Electronic Supporting Information

Influence of the reducing-end anomeric configuration of the Man_9 epitope on DC-SIGN recognition.

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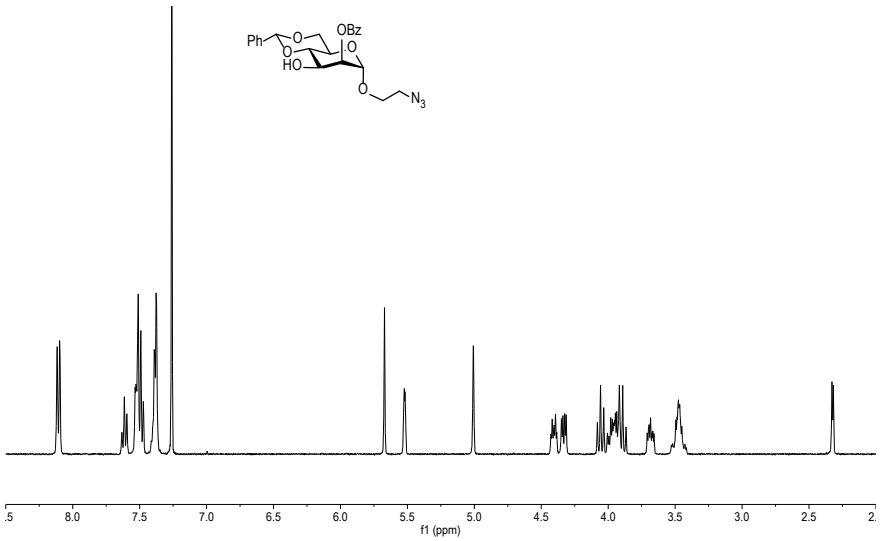
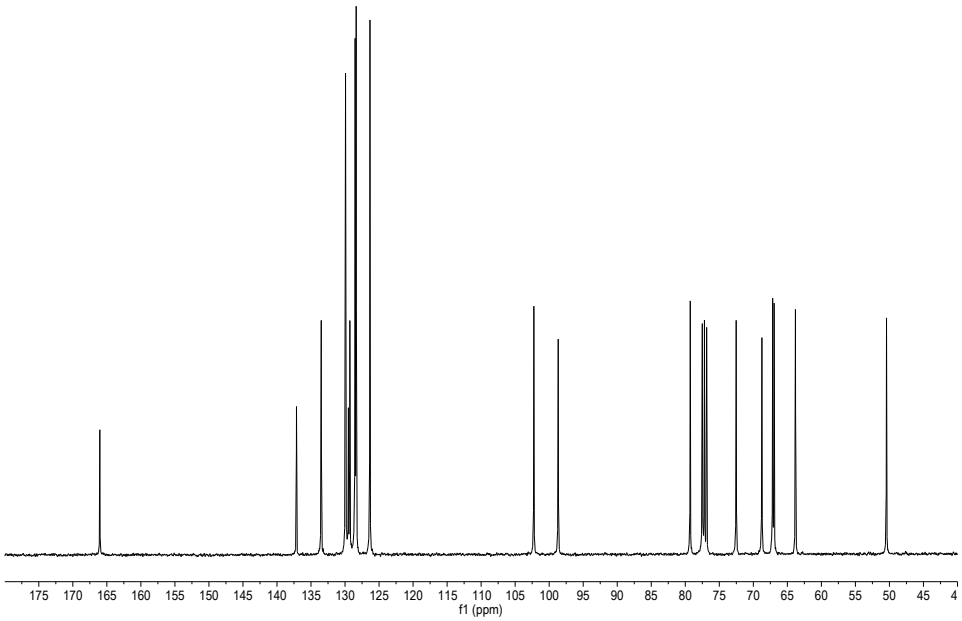
^{1}H and ^{13}C NMR spectra and selected HSQC and MS spectra

Compound 6

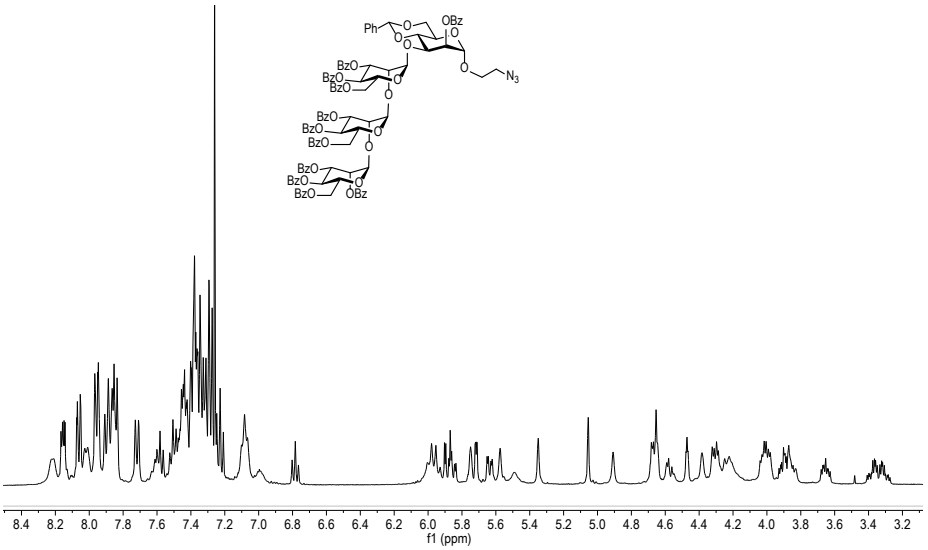


^{1}H-NMR (400 MHz, $CDCl_3$): compound **6**.

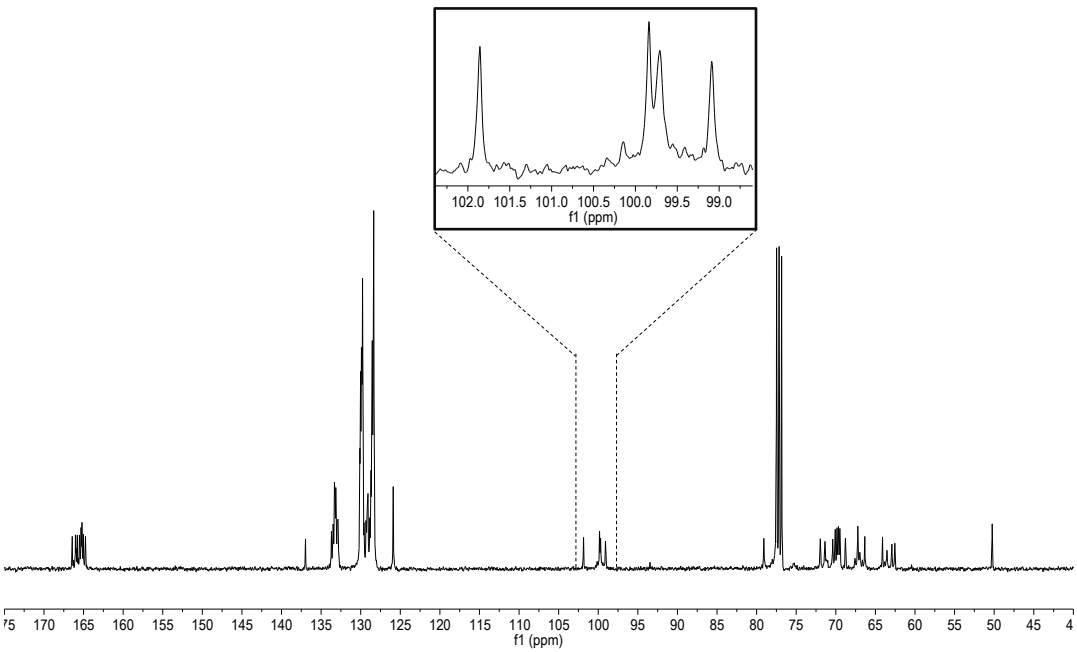


^{13}C-RMN (100 MHz, $CDCl_3$): compound **6**.

