Hidemasa Kondo

List of Publications by Year
in descending order

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52 papers	2,188 citations	218381 26 h-index	223531 46 g-index
53 all docs	53 docs citations	53 times ranked	2317 citing authors

#	Article	IF	Citations
1	Tetra-n-butylammonium bromideâ€"water (1/38). Acta Crystallographica Section C: Crystal Structure Communications, 2005, 61, o65-o66.	0.4	214
2	Highly efficient recovery of functional single-chain Fv fragments from inclusion bodies overexpressed in Escherichia coli by controlled introduction of oxidizing reagentâ€"application to a human single-chain Fv fragment. Journal of Immunological Methods, 1998, 219, 119-129.	0.6	190
3	Antifreeze proteins from snow mold fungi. Canadian Journal of Botany, 2003, 81, 1175-1181.	1.2	108
4	Thermal Stabilization of Bacillus subtilis Family-11 Xylanase by Directed Evolution. Journal of Biological Chemistry, 2006, 281, 10236-10242.	1.6	106
5	Ice-binding site of snow mold fungus antifreeze protein deviates from structural regularity and high conservation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9360-9365.	3.3	92
6	Escherichia coli positive regulator OmpR has a large loop structure at the putative RNA polymerase interaction site. Nature Structural and Molecular Biology, 1997, 4, 28-31.	3.6	87
7	Thermodynamic Consequences of Mutations in Vernier Zone Residues of a Humanized Anti-human Epidermal Growth Factor Receptor Murine Antibody, 528. Journal of Biological Chemistry, 2008, 283, 1156-1166.	1.6	86
8	Comparison of functional properties of two fungal antifreeze proteins from <i>Antarctomycesâ€ƒpsychrotrophicus</i> and <i>Typhulaâ€ƒishikariensis</i>. FEBS Journal, 2010, 277, 394-403.	2.2	76
9	Alternate conformations observed in catalytic serine ofBacillus subtilislipase determined at 1.3â€…Ã… resolution. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1168-1174.	2.5	67
10	Crystal Structure and Mutational Analysis of Ca2+-Independent Type II Antifreeze Protein from Longsnout Poacher, Brachyopsis rostratus. Journal of Molecular Biology, 2008, 382, 734-746.	2.0	66
11	Cold adaptation of fungi obtained from soil and lake sediment in the Skarvsnes ice-free area, Antarctica. FEMS Microbiology Letters, 2013, 346, 121-130.	0.7	64
12	Hyperactive antifreeze protein from an <scp>A</scp>ntarctic sea ice bacterium <i><scp>C</scp>olwellia</i> sp. has a compound iceâ€binding site without repetitive sequences. FEBS Journal, 2014, 281, 3576-3590.	2.2	64
13	Crystal Structure of Anti-Hen Egg White Lysozyme Antibody (HyHEL-10) Fv-Antigen Complex. Journal of Biological Chemistry, 1999, 274, 27623-27631.	1.6	63
14	The Role of Hydrogen Bonding via Interfacial Water Molecules in Antigen-Antibody Complexation. Journal of Biological Chemistry, 2003, 278, 5410-5418.	1.6	60
15	Relationship between the Size of the Bottleneck 15 Ã… from Iron in the Main Channel and the Reactivity of Catalase Corresponding to the Molecular Size of Substratesâ€¡. Biochemistry, 2007, 46, 11-22.	1.2	54
16	The Structural Basis for the Exo-mode of Action in GH74 Oligoxyloglucan Reducing End-specific Cellobiohydrolase. Journal of Molecular Biology, 2007, 370, 53-62.	2.0	52
17	Hydrophobic ice-binding sites confer hyperactivity of an antifreeze protein from a snow mold fungus. Biochemical Journal, 2016, 473, 4011-4026.	1.7	49
18	Critical contribution of VHâ€"VL interaction to reshaping of an antibody: The case of humanization of antiâ€lysozyme antibody, HyHELâ€10. Protein Science, 2008, 17, 261-270.	3.1	48

