SUPPLEMENTARY DATA

Structural comparison of exopolysaccharides from the two-potential probiotic *Limosilactobacillus fermentum* strains MC1 and D12

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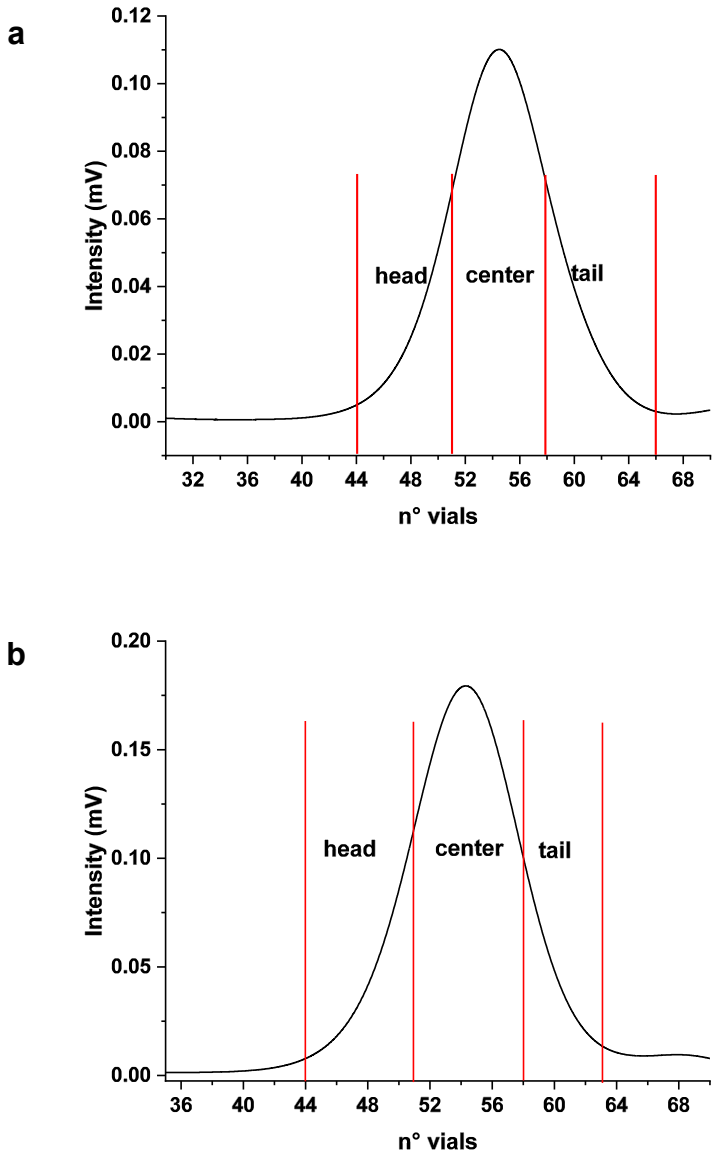

Figure S1: Elution profiles of D12 (a) and MC1 (b) EPSs obtained by middle pressure size exclusion chromatography on a Sephacryl S-300 HR column.

