

Zui Fujimoto

List of Publications by Year in descending order

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110
papers

3,208
citations

136740

32
h-index

168136

53
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111
all docs

111
docs citations

111
times ranked

3281
citing authors

#	ARTICLE	IF	CITATIONS
1	Substrate Specificities of GH8, GH39, and GH52 β -xylosidases from <i>Bacillus halodurans</i> C-125 Toward Substituted Xylooligosaccharides. <i>Applied Biochemistry and Biotechnology</i> , 2021, 193, 1042-1055.	1.4	9
2	Tetramer formation of <i>Bacillus subtilis</i> YabJ protein that belongs to YjgF/YER057c/UK114 family. <i>Bioscience, Biotechnology and Biochemistry</i> , 2021, 85, 297-306.	0.6	2
3	Structure-based substrate specificity analysis of GH11 xylanase from <i>Streptomyces olivaceoviridis</i> E-86. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 1943-1952.	1.7	10
4	Crystal structure of the ferredoxin reductase component of carbazole 1,9a-dioxygenase from <i>Janthinobacterium</i> sp. J3. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 921-932.	1.1	1
5	Discovery of an Antibiotic-Related Small Protein of Biocontrol Strain <i>Pseudomonas</i> sp. Os17 by a Genome-Mining Strategy. <i>Frontiers in Microbiology</i> , 2020, 11, 605705.	1.5	1
6	Development of immunogenic chimeric virus-like particles based on bovine papillomavirus type 6. <i>Vaccine</i> , 2020, 38, 7774-7779.	1.7	2
7	Unique active-site and subsite features in the arabinogalactan-degrading GH43 exo- β -1,3-galactanase from <i>Phanerochaete chrysosporium</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 18539-18552.	1.6	3
8	GH30 Glucuronoxylan-Specific Xylanase from <i>Streptomyces turgidiscabies</i> C56. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	29
9	Enhanced Azidolysis by the Formation of Stable Ser ^H His Catalytic Dyad in a Glycoside Hydrolase Family 10 Xylanase Mutant. <i>Journal of Applied Glycoscience</i> (1999), 2018, 65, 1-8.	0.3	4
10	<i>Paenibacillus</i> sp. 598K β -glucosyltransferase is essential for cycloisomaltooligosaccharide synthesis from β -D-glucan. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 4115-4128.	1.7	19
11	Crystal structure of metagenomic β -xylosidase/ β -l-arabinofuranosidase activated by calcium. <i>Journal of Biochemistry</i> , 2017, 162, 173-181.	0.9	22
12	Isomaltooligosaccharide-binding structure of <i>Paenibacillus</i> sp. 598K cycloisomaltooligosaccharide glucanotransferase. <i>Bioscience Reports</i> , 2017, 37, .	1.1	16
13	Carbohydrate-binding architecture of the multi-modular β -1,6-glucosyltransferase from <i>Paenibacillus</i> sp. 598K, which produces β -1,6-glucosyl- β -glucosaccharides from starch. <i>Biochemical Journal</i> , 2017, 474, 2763-2778.	1.7	21
14	Crystal structure of thermophilic dextranase from <i>Thermoanaerobacter pseudethanolicus</i> . <i>Journal of Biochemistry</i> , 2016, 159, mvv104.	0.9	12
15	Optimized inhibition assays reveal different inhibitory responses of hydroxylamine oxidoreductases from beta- and gamma-proteobacterial ammonium-oxidizing bacteria. <i>Biochemical and Biophysical Research Communications</i> , 2016, 476, 127-133.	1.0	14
16	Structural similarities and differences in H _{NS} family proteins revealed by the N-terminal structure of TurB in <i>Pseudomonas putida</i> KT2440. <i>FEBS Letters</i> , 2016, 590, 3583-3594.	1.3	12
17	Molecular engineering of cycloisomaltooligosaccharide glucanotransferase from <i>Bacillus circulans</i> T-3040: structural determinants for the reaction product size and reactivity. <i>Biochemical Journal</i> , 2015, 467, 259-270.	1.7	7
18	Structural Elucidation of the Cyclization Mechanism of β -1,6-Glucan by <i>Bacillus circulans</i> T-3040 Cycloisomaltooligosaccharide Glucanotransferase. <i>Journal of Biological Chemistry</i> , 2014, 289, 12040-12051.	1.6	34

