

Propargylation of CoQ0 through the Redox Chain Reaction

Robert Pawlowski, Maciej Stodulski*, and Jacek Mlynarski*

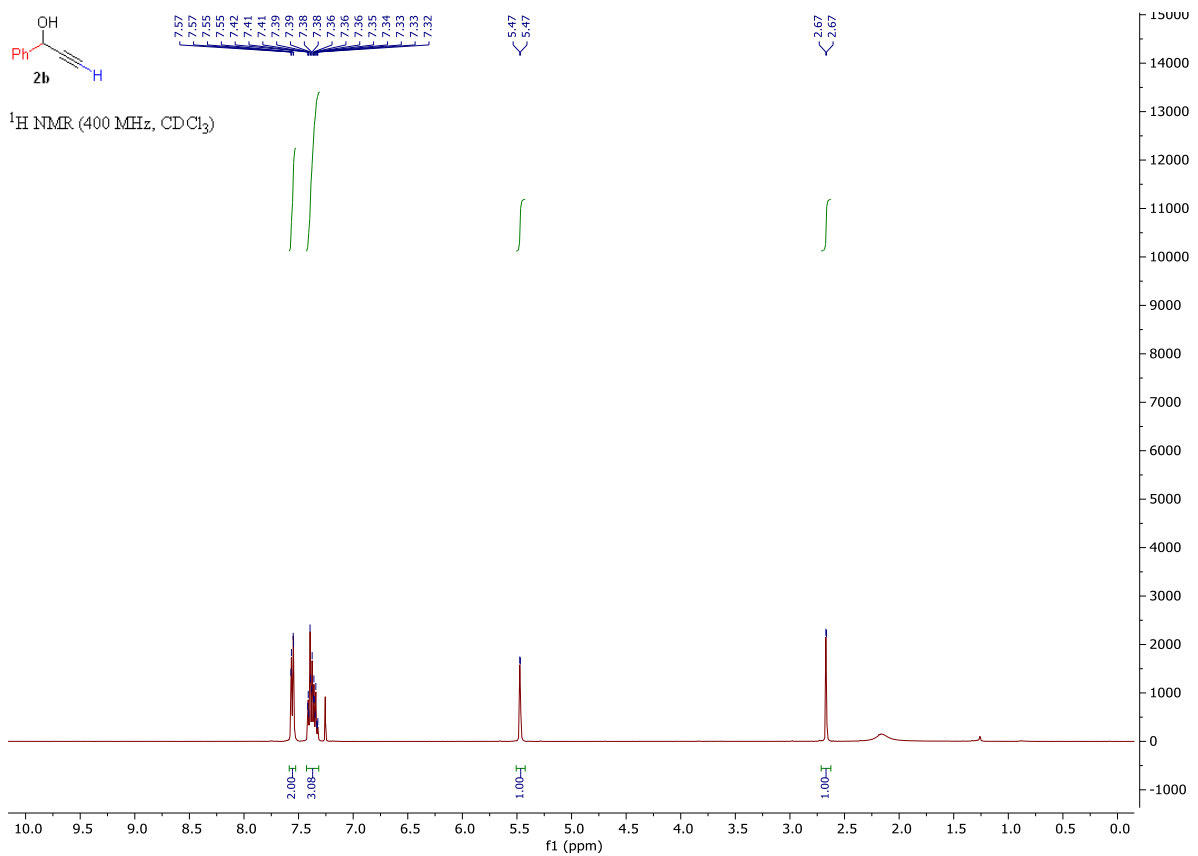
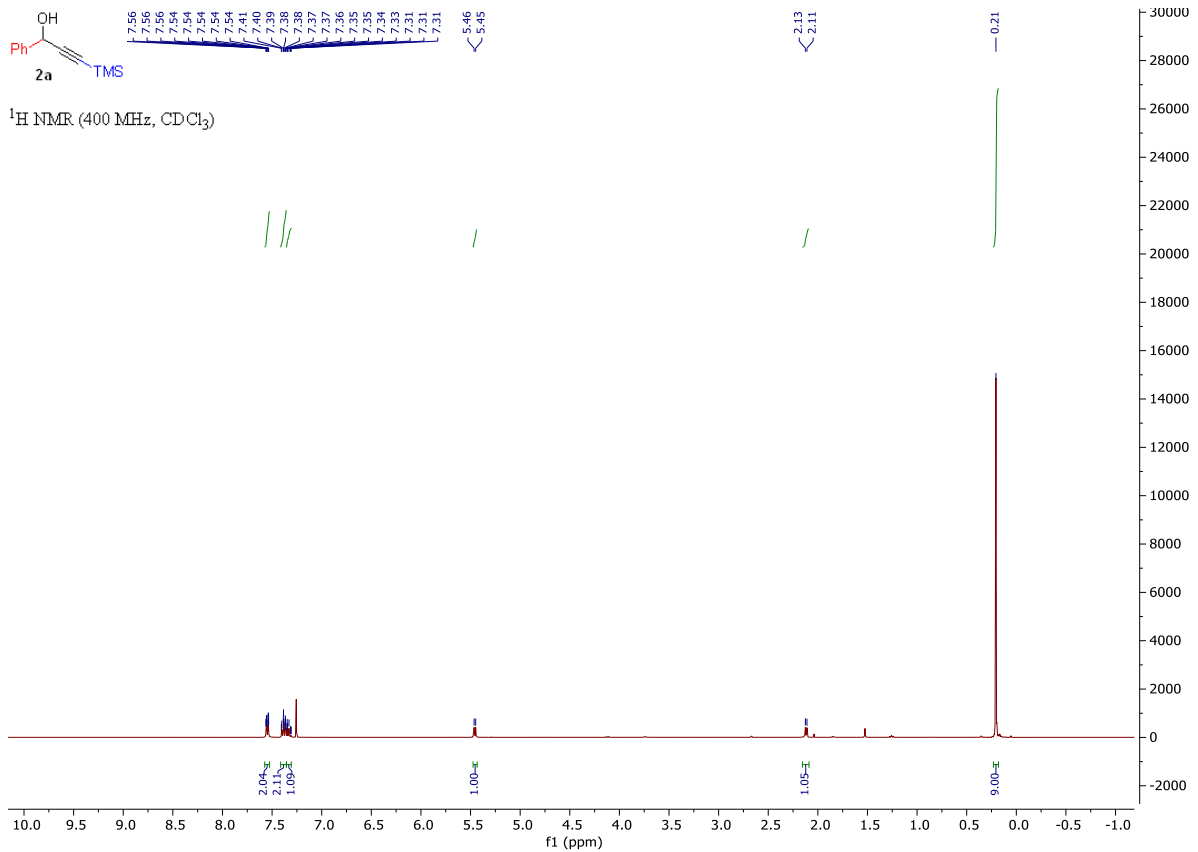
Institute of Organic Chemistry, Polish Academy of Sciences, Kasprzaka 44/52, 01-224 Warsaw, Poland

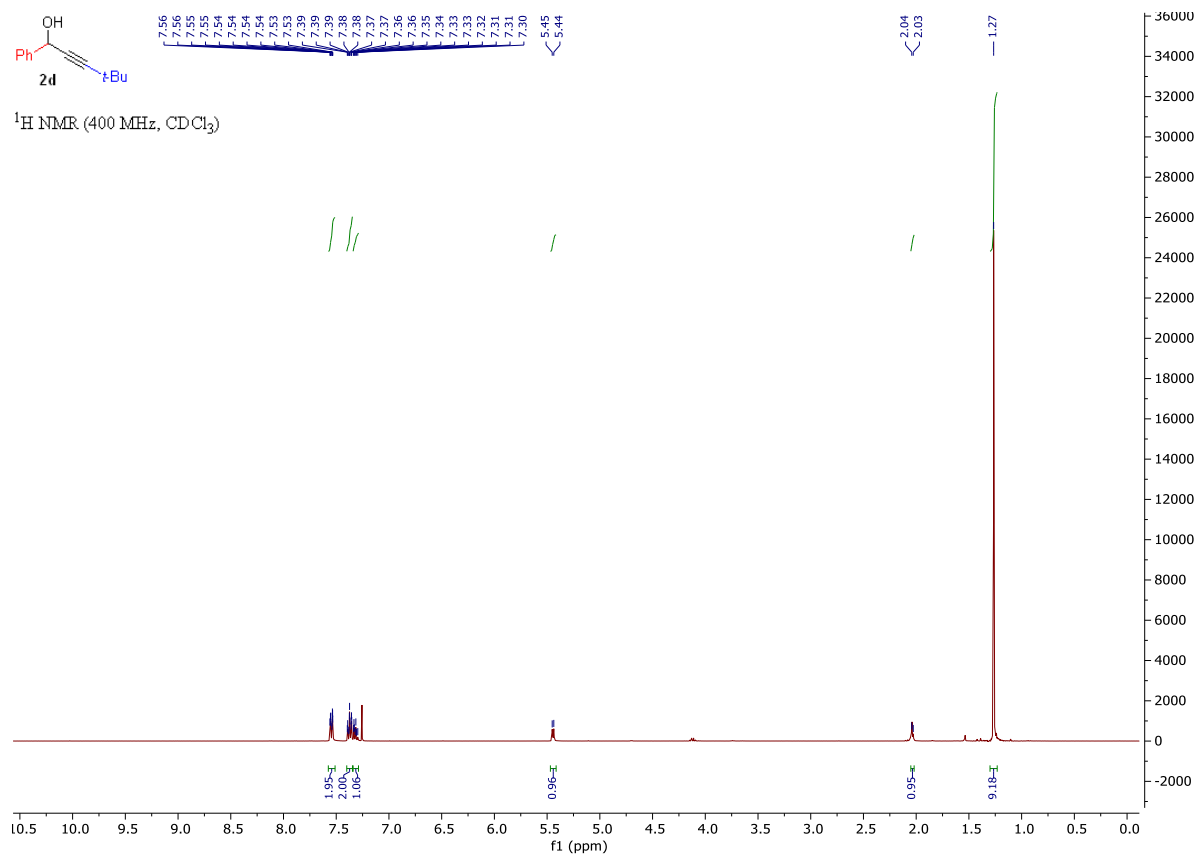
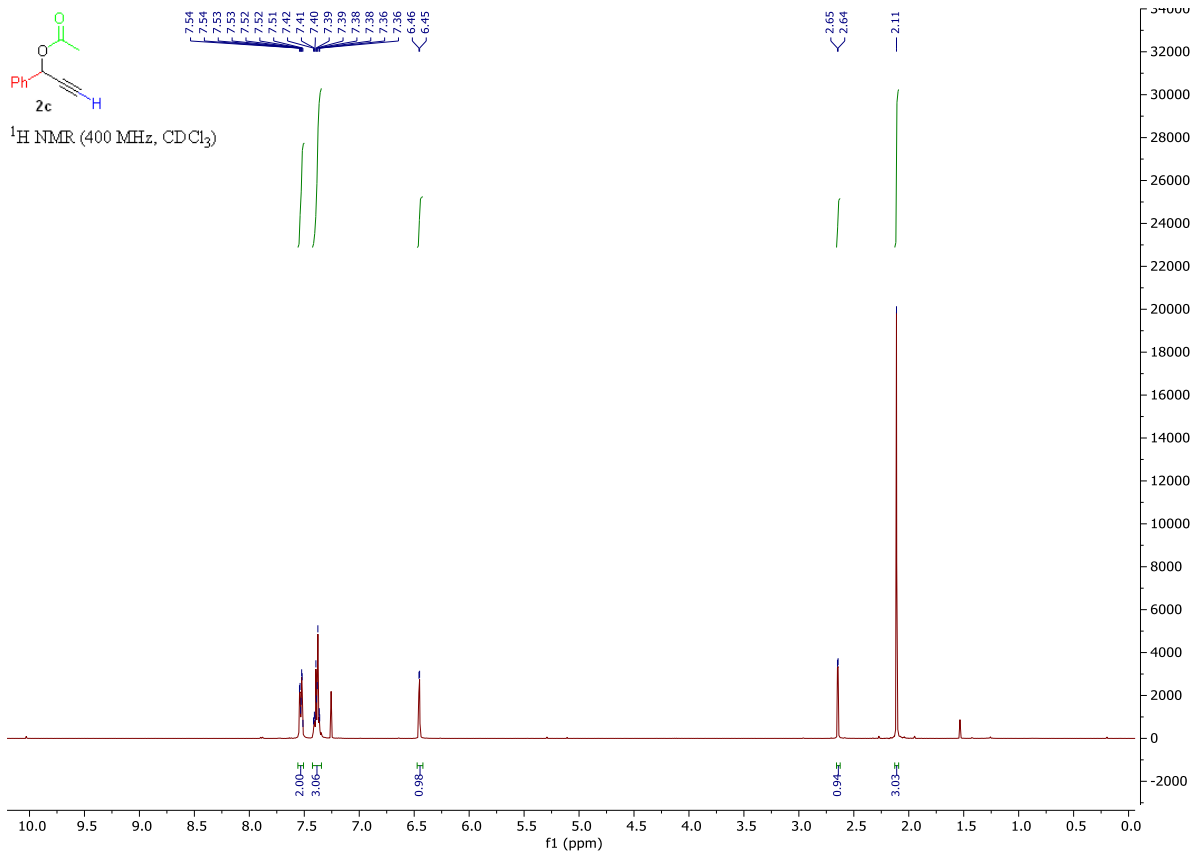
Supporting Information

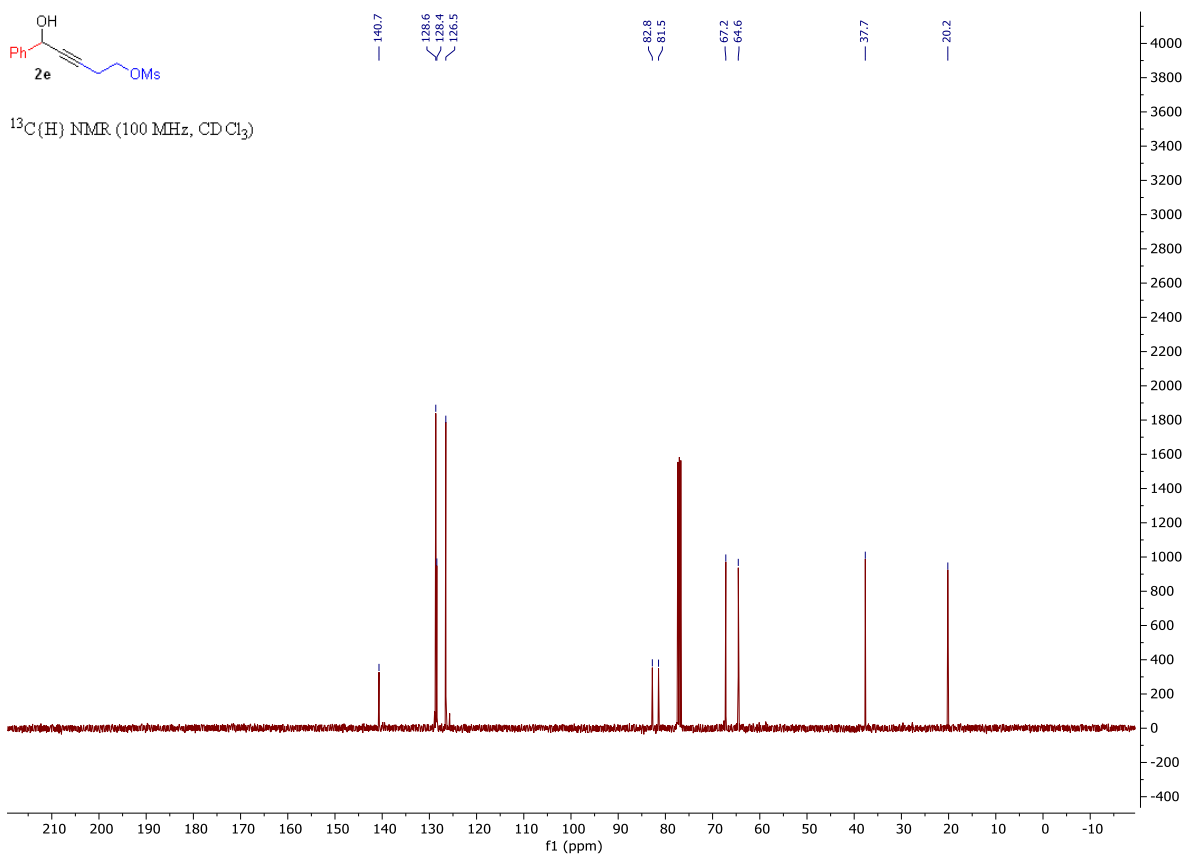
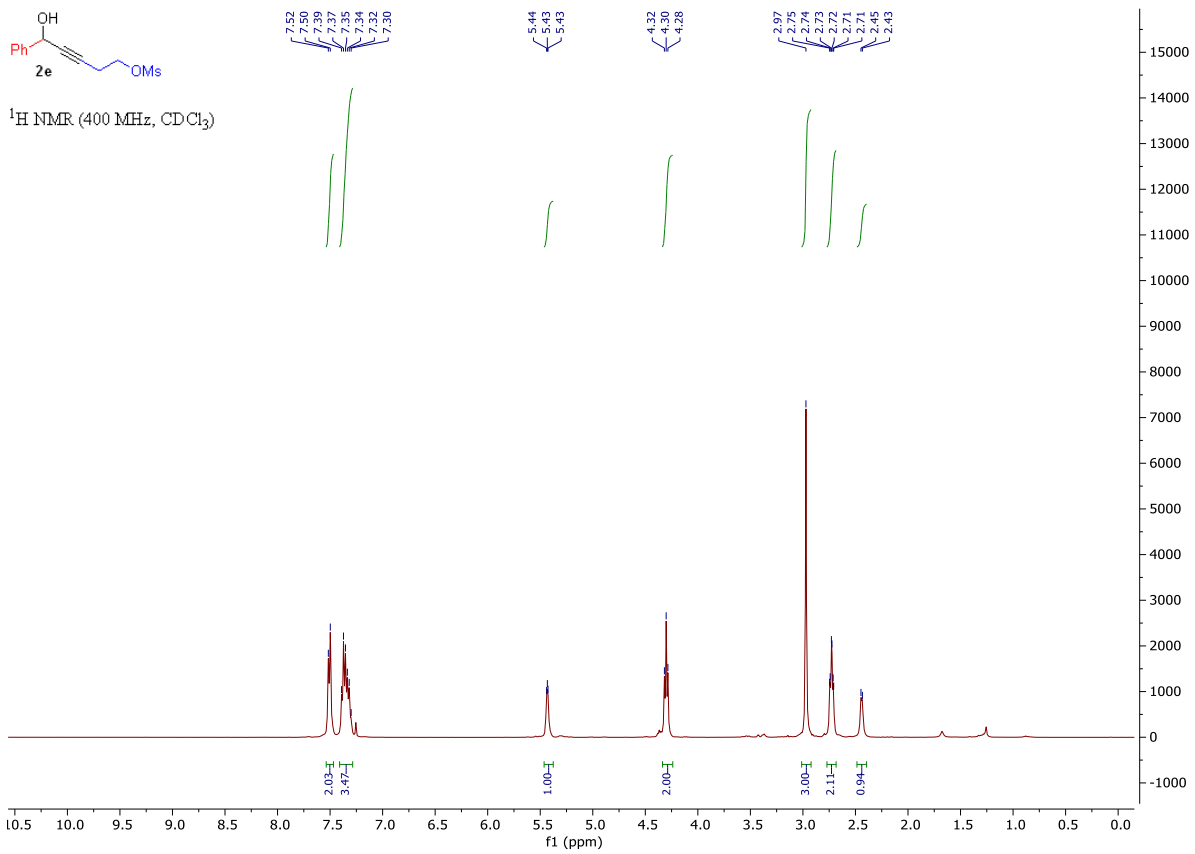
Table of Contents

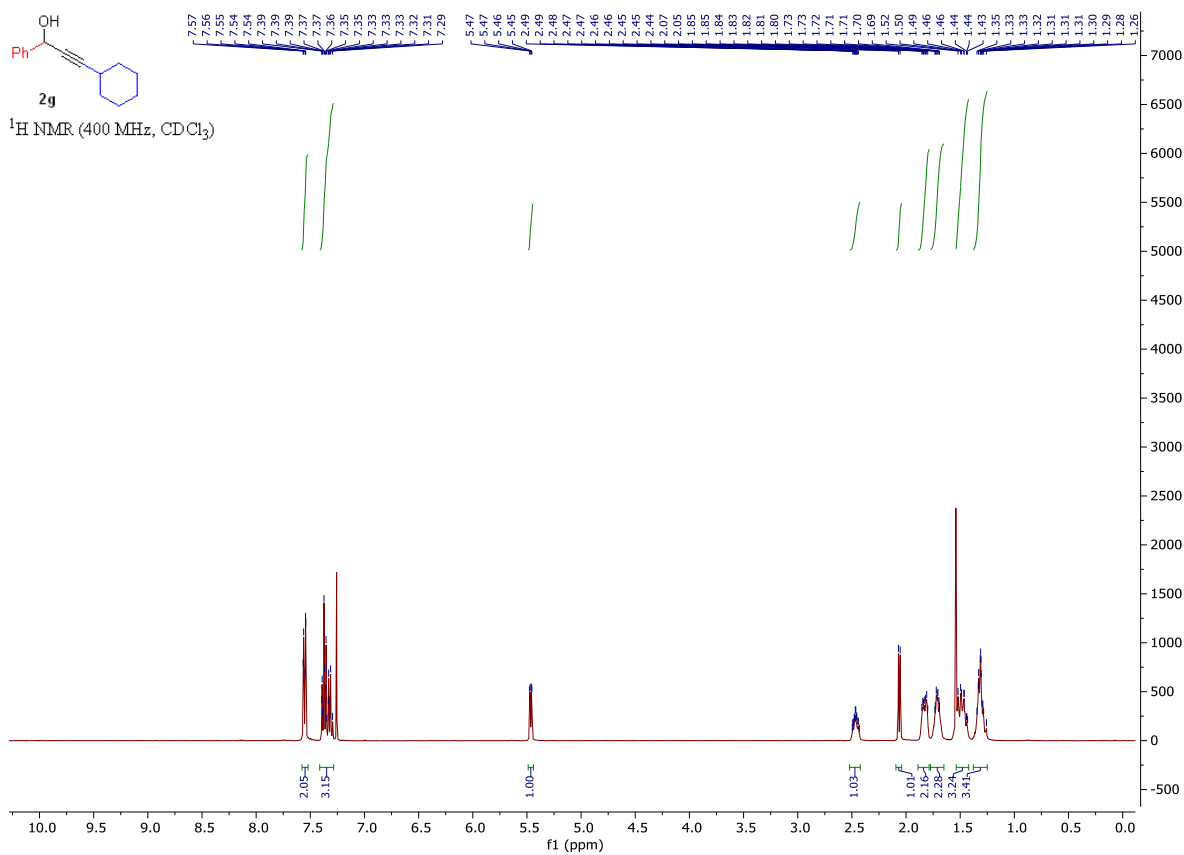
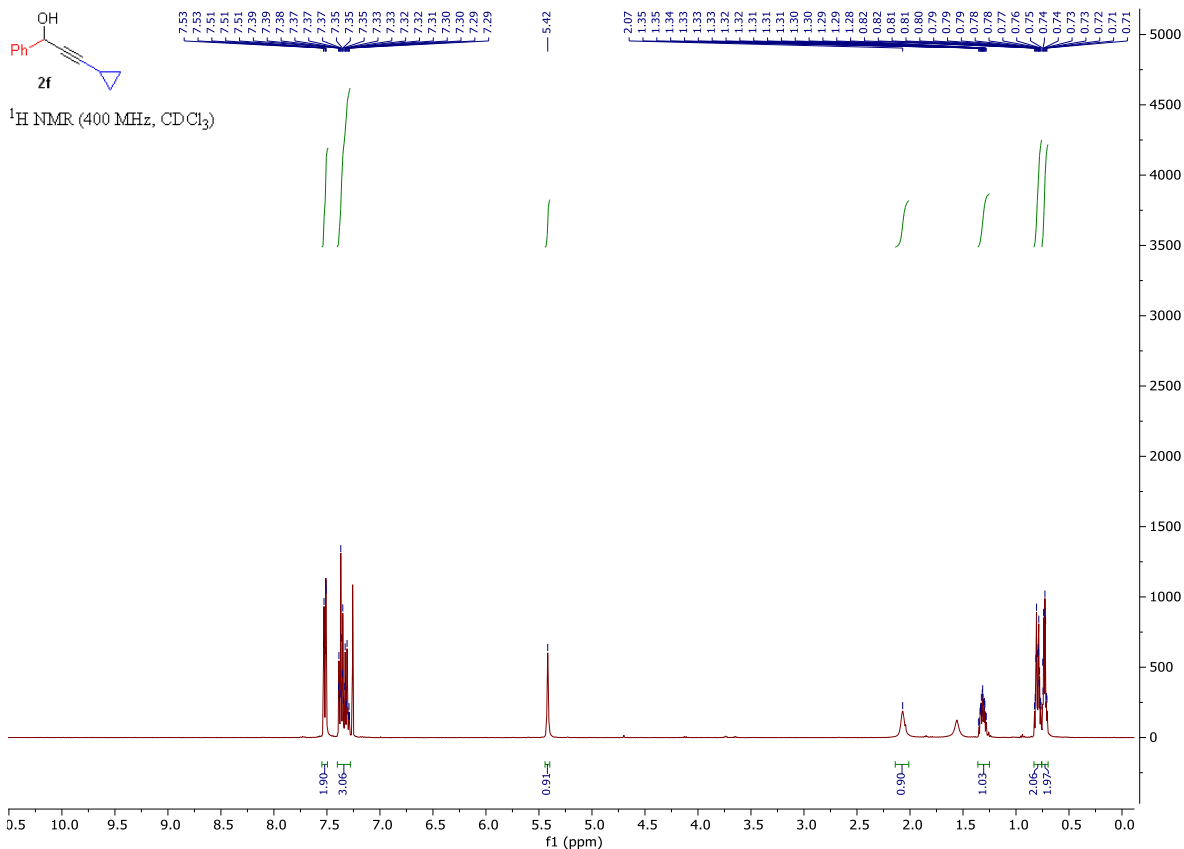
| | |
|---|-----|
| 1. Copies of ^1H and ^{13}C NMR spectra | S2 |
| 2. Mechanistic studies – LCMS analysis of raw reaction mixture..... | S40 |