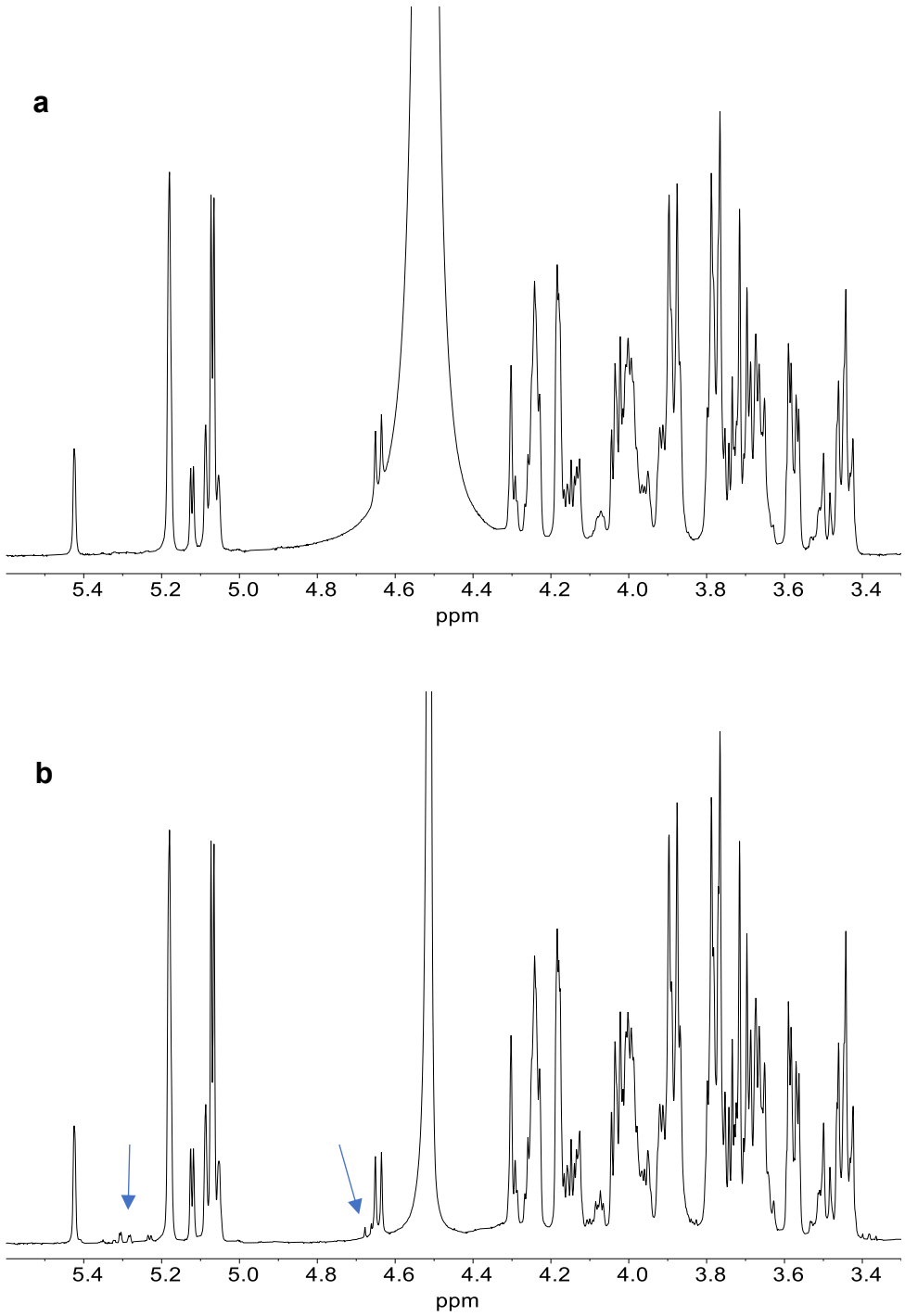

Figure S2: ^{1}H NMR spectra of D12 (a) and MC1 (b) EPSs isolated from the cell surface and extracted with 2 M NaOH. Arrows indicate resonances present in MC1 sample only. Spectra were recorded in D_2O, at 50 °C and 500 MHz.