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19	Lectin Structures: Classification Based on the 3-D Structures. <i>Methods in Molecular Biology</i> , 2014, 1200, 579-606.	0.4	45
20	Niemann-Pick type C2 protein mediating chemical communication in the worker ant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3847-3852.	3.3	90
21	Structural Basis of the Divergent Oxygenation Reactions Catalyzed by the Rieske Nonheme Iron Oxygenase Carbazole 1,9a-Dioxygenase. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2821-2832.	1.4	12
22	Crystallization and preliminary X-ray diffraction analyses of the redox-controlled complex of terminal oxygenase and ferredoxin components in the Rieske nonhaem iron oxygenase carbazole 1,9a-dioxygenase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1406-1409.	0.4	0
23	Evidence for cycloisomaltooligosaccharide production from starch by <i>Bacillus circulans</i> T-3040. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3947-3954.	1.7	8
24	Crystal Structure and Characterization of the Glycoside Hydrolase Family 62 β -L-Arabinofuranosidase from <i>Streptomyces coelicolor</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 7962-7972.	1.6	42
25	Basic Procedure of X-Ray Crystallography for Analysis of Lectin-Sugar Interactions. <i>Methods in Molecular Biology</i> , 2014, 1200, 481-490.	0.4	1
26	Expression, crystallization and preliminary X-ray analysis of rice L-galactose dehydrogenase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 809-811.	0.7	5
27	Crystallization and preliminary X-ray crystallographic analysis of cycloisomaltooligosaccharide glucanotransferase from <i>Bacillus circulans</i> T-3040. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 946-949.	0.7	2
28	Crystallization and preliminary X-ray diffraction studies of the reduced form of the terminal oxygenase component of the Rieske nonhaem iron oxygenase system carbazole 1,9a-dioxygenase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1284-1287.	0.7	1
29	Structure and Function of Carbohydrate-Binding Module Families 13 and 42 of Glycoside Hydrolases, Comprising a β^2 -Trefoil Fold. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 1363-1371.	0.6	46
30	Characterization of an α -L-Rhamnosidase from <i>Streptomyces avermitilis</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 213-216.	0.6	31
31	The Structure of a <i>Streptomyces avermitilis</i> α -L-Rhamnosidase Reveals a Novel Carbohydrate-binding Module CBM67 within the Six-domain Arrangement. <i>Journal of Biological Chemistry</i> , 2013, 288, 12376-12385.	1.6	67
32	Crystal Structure of Silkworm <i>Bombyx mori</i> JHBP in Complex With 2-Methyl-2,4-Pentanediol: Plasticity of JH-Binding Pocket and Ligand-Induced Conformational Change of the Second Cavity in JHBP. <i>PLoS ONE</i> , 2013, 8, e56261.	1.1	13
33	Studies on crenarchaeal tyrosylation accuracy with mutational analyses of tyrosyl-tRNA synthetase and tyrosine tRNA from <i>Aeropyrum pernix</i> . <i>Journal of Biochemistry</i> , 2012, 152, 539-548.	0.9	2
34	Structural and Biochemical Characterization of Glycoside Hydrolase Family 79 β -D-Glucuronidase from <i>Acidobacterium capsulatum</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 14069-14077.	1.6	39
35	Novel Dextranase Catalyzing Cycloisomaltooligosaccharide Formation and Identification of Catalytic Amino Acids and Their Functions Using Chemical Rescue Approach. <i>Journal of Biological Chemistry</i> , 2012, 287, 19927-19935.	1.6	19
36	Structural Elucidation of Dextran Degradation Mechanism by <i>Streptococcus mutans</i> Dextranase Belonging to Glycoside Hydrolase Family 66. <i>Journal of Biological Chemistry</i> , 2012, 287, 19916-19926.	1.6	42

