

# Shigehiro Kamitori

## List of Publications by Year in descending order

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108  
papers

2,944  
citations

147566

31  
h-index

189595

50  
g-index

109  
all docs

109  
docs citations

109  
times ranked

3093  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of the 2:1 complex between d(GAAGCTTC) and the anticancer drug actinomycin D. <i>Journal of Molecular Biology</i> , 1992, 225, 445-456.	2.0	157
2	Crystal structure of <i>Thermoactinomyces vulgaris</i> R-47 Î±-amylase II (TVAII) hydrolyzing cyclodextrins and pullulan at 2.6 Å... resolution. <i>Journal of Molecular Biology</i> , 1999, 287, 907-921.	2.0	114
3	Crystal Structure of S-Adenosylmethionine Synthetase. <i>Journal of Biological Chemistry</i> , 1996, 271, 136-147.	1.6	112
4	Crystal and molecular structures of double macrocyclic inclusion complexes composed of cyclodextrins, crown ethers, and cations. <i>Journal of the American Chemical Society</i> , 1987, 109, 2409-2414.	6.6	100
5	A [2]Rotaxane Capped by a Cyclodextrin and a Guest:Â Formation of Supramolecular [2]Rotaxane Polymer. <i>Journal of the American Chemical Society</i> , 2005, 127, 2034-2035.	6.6	100
6	Complex Structures of <i>Thermoactinomyces vulgaris</i> R-47 Î±-Amylase 1 with Malto-oligosaccharides Demonstrate the Role of Domain N Acting as a Starch-binding Domain. <i>Journal of Molecular Biology</i> , 2004, 335, 811-822.	2.0	91
7	Structural analysis of fungus-derived FAD glucose dehydrogenase. <i>Scientific Reports</i> , 2015, 5, 13498.	1.6	89
8	Multiple Binding Modes of Anticancer Drug Actinomycin D: X-ray, Molecular Modeling, and Spectroscopic Studies of d(GAAGCTTC) <sub>2</sub> -Actinomycin D Complexes and Its Host DNA. <i>Journal of the American Chemical Society</i> , 1994, 116, 4154-4165.	6.6	88
9	Crystal Structures of d-Tagatose 3-Epimerase from <i>Pseudomonas cichorii</i> and Its Complexes with d-Tagatose and d-Fructose. <i>Journal of Molecular Biology</i> , 2007, 374, 443-453.	2.0	86
10	A Novel Pseudo-Polyrotaxane Structure Composed of Cyclodextrins and a Straight-Chain Polymer:Â Crystal Structures of Inclusion Complexes of Î²-Cyclodextrin with Poly(trimethylene oxide) and Poly(propylene glycol). <i>Macromolecules</i> , 2000, 33, 1500-1502.	2.2	85
11	Crystal structure of the E166A mutant of extended-spectrum Î²-lactamase toho-1 at 1.8 Å... resolution 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 285, 2079-2087.	2.0	83
12	A Real Knot in Protein. <i>Journal of the American Chemical Society</i> , 1996, 118, 8945-8946.	6.6	80
13	Three-Dimensional Structures of Aspartate Aminotransferase from <i>Escherichia coli</i> and Its Mutant Enzyme at 2.5 Å... Resolution. <i>Journal of Biochemistry</i> , 1990, 108, 175-184.	0.9	78
14	Functional and structural bases of a cysteine-less mutant as a long-lasting substitute for galectin-1. <i>Glycobiology</i> , 2008, 18, 1065-1073.	1.3	68
15	Chemoenzymatic Synthesis of the Immunoglobulin Domain of Timâ€³ Carrying a Complexâ€¢Type Nâ€¢Glycan by Using a Oneâ€¢pot Ligation. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 9733-9737.	7.2	60
16	Silicon-carbon unsaturated compounds. 19. Nickel-catalyzed reactions of silacyclopropenes and (phenylethynyl)polysilanes with phenyl(trimethylsilyl)acetylene and molecular structure of 1,4,4-trimethyl-3,6-diphenyl-1-1,2,5-tris(trimethylsilyl)-1,4-disilacyclohexa-2,5-diene. <i>Organometallics</i> , 1985, 4, 2040-2046.	1.1	58
17	Crystal Structures and Structural Comparison of <i>Thermoactinomyces vulgaris</i> R-47 Î±-Amylase 1 (TVAI) at 1.6Å... Resolution and Î±-Amylase 2 (TVAII) at 2.3Å... Resolution. <i>Journal of Molecular Biology</i> , 2002, 318, 443-453.	2.0	57
18	X-ray Structures of NADPH-dependent Carbonyl Reductase from <i>Sporobolomyces salmonicolor</i> Provide Insights into Stereoselective Reductions of Carbonyl Compounds. <i>Journal of Molecular Biology</i> , 2005, 352, 551-558.	2.0	54

