

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
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101
all docs

101
docs citations

101
times ranked

2165
citing authors

#	ARTICLE	IF	CITATIONS
1	Current knowledge on enzymatic PET degradation and its possible application to waste stream management and other fields. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 4253-4268.	1.7	366
2	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
3	Current State and Perspectives Related to the Polyethylene Terephthalate Hydrolases Available for Biorecycling. <i>ACS Sustainable Chemistry and Engineering</i> , 2020, 8, 8894-8908.	3.2	181
4	Thermodynamics of specific and non-specific DNA binding by the c-myc DNA-binding domain. <i>Journal of Molecular Biology</i> , 1998, 276, 571-590.	2.0	100
5	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
6	Structure of ¹²⁵ I-Glucan Oligomer from Laminarin and Its Effect on Human Monocytes to Inhibit the Proliferation of U937 Cells. <i>Bioscience, Biotechnology and Biochemistry</i> , 2005, 69, 553-558.	0.6	80
7	Enzymatic hydrolysis of PET: functional roles of three Ca ²⁺ ions bound to a cutinase-like enzyme, Cut190*, and its engineering for improved activity. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 10067-10077.	1.7	78
8	Exploring the Energy Landscape of Antibody-Antigen Complexes: Protein Dynamics, Flexibility, and Molecular Recognition. <i>Biochemistry</i> , 2008, 47, 7237-7247.	1.2	69
9	Thermodynamic and kinetic analyses for understanding sequence-specific DNA recognition. <i>Genes To Cells</i> , 2000, 5, 319-326.	0.5	67
10	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
11	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. <i>Biochemistry</i> , 2018, 57, 5289-5300.	1.2	59
12	Thermodynamic and kinetic aspects of antibody evolution during the immune response to hapten. <i>Molecular Immunology</i> , 2003, 39, 801-808.	1.0	55
13	Metal-ion-dependent GFP Emission in Vivo by Combining a Circularly Permutated Green Fluorescent Protein with an Engineered Metal-Ion-Binding Coiled-coil. <i>Journal of the American Chemical Society</i> , 2007, 129, 11378-11383.	6.6	53
14	Mutational analysis of cutinase-like enzyme, Cut190, based on the 3D docking structure with model compounds of polyethylene terephthalate. <i>Journal of Bioscience and Bioengineering</i> , 2017, 124, 28-35.	1.1	51
15	Regional and segmental flexibility of antibodies in interaction with antigens of different size. <i>FEBS Journal</i> , 2006, 273, 1476-1487.	2.2	42
16	Adaptive Mutations Alter Antibody Structure and Dynamics during Affinity Maturation. <i>Biochemistry</i> , 2015, 54, 2085-2093.	1.2	37
17	Effects of antibody affinity and antigen valence on molecular forms of immune complexes. <i>Molecular Immunology</i> , 2009, 47, 357-364.	1.0	34
18	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

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19	Thermodynamic effects of multiple protein conformations on stability and DNA binding. Archives of Biochemistry and Biophysics, 2013, 537, 225-232.	1.4	32
20	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
21	Protein Dynamics and the Diversity of an Antibody Response. Journal of Biological Chemistry, 2012, 287, 27139-27147.	1.6	30
22	Segmental flexibility and avidity of IgM in the interaction of polyvalent antigens. Molecular Immunology, 2004, 40, 803-811.	1.0	29
23	A role for the P1 anchor residue in the thermal stability of MHC class II molecule I-Ab. Immunology Letters, 2003, 85, 47-52.	1.1	25
24	Quantitative analysis by surface plasmon resonance of CD28 interaction with cytoplasmic adaptor molecules Grb2, Gads and p85 PI3K. Immunological Investigations, 2014, 43, 278-291.	1.0	23
25	Investigation of the Pyrimidine Preference by the c-Myb DNA-binding Domain at the Initial Base of the Consensus Sequence. Journal of Biological Chemistry, 1997, 272, 17966-17971.	1.6	20
26	Molecular characterization of endo-1,3- β -glucanase from Cellulosimicrobium cellulans: Effects of carbohydrate-binding module on enzymatic function and stability. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 1713-1719.	1.1	20
27	Kinetic study of the enzymatic cycling reaction conducted with 3 β -hydroxysteroid dehydrogenase in the presence of excessive thio-NAD ⁺ and NADH. Analytical Biochemistry, 2004, 332, 84-89.	1.1	19
28	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
29	Structural and physical properties of collagen extracted from moon jellyfish under neutral pH conditions. Bioscience, Biotechnology and Biochemistry, 2015, 79, 1603-1607.	0.6	18
30	Crystal Structures and Thermodynamic Analysis Reveal Distinct Mechanisms of CD28 Phosphopeptide Binding to the Src Homology 2 (SH2) Domains of Three Adaptor Proteins. Journal of Biological Chemistry, 2017, 292, 1052-1060.	1.6	18
31	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
32	Structural basis of mutants of PET-degrading enzyme from <i>Saccharomonospora viridis</i> AHK190 with high activity and thermal stability. Proteins: Structure, Function and Bioinformatics, 2021, 89, 502-511.	1.5	17
33	High Resolution Crystal Structure of the Grb2 SH2 Domain with a Phosphopeptide Derived from CD28. PLoS ONE, 2013, 8, e74482.	1.1	17
34	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
35	Apo- and Holo-structures of 3 β -Hydroxysteroid Dehydrogenase from <i>Pseudomonas</i> B-0831. Journal of Biological Chemistry, 2006, 281, 31876-31884.	1.6	16
36	Structural dynamics of a single-chain Fv antibody against (4-hydroxy-3-nitrophenyl)acetyl. International Journal of Biological Macromolecules, 2016, 91, 151-157.	3.6	15