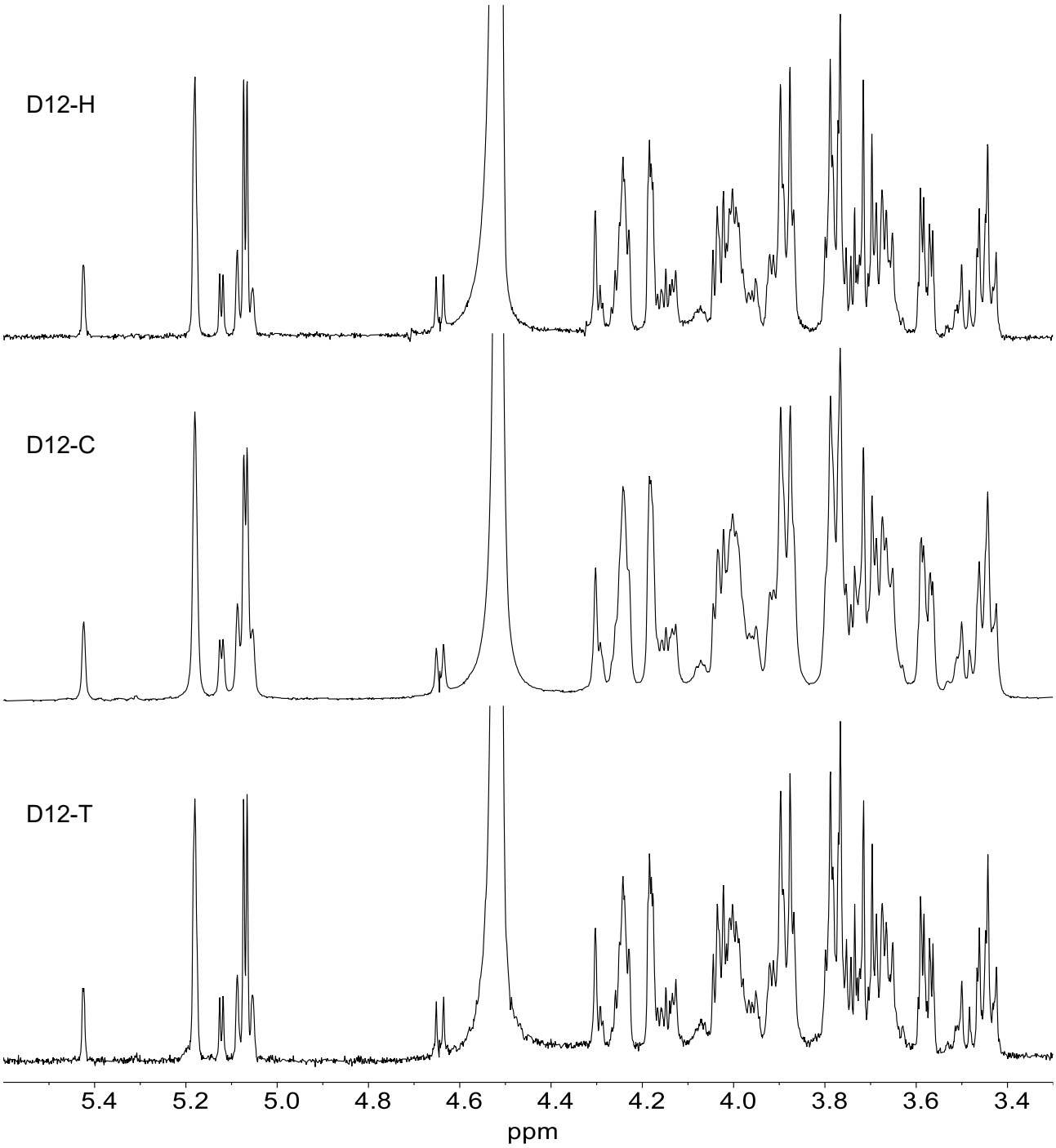

Figure S3: ^{1}H NMR spectra of the three fractions, head, center and tail, obtained after size exclusion chromatography of D12 EPS. Spectra were recorded in D_2O, at 50 °C and 500 MHz.

