Edward A Bayer

List of Publications by Year
in descending order

170 papers	12,573 citations	22153 59 h-index	29157 104 g-index
177 all docs	177 docs citations	177 times ranked	7978 citing authors

#	Article	IF	Citations
1	Mapping the deformability of natural and designed cellulosomes in solution. , 2022, 15, .		4
2	Novel clostridial cell-surface hemicellulose-binding CBM3 proteins. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 95-104.	0.8	1
3	NMR chemical shift assignments of a module of unknown function in the cellulosomal secondary scaffoldin ScaF from Clostridium thermocellum. Biomolecular NMR Assignments, 2021, 15, 329-334.	0.8	0
4	Coordinated Î²-glucosidase activity with the cellulosome is effective for enhanced lignocellulose saccharification. Bioresource Technology, 2021, 337, 125441.	9.6	26
5	Surface Display of Designer Protein Scaffolds on Genome-Reduced Strains of <i>Pseudomonas putida</i>. ACS Synthetic Biology, 2020, 9, 2749-2764.	3.8	16
6	Understanding Cellulosome Interaction with Cellulose by High-Resolution Imaging. ACS Central Science, 2020, 6, 1034-1036.	11.3	11
7	Impact of scaffoldin mechanostability on cellulosomal activity. Biomaterials Science, 2020, 8, 3601-3610.	5.4	7
8	Rapid adaptation for fibre degradation by changes in plasmid stoichiometry within <i>Lactobacillus plantarum</i> at the synthetic community level. Microbial Biotechnology, 2020, 13, 1748-1764.	4.2	5
9	Minimalistic Cellulosome of the Butanologenic Bacterium Clostridium saccharoperbutylacetonicum. MBio, 2020, 11, .	4.1	7
10	Mechanisms of Nanonewton Mechanostability in a Protein Complex Revealed by Molecular Dynamics Simulations and Single-Molecule Force Spectroscopy. Journal of the American Chemical Society, 2019, 141, 14752-14763.	13.7	55
11	Directed Evolution of Clostridium thermocellum Î²-Glucosidase A Towards Enhanced Thermostability. International Journal of Molecular Sciences, 2019, 20, 4701.	4.1	26
12	The Cellulosome Paradigm in An Extreme Alkaline Environment. Microorganisms, 2019, 7, 347.	3.6	20
13	Cell-surface display of designer cellulosomes by Lactobacillus plantarum. Methods in Enzymology, 2019, 617, 241-263.	1.0	6
14	Alternative ÏƒI/anti-ÏƒI factors represent a unique form of bacterial Ïƒ/anti-Ïƒ complex. Nucleic Acids Research, 2019, 47, 5988-5997.	14.5	19
15	Unraveling essential cellulosomal components of the (Pseudo)Bacteroides cellulosolvens reveals an extensive reservoir of novel catalytic enzymes. Biotechnology for Biofuels, 2019, 12, 115.	6.2	11
16	Creation of a functional hyperthermostable designer cellulosome. Biotechnology for Biofuels, 2019, 12, 44.	6.2	39
17	The cohesin module is a major determinant of cellulosome mechanical stability. Journal of Biological Chemistry, 2018, 293, 7139-7147.	3.4	15
18	Assembly of Synthetic Functional Cellulosomal Structures onto the Cell Surface of Lactobacillus plantarum, a Potent Member of the Gut Microbiome. Applied and Environmental Microbiology, 2018, 84, .	3.1	33

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19	Colocalization and Disposition of Cellulosomes in <i>Clostridium clariflavum</i> as Revealed by Correlative Superresolution Imaging. MBio, 2018, 9, .	4.1	15
20	Molecular simulations reveal that a short helical loop regulates thermal stability of type I cohesinâ€"dockerin complexes. Physical Chemistry Chemical Physics, 2018, 20, 28445-28451.	2.8	3
21	Crystal structure of afifavidin reveals common features of molecular assemblage in the bacterial dimeric avidins. FEBS Journal, 2018, 285, 4617-4630.	4.7	6
22	Advanced Cloning Tools for Construction of Designer Cellulosomes. Methods in Molecular Biology, 2018, 1796, 135-151.	0.9	5
23	Dual binding in cohesin-dockerin complexes: the energy landscape and the role of short, terminal segments of the dockerin module. Scientific Reports, 2018, 8, 5051.	3.3	9