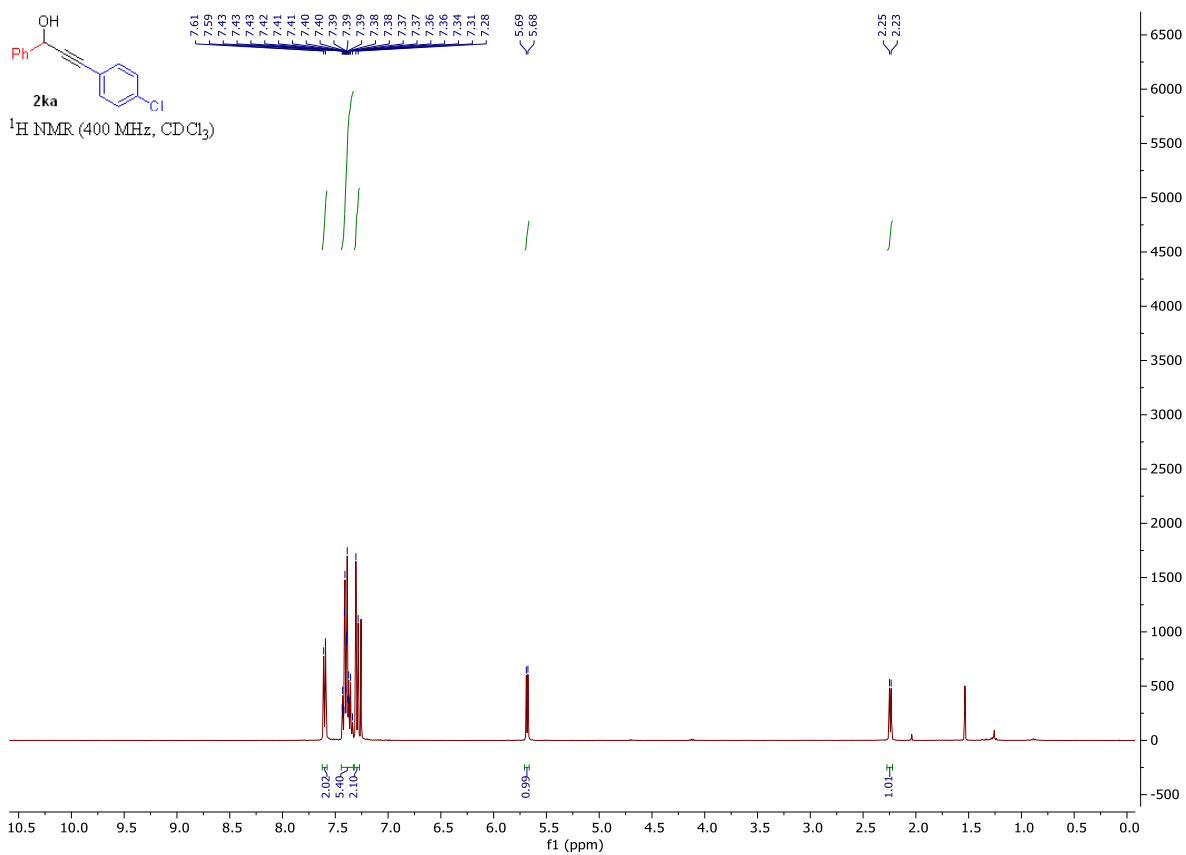
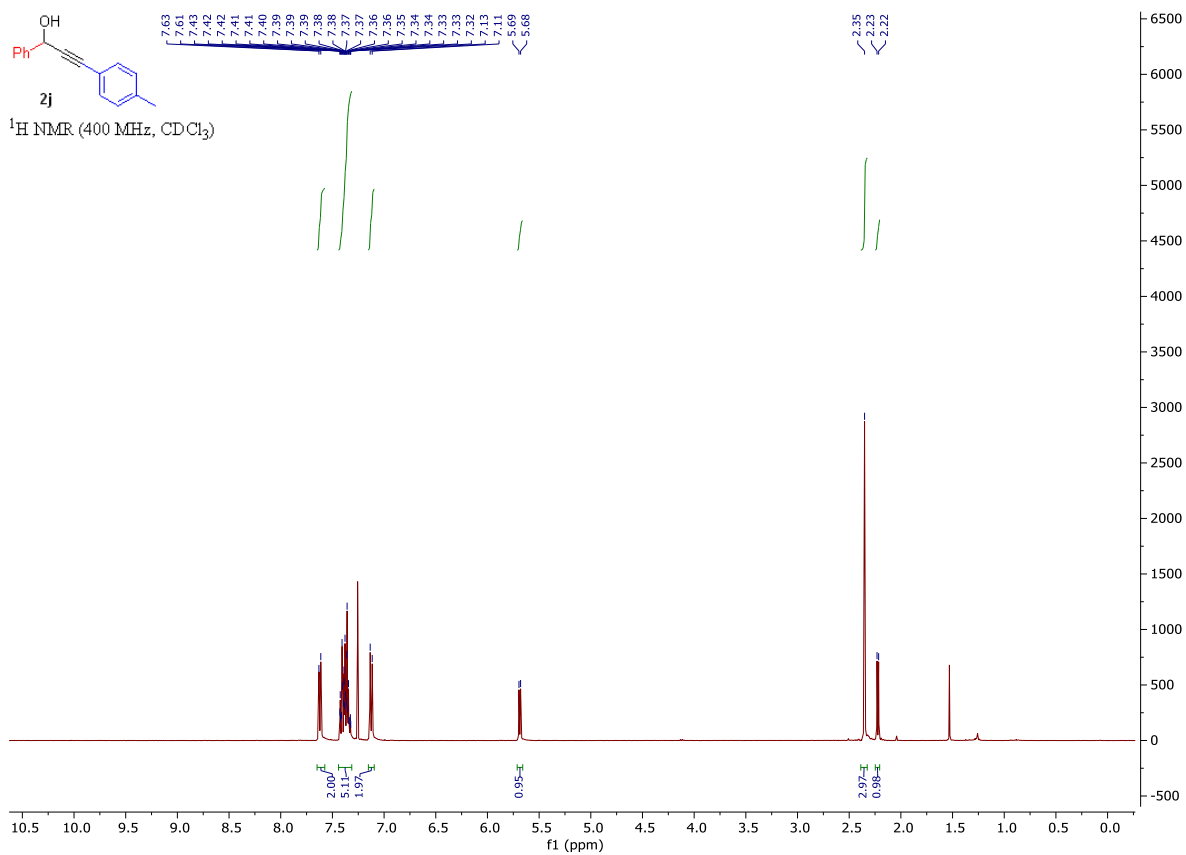
1. Copies of ^1H and ^{13}C NMR spectra

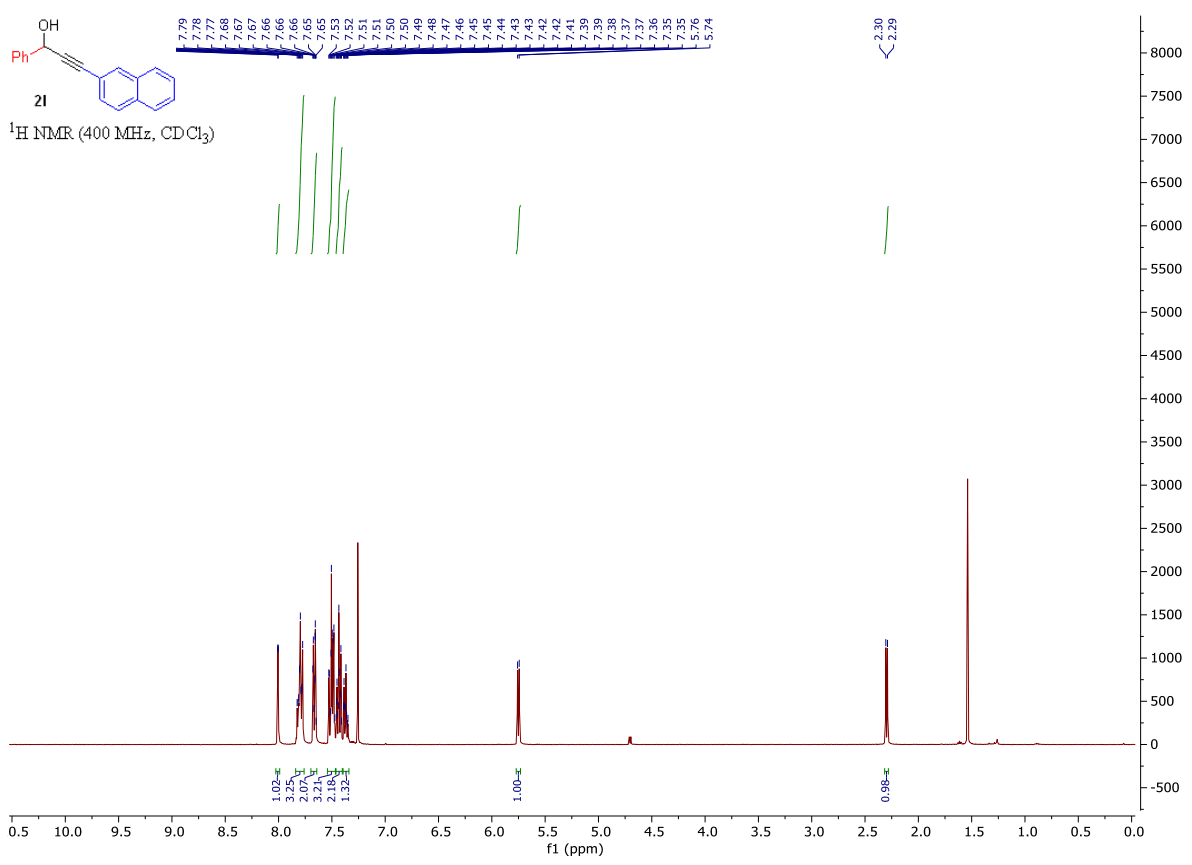
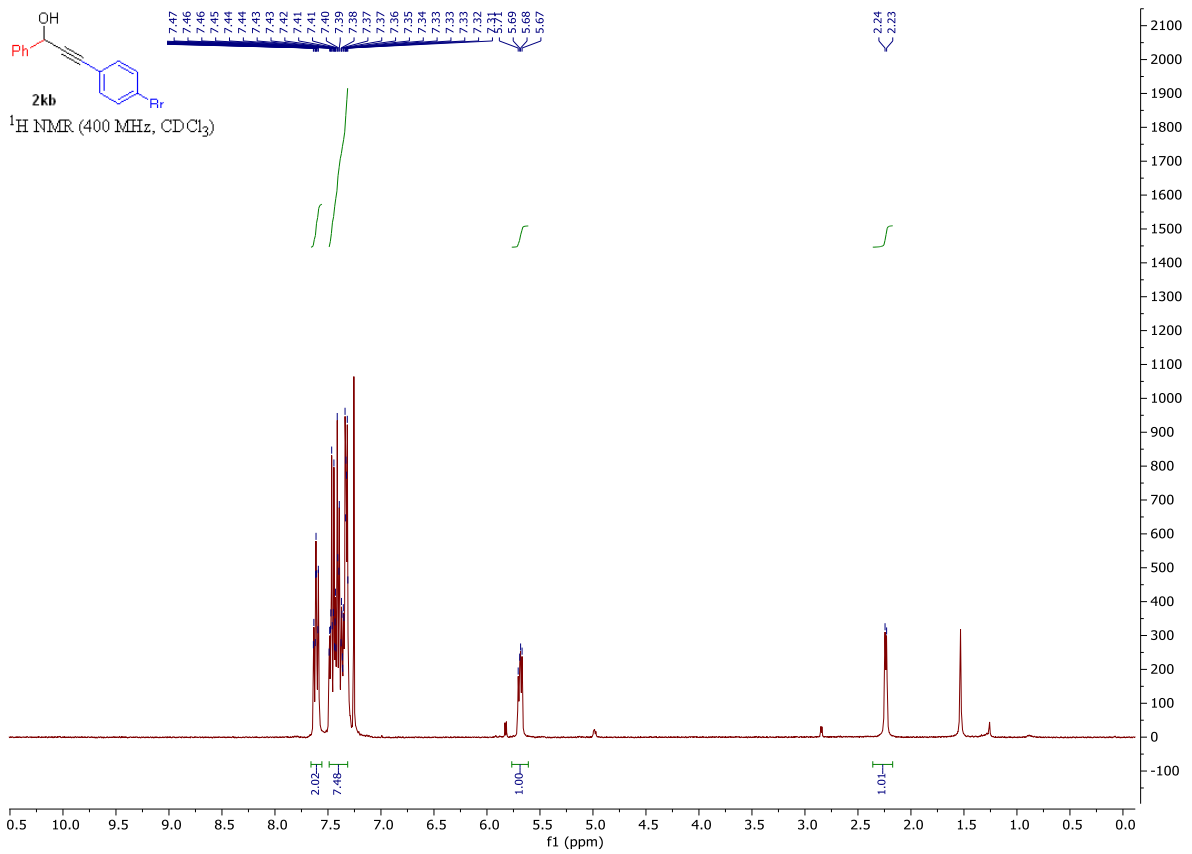


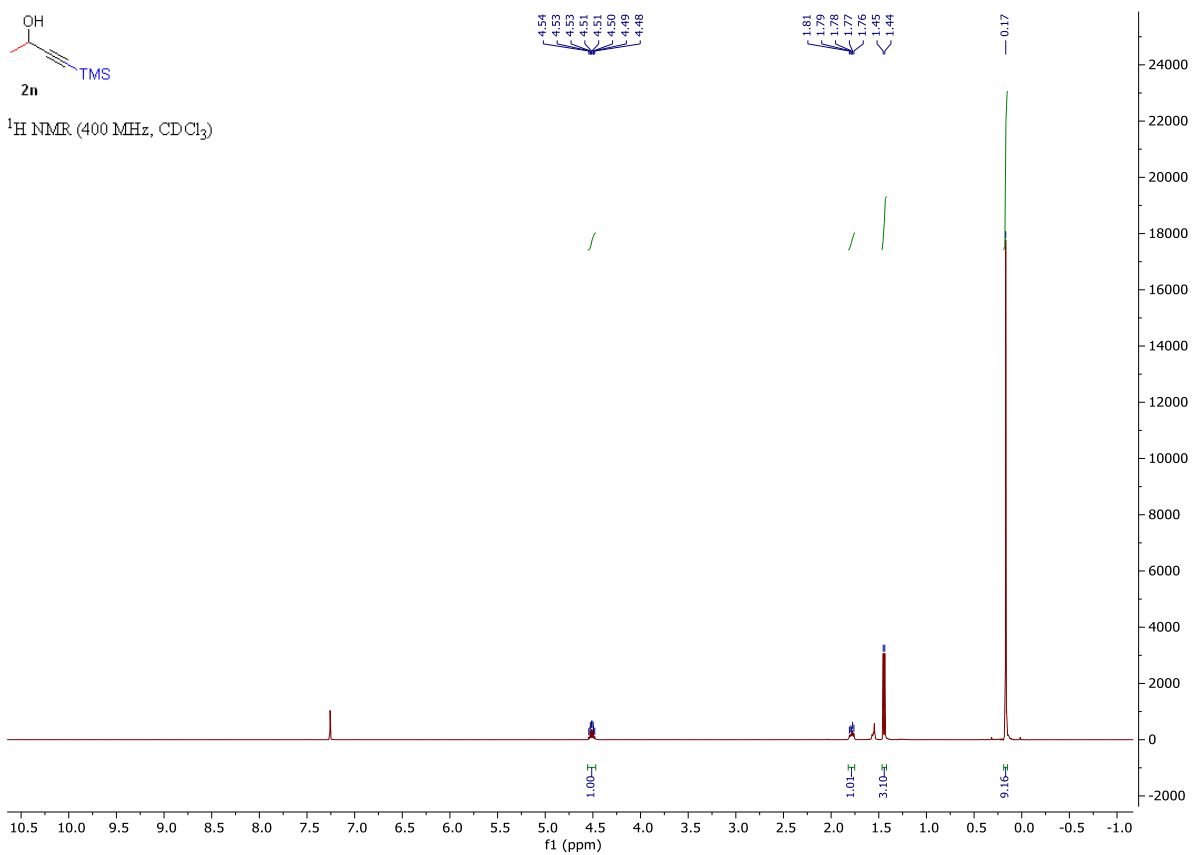
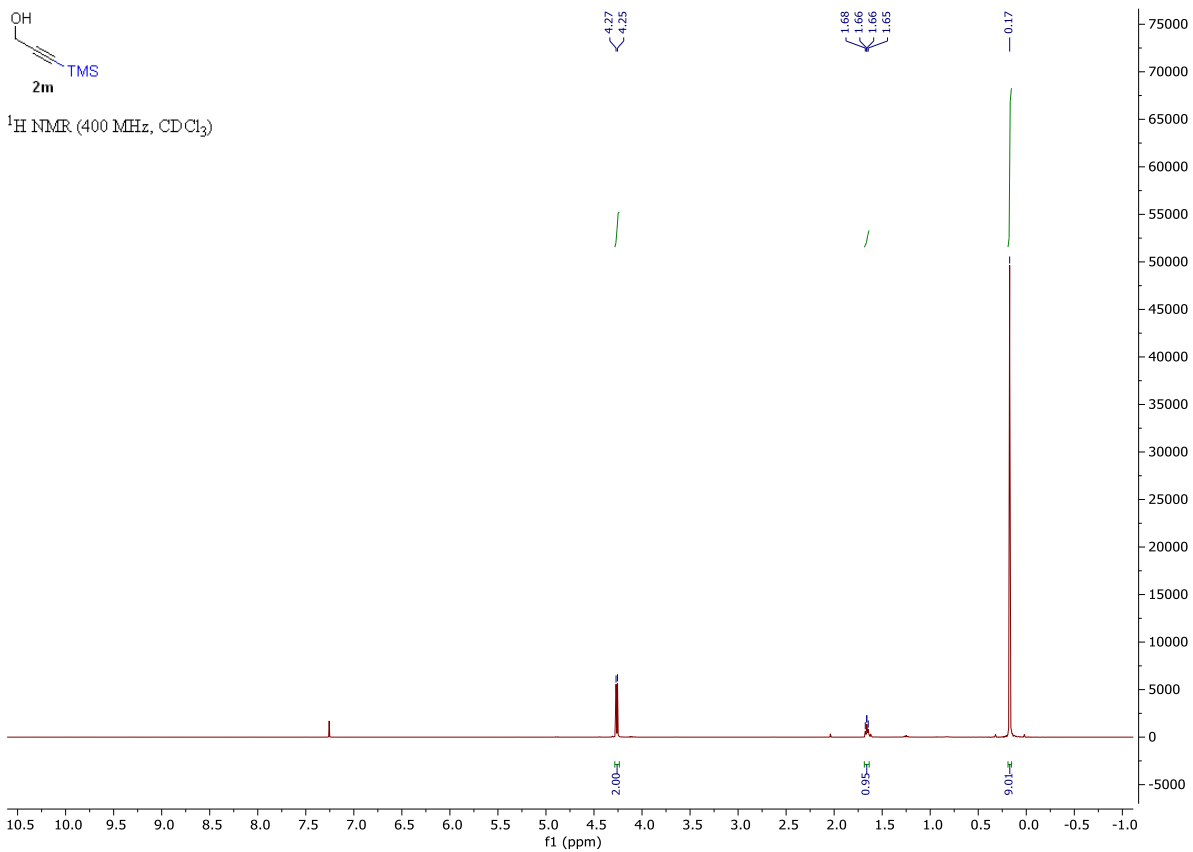


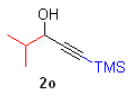




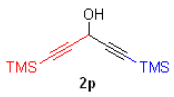
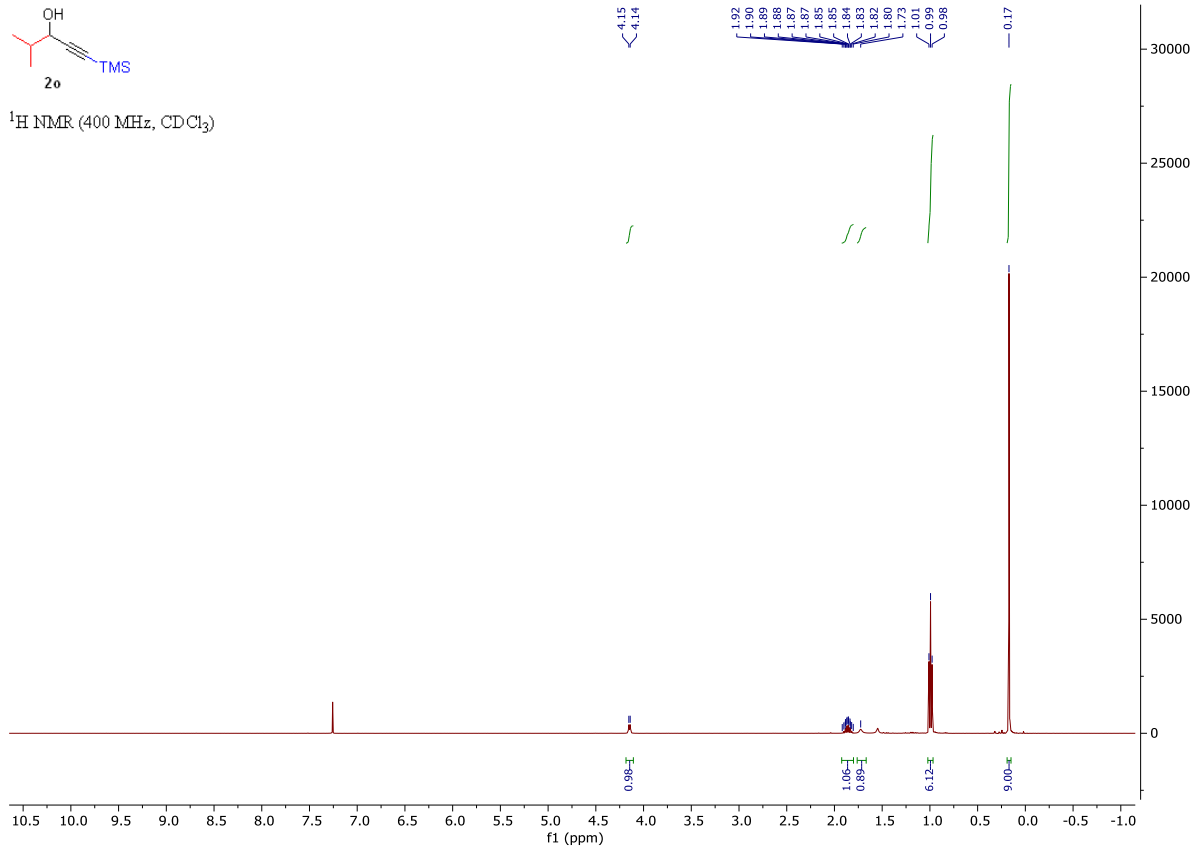




