

Supporting Information

For

‘Clickable’ 2,5-diketopiperazines as scaffolds for ligation of biomolecules: use in A β inhibitor’s assembly

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S1. Kinetic studies of A β ₄₀ fibril formation in presence of DKPs

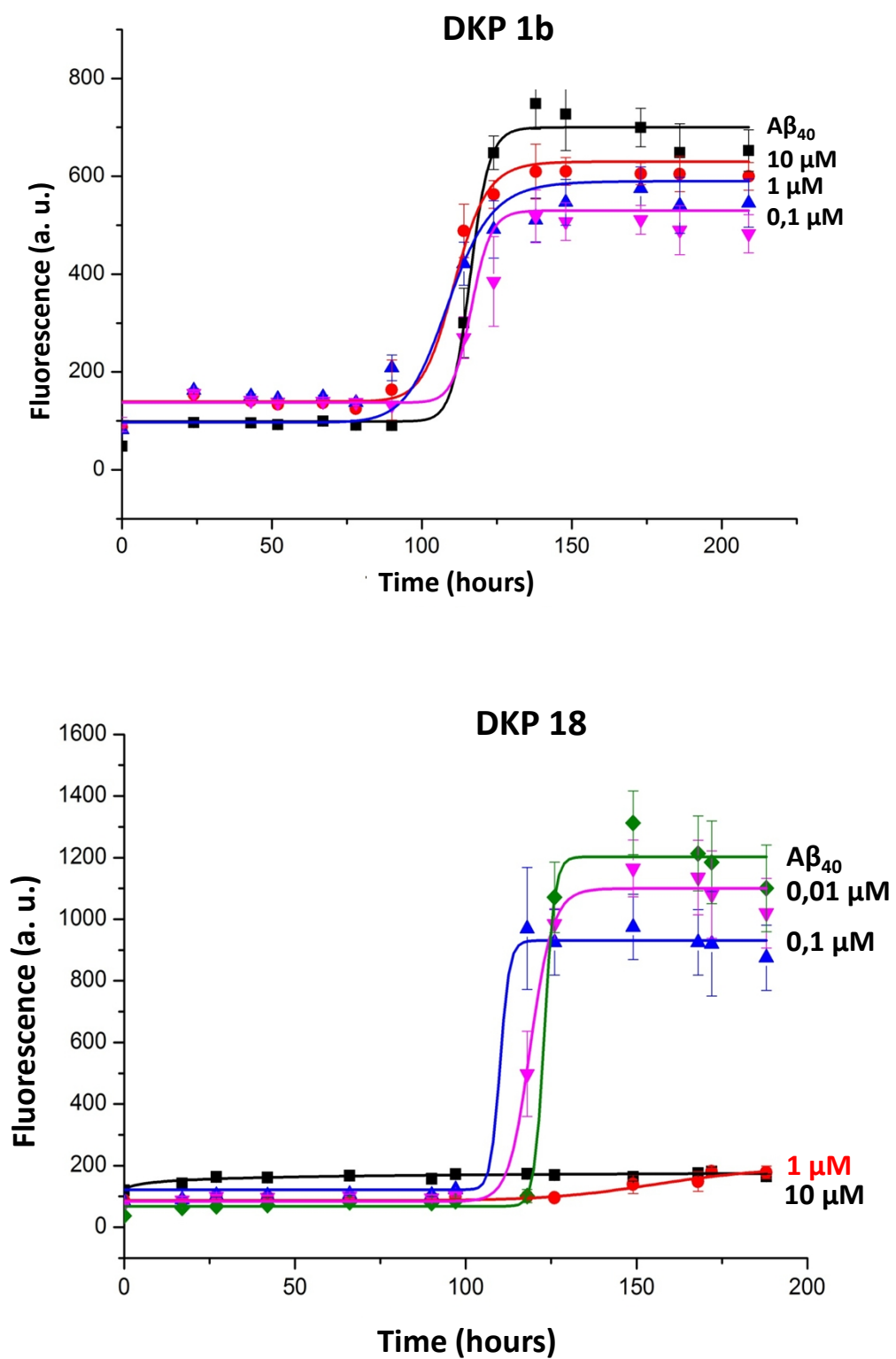
Materials and methods

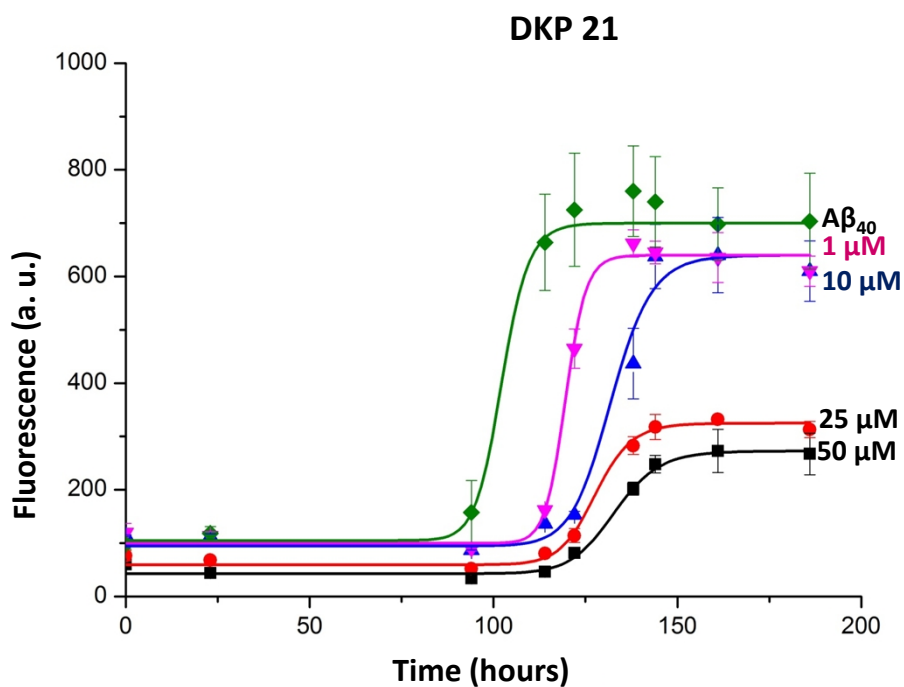
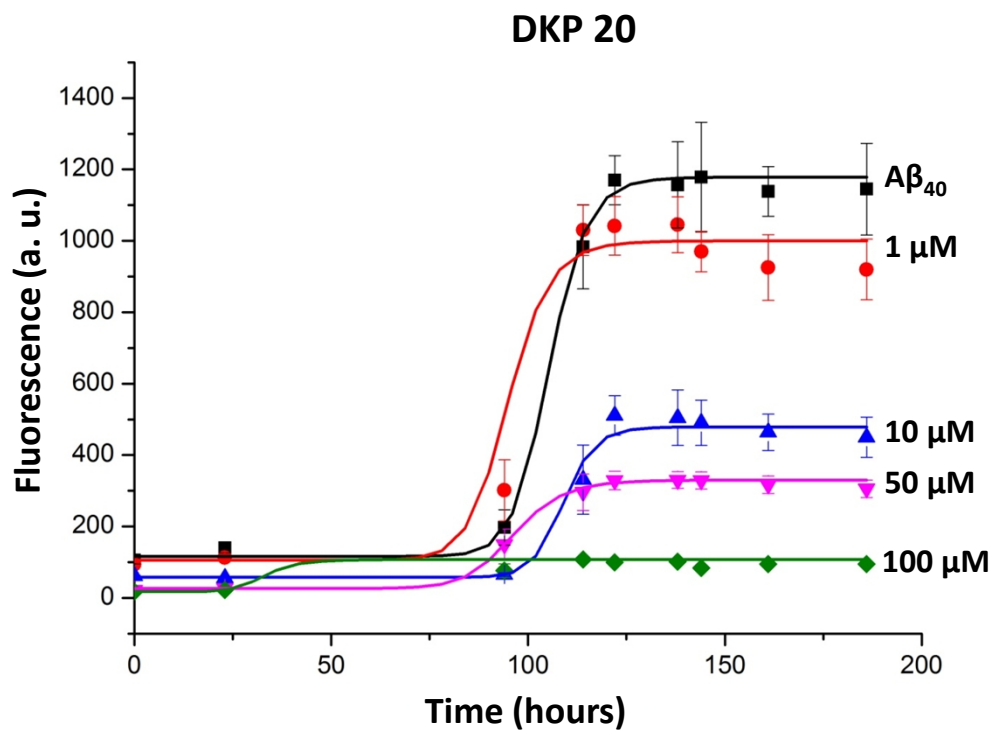
We used for the kinetic assays the same materials and conditions as we have previously described (G. T. Dolphin, S. Chierici, M. Ouberaï, P. Dumy and J. Garcia, *ChemBioChem*, 2008, **9**, 952. These conditions are mentioned below.

Preparation of synthetic A β ₄₀ peptide: A β ₄₀ was synthesized on an Applied Biosystems 433A peptide synthesizer using Fmoc-Val-Novasyn-TGA resin (loading 0.24 mmol/g). The peptide was assembled using standard solid phase methods but coupling reaction times of 60 min were used and difficult residues were coupled twice. Removal of protecting groups and cleavage from the resin were carried out with a mixture of TFA/TIS/H₂O/EDT (94:2:2:2), with swirling for 2 h. After filtration, TFA was removed under *vacuum* and the peptide was precipitated in Et₂O. A β ₄₀ peptide was obtained after purification by RP-HPLC (C5, 214 nm, 10-90% B in 30 min) and lyophilization, and was stored at -20 °C. RP-HPLC (C18, 214 nm, 5-100% solvent B in 20 min) t_R = 12 min. ESI-MS calcd 4328, found 4329.7.