24	Regulation of biomass degradation by alternative Ïƒ factors in cellulolytic clostridia. Scientific Reports, 2018, 8, 11036.	3.3	24
25	Complexity of the Ruminococcus flavefaciens FD-1 cellulosome reflects an expansion of family-related protein-protein interactions. Scientific Reports, 2017, 7, 42355.	3.3	31
26	Continually emerging mechanistic complexity of the multi-enzyme cellulosome complex. Current Opinion in Structural Biology, 2017, 44, 151-160.	5.7	47
27	Carbohydrate Depolymerization by Intricate Cellulosomal Systems. Methods in Molecular Biology, 2017, 1588, 93-116.	0.9	8
28	Cellulosomes: bacterial nanomachines for dismantling plant polysaccharides. Nature Reviews Microbiology, 2017, 15, 83-95.	28.6	336
29	Assembly of Ruminococcus flavefaciens cellulosome revealed by structures of two cohesin-dockerin complexes. Scientific Reports, 2017, 7, 759.	3.3	20
30	Cellulosomes and designer cellulosomes: why toy with <scp>N</scp>ature?. Environmental Microbiology Reports, 2017, 9, 14-15.	2.4	14
31	Broad phylogeny and functionality of cellulosomal components in the bovine rumen microbiome. Environmental Microbiology, 2017, 19, 185-197.	3.8	32
32	Unique organization and unprecedented diversity of the Bacteroides (Pseudobacteroides) cellulosolvens cellulosome system. Biotechnology for Biofuels, 2017, 10, 211.	6.2	29
33	How does cellulosome composition influence deconstruction of lignocellulosic substrates in Clostridium (Ruminiclostridium) thermocellum DSM 1313?. Biotechnology for Biofuels, 2017, 10, 222.	6.2	47
34	Pan-Cellulosomics of Mesophilic Clostridia: Variations on a Theme. Microorganisms, 2017, 5, 74.	3.6	17
35	Dramatic performance of <i>Clostridium thermocellum</i> explained by its wide range of cellulase modalities. Science Advances, 2016, 2, e1501254.	10.3	99
36	Application of Long Sequence Reads To Improve Genomes for Clostridium thermocellum AD2, Clostridium thermocellum LQRI, and Pelosinus fermentans R7. Genome Announcements, 2016, 4, .	0.8	2

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37	Lysozyme activity of the <scp><i>R</i></scp><i>uminococcus champanellensis</i> cellulosome. Environmental Microbiology, 2016, 18, 5112-5122.	3.8	19
38	Single versus dual-binding conformations in cellulosomal cohesinâ€"dockerin complexes. Current Opinion in Structural Biology, 2016, 40, 89-96.	5.7	34
39	Toward combined delignification and saccharification of wheat straw by a laccase-containing designer cellulosome. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10854-10859.	7.1	77
40	Enhancement of cellulosome-mediated deconstruction of cellulose by improving enzyme thermostability. Biotechnology for Biofuels, 2016, 9, 164.	6.2	49
41	Enzymatic profiling of cellulosomal enzymes from the human gut bacterium, <scp><i>R</i></scp><i>uminococcus champanellensis</i>, reveals a fineâ€tuned system for cohesinâ€dockerin recognition. Environmental Microbiology, 2016, 18, 542-556.	3.8	57
42	Cellulosomal expansin: functionality and incorporation into the complex. Biotechnology for Biofuels, 2016, 9, 61.	6.2	29
43	Adaptor Scaffoldins: An Original Strategy for Extended Designer Cellulosomes, Inspired from Nature. MBio, 2016, 7, e00083.	4.1	50
44	Nanoscale Engineering of Designer Cellulosomes. Advanced Materials, 2016, 28, 5619-5647.	21.0	42
45	Decoding Biomass-Sensing Regulons of Clostridium thermocellum Alternative Sigma-I Factors in a Heterologous Bacillus subtilis Host System. PLoS ONE, 2016, 11, e0146316.	2.5	31
46	Near-Complete Genome Sequence of the Cellulolytic Bacterium <i>Bacteroides</i> () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 Td (<i>P	0.8	12
47	Resolving dual binding conformations of cellulosome cohesin-dockerin complexes using single-molecule force spectroscopy. ELife, 2015, 4, .	6.0	39
