

# Shigehiro Kamitori

## List of Publications by Year in descending order

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108  
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2,944  
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147801

31  
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189892

50  
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109  
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109  
docs citations

109  
times ranked

3093  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure and conformational stability of a galectin-1 tandem-repeat mutant with a short linker. <i>Glycobiology</i> , 2022, 32, 251-259.	2.5	1
2	Structural and biochemical characterizations of the novel autolysin Acd24020 from <i>Clostridioides difficile</i> and its full-function catalytic domain as a lytic enzyme. <i>Molecular Microbiology</i> , 2021, 115, 684-698.	2.5	9
3	Crystal structure of a novel homodimeric <i>Methylobacterium</i> ribulose 3-epimerase from <i>Methylobacterium</i> sp.. <i>FEBS Open Bio</i> , 2021, 11, 1621-1637.	2.3	8
4	X-ray structures of <i>Clostridium perfringens</i> sortase C with C-terminal cell wall sorting motif of LPST demonstrate role of subsite for substrate-binding and structural variations of catalytic site. <i>Biochemical and Biophysical Research Communications</i> , 2021, 554, 138-144.	2.1	1
5	Modulation of the carbohydrate-binding specificity of two <i>Xenopus</i> proto-type galectins by site-directed mutagenesis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140684.	2.3	3
6	Structural and biochemical characterization of the <i>Clostridium perfringens</i> -specific Zn <sup>2+</sup> -dependent amidase endolysin, Psa, catalytic domain. <i>Biochemical and Biophysical Research Communications</i> , 2021, 576, 66-72.	2.1	3
7	X-ray crystal structures of $\alpha$ -cyclodextrin-5-hydroxypentanoic acid, $\beta$ -cyclodextrin-5-hydroxypentanoic acid, $\beta$ -cyclodextrin- $\mu$ -caprolactone, and $\beta$ -cyclodextrin- $\mu$ -caprolactam inclusion complexes. <i>Journal of Inclusion Phenomena and Macrocyclic Chemistry</i> , 2020, 96, 93-99.	1.6	2
8	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.	2.1	6
9	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.	2.3	7
10	X-ray structure of the direct electron transfer-type FAD glucose dehydrogenase catalytic subunit complexed with a hitchhiker protein. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 841-851.	2.3	18
11	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.	0.8	5
12	Mutagenesis-induced conformational change in domain B of a pullulan-hydrolyzing $\alpha$ -amylase TVA I. <i>Amylase</i> , 2018, 2, 1-10.	1.6	3
13	Three-Dimensional Structures of Galectins. <i>Trends in Glycoscience and Glycotechnology</i> , 2018, 30, SE41-SE50.	0.1	20
14	X-ray structure of <i>Arthrobacter globiformis</i> M30 ketose 3-epimerase for the production of <i>D</i> -allulose from <i>D</i> -fructose. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 669-676.	0.8	18
15	Three-Dimensional Structures of Galectins. <i>Trends in Glycoscience and Glycotechnology</i> , 2018, 30, SJ1-SJ10.	0.1	1
16	Structural and biochemical characterization of the <i>Clostridium perfringens</i> autolysin catalytic domain. <i>FEBS Letters</i> , 2017, 591, 231-239.	2.8	9
17	X-ray structure of <i>Clostridium perfringens</i> sortase B cysteine transpeptidase. <i>Biochemical and Biophysical Research Communications</i> , 2017, 493, 1267-1272.	2.1	5
18	X-ray structures of fructosyl peptide oxidases revealing residues responsible for gating oxygen access in the oxidative half reaction. <i>Scientific Reports</i> , 2017, 7, 2790.	3.3	13