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37	<i>Bacteroides</i> VPI 5482 glycoside hydrolase family 66 homolog catalyzes dextranolytic and cyclization reactions. <i>FEBS Journal</i> , 2012, 279, 3185-3191.	2.2	20
38	Interdomain Disulfide Bridge in the Rice Granule Bound Starch Synthase I Catalytic Domain as Elucidated by X-Ray Structure Analysis. <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 1591-1595.	0.6	52
39	Biochemical characterization of a novel cycloisomaltooligosaccharide glucanotransferase from <i>Paenibacillus</i> sp. 598K. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 919-924.	1.1	21
40	Structural insight into the substrate- and dioxygen-binding manner in the catalytic cycle of rieske nonheme iron oxygenase system, carbazole 1,9a-dioxygenase. <i>BMC Structural Biology</i> , 2012, 12, 15.	2.3	41
41	Crystal structure of bacteriophage ϕ -NIT1 zinc peptidase PghP that hydrolyzes β -glutamyl linkage of bacterial poly β -glutamate. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 722-732.	1.5	7
42	Structure-based engineering of glucose specificity in a family 10 xylanase from <i>Streptomyces olivaceoviridis</i> E-86. <i>Process Biochemistry</i> , 2012, 47, 358-365.	1.8	12
43	Structural mechanism of JH delivery in hemolymph by JHBP of silkworm, <i>Bombyx mori</i> . <i>Scientific Reports</i> , 2011, 1, 133.	1.6	57
44	Truncation of N- and C-terminal regions of <i>Streptococcus mutans</i> dextranase enhances catalytic activity. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 329-339.	1.7	41
45	Crystallization and preliminary crystallographic analysis of the glycoside hydrolase family 115 β -glucuronidase from <i>Streptomyces pristinaespiralis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 68-71.	0.7	11
46	Crystallization and preliminary crystallographic analysis of dextranase from <i>Streptococcus mutans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1542-1544.	0.7	7
47	Deletion analysis of regions at the C-terminal part of cycloisomaltooligosaccharide glucanotransferase from <i>Bacillus circulans</i> T-3040. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 428-434.	1.1	19
48	Crystallization and preliminary X-ray diffraction studies of a ferredoxin reductase component of carbazole 1,9a-dioxygenase from <i>Novosphingobium</i> sp. KA1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 712-714.	0.7	4
49	Crystallization and preliminary X-ray diffraction studies of a terminal oxygenase of carbazole 1,9a-dioxygenase from <i>Novosphingobium</i> sp. KA1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1480-1483.	0.7	3
50	Crystal Structure of an Exo-1,5- β -l-arabinofuranosidase from <i>Streptomyces avermitilis</i> Provides Insights into the Mechanism of Substrate Discrimination between Exo- and Endo-type Enzymes in Glycoside Hydrolase Family 43*. <i>Journal of Biological Chemistry</i> , 2010, 285, 34134-34143.	1.6	38
51	Crystallographic analysis reveals a unique conformation of the ADP-bound novel rice kinesin K16. <i>Biochemical and Biophysical Research Communications</i> , 2010, 401, 251-256.	1.0	3
52	Enzymatic Degradation of Poly-Gamma-Glutamic Acid. <i>Microbiology Monographs</i> , 2010, , 95-117.	0.3	15
53	Substrate Recognition of a Family 10 Xylanase from <i>Streptomyces olivaceoviridis</i> E-86: A Study by Site-directed Mutagenesis to Make an Hindrance around the Entrance toward the Substrate-binding Cleft. <i>Journal of Applied Glycoscience</i> (1999), 2009, 56, 173-179.	0.3	7
54	A β -l-Arabinopyranosidase from <i>Streptomyces avermitilis</i> Is a Novel Member of Glycoside Hydrolase Family 27. <i>Journal of Biological Chemistry</i> , 2009, 284, 25097-25106.	1.6	52

