

Identification and Characterization of a Novel Endo- β -1,4-Xylanase from *Streptomyces* sp. T7
and its Application in Xylo-oligosaccharide Production

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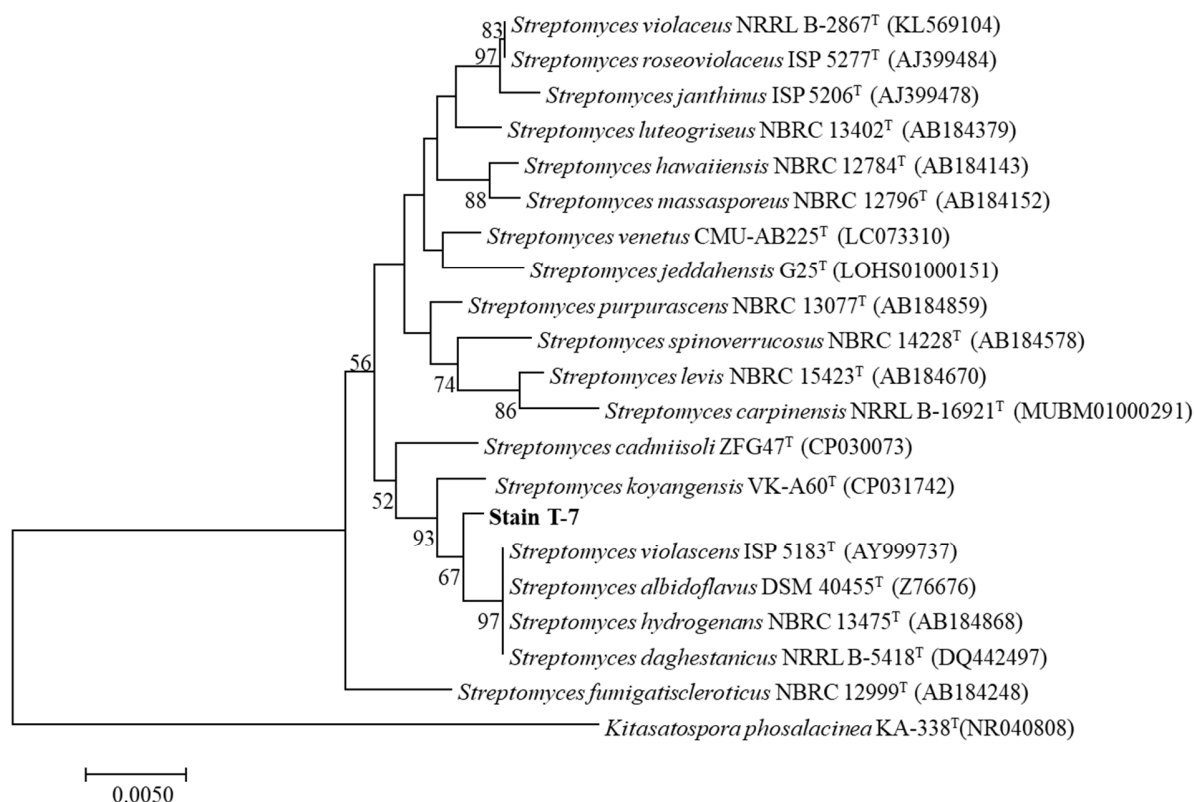


Figure S1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the position of strain T7 among its phylogenetic neighbours. *Kitasatospora phosalacinea* KA-338^T was used as outgroup. Bootstrap values (>50 %) based on 1000 replications are shown at branch nodes. Bar, 0.005 substitutions per nucleotide position.