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19	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.	2.1	5
20	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.	2.2	5
21	X-ray structures of the <i>Pseudomonas cichorii</i> D-tagatose 3-epimerase mutant form C66S recognizing deoxy sugars as substrates. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 10403-10415.	3.6	11
22	Structural analysis of fungus-derived FAD glucose dehydrogenase. <i>Scientific Reports</i> , 2015, 5, 13498.	3.3	89
23	Essentiality of tetramer formation of <i>Cellulomonas parahominis</i> L-ribose isomerase involved in novel L-ribose metabolic pathway. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 6303-6313.	3.6	13
24	Crystal structure of a <i>Xenopus laevis</i> skin proto-type galectin, close to but distinct from galectin-1. <i>Glycobiology</i> , 2015, 25, 792-803.	2.5	10
25	Structure-Function Relationship of Bacterial SH3 Domains. , 2015, , 71-89.		10
26	X-ray structure of a novel endolysin encoded by episomal phage $\phi$ SM101 of <i>Clostridium perfringens</i> . <i>Molecular Microbiology</i> , 2014, 92, 326-337.	2.5	42
27	X-ray structure of a novel L-ribose isomerase acting on a non-natural sugar L-ribose as its ideal substrate. <i>FEBS Journal</i> , 2014, 281, 3150-3164.	4.7	14
28	Purification, crystallization and preliminary X-ray analysis of an HA17-HA70 (HA2-HA3) complex from <i>Clostridium botulinum</i> type C progenitor toxin. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 64-67.	0.8	3
29	Chemoenzymatic Synthesis of the Immunoglobulin Domain of Tim $\beta$ Carrying a Complex Type N-Glycan by Using a One-pot Ligation. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 9733-9737.	13.8	60
30	Structure of L-ribose isomerase in complex with L-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.	2.3	8
31	Self-association of the galectin-9 C-terminal domain via the opposite surface of the sugar-binding site. <i>Journal of Biochemistry</i> , 2013, 153, 463-471.	1.7	10
32	X-ray structure of a protease-resistant mutant form of human galectin-9 with two carbohydrate recognition domains. <i>FEBS Journal</i> , 2012, 279, 3937-3951.	4.7	34
33	Carbohydrate recognition mechanism of HA70 from <i>Clostridium botulinum</i> deduced from X-ray structures in complexes with sialylated oligosaccharides. <i>FEBS Letters</i> , 2012, 586, 2404-2410.	2.8	29
34	Monooxygenation by a thermophilic cytochrome P450 via direct electron donation from NADH. <i>Metallomics</i> , 2011, 3, 389.	2.4	6
35	Overexpression, crystallization and preliminary X-ray diffraction analysis of L-ribose isomerase from <i>Acinetobacter</i> sp. strain DL-28. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1281-1284.	0.7	2
36	Crystal structures of rare disaccharides, $\beta$ -D-glucopyranosyl $\beta$ -D-psicofuranoside, and $\beta$ -D-galactopyranosyl $\beta$ -D-psicofuranoside. <i>Carbohydrate Research</i> , 2011, 346, 1182-1185.	2.3	7

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37	X-ray structures of <i>Bacillus pallidus</i> d-arabinose isomerase and its complex with l-fucitol. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 1359-1368.	2.3	17
38	Catalytic reaction mechanism of <i>Pseudomonas stutzeri</i> l-rhamnose isomerase deduced from X-ray structures. <i>FEBS Journal</i> , 2010, 277, 1045-1057.	4.7	19
39	X-ray Structures of Human Galectin-9 C-terminal Domain in Complexes with a Biantennary Oligosaccharide and Sialyllactose. <i>Journal of Biological Chemistry</i> , 2010, 285, 36969-36976.	3.4	43
40	Elucidation of the role of Ser329 and the C-terminal region in the catalytic activity of <i>Pseudomonas stutzeri</i> l-rhamnose isomerase. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 919-927.	2.1	6
41	Crystallization and preliminary X-ray diffraction analysis of a protease-resistant mutant form of human galectin-8. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 512-514.	0.7	2
42	Crystallization and preliminary X-ray analysis of AAMS amidohydrolase, the final enzyme in degradation pathway I of pyridoxine. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 829-831.	0.7	0
43	Crystal structures of open and closed forms of cyclomaltodextrin-binding protein. <i>FEBS Journal</i> , 2009, 276, 3008-3019.	4.7	25
44	$\beta$ -D-Altrose. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2009, 65, o280-o280.	0.2	1
45	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
46	Overexpression, purification, crystallization and preliminary X-ray crystal analysis of <i>Bacillus pallidus</i> d-arabinose isomerase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 945-948.	0.7	4
47	Crystal Structure of <i>Aspergillus niger</i> Isopullulanase, a Member of Glycoside Hydrolase Family 49. <i>Journal of Molecular Biology</i> , 2008, 376, 210-220.	4.2	23
48	Structural Insights into the Substrate Specificity and Function of <i>Escherichia coli</i> K12 YgjK, a Glucosidase Belonging to the Glycoside Hydrolase Family 63. <i>Journal of Molecular Biology</i> , 2008, 381, 116-128.	4.2	42
49	Functional and structural bases of a cysteine-less mutant as a long-lasting substitute for galectin-1. <i>Glycobiology</i> , 2008, 18, 1065-1073.	2.5	68
50	The Structures of l-Rhamnose Isomerase from <i>Pseudomonas stutzeri</i> in Complexes with l-Rhamnose and d-Allose Provide Insights into Broad Substrate Specificity. <i>Journal of Molecular Biology</i> , 2007, 365, 1505-1516.	4.2	32
51	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.	4.2	86
52	Purification, crystallization and preliminary X-ray diffraction studies of d-tagatose 3-epimerase from <i>Pseudomonas cichorii</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 123-125.	0.7	9
53	Structural basis for cyclodextrin recognition by <i>Thermoactinomyces vulgaris</i> cyclomaltodextrin-binding protein. <i>FEBS Journal</i> , 2007, 274, 2109-2120.	4.7	20
54	X-ray Structures of the Microglia/Macrophage-specific Protein Iba1 from Human and Mouse Demonstrate Novel Molecular Conformation Change Induced by Calcium binding. <i>Journal of Molecular Biology</i> , 2006, 364, 449-457.	4.2	23