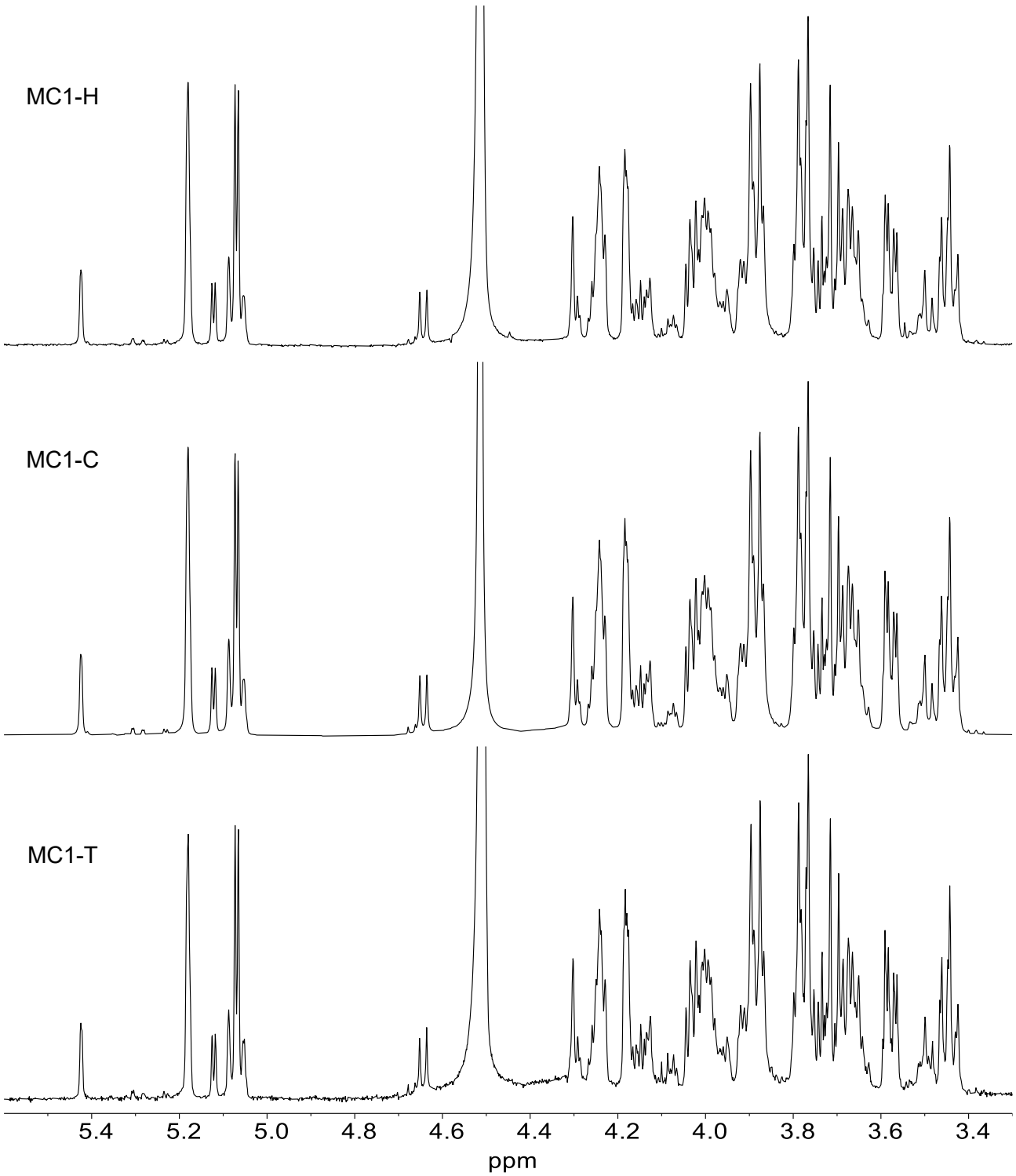

Figure S4: ^{1}H NMR spectra of the three fractions, head, center and tail, obtained after size exclusion chromatography of MC1 EPS. Spectra were recorded in D_2O, at 50 °C and 500 MHz.