48	Significance of Relative Position of Cellulases in Designer Cellulosomes for Optimized Cellulolysis. PLoS ONE, 2015, 10, e0127326.	2.5	43
49	Combined Crystal Structure of a Type I Cohesin. Journal of Biological Chemistry, 2015, 290, 16215-16225.	3.4	10
50	Hoefavidin: A dimeric bacterial avidin with a C-terminal binding tail. Journal of Structural Biology, 2015, 191, 139-148.	2.8	17
51	Cell-surface Attachment of Bacterial Multienzyme Complexes Involves Highly Dynamic Protein-Protein Anchors. Journal of Biological Chemistry, 2015, 290, 13578-13590.	3.4	22
52	Standalone cohesin as a molecular shuttle in cellulosome assembly. FEBS Letters, 2015, 589, 1569-1576.	2.8	14
53	Functional phylotyping approach for assessing intraspecific diversity of Ruminococcus albus within the rumen microbiome. FEMS Microbiology Letters, 2015, 362, 1-10.	1.8	12
54	Ruminococcal cellulosome systems from rumen to human. Environmental Microbiology, 2015, 17, 3407-3426.	3.8	104

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55	Unique Organization of Extracellular Amylases into Amylosomes in the Resistant Starch-Utilizing Human Colonic <i>Firmicutes</i> Bacterium Ruminococcus bromii. MBio, 2015, 6, e01058-15.	4.1	145
56	Clostridium clariflavum: Key Cellulosome Players Are Revealed by Proteomic Analysis. MBio, 2015, 6, e00411-15.	4.1	57
57	Crucial Roles of Single Residues in Binding Affinity, Specificity, and Promiscuity in the Cellulosomal Cohesin-Dockerin Interface. Journal of Biological Chemistry, 2015, 290, 13654-13666.	3.4	14
58	Mapping Mechanical Force Propagation through Biomolecular Complexes. Nano Letters, 2015, 15, 7370-7376.	9.1	83
59	Three cellulosomal xylanase genes in<i>Clostridium thermocellum</i> are regulated by both vegetative SigA (Ïƒ^A) and alternative SigI6 (Ïƒ^{I6}) factors. FEBS Letters, 2015, 589, 3133-3140.	2.8	19
60	Reassembly and co-crystallization of a family 9 processive endoglucanase from its component parts: structural and functional significance of the intermodular linker. PeerJ, 2015, 3, e1126.	2.0	29
61	Rumen Cellulosomics: Divergent Fiber-Degrading Strategies Revealed by Comparative Genome-Wide Analysis of Six Ruminococcal Strains. PLoS ONE, 2014, 9, e99221.	2.5	73
62	Ultrastable cellulosome-adhesion complex tightens under load. Nature Communications, 2014, 5, 5635.	12.8	92
63	Revisiting the NMR solution structure of the Cel48S type-I dockerin module from Clostridium thermocellum reveals a cohesin-primed conformation. Journal of Structural Biology, 2014, 188, 188-193.	2.8	21
64	A combined cell-consortium approach for lignocellulose degradation by specialized Lactobacillus plantarumcells. Biotechnology for Biofuels, 2014, 7, 112.	6.2	40
65	Overexpression, crystallization and preliminary X-ray characterization ofRuminococcus flavefaciensscaffoldin C cohesin in complex with a dockerin from an uncharacterized CBM-containing protein. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1061-1064.	0.8	2
66	Structural characterization of a novel autonomous cohesin from<i>Ruminococcus flavefaciens</i>. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 450-456.	0.8	3
67	Thermophilic lignocellulose deconstruction. FEMS Microbiology Reviews, 2014, 38, 393-448.	8.6	145
68	Fine-structural variance of family 3 carbohydrate-binding modules as extracellular biomass-sensing components of<i>Clostridium thermocellum</i>anti-Ïƒ^Ifactors. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 522-534.	2.5	26
69	Towards lactic acid bacteria-based biorefineries. Biotechnology Advances, 2014, 32, 1216-1236.	11.7	152
70	Insights into enhanced thermostability of a cellulosomal enzyme. Carbohydrate Research, 2014, 389, 78-84.	2.3	12
