

Takashi Tonozuka

List of Publications by Year in descending order

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101
papers

1,973
citations

236612

25
h-index

288905

40
g-index

104
all docs

104
docs citations

104
times ranked

1874
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanism of Phosphorylation-Dependent Binding of APC to β -Catenin and Its Role in β -Catenin Degradation. <i>Molecular Cell</i> , 2004, 15, 511-521.	4.5	288
2	Crystal structure of <i>Thermoactinomyces vulgaris</i> R-47 β -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	Complex Structures of <i>Thermoactinomyces vulgaris</i> R-47 β -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
4	A Neopullulanase-type β -Amylase Gene from <i>Thermoactinomyces vulgaris</i> R-47. <i>Bioscience, Biotechnology and Biochemistry</i> , 1993, 57, 395-401.	0.6	72
5	Crystal Structures and Structural Comparison of <i>Thermoactinomyces vulgaris</i> R-47 β -Amylase 1 (TVAI) at 1.6Å... Resolution and β -Amylase 2 (TVAII) at 2.3Å... Resolution. <i>Journal of Molecular Biology</i> , 2002, 318, 443-453.	2.0	57
6	Comparison of primary structures and substrate specificities of two pullulan-hydrolyzing β -amylases, TVA I and TVA II, from <i>Thermoactinomyces vulgaris</i> R-47. <i>BBA - Proteins and Proteomics</i> , 1995, 1252, 35-42.	2.1	54
7	Sugar-binding Sites of the HA1 Subcomponent of <i>Clostridium botulinum</i> Type C Progenitor Toxin. <i>Journal of Molecular Biology</i> , 2008, 376, 854-867.	2.0	48
8	Structural Insights into Substrate Specificity and Function of Glucodextranase. <i>Journal of Biological Chemistry</i> , 2004, 279, 10575-10583.	1.6	43
9	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.	2.0	42
10	Mechanism of active site exclusion in a site-specific recombinase: role of the DNA substrate in conferring half-of-the-sites activity. <i>Genes and Development</i> , 1997, 11, 3061-3071.	2.7	38
11	Crystal Structure of the HA3 Subcomponent of <i>Clostridium botulinum</i> Type C Progenitor Toxin. <i>Journal of Molecular Biology</i> , 2009, 385, 1193-1206.	2.0	37
12	Complexes of <i>Thermoactinomyces vulgaris</i> R-47 β -amylase 1 and pullulan model oligosaccharides provide new insight into the mechanism for recognizing substrates with β -(1,6) glycosidic linkages. <i>FEBS Journal</i> , 2005, 272, 6145-6153.	2.2	35
13	Novel glucoamylase-type enzymes from <i>Thermoactinomyces vulgaris</i> and <i>Methanococcus jannaschii</i> whose genes are found in the flanking region of the β -amylase genes. <i>Applied Microbiology and Biotechnology</i> , 2001, 56, 465-473.	1.7	34
14	Crystal structure of a lactosucrose-producing enzyme, <i>Arthrobacter</i> sp. K-1 β -fructofuranosidase. <i>Enzyme and Microbial Technology</i> , 2012, 51, 359-365.	1.6	33
15	Cell internalization and traffic pathway of <i>Clostridium botulinum</i> type C neurotoxin in HT-29 cells. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2006, 1763, 120-128.	1.9	32
16	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.	1.3	29
17	Structures of <i>Thermoactinomyces vulgaris</i> R-47 β -Amylase II Complexed with Substrate Analogues. <i>Bioscience, Biotechnology and Biochemistry</i> , 2001, 65, 619-626.	0.6	28
18	Crystal structure of a glycoside hydrolase family 6 enzyme, CcCel6C, a cellulase constitutively produced by <i>Coprinopsis cinerea</i> . <i>FEBS Journal</i> , 2010, 277, 1532-1542.	2.2	28

