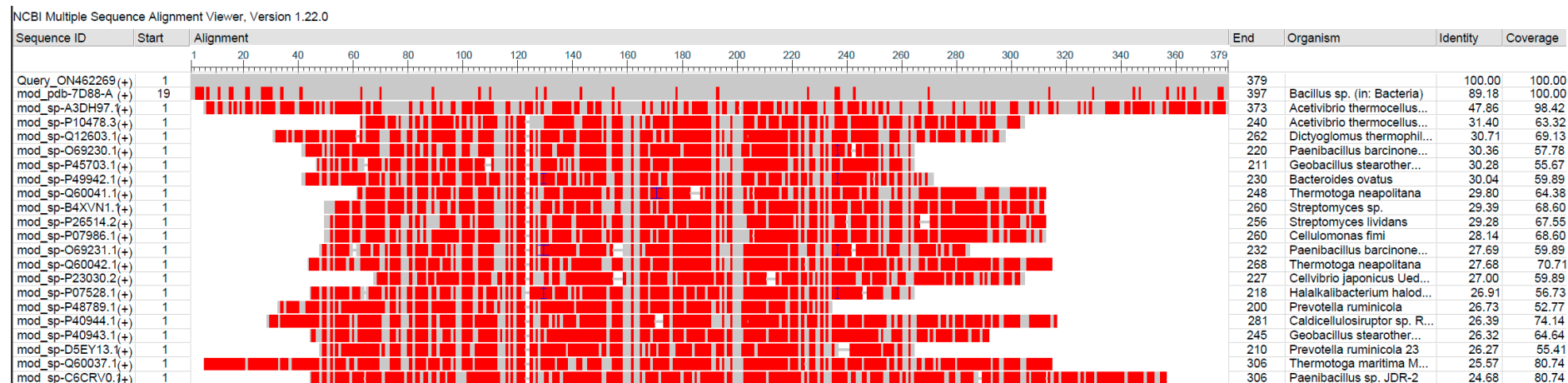


Supplementary Figure S3



Aminoacid sequence alignment of BsXyn10 with other bacterial GH10 endo-xylanases, using NCBI Multiple Sequence Alignment Viewer Version 1.22.0.

Used sequences were obtained from PDB and UniprotKB/Swiss-Prot databases based on maximum sequence identity with BsXyn10. Identical aminoacids are depicted in grey bars.