA Binding Specificity. <i>Biochemical and Biophysical Research Communications</i> , 1999, 262, 94-97.	1.0	12
99	Thermodynamics of specific and non-specific DNA binding by the c-myb DNA-binding domain. <i>Journal of Molecular Biology</i> , 1998, 276, 571-590.	2.0	100
100	Investigation of the Pyrimidine Preference by the c-Myb DNA-binding Domain at the Initial Base of the Consensus Sequence. <i>Journal of Biological Chemistry</i> , 1997, 272, 17966-17971.	1.6	20