Compound 9

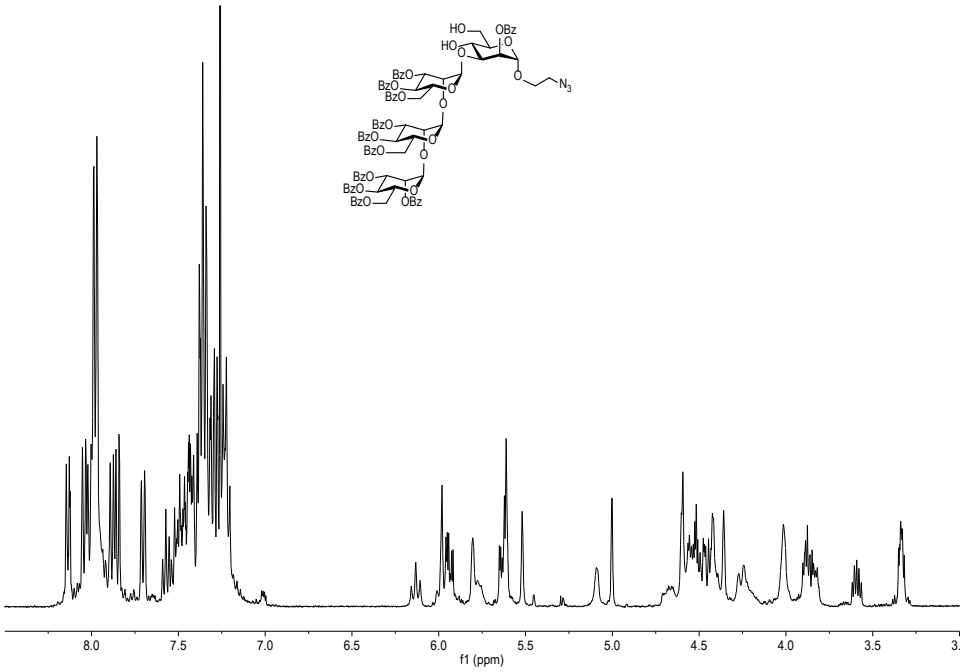


^{1}H-NMR (400 MHz, $CDCl_3$): compound **9**.

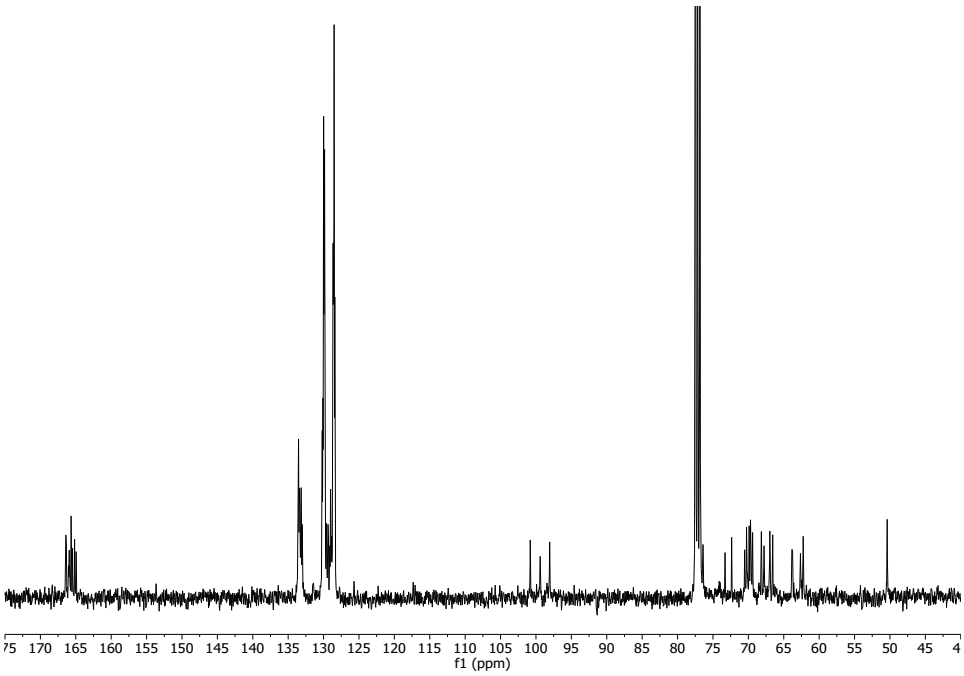


^{13}C-NMR (100 MHz, $CDCl_3$): compound **9**.

Compound 10

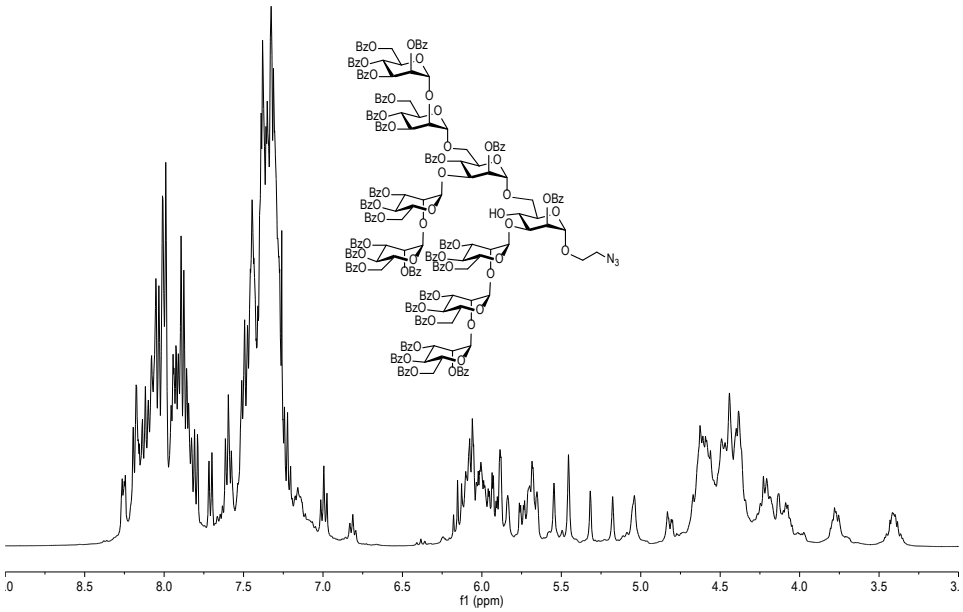


^{1}H-NMR (400 MHz, $CDCl_3$): compound **10**.

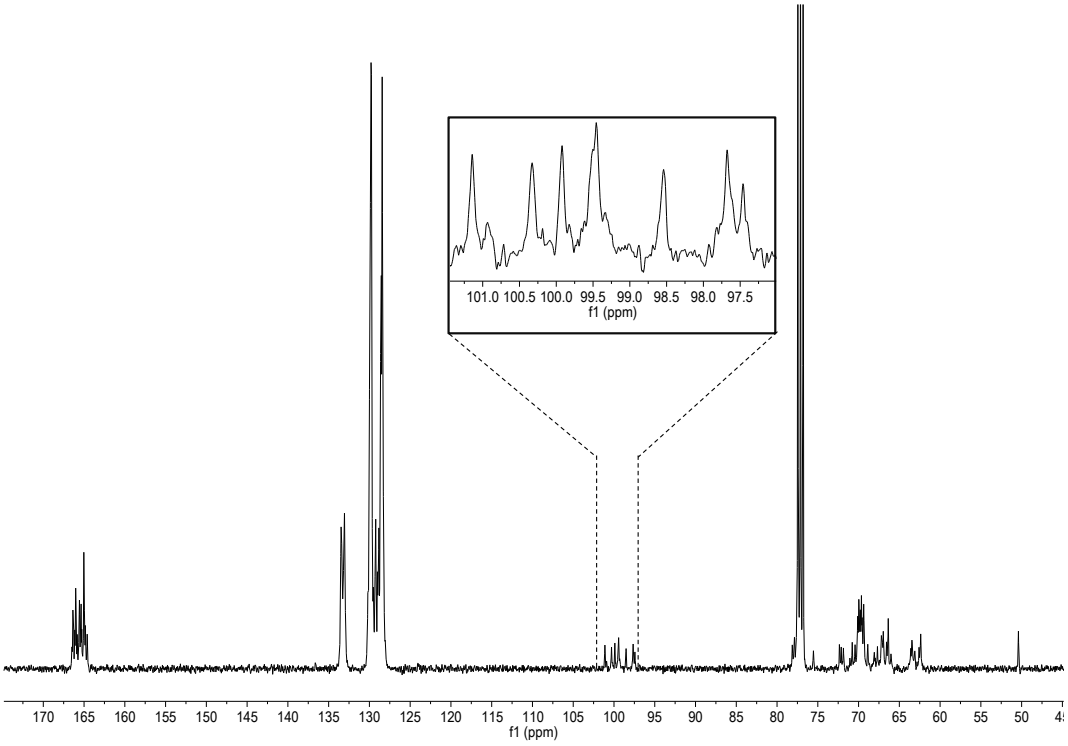


^{13}C-NMR (100 MHz, $CDCl_3$): compound **10**.

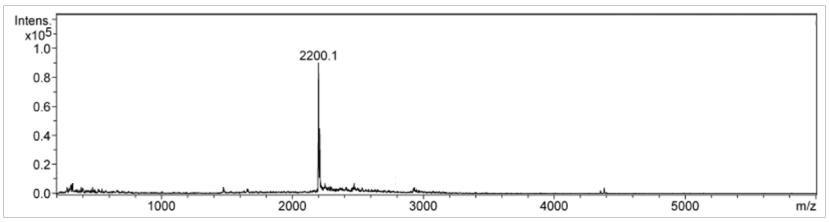
Compound 11



^{1}H-NMR (400 MHz, $CDCl_3$): compound **11**.

