

Yuval Shoham

List of Publications by Year in descending order

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44069

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all docs

118
docs citations

118
times ranked

5053
citing authors

#	ARTICLE	IF	CITATIONS
1	The Cellulosomes: Multienzyme Machines for Degradation of Plant Cell Wall Polysaccharides. Annual Review of Microbiology, 2004, 58, 521-554.	7.3	834
2	Microbial hemicellulases. Current Opinion in Microbiology, 2003, 6, 219-228.	5.1	580
3	Cellulose, cellulases and cellulosomes. Current Opinion in Structural Biology, 1998, 8, 548-557.	5.7	520
4	Cellulosomesâ€™ Structure and Ultrastructure. Journal of Structural Biology, 1998, 124, 221-234.	2.8	306
5	The cellulosome concept as an efficient microbial strategy for the degradation of insoluble polysaccharides. Trends in Microbiology, 1999, 7, 275-281.	7.7	287
6	Degradation of Cellulose Substrates by Cellulosome Chimeras. Journal of Biological Chemistry, 2002, 277, 49621-49630.	3.4	254
7	Species-specificity of the cohesin-dockerin interaction between <i>Clostridium thermocellum</i> and <i>Clostridium cellulolyticum</i> : Prediction of specificity determinants of the dockerin domain. Proteins: Structure, Function and Bioinformatics, 1997, 29, 517-527.	2.6	192
8	Design and Production of Active Cellulosome Chimeras. Journal of Biological Chemistry, 2001, 276, 21257-21261.	3.4	182
9	Cellulosomal Scaffoldin-Like Proteins from <i>Ruminococcus flavefaciens</i> . Journal of Bacteriology, 2001, 183, 1945-1953.	2.2	166
10	Expression, purification and subunit-binding properties of cohesins 2 and 3 of the <i>Clostridium thermocellum</i> cellulosome. FEBS Letters, 1995, 360, 121-124.	2.8	135
11	The Structure of an Inverting GH43 Î²-Xylosidase from <i>Geobacillus stearothermophilus</i> with its Substrate Reveals the Role of the Three Catalytic Residues. Journal of Molecular Biology, 2006, 359, 97-109.	4.2	132
12	The Glucuronic Acid Utilization Gene Cluster from <i>Bacillus stearothermophilus</i> T-6. Journal of Bacteriology, 1999, 181, 3695-3704.	2.2	130
13	Crystal structure and snapshots along the reaction pathway of a family 51 Î±-L-arabinofuranosidase. EMBO Journal, 2003, 22, 4922-4932.	7.8	127
14	Mapping glycoside hydrolase substrate subsites by isothermal titration calorimetry. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11275-11280.	7.1	120
15	A cohesin domain from <i>Clostridium thermocellum</i> : the crystal structure provides new insights into cellulosome assembly. Structure, 1997, 5, 381-390.	3.3	119
16	Cell, a Noncellulosomal Family 9 Enzyme from <i>Clostridium thermocellum</i> , Is a Processive Endoglucanase That Degrades Crystalline Cellulose. Journal of Bacteriology, 2003, 185, 391-398.	2.2	119
17	<i>Clostridium thermocellum</i> cellulosomal genes are regulated by extracytoplasmic polysaccharides via alternative sigma factors. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18646-18651.	7.1	114
18	Cohesin-Dockerin Interaction in Cellulosome Assembly. Journal of Biological Chemistry, 2001, 276, 9883-9888.	3.4	100