71	Integration of bacterial lytic polysaccharide monooxygenases into designer cellulosomes promotes enhanced cellulose degradation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9109-9114.	7.1	96
72	Biomass Utilization by Gut Microbiomes. Annual Review of Microbiology, 2014, 68, 279-296.	7.3	161

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73	Cellulosomics of the cellulolytic thermophile Clostridium clariflavum. Biotechnology for Biofuels, 2014, 7, 100.	6.2	53
74	Elaborate cellulosome architecture of<i>Acetivibrio cellulolyticus</i>revealed by selective screening of cohesinâ€“dockerin interactions. PeerJ, 2014, 2, e636.	2.0	29
75	Structure and regulation of the cellulose degradome in Clostridium cellulolyticum. Biotechnology for Biofuels, 2013, 6, 73.	6.2	49
76	A synthetic biology approach for evaluating the functional contribution of designer cellulosome components to deconstruction of cellulosic substrates. Biotechnology for Biofuels, 2013, 6, 182.	6.2	76
77	Atypical Cohesin-Dockerin Complex Responsible for Cell Surface Attachment of Cellulosomal Components. Journal of Biological Chemistry, 2013, 288, 16827-16838.	3.4	38
78	Insights into cellulosome assembly and dynamics: from dissection to reconstruction of the supramolecular enzyme complex. Current Opinion in Structural Biology, 2013, 23, 686-694.	5.7	66
79	Lignocellulose-Decomposing Bacteria and Their Enzyme Systems. , 2013, , 215-266.		25
80	Fungal cellulases and complexed cellulosomal enzymes exhibit synergistic mechanisms in cellulose deconstruction. Energy and Environmental Science, 2013, 6, 1858.	30.8	128
81	Small Angle X-ray Scattering Analysis of Clostridium thermocellum Cellulosome N-terminal Complexes Reveals a Highly Dynamic Structure. Journal of Biological Chemistry, 2013, 288, 7978-7985.	3.4	22
82	Establishment of a Simple Lactobacillus plantarum Cell Consortium for Cellulase-Xylanase Synergistic Interactions. Applied and Environmental Microbiology, 2013, 79, 5242-5249.	3.1	42
83	Crystal Structure of an Uncommon Cellulosome-Related Protein Module from Ruminococcus flavefaciens That Resembles Papain-Like Cysteine Peptidases. PLoS ONE, 2013, 8, e56138.	2.5	19
84	Deconstruction of Lignocellulose into Soluble Sugars by Native and Designer Cellulosomes. MBio, 2012, 3, .	4.1	92
85	How Does Plant Cell Wall Nanoscale Architecture Correlate with Enzymatic Digestibility?. Science, 2012, 338, 1055-1060.	12.6	646
86	Single-molecule dissection of the high-affinity cohesinâ€“dockerin complex. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20431-20436.	7.1	104
87	Scaffoldin Conformation and Dynamics Revealed by a Ternary Complex from the Clostridium thermocellum Cellulosome. Journal of Biological Chemistry, 2012, 287, 26953-26961.	3.4	33
88	Approaches for Improving Thermostability Characteristics in Cellulases. Methods in Enzymology, 2012, 510, 261-271.	1.0	19
89	Indirect ELISAâ€based approach for comparative measurement of highâ€affinity cohesinâ€“dockerin interactions. Journal of Molecular Recognition, 2012, 25, 616-622.	2.1	16
90	Genome-wide analysis of Acetivibrio cellulolyticus provides a blueprint of an elaborate cellulosome system. BMC Genomics, 2012, 13, 210.	2.8	54

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91	Designer Cellulosomes for Enhanced Hydrolysis of Cellulosic Substrates. Methods in Enzymology, 2012, 510, 429-452.	1.0	43
92	Improved Thermostability of Clostridium thermocellum Endoglucanase Cel8A by Using Consensus-Guided Mutagenesis. Applied and Environmental Microbiology, 2012, 78, 3458-3464.	3.1	114
93	Enhanced cellulose degradation by targeted integration of a cohesin-fused Î²-glucosidase into the <i>Clostridium thermocellum</i> cellulosome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10298-10303.	7.1	109
