

# 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	Discovery of Hyperactive Antifreeze Protein from Phylogenetically Distant Beetles Questions Its Evolutionary Origin. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3637.	4.1	8
2	Characterization of microbial antifreeze protein with intermediate activity suggests that a bound-water network is essential for hyperactivity. <i>Scientific Reports</i> , 2021, 11, 5971.	3.3	15
3	Subzero Nonfreezing Hypothermia with Insect Antifreeze Protein Dramatically Improves Survival Rate of Mammalian Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12680.	4.1	8
4	An Ice-Binding Protein from an Antarctic Ascomycete Is Fine-Tuned to Bind to Specific Water Molecules Located in the Ice Prism Planes. <i>Biomolecules</i> , 2020, 10, 759.	4.0	8
5	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
6	Calcium-Binding Generates the Semi-Clathrate Waters on a Type II Antifreeze Protein to Adsorb onto an Ice Crystal Surface. <i>Biomolecules</i> , 2019, 9, 162.	4.0	15
7	Ice recrystallization is strongly inhibited when antifreeze proteins bind to multiple ice planes. <i>Scientific Reports</i> , 2019, 9, 2212.	3.3	43
8	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
9	Multiple binding modes of a moderate ice-binding protein from a polar microalga. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 25295-25303.	2.8	14
10	Poly-pentagonal 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
11	Concentration-dependent oligomerization of an alpha-helical antifreeze polypeptide makes it hyperactive. <i>Scientific Reports</i> , 2017, 7, 42501.	3.3	35
12	Hydrophobic ice-binding sites confer hyperactivity of an antifreeze protein from a snow mold fungus. <i>Biochemical Journal</i> , 2016, 473, 4011-4026.	3.7	49
13	Title is missing!. <i>Kagaku To Seibutsu</i> , 2014, 52, 10-12.	0.0	0
14	Hyperactive antifreeze protein from an Antarctic sea ice bacterium <i>Colwellia</i> sp. has a compound ice-binding site without repetitive sequences. <i>FEBS Journal</i> , 2014, 281, 3576-3590.	4.7	64
15	Annealing condition influences thermal hysteresis of fungal type ice-binding proteins. <i>Cryobiology</i> , 2014, 68, 159-161.	0.7	17
16	Cold adaptation of fungi obtained from soil and lake sediment in the Skarvsnes ice-free area, Antarctica. <i>FEMS Microbiology Letters</i> , 2013, 346, 121-130.	1.8	64
17	Ice-binding site of snow mold fungus antifreeze protein deviates from structural regularity and high conservation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9360-9365.	7.1	92
18	ä,ê,î,ã,î,f³ãf'ã,`è³æ ©ÿèf½ãã¿œç". <i>Kagaku To Seibutsu</i> , 2010, 48, 381-388.	0.0	2

#	ARTICLE	IF	CITATIONS
19	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
20	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.	3.4	18
21	Crystal structure and enhanced activity of a cutinase-like enzyme from <i>Cryptococcus</i> sp. strain Sâ€2. Proteins: Structure, Function and Bioinformatics, 2009, 77, 710-717.	2.6	40
22	The crystal structure of a xyloglucan-specific endo-1,4-glucanase from <i>Geotrichum</i> sp. M128 xyloglucanase reveals a key amino acid residue for substrate specificity. FEBS Journal, 2009, 276, 5094-5100.	4.7	24
23	ONIOM Study of the Mechanism of the Enzymatic Hydrolysis of Biodegradable Plastics. Bulletin of the Chemical Society of Japan, 2009, 82, 338-346.	3.2	6
24	Critical contribution of VH-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
25	Crystal Structure and Mutational Analysis of Ca <sup>2+</sup> -Independent Type II Antifreeze Protein from Longsnout Poacher, <i>Brachyopsis rostratus</i> . Journal of Molecular Biology, 2008, 382, 734-746.	4.2	66
26	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
27	Mass preparation and technological development of an antifreeze protein. Synthesiology, 2008, 1, 7-14.	0.2	23
28	ä,â†èç™1/2è3âââšé†ç23/4è1/2ã•æ-°ãÿã•â¿œç”é-æ<“i1/4â®ÿç”âCE-ã,æCE†âã™ã,èèç™1/2è3âç”ç©¶1/4• Synthesiology, 2008, 1, 7-14.		
29	Structural Consequences of Mutations in Interfacial Tyr Residues of a Protein Antigen-Antibody Complex. Journal of Biological Chemistry, 2007, 282, 6783-6791.	3.4	44
30	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
31	A Human Antibody Fragment with High Affinity for Biodegradable Polymer Film. Bioconjugate Chemistry, 2007, 18, 645-651.	3.6	16
32	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 Substratesâ€j. Biochemistry, 2007, 46, 11-22.	2.5	54
33	Crystallization and preliminary X-ray crystallographic analysis of Ca <sup>2+</sup> -independent and Ca <sup>2+</sup> -dependent species of the type II antifreeze protein. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 538-541.	0.7	7
34	Thermal Stabilization of <i>Bacillus subtilis</i> Family-11 Xylanase by Directed Evolution. Journal of Biological Chemistry, 2006, 281, 10236-10242.	3.4	106
35	Tetra-n-butylammonium bromideâ€“water (1/38). Acta Crystallographica Section C: Crystal Structure Communications, 2005, 61, o65-o66.	0.4	214
36	Functions and Structures of Xyloglucan Hydrolases Belonging to Glycoside Hydrolase Family 74. Journal of Applied Glycoscience (1999), 2005, 52, 169-176.	0.7	3