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55	Crystallographic Snapshots of an Entire Reaction Cycle for a Retaining Xylanase from <i>Streptomyces olivaceoviridis</i> E-86. <i>Journal of Biochemistry</i> , 2009, 146, 61-70.	0.9	16
56	NMR assignments of juvenile hormone binding protein in complex with JH III. <i>Biomolecular NMR Assignments</i> , 2009, 3, 73-76.	0.4	8
57	Sugar-complex structures of the C-half domain of the galactose-binding lectin EW29 from the earthworm <i>Lumbricus terrestris</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 49-57.	2.5	25
58	Crystallization and preliminary crystallographic analysis of β -L-arabinopyranosidase from <i>Streptomyces avermitilis</i> NBRC14893. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 632-634.	0.7	10
59	Crystallization and preliminary crystallographic analysis of poly- β -glutamate hydrolase from bacteriophage ϕ NIT1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 913-916.	0.7	5
60	Crystallization of selenomethionyl α -1,3-galactanase from the basidiomycete <i>Phanerochaete chrysosporium</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1274-1276.	0.7	8
61	Specific Interactions between the Ferredoxin and Terminal Oxygenase Components of a Class IIB Rieske Nonheme Iron Oxygenase, Carbazole 1,9a-Dioxygenase. <i>Journal of Molecular Biology</i> , 2009, 392, 436-451.	2.0	28
62	The Tetramer Structure of the Glycoside Hydrolase Family 27 β -Galactosidase I from <i>Umbelopsis vinacea</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2009, 73, 2360-2364.	0.6	14
63	Importance of Interactions of the α -Helices in the Catalytic Domain N- and C-Terminals of the Family 10 Xylanase from <i>Streptomyces olivaceoviridis</i> E-86 to the Stability of the Enzyme. <i>Journal of Applied Glycoscience</i> (1999), 2009, 56, 165-171.	0.3	7
64	Characterization of a modular enzyme of α -1,5-L-arabinofuranosidase and arabinan binding module from <i>Streptomyces avermitilis</i> NBRC14893. <i>Applied Microbiology and Biotechnology</i> , 2008, 80, 399-408.	1.7	54
65	Structures of pseudechetoxin and pseudecin, two snake-venom cysteine-rich secretory proteins that target cyclic nucleotide-gated ion channels: implications for movement of the C-terminal cysteine-rich domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1034-1042.	2.5	59
66	Crystallization and preliminary X-ray diffraction studies of a novel ferredoxin involved in the dioxygenation of carbazole by <i>Novosphingobium</i> sp. KA1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 632-635.	0.7	5
67	Crystallization and preliminary crystallographic analysis of α -1,5-L-arabinofuranosidase from <i>Streptomyces avermitilis</i> NBRC14893. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 1007-1009.	0.7	4
68	Crystallization and preliminary X-ray diffraction studies of the ferredoxin reductase component in the Rieske nonhaem iron oxygenase system carbazole 1,9a-dioxygenase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 499-502.	0.7	9
69	Crystallization and preliminary crystallographic analysis of the ferredoxin component of carbazole 1,9a-dioxygenase from <i>Nocardioides aromaticivorans</i> IC177. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 855-857.	0.7	5
70	Crystallization and preliminary X-ray diffraction studies of the terminal oxygenase component of carbazole 1,9a-dioxygenase from <i>Nocardioides aromaticivorans</i> IC177. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1212-1214.	0.7	6
71	Tailoring a Novel Sialic Acid-Binding Lectin from a Ricin-B Chain-like Galactose-Binding Protein by Natural Evolution-Mimicry. <i>Journal of Biochemistry</i> , 2006, 141, 389-399.	0.9	60
72	Electron Transfer Complex Formation between Oxygenase and Ferredoxin Components in Rieske Nonheme Iron Oxygenase System. <i>Structure</i> , 2006, 14, 1779-1789.	1.6	65