94	Affinity Electrophoresis as a Method for Determining Substrate-Binding Specificity of Carbohydrate-Active Enzymes for Soluble Polysaccharides. , 2012, 908, 119-127.		2
95	Assembly of Xylanases into Designer Cellulosomes Promotes Efficient Hydrolysis of the Xylan Component of a Natural Recalcitrant Cellulosic Substrate. MBio, 2011, 2, .	4.1	62
96	The unique set of putative membrane-associated anti-Ïƒ factors in Clostridium thermocellumâ€ƒsuggests a novel extracellular carbohydrate-sensing mechanism involved in gene regulation. FEMS Microbiology Letters, 2010, 308, 84-93.	1.8	73
97	Abundance and Diversity of Dockerin-Containing Proteins in the Fiber-Degrading Rumen Bacterium, Ruminococcus flavefaciens FD-1. PLoS ONE, 2010, 5, e12476.	2.5	65
98	Interplay between <i>Clostridium thermocellum</i> Family 48 and Family 9 Cellulases in Cellulosomal versus Noncellulosomal States. Applied and Environmental Microbiology, 2010, 76, 3236-3243.	3.1	64
99	Microbial enzyme systems for biomass conversion: emerging paradigms. Biofuels, 2010, 1, 323-341.	2.4	175
100	Cellulase-Xylanase Synergy in Designer Cellulosomes for Enhanced Degradation of a Complex Cellulosic Substrate. MBio, 2010, 1, .	4.1	99
101	<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
102	Homology swapping of intrinsic secondary structural elements between cellulosomal types I and II cohesins and their effect on dockerin binding. Pure and Applied Chemistry, 2010, 82, 193-204.	1.9	1
103	Insights into Higher-Order Organization of the Cellulosome Revealed by a Dissect-and-Build Approach: Crystal Structure of Interacting Clostridium thermocellum Multimodular Components. Journal of Molecular Biology, 2010, 396, 833-839.	4.2	34
104	Modular Arrangement of a Cellulosomal Scaffoldin Subunit Revealed from the Crystal Structure of a Cohesin Dyad. Journal of Molecular Biology, 2010, 399, 294-305.	4.2	24
105	Cellodextrin and Laminaribiose ABC Transporters in <i>Clostridium thermocellum</i>. Journal of Bacteriology, 2009, 191, 203-209.	2.2	83
106	Effect of Linker Length and Dockerin Position on Conversion of a <i>Thermobifida fusca</i> Endoglucanase to the Cellulosomal Mode. Applied and Environmental Microbiology, 2009, 75, 7335-7342.	3.1	67
107	Remembering Mary (1917 to 2008): editorial introduction to the thematic series on the life and lifework of Mary Mandels, first lady of cellulase research. Biotechnology for Biofuels, 2009, 2, 23.	6.2	4
108	Lignocellulose conversion to biofuels: current challenges, global perspectives. Current Opinion in Biotechnology, 2009, 20, 316-317.	6.6	106

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109	Intermodular Linker Flexibility Revealed from Crystal Structures of Adjacent Cellulosomal Cohesins of Acetivibrio cellulolyticus. Journal of Molecular Biology, 2009, 391, 86-97.	4.2	23
110	Cohesinâ€dockerin microarray: Diverse specificities between two complementary families of interacting protein modules. Proteomics, 2008, 8, 968-979.	2.2	90
111	From cellulosomes to cellulosomics. Chemical Record, 2008, 8, 364-377.	5.8	267
112	The Clostridium cellulolyticum Dockerin Displays a Dual Binding Mode for Its Cohesin Partner. Journal of Biological Chemistry, 2008, 283, 18422-18430.	3.4	71
113	Evidence for a dual binding mode of dockerin modules to cohesins. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3089-3094.	7.1	124
114	The potential of cellulases and cellulosomes for cellulosic waste management. Current Opinion in Biotechnology, 2007, 18, 237-245.	6.6	283
115	Thermobifida fuscafamily-6 cellulases as potential designer cellulosome components. Biocatalysis and Biotransformation, 2006, 24, 3-12.	2.0	46
116	The Use of the Avidin-Biotin Complex as a Tool in Molecular Biology. Methods of Biochemical Analysis, 2006, 26, 1-45.	0.2	523