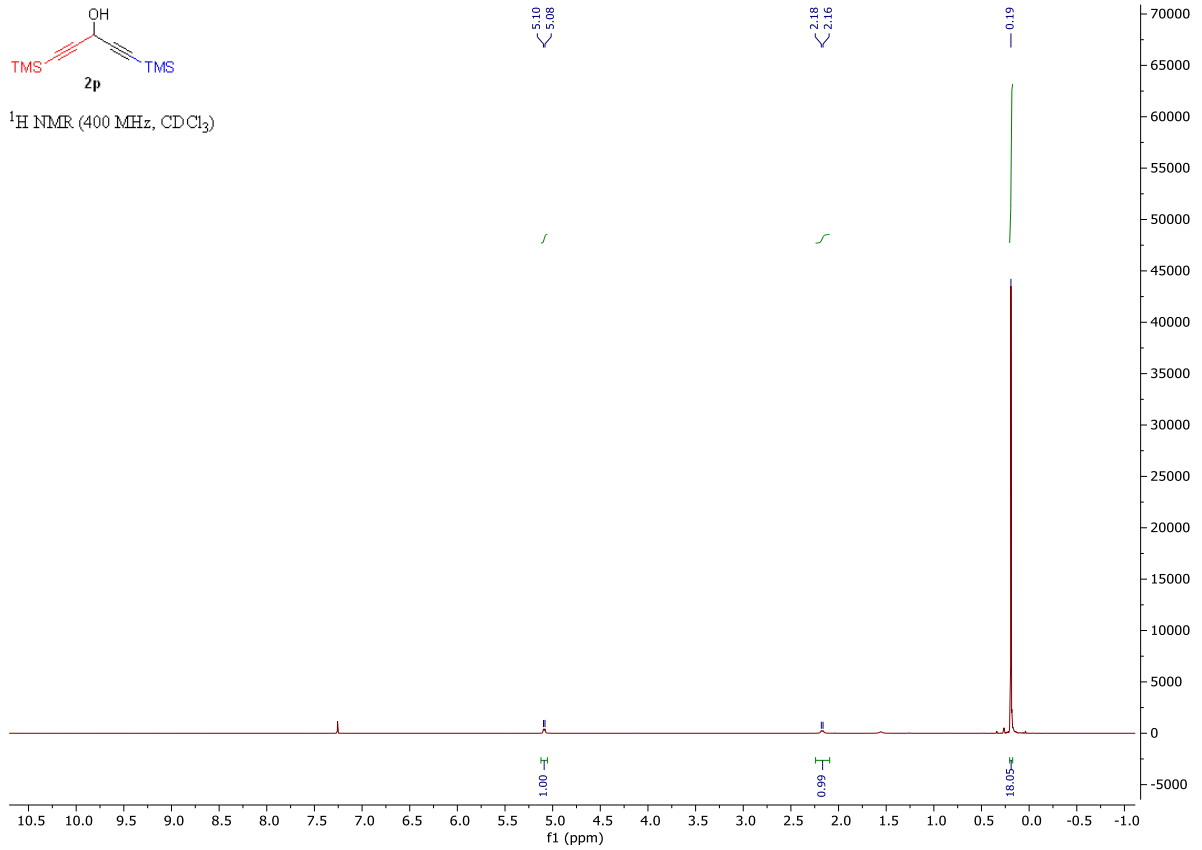


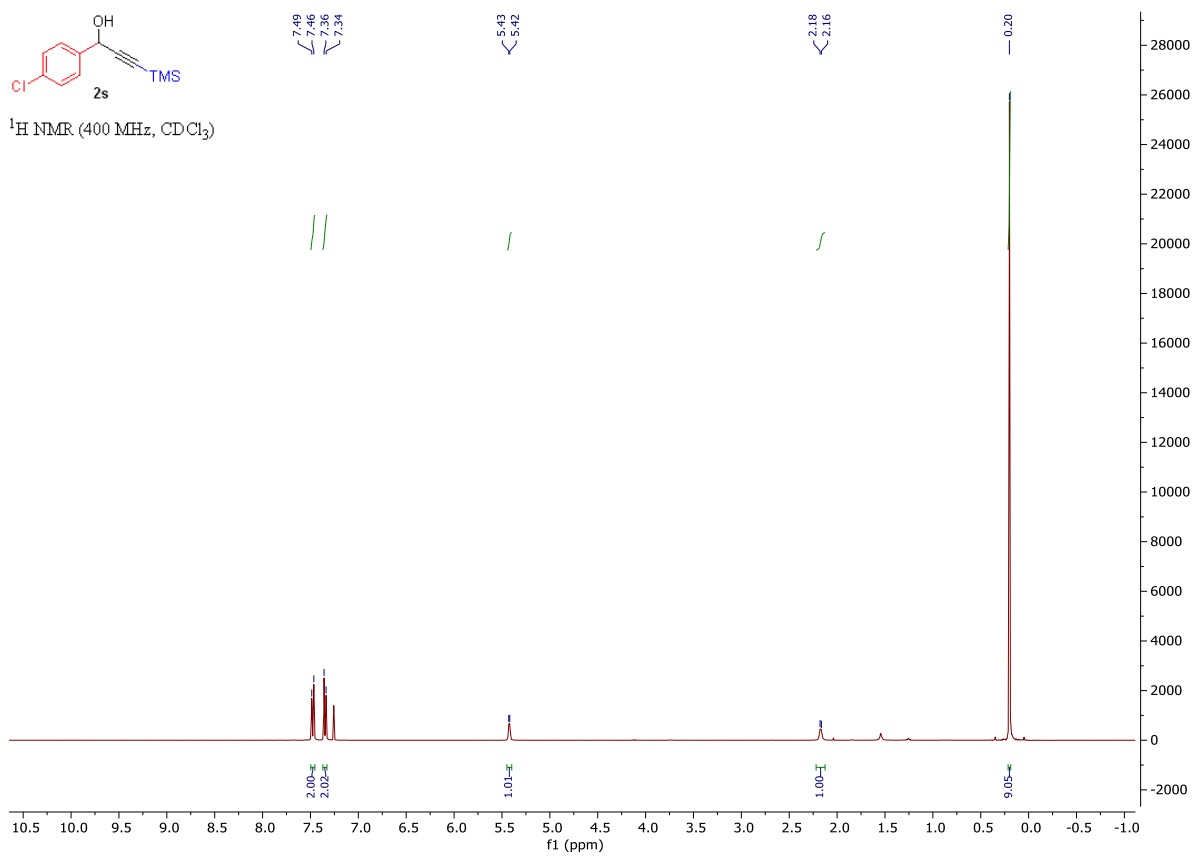
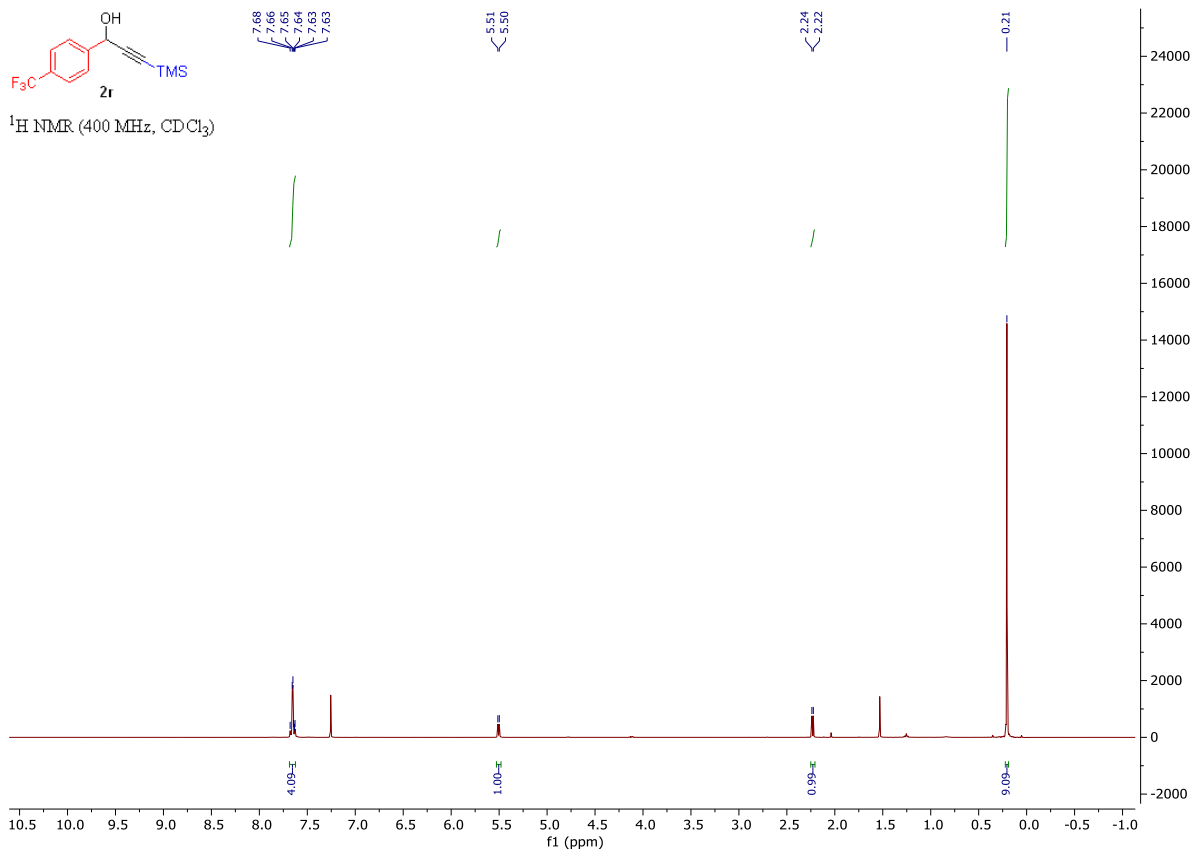


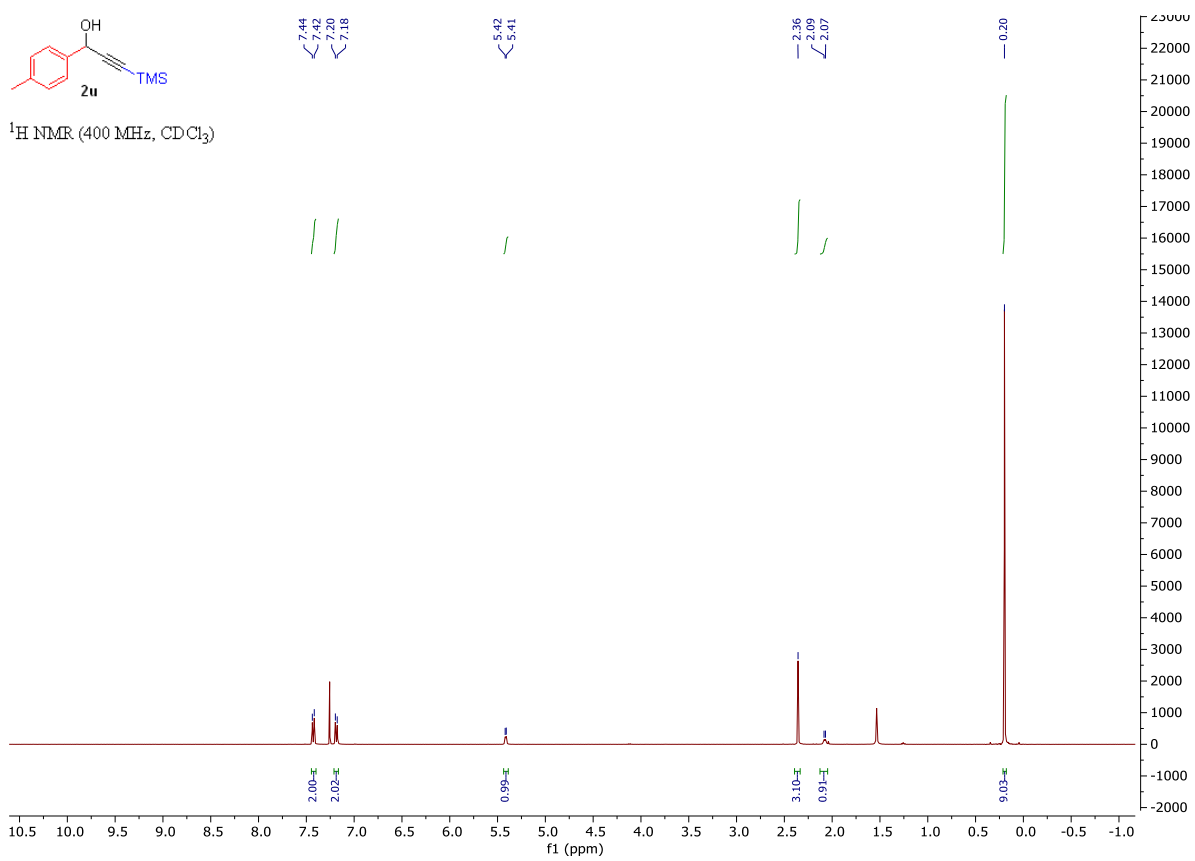
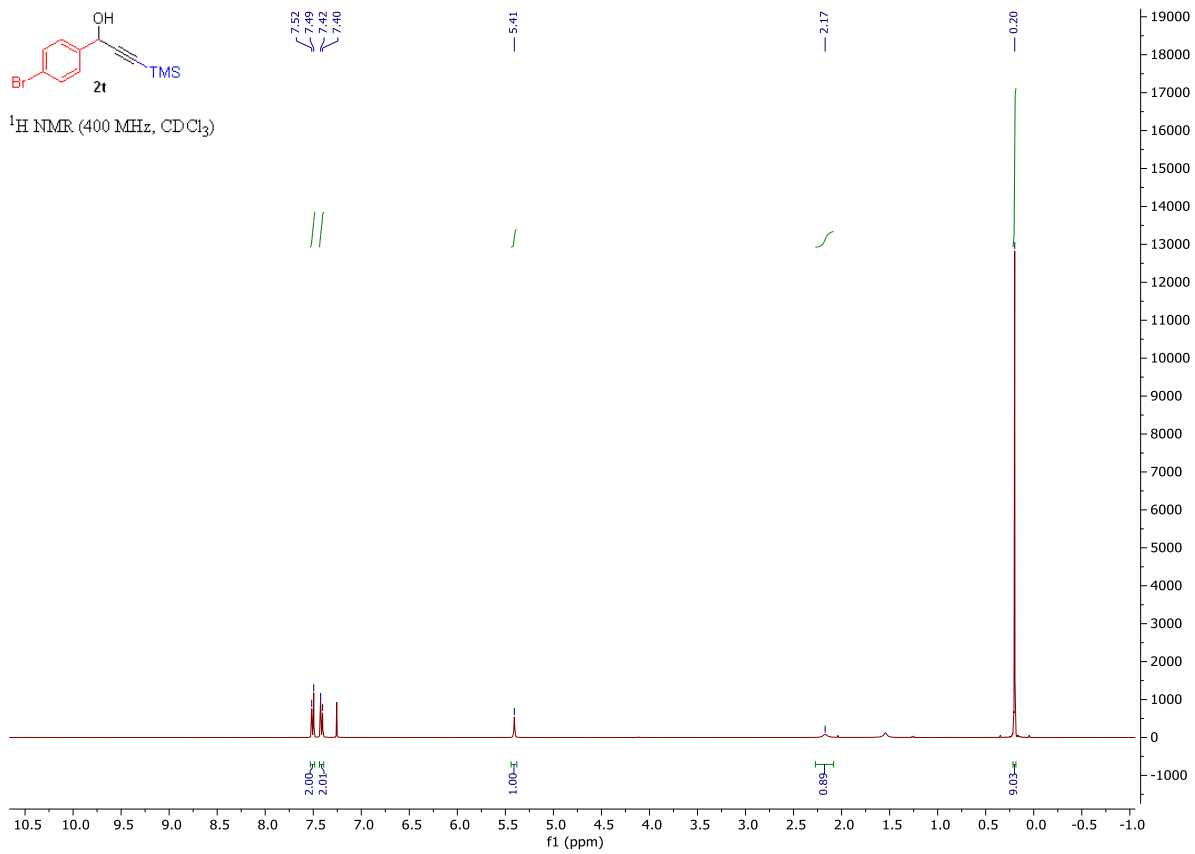
¹H NMR (400 MHz, CDCl₃)

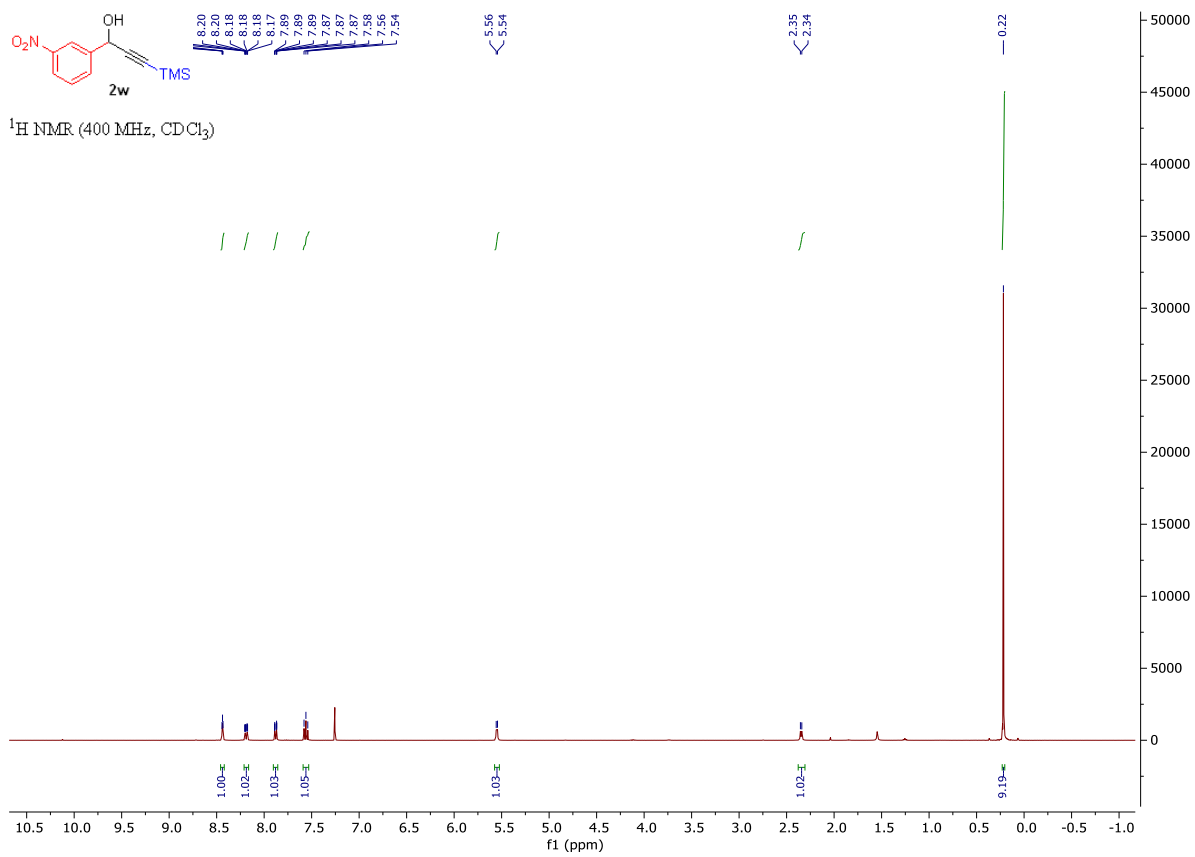
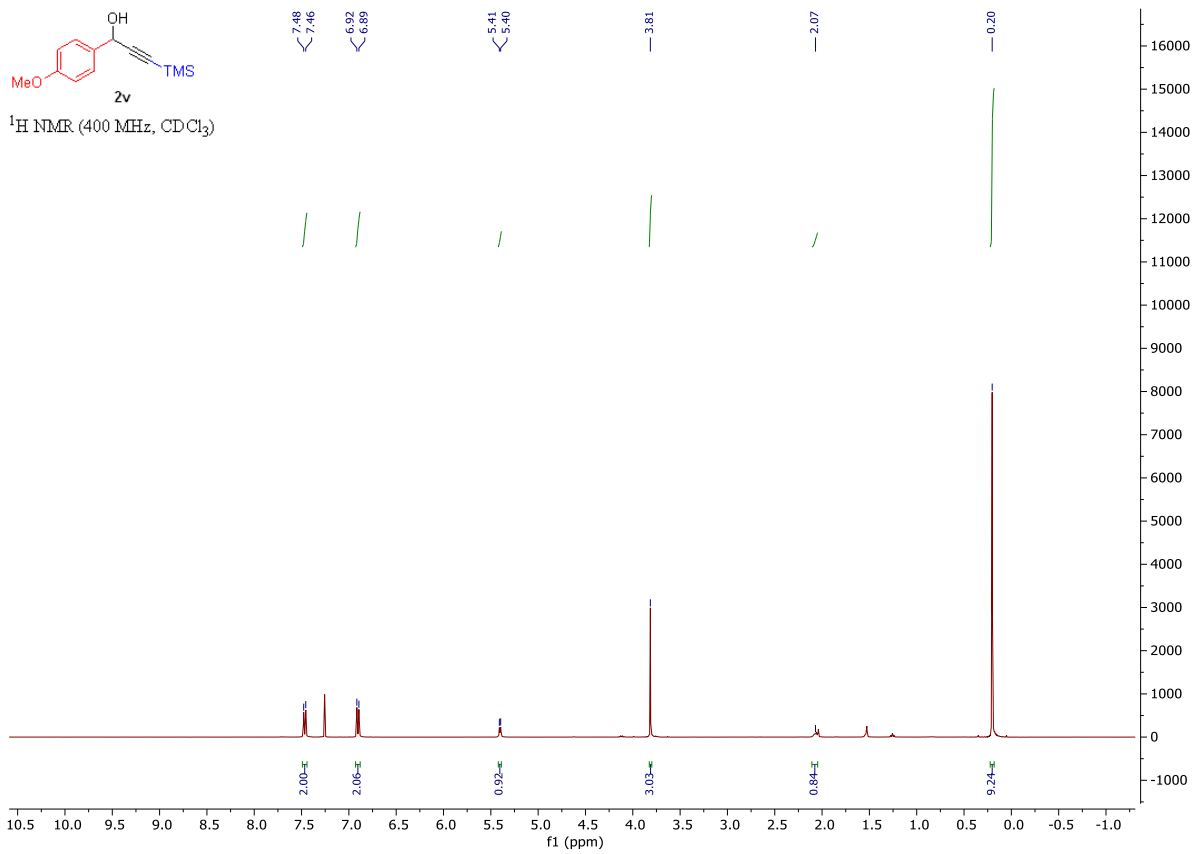


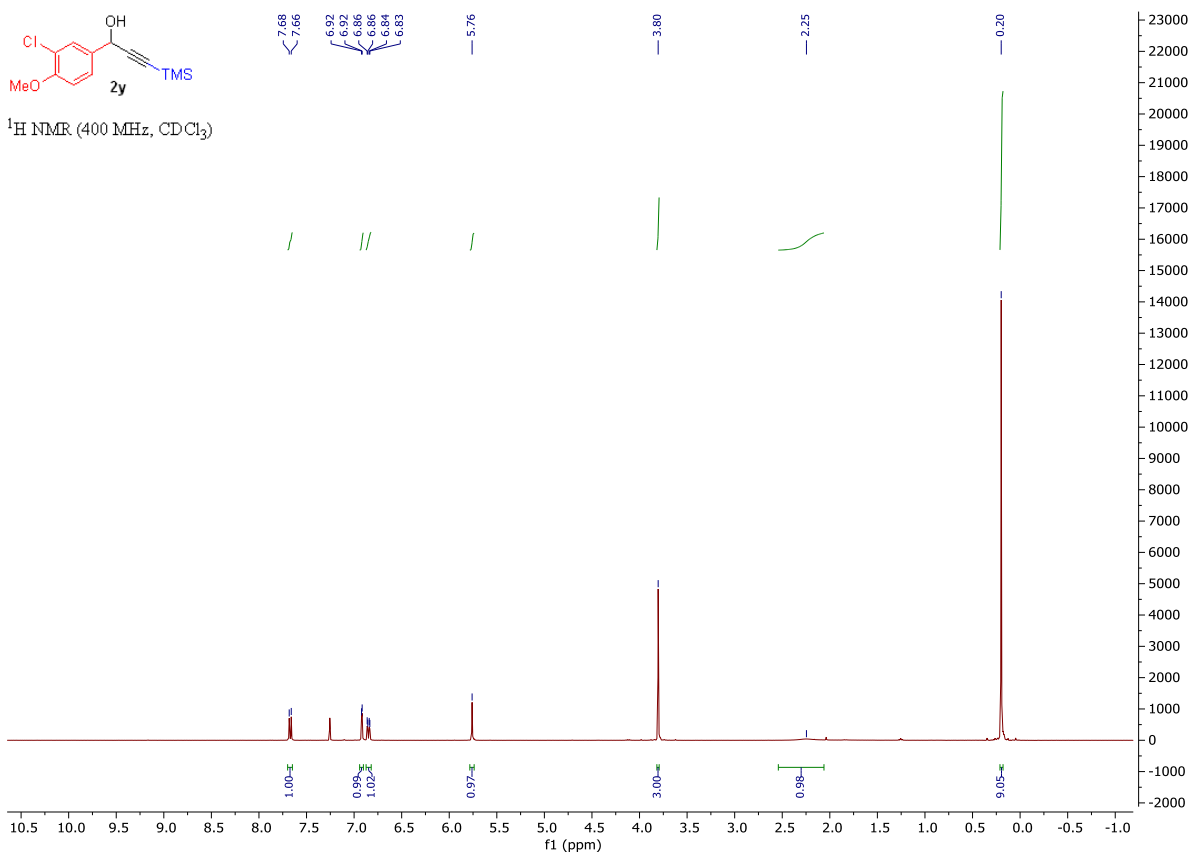
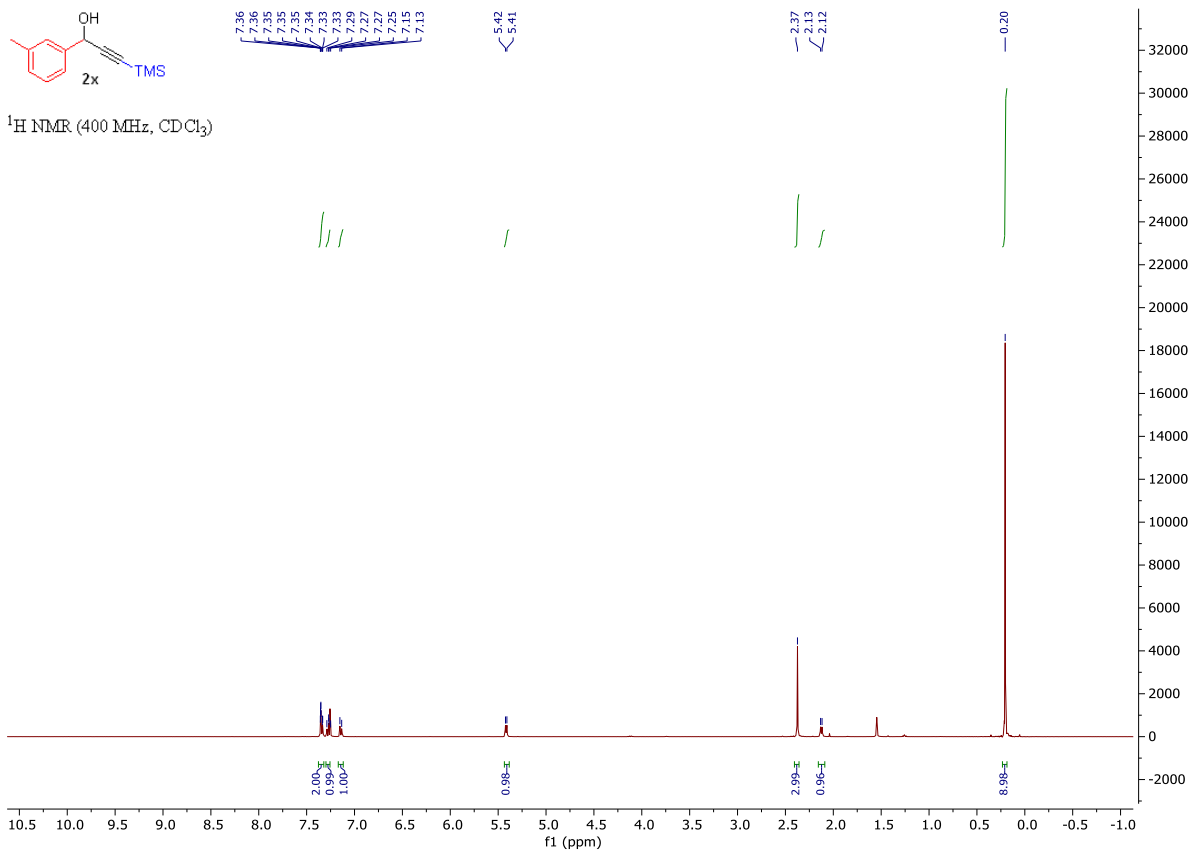
¹H NMR (400 MHz, CDCl₃)

