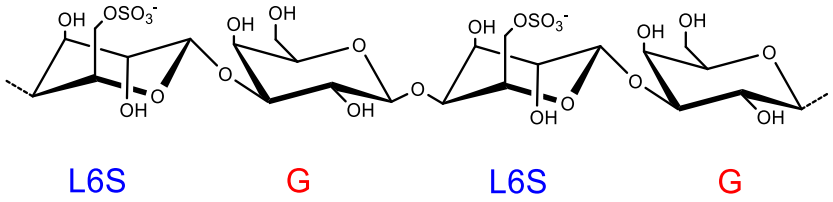
(A)



(B)

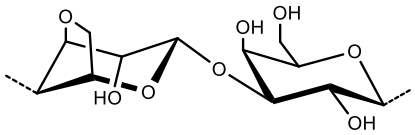


Figure S1. (A) Structure of porphyran, which is composed of alternating 4-linked α-L-galactopyranose-6-sulfate (L6S) residues and 3-linked β-D-galactopyranose (G) residues. (B) Structure of agarose disaccharide moiety, which is composed of alternating 4-linked 3,6-anhydro-α-L-galactopyranose (LA) residues and 3-linked β-D-galactopyranose (G) residues.

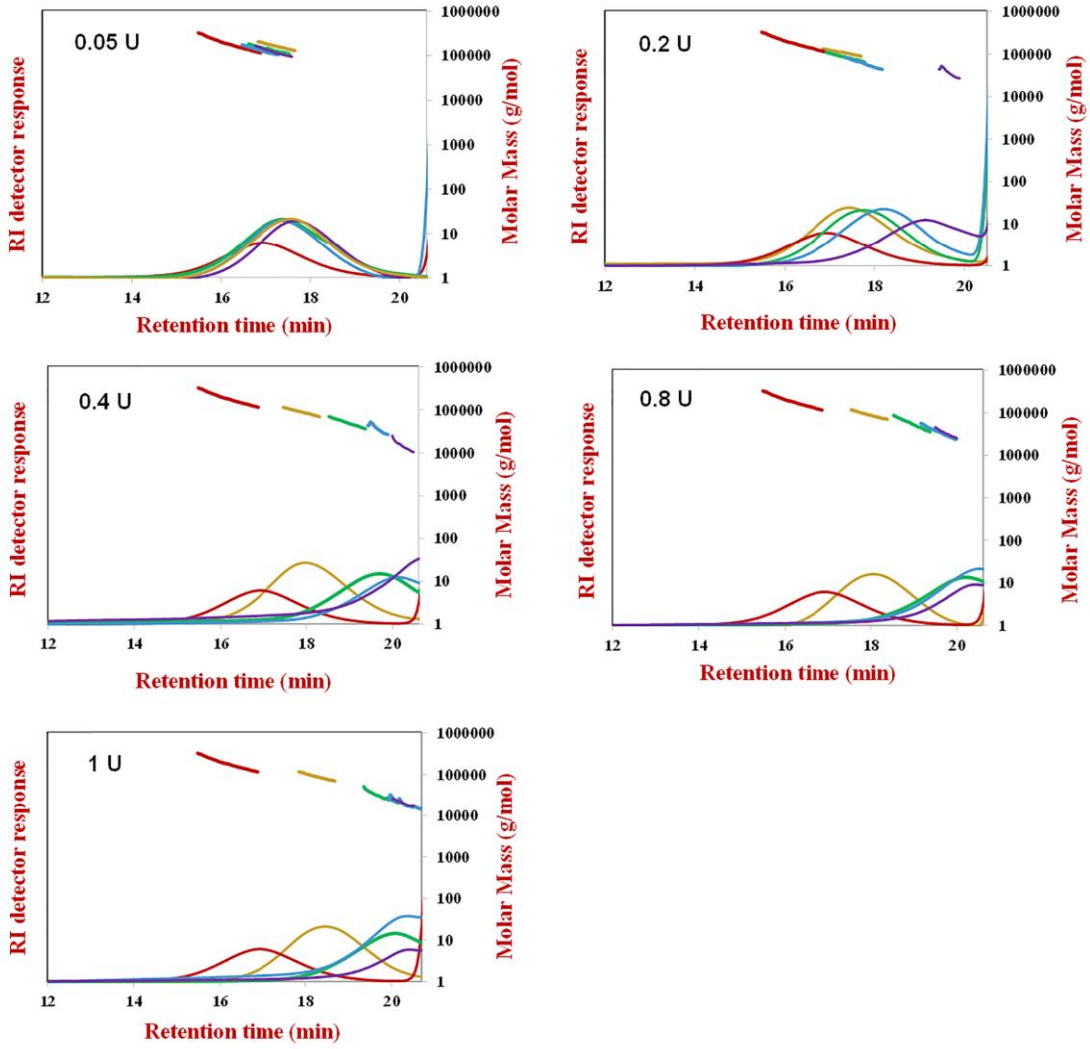


Figure S2. HPSEC-MALLS-RI analysis of the molecular weights of hydrolysis products prepared by incubating porphyran with Por16A_Wf. Enzyme dose was noted into each chromatogram. Plots of samples obtained at the incubation time of 0, 1, 5, 10 and 20 minutes were respectively colored by red, yellow, green, blue and purple.

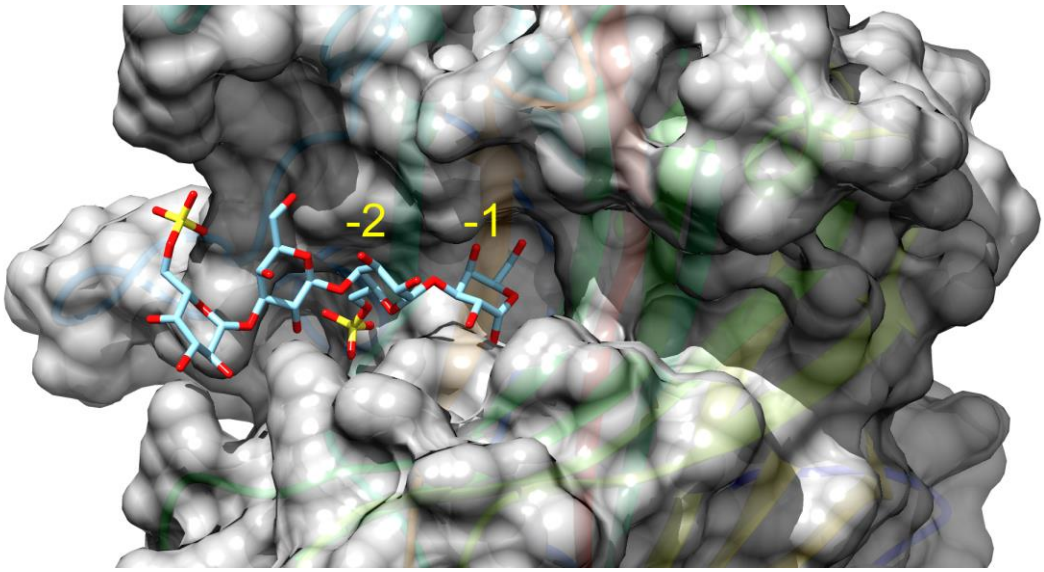


Figure S3. The predicted structure of Por16A_Wf. The structure was aligned to that of PorA (3ILF) using the Match Maker function of UCSF Chimera (version 1.13.1). The ligand in PorA was shown for indicating the subsite -2 and -1 in Por16A_Wf.