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19	Silicon-carbon unsaturated compounds. 20. Formation and reactions of disilacyclopropanes and molecular structure of 3-(hydroxydimethylsilyl)-1,1-dimethyl-2,2-bis(trimethylsilyl)-1-silacyclopropane. Journal of the American Chemical Society, 1985, 107, 7706-7710.	6.6	53
20	Structure and direct electrochemistry of cytochrome P450 from the thermoacidophilic crenarchaeon, Sulfolobus tokodaii strain 7. Journal of Inorganic Biochemistry, 2004, 98, 1194-1199.	1.5	50
21	Structural Insights into Substrate Specificity and Function of Glucodextranase. Journal of Biological Chemistry, 2004, 279, 10575-10583.	1.6	43
22	X-ray Structures of Human Galectin-9 C-terminal Domain in Complexes with a Biantennary Oligosaccharide and Sialyllactose. Journal of Biological Chemistry, 2010, 285, 36969-36976.	1.6	43
23	Structural Insights into the Substrate Specificity and Function of Escherichia coli K12 YgjK, a Glucosidase Belonging to the Glycoside Hydrolase Family 63. Journal of Molecular Biology, 2008, 381, 116-128.	2.0	42
24	X-ray structure of a novel endolysin encoded by episomal phage phiSM101 of Clostridium perfringens. Molecular Microbiology, 2014, 92, 326-337.	1.2	42
25	Crystal and molecular structure of the Î³-cyclodextrin-12-crown-4 1 : 1 inclusion complex. Journal of the Chemical Society Chemical Communications, 1986, , 690-691.	2.0	41
26	Crystal Structure of the Complex of Î²-Cyclodextrin with Bithiophene and Their Oxidative Polymerization in Water. Macromolecules, 2004, 37, 3962-3964.	2.2	40
27	Three-Dimensional Structure of Aspartate Aminotransferase from Escherichia coli at 2.8 Å... Resolution. Journal of Biochemistry, 1988, 104, 317-318.	0.9	38
28	Complexes of Thermoactinomyces vulgaris R-47 Î±-amylase 1 and pullulan model oligosaccharides provide new insight into the mechanism for recognizing substrates with Î±-(1,6) glycosidic linkages. FEBS Journal, 2005, 272, 6145-6153.	2.2	35
29	X-ray structure of a protease-resistant mutant form of human galectin-8 with two carbohydrate recognition domains. FEBS Journal, 2012, 279, 3937-3951.	2.2	34
30	The Structures of l-Rhamnose Isomerase from Pseudomonas stutzeri in Complexes with l-Rhamnose and d-Allose Provide Insights into Broad Substrate Specificity. Journal of Molecular Biology, 2007, 365, 1505-1516.	2.0	32
31	Average Crystal Structure of (Pro-Pro-Gly) <sub>9</sub> at 1.0Å... Resolution. Polymer Journal, 2001, 33, 812.	1.3	32
32	Carbohydrate recognition mechanism of HA70 from Clostridium botulinum deduced from X-ray structures in complexes with sialylated oligosaccharides. FEBS Letters, 2012, 586, 2404-2410.	1.3	29
33	Crystal and Molecular Structure of Double Macrocyclic Inclusion Complexes, Î³-Cyclodextrin-12-Crown-4-NaCl, a Model for the Transport of Ions through Membranes. Bulletin of the Chemical Society of Japan, 1988, 61, 3825-3830.	2.0	28
34	Role of D-Valine Residues in the Antitumor Drug Actinomycin D: Replacement of D-Valines with Other D-Amino Acids Changes the DNA Binding Characteristics and Transcription Inhibitory Activities. Journal of the American Chemical Society, 1994, 116, 7971-7982.	6.6	28
35	Structures of Thermoactinomyces vulgaris R-47 Î±-Amylase II Complexed with Substrate Analogues. Bioscience, Biotechnology and Biochemistry, 2001, 65, 619-626.	0.6	28
36	Complex Structures of Thermoactinomyces vulgaris R-47 Î±-Amylase 2 with Acarbose and Cyclodextrins Demonstrate the Multiple Substrate Recognition Mechanism. Journal of Biological Chemistry, 2004, 279, 31033-31040.	1.6	27