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19	Cellulase-Xylanase Synergy in Designer Cellulosomes for Enhanced Degradation of a Complex Cellulosic Substrate. <i>MBio</i> , 2010, 1, .	4.1	99
20	Isolation of a <i>Bacillus</i> sp. capable of transforming isoeugenol to vanillin. <i>Journal of Biotechnology</i> , 2000, 78, 1-9.	3.8	97
21	Biochemical Characterization and Identification of the Catalytic Residues of a Family 43 β -D-Xylosidase from <i>Geobacillus stearothermophilus</i> T-6. <i>Biochemistry</i> , 2005, 44, 387-397.	2.5	93
22	A Novel Cellulosomal Scaffoldin from <i>Acetivibrio cellulolyticus</i> That Contains a Family 9 Glycosyl Hydrolase. <i>Journal of Bacteriology</i> , 1999, 181, 6720-6729.	2.2	93
23	Matching fusion protein systems for affinity analysis of two interacting families of proteins: the cohesin-dockerin interaction. <i>Journal of Molecular Recognition</i> , 2005, 18, 491-501.	2.1	92
24	Deconstruction of Lignocellulose into Soluble Sugars by Native and Designer Cellulosomes. <i>MBio</i> , 2012, 3, .	4.1	92
25	Cohesin-dockerin microarray: Diverse specificities between two complementary families of interacting protein modules. <i>Proteomics</i> , 2008, 8, 968-979.	2.2	90
26	The Cellulosome System of <i>Acetivibrio cellulolyticus</i> Includes a Novel Type of Adaptor Protein and a Cell Surface Anchoring Protein. <i>Journal of Bacteriology</i> , 2003, 185, 4548-4557.	2.2	84
27	Cohesin-dockerin recognition in cellulosome assembly: Experiment versus hypothesis. , 2000, 39, 170-177.		83
28	Detailed Kinetic Analysis and Identification of the Nucleophile in β -L-Arabinofuranosidase from <i>Geobacillus stearothermophilus</i> T-6, a Family 51 Glycoside Hydrolase. <i>Journal of Biological Chemistry</i> , 2002, 277, 43667-43673.	3.4	83
29	Cellodextrin and Laminaribiose ABC Transporters in <i>Clostridium thermocellum</i> . <i>Journal of Bacteriology</i> , 2009, 191, 203-209.	2.2	83
30	Novel Organization and Divergent Dockerin Specificities in the Cellulosome System of <i>Ruminococcus flavefaciens</i> . <i>Journal of Bacteriology</i> , 2003, 185, 703-713.	2.2	78
31	Digestion of crystalline cellulose substrates by the <i>Clostridium thermocellum</i> cellulosome: structural and morphological aspects. <i>Biochemical Journal</i> , 1999, 340, 829-835.	3.7	72
32	The identification of the acid-base catalyst of β -arabinofuranosidase from <i>Geobacillus stearothermophilus</i> T-6, a family 51 glycoside hydrolase. <i>FEBS Letters</i> , 2002, 514, 163-167.	2.8	72
33	Regulation of the Cellulosomal <i>celS</i> (<i>cel48A</i>) Gene of <i>Clostridium thermocellum</i> Is Growth Rate Dependent. <i>Journal of Bacteriology</i> , 2003, 185, 3042-3048.	2.2	72
34	Architecture of the <i>Bacteroides cellulosolvens</i> Cellulosome: Description of a Cell Surface-Anchoring Scaffoldin and a Family 48 Cellulase. <i>Journal of Bacteriology</i> , 2004, 186, 968-977.	2.2	70
35	A Scaffoldin of the <i>Bacteroides cellulosolvens</i> Cellulosome That Contains 11 Type II Cohesins. <i>Journal of Bacteriology</i> , 2000, 182, 4915-4925.	2.2	68
36	Enzyme-Substrate Complex Structures of a GH39 β -Xylosidase from <i>Geobacillus stearothermophilus</i> . <i>Journal of Molecular Biology</i> , 2005, 353, 838-846.	4.2	67