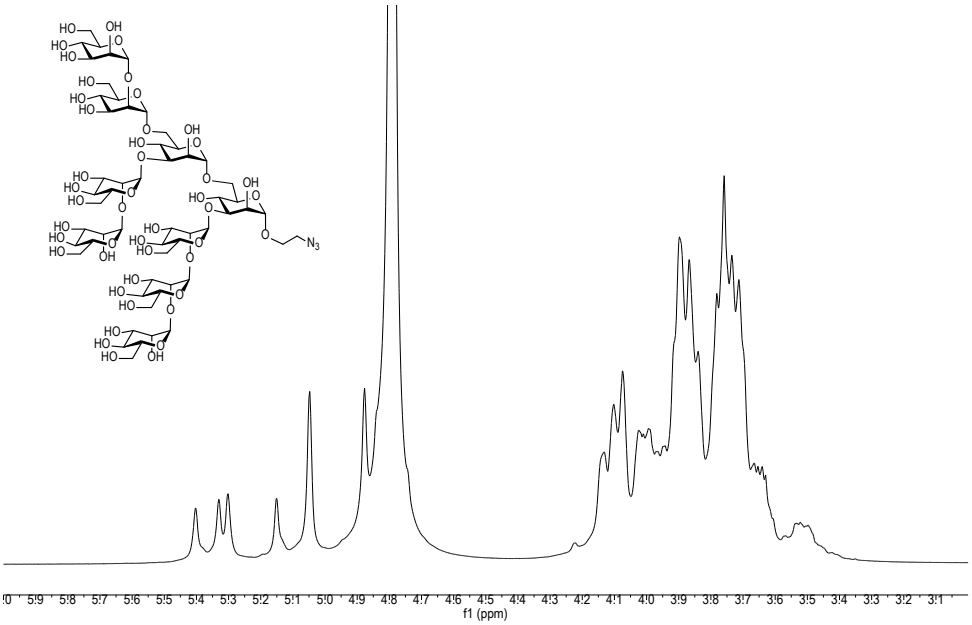


^{13}C-NMR (100 MHz, $CDCl_3$): compound **11**.

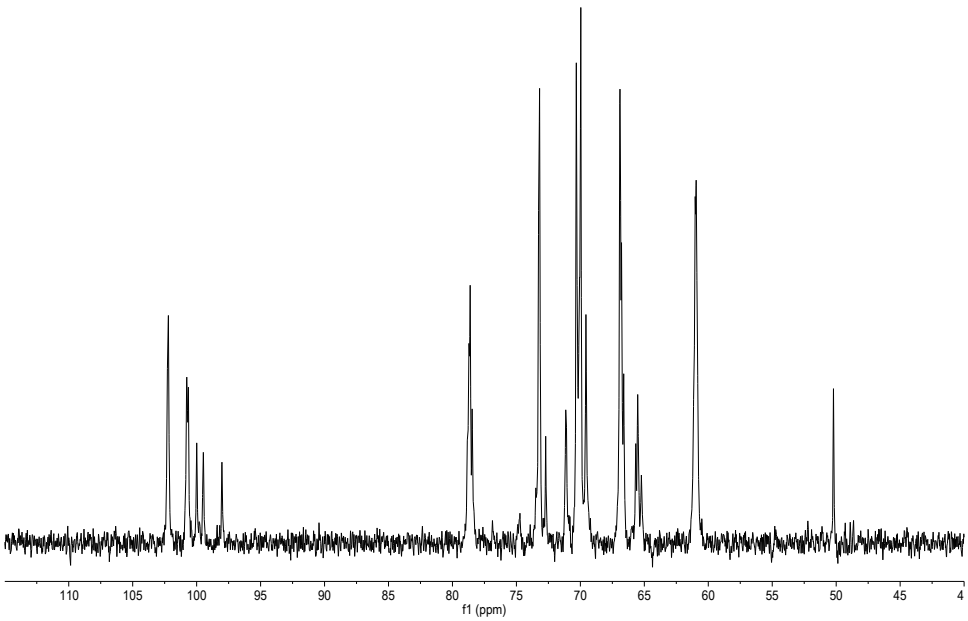


ESI-MS: compound **11**.

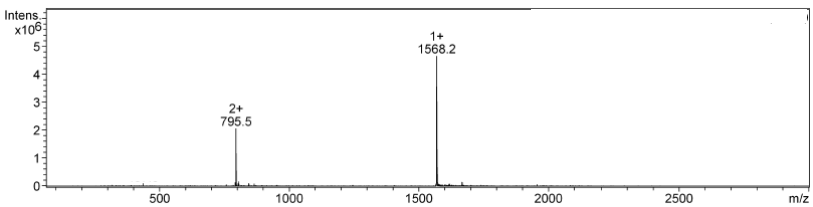
Compound 12



^{1}H-NMR (400 MHz, D_2O): compound **12**.

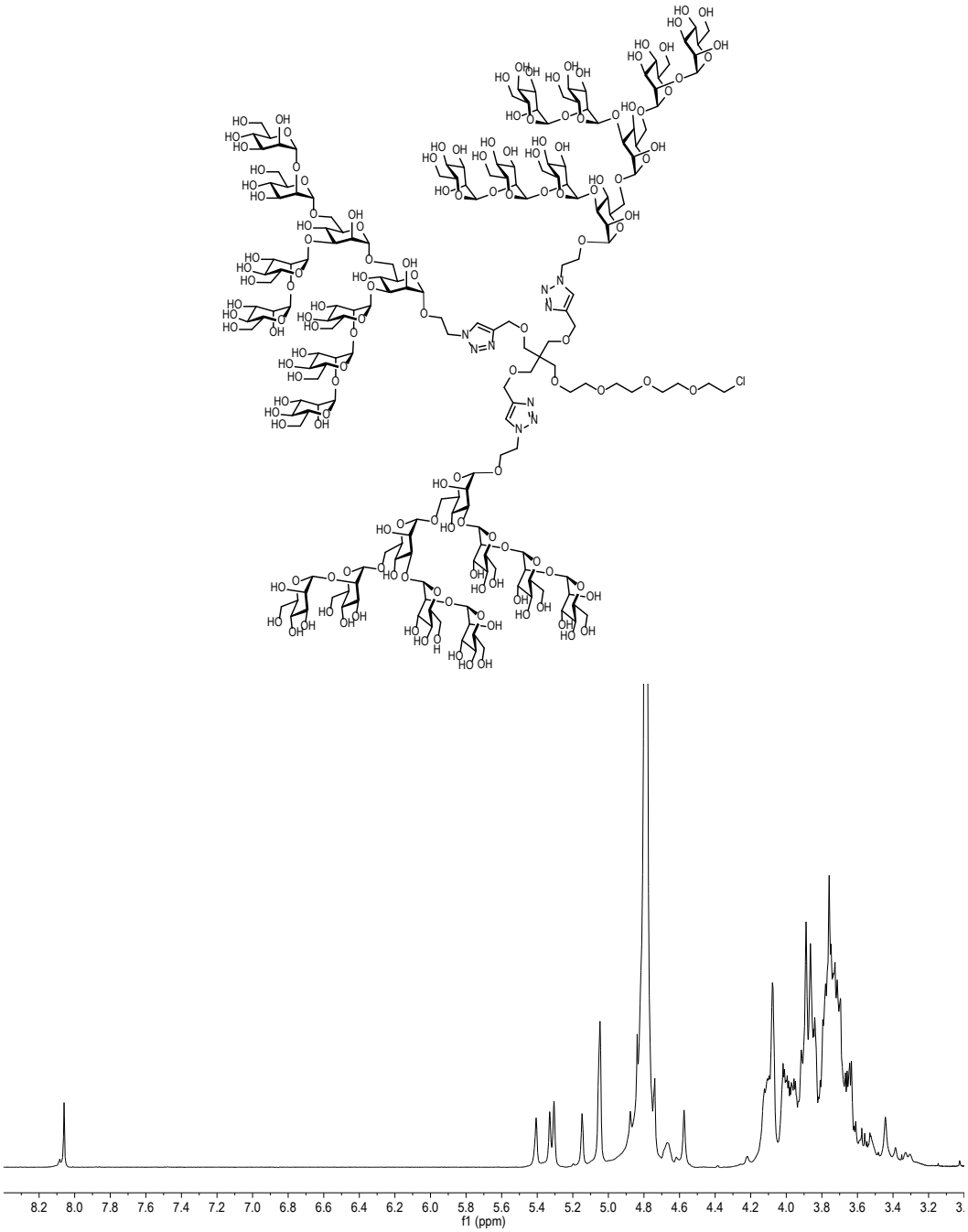


^{13}C-NMR (100 MHz, D_2O): compound **12**.