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19	Complex Structures of <i>Thermoactinomyces vulgaris</i> R-47 α -Amylase 2 with Acarbose and Cyclodextrins Demonstrate the Multiple Substrate Recognition Mechanism. <i>Journal of Biological Chemistry</i> , 2004, 279, 31033-31040.	1.6	27
20	Molecular diversity of the two sugar-binding sites of the β -trefoil lectin HA33/C (HA1) from <i>Clostridium botulinum</i> type C neurotoxin. <i>Archives of Biochemistry and Biophysics</i> , 2011, 512, 69-77.	1.4	27
21	A convenient enzymatic synthesis of 42- α -isomaltosylisomaltose using <i>Thermoactinomyces vulgaris</i> R-47 α -amylase II (TVA II). <i>Carbohydrate Research</i> , 1994, 261, 157-162.	1.1	26
22	Construction of chimeric cyclodextrin glucanotransferases from <i>Bacillus circulans</i> A11 and <i>Paenibacillus macerans</i> IAM1243 and analysis of their product specificity. <i>Carbohydrate Research</i> , 2005, 340, 2279-2289.	1.1	26
23	Structural and biochemical characterization of novel bacterial α -galactosidases belonging to glycoside hydrolase family 31. <i>Biochemical Journal</i> , 2015, 469, 145-158.	1.7	26
24	Crystal structure of a β -fructofuranosidase with high transfructosylation activity from <i>Aspergillus kawachii</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 1786-1795.	0.6	26
25	Crystal structures of open and closed forms of cyclo/maltodextrin-binding protein. <i>FEBS Journal</i> , 2009, 276, 3008-3019.	2.2	25
26	Crystal structure of the catalytic domain of a GH16 β -agarase from a deep-sea bacterium, <i>Microbulbifer thermotolerans</i> JAMB-A94. <i>Bioscience, Biotechnology and Biochemistry</i> , 2015, 79, 625-632.	0.6	25
27	Jaw1/LRMP has a role in maintaining nuclear shape via interaction with SUN proteins. <i>Journal of Biochemistry</i> , 2018, 164, 303-311.	0.9	24
28	The Deletion of Amino-Terminal Domain in <i>Thermoactinomyces vulgaris</i> R-47 α -Amylases: Effects of domain N on Activity, Specificity, Stability and Dimerization. <i>Bioscience, Biotechnology and Biochemistry</i> , 2001, 65, 401-408.	0.6	23
29	Binding properties of <i>Clostridium botulinum</i> type C progenitor toxin to mucins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2007, 1770, 551-555.	1.1	23
30	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.	2.0	23
31	The crystal structure of <i>Thermoactinomyces vulgaris</i> R-47 α -amylase II (TVA II) complexed with transglycosylated product. <i>FEBS Journal</i> , 2004, 271, 2530-2538.	0.2	21
32	Kinetic Studies of Site-Directed Mutational Isomalto-dextranase-Catalyzed Hydrolytic Reactions on a 27 MHz Quartz-Crystal Microbalance. <i>Biochemistry</i> , 2005, 44, 9456-9461.	1.2	21
33	Crystal Structure and Mutational Analysis of Isomalto-dextranase, a Member of Glycoside Hydrolase Family 27. <i>Journal of Biological Chemistry</i> , 2015, 290, 26339-26349.	1.6	21
34	Studies on the Hydrolyzing Mechanism for Cyclodextrins of <i>Thermoactinomyces vulgaris</i> R-47 α -Amylase 2 (TVAII). X-Ray Structure of the Mutant E354A Complexed with α -Cyclodextrin, and Kinetic Analyses on Cyclodextrins. <i>Journal of Biochemistry</i> , 2001, 129, 423-428.	0.9	20
35	Structure of a complex of <i>Thermoactinomyces vulgaris</i> R-47 α -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.	1.1	20
36	Structural basis for cyclodextrin recognition by <i>Thermoactinomyces vulgaris</i> cyclo/maltodextrin-binding protein. <i>FEBS Journal</i> , 2007, 274, 2109-2120.	2.2	20