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37	Regulation of Expression of Scaffoldin-Related Genes in <i>Clostridium thermocellum</i> . <i>Journal of Bacteriology</i> , 2003, 185, 5109-5116.	2.2	63
38	Crystal Structures of <i>Geobacillus stearothermophilus</i> β -Glucuronidase Complexed with Its Substrate and Products. <i>Journal of Biological Chemistry</i> , 2004, 279, 3014-3024.	3.4	62
39	A Two-Component System Regulates the Expression of an ABC Transporter for Xylo-Oligosaccharides in <i>Geobacillus stearothermophilus</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 874-884.	3.1	62
40	Assembly of Xylanases into Designer Cellulosomes Promotes Efficient Hydrolysis of the Xylan Component of a Natural Recalcitrant Cellulosic Substrate. <i>MBio</i> , 2011, 2, .	4.1	62
41	Two Active Forms of <i>Zymomonas mobilis</i> Levansucrase. <i>Journal of Biological Chemistry</i> , 2008, 283, 32209-32217.	3.4	59
42	Cellulose-decomposing Bacteria and Their Enzyme Systems. , 2006, , 578-617.		56
43	Detailed Kinetic Analysis of a Family 52 Glycoside Hydrolase: A β -Xylosidase from <i>Geobacillus stearothermophilus</i> . <i>Biochemistry</i> , 2003, 42, 10528-10536.	2.5	54
44	Crystal structure of an inverting GH 43 1,5- β -D-arabinanase from <i>Geobacillus stearothermophilus</i> complexed with its substrate. <i>Biochemical Journal</i> , 2009, 422, 73-82.	3.7	54
45	Identification of the Catalytic Residues in Family 52 Glycoside Hydrolase, a β -Xylosidase from <i>Geobacillus stearothermophilus</i> T-6. <i>Journal of Biological Chemistry</i> , 2003, 278, 26742-26749.	3.4	53
46	Delignification of wood pulp by a thermostable xylanase from <i>Bacillus stearothermophilus</i> strain T-6. <i>Biodegradation</i> , 1992, 3, 207-218.	3.0	52
47	Glycosynthase Activity of <i>Geobacillus stearothermophilus</i> GH52 β -Xylosidase: Efficient Synthesis of Xylooligosaccharides from β -D-Xylopyranosyl Fluoride through a Conjugated Reaction. <i>ChemBioChem</i> , 2007, 8, 2145-2151.	2.6	52
48	Contribution of a Xylan-Binding Module to the Degradation of a Complex Cellulosic Substrate by Designer Cellulosomes. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3787-3796.	3.1	52
49	A New Family of Carbohydrate Esterases Is Represented by a GDSL Hydrolase/Acetylxylan Esterase from <i>Geobacillus stearothermophilus</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 41993-42001.	3.4	52
50	Biochemical characterization and identification of catalytic residues in β -glucuronidase from <i>Bacillus stearothermophilus</i> T-6. <i>FEBS Journal</i> , 2001, 268, 3006-3016.	0.2	51
51	Novel architecture of family-9 glycoside hydrolases identified in cellulosomal enzymes of <i>Acetivibrio cellulolyticus</i> and <i>Clostridium thermocellum</i> . <i>FEMS Microbiology Letters</i> , 2006, 254, 308-316.	1.8	50
52	Structure of a family IIIa scaffoldin CBD from the cellulosome of <i>Clostridium cellulolyticum</i> at 2.2-Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1560-1568.	2.5	48
53	Optimization of protein-production by the baculovirus expression vector system in shake flasks. <i>Applied Microbiology and Biotechnology</i> , 1992, 37, 74-8.	3.6	47
54	The β -Arabinan Utilization System of <i>Geobacillus stearothermophilus</i> . <i>Journal of Bacteriology</i> , 2011, 193, 2838-2850.	2.2	47