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37	Crystal structures of open and closed forms of cyclo/maltodextrin-binding protein. FEBS Journal, 2009, 276, 3008-3019.	2.2	25
38	7/2-Helical model for collagen " Evidence from model peptides. Journal of Chemical Sciences, 1999, 111, 19-34.	0.7	24
39	Molecular and Crystal Structures of Dodecyltrimethylammonium Bromide and its Complex with <i>p</i> -Phenylphenol. Molecular Crystals and Liquid Crystals, 1997, 300, 31-43.	0.3	23
40	The Deletion of Amino-Terminal Domain in Thermoactinomyces vulgaris R-47 $\alpha$ -Amylases: Effects of domain N on Activity, Specificity, Stability and Dimerization. Bioscience, Biotechnology and Biochemistry, 2001, 65, 401-408.	0.6	23
41	X-ray Structures of the Microglia/Macrophage-specific Protein Iba1 from Human and Mouse Demonstrate Novel Molecular Conformation Change Induced by Calcium binding. Journal of Molecular Biology, 2006, 364, 449-457.	2.0	23
42	Crystal Structure of Aspergillus niger Isopullulanase, a Member of Glycoside Hydrolase Family 49. Journal of Molecular Biology, 2008, 376, 210-220.	2.0	23
43	Complex Formation of Cyclodextrins with Various Thiophenes and their Polymerization in Water: Preparation of Poly-pseudo-rotaxanes containing Poly(thiophene)s. Journal of Inclusion Phenomena and Macrocyclic Chemistry, 2006, 56, 45-53.	1.6	22
44	The crystal structure of Thermoactinomyces vulgaris R-47 $\alpha$ -amylase II (TVA II) complexed with transglycosylated product. FEBS Journal, 2004, 271, 2530-2538.	0.2	21
45	Structure of a complex of Thermoactinomyces vulgaris R-47 $\alpha$ -amylase 2 with maltohexaose demonstrates the important role of aromatic residues at the reducing end of the substrate binding cleft. Carbohydrate Research, 2006, 341, 1041-1046.	1.1	20
46	Structural basis for cyclodextrin recognition by Thermoactinomyces vulgaris cyclo/maltodextrin-binding protein. FEBS Journal, 2007, 274, 2109-2120.	2.2	20
47	Three-Dimensional Structures of Galectins. Trends in Glycoscience and Glycotechnology, 2018, 30, SE41-SE50.	0.0	20
48	Catalytic reaction mechanism of <i>Pseudomonas</i> <i>f</i> <i>stutzeri</i> $\alpha$ -D-fructanose isomerase deduced from X-ray structures. FEBS Journal, 2010, 277, 1045-1057.	2.2	19
49	Toward the Design of an RNA:DNA Hybrid Binding Agent. Journal of the American Chemical Society, 1994, 116, 2243-2253.	6.6	18
50	Role of Phe286 in the recognition mechanism of cyclomaltooligosaccharides (cyclodextrins) by Thermoactinomyces vulgaris R-47 $\alpha$ -amylase 2 (TVAII). X-ray structures of the mutant TVAIIs, F286A and F286Y, and kinetic analyses of the Phe286-replaced mutant TVAIIs. Carbohydrate Research, 2001, 334, 309-313.	1.1	18
51	Spectroscopic study on the interaction of cyclodextrins with naphthyl groups attached to poly(acrylamide) backbone. Journal of Photochemistry and Photobiology A: Chemistry, 2006, 179, 13-19.	2.0	18
52	X-ray structure of <i>Arthrobacter globiformis</i> M30 ketose 3-epimerase for the production of D-allulose from D-fructose. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 669-676.	0.4	18
53	X-ray structure of the direct electron transfer-type FAD glucose dehydrogenase catalytic subunit complexed with a hitchhiker protein. Acta Crystallographica Section D: Structural Biology, 2019, 75, 841-851.	1.1	18
54	X-ray structures of Bacillus pallidus d-arabinose isomerase and its complex with l-fucitol. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 1359-1368.	1.1	17