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37	The relative contribution of mannose salvage pathways to glycosylation in PMI-deficient mouse embryonic fibroblast cells. <i>FEBS Journal</i> , 2008, 275, 788-798.	2.2	20
38	A glycoside hydrolase family 31 dextranase with high transglucosylation activity from <i>Flavobacterium johnsoniae</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2016, 80, 1562-1567.	0.6	20
39	Characterization of fructooligosaccharide metabolism and fructooligosaccharide-degrading enzymes in human commensal butyrate producers. <i>Gut Microbes</i> , 2021, 13, 1-20.	4.3	20
40	Role of Phe286 in the recognition mechanism of cyclomaltooligosaccharides (cyclodextrins) by <i>Thermoactinomyces vulgaris</i> R-47 α -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.	1.1	18
41	Enhancing thermostability and the structural characterization of <i>Microbacterium saccharophilum</i> K-1 β -fructofuranosidase. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 6667-6677.	1.7	18
42	Comparison of the structural changes in two cellobiohydrolases, CcCel6A and CcCel6C, from <i>Coprinopsis cinerea</i> α -f α tweezer-like motion in the structure of CcCel6C. <i>FEBS Journal</i> , 2012, 279, 1871-1882.	2.7	17
43	Structural insights into polysaccharide recognition by <i>Flavobacterium johnsoniae</i> dextranase, a member of glycoside hydrolase family 31. <i>FEBS Journal</i> , 2020, 287, 1195-1207.	2.2	17
44	Insights into the reaction mechanism of glycosyl hydrolase family 49. Site-directed mutagenesis and substrate preference of isopullulanase. <i>FEBS Journal</i> , 2004, 271, 4420-4427.	0.2	16
45	Heterologous expression and characterization of processing β -glucosidase I from <i>Aspergillus brasiliensis</i> ATCC 9642. <i>Glycoconjugate Journal</i> , 2011, 28, 563-571.	1.4	16
46	Purification, Characterization, and Subsite Affinities of <i>Thermoactinomyces vulgaris</i> R-47 Maltooligosaccharide-metabolizing Enzyme Homologous to Glucoamylases. <i>Bioscience, Biotechnology and Biochemistry</i> , 2004, 68, 413-420.	0.6	15
47	Structure of the Catalytic Domain of β -L-Arabinofuranosidase from <i>Coprinopsis cinerea</i> , CcAbf62A, Provides Insights into Structure-Function Relationships in Glycoside Hydrolase Family 62. <i>Applied Biochemistry and Biotechnology</i> , 2017, 181, 511-525.	1.4	14
48	The phosphorylation of sorting nexin 5 at serine 226 regulates retrograde transport and macropinocytosis. <i>PLoS ONE</i> , 2018, 13, e0207205.	1.1	14
49	Characterization of Glycoside Hydrolase Family 6 Enzymes from <i>Coprinopsis cinerea</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2009, 73, 1432-1434.	0.6	13
50	Deglycosylated Isopullulanase Retains Enzymatic Activity.. <i>Journal of Applied Glycoscience</i> (1999), 2000, 47, 287-292.	0.3	13
51	Construction of an Efficient Expression System for <i>Aspergillus</i> Isopullulanase in <i>Pichia pastoris</i> , and a Simple Purification Method. <i>Bioscience, Biotechnology and Biochemistry</i> , 2003, 67, 1149-1153.	0.6	11
52	Crystal structure of a glycoside hydrolase family 68 β -fructosyltransferase from <i>Beijerinckia indica</i> subsp. <i>indica</i> in complex with fructose. <i>Bioscience, Biotechnology and Biochemistry</i> , 2020, 84, 2508-2520.	0.6	11
53	Cloning and Nucleotide Sequence of the Pullulanase Gene of <i>Thermus thermophilus</i> HB8 and Production of the Enzyme in <i>Escherichia coli</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2001, 65, 2090-2094.	0.6	10
54	Heterologous Expression, Purification, and Characterization of an α -Mannosidase Belonging to Glycoside Hydrolase Family 99 of <i>Shewanella amazonensis</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2011, 75, 797-799.	0.6	10