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55	Thermobifida fusca family-6 cellulases as potential designer cellulosome components. <i>Biocatalysis and Biotransformation</i> , 2006, 24, 3-12.	2.0	46
56	Effect of Dimer Dissociation on Activity and Thermostability of the β -Glucuronidase from <i>Geobacillus stearothermophilus</i> : Dissecting the Different Oligomeric Forms of Family 67 Glycoside Hydrolases. <i>Journal of Bacteriology</i> , 2004, 186, 6928-6937.	2.2	45
57	Regulation of Major Cellulosomal Endoglucanases of <i>Clostridium thermocellum</i> Differs from That of a Prominent Cellulosomal Xylanase. <i>Journal of Bacteriology</i> , 2005, 187, 2261-2266.	2.2	44
58	Biotransformations of propenylbenzenes by an <i>Arthrobacter</i> sp. and its t-anethole blocked mutants. <i>Journal of Biotechnology</i> , 2003, 105, 61-70.	3.8	43
59	A Novel <i>Acetivibrio cellulolyticus</i> Anchoring Scaffoldin That Bears Divergent Cohesins. <i>Journal of Bacteriology</i> , 2004, 186, 5782-5789.	2.2	43
60	Physical association of the catalytic and helper modules of a family 9 glycoside hydrolase is essential for activity. <i>FEBS Letters</i> , 2009, 583, 879-884.	2.8	42
61	Stereochemistry of family 52 glycosyl hydrolases: a β -xylosidase from <i>Bacillus stearothermophilus</i> T-6 is a retaining enzyme. <i>FEBS Letters</i> , 2001, 495, 39-43.	2.8	41
62	Glycoside hydrolases as components of putative carbohydrate biosensor proteins in <i>Clostridium thermocellum</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2011, 38, 825-832.	3.0	41
63	Novel Methodology for Enzymatic Removal of Atrazine from Water by CBD-Fusion Protein Immobilized on Cellulose. <i>Environmental Science & Technology</i> , 2000, 34, 1292-1296.	10.0	39
64	A Simple and Rapid Method for Preparing a Cell-Free Bacterial Lysate for Protein Synthesis. <i>PLoS ONE</i> , 2016, 11, e0165137.	2.5	38
65	Glutamic acid 160 is the acid-base catalyst of β -xylosidase from <i>Bacillus stearothermophilus</i> T-6: a family 39 glycoside hydrolase. <i>FEBS Letters</i> , 2001, 495, 115-119.	2.8	36
66	Cohesin-dockerin interaction in cellulosome assembly: a single Asp-to-Asn mutation disrupts high-affinity cohesin-dockerin binding. <i>FEBS Letters</i> , 2004, 572, 195-200.	2.8	36
67	Functional characterization of the galactan utilization system of <i>Geobacillus stearothermophilus</i> . <i>FEBS Journal</i> , 2013, 280, 950-964.	4.7	33
68	Assembly of Synthetic Functional Cellulosomal Structures onto the Cell Surface of <i>Lactobacillus plantarum</i> , a Potent Member of the Gut Microbiome. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	33
69	Decoding Biomass-Sensing Regulons of <i>Clostridium thermocellum</i> Alternative Sigma-I Factors in a Heterologous <i>Bacillus subtilis</i> Host System. <i>PLoS ONE</i> , 2016, 11, e0146316.	2.5	31
70	A unique octameric structure of Axe2, an intracellular acetyl-xylooligosaccharide esterase from <i>Geobacillus stearothermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 261-278.	2.5	30
71	Reassembly and co-crystallization of a family 9 processive endoglucanase from its component parts: structural and functional significance of the intermodular linker. <i>PeerJ</i> , 2015, 3, e1126.	2.0	29
72	Functional Association of Catalytic and Ancillary Modules Dictates Enzymatic Activity in Glycoside Hydrolase Family 43 β -Xylosidase. <i>Journal of Biological Chemistry</i> , 2012, 287, 9213-9221.	3.4	28