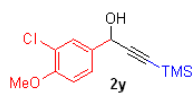




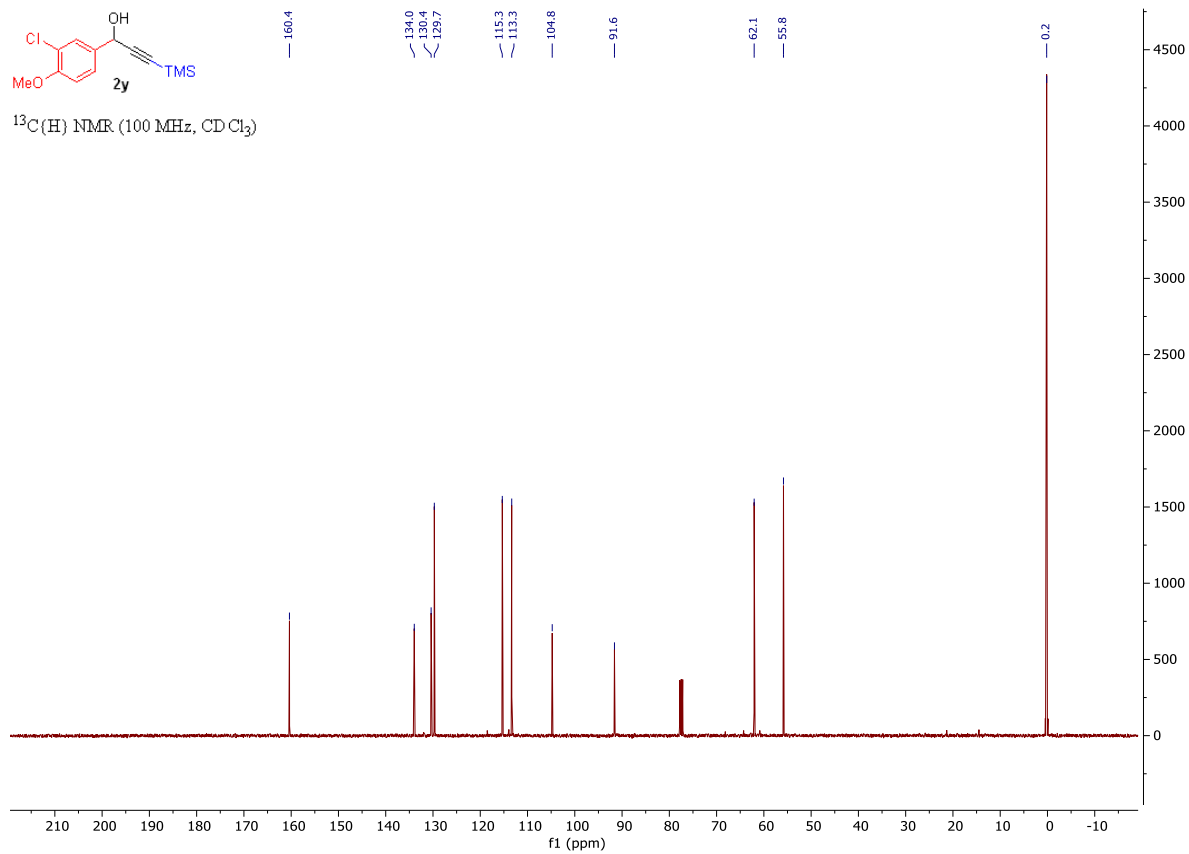




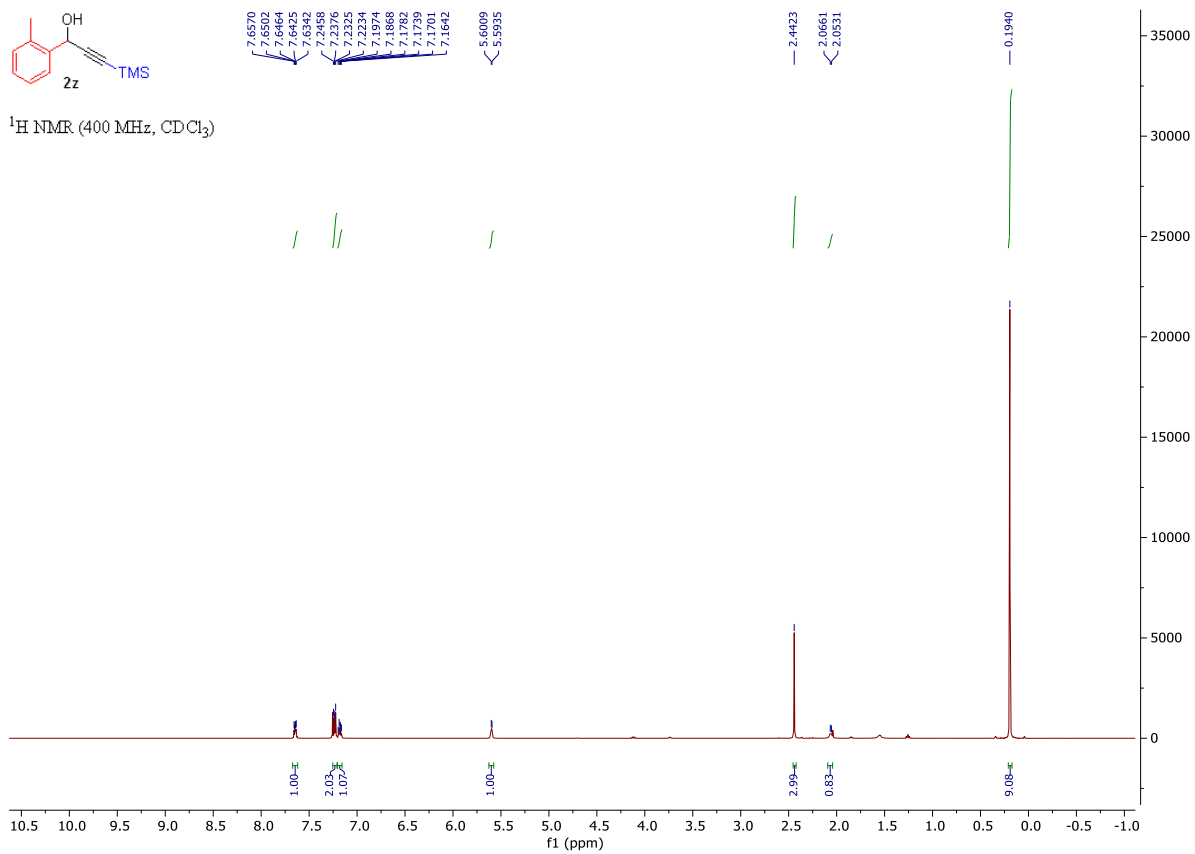


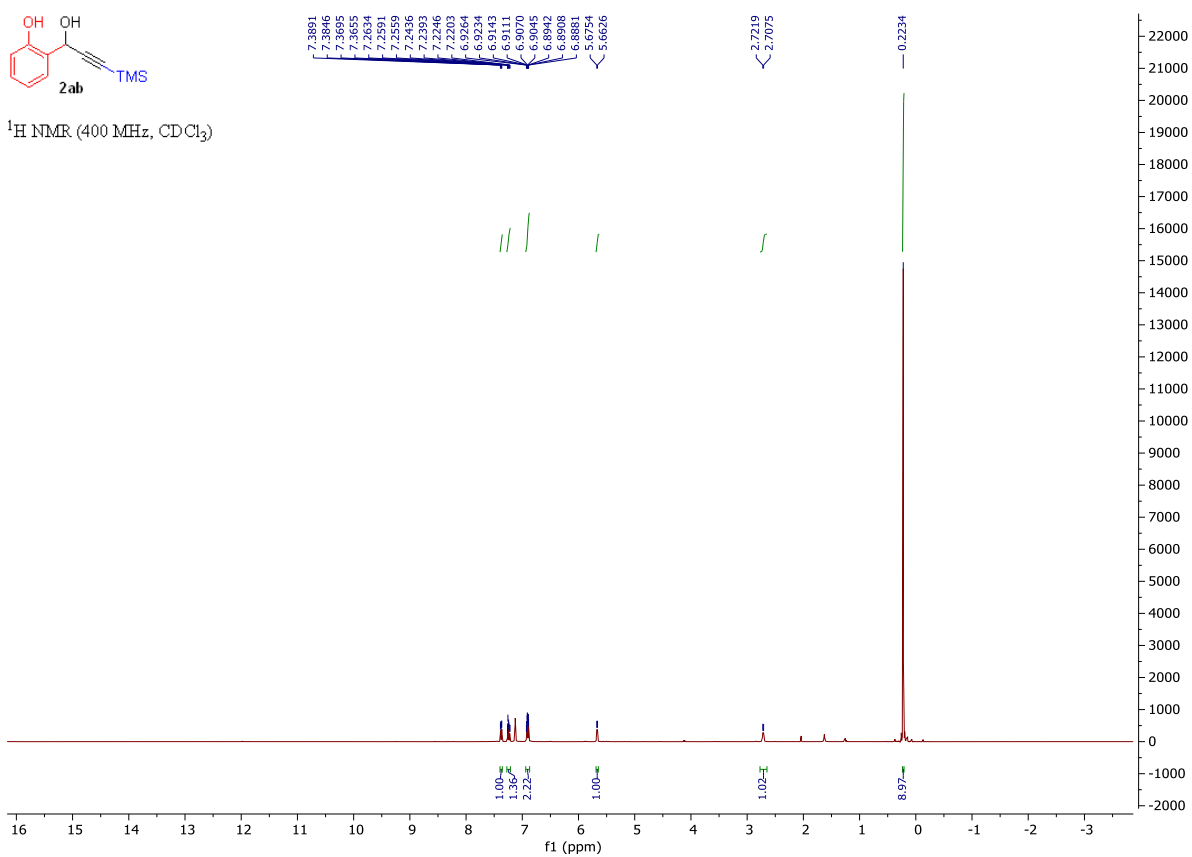
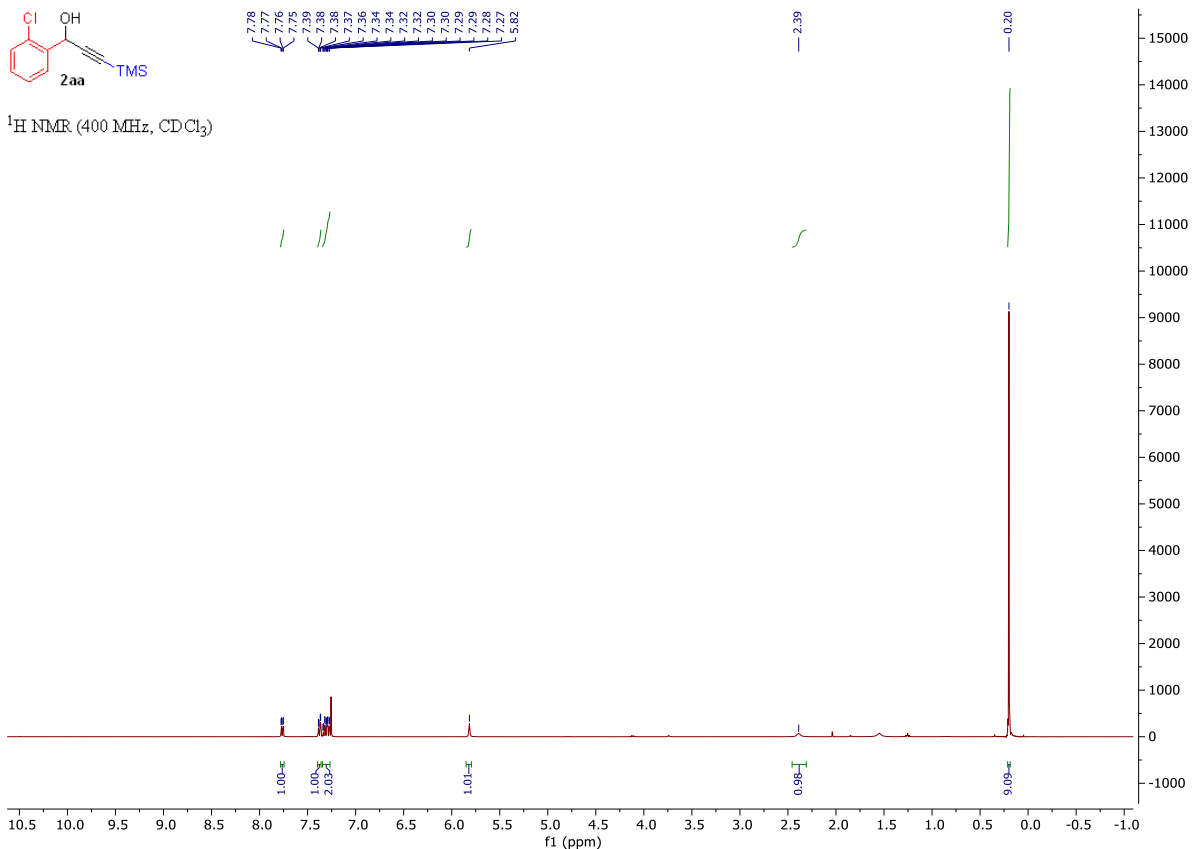


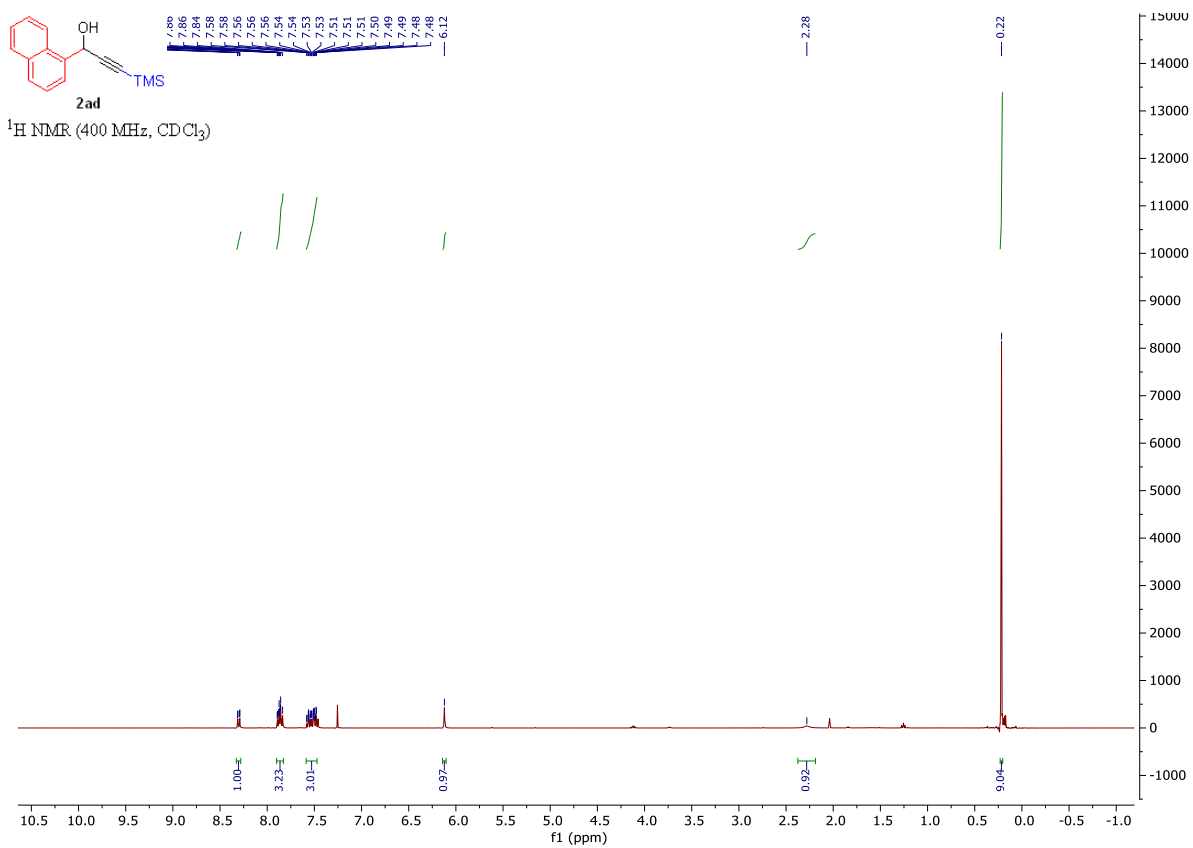
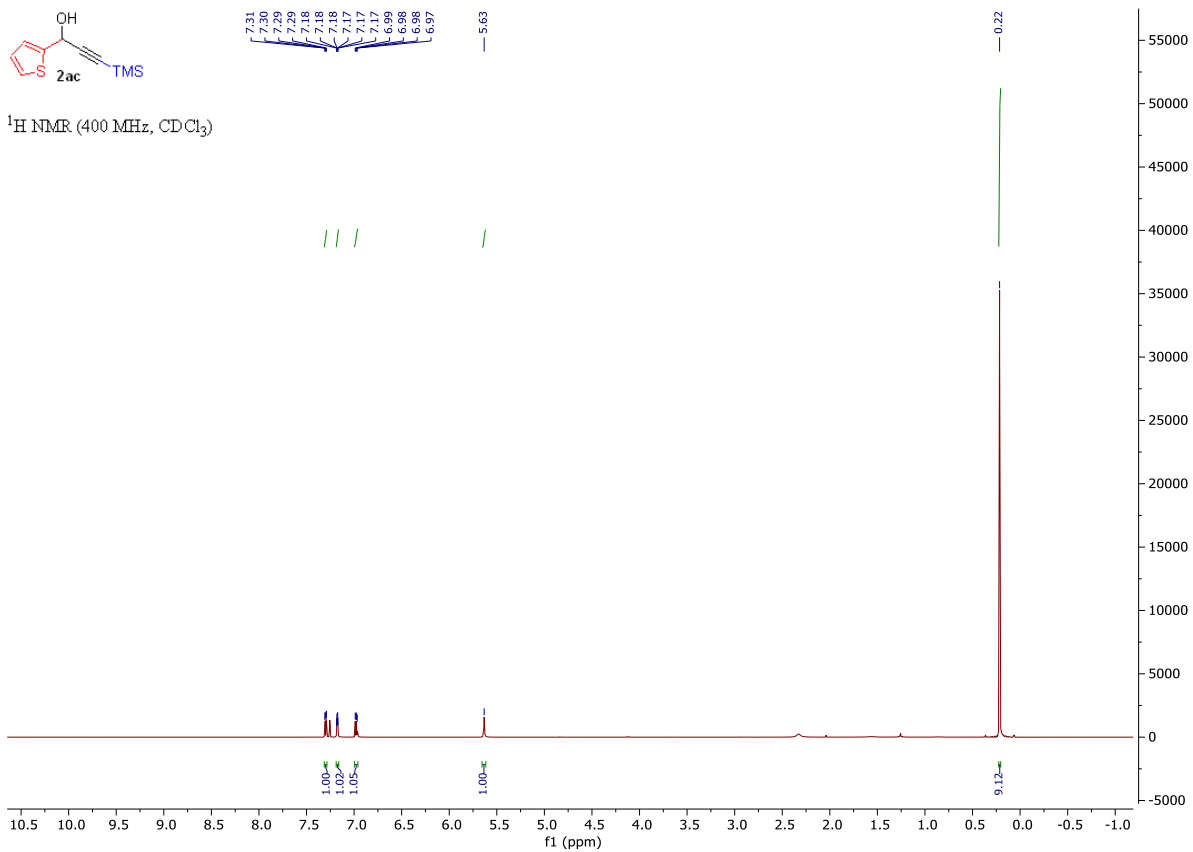
$^{13}\text{C}\{^1\text{H}\}$ NMR (100 MHz, CDCl_3)

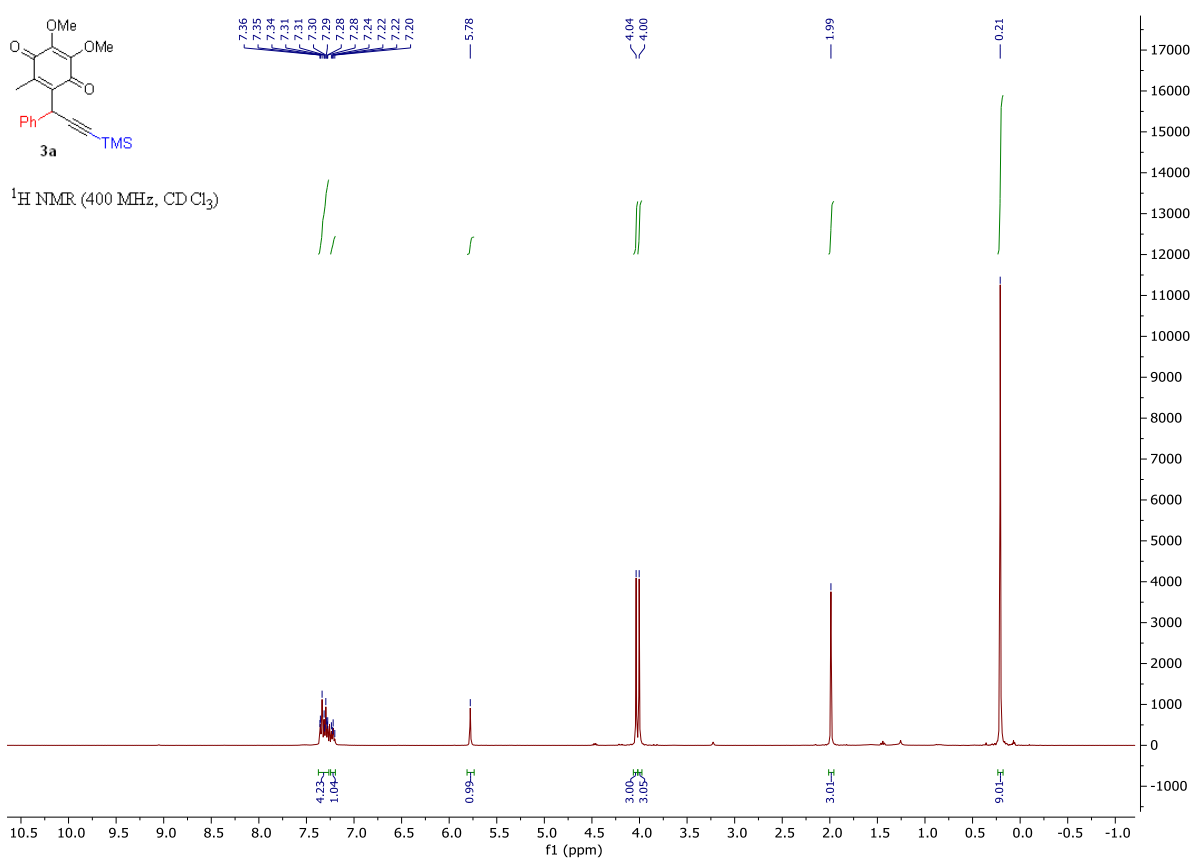
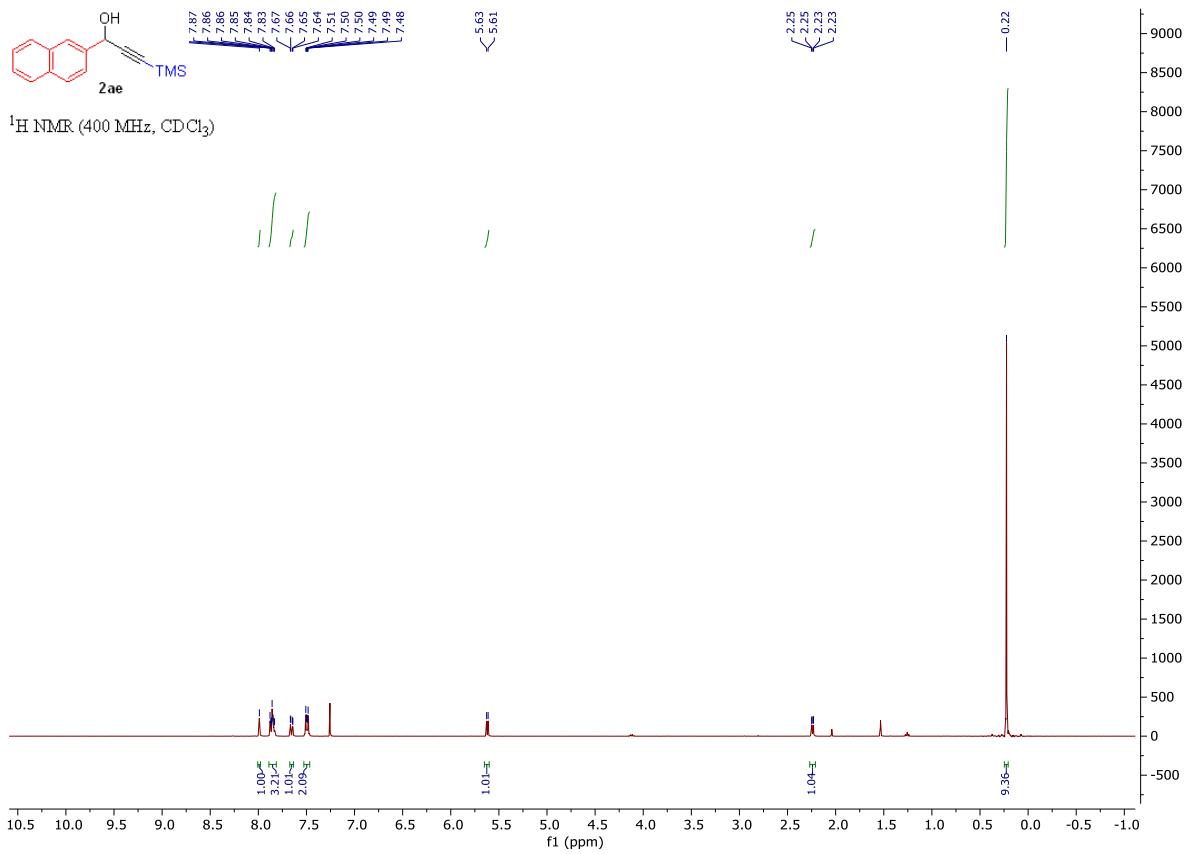