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37	Structural and functional properties of Grb2 SH2 dimer in CD28 binding. <i>Biophysics and Physicobiology</i> , 2019, 16, 80-88.	0.5	15
38	Functional characterizations of polyethylene terephthalate-degrading cutinase-like enzyme Cut190 mutants using bis(2-hydroxyethyl) terephthalate as the model substrate. <i>AIMS Biophysics</i> , 2018, 5, 290-302.	0.3	15
39	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
40	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. <i>FEBS Journal</i> , 2004, 271, 1774-1780.	0.2	14
41	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
42	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
43	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
44	Identification and characterization of a multispecific monoclonal antibody G2 against chicken prion protein. <i>Protein Science</i> , 2014, 23, 1050-1059.	3.1	13
45	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
46	Thermodynamic and Structural Basis for Transition-State Stabilization in Antibody-Catalyzed Hydrolysis. <i>Journal of Molecular Biology</i> , 2007, 369, 198-209.	2.0	12
47	Molecular dynamics simulations of inclusion complexation of glycyrrhizic acid and cyclodextrins (1:1) in water. <i>Journal of Inclusion Phenomena and Macrocyclic Chemistry</i> , 2016, 85, 271-279.	0.9	12
48	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
49	Functional conformer of c-Myb DNA-binding domain revealed by variable temperature studies. <i>FEBS Journal</i> , 2015, 282, 4497-4514.	2.2	11
50	Structural and binding properties of laminarin revealed by analytical ultracentrifugation and calorimetric analyses. <i>Carbohydrate Research</i> , 2016, 431, 33-38.	1.1	11
51	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
52	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
53	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
54	Effect of a salt-bridge between inter-repeats on the 3D structure of the c-Myb DNA-binding domain revealed by thermodynamic analysis. <i>Journal of Thermal Analysis and Calorimetry</i> , 2018, 131, 335-341.	2.0	8

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55	Binding thermodynamics of metal ions to HIV-1 ribonuclease H domain. <i>Journal of Thermal Analysis and Calorimetry</i> , 2019, 135, 2647-2653.	2.0	8
56	Na ⁺ -ve 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
57	Cutinases from thermophilic bacteria (actinomycetes): From identification to functional and structural characterization. <i>Methods in Enzymology</i> , 2021, 648, 159-185.	0.4	8
58	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
59	Crystallization and preliminary X-ray analysis of the complex of NADH and 3 β -hydroxysteroid dehydrogenase from <i>Pseudomonas</i> B-0831. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 569-571.	0.7	7
60	Critical roles of Asp270 and Trp273 in the β -repeat of the carbohydrate-binding module of endo-1,3- β -glucanase for laminarin-binding avidity. <i>Glycoconjugate Journal</i> , 2012, 29, 77-85.	1.4	7
61	Folding thermodynamics of c-Myb DNA-binding domain in correlation with its β -helical contents. <i>International Journal of Biological Macromolecules</i> , 2016, 82, 725-732.	3.6	7
62	First observation of metal ion-induced structural fluctuations of β -helical peptides by using diffracted X-ray tracking. <i>Biophysical Chemistry</i> , 2017, 228, 81-86.	1.5	7
63	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. <i>Molecular Immunology</i> , 2019, 114, 545-552.	1.0	7
64	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
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	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
67	DNA-binding induced conformational change of c-Myb R2R3 analyzed using diffracted X-ray tracking. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 338-343.	1.0	6
68	Metal binding to cutinase-like enzyme from <i>Saccharomonospora viridis</i> AHK190 and its effects on enzyme activity and stability. <i>Journal of Biochemistry</i> , 2019, 166, 149-156.	0.9	6
69	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
70	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
71	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
72	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