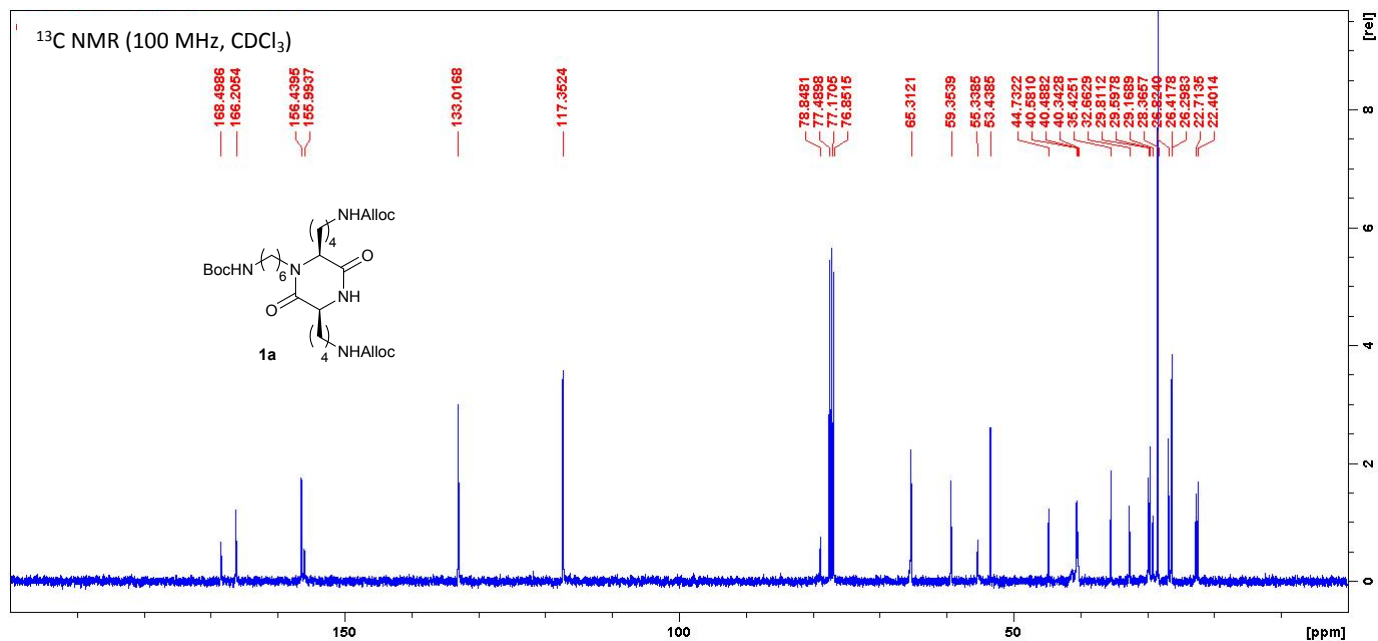
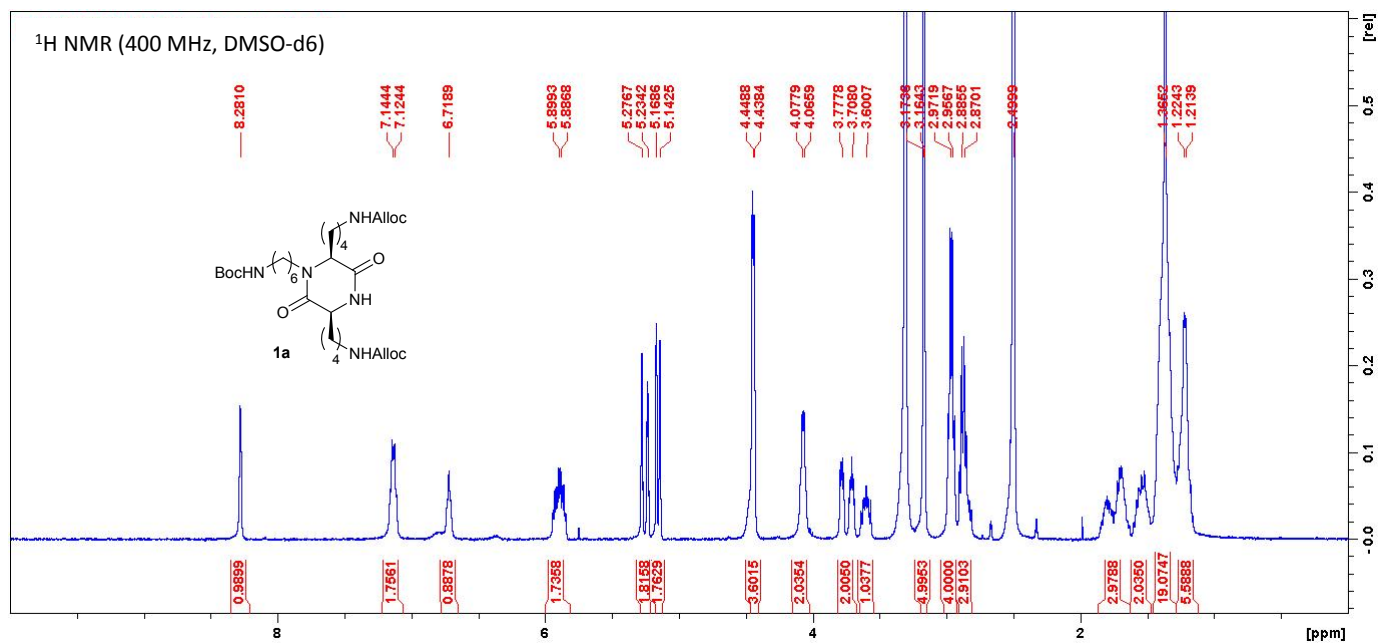
Preparation of inhibitor stock solutions: Inhibitors were dissolved in DMSO/H₂O (1/1). Stock solutions at 5 mM were first prepared, thereafter they were diluted with DMSO/H₂O (1/1) to afford a concentration range of 2.5 mM to 0.5 μ M. Final concentrations of DMSO in inhibition studies were less than 2%.

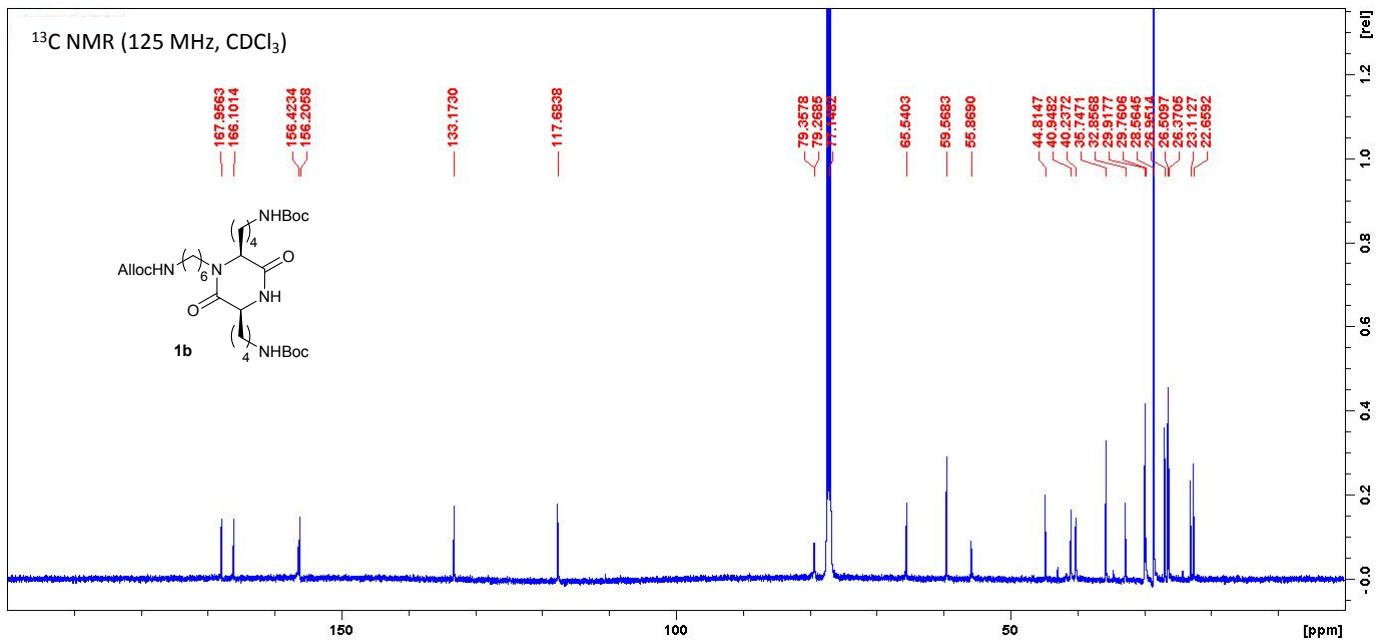
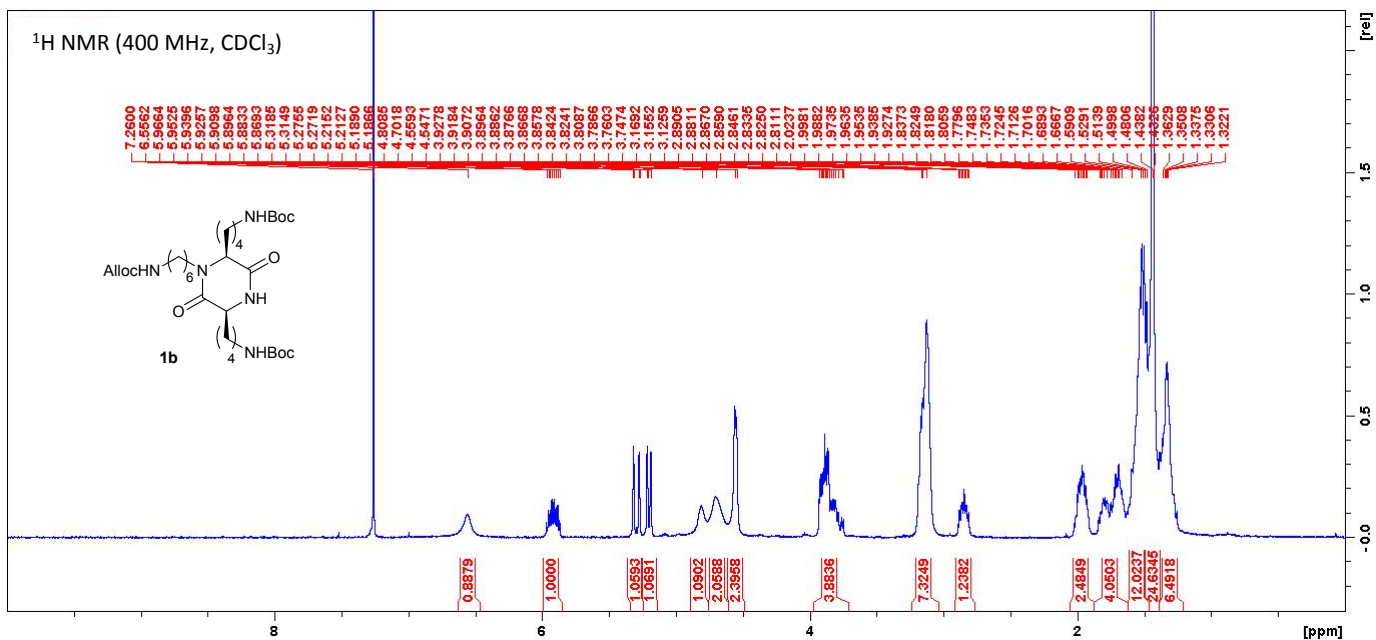
Aggregation measurement of A β ₄₀: A solution of A β ₄₀ was prepared as follows: 2.7 mg were dissolved in 200 μ L of 1,1,1,3,3,3-hexafluoro-2-propanol to disassemble preformed aggregates, thereafter it was lyophilized. One mL of pure water was added to the lyophilized peptide and the solution was centrifuged at 12 000 g to remove eventual aggregates. The concentration of A β ₄₀ was 500 μ M. Aggregation of A β ₄₀ was performed in 96-well black polypropylene microplates (Sterilin). To each well an aliquot of the A β ₄₀ peptide solution was mixed into the aggregation buffer giving a final composition of A β ₄₀ (50 μ M) and ThT (10 μ M) in sodium phosphate (50 mM) and NaCl (100 mM) pH 7.4. Aliquots of 2 μ L of the inhibitor compounds were added, giving the aggregation mixture a total volume of 100 μ L. The microplates were sealed with a plastic sheet and incubated at 37 °C. The ThT fluorescence intensity was recorded once or twice daily using bandpass filters of 445 nm for excitation and 485 nm for emission, and a cutoff filter of 475 nm, using a Molecular Devices Spectra MAX Gemini XS microplate reader. The data are the result of three experiments. Kinetic data were fitted with the stretched exponential function: $F(t)=F(\infty)-\Delta F\exp(-(kt)^n)$, where $F(t)$ is the fluorescence at time t , $F(\infty)$ is the fluorescence after complete fibril formation, ΔF is the difference in fluorescence between $t(0)$ and $t(\infty)$, k is the rate constant, and values larger than 1 for the parameter n indicate a sigmoidal transition with an initial lag-phase.