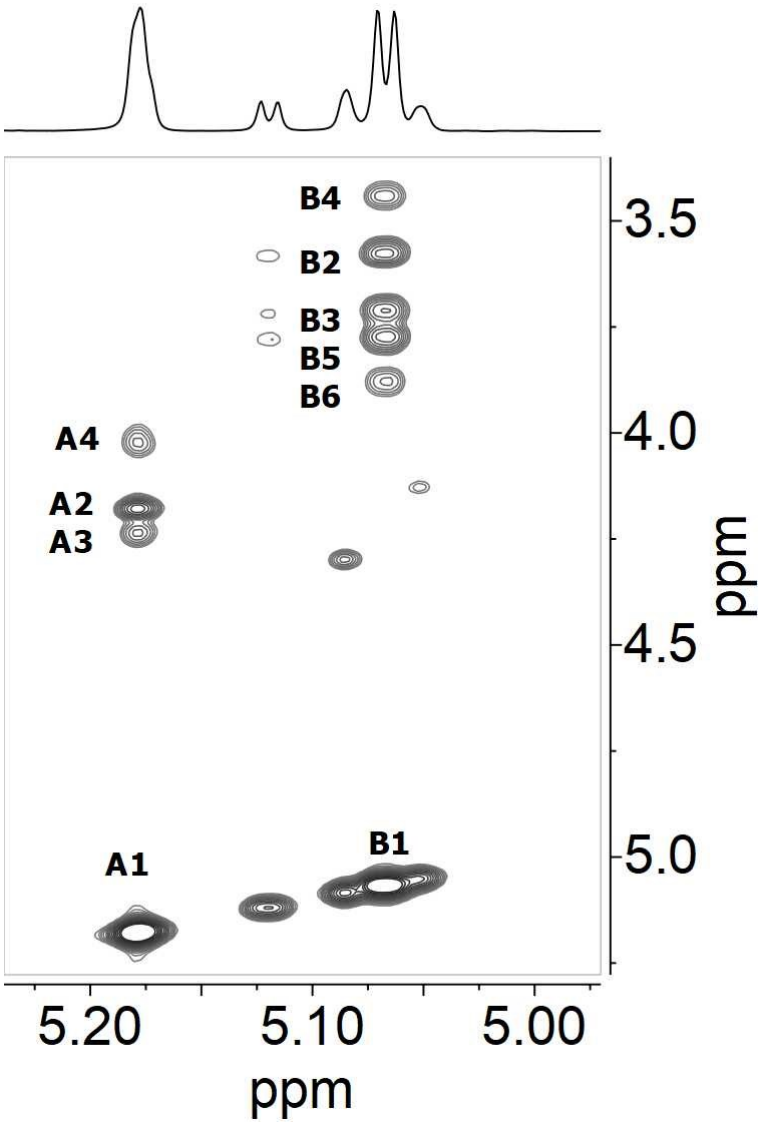

Figure S5: TOCSY spectrum of D12 EPS recorded in D_2O, at 50 °C and 500 MHz. Cross-peaks for spin systems **A** and **B** are indicated (as in Table 4).