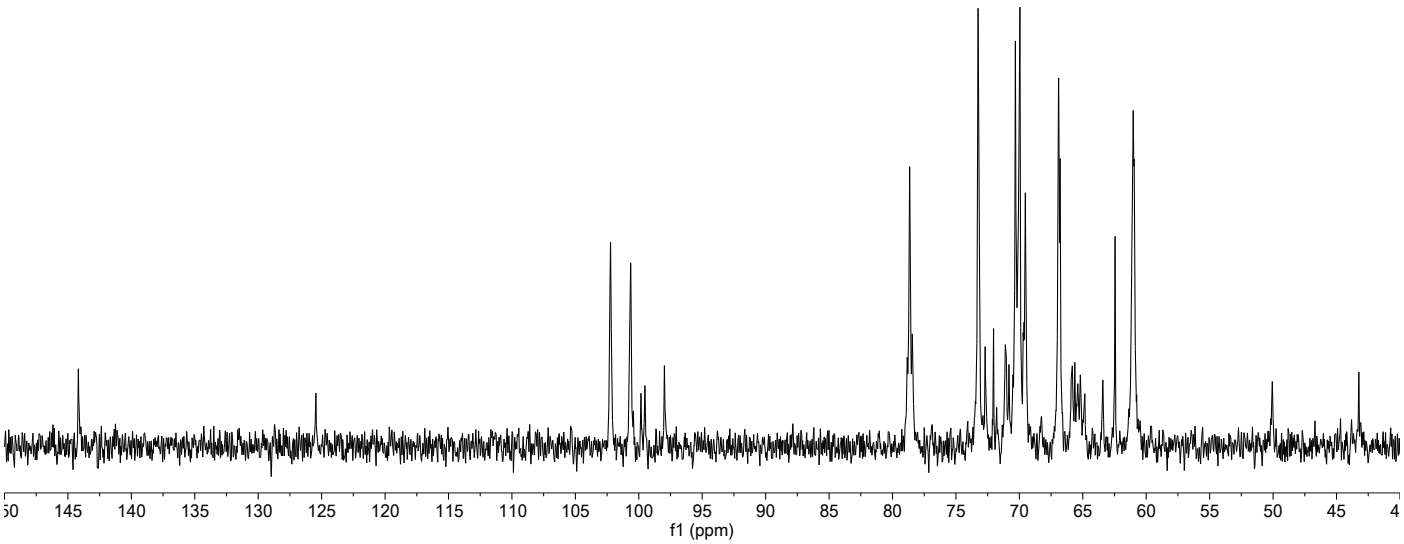


ESI-MS: compound **12**.

C**ompound 15**

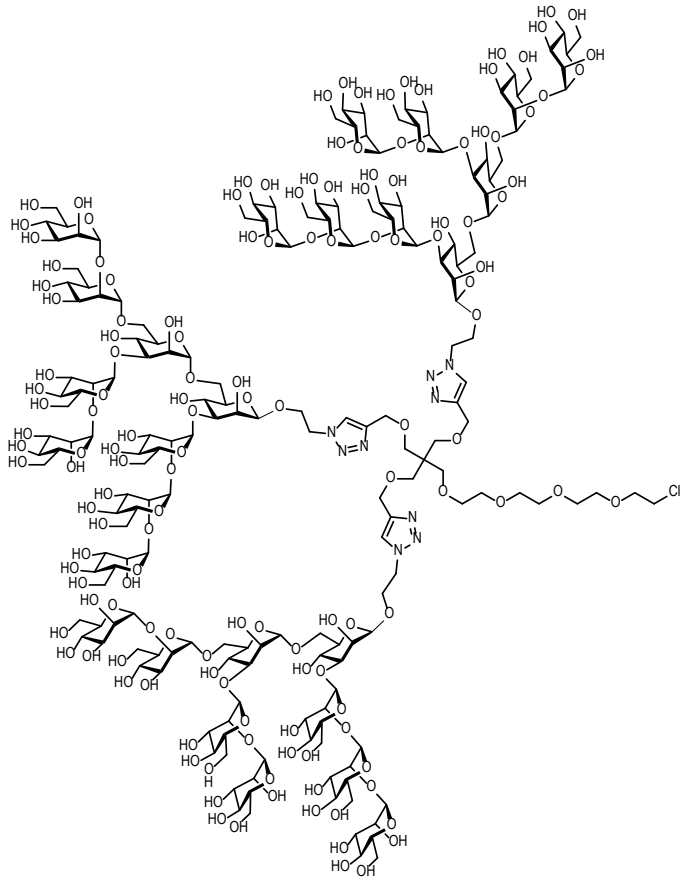


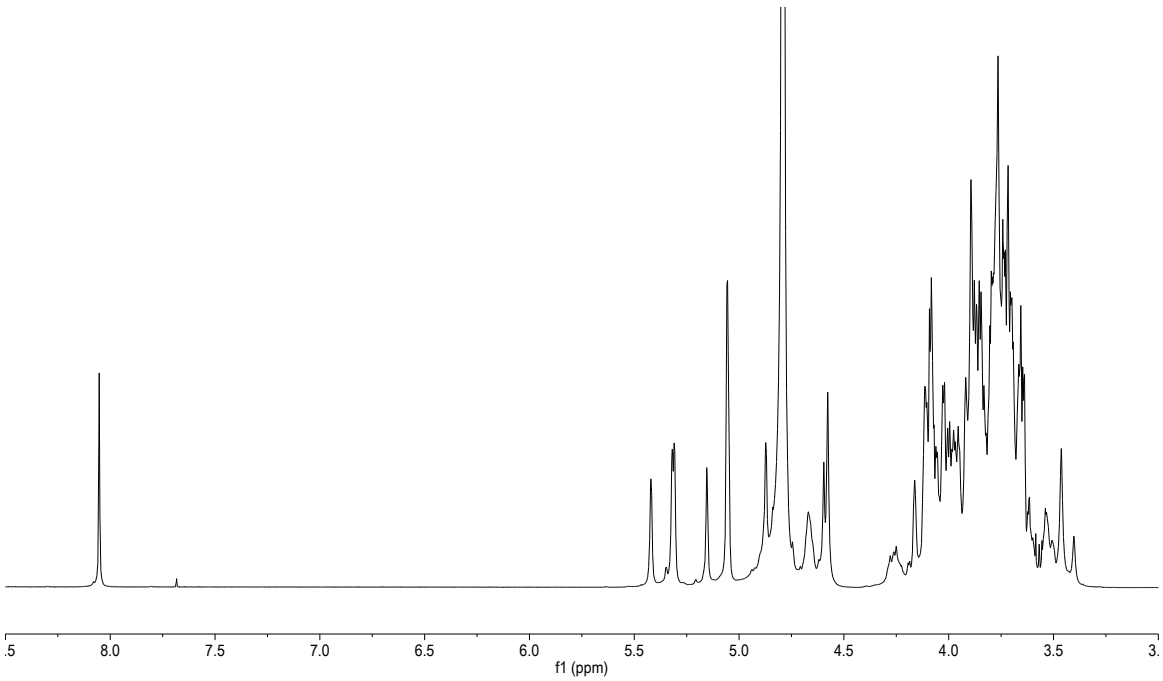
^{1}H-NMR (400 MHz, D_2O): compound **15**.



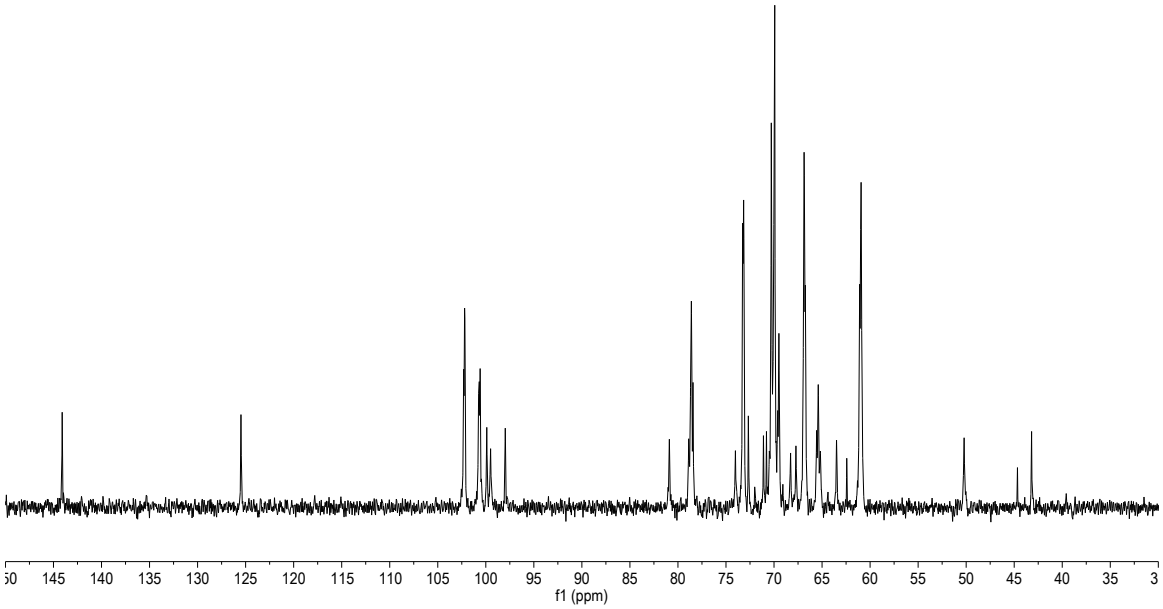
^{13}C-NMR (100 MHz, D_2O): compound **15**.