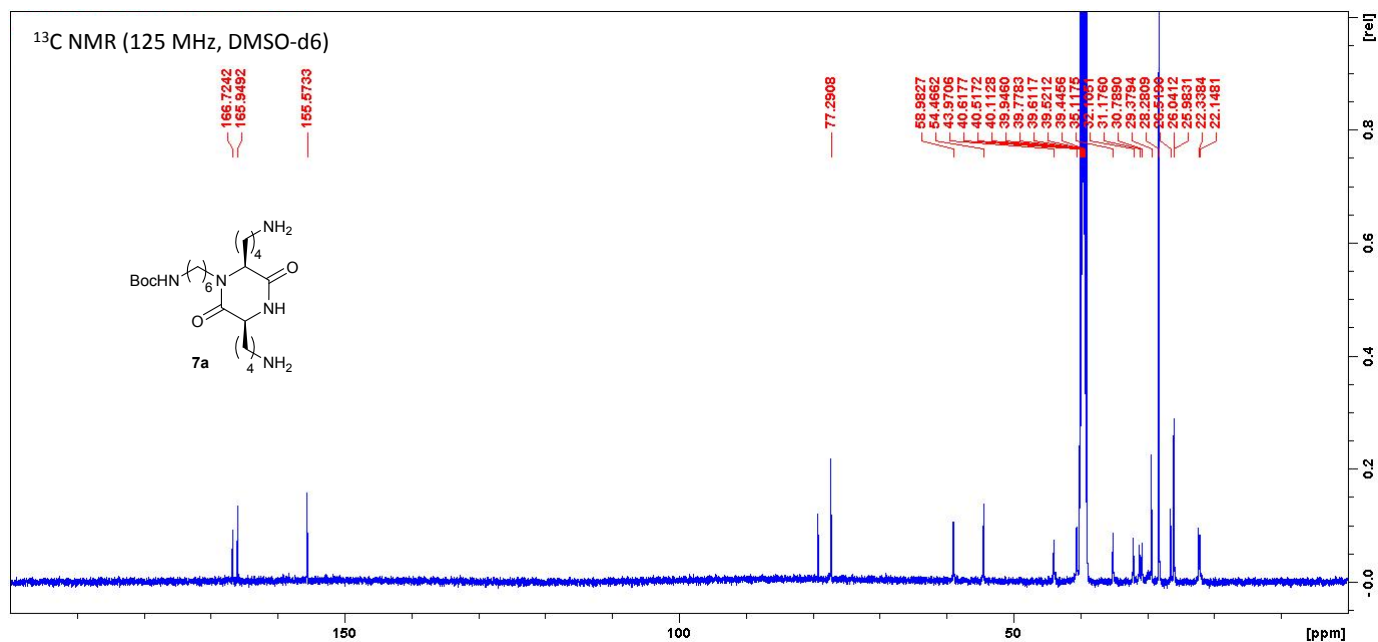
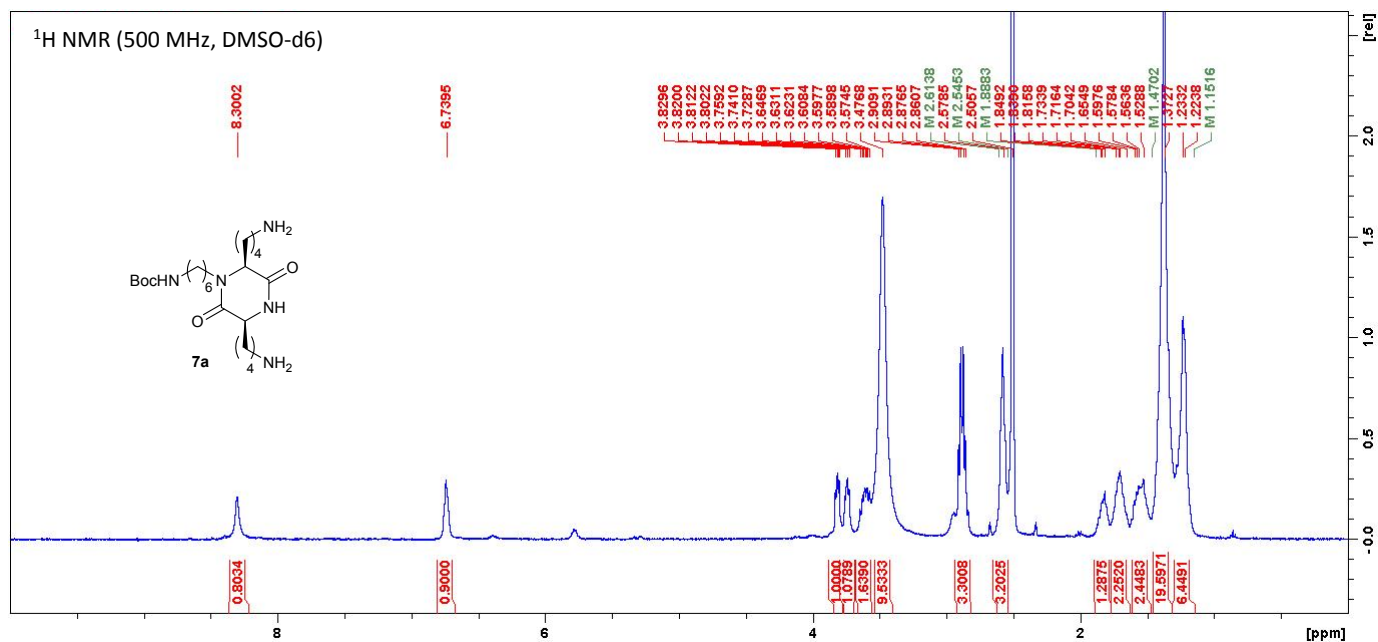


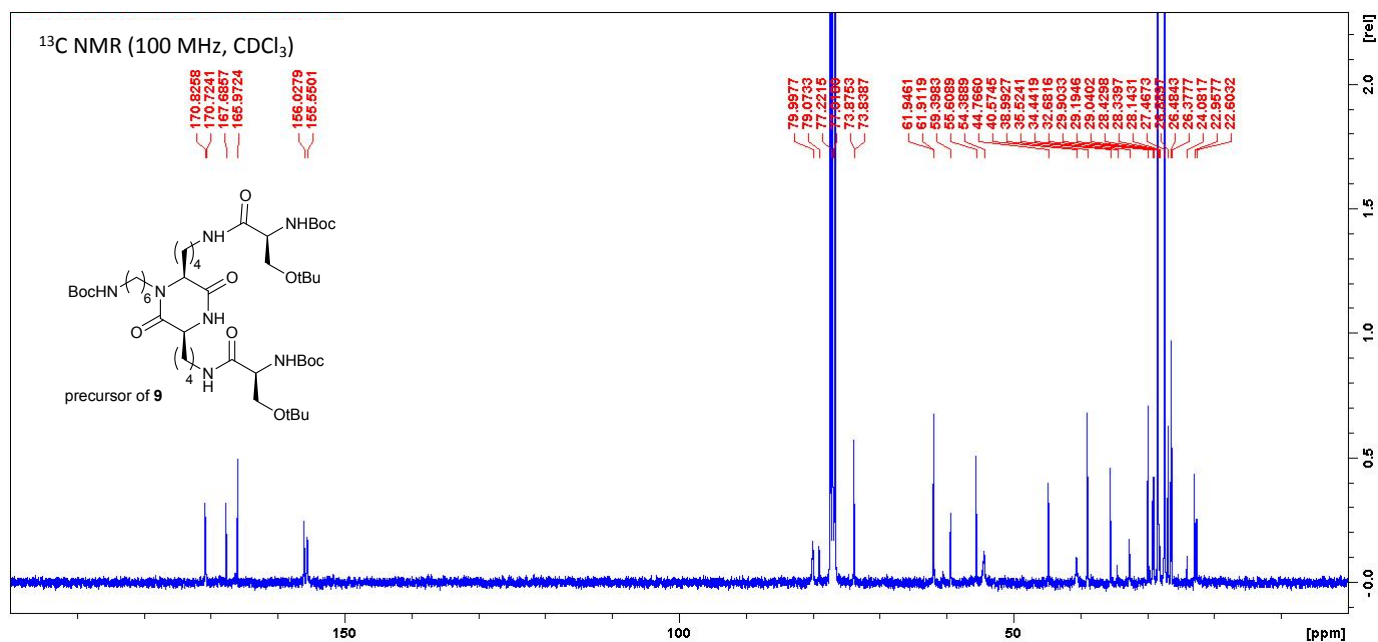
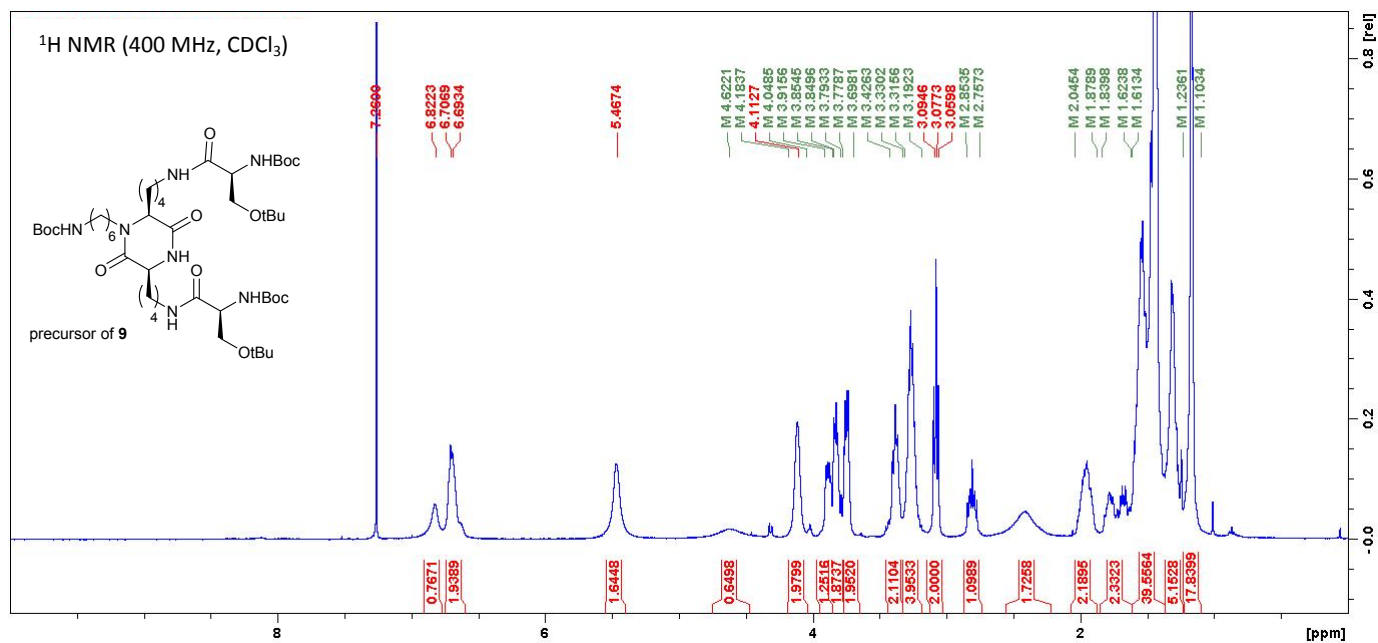