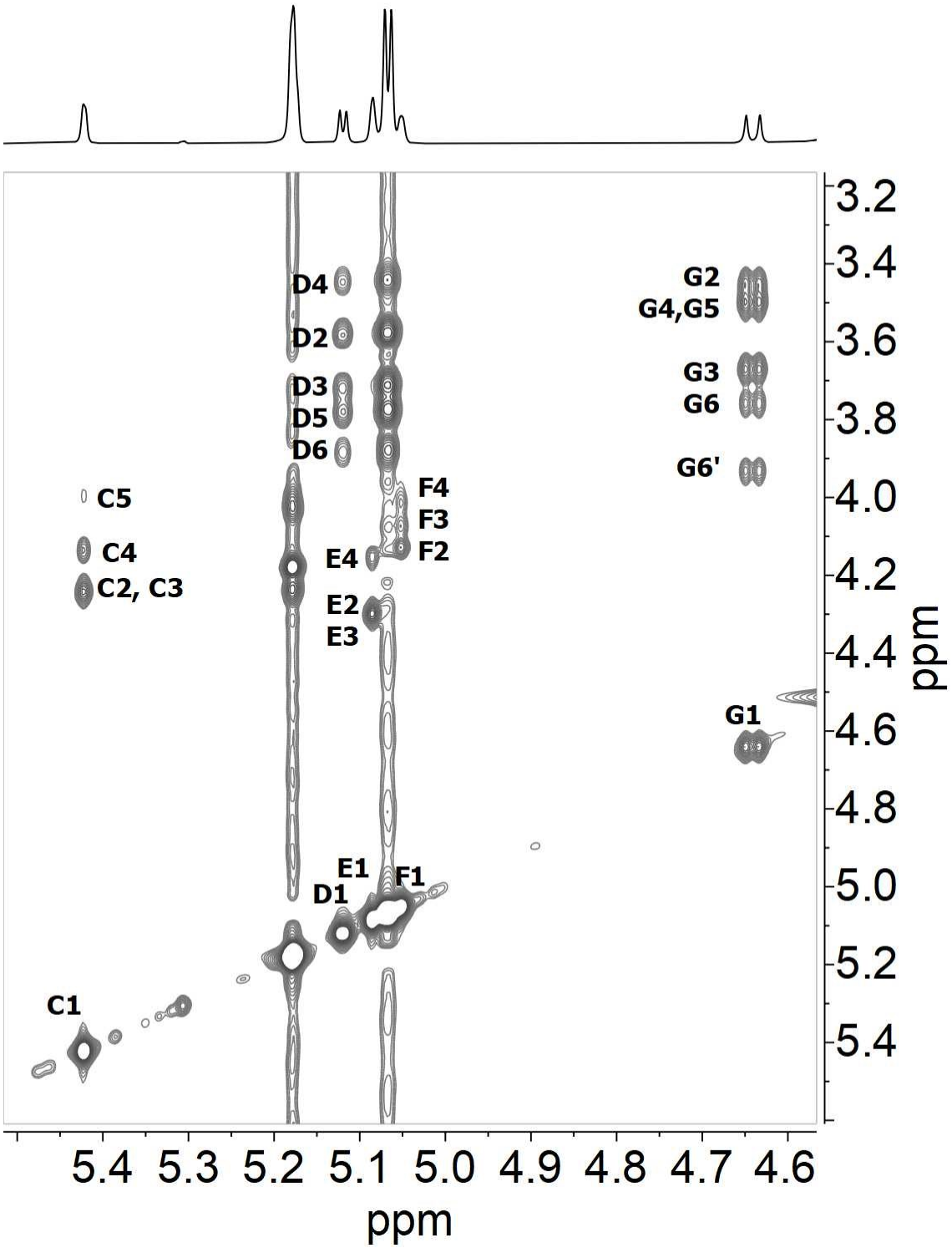

Figure S6: TOCSY spectrum of D12 EPS recorded in D2O, at 50 °C and 500 MHz. Cross-peaks for spin systems **C** to **G** are indicated (as in Table 4).

