

Hidemasa Kondo

List of Publications by Year in descending order

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52
papers

2,188
citations

218677

26
h-index

223800

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.	1.4	190
3	Antifreeze proteins from snow mold fungi. Canadian Journal of Botany, 2003, 81, 1175-1181.	1.1	108
4	Thermal Stabilization of Bacillus subtilis Family-11 Xylanase by Directed Evolution. Journal of Biological Chemistry, 2006, 281, 10236-10242.	3.4	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.	7.1	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.	8.2	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.	3.4	86
8	Comparison of functional properties of two fungal antifreeze proteins from <i>Antarctomyces psychrotrophicus</i> and <i>Typhula fishikariensis</i> . FEBS Journal, 2010, 277, 394-403.	4.7	76
9	Alternate conformations observed in catalytic serine of Bacillus subtilis lipase determined at 1.3 Å resolution. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1168-1174.	2.5	67
10	Crystal Structure and Mutational Analysis of Ca ²⁺ -Independent Type II Antifreeze Protein from Longsnout Poacher, <i>Brachyopsis rostratus</i> . Journal of Molecular Biology, 2008, 382, 734-746.	4.2	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.	1.8	64
12	Hyperactive antifreeze protein from an Antarctic sea ice bacterium <i>Colwellia</i> sp. has a compound ice-binding site without repetitive sequences. FEBS Journal, 2014, 281, 3576-3590.	4.7	64
13	Crystal Structure of Anti-Hen Egg White Lysozyme Antibody (HyHEL-10) Fv-Antigen Complex. Journal of Biological Chemistry, 1999, 274, 27623-27631.	3.4	63
14	The Role of Hydrogen Bonding via Interfacial Water Molecules in Antigen-Antibody Complexation. Journal of Biological Chemistry, 2003, 278, 5410-5418.	3.4	60
15	Relationship between the Size of the Bottleneck 15 Å from Iron in the Main Channel and the Reactivity of Catalase Corresponding to the Molecular Size of Substrates. Biochemistry, 2007, 46, 11-22.	2.5	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.	4.2	52
17	Hydrophobic ice-binding sites confer hyperactivity of an antifreeze protein from a snow mold fungus. Biochemical Journal, 2016, 473, 4011-4026.	3.7	49
18	Critical contribution of VHâ€“VL interaction to reshaping of an antibody: The case of humanization of anti-lysozyme antibody, HyHEL-10. Protein Science, 2008, 17, 261-270.	7.6	48

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19	NMR Analysis of Type III Antifreeze Protein Intramolecular Dimer. <i>Journal of Biological Chemistry</i> , 2001, 276, 1304-1310.	3.4	47
20	Tandem Repeat of a Seven-Bladed β^2 -Propeller Domain in Oligoxyloglucan Reducing-End-Specific Cellobiohydrolase. <i>Structure</i> , 2004, 12, 1209-1217.	3.3	45
21	Structural Consequences of Mutations in Interfacial Tyr Residues of a Protein Antigen-Antibody Complex. <i>Journal of Biological Chemistry</i> , 2007, 282, 6783-6791.	3.4	44
22	Ice recrystallization is strongly inhibited when antifreeze proteins bind to multiple ice planes. <i>Scientific Reports</i> , 2019, 9, 2212.	3.3	43
23	Crystal structure and enhanced activity of a cutinase-like enzyme from <i>Cryptococcus</i> sp. strain Sâ€². <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 710-717.	2.6	40
24	Structural Evidence for Entropic Contribution of Salt Bridge Formation to a Protein Antigen-Antibody Interaction. <i>Journal of Biological Chemistry</i> , 2001, 276, 23042-23050.	3.4	36
25	Concentration-dependent oligomerization of an alpha-helical antifreeze polypeptide makes it hyperactive. <i>Scientific Reports</i> , 2017, 7, 42501.	3.3	35
26	Polypentagonal ice-like water networks emerge solely in an activity-improved variant of ice-binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5456-5461.	7.1	32
27	Ice-binding proteins from the fungus <i>Antarctomyces psychrotrophicus</i> possibly originate from two different bacteria through horizontal gene transfer. <i>FEBS Journal</i> , 2019, 286, 946-962.	4.7	25
28	The crystal structure of a xyloglucan-specific endo- α -1,4-glucanase from <i>Geotrichum</i> sp. M128 xyloglucanase reveals a key amino acid residue for substrate specificity. <i>FEBS Journal</i> , 2009, 276, 5094-5100.	4.7	24
29	Mass preparation and technological development of an antifreeze protein. <i>Synthesiology</i> , 2008, 1, 7-14.	0.2	23
30	Can lipases hydrolyze a peptide bond?. <i>Enzyme and Microbial Technology</i> , 2003, 32, 655-657.	3.2	19
31	Contribution of Asparagine Residues to the Stabilization of a Proteinaceous Antigen-Antibody Complex, HyHEL-10-Hen Egg White Lysozyme. <i>Journal of Biological Chemistry</i> , 2010, 285, 7686-7696.	3.4	18
32	Annealing condition influences thermal hysteresis of fungal type ice-binding proteins. <i>Cryobiology</i> , 2014, 68, 159-161.	0.7	17
33	Fish-Derived Antifreeze Proteins and Antifreeze Glycoprotein Exhibit a Different Ice-Binding Property with Increasing Concentration. <i>Biomolecules</i> , 2020, 10, 423.	4.0	17
34	Identification of the fatty acid binding site on glutathione S-transferase P. <i>Biochemical and Biophysical Research Communications</i> , 1992, 189, 197-205.	2.1	16
35	A Human Antibody Fragment with High Affinity for Biodegradable Polymer Film. <i>Bioconjugate Chemistry</i> , 2007, 18, 645-651.	3.6	16
36	The Absolute Stereochemistry of Okamurallene and Its Congeners, Halogenated C ₁₅ Nonterpenoids from the Red Alga <i>Laurencia intricata</i> . <i>Chemistry Letters</i> , 1991, 20, 33-34.	1.3	15