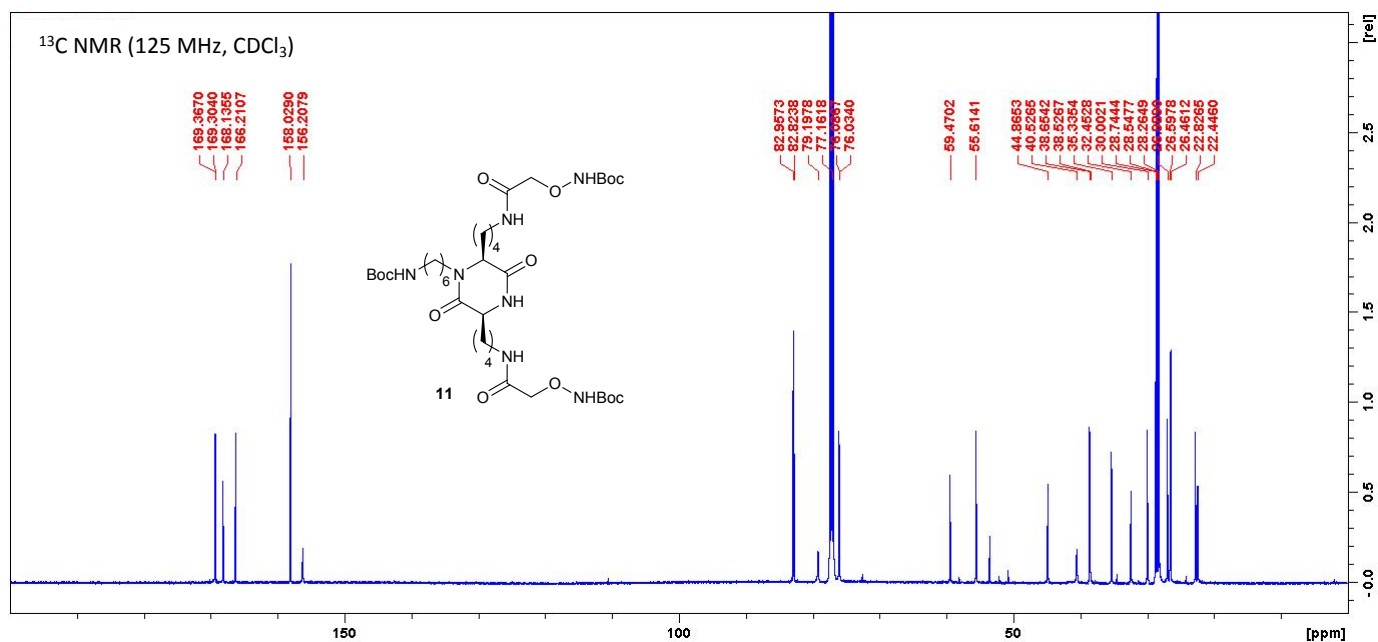
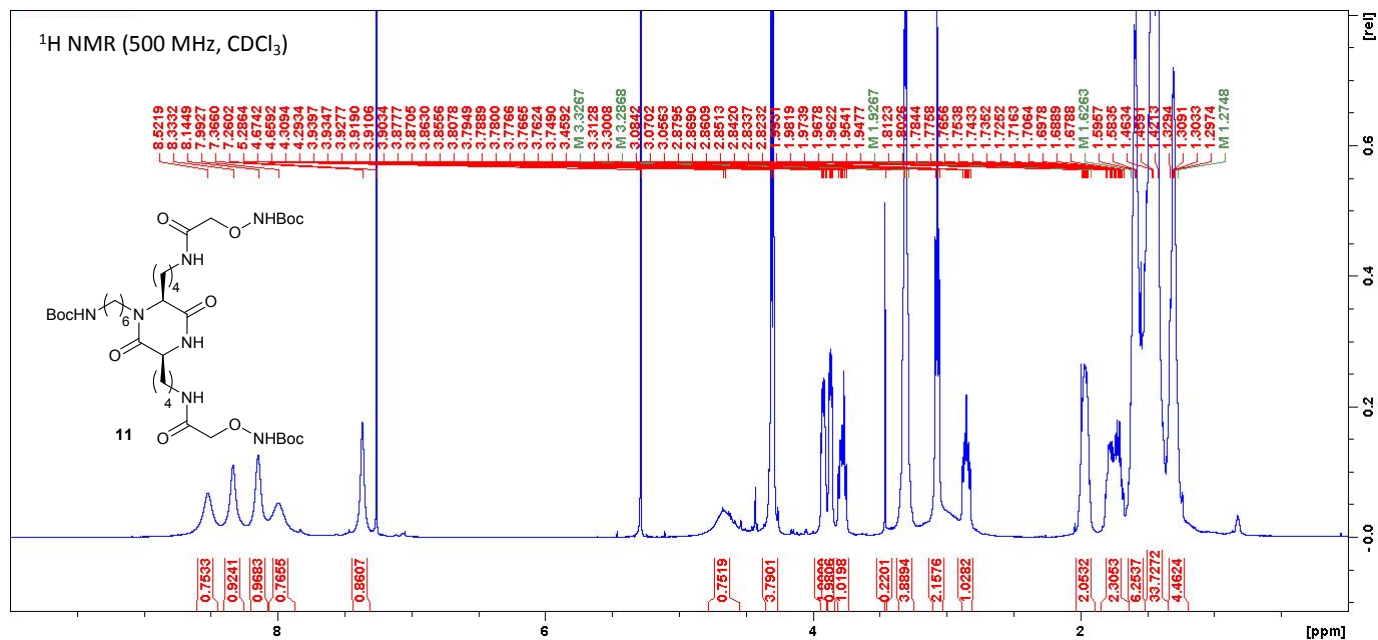
S2. Copies of NMR spectra

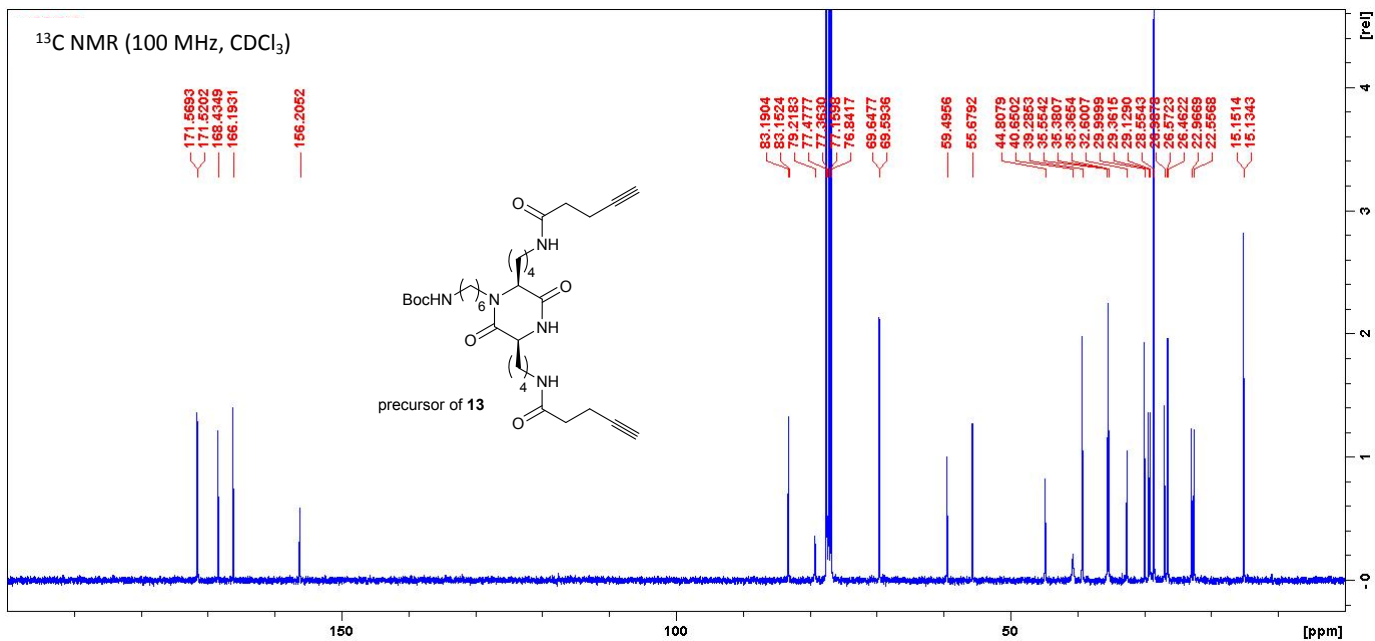
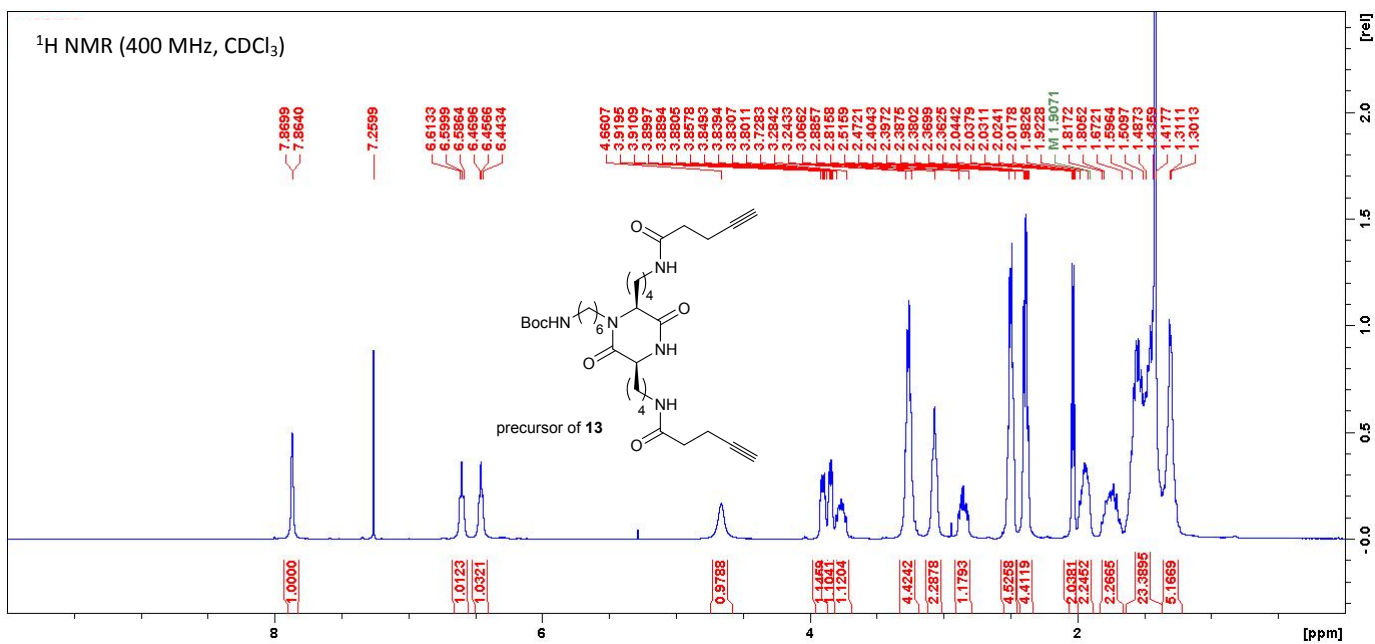