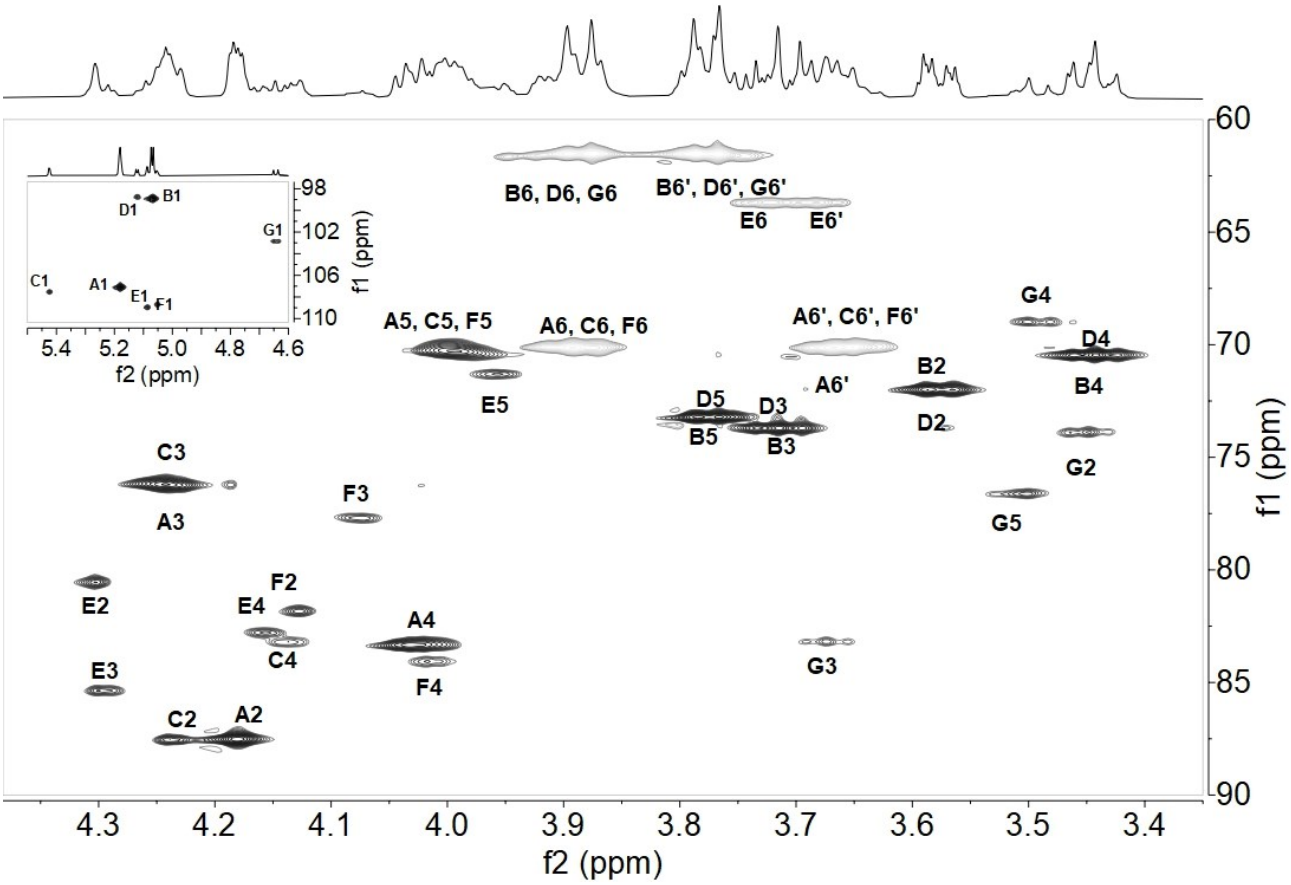

Figure S7: HSQC spectrum of MC1 EPS recorded in D_2O, at 50 °C and 500 MHz. Anomeric region is shown in the inset. Cross-peaks for spin systems **A** to **G** are indicated (as in Table 4).

Oligosaccharide subjected to chemical shift simulation:

α-D-Glc*p*(1→2)-β-D-Gal*f*-(1→6)[α-D-Glc*p*(1→2)]-β-D-Gal*f*-(1→6)[α-D-Glc*p*(1→2)]-β-D-Gal*f*-OMe

Table S1: ^{13}C chemical shifts obtained using the simulation tool for 13C nucleus at the Carbohydrate Structure Database (CSDB), the CSDB structural ranking tool and empirical chemical shift simulation.

