

Elizabeth Ficko-Blean

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

1,349
citations

393982

19
h-index

360668

35
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37
all docs

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docs citations

37
times ranked

1759
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic comparison of eight methods for preparation of high purity sulfated fucans extracted from the brown alga <i>Pelvetia canaliculata</i> . <i>International Journal of Biological Macromolecules</i> , 2022, 201, 143-157.	3.6	1
2	In-depth structural characterization of oligosaccharides released by GH107 endofucanase <i>FcnA</i> reveals enzyme subsite specificity and sulfated fucan substructural features. <i>Glycobiology</i> , 2022, 32, 276-288.	1.3	2
3	Architecturally complex <i>O</i> -glycopeptidases are customized for mucin recognition and hydrolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	20
4	A fresh trim provides a new look at the human mannose receptor. <i>Journal of Biological Chemistry</i> , 2021, 297, 100922.	1.6	0
5	To gel or not to gel: differential expression of carrageenan-related genes between the gametophyte and tetrasporophyte life cycle stages of the red alga <i>Chondrus crispus</i> . <i>Scientific Reports</i> , 2020, 10, 11498.	1.6	24
6	Red Algal Molecules - Synthesis of Methyl Neo- β -carrabioside and Its S-Linked Variant via Two Synthetic Routes: A Late Stage Ring Closure and Using a 3,6-Anhydro-d-galactosyl Donor. <i>Journal of Organic Chemistry</i> , 2020, 85, 16182-16195.	1.7	1
7	Trehalose and (iso)floridoside production under desiccation stress in red alga <i>Porphyra umbilicalis</i> and the genes involved in their synthesis. <i>Journal of Phycology</i> , 2020, 56, 1468-1480.	1.0	6
8	Characterisation of an exo- $(\pm 1,3)$ -3,6-anhydro-d-galactosidase produced by the marine bacterium <i>Zobellia galactanivorans</i> DsjT: Insight into enzyme preference for natural carrageenan oligosaccharides and kinetic characterisation on a novel chromogenic substrate. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 1471-1479.	3.6	9
9	Recognition of protein-linked glycans as a determinant of peptidase activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E679-E688.	3.3	70
10	Probing the Complex Architecture of Multimodular Carbohydrate-Active Enzymes Using a Combination of Small Angle X-Ray Scattering and X-Ray Crystallography. <i>Methods in Molecular Biology</i> , 2017, 1588, 239-253.	0.4	3
11	Insights into the red algae and eukaryotic evolution from the genome of <i>Porphyra umbilicalis</i> (Bangiophyceae, Rhodophyta). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6361-E6370.	3.3	233
12	Carrageenan catabolism is encoded by a complex regulon in marine heterotrophic bacteria. <i>Nature Communications</i> , 2017, 8, 1685.	5.8	131
13	Unraveling the multivalent binding of a marine family 6 carbohydrate-binding module with its native laminarin ligand. <i>FEBS Journal</i> , 2016, 283, 1863-1879.	2.2	16
14	Sweet and sour sugars from the sea: the biosynthesis and remodeling of sulfated cell wall polysaccharides from marine macroalgae. <i>Perspectives in Phycology</i> , 2015, 2, 51-64.	1.9	58
15	Biochemical and structural investigation of two paralogous glycoside hydrolases from <i>Zobellia galactanivorans</i> : novel insights into the evolution, dimerization plasticity and catalytic mechanism of the GH117 family. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 209-223.	2.5	18
16	Tampering with Cell Division by Using Small-Molecule Inhibitors of CDK-CKS Protein Interactions. <i>ChemBioChem</i> , 2015, 16, 432-439.	1.3	6
17	<i>Chondrus crispus</i> – A Present and Historical Model Organism for Red Seaweeds. <i>Advances in Botanical Research</i> , 2014, 71, 53-89.	0.5	37
18	An Unusual Mode of Galactose Recognition by a Family 32 Carbohydrate-Binding Module. <i>Journal of Molecular Biology</i> , 2014, 426, 869-880.	2.0	18