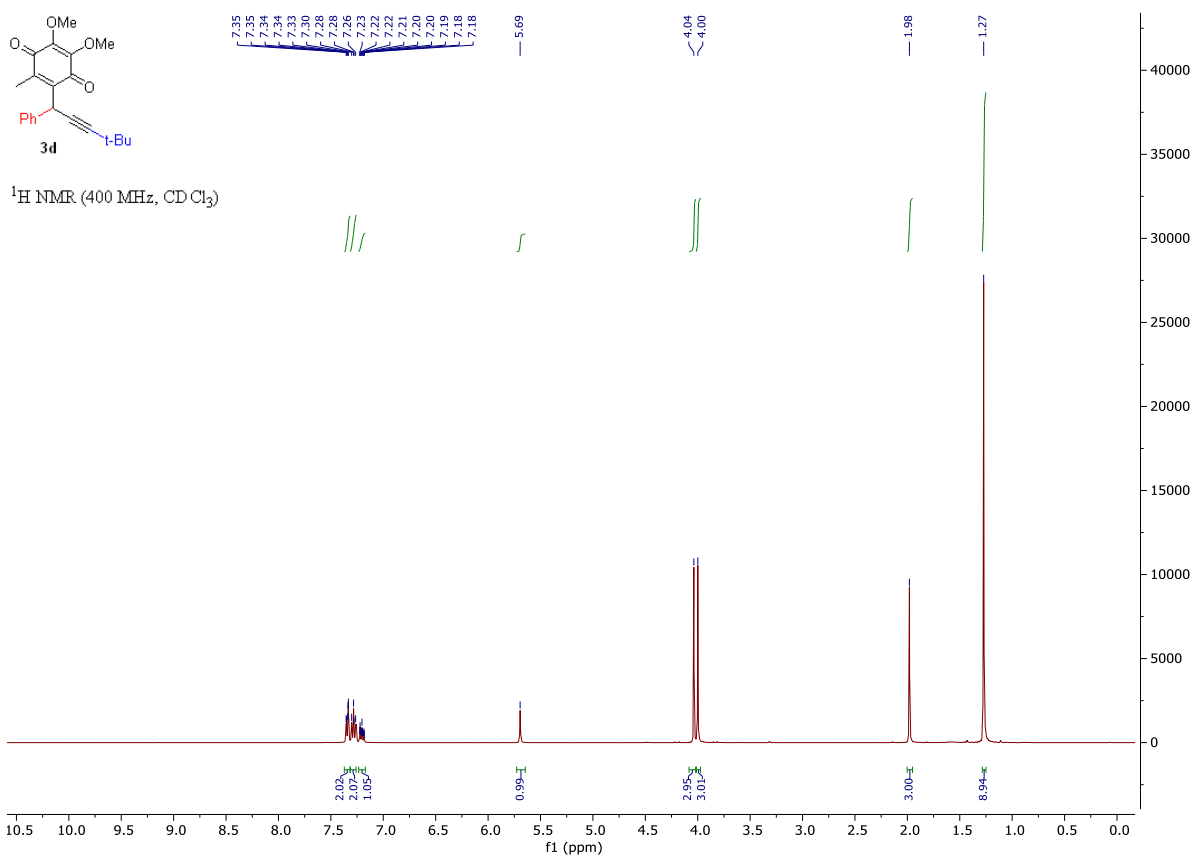
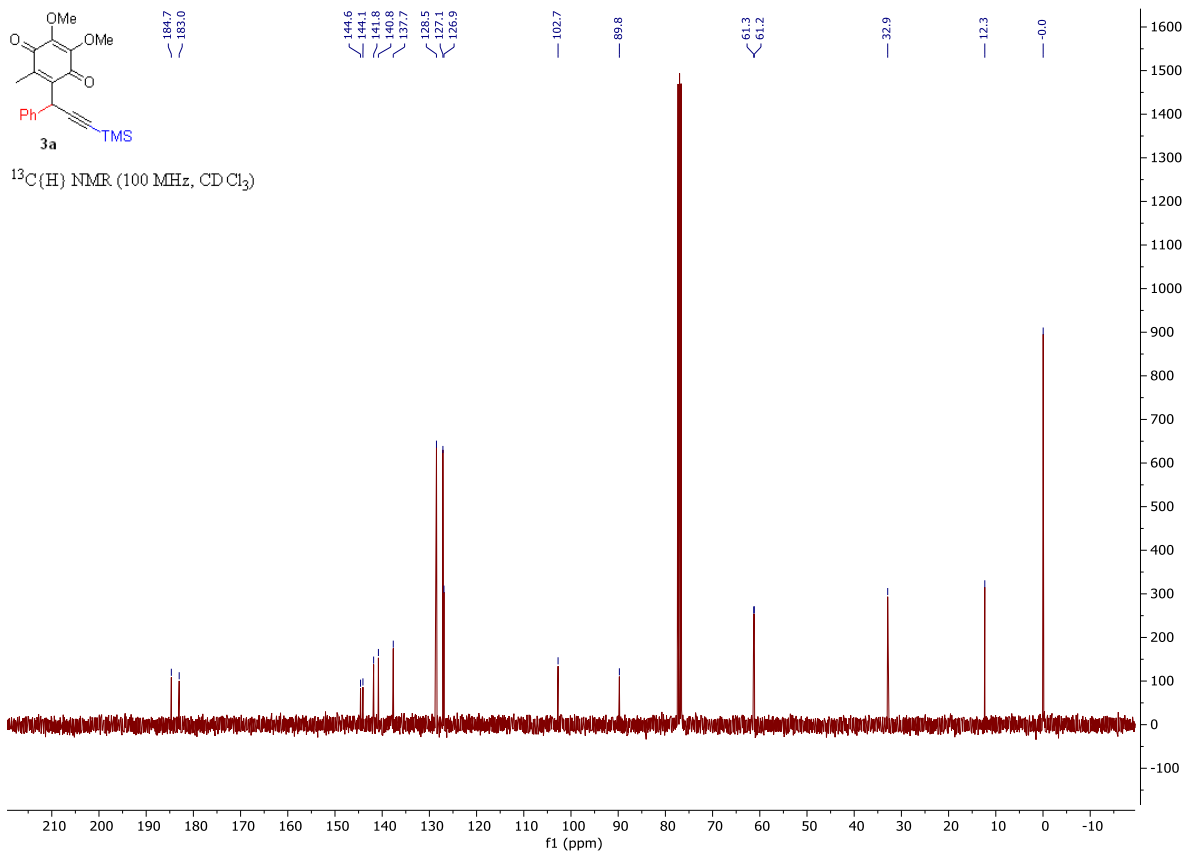
^1H NMR (400 MHz, CDCl_3)

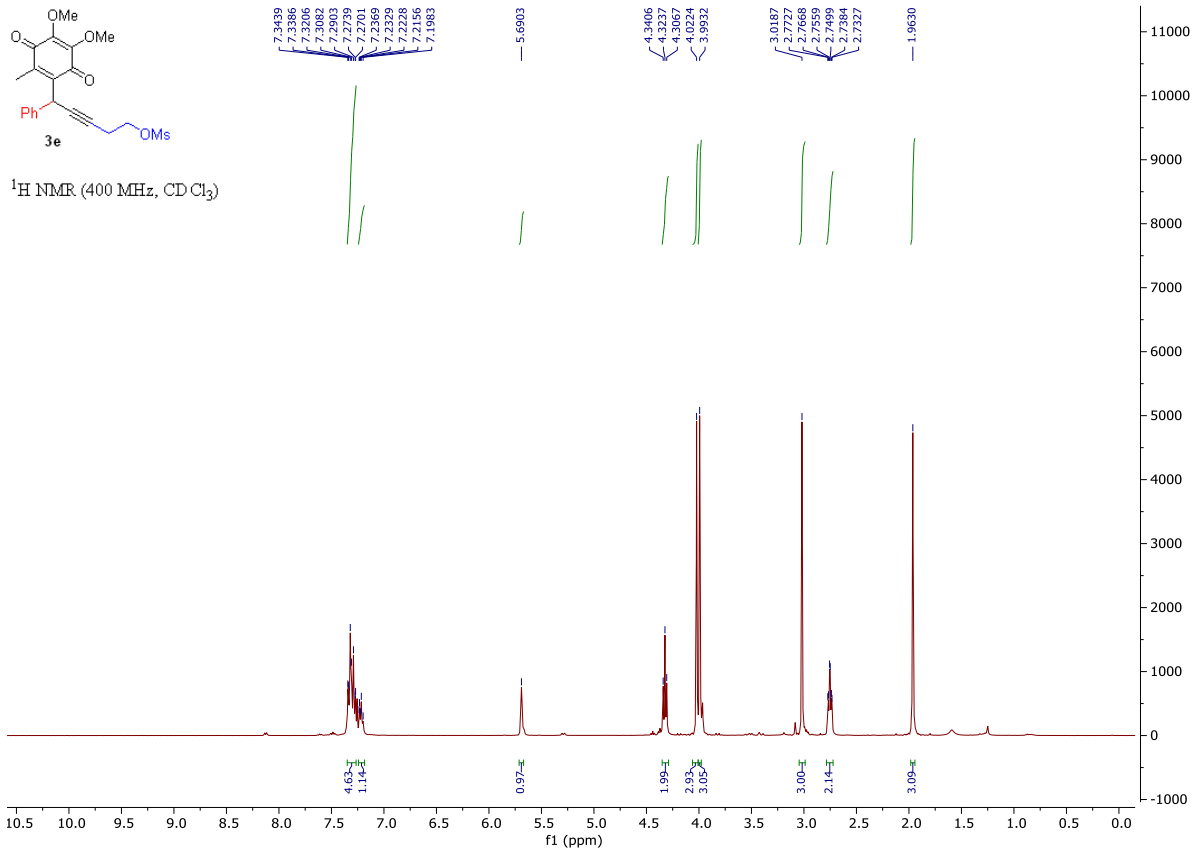
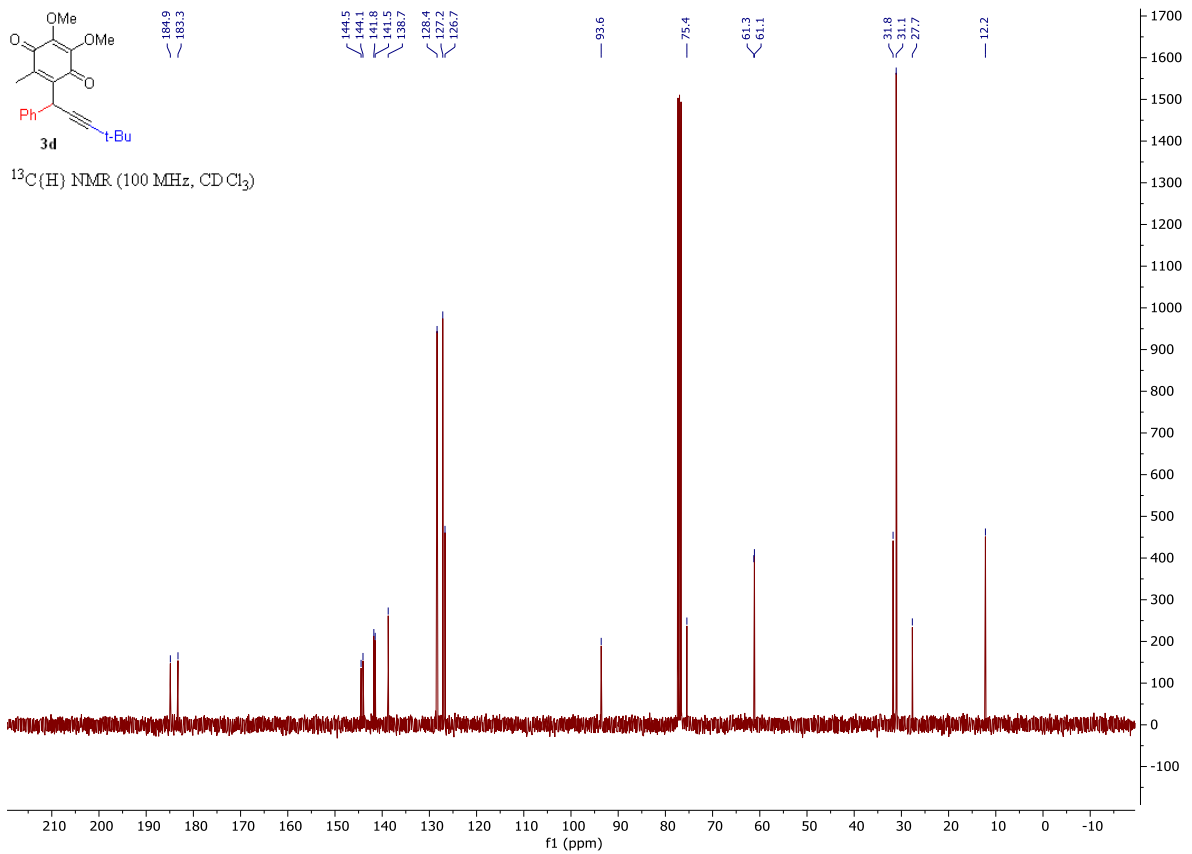


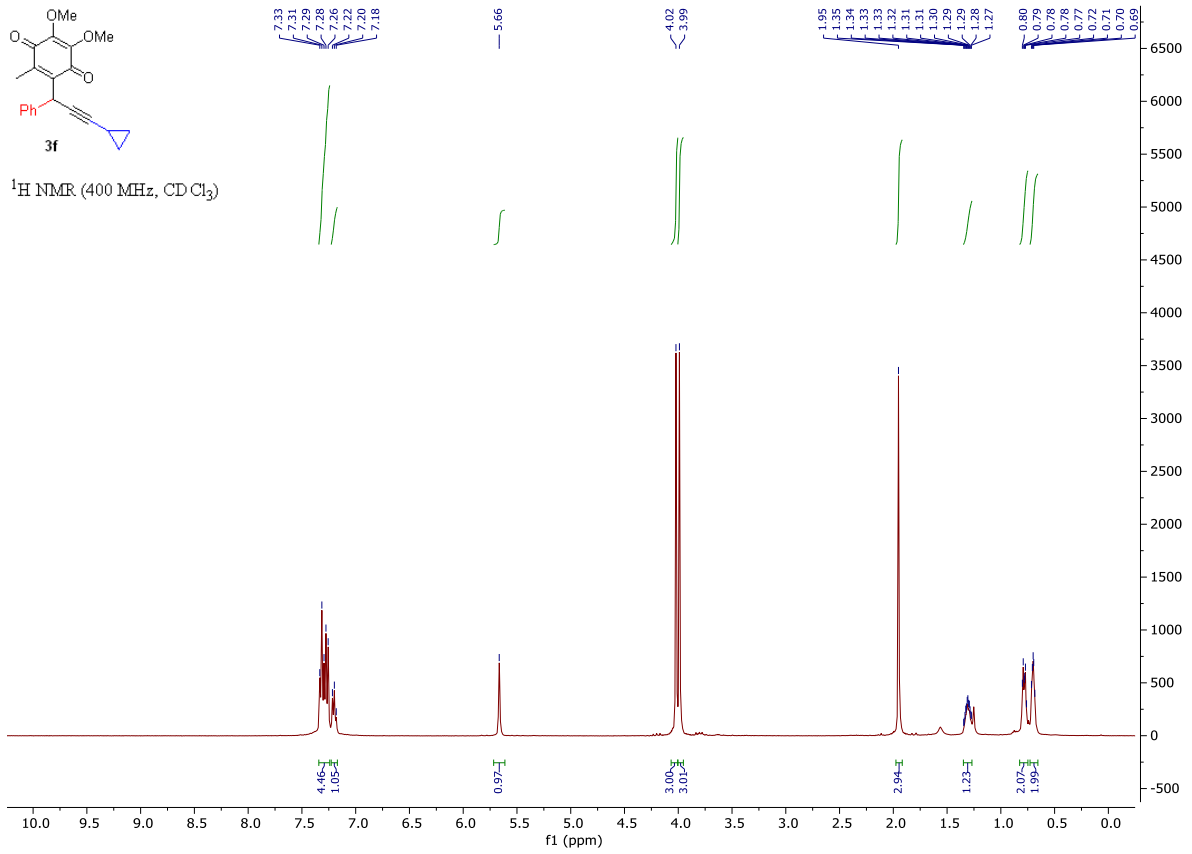
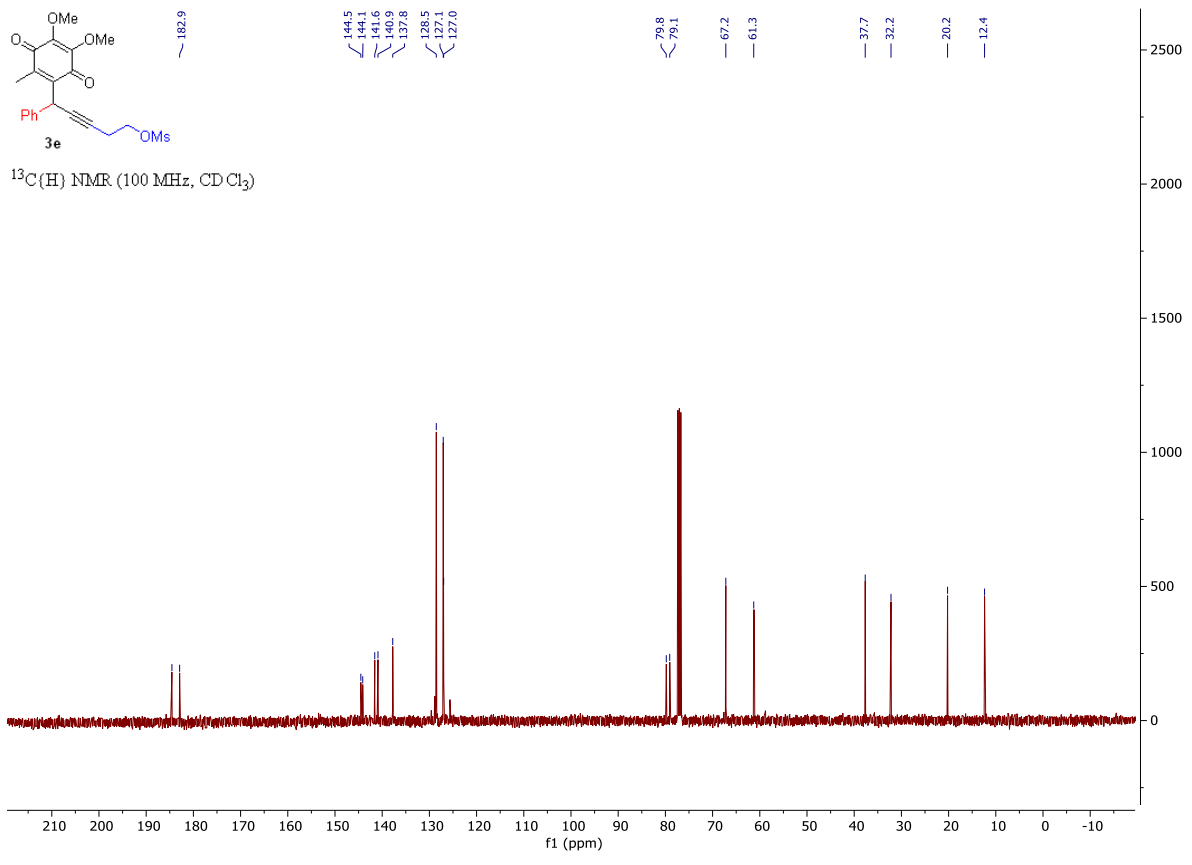


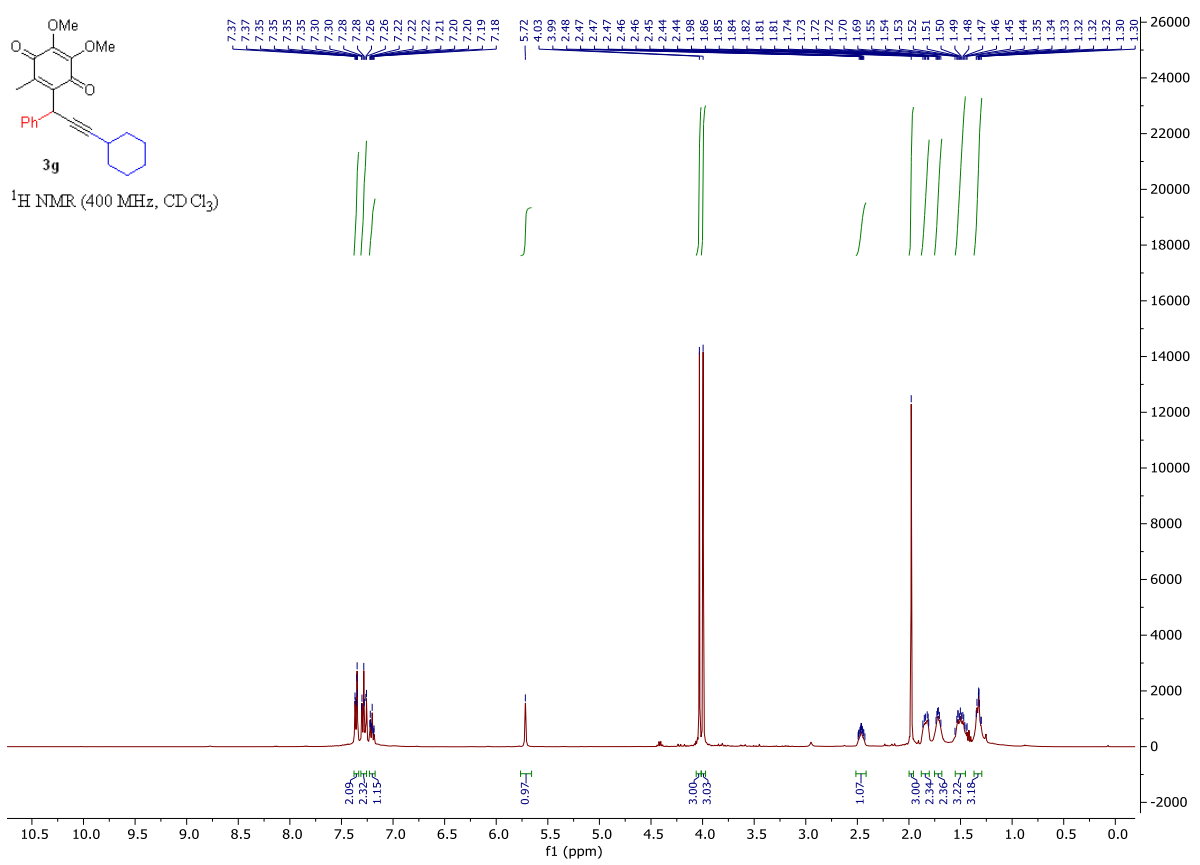
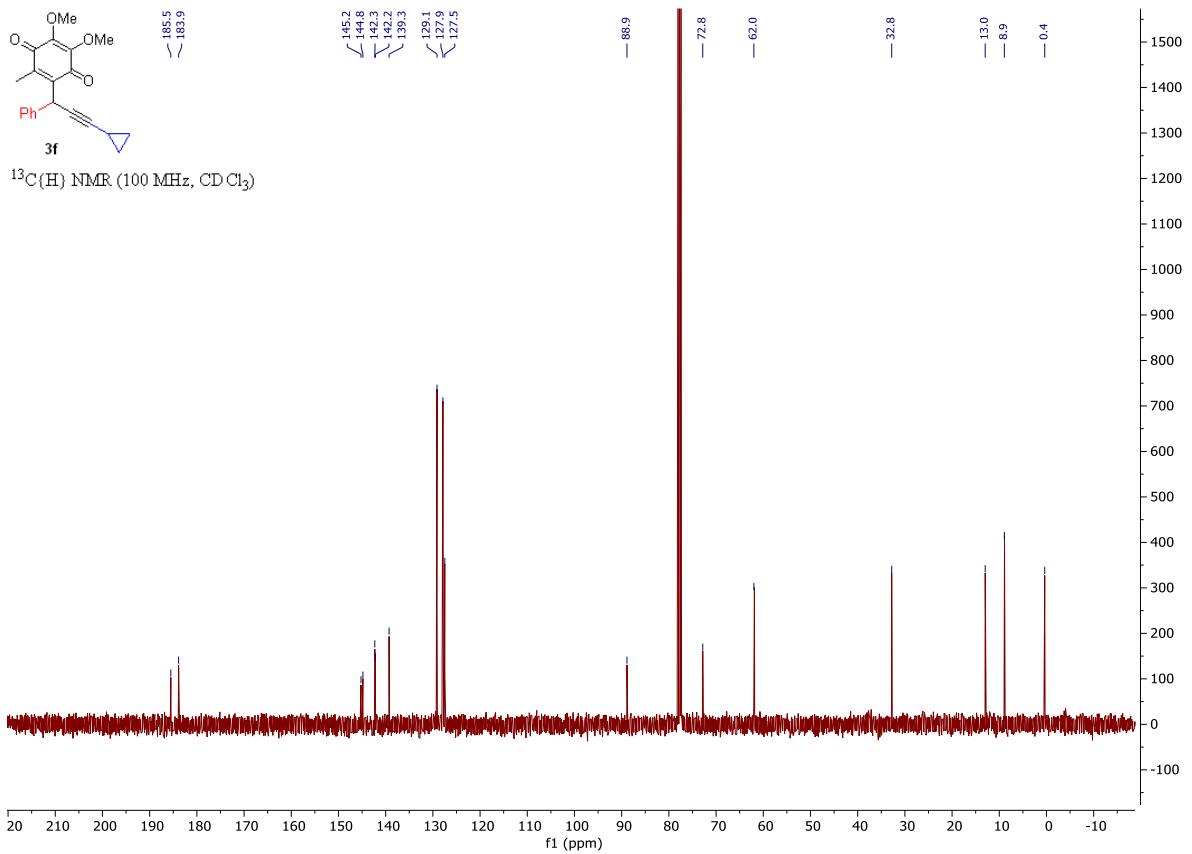


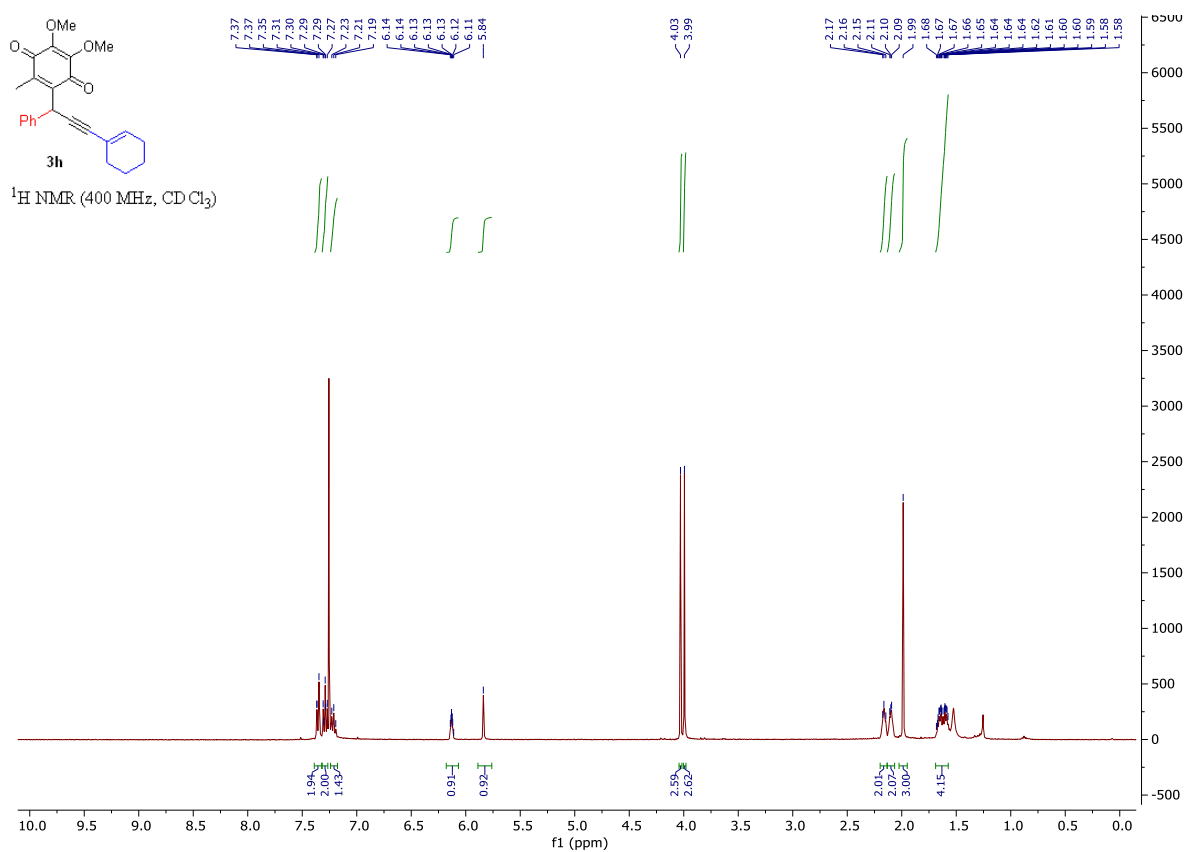
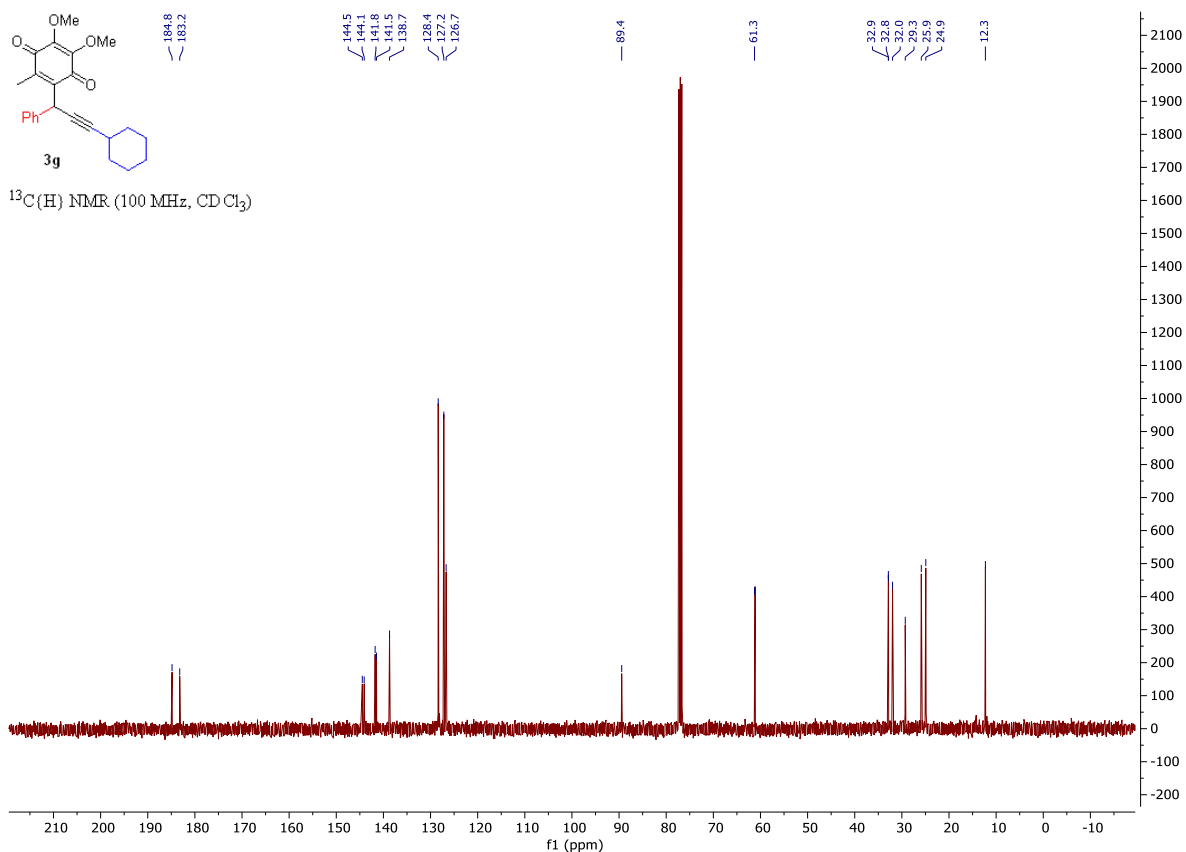