Position[a]	Residue	Trust	C1	C2	C3	C4	C5	C6
1	β-D-Gal*f*-OMe	25%	108.9	87.7	76.6	83.5	70.5	70.3
2	α-D-Glcp	93%	99.2	72.5	73.9	70.7	73.5	61.8
3	β-D-Gal*f*	79%	107.4	87.8	76.6	83.5	70.7	70.4
4	α-D-Glcp	93%	99.2	72.5	73.9	70.7	73.5	61.8
5	β-D-Gal*f*	69%	107.4	87.8	76.4	83.4	71.3	63.4
6	α-D-Glcp	93%	99.2	72.5	73.9	70.7	73.5	61.8

[a] Residue position in the oligosaccharide chain starting from β-D-Gal*f*-OMe

Oligosaccharide subjected to chemical shift simulation:

β-D-Gal*f*-(1→6)-β-D-Gal*f*-(1→6)-β-D-Gal*f*-OMe

Table S2: ^{13}C chemical shifts obtained using the simulation tool for 13C nucleus at the Carbohydrate Structure Database (CSDB), the CSDB structural ranking tool and empirical chemical shift simulation.

Position[a]	Residue	Trust	C1	C2	C3	C4	C5	C6
1	β-D-Gal*f*-OMe	46%	111.4	81.9	77.8	83.7	70.6	70.1
2	β-D-Gal*f*-OMe	83%	109.4	81.5	78.2	84.6	71.0	70.2
3	β-D-Gal*f*-OMe	87%	109.6	81.4	78.1	84.3	71.4	63.4

[a] Residue position in the oligosaccharide chain starting from β-D-Gal*f*-OMe

Oligosaccharide subjected to chemical shift simulation (3 repeating units):

β-D-Glc*p*-(1→3)-β-D-Gal*f*-(1→6)[α-D-Glc*p*(1→2)]-β-D-Gal*f*-(1→3)-β-D-Glc*p*-(1→3)-β-D-Gal*f*-(1→6)[α-D-Glc*p*(1→2)]-β-D-Gal*f*-(1→3)-β-D-Glc*p*-(1→3)-β-D-Gal*f*-(1→6)[α-D-Glc*p*(1→2)]-β-D-Gal*f*-OMe

Table S3: ^{13}C chemical shifts obtained using the simulation tool for 13C nucleus at the Carbohydrate Structure Database (CSDB), the CSDB structural ranking tool and empirical chemical shift simulation.

Position[a]	Residue	Trust	C1	C2	C3	C4	C5	C6
1	β-D-Gal*f*-OMe	25%	108.9	87.7	76.6	83.5	70.5	70.3
2	α-D-Glcp	93%	99.2	72.5	73.9	70.7	73.5	61.8
3	β-D-Gal*f*	61%	108.5	80.1	84.9	82.5	70.8	63.3
4	β-D-Glcp	78%	102.9	74.2	83.3	69.3	76.9	61.9
5	β-D-Gal*f*	68%	107.0	87.3	75.8	83.0	69.9	69.7
6	α-D-Glcp	93%	99.2	72.5	73.9	70.7	73.5	61.8
7	β-D-Gal*f*	61%	108.5	80.1	84.9	82.5	70.8	63.3
8	β-D-Glcp	78%	102.9	74.2	83.3	69.3	76.9	61.9
9	β-D-Gal*f*	68%	107.0	87.3	75.8	83.0	69.9	69.7
10	α-D-Glcp	93%	99.2	72.5	73.9	70.7	73.5	61.8
11	β-D-Gal*f*	61%	108.5	80.1	84.9	82.5	70.8	63.3
12	β-D-Glcp	92%	103.1	73.9	76.4	70.4	76.8	61.6

[a] Residue position in the oligosaccharide chain starting from β-D-Gal*f*-OMe