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73	Crystallization and preliminary X-ray analysis of coagulation factor IX-binding protein from habu snake venom at pH 6.5 and 4.6. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 147-149.	0.7	3
74	Crystallization and preliminary X-ray crystallographic studies of XynX, a family 10 xylanase from <i>Aeromonas punctata</i> ME-1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 255-257.	0.7	0
75	Crystallization and preliminary X-ray diffraction analysis of the electron-transfer complex between the terminal oxygenase component and ferredoxin in the Rieske non-haem iron oxygenase system carbazole 1,9a-dioxygenase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 577-580.	0.7	17
76	Crystallization and preliminary X-ray diffraction analyses of pseudochetoxin and pseudodecin, two snake-venom cysteine-rich secretory proteins that target cyclic nucleotide-gated ion channels. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 750-752.	0.7	5
77	Overexpression, purification and crystallization of tyrosyl-tRNA synthetase from the hyperthermophilic archaeon <i>Aeropyrum pernix</i> K1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 1003-1005.	0.7	3
78	Crystal structure of the ferredoxin component of carbazole 1,9a-dioxygenase of <i>Pseudomonas resinovorans</i> strain CA10, a novel Rieske non-heme iron oxygenase system. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 58, 779-789.	1.5	40
79	Complicated water orientations in the minor groove of the B-DNA decamer d(CCATTAATGG) ₂ observed by neutron diffraction measurements. <i>Nucleic Acids Research</i> , 2005, 33, 3017-3024.	6.5	108
80	Structure of the Terminal Oxygenase Component of Angular Dioxygenase, Carbazole 1,9a-Dioxygenase. <i>Journal of Molecular Biology</i> , 2005, 351, 355-370.	2.0	86
81	pH-Dependent Structural Changes at Ca ²⁺ -binding Sites of Coagulation Factor IX-binding Protein. <i>Journal of Molecular Biology</i> , 2005, 353, 80-87.	2.0	14
82	Structure and Function of a Family 10 β -Xylanase Chimera of <i>Streptomyces olivaceoviridis</i> E-86 FXYN and <i>Cellulomonas fimi</i> Cex. <i>Journal of Biological Chemistry</i> , 2004, 279, 26619-26626.	1.6	30
83	Crystal Structures of Decorated Xylooligosaccharides Bound to a Family 10 Xylanase from <i>Streptomyces olivaceoviridis</i> E-86. <i>Journal of Biological Chemistry</i> , 2004, 279, 9606-9614.	1.6	80
84	Crystal Structure of Activated HutP. <i>Structure</i> , 2004, 12, 1269-1280.	1.6	28
85	Crystallization and preliminary X-ray crystallographic studies of the C-terminal domain of galactose-binding lectin EW29 from the earthworm <i>Lumbricus terrestris</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1895-1896.	2.5	6
86	Crystallization and preliminary crystallographic analysis of the ϵ -aminobiphenyl-2,3-diol 1,2-dioxygenase from the carbazole-degrader <i>Pseudomonas resinovorans</i> strain CA10. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2340-2342.	2.5	2
87	Expression, crystallization and preliminary X-ray crystallographic studies of <i>Klebsiella pneumoniae</i> maltose-producing α -amylase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2352-2354.	2.5	1
88	Crystallization and preliminary X-ray analysis of the <i>Streptomyces olivaceoviridis</i> NgcE binding protein of the ABC transporter for N-acetylglucosamine. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2358-2360.	2.5	1
89	Crystal Structure of Aspartic Proteinase from <i>Irpex lacteus</i> in Complex with Inhibitor Pepstatin. <i>Journal of Molecular Biology</i> , 2004, 341, 1227-1235.	2.0	26
90	The Atomic Structure of Rice dwarf Virus Reveals the Self-Assembly Mechanism of Component Proteins. <i>Structure</i> , 2003, 11, 1227-1238.	1.6	144