Compound 16



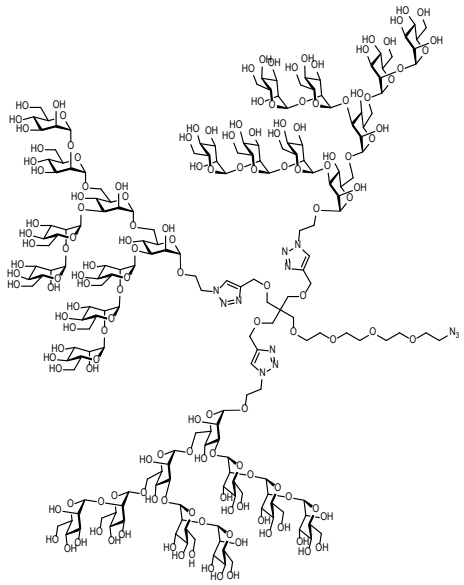


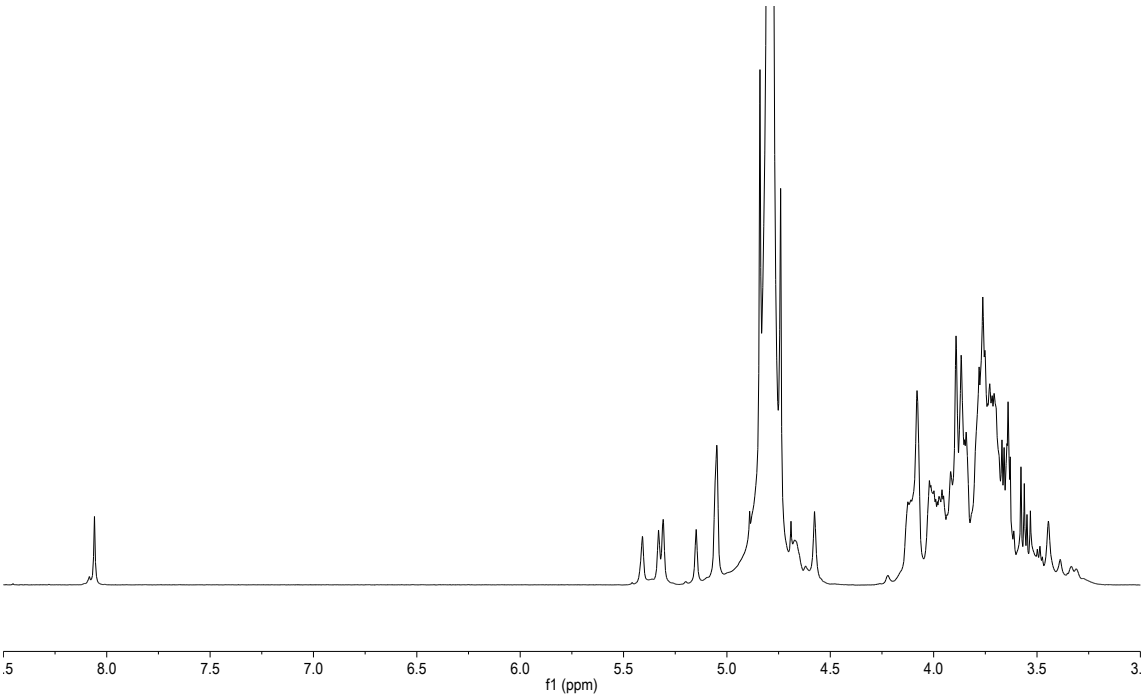
^{1}H-NMR (400 MHz, D_2O): compound **16**.



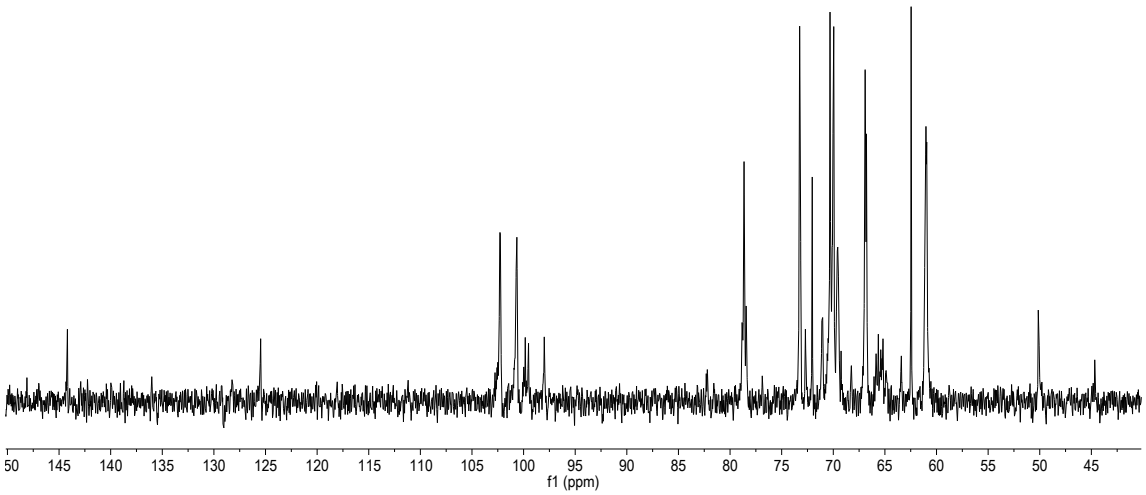
^{13}C-NMR (100 MHz, D_2O): compound **16**.

Compound 17

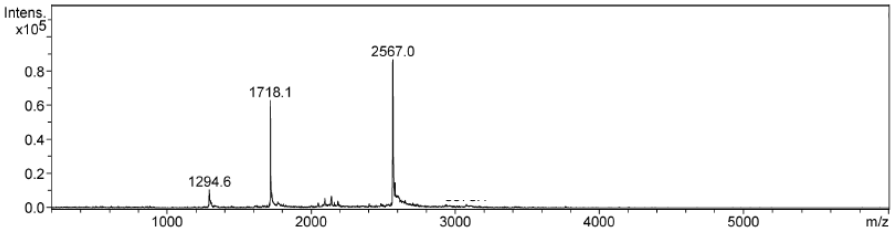




^{1}H-NMR (400 MHz, D_2O): compound **17**.

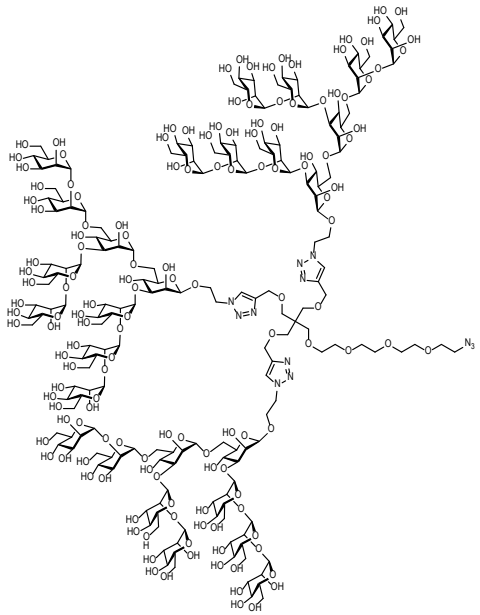


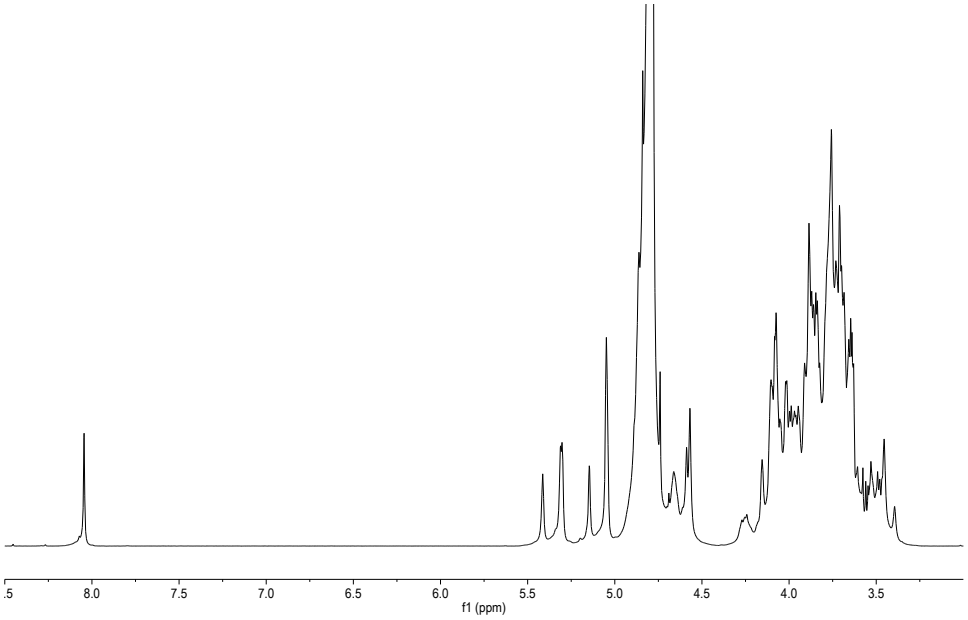
^{13}C-NMR (100 MHz, D_2O): compound **17**.