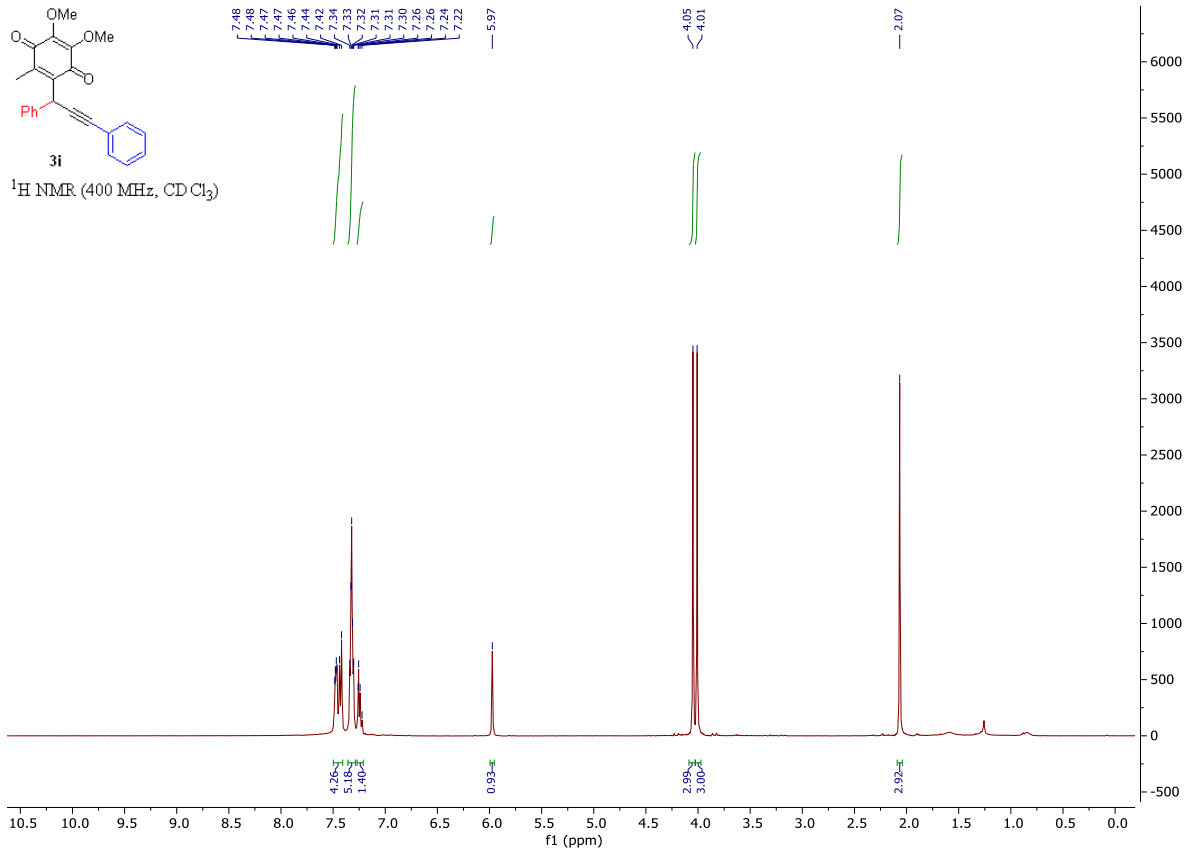
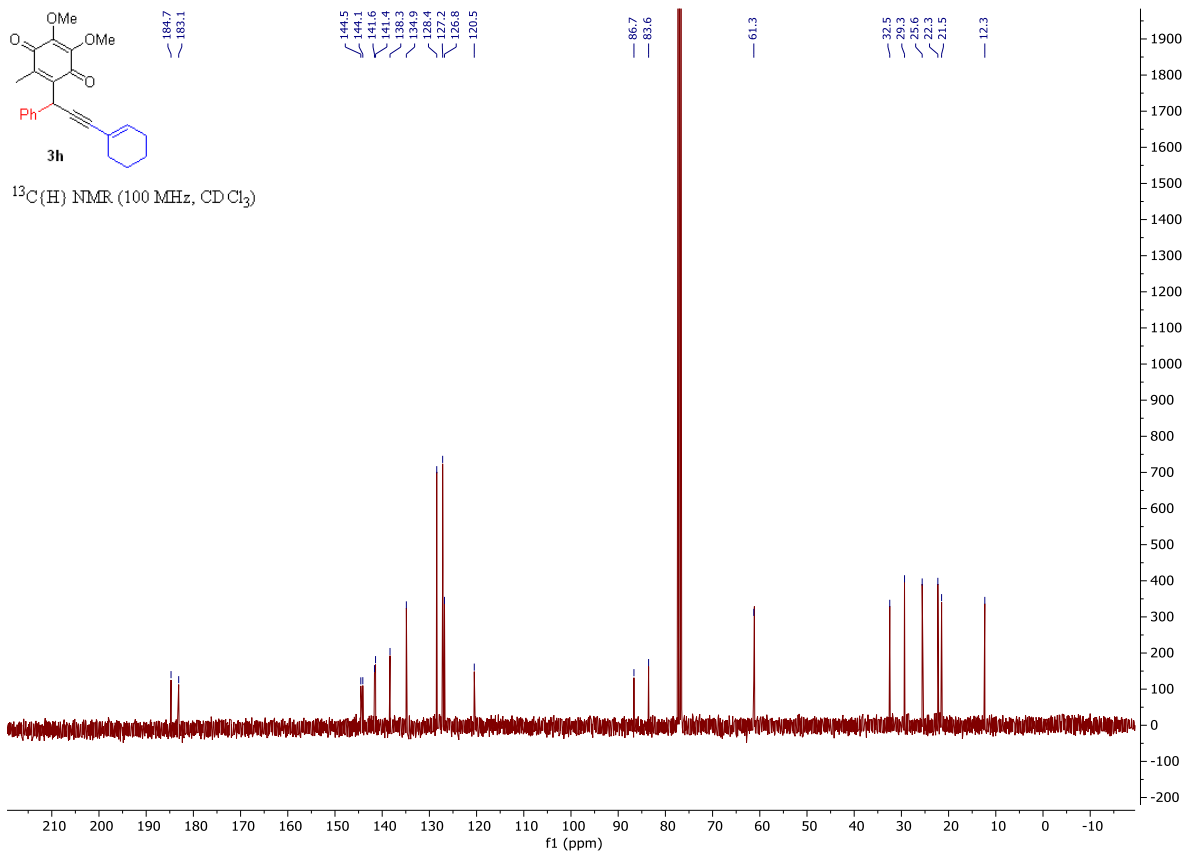


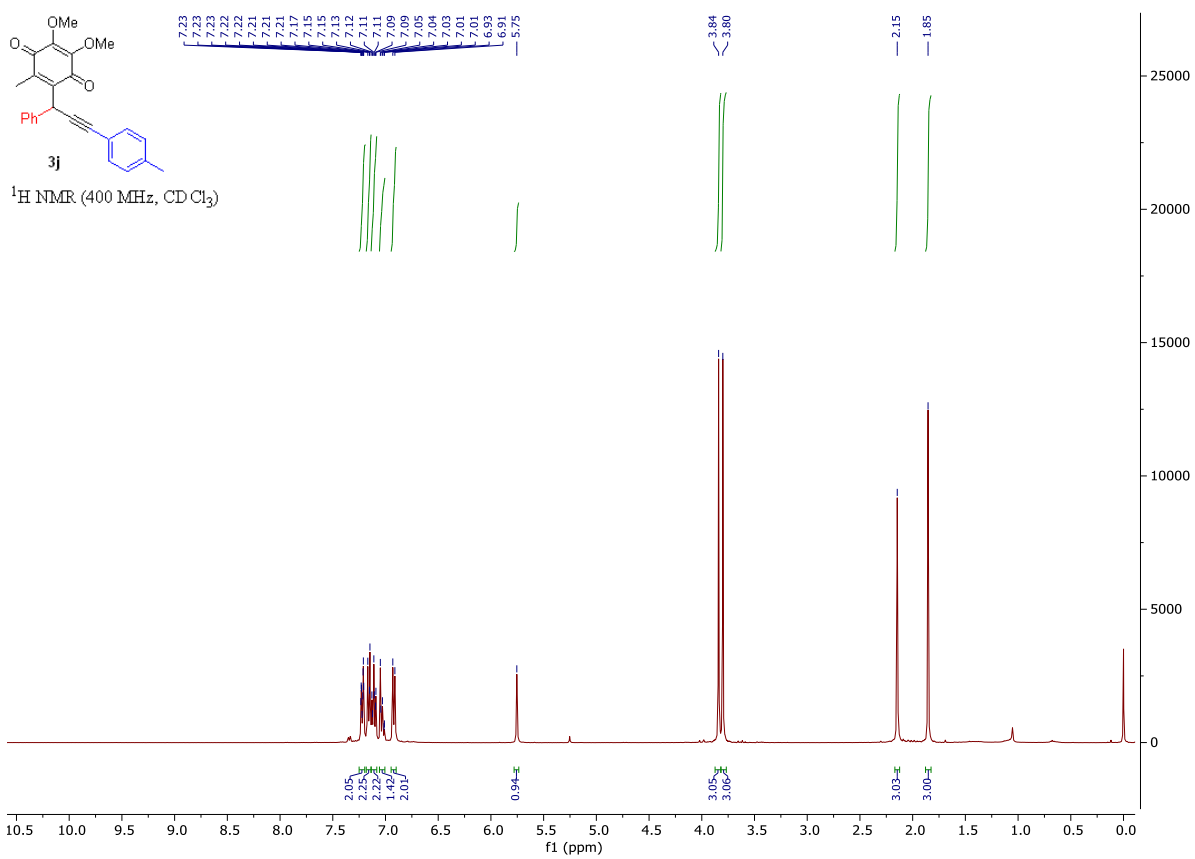
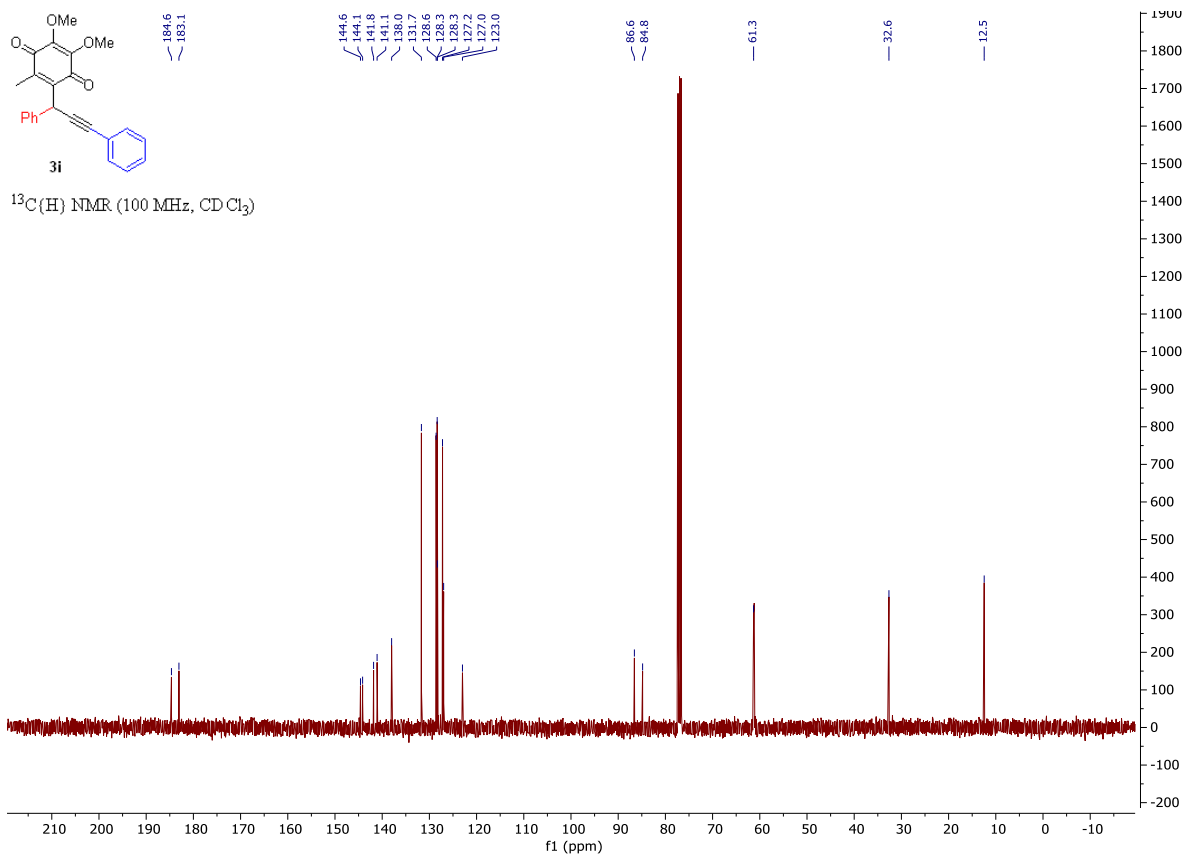


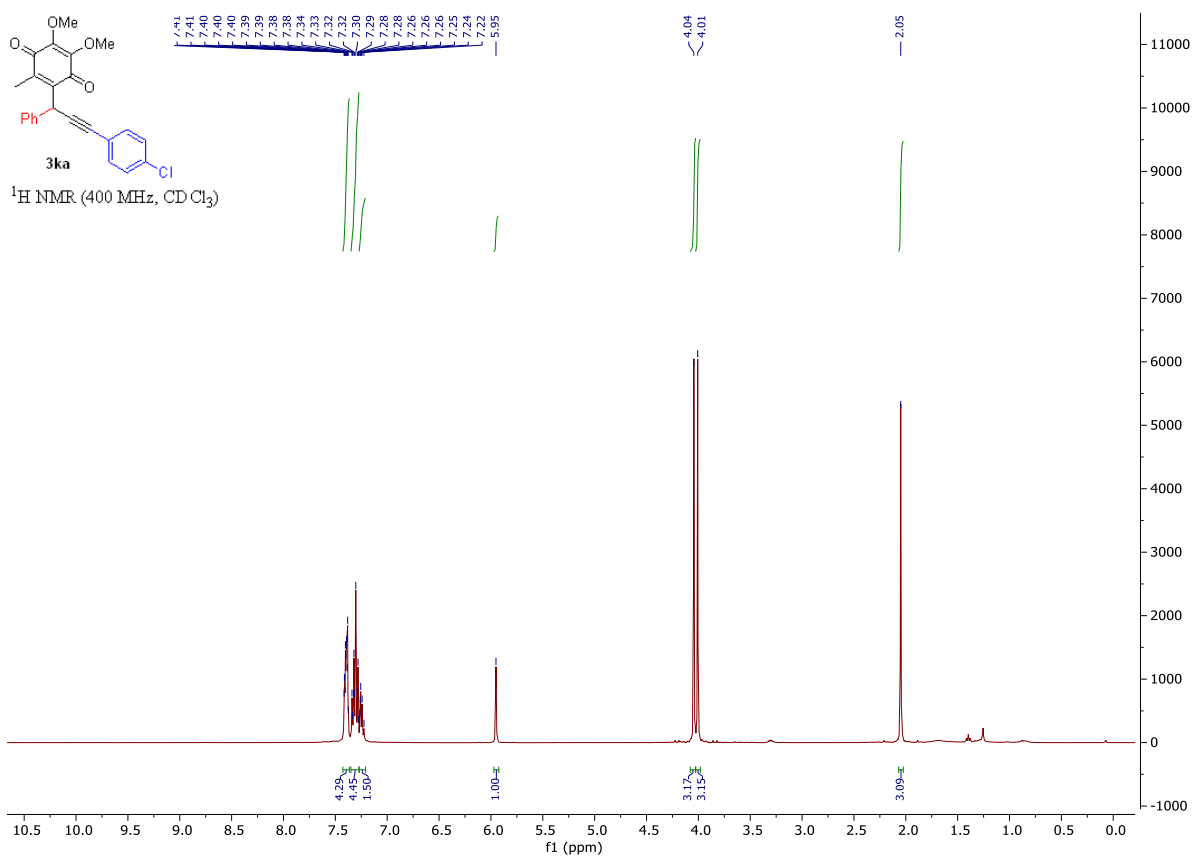
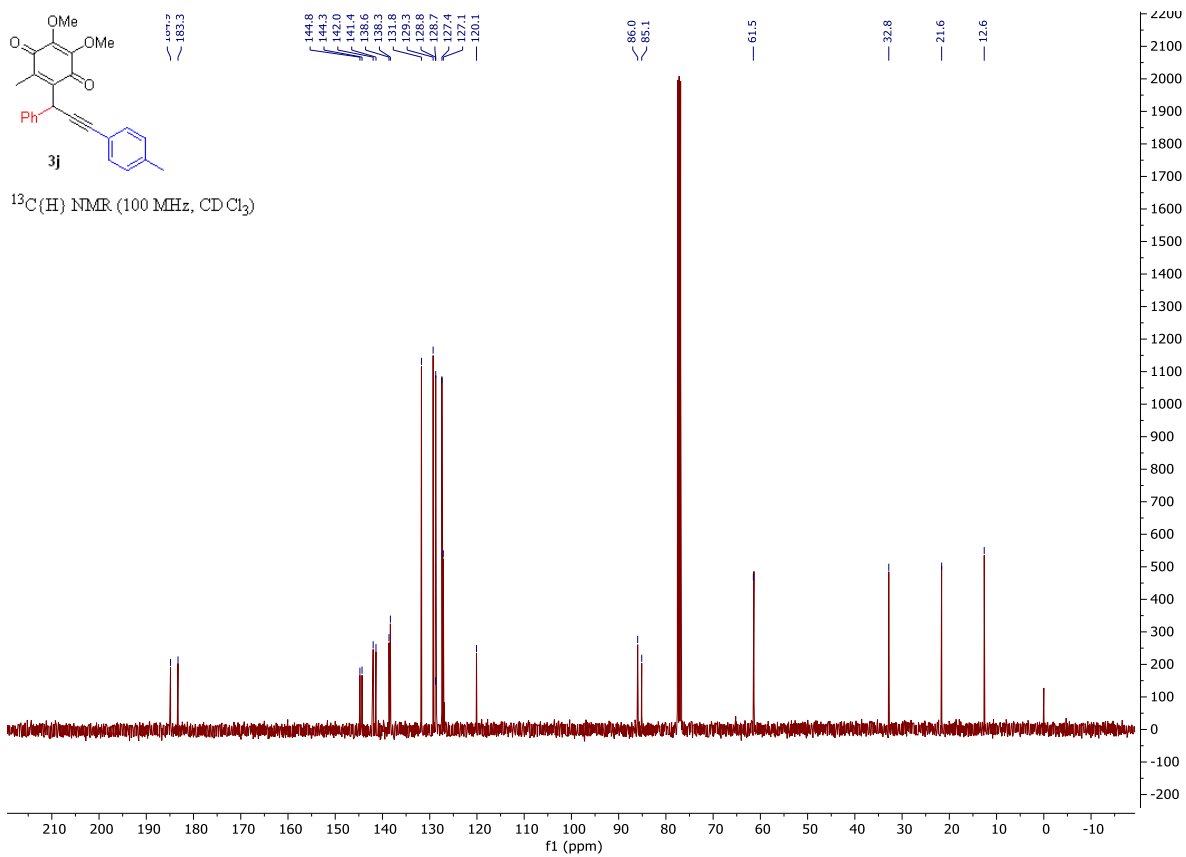


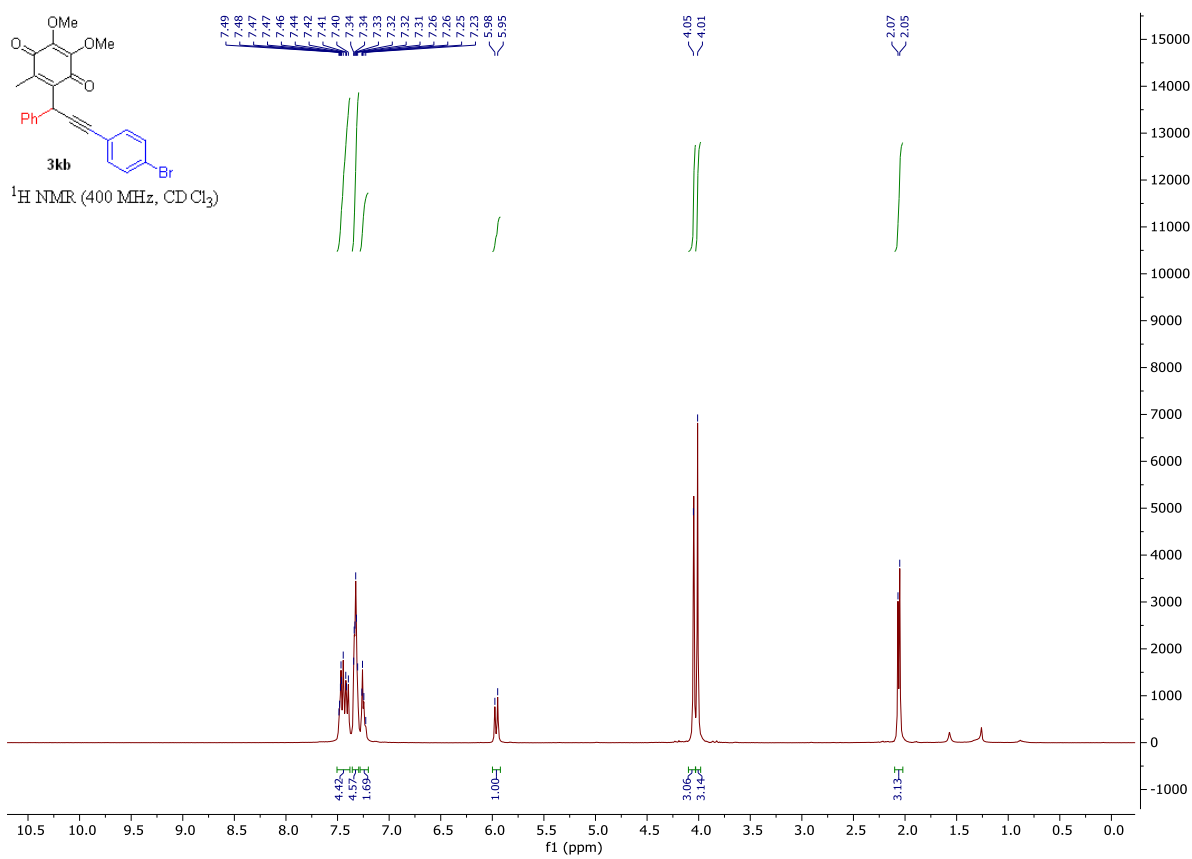
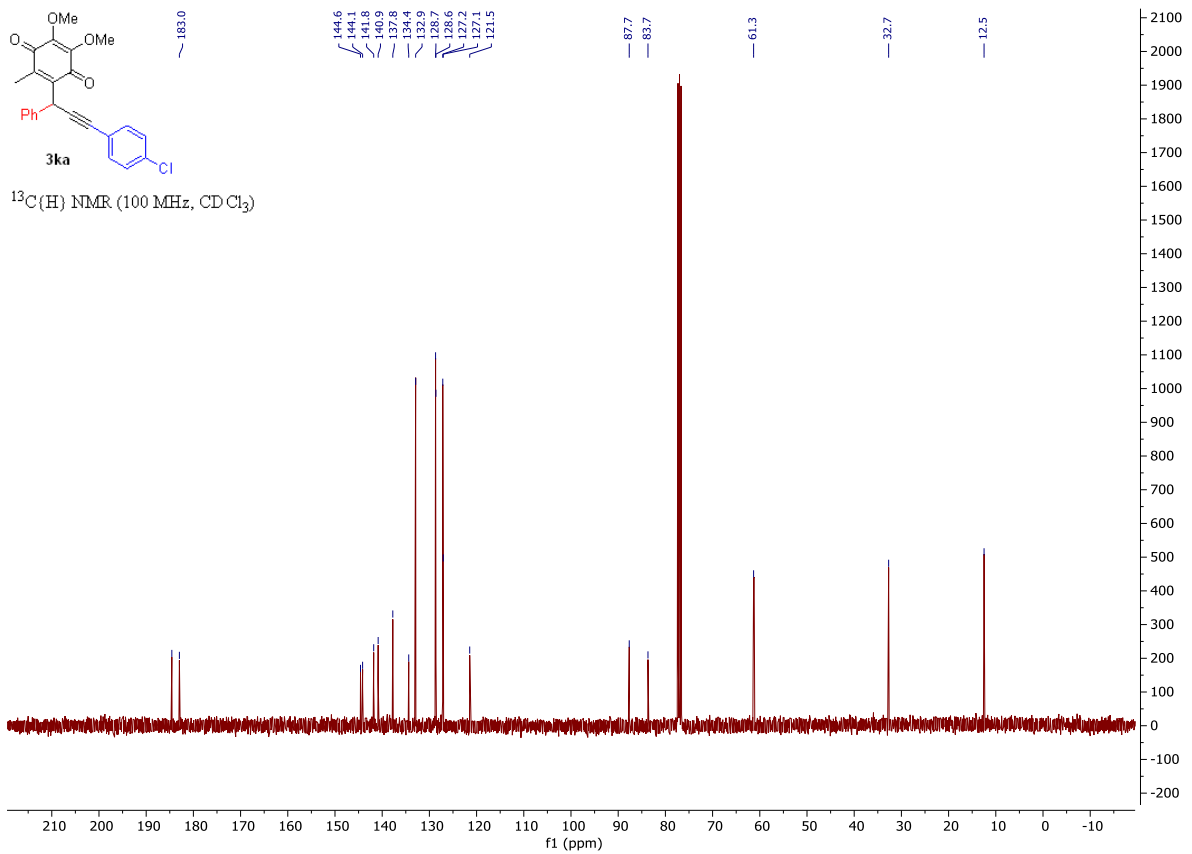