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55	Crystallization and preliminary X-ray diffraction studies of L-rhamnose isomerase from <i>Pseudomonas stutzeri</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 550-552.	0.7	4
56	Structure of a complex of <i>Thermoactinomyces vulgaris</i> R-47 $\alpha$ -amylase 2 with maltohexaose demonstrates the important role of aromatic residues at the reducing end of the substrate binding cleft. <i>Carbohydrate Research</i> , 2006, 341, 1041-1046.	2.3	20
57	Spectroscopic study on the interaction of cyclodextrins with naphthyl groups attached to poly(acrylamide) backbone. <i>Journal of Photochemistry and Photobiology A: Chemistry</i> , 2006, 179, 13-19.	3.9	18
58	Complex Formation of Cyclodextrins with Various Thiophenes and their Polymerization in Water: Preparation of Poly-pseudo-rotaxanes containing Poly(thiophene)s. <i>Journal of Inclusion Phenomena and Macrocyclic Chemistry</i> , 2006, 56, 45-53.	1.6	22
59	Complexes of <i>Thermoactinomyces vulgaris</i> R-47 $\alpha$ -amylase 1 and pullulan model oligosaccharides provide new insight into the mechanism for recognizing substrates with $\alpha$ -(1,6) glycosidic linkages. <i>FEBS Journal</i> , 2005, 272, 6145-6153.	4.7	35
60	Crystallization and preliminary X-ray analysis of <i>Thermoactinomyces vulgaris</i> R-47 maltooligosaccharide-metabolizing enzyme homologous to glucoamylase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 302-304.	0.7	3
61	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.	4.2	54
62	A [2]Rotaxane Capped by a Cyclodextrin and a Guest: $\alpha$ Formation of Supramolecular [2]Rotaxane Polymer. <i>Journal of the American Chemical Society</i> , 2005, 127, 2034-2035.	13.7	100
63	Mutagenesis and Structural Analysis of <i>Thermoactinomyces vulgaris</i> R-47 $\alpha$ -Amylase II (TVA II). <i>Journal of Applied Glycoscience</i> (1999), 2005, 52, 225-231.	0.7	1
64	X-ray Crystallographic Study of Glucodextranase from a Gram-positive Bacterium, <i>Arthrobacter globiformis</i> I42. <i>Journal of Applied Glycoscience</i> (1999), 2005, 52, 145-151.	0.7	0
65	Structural Insights into Substrate Specificity and Function of Glucodextranase. <i>Journal of Biological Chemistry</i> , 2004, 279, 10575-10583.	3.4	43
66	Complex Structures of <i>Thermoactinomyces vulgaris</i> R-47 $\alpha$ -Amylase 2 with Acarbose and Cyclodextrins Demonstrate the Multiple Substrate Recognition Mechanism. <i>Journal of Biological Chemistry</i> , 2004, 279, 31033-31040.	3.4	27
67	The crystal structure of <i>Thermoactinomyces vulgaris</i> R-47 $\alpha$ -amylase II (TVA II) complexed with transglycosylated product. <i>FEBS Journal</i> , 2004, 271, 2530-2538.	0.2	21
68	Structure and direct electrochemistry of cytochrome P450 from the thermoacidophilic crenarchaeon, <i>Sulfolobus tokodaii</i> strain 7. <i>Journal of Inorganic Biochemistry</i> , 2004, 98, 1194-1199.	3.5	50
69	Crystallization and preliminary X-ray crystallographic analysis of macrophage/microglia-specific calcium-binding protein Iba1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 569-571.	2.5	1
70	Crystal Structure of the Complex of $\beta$ -Cyclodextrin with Bithiophene and Their Oxidative Polymerization in Water. <i>Macromolecules</i> , 2004, 37, 3962-3964.	4.8	40
71	Complex Structures of <i>Thermoactinomyces vulgaris</i> R-47 $\alpha$ -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.	4.2	91
72	Crystal structure of chartreusin derivative A132. <i>Carbohydrate Research</i> , 2003, 338, 1523-1525.	2.3	2