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73	DNA-binding function of c-Myb R2R3 around thermal denaturation temperature. Biophysics and Physicobiology, 2021, 18, 78-84.	0.5	4
74	Pivotal role of a conserved histidine in <i>Escherichia coli</i> ribonuclease HI as proposed by X-ray crystallography. Acta Crystallographica Section D: Structural Biology, 2022, 78, 390-398.	1.1	4
75	A Trade-off Between Thermostability and Binding Affinity of Anti-(4-hydroxy-3-nitrophenyl)Acetyl Antibodies During the Course of Affinity Maturation. Protein Journal, 2022, 41, 293-303.	0.7	4
76	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
77	Structure and Dynamics of Stacking Interactions in an Antibody Binding Site. Biochemistry, 2019, 58, 2987-2995.	1.2	3
78	Effects of substrate conformational strain on binding kinetics of catalytic antibodies. Biophysics and Physicobiology, 2016, 13, 135-138.	0.5	2
79	Tryptophan introduction can change β -glucan binding ability of the carbohydrate-binding module of endo-1,3- β -glucanase. Bioscience, Biotechnology and Biochemistry, 2017, 81, 951-957.	0.6	2
80	Effects of active site residues of β -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
81	Conformational changes of α -helical peptides with different hydrophobic residues induced by metal-ion binding. Biophysical Chemistry, 2021, 277, 106661.	1.5	2
82	Structural dynamics of a DNA-binding protein analyzed using diffracted X-ray tracking. Biophysical Chemistry, 2021, 278, 106669.	1.5	2
83	Structural and functional evaluation of single-chain Fv antibody HyC1 recognizing the residual native structure of hen egg lysozyme. Bioscience, Biotechnology and Biochemistry, 2020, 84, 358-364.	0.6	1
84	Single-chain Fv antibody covalently linked to antigen peptides and its structural evaluation. Analytical Biochemistry, 2021, 629, 114312.	1.1	1
85	Effects of chain length, temperature, and ionic strength on association and dissociation thermodynamics of DNA. Chemical Thermodynamics and Thermal Analysis, 2021, 3-4, 100015.	0.7	1
86	Interdomain interactions in Grb2 revealed by the conformational stability and CD28 binding analysis. Biophysical Chemistry, 2022, 284, 106792.	1.5	1
87	1P006 Molecular dynamics simulation of β -hydroxysteroid dehydrogenase with NADH : Structural changes in the substrate-binding loop(Proteins-structure and structure-function relationship,Oral) Tj ETQq1 1 0.784314 rgBTd/Overlock	0.0	0
88	3P352 Inclusion complexation of gymnemic acid by β -cyclodextrin(Bioimaging. Behavior. Development and) Tj ETQq0 0 0 rgBTd/Overlock	0.0	0
89	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
90	S04H6 Antigen recognition and hydrolytic mechanism of catalytic antibody(Thermodynamic) Tj ETQq0 0 0 rgBTd/Overlock 10 Tf 50 67 T Seibutsu Butsuri, 2007, 47, S6.	0.0	0

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91	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
92	1P-067 Roles of the catalytic residues in 3alpha-hydroxysteroid dehydrogenase for the cofactor binding and catalytic activity(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S31.	0.0	0
93	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). Seibutsu Butsuri, 2008, 48, S75.	0.0	0
94	2P-037 Structural and biochemical analysis for the cofactor-induced conformational change of 3alpha-hydroxysteroid dehydrogenase(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S80-S81.	0.0	0
95	Site-specific observation of the conformational change of a protein with 15N-labeled Tyr residues using NMR. Analytical Biochemistry, 2019, 574, 34-38.	1.1	0
96	2P-024 Analysis of conformational change of 3alpha-hydroxysteroid dehydrogenase using single-molecule detection system with X-rays(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S31.	0.0	0
97	Varying the Directionality of Protein Catalysts for Aldol and Retroaldol Reactions. ChemBioChem, 2021, , .	1.3	0
98	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
99	Structural Analysis of Hen Egg Lysozyme Refolded after Denaturation at Acidic pH. Protein Journal, 2022, 41, 71.	0.7	0
100	Thermodynamics of nucleic acids. Drug Delivery System, 2021, 36, 353-359.	0.0	0