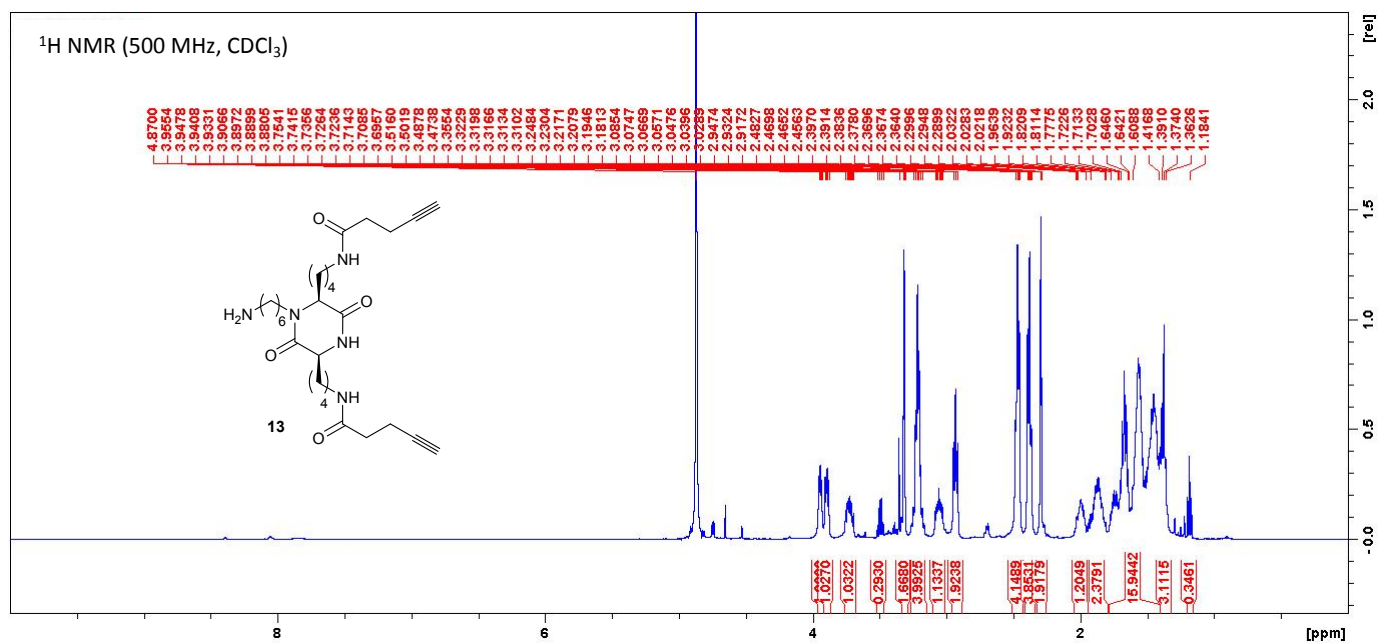


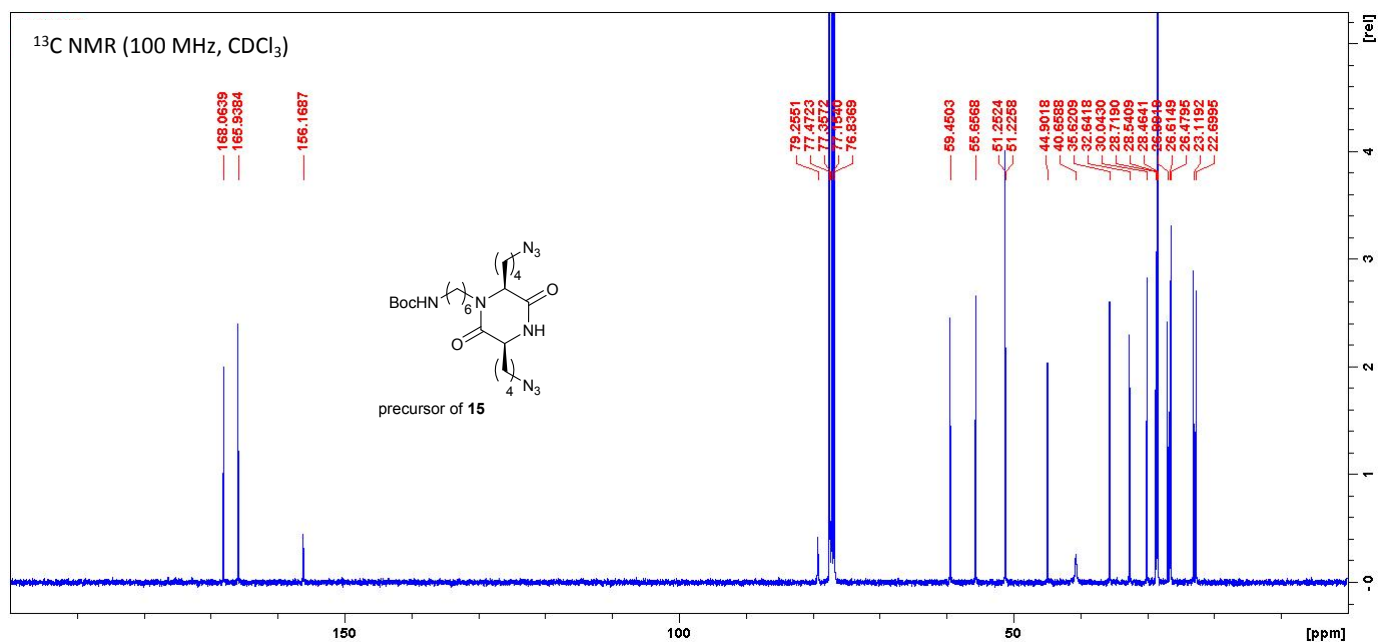
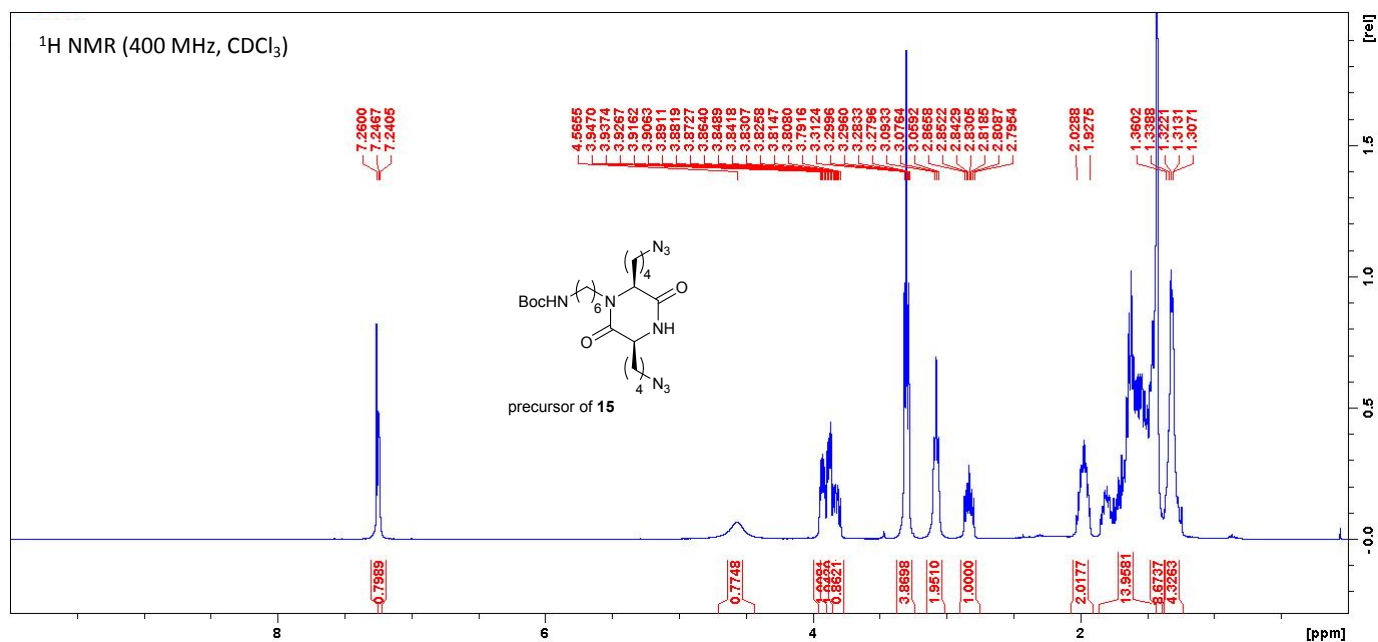


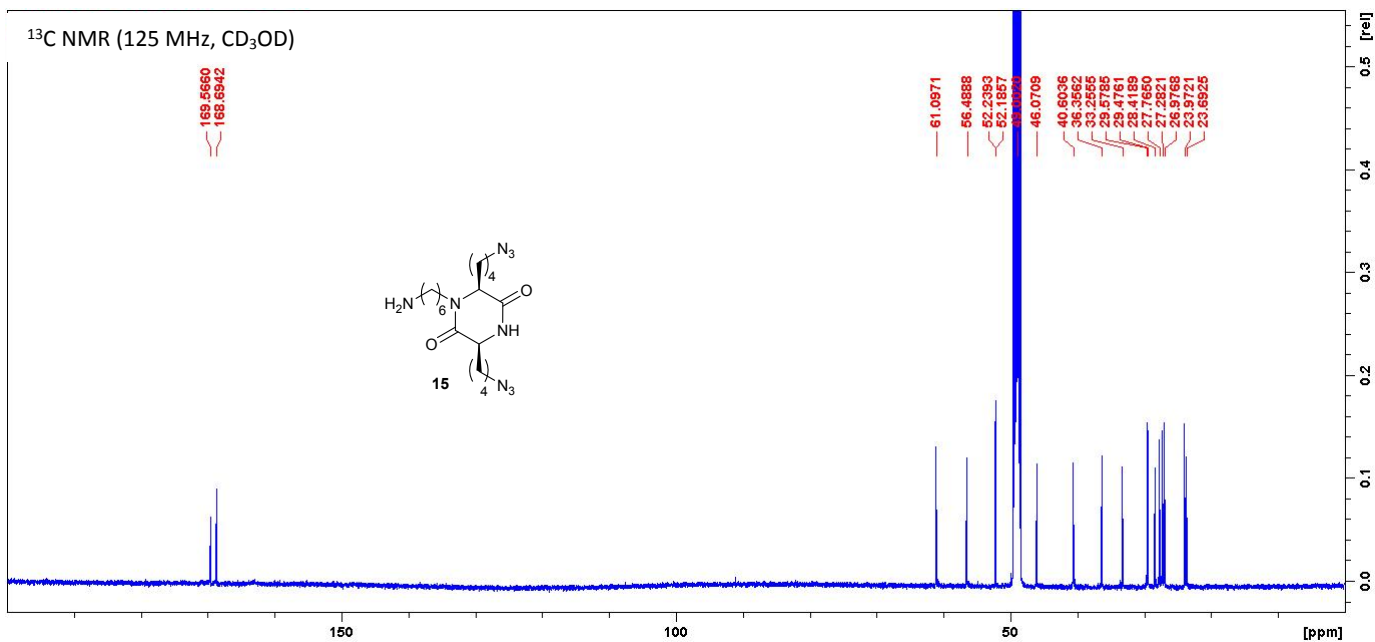
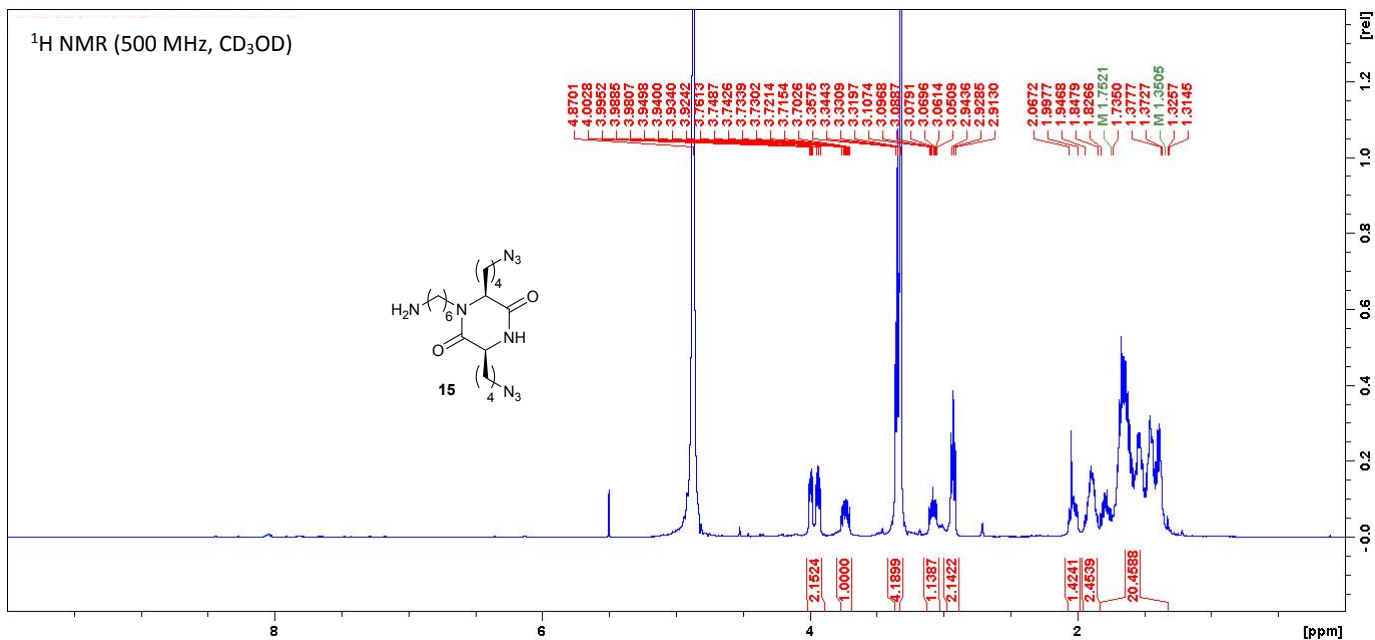