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19	Conformational Analysis of StrH, the Surface-Attached exo- β -D-N-Acetylglucosaminidase from <i>Streptococcus pneumoniae</i> . <i>Journal of Molecular Biology</i> , 2013, 425, 334-349.	2.0	14
20	Structural analysis of a bacterial exo- β -D-N-acetylglucosaminidase in complex with an unusual disaccharide found in class III mucin. <i>Glycobiology</i> , 2012, 22, 590-595.	1.3	11
21	Insights into the recognition of the human glycome by microbial carbohydrate-binding modules. <i>Current Opinion in Structural Biology</i> , 2012, 22, 570-577.	2.6	48
22	^1H , ^{15}N and ^{13}C backbone and side-chain resonance assignments of a family 32 carbohydrate-binding module from the <i>Clostridium perfringens</i> NagH. <i>Biomolecular NMR Assignments</i> , 2012, 6, 139-142.	0.4	5
23	Carbohydrate Recognition by an Architecturally Complex β -N-Acetylglucosaminidase from <i>Clostridium perfringens</i> . <i>PLoS ONE</i> , 2012, 7, e33524.	1.1	42
24	The Overall Architecture and Receptor Binding of Pneumococcal Carbohydrate-Antigen-Hydrolyzing Enzymes. <i>Journal of Molecular Biology</i> , 2011, 411, 1017-1036.	2.0	24
25	The Conformation and Function of a Multimodular Glycogen-Degrading Pneumococcal Virulence Factor. <i>Structure</i> , 2011, 19, 640-651.	1.6	42
26	Structural analysis of CPF_2247, a novel β -amylase from <i>Clostridium perfringens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2771-2777.	1.5	22
27	Portrait of an Enzyme, a Complete Structural Analysis of a Multimodular β -N-Acetylglucosaminidase from <i>Clostridium perfringens</i> . <i>Journal of Biological Chemistry</i> , 2009, 284, 9876-9884.	1.6	40
28	Analysis of the Structural and Functional Diversity of Plant Cell Wall Specific Family 6 Carbohydrate Binding Modules. <i>Biochemistry</i> , 2009, 48, 10395-10404.	1.2	36
29	N-Acetylglucosamine Recognition by a Family 32 Carbohydrate-Binding Module from <i>Clostridium perfringens</i> NagH. <i>Journal of Molecular Biology</i> , 2009, 390, 208-220.	2.0	35
30	Three-dimensional Structure of a Putative Non-cellulosomal Cohesin Module from a <i>Clostridium perfringens</i> Family 84 Glycoside Hydrolase. <i>Journal of Molecular Biology</i> , 2008, 375, 20-28.	2.0	16
31	Structural and mechanistic insight into the basis of mucopolysaccharidosis IIIB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6560-6565.	3.3	79
32	Carbohydrate Recognition by a Large Sialidase Toxin from <i>Clostridium perfringens</i> . <i>Biochemistry</i> , 2007, 46, 11352-11360.	1.2	84
33	NMR assignment of backbone and side chain resonances for a putative protein-protein interaction module from a family 84 glycoside hydrolase of <i>Clostridium perfringens</i> . <i>Biomolecular NMR Assignments</i> , 2007, 1, 7-9.	0.4	3
34	A Structural and Functional Analysis of β -Glucan Recognition by Family 25 and 26 Carbohydrate-binding Modules Reveals a Conserved Mode of Starch Recognition. <i>Journal of Biological Chemistry</i> , 2006, 281, 587-598.	1.6	90
35	The Interaction of a Carbohydrate-binding Module from a <i>Clostridium perfringens</i> N-Acetyl- β -hexosaminidase with Its Carbohydrate Receptor. <i>Journal of Biological Chemistry</i> , 2006, 281, 37748-37757.	1.6	84
36	Cloning, recombinant production, crystallization and preliminary X-ray diffraction studies of a family 84 glycoside hydrolase from <i>Clostridium perfringens</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 834-836.	0.7	21

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37	NMR assignment of backbone and side chain resonances for a putative protein-protein interaction module from a family 84 glycoside hydrolase of <i>Clostridium perfringens</i> . Journal of Biomolecular NMR, 0, , .	1.6	0