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55	Crystal structures of cyclomaltohexaose ( $\alpha$ -cyclodextrin) complexes with p-bromophenol and m-bromophenol. Carbohydrate Research, 2001, 332, 235-240.	1.1	16
56	Crystal Structures of <i>Aspergillus oryzae</i> Aspartic Proteinase and its Complex with an Inhibitor Pepstatin at 1.9Å... Resolution. Journal of Molecular Biology, 2003, 326, 1503-1511.	2.0	16
57	Crystal structures of two forms of a 2:1 cyclomaltohexaose ( $\alpha$ -cyclodextrin)/4,4'-biphenyldicarboxylic acid inclusion complex. Carbohydrate Research, 1998, 312, 177-181.	1.1	15
58	Structure of Ursodeoxycholic Acid. Yakugaku Zasshi, 1985, 105, 1115-1121.	0.0	14
59	Crystal structures of cyclomaltohexaose ( $\alpha$ -cyclodextrin) complexes with p-chlorophenol and p-cresol. Carbohydrate Research, 1999, 320, 261-266.	1.1	14
60	X-ray structure of a novel L-ribose isomerase acting on a non-natural sugar D-ribose as its ideal substrate. FEBS Journal, 2014, 281, 3150-3164.	2.2	14
61	Formation and reactions of 1-silacyclobut-2-en-1-ylidene and molecular structures of methanol and diene adducts. Organometallics, 1986, 5, 2447-2451.	1.1	13
62	Essentiality of tetramer formation of <i>Cellulomonas parahominis</i> L-ribose isomerase involved in novel L-ribose metabolic pathway. Applied Microbiology and Biotechnology, 2015, 99, 6303-6313.	1.7	13
63	X-ray structures of fructosyl peptide oxidases revealing residues responsible for gating oxygen access in the oxidative half reaction. Scientific Reports, 2017, 7, 2790.	1.6	13
64	Resolution and structural determination of unsymmetrically 6A6D-disubstituted $\beta$ -cyclodextrin. Journal of the American Chemical Society, 1985, 107, 1790-1791.	6.6	12
65	Crystallization and Preliminary X-Ray Characterization of Branched-Chain Amino Acid Aminotransferase from <i>Escherichia coli</i> . Journal of Biochemistry, 1989, 105, 671-672.	0.9	11
66	X-ray structures of the <i>Pseudomonas cichorii</i> D-tagatose 3-epimerase mutant form C66S recognizing deoxy sugars as substrates. Applied Microbiology and Biotechnology, 2016, 100, 10403-10415.	1.7	11
67	Self-association of the galectin-9 C-terminal domain via the opposite surface of the sugar-binding site. Journal of Biochemistry, 2013, 153, 463-471.	0.9	10
68	Crystal structure of a <i>Xenopus laevis</i> skin proto-type galectin, close to but distinct from galectin-1. Glycobiology, 2015, 25, 792-803.	1.3	10
69	Structure-Function Relationship of Bacterial SH3 Domains. , 2015, , 71-89.		10
70	Purification, crystallization and preliminary X-ray diffraction studies of D-tagatose 3-epimerase from <i>Pseudomonas cichorii</i> . Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 123-125.	0.7	9
71	Structural and biochemical characterization of the <i>Clostridium perfringens</i> autolysin catalytic domain. FEBS Letters, 2017, 591, 231-239.	1.3	9
72	Structural and biochemical characterizations of the novel autolysin Acd24020 from <i>Clostridioides difficile</i> and its full-function catalytic domain as a lytic enzyme. Molecular Microbiology, 2021, 115, 684-698.	1.2	9