117	Structural Basis of Cellulosome Efficiency Explored by Small Angle X-ray Scattering. Journal of Biological Chemistry, 2005, 280, 38562-38568.	3.4	95
118	Matching fusion protein systems for affinity analysis of two interacting families of proteins: the cohesin-dockerin interaction. Journal of Molecular Recognition, 2005, 18, 491-501.	2.1	92
119	Action of Designer Cellulosomes on Homogeneous Versus Complex Substrates. Journal of Biological Chemistry, 2005, 280, 16325-16334.	3.4	214
120	Unconventional Mode of Attachment of the Ruminococcus flavefaciens Cellulosome to the Cell Surface. Journal of Bacteriology, 2005, 187, 7569-7578.	2.2	87
121	Ordered arrays of quantum dots using cellulosomal proteins. Industrial Biotechnology, 2005, 1, 198-206.	0.8	6
122	Effect of Rational Mutagenesis of Selected Cohesin Residues on the High-Affinity Cohesin-Dockerin Interaction. ACS Symposium Series, 2004, , 194-206.	0.5	4
123	The Cellulosomes: Multienzyme Machines for Degradation of Plant Cell Wall Polysaccharides. Annual Review of Microbiology, 2004, 58, 521-554.	7.3	834
124	Regulation of the Cellulosomal celS (cel48A) Gene of Clostridium thermocellum Is Growth Rate Dependent. Journal of Bacteriology, 2003, 185, 3042-3048.	2.2	72
125	Regulation of Expression of Scaffoldin-Related Genes in Clostridium thermocellum. Journal of Bacteriology, 2003, 185, 5109-5116.	2.2	63
126	Degradation of Cellulose Substrates by Cellulosome Chimeras. Journal of Biological Chemistry, 2002, 277, 49621-49630.	3.4	254

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127	Nonproteolytic Clevage of Aspartyl Proline Bonds in the Cellulosomal Scaffoldin Subunit from Clostridium thermocellum. Applied Biochemistry and Biotechnology, 2001, 90, 67-74.	2.9	23
128	Design and Production of Active Cellulosome Chimeras. Journal of Biological Chemistry, 2001, 276, 21257-21261.	3.4	182
129	Phage Display of Cellulose Binding Domains for Biotechnological Application. ACS Symposium Series, 2000, , 168-189.	0.5	2
130	Cohesin-dockerin recognition in cellulosome assembly: Experiment versus hypothesis. , 2000, 39, 170-177.		83
131	Recombinant NeutraLite Avidin: a non-glycosylated, acidic mutant of chicken avidin that exhibits high affinity for biotin and low non-specific binding properties. FEBS Letters, 2000, 467, 31-36.	2.8	93
132	Novel Methodology for Enzymatic Removal of Atrazine from Water by CBD-Fusion Protein Immobilized on Cellulose. Environmental Science & Technology, 2000, 34, 1292-1296.	10.0	39
133	The cellulosome concept as an efficient microbial strategy for the degradation of insoluble polysaccharides. Trends in Microbiology, 1999, 7, 275-281.	7.7	287
134	Mutation of a critical tryptophan to lysine in avidin or streptavidin may explain why sea urchin fibropellin adopts an avidin-like domain. FEBS Letters, 1999, 461, 52-58.	2.8	54
135	Cellulosome-like sequences inArchaeoglobus fulgidus: an enigmatic vestige of cohesin and dockerin domains. FEBS Letters, 1999, 463, 277-280.	2.8	23
136	Digestion of crystalline cellulose substrates by the Clostridium thermocellum cellulosome: structural and morphological aspects. Biochemical Journal, 1999, 340, 829-835.	3.7	72
137	Cellulose, cellulases and cellulosomes. Current Opinion in Structural Biology, 1998, 8, 548-557.	5.7	520
138	Engineering of chicken avidin: a progressive series of reduced charge mutants. FEBS Letters, 1998, 441, 313-317.	2.8	39
139	Cellulosomesâ€”Structure and Ultrastructure. Journal of Structural Biology, 1998, 124, 221-234.	2.8	306
140	Species-specificity of the cohesin-dockerin interaction betweenClostridium thermocellum andClostridium cellulolyticum: Prediction of specificity determinants of the dockerin domain. Proteins: Structure, Function and Bioinformatics, 1997, 29, 517-527.	2.6	192