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73	Multiple Regulatory Mechanisms Control the Expression of the <i>Geobacillus stearothermophilus</i> Gene for Extracellular Xylanase. <i>Journal of Biological Chemistry</i> , 2014, 289, 25957-25975.	3.4	28
74	Spectroscopic FTIR and NMR study of the interactions of sugars with proteins. <i>Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy</i> , 2019, 222, 116861.	3.9	28
75	Draft Genome Sequences for <i>Clostridium thermocellum</i> Wild-Type Strain YS and Derived Cellulose Adhesion-Defective Mutant Strain AD2. <i>Journal of Bacteriology</i> , 2012, 194, 3290-3291.	2.2	27
76	Fine-structural variance of family 3 carbohydrate-binding modules as extracellular biomass-sensing components of <i>Clostridium thermocellum</i> anti- β factors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 522-534.	2.5	26
77	Lignocellulose-Decomposing Bacteria and Their Enzyme Systems. , 2013, , 215-266.		25
78	Dissociation of the cellulosome of <i>Clostridium thermocellum</i> under nondenaturing conditions. <i>Journal of Biotechnology</i> , 1996, 51, 235-242.	3.8	24
79	Digestion of crystalline cellulose substrates by the <i>Clostridium thermocellum</i> cellulosome: structural and morphological aspects. <i>Biochemical Journal</i> , 1999, 340, 829.	3.7	24
80	Structural and Mechanistic Investigation of 3-Deoxy-d-manno-octulosonate-8-phosphate Synthase by Solid-State REDOR NMR. <i>Biochemistry</i> , 2000, 39, 14865-14876.	2.5	24
81	Regulation of biomass degradation by alternative β factors in cellulolytic clostridia. <i>Scientific Reports</i> , 2018, 8, 11036.	3.3	24
82	Nonproteolytic Cleavage of Aspartyl Proline Bonds in the Cellulosomal Scaffoldin Subunit from <i>Clostridium thermocellum</i> . <i>Applied Biochemistry and Biotechnology</i> , 2001, 90, 67-74.	2.9	23
83	Crystallization and preliminary crystallographic analysis of GanB, a GH42 intracellular β -galactosidase from <i>Geobacillus stearothermophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1114-1119.	0.7	21
84	Structure-function relationships in Gan42B, an intracellular GH42 β -galactosidase from <i>Geobacillus stearothermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2433-2448.	2.5	19
85	Three cellulosomal xylanase genes in <i>Clostridium thermocellum</i> are regulated by both vegetative SigA (β A) and alternative Sig16 (β 16) factors. <i>FEBS Letters</i> , 2015, 589, 3133-3140.	2.8	19
86	Crystallization and preliminary X-ray analysis of β -D-glucuronidase from <i>Bacillus stearothermophilus</i> AT-6. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 869-872.	2.5	18
87	A new crystal form of XT6 enables a significant improvement of its diffraction quality and resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 545-549.	2.5	18
88	Functional asymmetry in cohesin binding belies inherent symmetry of the dockerin module: insight into cellulosome assembly revealed by systematic mutagenesis. <i>Biochemical Journal</i> , 2008, 410, 331-338.	3.7	17
89	Crystallization and preliminary crystallographic analysis of Axe2, an acetylxylan esterase from <i>Geobacillus stearothermophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 430-434.	0.7	17
90	The <i>abp</i> gene in <i>Geobacillus stearothermophilus</i> encodes a GH27 β -arabinopyranosidase. <i>FEBS Letters</i> , 2012, 586, 2436-2442.	2.8	16