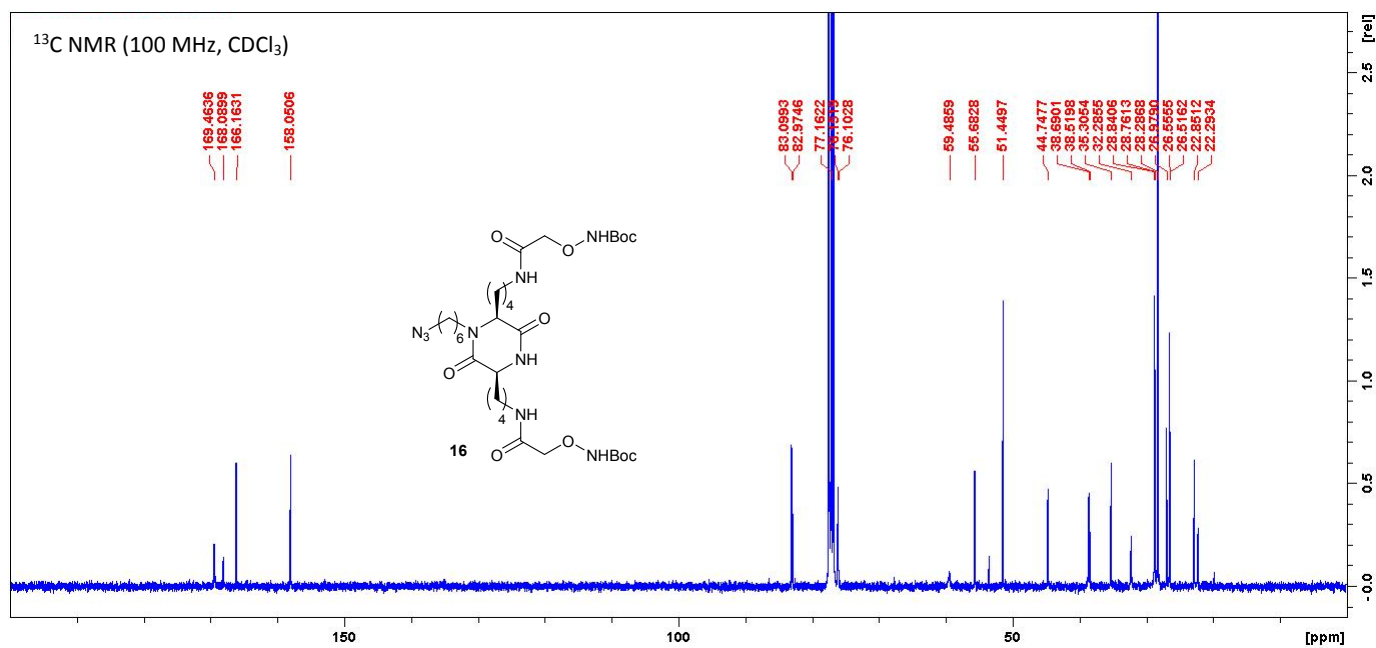
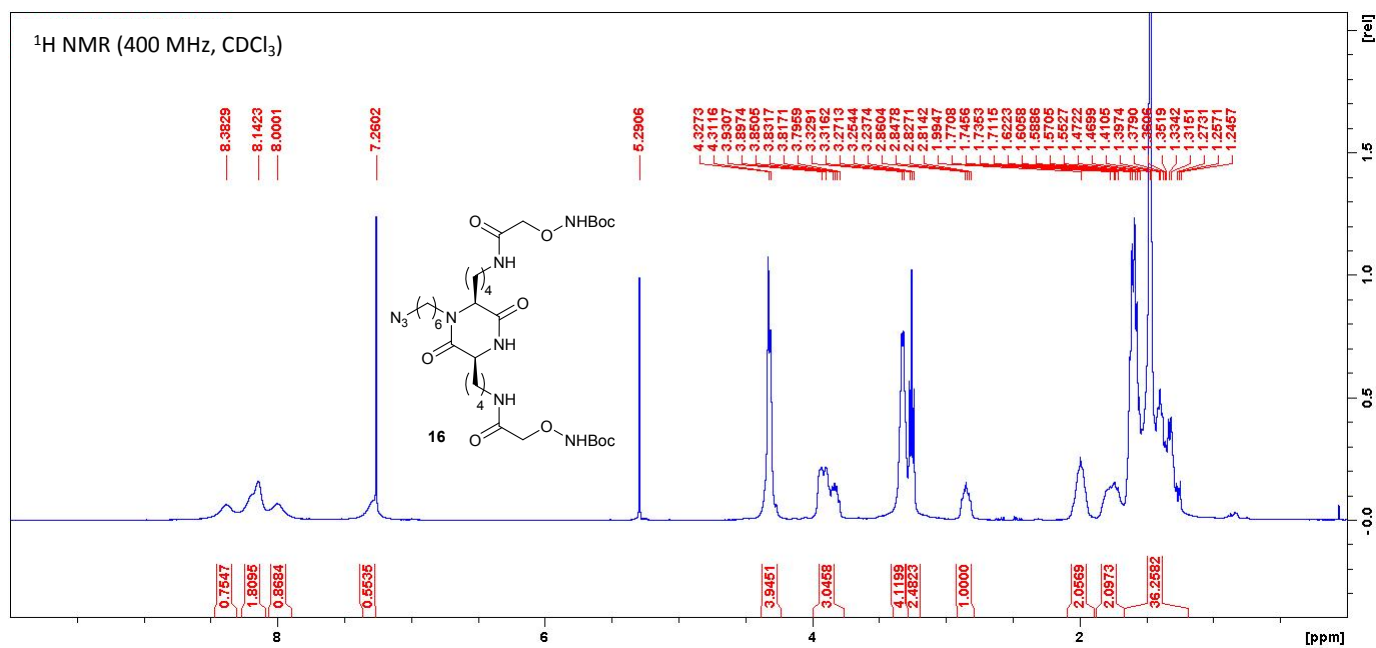






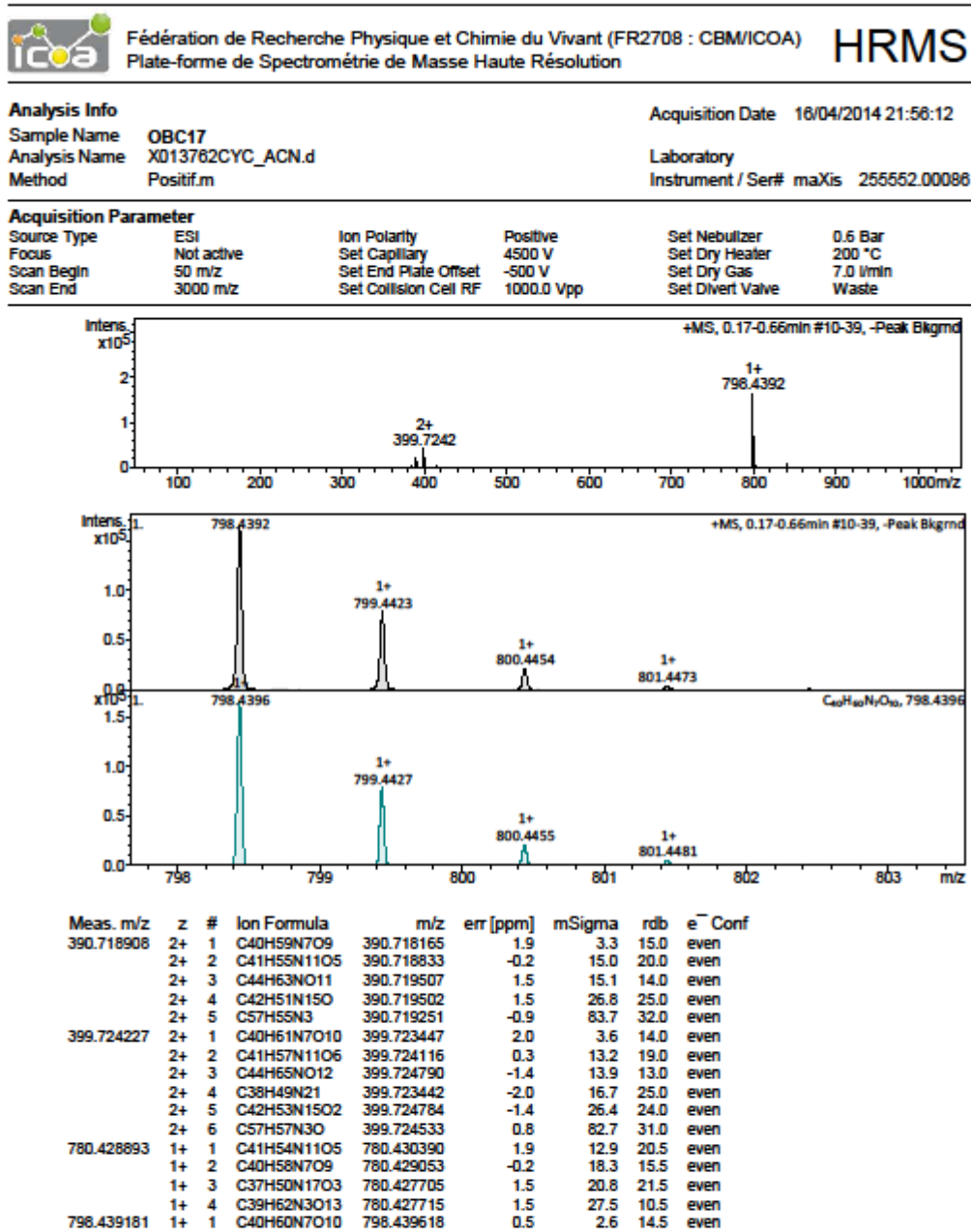






S3. Copies of MS and HRMS spectra

Compound 17, HRMS (ESI)



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Compound **17**, Mass spectra (ESI)