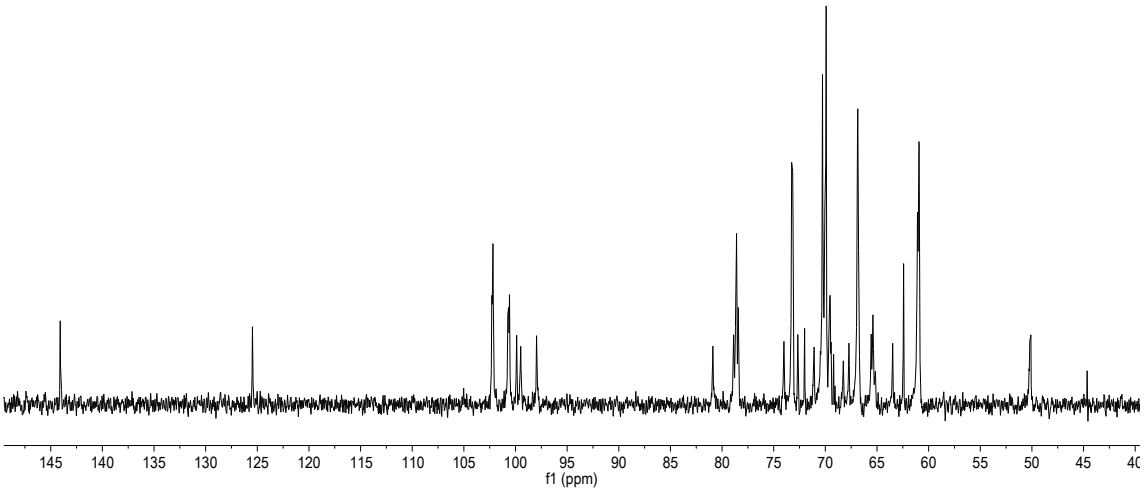
ESI-MS: compound **17**.

Compound 18

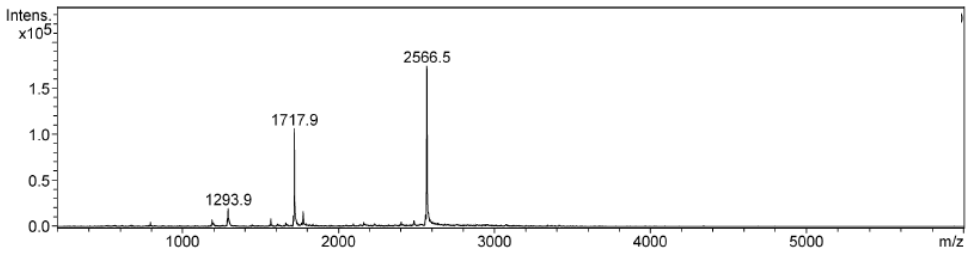




^{1}H-NMR (400 MHz, D_2O): compound **18**.

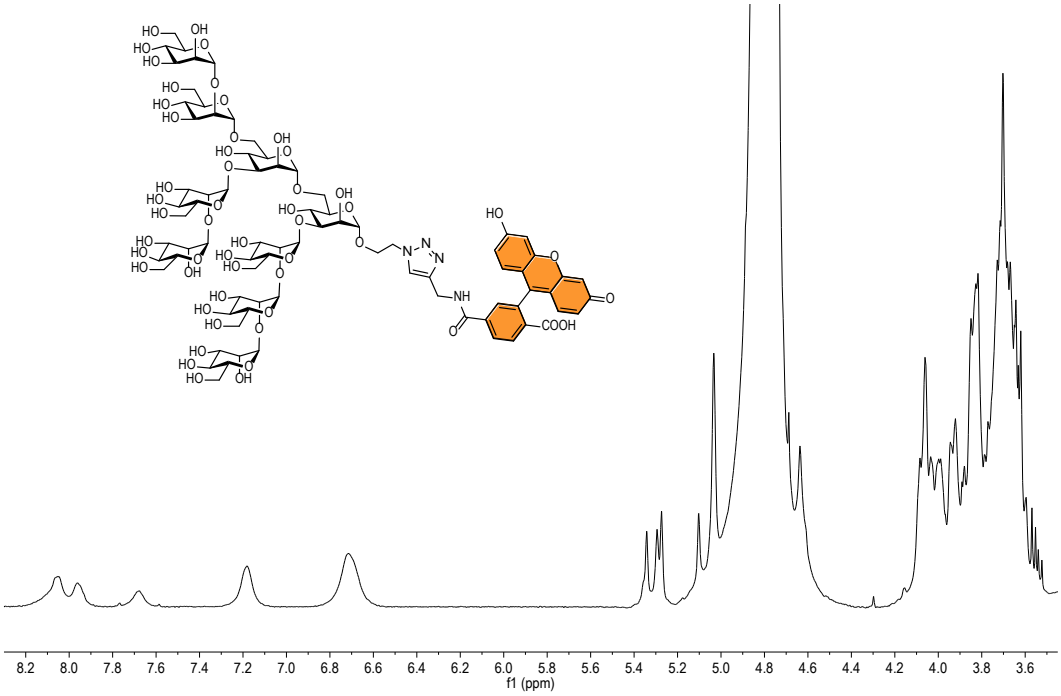


^{13}C-NMR (100 MHz, D_2O): compound **18**.

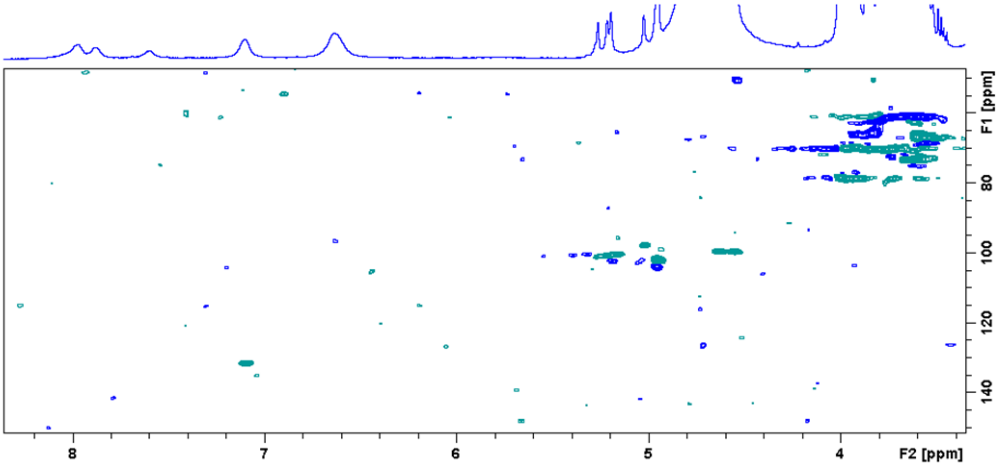


ESI-MS: compound **18**.

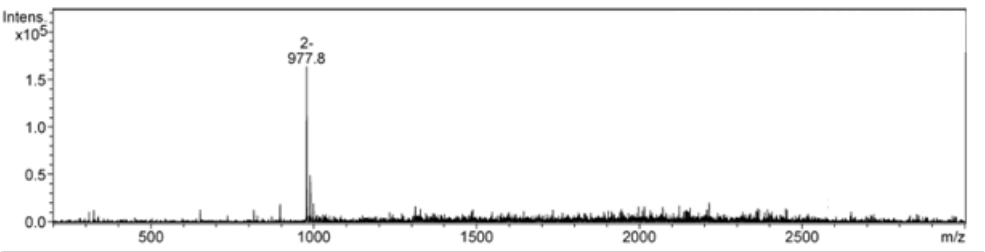
Compound 20



^{1}H-NMR (400 MHz, D_2O): compound **20**.

