

Christina M Payne

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

49
papers

2,134
citations

21
h-index

46
g-index

53
ext. papers

2,515
ext. citations

6.4
avg, IF

4.65
L-index

#	Paper	IF	Citations
49	Machine learning reveals sequence-function relationships in family 7 glycoside hydrolases. <i>Journal of Biological Chemistry</i> , 2021 , 297, 100931	5.4	2
48	Characterization and engineering of a two-enzyme system for plastics depolymerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 25476-25485	11.5	90
47	Improving Enzyme Optimum Temperature Prediction with Resampling Strategies and Ensemble Learning. <i>Journal of Chemical Information and Modeling</i> , 2020 , 60, 4098-4107	6.1	7
46	Polar residues lining the binding cleft of a <i>Serratia marcescens</i> family 18 chitinase position the substrate for attack and stabilize associative interactions. <i>Molecular Physics</i> , 2019 , 117, 3664-3682	1.7	2
45	Inhibition Mechanisms of 2-Hydroxybiphenyl-2-sulfinate Desulfinate. <i>Journal of Physical Chemistry B</i> , 2019 , 123, 9054-9065	3.4	3
44	Kinetic and molecular dynamics study of inhibition and transglycosylation in family 3 β -glucosidases. <i>Journal of Biological Chemistry</i> , 2019 , 294, 3169-3180	5.4	3
43	Enabling microbial syringol conversion through structure-guided protein engineering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 13970-13976	11.5	22
42	Thermodynamic Signatures of Substrate Binding for Three <i>Thermobifida fusca</i> Cellulases with Different Modes of Action. <i>Biochemistry</i> , 2019 , 58, 1648-1659	3.2	8
41	Structural and molecular dynamics studies of a C1-oxidizing lytic polysaccharide monooxygenase from <i>Heterobasidion irregulare</i> reveal amino acids important for substrate recognition. <i>FEBS Journal</i> , 2018 , 285, 2225-2242	5.7	26
40	The role of catalytic residue pK on the hydrolysis/transglycosylation partition in family 3 β -glucosidases. <i>Organic and Biomolecular Chemistry</i> , 2018 , 16, 316-324	3.9	6
39	Correlation of structure, function and protein dynamics in GH7 cellobiohydrolases from <i>Trichoderma reesei</i> and <i>Aspergillus niger</i> . <i>Biotechnology for Biofuels</i> , 2018 , 11, 5	7.8	18
38	Cellulose-specific Type B carbohydrate binding modules: understanding oligomeric and non-crystalline substrate recognition mechanisms. <i>Biotechnology for Biofuels</i> , 2018 , 11, 319	7.8	1
37	Hydrolysis and Transglycosylation Transition States of Glycoside Hydrolase Family 3 β -glucosidases Differ in Charge and Puckering Conformation. <i>Journal of Physical Chemistry B</i> , 2018 , 122, 9452-9459	3.4	8
36	Molecular Determinants of Substrate Affinity and Enzyme Activity of a Cytochrome P450 Variant. <i>Biophysical Journal</i> , 2018 , 115, 1251-1263	2.9	2
35	Inhibition of Mammalian Glycoprotein YKL-40: IDENTIFICATION OF THE PHYSIOLOGICAL LIGAND. <i>Journal of Biological Chemistry</i> , 2017 , 292, 2624-2636	5.4	15
34	Desulfination by 2-Hydroxybiphenyl-2-sulfinate desulfinate proceeds electrophilic aromatic substitution by the cysteine-27 proton. <i>Chemical Science</i> , 2017 , 8, 5078-5086	9.4	7
33	CHARMM force field parameters for 2-Hydroxybiphenyl-2-sulfinate, 2-hydroxybiphenyl, and related analogs. <i>Journal of Molecular Graphics and Modelling</i> , 2017 , 72, 32-42	2.8	8