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73	Mutual conversion of substrate specificities of <i>Thermoactinomyces vulgaris</i> R-47 $\hat{\pm}$ -amylases TVAI and TVAll by site-directed mutagenesis. <i>Carbohydrate Research</i> , 2003, 338, 1553-1558.	2.3	6
74	Crystal Structures of <i>Aspergillus oryzae</i> Aspartic Proteinase and its Complex with an Inhibitor Pepstatin at 1.9Å... Resolution. <i>Journal of Molecular Biology</i> , 2003, 326, 1503-1511.	4.2	16
75	Crystal Structures and Structural Comparison of <i>Thermoactinomyces vulgaris</i> R-47 $\hat{\pm}$ -Amylase 1 (TVAI) at 1.6Å... Resolution and $\hat{\pm}$ -Amylase 2 (TVAll) at 2.3Å... Resolution. <i>Journal of Molecular Biology</i> , 2002, 318, 443-453.	4.2	57
76	Role of Phe286 in the recognition mechanism of cyclomaltooligosaccharides (cyclodextrins) by <i>Thermoactinomyces vulgaris</i> R-47 $\hat{\pm}$ -amylase 2 (TVAll). X-ray structures of the mutant TVAlls, F286A and F286Y, and kinetic analyses of the Phe286-replaced mutant TVAlls. <i>Carbohydrate Research</i> , 2001, 334, 309-313.	2.3	18
77	Crystal structures of cyclomaltohexaose ( $\hat{\pm}$ -cyclodextrin) complexes with p-bromophenol and m-bromophenol. <i>Carbohydrate Research</i> , 2001, 332, 235-240.	2.3	16
78	Structures of <i>Thermoactinomyces vulgaris</i> R-47 $\hat{\pm}$ -Amylase II Complexed with Substrate Analogues. <i>Bioscience, Biotechnology and Biochemistry</i> , 2001, 65, 619-626.	1.3	28
79	The Deletion of Amino-Terminal Domain in <i>Thermoactinomyces vulgaris</i> R-47 $\hat{\pm}$ -Amylases: Effects of domain N on Activity, Specificity, Stability and Dimerization. <i>Bioscience, Biotechnology and Biochemistry</i> , 2001, 65, 401-408.	1.3	23
80	Average Crystal Structure of (Pro-Pro-Gly) <sub>9</sub> at 1.0Å... Resolution. <i>Polymer Journal</i> , 2001, 33, 812.	2.7	32
81	Crystal Structures and Functions of Two Pullulan-hydrolyzing .ALPHA.-Amylases from a Thermophilic Actinomycete, <i>Thermoactinomyces vulgaris</i> .. <i>Journal of Applied Glycoscience</i> (1999), 2001, 48, 163-169.	0.7	0
82	A Novel Pseudo-Polyrotaxane Structure Composed of Cyclodextrins and a Straight-Chain Polymer:Å Crystal Structures of Inclusion Complexes of $\hat{\pm}$ -Cyclodextrin with Poly(trimethylene oxide) and Poly(propylene glycol). <i>Macromolecules</i> , 2000, 33, 1500-1502.	4.8	85
83	Crystal structures of cyclomaltohexaose ( $\hat{\pm}$ -cyclodextrin) complexes with p-chlorophenol and p-cresol. <i>Carbohydrate Research</i> , 1999, 320, 261-266.	2.3	14
84	Crystal structure of the E166A mutant of extended-spectrum $\hat{\pm}$ -lactamase toho-1 at 1.8 Å... resolution 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 285, 2079-2087.	4.2	83
85	Crystal structure of <i>Thermoactinomyces vulgaris</i> R-47 $\hat{\pm}$ -amylase II (TVAll) hydrolyzing cyclodextrins and pullulan at 2.6 Å... resolution. <i>Journal of Molecular Biology</i> , 1999, 287, 907-921.	4.2	114
86	7/2-Helical model for collagen $\hat{\pm}$ " Evidence from model peptides. <i>Journal of Chemical Sciences</i> , 1999, 111, 19-34.	1.5	24
87	Crystal structures of two forms of a 2:1 cyclomaltohexaose ( $\hat{\pm}$ -cyclodextrin)/4,4- $\hat{\pm}$ -biphenyldicarboxylic acid inclusion complex. <i>Carbohydrate Research</i> , 1998, 312, 177-181.	2.3	15
88	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.	1.3	3
89	Molecular and Crystal Structures of Dodecyltrimethylammonium Bromide and its Complex with <i>p</i> -Phenylphenol. <i>Molecular Crystals and Liquid Crystals</i> , 1997, 300, 31-43.	0.3	23
90	A Real Knot in Protein. <i>Journal of the American Chemical Society</i> , 1996, 118, 8945-8946.	13.7	80