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55	Cloning and Expression of .BETA.-Fructofuranosidase Gene from <i>Arthrobacter</i> sp. K-1.. <i>Journal of Applied Glycoscience</i> (1999), 2002, 49, 291-296.	0.3	9
56	Facile construction of 1,2-cis glucosidic linkage using sequential oxidationâ€“reduction route for synthesis of an ER processing Î±-glucosidase I substrate. <i>Tetrahedron Letters</i> , 2012, 53, 4452-4456.	0.7	9
57	Analysis of Transglucosylation Products of <i>Aspergillus niger&/i>; Î±-Glucosidase that Catalyzes the Formation of Î±-1,2- and Î±-1,3-Linked Oligosaccharides. <i>Journal of Applied Glycoscience</i> (1999), 2020, 67, 41-49.	0.3	9
58	Crystal structure and substrate-binding mode of GH63 mannosylglycerate hydrolase from <i>Thermus thermophilus</i> HB8. <i>Journal of Structural Biology</i> , 2015, 190, 21-30.	1.3	8
59	The side chain of a glycosylated asparagine residue is important for the stability of isopullulanase. <i>Journal of Biochemistry</i> , 2015, 157, 225-234.	0.9	8
60	Analysis of Catalytic Residues of <i>Thermoactinomyces vulgaris</i> R-47 Î±-Amylase II (TVA II) by Site-directed Mutagenesis. <i>Bioscience, Biotechnology and Biochemistry</i> , 2000, 64, 2692-2695.	0.6	7
61	Rapid evaluation of 1-kestose producing Î²-fructofuranosidases from <i>Aspergillus</i> species and enhancement of 1-kestose production using a PgsA surface-display system. <i>Bioscience, Biotechnology and Biochemistry</i> , 2018, 82, 1599-1605.	0.6	7
62	A Novel Î±-Glucosidase of the Glycoside Hydrolase Family 31 from <i>Aspergillus sojae</i>. <i>Journal of Applied Glycoscience</i> (1999), 2019, 66, 73-81.	0.3	7
63	Structure of a bacterial glycoside hydrolase family 63 enzyme in complex with its glycosynthase product, and insights into the substrate specificity. <i>FEBS Journal</i> , 2013, 280, 4560-4571.	2.2	7
64	Crystallization and Preliminary X-Ray Analysis of <i>Thermoactinomyces vulgaris</i> R-47 Î±-Amylase II. <i>Journal of Structural Biology</i> , 1995, 114, 229-231.	1.3	6
65	Mutual conversion of substrate specificities of <i>Thermoactinomyces vulgaris</i> R-47 Î±-amylases TVA I and TVA II by site-directed mutagenesis. <i>Carbohydrate Research</i> , 2003, 338, 1553-1558.	1.1	6
66	Crystal structure of the N-terminal domain of a glycoside hydrolase family 131 protein from <i>Coprinopsis cinerea</i>. <i>FEBS Letters</i> , 2013, 587, 2193-2198.	1.3	6
67	Crystal structure of the enzyme-product complex reveals sugar ring distortion during catalysis by family 63 inverting Î±-glucosidase. <i>Journal of Structural Biology</i> , 2016, 196, 479-486.	1.3	6
68	Jaw1/LRMP increases Ca ²⁺ influx upon GPCR stimulation with heterogeneous effect on the activity of each ITPR subtype. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
69	Crystallization and preliminary X-ray analysis of the HA3 component of <i>Clostridium botulinum</i> type C progenitor toxin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 1038-1040.	0.7	5
70	Heterologous expression, crystallization and preliminary X-ray characterization of CcCel6C, a glycoside hydrolase family 6 enzyme from the basidiomycete <i>Coprinopsis cinerea</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 140-143.	0.7	5
71	Enzymatic synthesis of novel branched sugar alcohols mediated by the transglycosylation reaction of pullulan-hydrolyzing amylase II (TVA II) cloned from <i>Thermoactinomyces vulgaris</i> R-47. <i>Carbohydrate Research</i> , 2011, 346, 1842-1847.	1.1	5
72	The N-terminal region of Jaw1 has a role to inhibit the formation of organized smooth endoplasmic reticulum as an intrinsically disordered region. <i>Scientific Reports</i> , 2021, 11, 753.	1.6	5