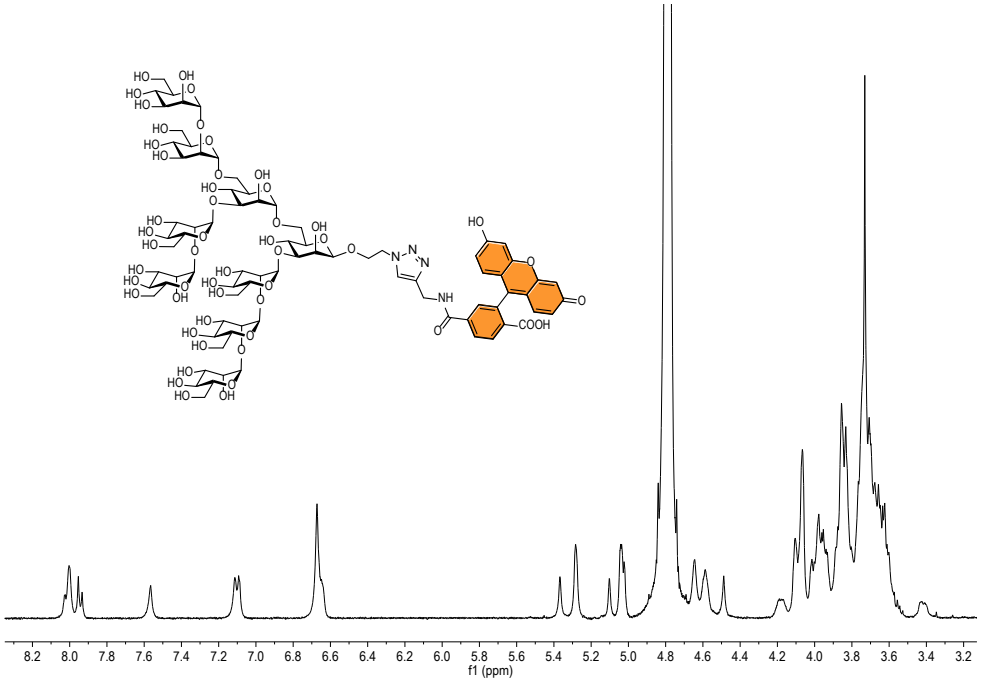


HSQC-NMR (D_2O): compound **20**.



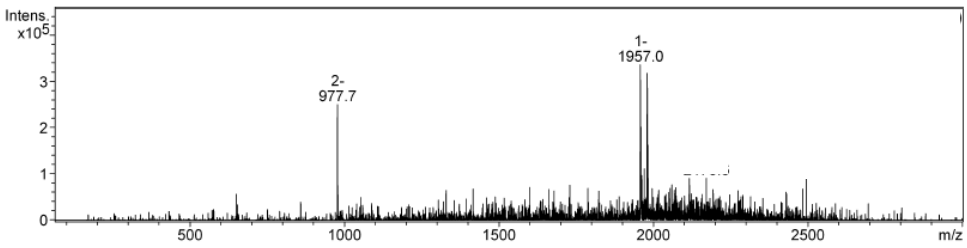
ESI-MS: compound **20**.

Compound 21



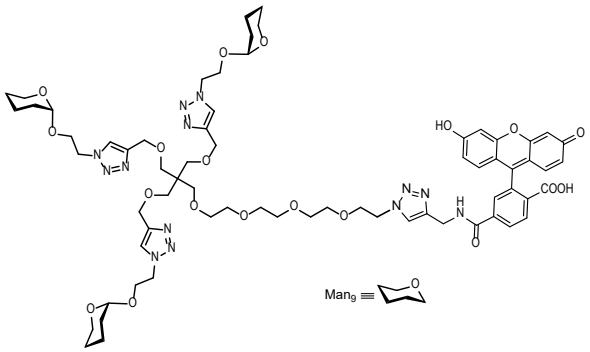
^{1}H-NMR (400 MHz, D_2O): compound **21**.

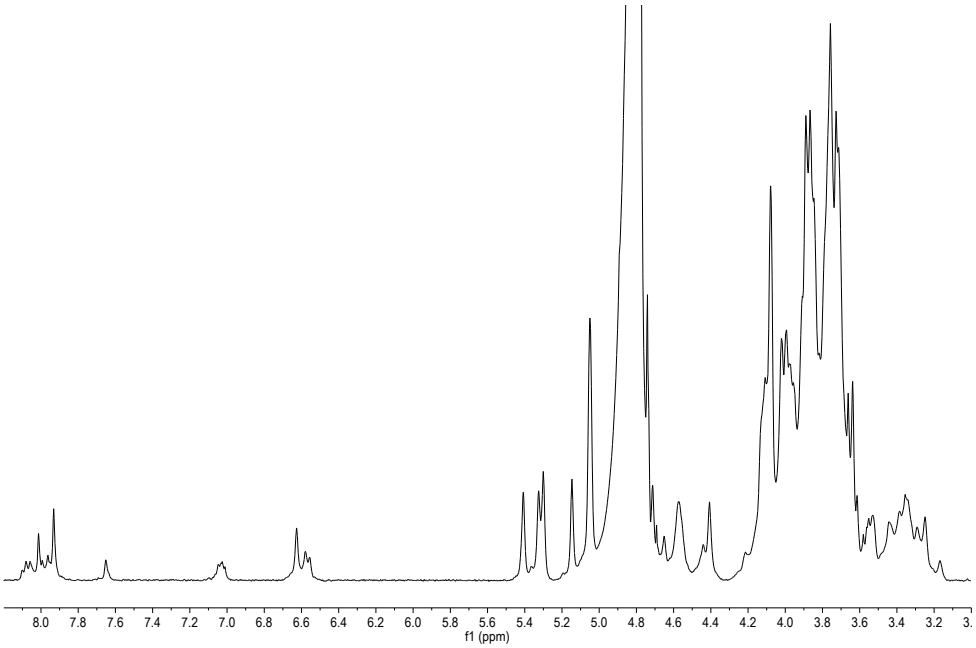
HSQC-NMR (D_2O): compound **21**.



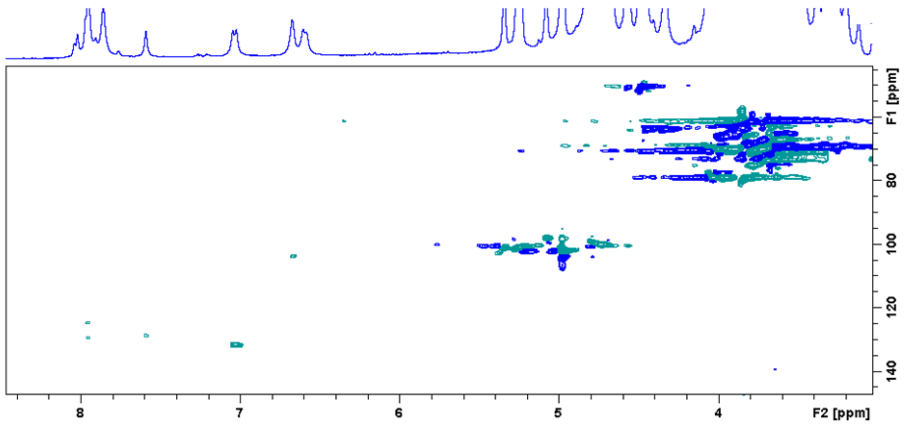
ESI-MS: compound **21**.

Compound 22

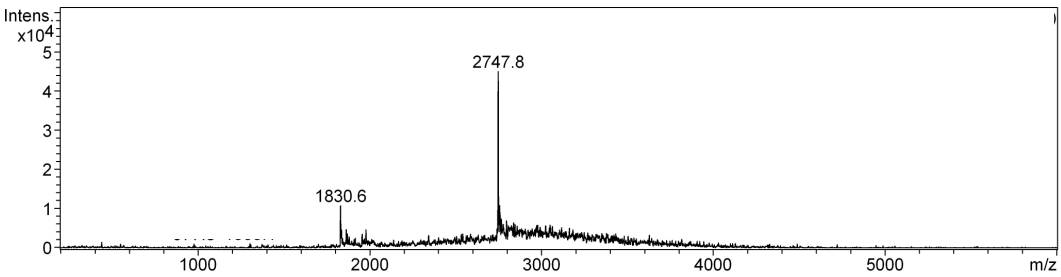




^{1}H-NMR (400 MHz, D_2O): compound **22**.

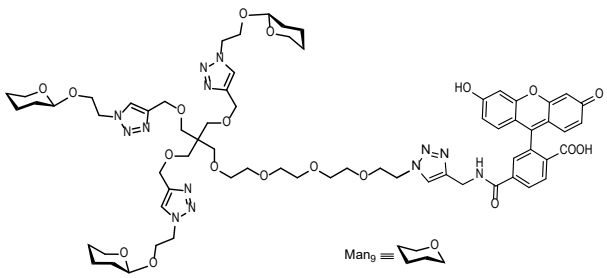


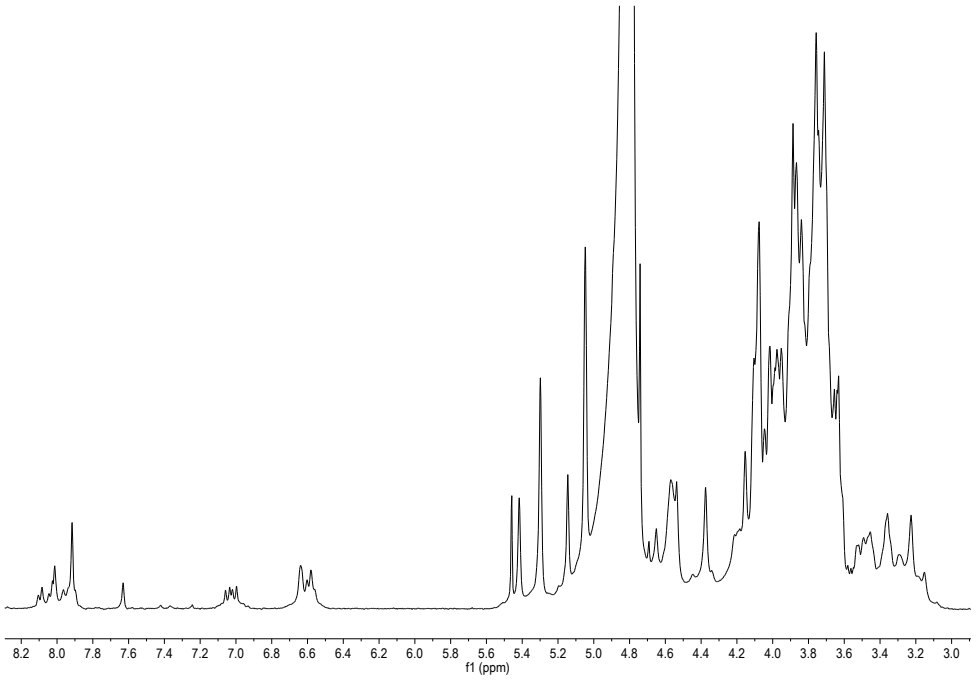
HSQC-NMR (D_2O): compound **22**.