Display Report

Analysis Info

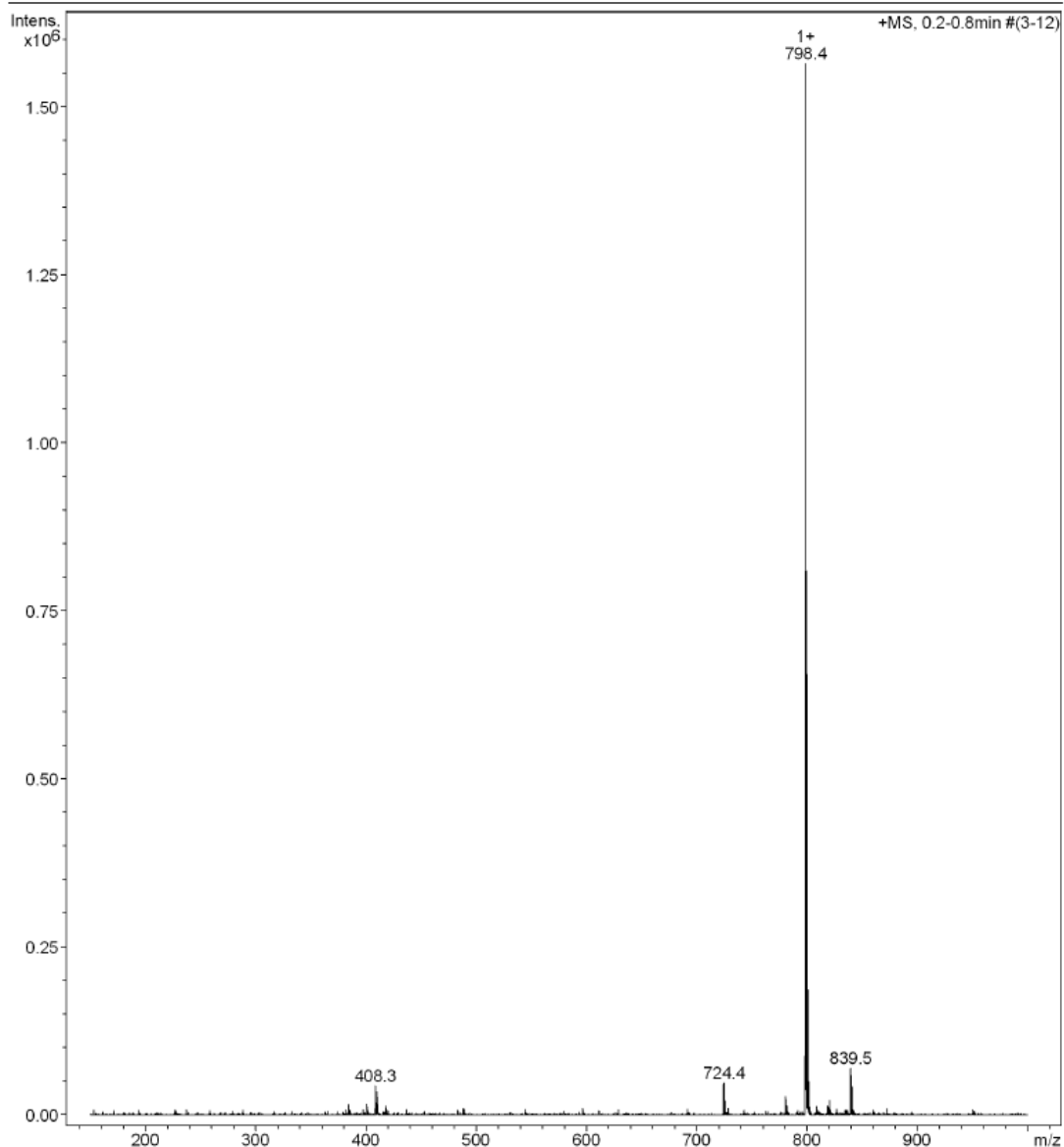
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dilue 1/100 eau/acn/hcooh

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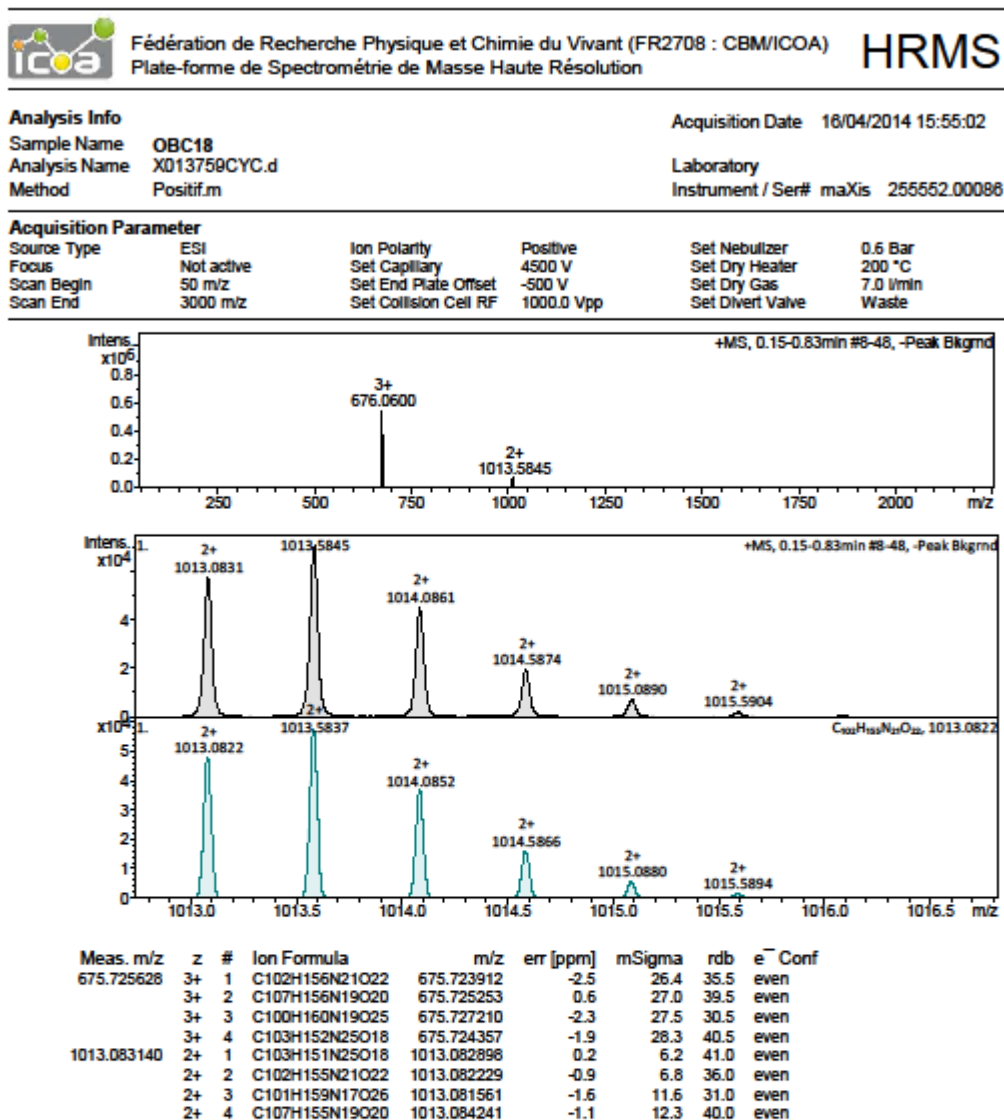
Operator Rodolphe
Instrument esquire3000 plus

Acquisition Parameter

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Mass Range Mode	Std/Enhanced	Scan Begin	150 m/z	Scan End	1000 m/z
Capillary Exit	136.0 Volt	Skim 1	40.0 Volt	Trap Drive	83.1
Accumulation Time	511 μ s	Averages	20 Spectra	Auto MS/MS	off



Compound **18**, HRMS (ESI)



Compound **18**, Mass spectra (ESI)

Mass Spectrum Deconvolution Report

Analysis Info

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Method Standby.m
Sample Name emilie dufour
Comment edufB39 tr=15.9

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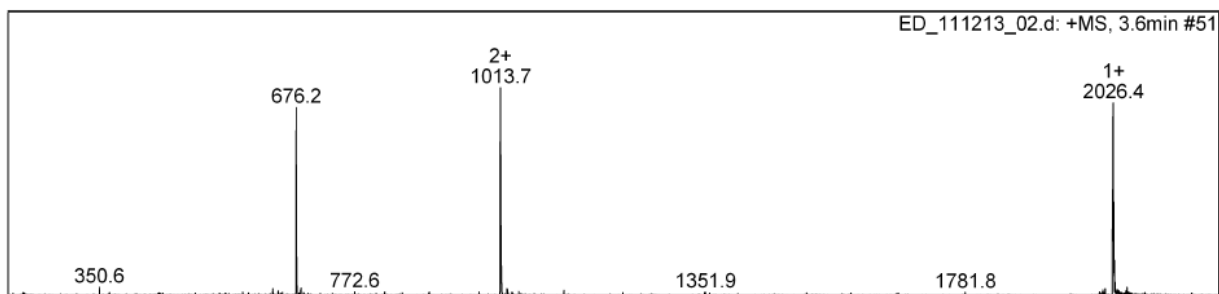
Operator Rodolphe
Instrument esquire3000 plus

Acquisition Parameter

Ion Source Type ESI
Mass Range Mode Std/Normal
Capillary Exit 151.0 Volt
Accumulation Time 42 µs

Ion Polarity Positive
Scan Begin 200 m/z
Skim 1 40.0 Volt
Averages 20 Spectra

Alternating Ion Polarity off
Scan End 2200 m/z
Trap Drive 101.1
Auto MS/MS off



Component	Molecular Mass	Molecule	Absolute Abundance	Relative Abundance
A	2025.4	2026.7 [M + H] ⁺	5242157	100.00