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73	Heterologous Production and Characterization of <i>Arthrobacter globiformis</i> T6 Isomalto-dextranase. <i>Journal of Applied Glycoscience</i> (1999), 2004, 51, 27-32.	0.3	5
74	Crystallization and preliminary X-ray analysis of <i>Escherichia coli</i> K12 YgjK protein, a member of glycosyl hydrolase family 63. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1284-1285.	2.5	4
75	Cloning of a Gene Cluster for Dextrin Utilization from <i>Thermoactinomyces vulgaris</i> R-47 and Characterization of the Cyclodextrin-binding Protein.. <i>Journal of Applied Glycoscience</i> (1999), 2002, 49, 107-114.	0.3	4
76	Enzymatic and structural characterization of β -fructofuranosidase from the honeybee gut bacterium <i>Frischella perrara</i> . <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 2455-2470.	1.7	4
77	Structural basis for proteolytic processing of <i>Aspergillus sojae</i> β -glucosidase L with strong transglucosylation activity. <i>Journal of Structural Biology</i> , 2022, 214, 107874.	1.3	4
78	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
79	Molecular Cloning and Characterization of an Enzyme Hydrolyzing <i>p</i> -Nitrophenyl β -D-Glucoside from <i>Bacillus stearothermophilus</i> SA0301. <i>Bioscience, Biotechnology and Biochemistry</i> , 2006, 70, 495-499.	0.6	3
80	Mutagenesis-induced conformational change in domain B of a pullulan-hydrolyzing β -amylase TVA I. <i>Amylase</i> , 2018, 2, 1-10.	0.7	3
81	Modification of the transglucosylation properties of β -glucosidases from <i>Aspergillus oryzae</i> and <i>Aspergillus sojae</i> via a single critical amino acid replacement. <i>Bioscience, Biotechnology and Biochemistry</i> , 2021, 85, 1706-1710.	0.6	3
82	Purification, crystallization and preliminary X-ray analysis of an HA17 α -HA70 (HA2 α -HA3) complex from <i>Clostridium botulinum</i> type C progenitor toxin. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 64-67.	0.4	3
83	Glycan detecting tools developed from the <i>Clostridium botulinum</i> whole hemagglutinin complex. <i>Scientific Reports</i> , 2021, 11, 21973.	1.6	3
84	Novel protocol to observe the intestinal tuft cell using transmission electron microscopy. <i>Biology Open</i> , 2022, 11, .	0.6	3
85	Crystallization and preliminary X-ray study of isomaltodextranase from <i>Arthrobacter globiformis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 572-573.	2.5	2
86	Structural Similarity between a Starch-hydrolyzing Enzyme and an N-Glycan-Hydrolyzing Enzyme: Exohydrolases Cleaving β -1,4-Glucosidic Linkages to Produce β -Glucose. <i>Trends in Glycoscience and Glycotechnology</i> , 2011, 23, 93-102.	0.0	1
87	Enzymes for Cellulosic Biomass Conversion. , 2014, , 225-242.		1
88	A Surface Loop in the N-Terminal Domain of <i>Pedobacter heparinus</i> Heparin Lyase II is Important for Activity. <i>Journal of Applied Glycoscience</i> (1999), 2016, 63, 7-11.	0.3	1
89	Differences in the Characteristics of the Bacterial Community in the Epilithon and River Water as Demonstrated by Plate Counts Using Different Temperatures and Staining Methods.. <i>Japanese Journal of Limnology</i> , 1994, 55, 193-199.	0.1	1
90	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.	0.3	1

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91	Inactivation of .ALPHA.-Amylases from <i>Thermoactinomyces vulgaris</i> R-47, TVA I and TVA II, by .OMEGA.-Epoxyalkyl .ALPHA.-D-Glucopyranoside. <i>Journal of Applied Glycoscience</i> (1999), 2005, 52, 273-276.	0.3	1
92	Study on Structure and Function of Enzymes Acting on Pullulan and Related Saccharides. <i>Journal of Applied Glycoscience</i> (1999), 2009, 56, 29-33.	0.3	1
93	Purification and Properties of <i>Bacillus sectorramus</i> FERM-P8973 Pullulanase.. <i>Journal of the Japanese Society of Starch Science</i> , 1992, 39, 7-9.	0.1	1
94	Differences in the characteristics of the bacterial community in the epilithon and river water as demonstrated by plate count and staining methods. <i>Verhandlungen Der Internationalen Vereinigung Fur Theoretische Und Angewandte Limnologie International Association of Theoretical and Applied Limnology</i> , 1998, 26, 1641-1644.	0.1	0
95	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.	0.3	0
96	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.	0.3	0
97	Site-Directed Mutagenesis of Tryptophan 622 of <i>Thermoactinomyces vulgaris</i> R-47 Glucoamylase: pH Optima and Activities of Five Mutants. <i>Journal of Applied Glycoscience</i> (1999), 2005, 52, 277-279.	0.3	0
98	[Review: Symposium on Applied Glycoscience] Novel Findings of the Structure and Substrate Specificity of Glucosidases Belonging to Glycoside Hydrolase Family 63. <i>Bulletin of Applied Glycoscience</i> , 2013, 3, 151-158.	0.0	0
99	Traffic of Botulinum Toxin Complex: The Crystal Structure and the Role of Toxin Complex. , 2014, , 1-5.		0
100	Study on Structure and Function of Pullulan-Hydrolyzing Enzymes.. <i>Journal of Applied Glycoscience</i> (1999), 1999, 46, 179-186.	0.3	0
101	Traffic of Botulinum Toxin Complex: Crystal Structure and Role of Toxin Complex. , 2015, , 955-958.		0