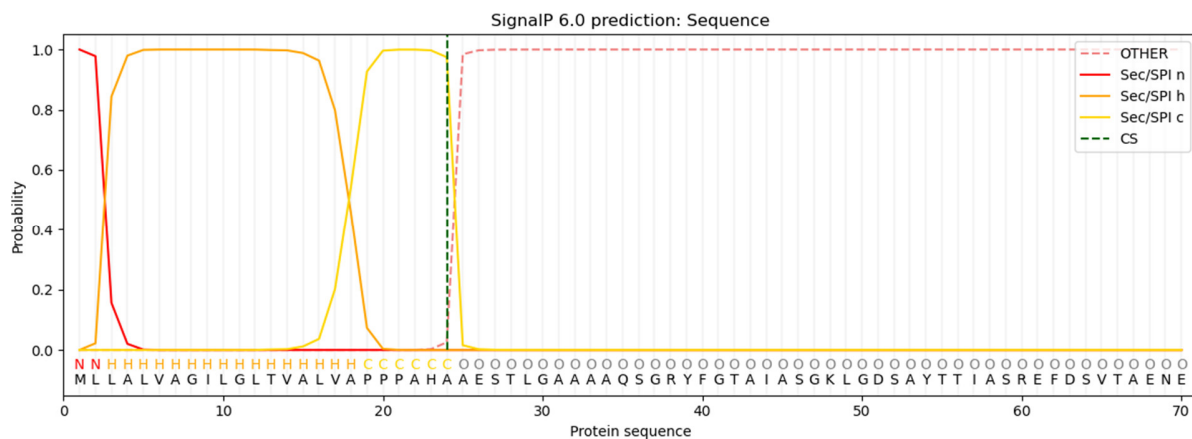


Figure S2. Predictive signal peptide sequence of xynST7

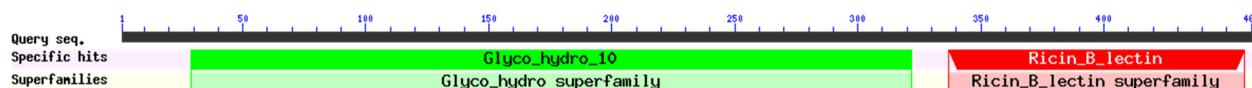


Figure S3. Conserved domains of xynST7

Amino acid composition:

Ala (A)	46	10.6%
Arg (R)	22	5.1%
Asn (N)	25	5.7%
Asp (D)	30	6.9%
Cys (C)	10	2.3%
Gln (Q)	26	6.0%
Glu (E)	9	2.1%
Gly (G)	52	12.0%
His (H)	5	1.1%
Ile (I)	14	3.2%
Leu (L)	26	6.0%
Lys (K)	14	3.2%
Met (M)	6	1.4%
Phe (F)	12	2.8%
Pro (P)	12	2.8%
Ser (S)	36	8.3%
Thr (T)	35	8.0%
Trp (W)	14	3.2%
Tyr (Y)	14	3.2%
Val (V)	27	6.2%
Pyl (O)	0	0.0%
Sec (U)	0	0.0%

Figure S4. Total amino acid composition (%) of xynST7. Total numbers of negatively (Asp + Glu) and positively (Arg + Lys) charged residues were 39 and 36, respectively.

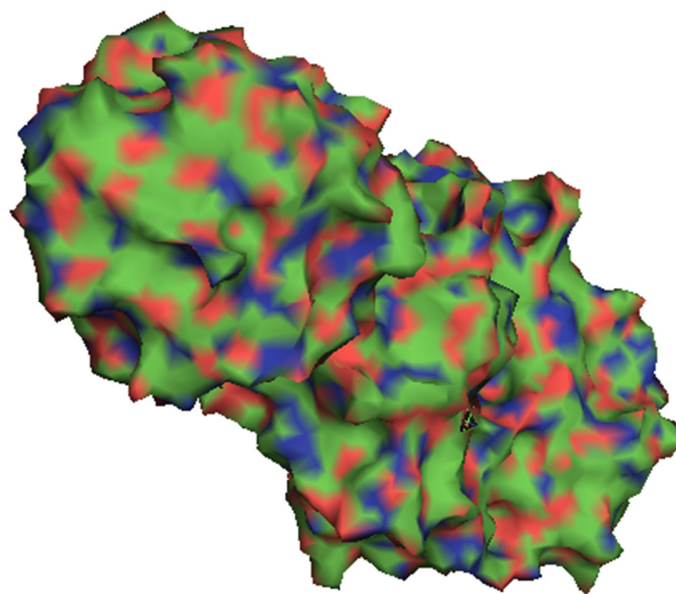


Figure S5. Surface representation of xynST7. Negatively and positively charged surfaces are coloured red and blue, respectively.