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91	Crystal Structure of S-Adenosylmethionine Synthetase. <i>Journal of Biological Chemistry</i> , 1996, 271, 136-147.	3.4	112
92	Molecular and crystal structures of two 1,6-anhydro- $\beta$ -maltotriose derivatives. <i>Carbohydrate Research</i> , 1995, 278, 195-203.	2.3	4
93	Crystallization and Preliminary X-Ray Analysis of <i>Thermoactinomyces vulgaris</i> R-47 $\beta$ -Amylase II. <i>Journal of Structural Biology</i> , 1995, 114, 229-231.	2.8	6
94	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.	13.7	88
95	Toward the Design of an RNA:DNA Hybrid Binding Agent. <i>Journal of the American Chemical Society</i> , 1994, 116, 2243-2253.	13.7	18
96	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. <i>Journal of the American Chemical Society</i> , 1994, 116, 7971-7982.	13.7	28
97	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.	4.2	157
98	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.	1.7	78
99	Crystallization and Preliminary X-Ray Characterization of Branched-Chain Amino Acid Aminotransferase from <i>Escherichia coli</i> . <i>Journal of Biochemistry</i> , 1989, 105, 671-672.	1.7	11
100	Crystal and Molecular Structure of Double Macrocyclic Inclusion Complexes, $\beta$ -Cyclodextrin- $\beta$ -12-Crown-4-NaCl, a Model for the Transport of Ions through Membranes. <i>Bulletin of the Chemical Society of Japan</i> , 1988, 61, 3825-3830.	3.2	28
101	Three-Dimensional Structure of Aspartate Aminotransferase from <i>Escherichia coli</i> at 2.8 Å... Resolution. <i>Journal of Biochemistry</i> , 1988, 104, 317-318.	1.7	38
102	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.	13.7	100
103	Crystal and molecular structure of the $\beta$ -cyclodextrin- $\beta$ -12-crown-4 1 : 1 inclusion complex. <i>Journal of the Chemical Society Chemical Communications</i> , 1986, , 690-691.	2.0	41
104	Formation and reactions of 1-silacyclobut-2-en-1-ylidene and molecular structures of methanol and diene adducts. <i>Organometallics</i> , 1986, 5, 2447-2451.	2.3	13
105	Structure of Ursodeoxycholic Acid. <i>Yakugaku Zasshi</i> , 1985, 105, 1115-1121.	0.2	14
106	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.	2.3	58
107	Resolution and structural determination of unsymmetrically 6A6D-disubstituted $\beta$ -cyclodextrin. <i>Journal of the American Chemical Society</i> , 1985, 107, 1790-1791.	13.7	12
108	Silicon-carbon unsaturated compounds. 20. Formation and reactions of disilacyclopropanes and molecular structure of 3-(hydroxydimesitylsilyl)-1,1-dimesityl-2,2-bis(trimethylsilyl)-1-silacyclopropane. <i>Journal of the American Chemical Society</i> , 1985, 107, 7706-7710.	13.7	53