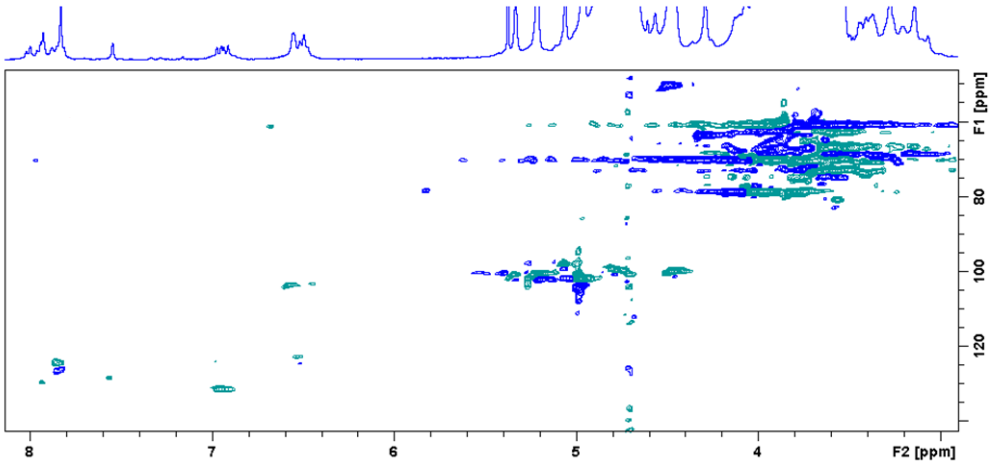
ESI-MS: compound **22**.

Compound 23

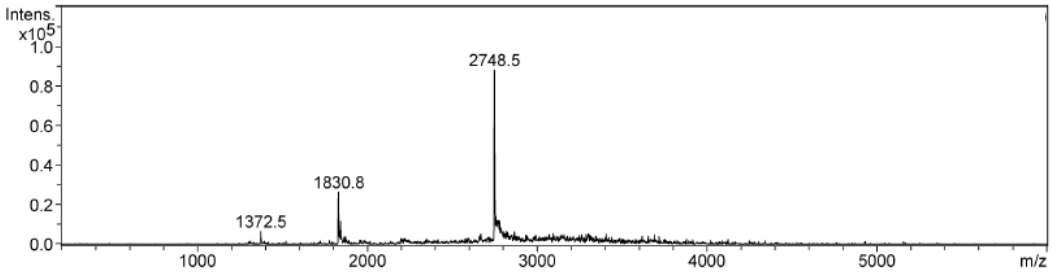




^{1}H-NMR (400 MHz, D_2O): compound **23**.



HSQC-NMR (D_2O): compound **23**.



ESI-MS: compound **23**.

Protocol for DC-SIGN ECD purification

DC-SIGN ECD sample, used for this work, was purified using a routine 2 steps automated protocol on Akta Xpress derived from the reference J Biol Chem 2009, 284, 21229-40 (https://pubmed.ncbi.nlm.nih.gov/19502234/), in which we demonstrated that DC-SIGN ECD is a tetramer. A Mannan-Agarose column to ensure its functionality, eluted with EDTA and after a Superose12 column to ensure its homogeneity, reload the carbohydrate recognition site with Ca and to remove aggregates.

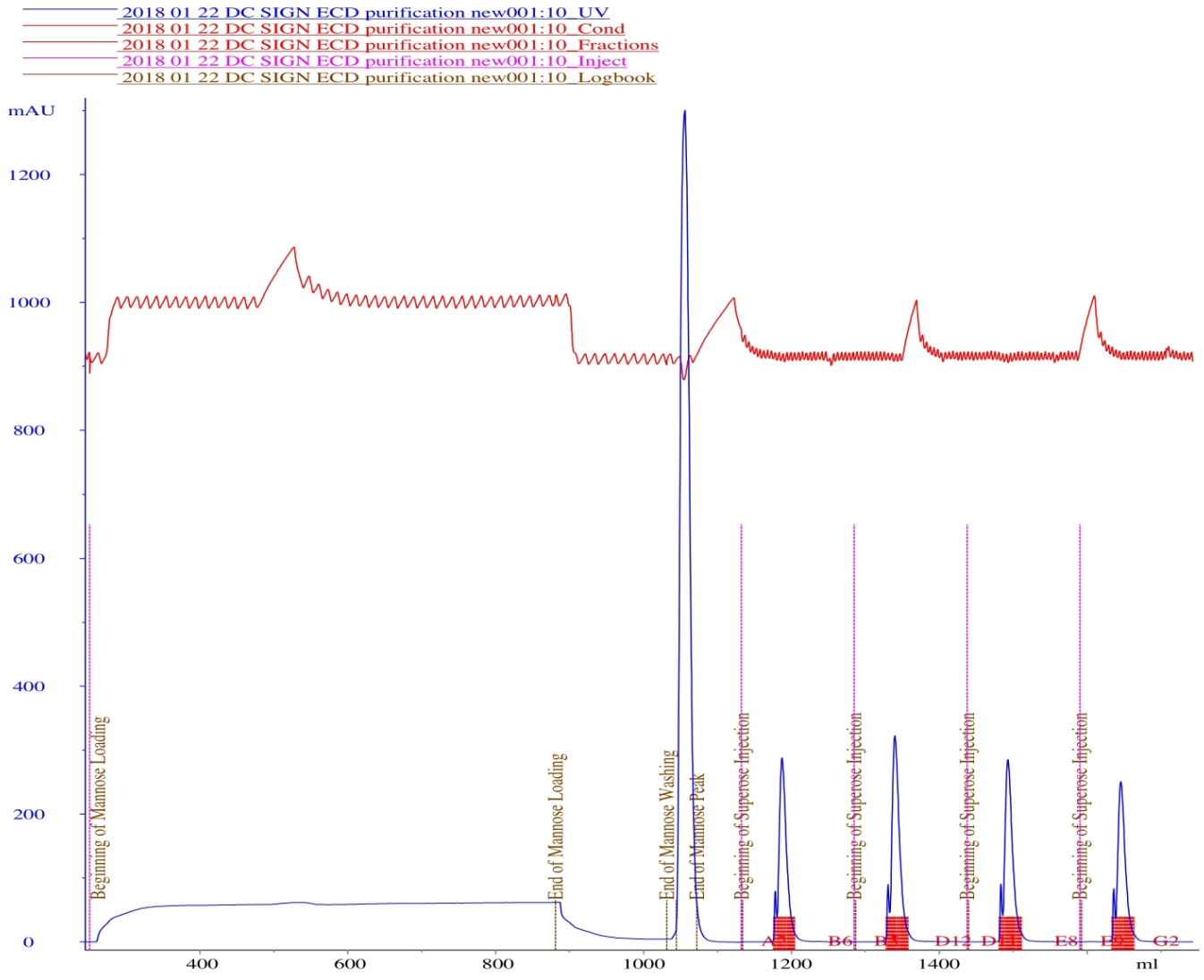
Chromatogram of the automated protocol for purification:

- loading of Mannan-Agarose column.

- washing of Mannan-Agarose column.

- elution of Mannan-Agarose column, with peak at ~1300 mAU, which was loaded into a storage loop and reinjected in fractions of 2mL on gel filtration.

- 4 cycles of gel filtration with injection of 2 mL of sample coming from storage loop.


2018 01 22 DC SIGN ECD purification new001:10_UV
2018 01 22 DC SIGN ECD purification new001:10_Cond
2018 01 22 DC SIGN ECD purification new001:10_Fractions
2018 01 22 DC SIGN ECD purification new001:10_Inject
2018 01 22 DC SIGN ECD purification new001:10_Logbook
mAU
1200
1000
800
600
400
200
0
Beginning of Mannose Loading
End of Mannose Loading
End of Mannose Washing
End of Mannose Peak
Beginning of Superose Injection
Beginning of Superose Injection
Beginning of Superose Injection
Beginning of Superose Injection
A
B6
D12
E8
G2
400
600
800
1000
1200
1400
ml