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73	Structure of <i>L</i> -rhamnose isomerase in complex with <i>L</i> -rhamnopyranose demonstrates the sugar ring opening mechanism and the role of a substrate sub-binding site. <i>FEBS Open Bio</i> , 2013, 3, 35-40.	1.0	8
74	Crystal structure of a novel homodimeric <i>D</i> -ribulose 3-epimerase from <i>Methylomonus</i> sp.. <i>FEBS Open Bio</i> , 2021, 11, 1621-1637.	1.0	8
75	Crystal structures of rare disaccharides, $\alpha$ -D-glucopyranosyl $\beta$ -D-psicofuranoside, and $\alpha$ -D-galactopyranosyl $\beta$ -D-psicofuranoside. <i>Carbohydrate Research</i> , 2011, 346, 1182-1185.	1.1	7
76	Structures of major pilins in <i>Clostridium perfringens</i> demonstrate dynamic conformational change. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 718-732.	1.1	7
77	Crystallization and Preliminary X-Ray Analysis of <i>Thermoactinomyces vulgaris</i> R-47 $\alpha$ -Amylase II. <i>Journal of Structural Biology</i> , 1995, 114, 229-231.	1.3	6
78	Mutual conversion of substrate specificities of <i>Thermoactinomyces vulgaris</i> R-47 $\alpha$ -amylases TVAI and TVAII by site-directed mutagenesis. <i>Carbohydrate Research</i> , 2003, 338, 1553-1558.	1.1	6
79	Structure of a putative molybdenum-cofactor biosynthesis protein C (MoaC) from <i>Sulfolobus tokodaii</i> (ST0472). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 589-592.	0.7	6
80	Elucidation of the role of Ser329 and the C-terminal region in the catalytic activity of <i>Pseudomonas stutzeri</i> -rhamnose isomerase. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 919-927.	1.0	6
81	Monooxygenation by a thermophilic cytochrome P450 via direct electron donation from NADH. <i>Metallicomics</i> , 2011, 3, 389.	1.0	6
82	Structures of human galectin-10/monosaccharide complexes demonstrate potential of monosaccharides as effectors in forming Charcot-Leyden crystals. <i>Biochemical and Biophysical Research Communications</i> , 2020, 525, 87-93.	1.0	6
83	X-ray structure of <i>Clostridium perfringens</i> sortase B cysteine transpeptidase. <i>Biochemical and Biophysical Research Communications</i> , 2017, 493, 1267-1272.	1.0	5
84	X-ray structure of a protease-resistant mutant form of human galectin-9 having two carbohydrate recognition domains with a metal-binding site. <i>Biochemical and Biophysical Research Communications</i> , 2017, 490, 1287-1293.	1.0	5
85	Role of the Tyr270 residue in 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase from <i>Mesorhizobium loti</i> . <i>Journal of Bioscience and Bioengineering</i> , 2017, 123, 154-162.	1.1	5
86	The first crystal structure of manganese superoxide dismutase from the genus <i>Staphylococcus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 135-142.	0.4	5
87	Molecular and crystal structures of two 1,6-anhydro- $\beta$ -maltotriose derivatives. <i>Carbohydrate Research</i> , 1995, 278, 195-203.	1.1	4
88	Crystallization and preliminary X-ray diffraction studies of <i>L</i> -rhamnose isomerase from <i>Pseudomonas stutzeri</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 550-552.	0.7	4
89	Overexpression, purification, crystallization and preliminary X-ray crystal analysis of <i>Bacillus pallidus</i> <i>D</i> -arabinose isomerase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 945-948.	0.7	4
90	Crystallization of (Pro-Hyp-Gly) <sub>10</sub> and Its Triple-Helical Structure Deduced from Cylindrical Patterson Map. <i>Chemistry Letters</i> , 1998, 27, 385-386.	0.7	3