141	Species-specificity of the cohesin-dockerin interaction between Clostridium thermocellum and Clostridium cellulolyticum: Prediction of specificity determinants of the dockerin domain. , 1997, 29, 517.		1
142	Species-specificity of the cohesin-dockerin interaction between Clostridium thermocellum and Clostridium cellulolyticum: Prediction of specificity determinants of the dockerin domain. , 1997, 29, 517.		1
143	Dissociation of the cellulosome of Clostridium thermocellum under nondenaturing conditions. Journal of Biotechnology, 1996, 51, 235-242.	3.8	24
144	Reversibility of biotin-binding by selective modification of tyrosine in avidin. Biochemical Journal, 1996, 316, 193-199.	3.7	93

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145	Sodium dodecyl sulfate-polyacrylamide gel electrophoretic method for assessing the quaternary state and comparative thermostability of avidin and streptavidin. Electrophoresis, 1996, 17, 1319-1324.	2.4	96
146	Isolation and properties of a thermostable endoglucanase from a thermophilic mutant strain ofTielavia terrestris. Applied Biochemistry and Biotechnology, 1995, 50, 137-143.	2.9	3
147	Preparation of deglycosylated egg white avidin. Applied Biochemistry and Biotechnology, 1995, 53, 1-9.	2.9	31
148	Expression, purification and subunit-binding properties of cohesins 2 and 3 of theClostridium thermocellumcellulosome. FEBS Letters, 1995, 360, 121-124.	2.8	135
149	The cellulosome â€" A treasure-trove for biotechnology. Trends in Biotechnology, 1994, 12, 379-386.	9.3	444
150	Streptavidin blocks immune reactions mediated by fibronectin-VLA-5 recognition through an Arg-Gly-Asp mimicking site. European Journal of Immunology, 1993, 23, 893-898.	2.9	17
151	The structure of the complex between avidin and the dye, 2-(4'-hydroxyazobenzene) benzoic acid (HABA). FEBS Letters, 1993, 328, 165-168.	2.8	58
152	Monoclonal anti-biotin antibodies simulate avidin m the recognition of biotin. FEBS Letters, 1993, 322, 47-50.	2.8	45
153	The cellulose paradox: pollutant par excellence and/or a reclaimable natural resource?. Biodegradation, 1992, 3, 171-188.	3.0	73
154	Identification of the cellulose-binding domain of the cellulosome subunit S1 fromClostridium thermocellumYS. FEMS Microbiology Letters, 1992, 99, 181-186.	1.8	74
155	Novel oligosaccharide constituents of the cellulase complex of Bacteroides cellulosolvens. FEBS Journal, 1992, 205, 799-808.	0.2	45
156	Identification of the cellulose-binding domain of the cellulosome subunit S1 from Clostridium thermocellum YS. FEMS Microbiology Letters, 1992, 99, 181-186.	1.8	45
157	Efficient cellulose solubilization by a combined cellulosome-Î²-glucosidase system. Applied Biochemistry and Biotechnology, 1991, 27, 173-183.	2.9	45
158	Anomalous dissociative behavior of the major glycosylated component of the cellulosome of clostridium thermocellum. Applied Biochemistry and Biotechnology, 1991, 30, 129-136.	2.9	11
159	Primary structure of O-linked carbohydrate chains in the cellulosome of different Clostridium thermocellum strains. FEBS Journal, 1991, 196, 115-122.	0.2	47
160	Cellulosome-like entities inBacteroides cellulosolvens. Current Microbiology, 1991, 22, 27-33.	2.2	43
161	Avidin column as a highly efficient and stable alternative for immobilization of ligands for affinity chromatography. Journal of Molecular Recognition, 1990, 3, 102-107.	2.1	14
162	[54] Avidin-biotin mediated immunoassays: Overview. Methods in Enzymology, 1990, , 467-469.	1.0	27

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163	[22] Enzymatic and radioactive assays for biotin, avidin, and streptavidin. Methods in Enzymology, 1990, 184, 208-217.	1.0	16
164	[3] Applications of avidin-biotin technology: Literature survey. Methods in Enzymology, 1990, 184, 14-45.	1.0	148
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