

Supplementary information

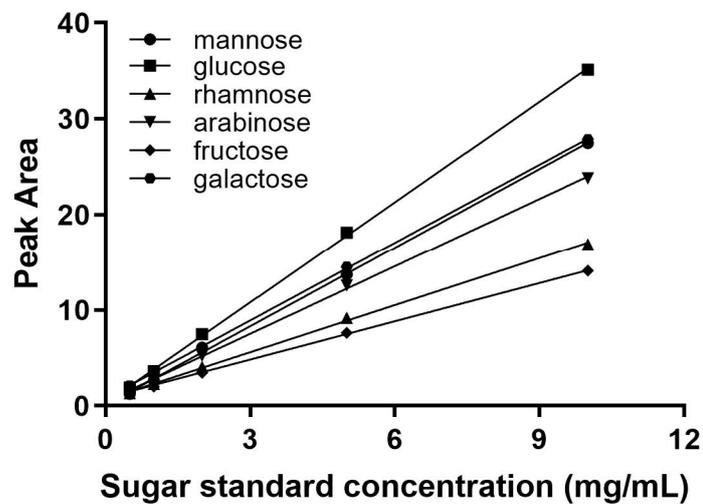
**Purification, characterization, and self-assembly of the polysaccharides from *Allium schoenoprasum***

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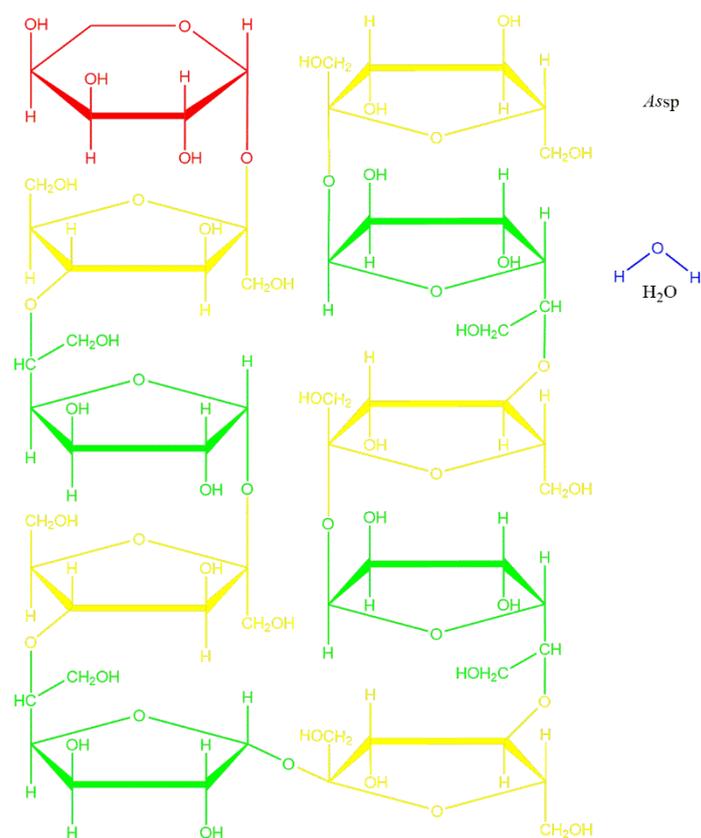
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**Figure S1.** The fitting curve of monosaccharide standard with HPLC peak area. The peak area of standard monosaccharide solutions with known concentrations were plotted against their corresponding concentrations to yield fitting curves for monosaccharide composition analysis.

**Table S1.** Fitting curve parameters of monosaccharide standards.

Sugar Standard	Fitting Curve	R <sup>2</sup>
rhamnose	$y = 1.6409x + 0.6746$	0.9990
arabinose	$y = 2.3535x + 0.4621$	0.9995
galactose	$y = 2.7162x + 0.768$	0.9996
glucose	$y = 3.4976x + 0.305$	0.9997
mannose	$y = 2.7423x + 0.0856$	0.9993
fructose	$y = 1.3325x + 0.8339$	0.9995



**Figure S2.** Coarse-grained model structure of AssP in aqueous solution. The coarse-grained model of the polysaccharide AssP and water molecules in an aqueous solution are represented by different beads. Red, arabinose residues; yellow, fructose residues; green, glucose or galactose residues; blue, water molecules.

**Table S2.** Repulsion parameters between monosaccharide residue beads.

<b>Bead</b>	<b>W</b>	<b>A</b>	<b>F</b>	<b>G</b>
W	25.000	-	-	-
A	88.586	25.000	-	-
F	83.606	25.505	25.000	-
G	92.185	25.037	25.286	25.000

A, arabinose residue; F, fructose residue; G, glucose or galactose residue; W, water.