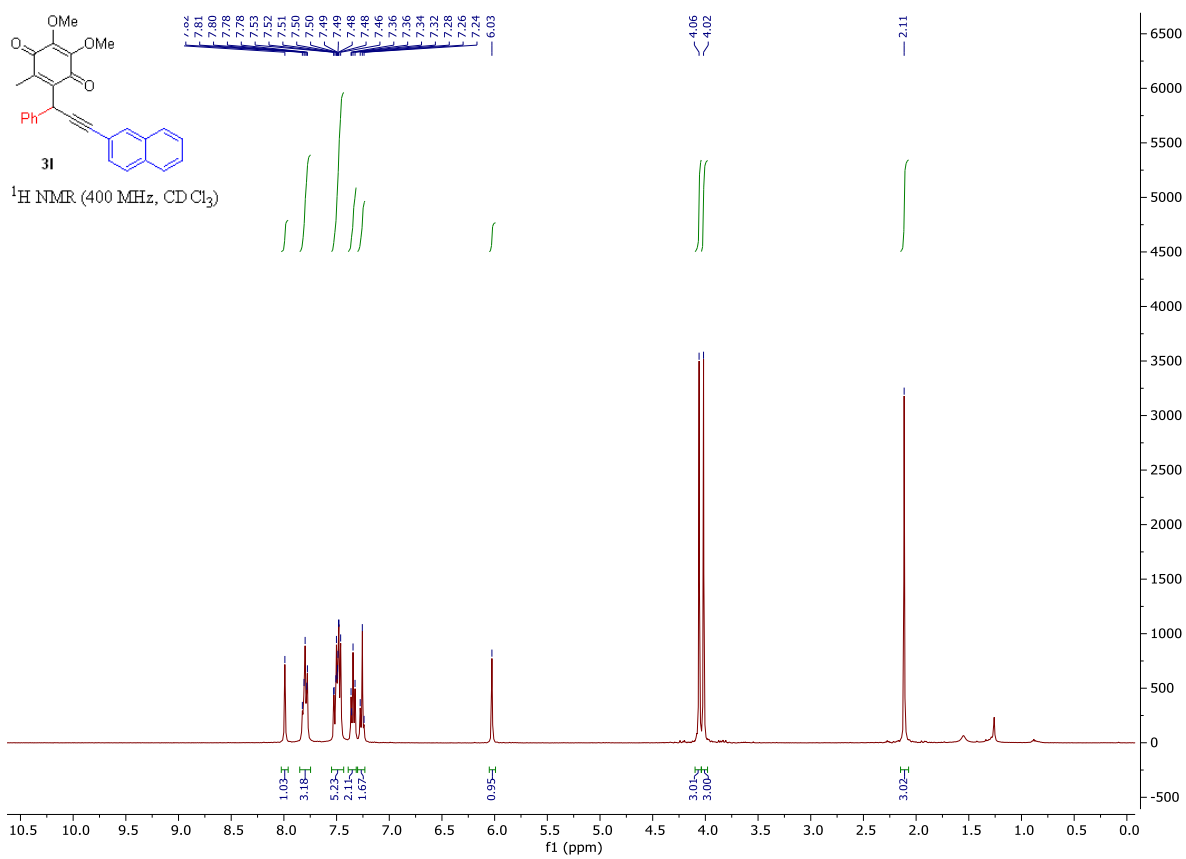
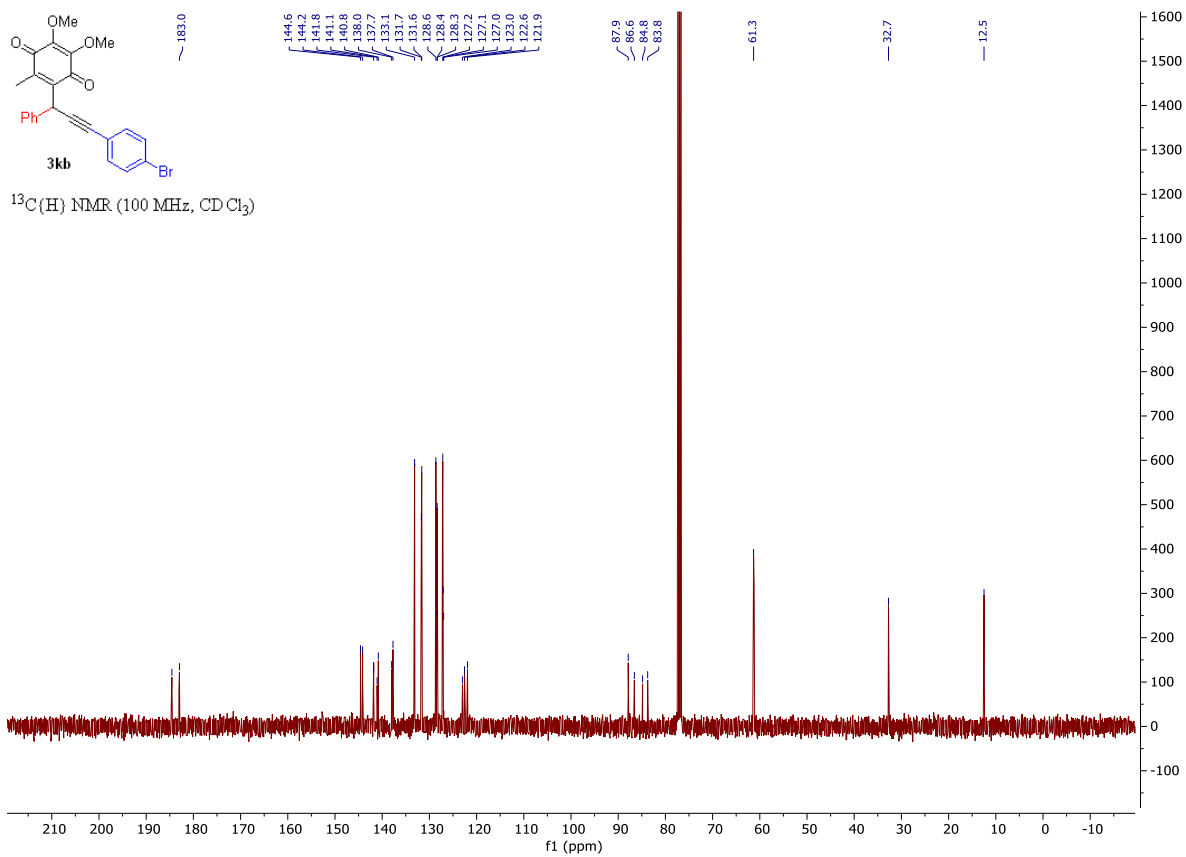


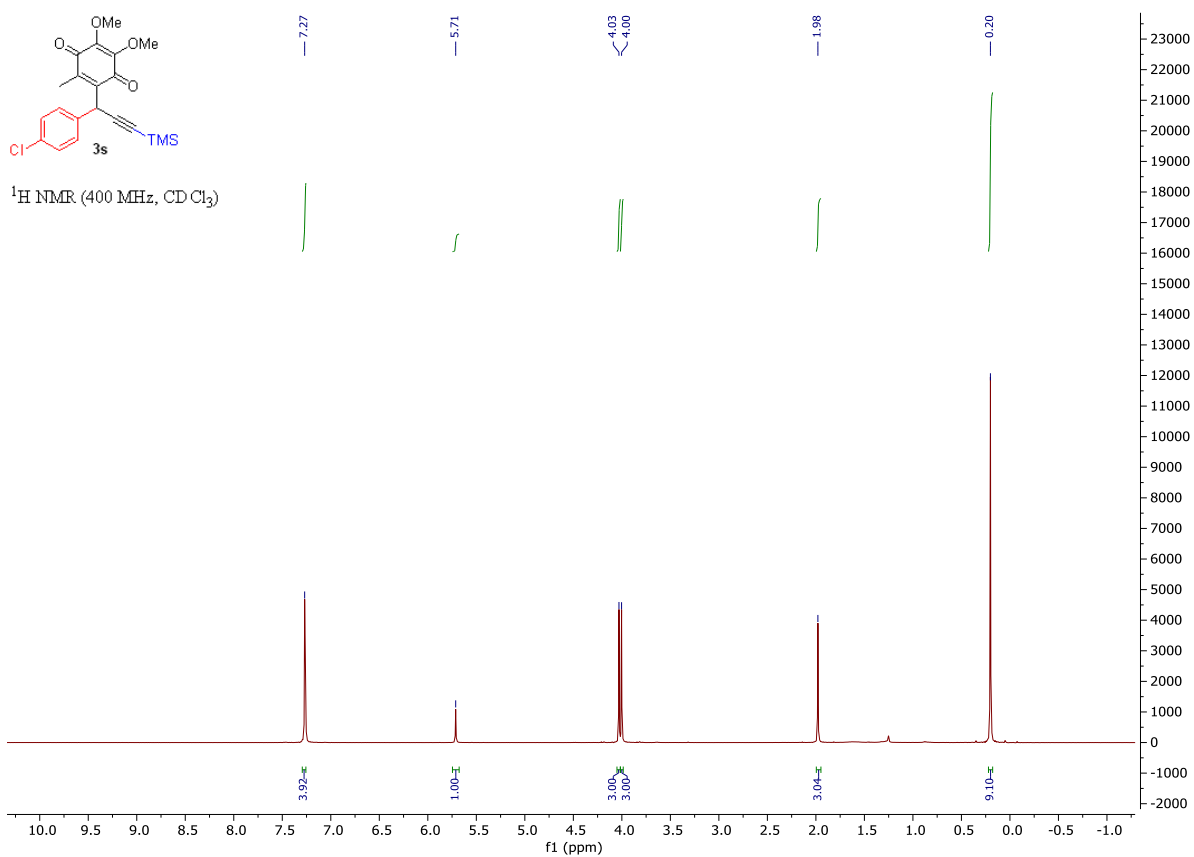
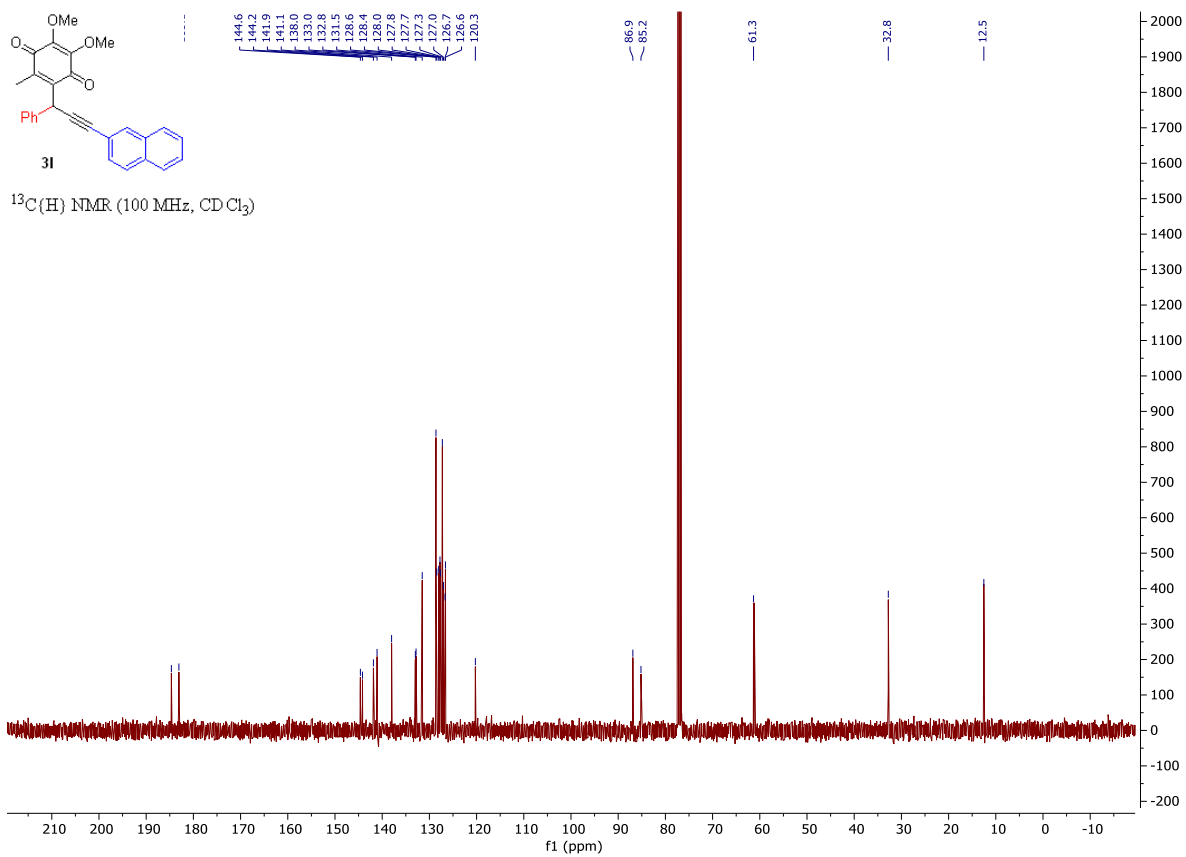


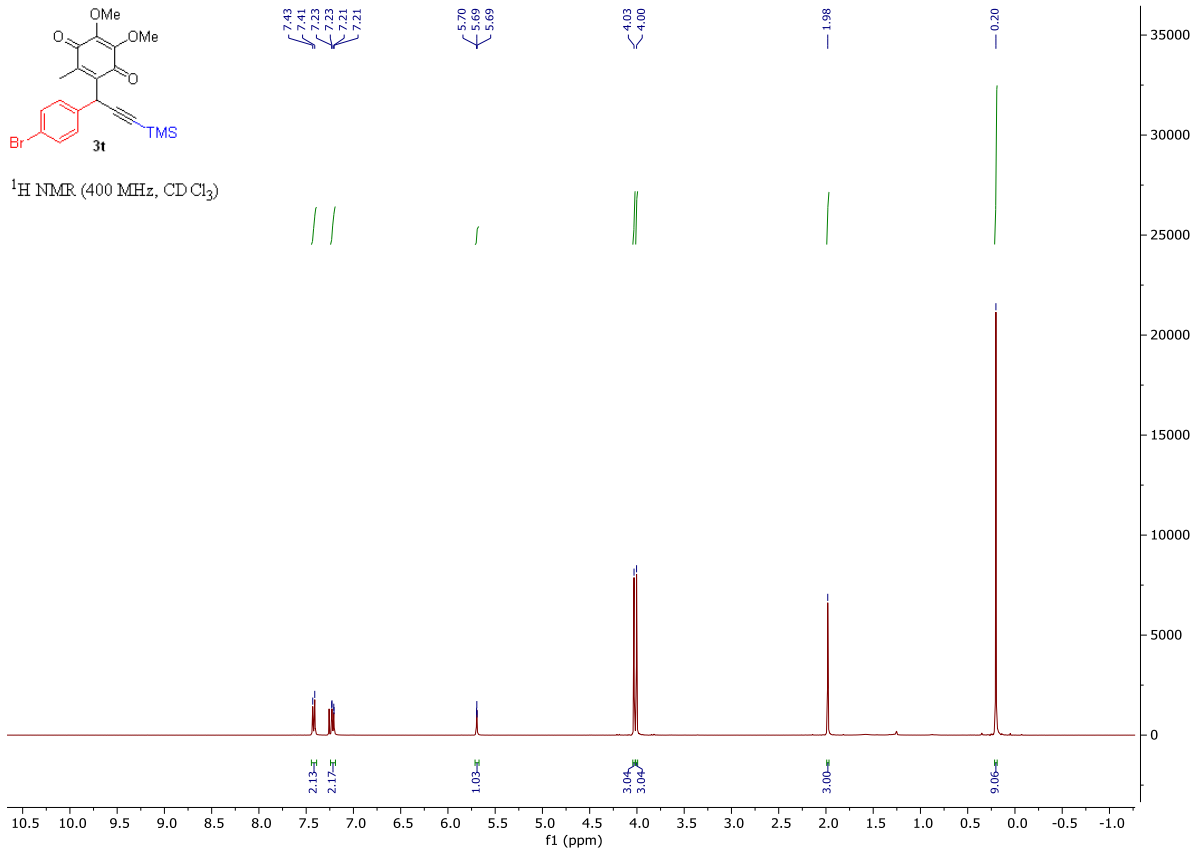
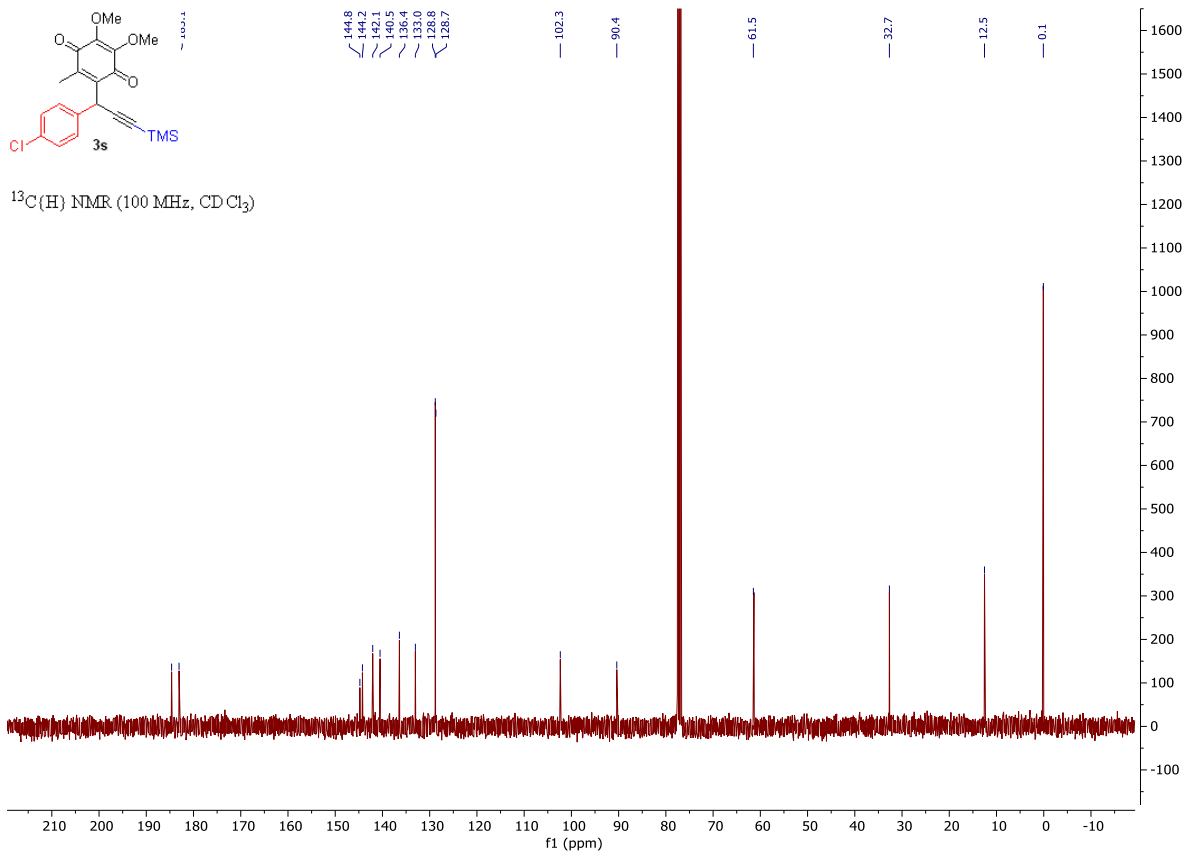


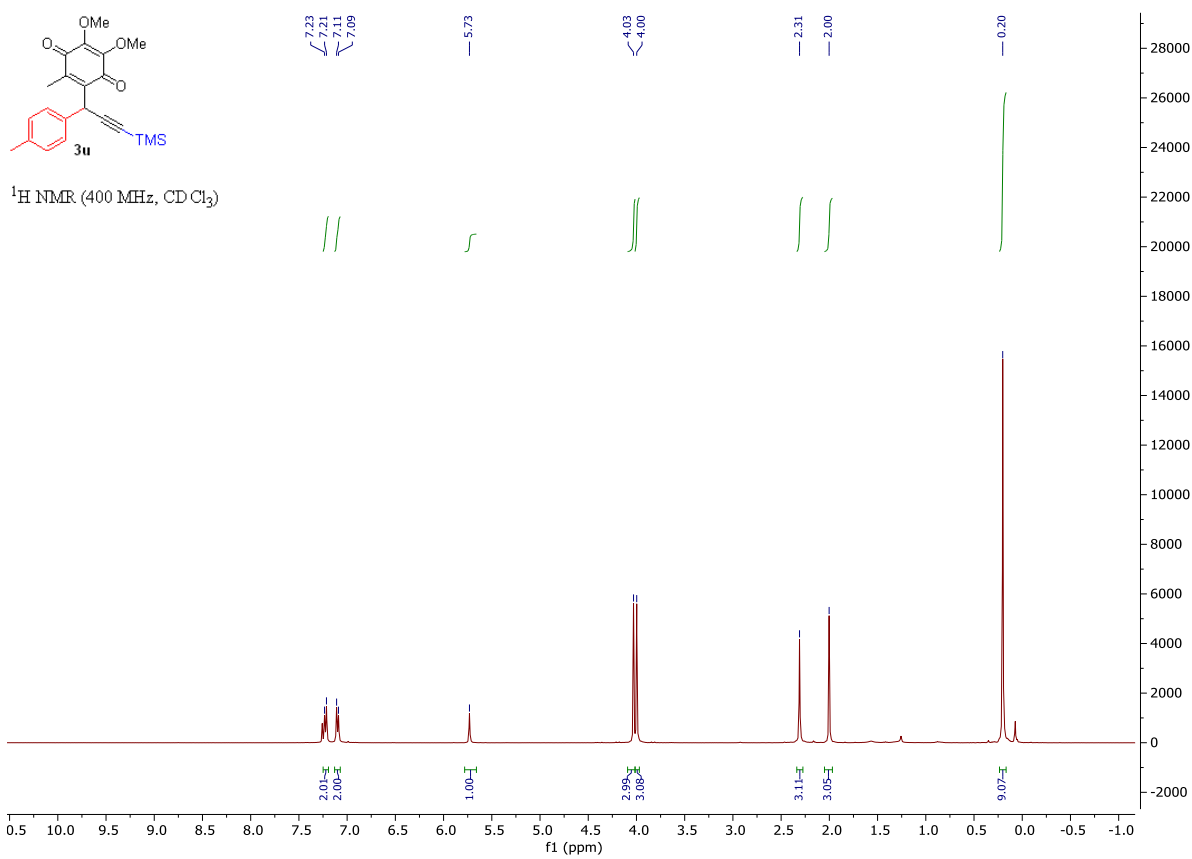
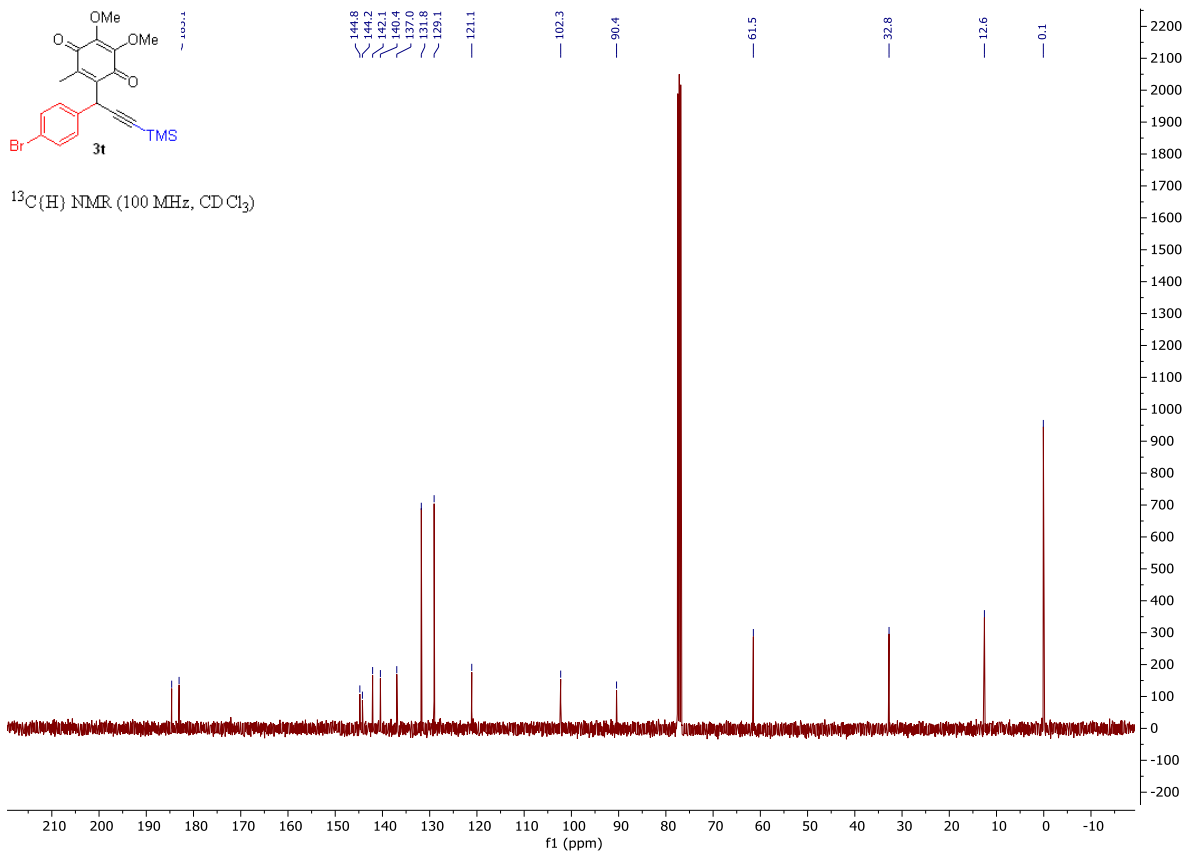