Component A Detail

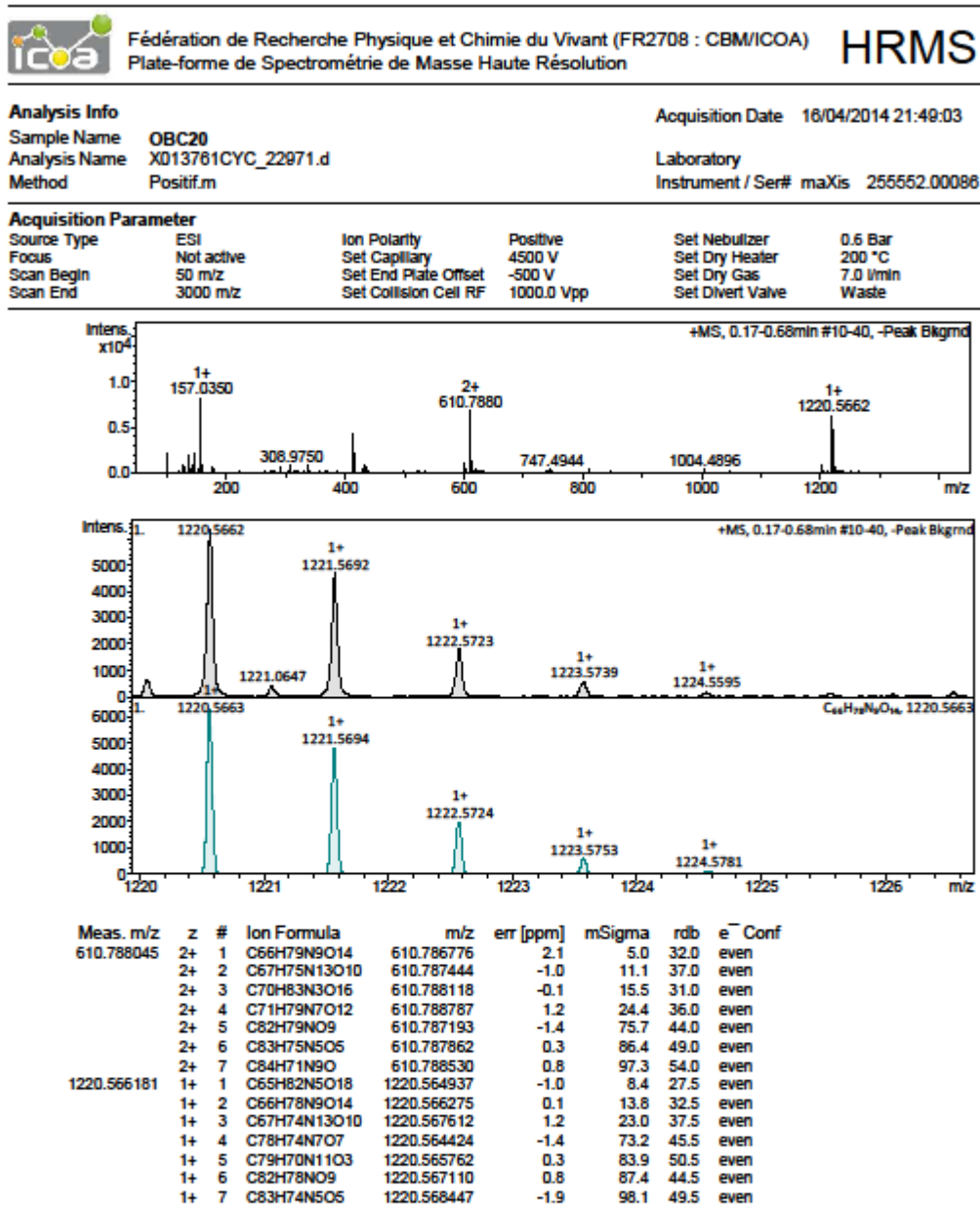
Actual Peak	Charge	Isotopic Mass ([M + H] ⁺)	Predicted Peak
1013.3	2+	2025.5	1013.2
1013.7	2+	2026.4	1013.7
1014.2	2+	2027.3	1014.2
1014.7	2+	2028.3	1014.7
1015.2	2+	2029.4	1015.2
1015.6	2+	2030.3	1015.7
1016.2	2+	2031.4	1016.2
1016.6	2+	2032.2	1016.7
2025.5	1+	2025.5	2025.4
2026.4	1+	2026.4	2026.4
2027.3	1+	2027.3	2027.4
2028.3	1+	2028.3	2028.4
2029.4	1+	2029.4	2029.4

Molecular Mass ([M + H]⁺): 2025.4
Average Mass ([M + H]⁺): 2026.7

Std. Deviation: 0.0918918

Compound **20**, HRMS (ESI)

For this analysis, an available solution of 20 at 500 µM in a water/DMSO mixture has been used justifying the background at low mass



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Compound **20**, Mass spectra (ESI)

Mass Spectrum Deconvolution Report

Analysis Info

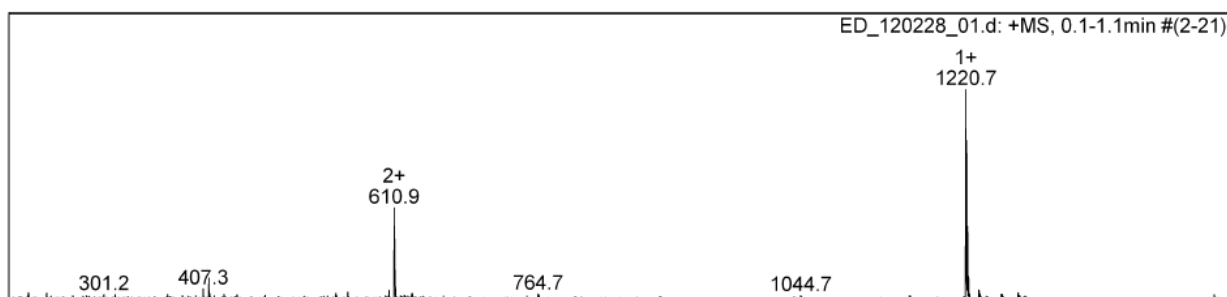
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Comment edufB70 tr=20.4

Acquisition Date 2/28/2012 9:27:47 AM

Operator Laure F
Instrument esquire3000 plus

Acquisition Parameter

Ion Source Type	ESI	Ion Polarity	Positive	Alternating Ion Polarity	off
Mass Range Mode	Std/Normal	Scan Begin	200 m/z	Scan End	1500 m/z
Capillary Exit	163.0 Volt	Skim 1	40.0 Volt	Trap Drive	117.0
Accumulation Time	860 µs	Averages	20 Spectra	Auto MS/MS	off



Component	Molecular Mass	Molecule	Absolute Abundance	Relative Abundance
A	1220.7	1221.6	[M + H] ⁺	955211
B	413.4	413.8	[M + H] ⁺	67748

Component A Detail

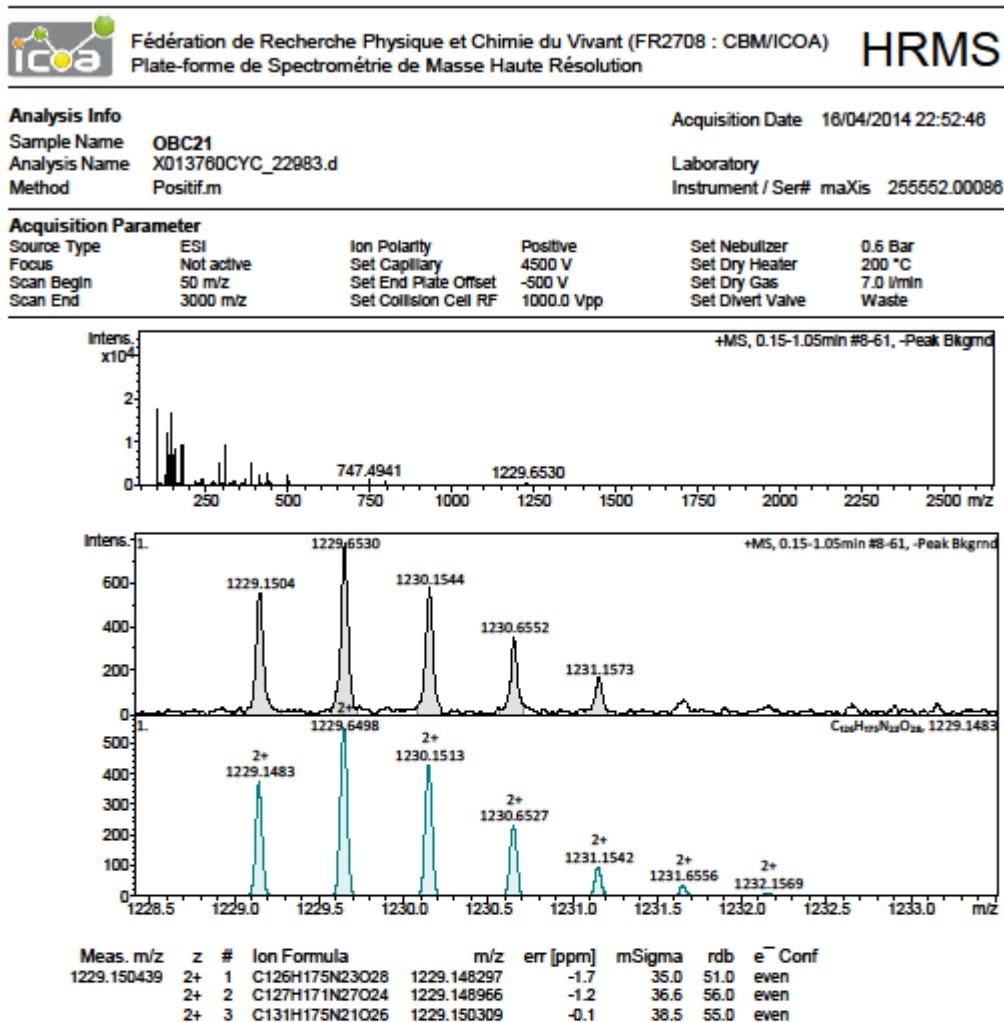
Actual Peak	Charge	Isotopic Mass ([M + H] ⁺)	Predicted Peak
610.9	2+	1220.8	610.9
611.4	2+	1221.8	611.4
611.9	2+	1222.8	611.9
612.4	2+	1223.8	612.4
612.8	2+	1224.7	612.9
613.4	2+	1225.8	613.4
1220.7	1+	1220.7	1220.7
1221.7	1+	1221.7	1221.7
1222.7	1+	1222.7	1222.7
1223.7	1+	1223.7	1223.7
1224.7	1+	1224.7	1224.8
1225.7	1+	1225.7	1225.8
1227.0	1+	1227.0	1226.8

Molecular Mass ([M + H]⁺): 1220.7
Average Mass ([M + H]⁺): 1221.6

Std. Deviation: 0.0968051

Compound **21**, HRMS (ESI)

For this analysis, an available solution of 21 at 500 µM in a water/DMSO mixture has been used justifying the background at low mass



Compound **21**, Mass spectra (ESI)

Mass Spectrum Deconvolution Report

Analysis Info

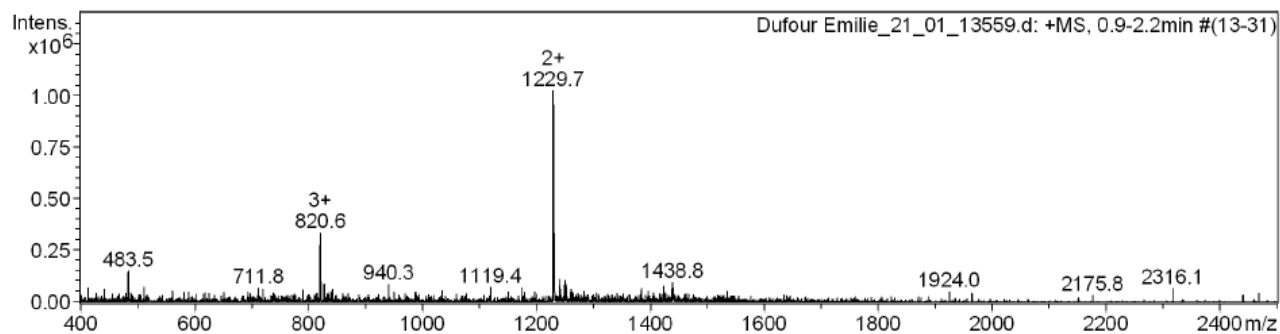
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conc hplc

Acquisition Date 6/14/2012 11:28:30 AM

Operator LF
Instrument esquire3000 plus

Acquisition Parameter

Ion Source Type	ESI	Ion Polarity	Positive	Alternating Ion Polarity	off
Mass Range Mode	Std/Normal	Scan Begin	400 m/z	Scan End	2500 m/z
Capillary Exit	163.0 Volt	Skim 1	40.0 Volt	Trap Drive	122.4
Accumulation Time	746 µs	Averages	20 Spectra	Auto MS/MS	off



Component	Molecular Mass	Molecule	Absolute Abundance	Relative Abundance
A	2457.4	2458.9 [M + H] ⁺	1311460	100.00

Component A Detail

Actual Peak	Charge	Isotopic Mass ([M + H] ⁺)	Predicted Peak
820.0	3+	2458.0	820.2
820.2	3+	2458.6	820.2
820.6	3+	2459.7	820.5
1229.2	2+	2457.4	1229.2
1229.7	2+	2458.4	1229.7
1230.2	2+	2459.5	1230.2
1230.7	2+	2460.5	1230.7
1231.1	2+	2461.3	1231.2

Molecular Mass ([M + H]⁺): 2457.4 Std. Deviation: 0.202472
Average Mass ([M + H]⁺): 2458.9