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91	Crystallization and preliminary X-ray analysis of Thermoactinomyces vulgaris R-47 maltotri-saccharide-metabolizing enzyme homologous to glucoamylase. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 302-304.	0.7	3
92	Mutagenesis-induced conformational change in domain B of a pullulan-hydrolyzing $\alpha$ -amylase TVA I. Amylase, 2018, 2, 1-10.	0.7	3
93	Modulation of the carbohydrate-binding specificity of two Xenopus proto-type galectins by site-directed mutagenesis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140684.	1.1	3
94	Structural and biochemical characterization of the Clostridium perfringens-specific Zn <sup>2+</sup> -dependent amidase endolysin, Psa, catalytic domain. Biochemical and Biophysical Research Communications, 2021, 576, 66-72.	1.0	3
95	Purification, crystallization and preliminary X-ray analysis of an HA17 $\alpha$ -HA70 (HA2 $\alpha$ -HA3) complex from Clostridium botulinum type C progenitor toxin. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 64-67.	0.4	3
96	Crystal structure of chartreusin derivative A132. Carbohydrate Research, 2003, 338, 1523-1525.	1.1	2
97	Crystallization and preliminary X-ray diffraction analysis of a protease-resistant mutant form of human galectin-8. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 512-514.	0.7	2
98	Overexpression, crystallization and preliminary X-ray diffraction analysis of <i>L</i> -ribose isomerase from Acinetobacter sp. strain DL-28. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1281-1284.	0.7	2
99	X-ray crystal structures of $\alpha$ -cyclodextrin $\alpha$ -5-hydroxypentanoic acid, $\beta$ -cyclodextrin $\alpha$ -5-hydroxypentanoic acid, $\beta$ -cyclodextrin $\alpha$ - $\mu$ -caprolactone, and $\beta$ -cyclodextrin $\alpha$ - $\mu$ -caprolactam inclusion complexes. Journal of Inclusion Phenomena and Macrocyclic Chemistry, 2020, 96, 93-99.	0.9	2
100	Crystallization and preliminary X-ray crystallographic analysis of macrophage/microglia-specific calcium-binding protein Iba1. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 569-571.	2.5	1
101	X-ray structures of Clostridium perfringens sortase C with C-terminal cell wall sorting motif of LPST demonstrate role of subsite for substrate-binding and structural variations of catalytic site. Biochemical and Biophysical Research Communications, 2021, 554, 138-144.	1.0	1
102	$\beta$ -D-Altrose. Acta Crystallographica Section E: Structure Reports Online, 2009, 65, o280-o280.	0.2	1
103	Crystal structure and conformational stability of a galectin-1 tandem-repeat mutant with a short linker. Glycobiology, 2022, 32, 251-259.	1.3	1
104	Mutagenesis and Structural Analysis of Thermoactinomyces vulgaris R-47 .ALPHA.-Amylase II (TVA II). Journal of Applied Glycoscience (1999), 2005, 52, 225-231.	0.3	1
105	Three-Dimensional Structures of Galectins. Trends in Glycoscience and Glycotechnology, 2018, 30, SJ1-SJ10.	0.0	1
106	Crystallization and preliminary X-ray analysis of AAMS amidohydrolase, the final enzyme in degradation pathway I of pyridoxine. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 829-831.	0.7	0
107	Crystal Structures and Functions of Two Pullulan-hydrolyzing .ALPHA.-Amylases from a Thermophilic Actinomycete, Thermoactinomyces vulgaris.. Journal of Applied Glycoscience (1999), 2001, 48, 163-169.	0.3	0
108	X-ray Crystallographic Study of Glucodextranase from a Gram-positive Bacterium, Arthrobacter globiformis I42. Journal of Applied Glycoscience (1999), 2005, 52, 145-151.	0.3	0