32	Improving the thermal stability of cellobiohydrolase Cel7A from by directed evolution. <i>Journal of Biological Chemistry</i> , 2017 , 292, 17418-17430	5.4	37
31	Effect of Mutation and Substrate Binding on the Stability of Cytochrome P450BM3 Variants. <i>Biochemistry</i> , 2016 , 55, 3594-606	3.2	12
30	Aromatic-Mediated Carbohydrate Recognition in Processive <i>Serratia marcescens</i> Chitinases. <i>Journal of Physical Chemistry B</i> , 2016 , 120, 1236-49	3.4	21
29	Plant α -glucan phosphatases SEX4 and LSF2 display different affinity for amylopectin and amylose. <i>FEBS Letters</i> , 2016 , 590, 118-28	3.8	17
28	Thermodynamic Relationships with Processivity in <i>Serratia marcescens</i> Family 18 Chitinases. <i>Journal of Physical Chemistry B</i> , 2015 , 119, 9601-13	3.4	20
27	Cello-oligomer-binding dynamics and directionality in family 4 carbohydrate-binding modules. <i>Glycobiology</i> , 2015 , 25, 1100-11	5.8	3
26	Effects of lytic polysaccharide monooxygenase oxidation on cellulose structure and binding of oxidized cellulose oligomers to cellulases. <i>Journal of Physical Chemistry B</i> , 2015 , 119, 6129-43	3.4	72
25	Structural and Functional Characterization of a Lytic Polysaccharide Monooxygenase with Broad Substrate Specificity. <i>Journal of Biological Chemistry</i> , 2015 , 290, 22955-69	5.4	131
24	Sequencing, biochemical characterization, crystal structure and molecular dynamics of cellobiohydrolase Cel7A from <i>Geotrichum candidum</i> 3C. <i>FEBS Journal</i> , 2015 , 282, 4515-37	5.7	27
23	Processivity, Substrate Positioning, and Binding: The Role of Polar Residues in a Family 18 Glycoside Hydrolase. <i>Biochemistry</i> , 2015 , 54, 7292-306	3.2	15
22	Fungal cellulases. <i>Chemical Reviews</i> , 2015 , 115, 1308-448	68.1	513
21	Towards a molecular-level theory of carbohydrate processivity in glycoside hydrolases. <i>Current Opinion in Biotechnology</i> , 2014 , 27, 96-106	11.4	73
20	Crystal structure and computational characterization of the lytic polysaccharide monooxygenase GH61D from the Basidiomycota fungus <i>Phanerochaete chrysosporium</i> . <i>Journal of Biological Chemistry</i> , 2013 , 288, 12828-39	5.4	131
19	Binding site dynamics and aromatic-carbohydrate interactions in processive and non-processive family 7 glycoside hydrolases. <i>Journal of Physical Chemistry B</i> , 2013 , 117, 4924-33	3.4	48
18	Glycoside hydrolase processivity is directly related to oligosaccharide binding free energy. <i>Journal of the American Chemical Society</i> , 2013 , 135, 18831-9	16.4	71
17	Structural, biochemical, and computational characterization of the glycoside hydrolase family 7 cellobiohydrolase of the tree-killing fungus <i>Heterobasidion irregulare</i> . <i>Journal of Biological Chemistry</i> , 2013 , 288, 5861-72	5.4	55
16	Structural characterization of a unique marine animal family 7 cellobiohydrolase suggests a mechanism of cellulase salt tolerance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 10189-94	11.5	70
15	Glycosylated linkers in multimodular lignocellulose-degrading enzymes dynamically bind to cellulose. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 14646-51	11.5	131

14	Uses of phage display in agriculture: a review of food-related protein-protein interactions discovered by biopanning over diverse baits. <i>Computational and Mathematical Methods in Medicine</i> , 2013 , 2013, 653759	2.8	5
13	Uses of phage display in agriculture: sequence analysis and comparative modeling of late embryogenesis abundant client proteins suggest protein-nucleic acid binding functionality. <i>Computational and Mathematical Methods in Medicine</i> , 2013 , 2013, 470390	2.8	5
12	Harnessing glycosylation to improve cellulase activity. <i>Current Opinion in Biotechnology</i> , 2012 , 23, 338-45	1.4	96
11	Hallmarks of processivity in glycoside hydrolases from crystallographic and computational studies of the <i>Serratia marcescens</i> chitinases. <i>Journal of Biological Chemistry</i> , 2012 , 287, 36322-30	5.4	81
10	Cellulase linkers are optimized based on domain type and function: insights from sequence analysis, biophysical measurements, and molecular simulation. <i>PLoS ONE</i> , 2012 , 7, e48615	3.7	76
9	Decrystallization of Oligosaccharides from the Cellulose II Surface with Molecular Simulation. <i>Journal of Physical Chemistry Letters</i> , 2011 , 2, 1546-1550	6.4	50
8	Multiple functions of aromatic-carbohydrate interactions in a processive cellulase examined with molecular simulation. <i>Journal of Biological Chemistry</i> , 2011 , 286, 41028-35	5.4	88
7	Controlled Translocation of DNA Segments through Nanoelectrode Gaps from Molecular Dynamics. <i>Journal of Physical Chemistry C</i> , 2008 , 112, 8-12	3.8	12
6	Molecular dynamics simulation of ss-DNA translocation between copper nanoelectrodes incorporating electrode charge dynamics. <i>Journal of Physical Chemistry B</i> , 2008 , 112, 1712-7	3.4	20
5	Electrophoresis of ssDNA through nanoelectrode gaps from molecular dynamics: impact of gap width and chain length. <i>Journal of Physical Chemistry B</i> , 2008 , 112, 12851-8	3.4	2
4	Molecular simulations of DNA transport in solution. <i>Molecular Simulation</i> , 2007 , 33, 399-403	2	3
3	Single-strand DNA molecule translocation through nanoelectrode gaps. <i>Nanotechnology</i> , 2007 , 18, 42401A	1.4	13
2	Evaluating the Thermodynamic Consistency of Experimental Data for HF + H ₂ O at 101.325 kPa. <i>Journal of Chemical & Engineering Data</i> , 2004 , 49, 306-310	2.8	5
1	Improving enzyme optimum temperature prediction with resampling strategies and ensemble learning		1