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91	Expression, crystallization and preliminary X-ray crystallographic studies of <i>Arthrobacter globiformis</i> inulin fructotransferase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2286-2288.	2.5	6
92	Crystallization and preliminary X-ray crystallographic studies of β -galactosidase I from <i>Mortierella vinacea</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2289-2291.	2.5	3
93	Crystal Structure of Trimestatin, a Disintegrin Containing a Cell Adhesion Recognition Motif RGD. <i>Journal of Molecular Biology</i> , 2003, 332, 1115-1122.	2.0	88
94	Crystal Structure of Rice β -Galactosidase Complexed with D-Galactose. <i>Journal of Biological Chemistry</i> , 2003, 278, 20313-20318.	1.6	102
95	Crystal Structure of <i>Bacillus subtilis</i> β -Amylase in Complex with Acarbose. <i>Journal of Bacteriology</i> , 2003, 185, 6981-6984.	1.0	34
96	Crystal Structure of Mg ²⁺ - and Ca ²⁺ -bound Gla Domain of Factor IX Complexed with Binding Protein. <i>Journal of Biological Chemistry</i> , 2003, 278, 24090-24094.	1.6	84
97	Crystal structures of the sugar complexes of <i>Streptomyces olivaceoviridis</i> E-86 xylanase: sugar binding structure of the family 13 carbohydrate binding module. <i>Journal of Molecular Biology</i> , 2002, 316, 65-78.	2.0	81
98	Crystallization and preliminary crystallographic studies of dimeric disintegrins from the venom of two Agkistrodon snakes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 145-147.	2.5	4
99	Crystallization and preliminary crystallographic analysis of the terminal oxygenase component of carbazole 1,9a-dioxygenase of <i>Pseudomonas resinovorans</i> strain CA10. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1350-1352.	2.5	8
100	Crystallization and preliminary X-ray crystallographic studies of rice β -galactosidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1374-1375.	2.5	4
101	Crystal structure of an anticoagulant protein in complex with the Gla domain of factor X. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 7230-7234.	3.3	131
102	Purification, crystallization and preliminary X-ray crystallographic study of β -amylase from <i>Bacillus stearothermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 200-202.	2.5	10
103	Module shuffling of a family F/10 xylanase: replacement of modules M4 and M5 of the FXYN of <i>Streptomyces olivaceoviridis</i> E-86 with those of the Cex of <i>Cellulomonas fimi</i> . <i>Protein Engineering, Design and Selection</i> , 2000, 13, 873-879.	1.0	23
104	Crystal structure of <i>Streptomyces olivaceoviridis</i> E-86 β -xylanase containing xylan-binding domain. <i>Journal of Molecular Biology</i> , 2000, 300, 575-585.	2.0	106
105	Novel sugar-binding specificity of the type XIII xylan-binding domain of a family F/10 xylanase from <i>Streptomyces olivaceoviridis</i> E-86. <i>FEBS Letters</i> , 2000, 482, 231-236.	1.3	27
106	An investigation of the nature and function of module 10 in a family F/10 xylanase FXYN of <i>Streptomyces olivaceoviridis</i> E-86 by module shuffling with the Cex of <i>Cellulomonas fimi</i> and by site-directed mutagenesis. <i>FEBS Letters</i> , 1999, 460, 61-66.	1.3	31
107	Crystal structure of coagulation factor IX-binding protein from habu snake venom at 2.6 Å: implication of central loop swapping based on deletion in the linker region 1. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 289, 103-112.	2.0	95
108	Characteristics of Two Forms of β -Amylases and Structural Implication. <i>Applied and Environmental Microbiology</i> , 1999, 65, 4652-4658.	1.4	52

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109	Crystal structure of a catalytic-site mutant $\hat{\alpha}$ -amylase from <i>Bacillus subtilis</i> complexed with maltopentaose. <i>Journal of Molecular Biology</i> , 1998, 277, 393-407.	2.0	126
110	Structure of coagulation factors IX/X-binding protein, a heterodimer of C-type lectin domains. <i>Nature Structural Biology</i> , 1997, 4, 438-441.	9.7	118