

Recombinant Enzyme Product Specification Sheet

Cat. No.:	PRO-E0051
LOT:	2008-0051
Activity:	β -Xylanase
Synonyms:	Endo-(1 \rightarrow 4)- β -xylan 4-xylanohydrolase; endo-1,4-xylanase; xylanase; β -1,4-xylanase; endo-1,4-xylanase; endo- β -1,4-xylanase; endo-1,4- β -D-xylanase; 1,4- β -xylan xylanohydrolase; β -xylanase; β -1,4-xylan xylanohydrolase; endo-1,4- β -xylanase; β -D-xylanase; 4- β -D-xylan xylanohydrolase
Nomenclature:	CmXyn10B, Xyn10B (former annotation xylanase 10C (XylC; XYLC; XynC; xynC)), GH10, GH 10, belongs to glycoside hydrolase family 10 (member of clan GH-A)
Source organism:	<i>Cellvibrio mixtus</i> ATCC 12120
Enzyme Commission No.:	3.2.1.8
Activity:	<div style="border: 1px solid black; padding: 5px;"> <p>NOTE: this product has been produced and is awaiting assay. It is thus currently available for purchase by the mg only. If you have a query, please contact us (technical@prozomix.com)</p> </div>
Specific activity:	
Purity:	> 95 % as judged by SDS-PAGE
Form and storage:	Supplied in 3.2 M ammonium sulphate, store at 4°C (shipped at room temperature)
pH optimum:	-
Temperature optimum:	-
[Protein]:	10 mg/mL
Sequence length:	370 amino acids (view sequence)
Accession No.:	AF049493 , O68541
Molecular weight:	42925.9 Da (theoretical) ~ 43000 Da (observed by SDS-PAGE) - (observed by mass spectrometry)
Biological function:	Efficient hydrolysis of especially decorated β -1,4-xylans
Potential application(s):	Biomass conversion , carbohydrate research
Comments:	This enzyme (comprising residues 11-379 of the native sequence) displays the highest catalytic activity towards both glucurono- and arabinoxylans so far observed. A notable feature revealed by X-ray

crystallographic analyses is a unique +1 subsite comprising two “hydrophobic walls”, as opposed to a single hydrophobic patch in other family 10 enzymes. This extensive hydrophobic feature, formed predominantly by Phe-336 and Phe-340, not only interacts with both the α - and β -faces of sugar residues located at the +1 subsite, but also forms a direct interaction (via Phe-340) with 4-O-MeGlcA side chains of substituted xylosyl residues occupying this subsite. The overall binding cleft comprises 6 major subsites running from -2 and +4. PDB: [1UQY](#), [1UQZ](#), [1UR1](#), [1UR2](#), [2CNC](#)

Usage: Agitate bottle sufficiently to fully homogenise enzyme precipitate before use

Assay: -

Primary sequence:

MLTSAGIAMGQASKLAAATKAAEQTGLKSAYKDNFLIGAALNATI ASGADERLNTLIAKEFN SITPENCMKWGVL
RDAQGQWNWKDADAFVAFGTKHNLHMVGH TLVWHSQIHDEVFKNADGSYISKAALQKKMEEHITTLAGRYKGKLA
AWDVVNEAVGDDLKMRD SHWYKIMGDDFIYNAFTLANEVDPKAHLMYNDYNIERTGKREATVEMIERLQKRGMPI
HGLGIQGHLGIDTPPIAEIEKSI IAFKLGRLRVHFTELDVDVLPVWELPVAEVSTRFEYKPERDPYTKGLPQEM
QDKLAKRYEDLFKLF IKHSDKIDRATFWGVSDDASWLN GFPIPGRTNYPLLFDRKLQPKDAYFRLLDLKR

Literature: 1. [Pell et al. \(2004\) J. Biol. Chem. 279, 9597-9605](#)