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91	Pinpoint Mapping of Recognition Residues on the Cohesin Surface by Progressive Homologue Swapping. <i>Journal of Biological Chemistry</i> , 2004, 279, 42881-42888.	3.4	14
92	Expression, purification and crystallization of a cohesin domain from the cellulosome of <i>Clostridium thermocellum</i> . <i>Journal of Biotechnology</i> , 1996, 51, 243-249.	3.8	12
93	Crystallization and preliminary X-ray analysis of a family 51 glycoside hydrolase, the β -L-arabinofuranosidase from <i>Geobacillus stearothermophilus</i> T-6. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 913-915.	2.5	12
94	Revisiting the Regulation of the Primary Scaffoldin Gene in <i>Clostridium thermocellum</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	10
95	Crystallization and preliminary crystallographic analysis of Abp, a GH27 β -L-arabinopyranosidase from <i>Geobacillus stearothermophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 695-699.	0.7	9
96	Structure-specificity relationships in Abp, a GH27 β -L-arabinopyranosidase from <i>Geobacillus stearothermophilus</i> T6. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2994-3012.	2.5	9
97	Purification, crystallization and preliminary crystallographic analysis of Gan1D, a GH1 6-phospho- β -galactosidase from <i>Geobacillus stearothermophilus</i> T1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 225-231.	0.8	9
98	Structural basis for enzyme bifunctionality – the case of Gan1D from <i>Geobacillus stearothermophilus</i> . <i>FEBS Journal</i> , 2017, 284, 3931-3953.	4.7	9
99	Cellulosome-Enhanced Conversion of Biomass: On the Road to Bioethanol. , 0, , 75-96.		9
100	Family of thiomeric derivatives of sugars: Synthesis, fungicidal/herbicidal activity, and application to the X-ray structure determination of the corresponding enzymes. <i>Israel Journal of Chemistry</i> , 2000, 40, 177-188.	2.3	8
101	Identifying critical unrecognized sugar-protein interactions in GH10 xylanases from <i>Geobacillus stearothermophilus</i> using STD NMR. <i>FEBS Journal</i> , 2013, 280, 4652-4665.	4.7	8
102	Preliminary crystallographic analysis of a double mutant of the acetyl xylo-oligosaccharide esterase Axe2 in its dimeric form. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 476-481.	0.8	8
103	Crystallization and preliminary crystallographic analysis of a thermostable family 52 β -D-xylosidase from <i>Geobacillus stearothermophilus</i> T-6. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1461-1463.	2.5	6
104	Cellulosome domains for novel biotechnological application. <i>Progress in Biotechnology</i> , 1995, , 251-259.	0.2	5
105	Cloning, purification and preliminary crystallographic analysis of Ara127N, a GH127 β -L-arabinofuranosidase from <i>Geobacillus stearothermophilus</i> T6. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1038-1045.	0.8	5
106	Carbohydrate-Binding Capability and Functional Conformational Changes of AbnE, an Arabino-oligosaccharide Binding Protein. <i>Journal of Molecular Biology</i> , 2020, 432, 2099-2120.	4.2	5
107	Crystallization and preliminary X-ray analysis of family 39 β -D-xylosidase from <i>Geobacillus stearothermophilus</i> T-6. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 583-585.	2.5	4
108	Effect of Rational Mutagenesis of Selected Cohesin Residues on the High-Affinity Cohesin-Dockerin Interaction. <i>ACS Symposium Series</i> , 2004, , 194-206.	0.5	4

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109	Crystallization and preliminary crystallographic analysis of a family 43 β -D-xylosidase from <i>Geobacillus stearothermophilus</i> T-6. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 1054-1057.	0.7	4
110	Cellulose to electricity conversion by an enzymatic biofuel cell. <i>Sustainable Energy and Fuels</i> , 2021, 5, 4580-4586.	4.9	4
111	Preliminary crystallographic analysis of Xyn52B2, a GH52 β -D-xylosidase from <i>Geobacillus stearothermophilus</i> T6. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1675-1682.	0.8	3
112	Integrative structure determination reveals functional global flexibility for an ultra-multimodular arabinanase. <i>Communications Biology</i> , 2022, 5, 465.	4.4	3
113	Phage Display of Cellulose Binding Domains for Biotechnological Application. <i>ACS Symposium Series</i> , 2000, , 168-189.	0.5	2
114	Cross-utilization of β -galactosides and cellobiose in <i>Geobacillus stearothermophilus</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 10766-10780.	3.4	2
115	Species-specificity of the cohesin-dockerin interaction between <i>Clostridium thermocellum</i> and <i>Clostridium cellulolyticum</i> : Prediction of specificity determinants of the dockerin domain. , 1997, 29, 517.		1
116	Species-specificity of the cohesin-dockerin interaction between <i>Clostridium thermocellum</i> and <i>Clostridium cellulolyticum</i> : Prediction of specificity determinants of the dockerin domain. , 1997, 29, 517.		1