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37	Tandem Repeat of a Seven-Bladed $\beta^2$ -Propeller Domain in Oligoxyloglucan Reducing-End-Specific Cellobiohydrolase. <i>Structure</i> , 2004, 12, 1209-1217.	3.3	45
38	Can lipases hydrolyze a peptide bond?. <i>Enzyme and Microbial Technology</i> , 2003, 32, 655-657.	3.2	19
39	Crystallization and preliminary X-ray crystallographic study on a xyloglucan-specific exo- $\beta^2$ -glycosidase, oligoxyloglucan reducing-end specific cellobiohydrolase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1838-1839.	2.5	6
40	Antifreeze proteins from snow mold fungi. <i>Canadian Journal of Botany</i> , 2003, 81, 1175-1181.	1.1	108
41	The Role of Hydrogen Bonding via Interfacial Water Molecules in Antigen-Antibody Complexation. <i>Journal of Biological Chemistry</i> , 2003, 278, 5410-5418.	3.4	60
42	Structural Consequences of Target Epitope-directed Functional Alteration of an Antibody. <i>Journal of Biological Chemistry</i> , 2003, 278, 24929-24936.	3.4	15
43	Alternate conformations observed in catalytic serine of <i>Bacillus subtilis</i> lipase determined at 1.3 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1168-1174.	2.5	67
44	NMR Analysis of Type III Antifreeze Protein Intramolecular Dimer. <i>Journal of Biological Chemistry</i> , 2001, 276, 1304-1310.	3.4	47
45	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
46	Crystal Structure of Anti-Hen Egg White Lysozyme Antibody (HyHEL-10) Fv-Antigen Complex. <i>Journal of Biological Chemistry</i> , 1999, 274, 27623-27631.	3.4	63
47	Highly efficient recovery of functional single-chain Fv fragments from inclusion bodies overexpressed in <i>Escherichia coli</i> by controlled introduction of oxidizing reagent application to a human single-chain Fv fragment. <i>Journal of Immunological Methods</i> , 1998, 219, 119-129.	1.4	190
48	Crystallization and Preliminary X-Ray Studies of Two Serine Proteinase Inhibitors, BGIA and BGIT, from the Seeds of Bitter Melon. <i>Journal of Structural Biology</i> , 1997, 120, 204-206.	2.8	2
49	<i>Escherichia coli</i> positive regulator OmpR has a large loop structure at the putative RNA polymerase interaction site. <i>Nature Structural and Molecular Biology</i> , 1997, 4, 28-31.	8.2	87
50	Crystallization and X-ray Studies of the DNA-binding Domain of OmpR Protein, a Positive Regulator Involved in Activation of Osmoregulatory Genes in <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1994, 235, 780-782.	4.2	12
51	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
52	The Absolute Stereochemistry of Okamurallene and Its Congeners, Halogenated C <sub>15</sub> Nonterpenoids from the Red Alga <i>Laurencia intricata</i> . <i>Chemistry Letters</i> , 1991, 20, 33-34.	1.3	15