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19	NMR Analysis of Type III Antifreeze Protein Intramolecular Dimer. Journal of Biological Chemistry, 2001, 276, 1304-1310.	1.6	47
20	Tandem Repeat of a Seven-Bladed Î²-Propeller Domain in Oligoxyloglucan Reducing-End-Specific Cellobiohydrolase. Structure, 2004, 12, 1209-1217.	1.6	45
21	Structural Consequences of Mutations in Interfacial Tyr Residues of a Protein Antigen-Antibody Complex. Journal of Biological Chemistry, 2007, 282, 6783-6791.	1.6	44
22	Ice recrystallization is strongly inhibited when antifreeze proteins bind to multiple ice planes. Scientific Reports, 2019, 9, 2212.	1.6	43
23	Crystal structure and enhanced activity of a cutinaseâ€like enzyme from <i>Cryptococcus</i> sp. strain Sâ€2. Proteins: Structure, Function and Bioinformatics, 2009, 77, 710-717.	1.5	40
24	Structural Evidence for Entropic Contribution of Salt Bridge Formation to a Protein Antigen-Antibody Interaction. Journal of Biological Chemistry, 2001, 276, 23042-23050.	1.6	36
25	Concentration-dependent oligomerization of an alpha-helical antifreeze polypeptide makes it hyperactive. Scientific Reports, 2017, 7, 42501.	1.6	35
26	Polypentagonal ice-like water networks emerge solely in an activity-improved variant of ice-binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 5456-5461.	3.3	32
27	Iceâ€binding proteins from the fungus <i>Antarctomyces psychrotrophicus</i> possibly originate from two different bacteria through horizontal gene transfer. FEBS Journal, 2019, 286, 946-962.	2.2	25
28	The crystal structure of a xyloglucanâ€specific endoâ€Î²â€1,4â€glucanase from <i>Geotrichum</i> sp. M128 xyloglucanase reveals a key amino acid residue for substrate specificity. FEBS Journal, 2009, 276, 5094-5100.	2.2	24
29	Mass preparation and technological development of an antifreeze protein. Synthesiology, 2008, 1, 7-14.	0.2	23
30	Can lipases hydrolyze a peptide bond?. Enzyme and Microbial Technology, 2003, 32, 655-657.	1.6	19
31	Contribution of Asparagine Residues to the Stabilization of a Proteinaceous Antigen-Antibody Complex, HyHEL-10-Hen Egg White Lysozyme. Journal of Biological Chemistry, 2010, 285, 7686-7696.	1.6	18
32	Annealing condition influences thermal hysteresis of fungal type ice-binding proteins. Cryobiology, 2014, 68, 159-161.	0.3	17
33	Fish-Derived Antifreeze Proteins and Antifreeze Glycoprotein Exhibit a Different Ice-Binding Property with Increasing Concentration. Biomolecules, 2020, 10, 423.	1.8	17
34	Identification of the fatty acid binding site on glutathione S-transferase P. Biochemical and Biophysical Research Communications, 1992, 189, 197-205.	1.0	16
35	A Human Antibody Fragment with High Affinity for Biodegradable Polymer Film. Bioconjugate Chemistry, 2007, 18, 645-651.	1.8	16
36	The Absolute Stereochemistry of Okamurallene and Its Congeners, Halogenated C15Nonterpenoids from the Red AlgaLaurencia intricata. Chemistry Letters, 1991, 20, 33-34.	0.7	15

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37	Structural Consequences of Target Epitope-directed Functional Alteration of an Antibody. Journal of Biological Chemistry, 2003, 278, 24929-24936.	1.6	15
38	Calcium-Binding Generates the Semi-Clathrate Waters on a Type II Antifreeze Protein to Adsorb onto an Ice Crystal Surface. Biomolecules, 2019, 9, 162.	1.8	15
39	Characterization of microbial antifreeze protein with intermediate activity suggests that a bound-water network is essential for hyperactivity. Scientific Reports, 2021, 11, 5971.	1.6	15
40	Multiple binding modes of a moderate ice-binding protein from a polar microalga. Physical Chemistry Chemical Physics, 2018, 20, 25295-25303.	1.3	14
41	Crystallization and X-ray Studies of the DNA-binding Domain of OmpR Protein, a Positive Regulator Involved in Activation of Osmoregulatory Genes in Escherichia coli. Journal of Molecular Biology, 1994, 235, 780-782.	2.0	12
42	An Ice-Binding Protein from an Antarctic Ascomycete Is Fine-Tuned to Bind to Specific Water Molecules Located in the Ice Prism Planes. Biomolecules, 2020, 10, 759.	1.8	8
43	Discovery of Hyperactive Antifreeze Protein from Phylogenetically Distant Beetles Questions Its Evolutionary Origin. International Journal of Molecular Sciences, 2021, 22, 3637.	1.8	8
44	Subzero Nonfreezing Hypothermia with Insect Antifreeze Protein Dramatically Improves Survival Rate of Mammalian Cells. International Journal of Molecular Sciences, 2021, 22, 12680.	1.8	8
45	Crystallization and preliminary X-ray crystallographic analysis of Ca2+-independent and Ca2+-dependent species of the type II antifreeze protein. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 538-541.	0.7	7
46	ä¸å‡†è›‹ç™½è³ªã®å§é‡ç²¾è£½ã¨æ–°ãŸãªå¿œç”¨é–‹æ‹“ ï¼å®Ÿç”¨åŒ–ã’æŒ‡åã™ã‚‹è›‹ç™½è³ªç”ç©¶ï¼š Synthesiology, 2008, 1, 7-1	0.2	7
47	Crystallization and preliminary X-ray crystallographic study on a xyloglucan-specific exo-Î²-glycosidase, oligoxyloglucan reducing-end specific cellobiohydrolase. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1838-1839.	2.5	6
48	ONIOM Study of the Mechanism of the Enzymatic Hydrolysis of Biodegradable Plastics. Bulletin of the Chemical Society of Japan, 2009, 82, 338-346.	2.0	6
49	Functions and Structures of Xyloglucan Hydrolases Belonging to Glycoside Hydrolase Family 74. Journal of Applied Glycoscience (1999), 2005, 52, 169-176.	0.3	3
50	Crystallization and Preliminary X-Ray Studies of Two Serine Proteinase Inhibitors, BGIA and BGIT, from the Seeds of Bitter Gourd. Journal of Structural Biology, 1997, 120, 204-206.	1.3	2
51	ä¸å‡†ã‚¿ãƒ³ãƒ'ã‚¯è³ª æ©Ÿèƒ½ã¨å¿œç”¨. Kagaku To Seibutsu, 2010, 48, 381-388.	0.0	2
52	Title is missing!. Kagaku To Seibutsu, 2014, 52, 10-12.	0.0	0