

# Liangwei Liu

## List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Terminal Amino Acids Disturb Xylanase Thermostability and Activity. <i>Journal of Biological Chemistry</i> , 2011, 286, 44710-44715.	1.6	56
2	Directed evolution of a mesophilic fungal xylanase by fusion of a thermophilic bacterial carbohydrate-binding module. <i>Process Biochemistry</i> , 2011, 46, 395-398.	1.8	22
3	Sandwich fusion of CBM9_2 to enhance xylanase thermostability and activity. <i>International Journal of Biological Macromolecules</i> , 2018, 117, 586-591.	3.6	19
4	Domain-swapping of mesophilic xylanase with hyper-thermophilic glucanase. <i>BMC Biotechnology</i> , 2012, 12, 28.	1.7	16
5	Rational pH-engineering of the thermostable xylanase based on computational model. <i>Process Biochemistry</i> , 2009, 44, 912-915.	1.8	12
6	Activity and thermostability increase of xylanase following transplantation with modules sub-divided from hyper-thermophilic CBM9_1-2. <i>Process Biochemistry</i> , 2012, 47, 853-857.	1.8	9
7	Computational analysis of di-peptides correlated with the optimal temperature in G/11 xylanase. <i>Process Biochemistry</i> , 2006, 41, 305-311.	1.8	8
8	Effect of Codon Message on Xylanase Thermal Activity. <i>Journal of Biological Chemistry</i> , 2012, 287, 27183-27188.	1.6	8
9	Non-Structured Amino-Acid Impact on GH11 Differs from GH10 Xylanase. <i>PLoS ONE</i> , 2012, 7, e45762.	1.1	8
10	C-Terminal carbohydrate-binding module 9_2 fused to the N-terminus of GH11 xylanase from <i>Aspergillus niger</i> . <i>Biotechnology Letters</i> , 2016, 38, 1739-1745.	1.1	7
11	Computational analysis of responsible dipeptides for optimum pH in G/11 xylanase. <i>Biochemical and Biophysical Research Communications</i> , 2004, 321, 391-396.	1.0	6
12	Principle component analysis in F/10 and G/11 xylanase. <i>Biochemical and Biophysical Research Communications</i> , 2004, 322, 277-280.	1.0	5
13	A novel model to determine the dipeptides responsible for optimum temperature in F/10 xylanase. <i>Process Biochemistry</i> , 2005, 40, 1389-1394.	1.8	5
14	Intra-Molecular Homologous Recombination of Scarless Plasmid. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1697.	1.8	4
15	Evolution of plasmid-construction. <i>International Journal of Biological Macromolecules</i> , 2022, 209, 1319-1326.	3.6	3
16	Abortive ligation intermediate blocks seamless repair of double-stranded breaks. <i>International Journal of Biological Macromolecules</i> , 2022, 209, 1498-1503.	3.6	3
17	Using signal peptide prediction with caution, a case study in <i>Aspergillus niger</i> xylanase. <i>Process Biochemistry</i> , 2012, 47, 2527-2530.	1.8	2