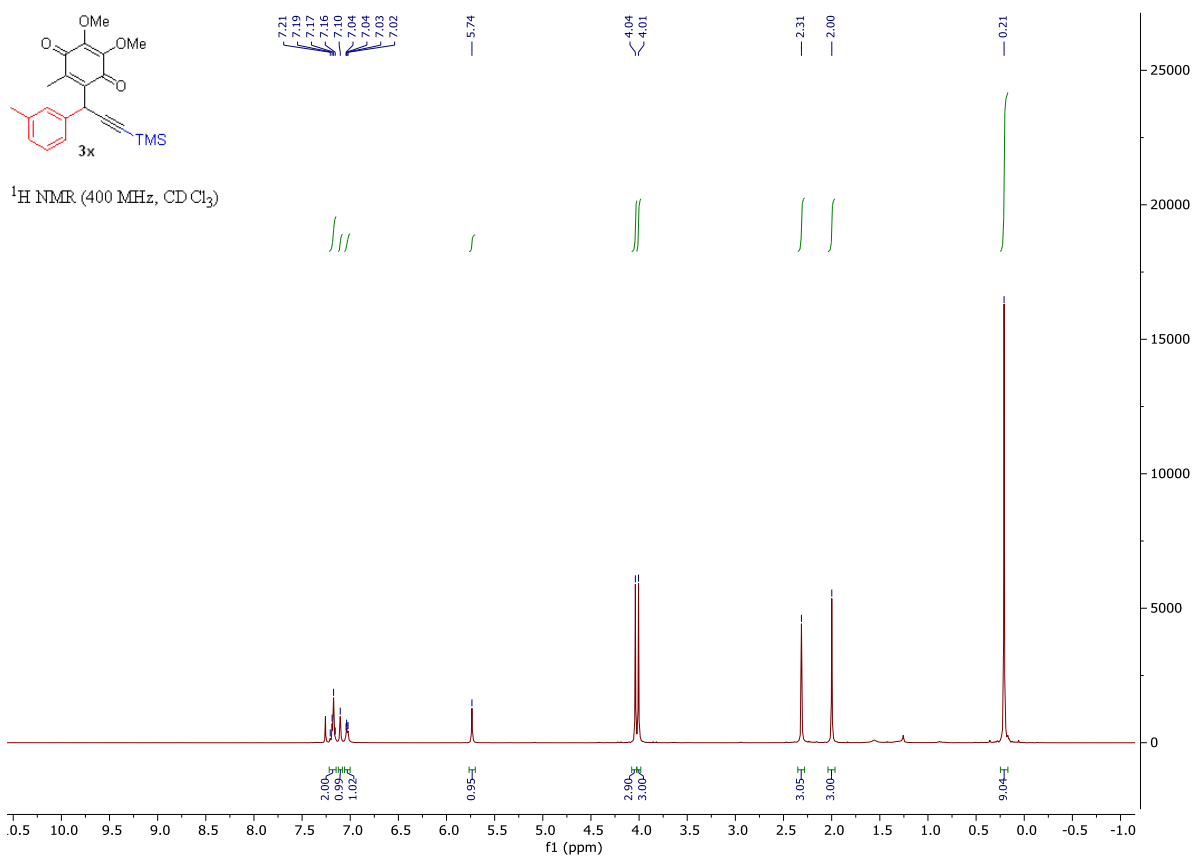
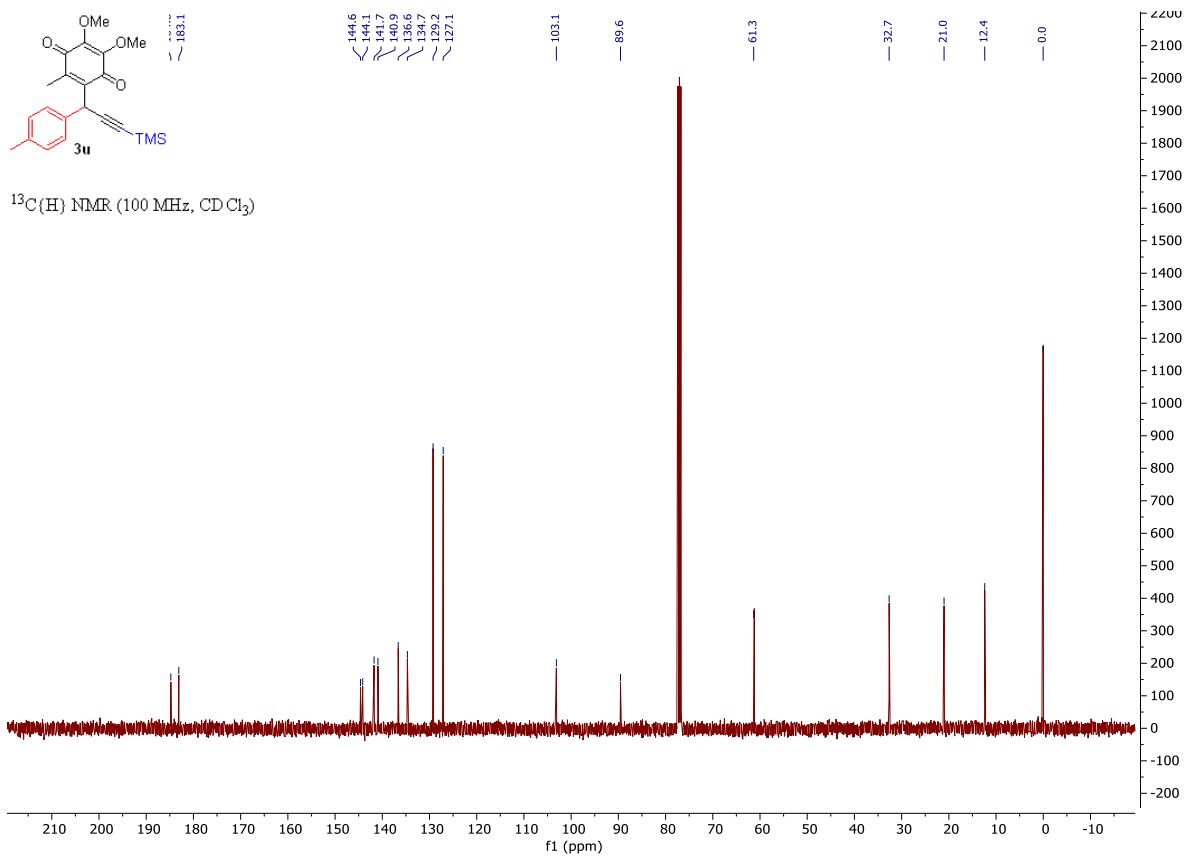


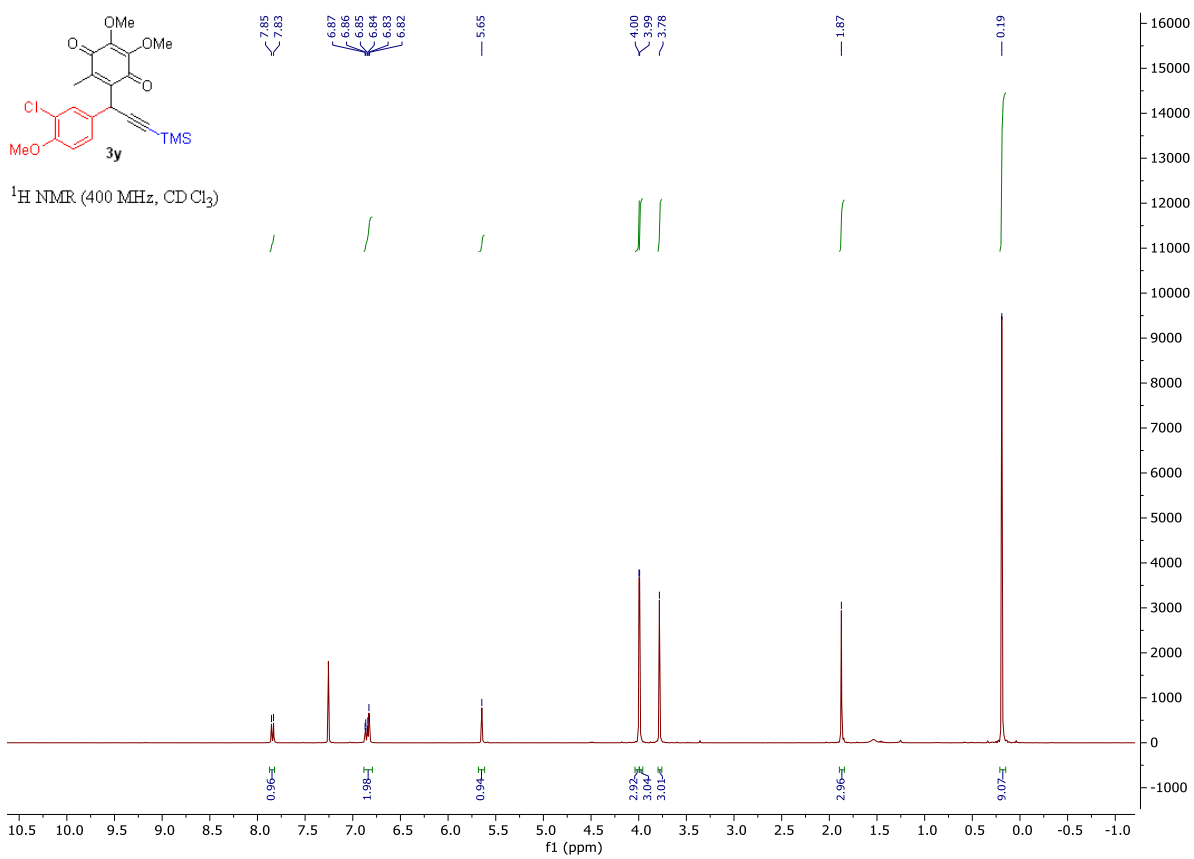
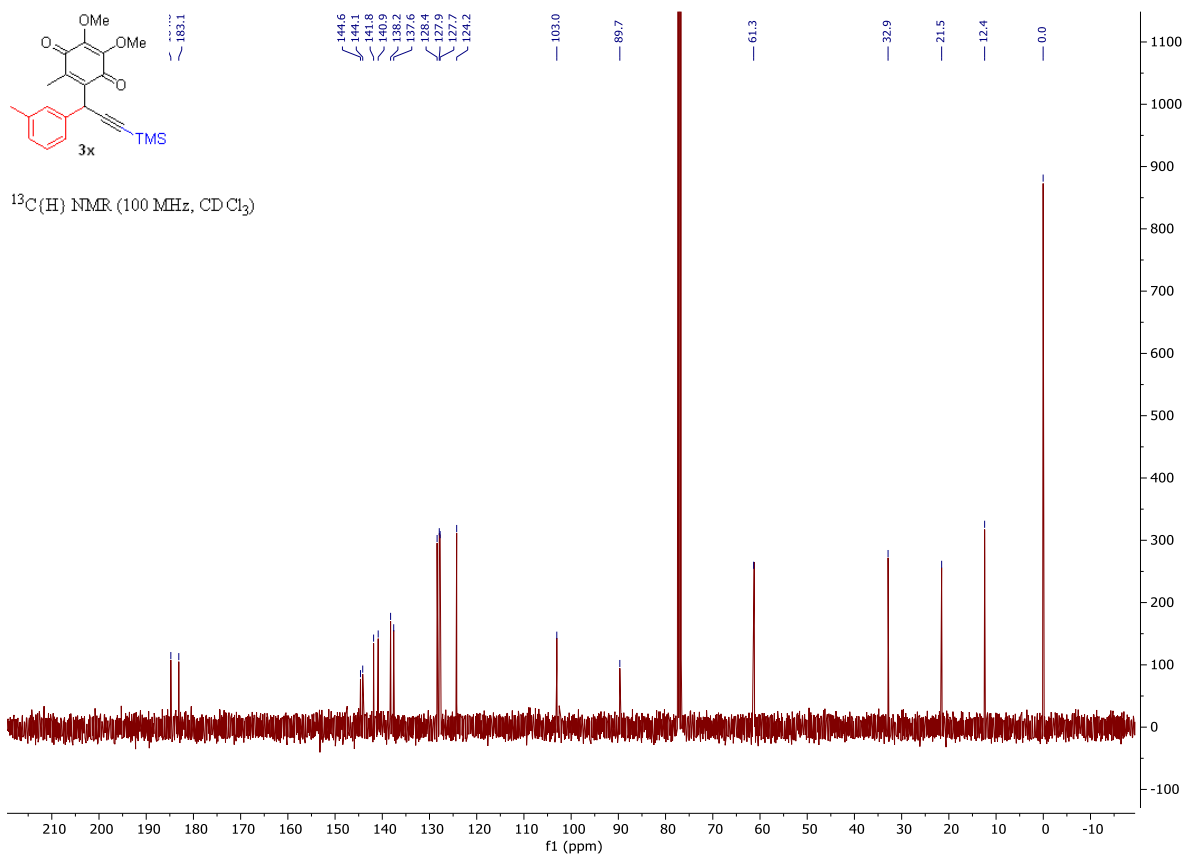


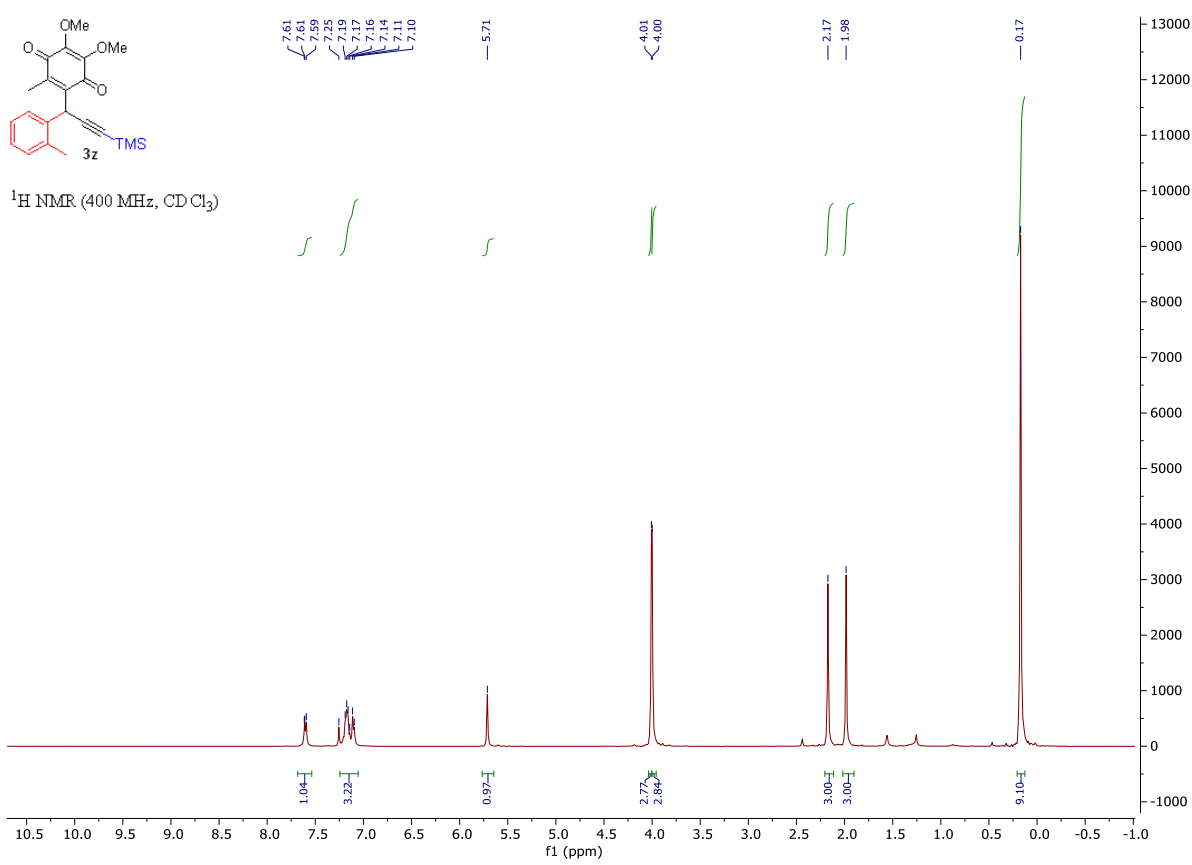
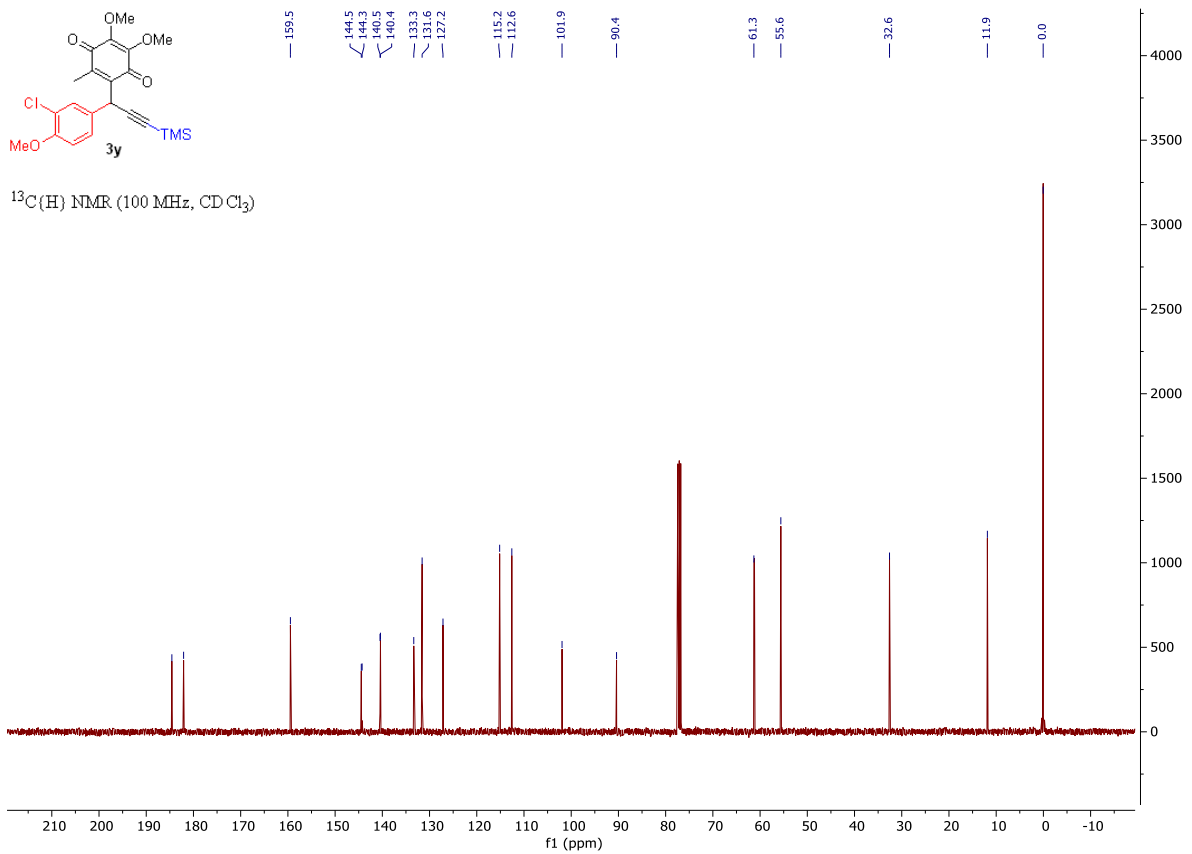


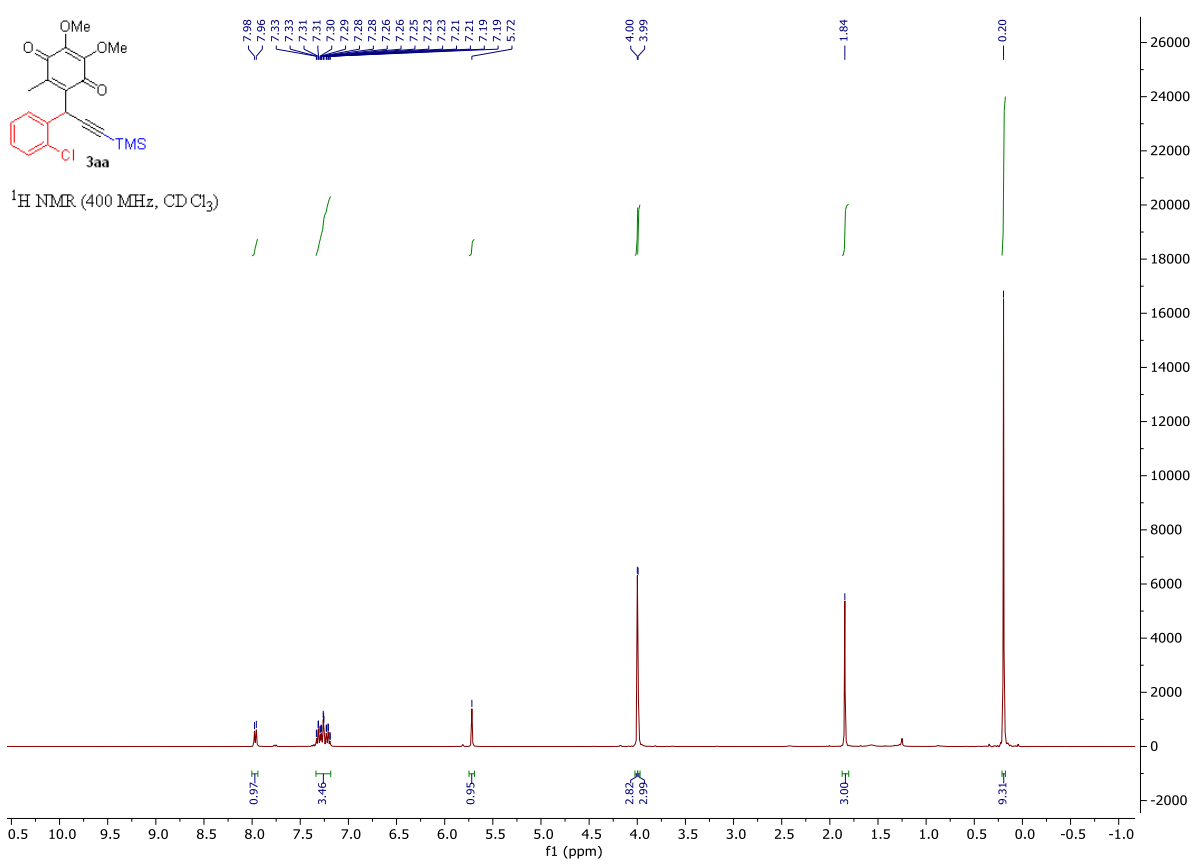
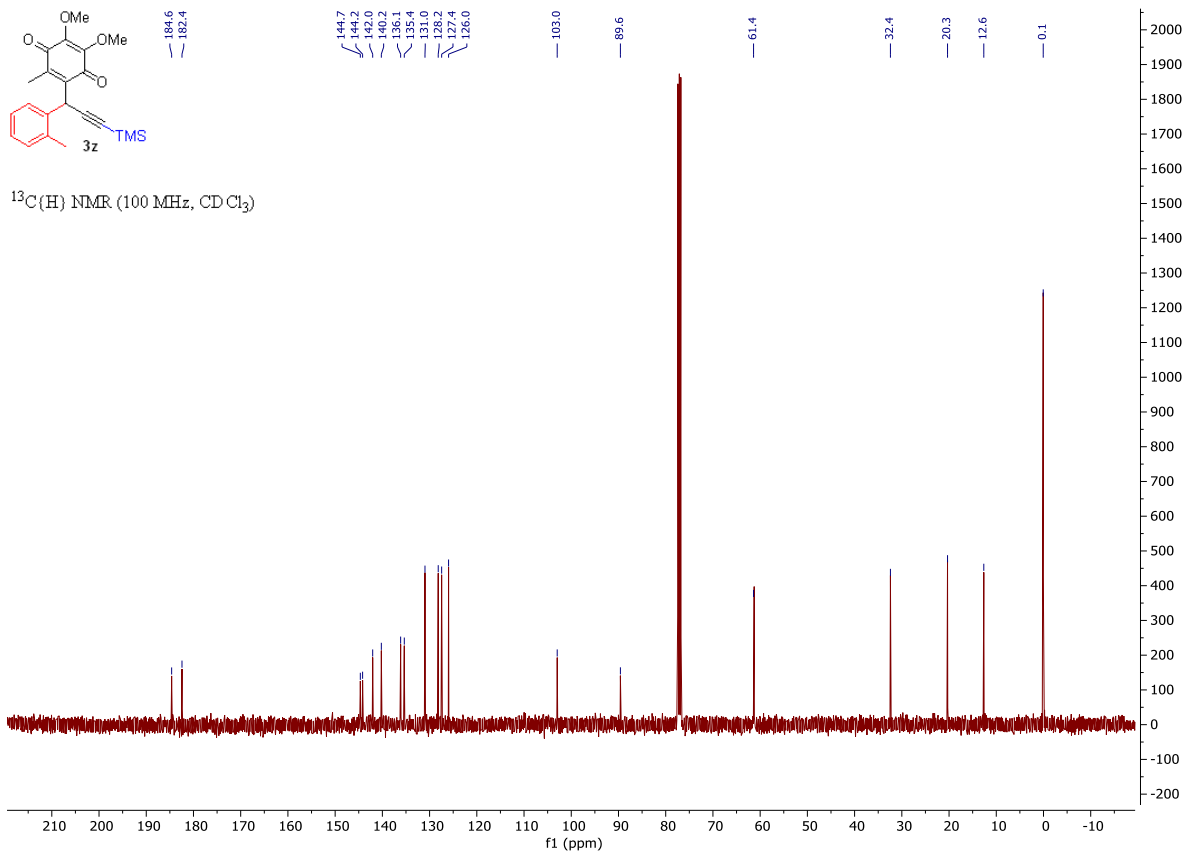


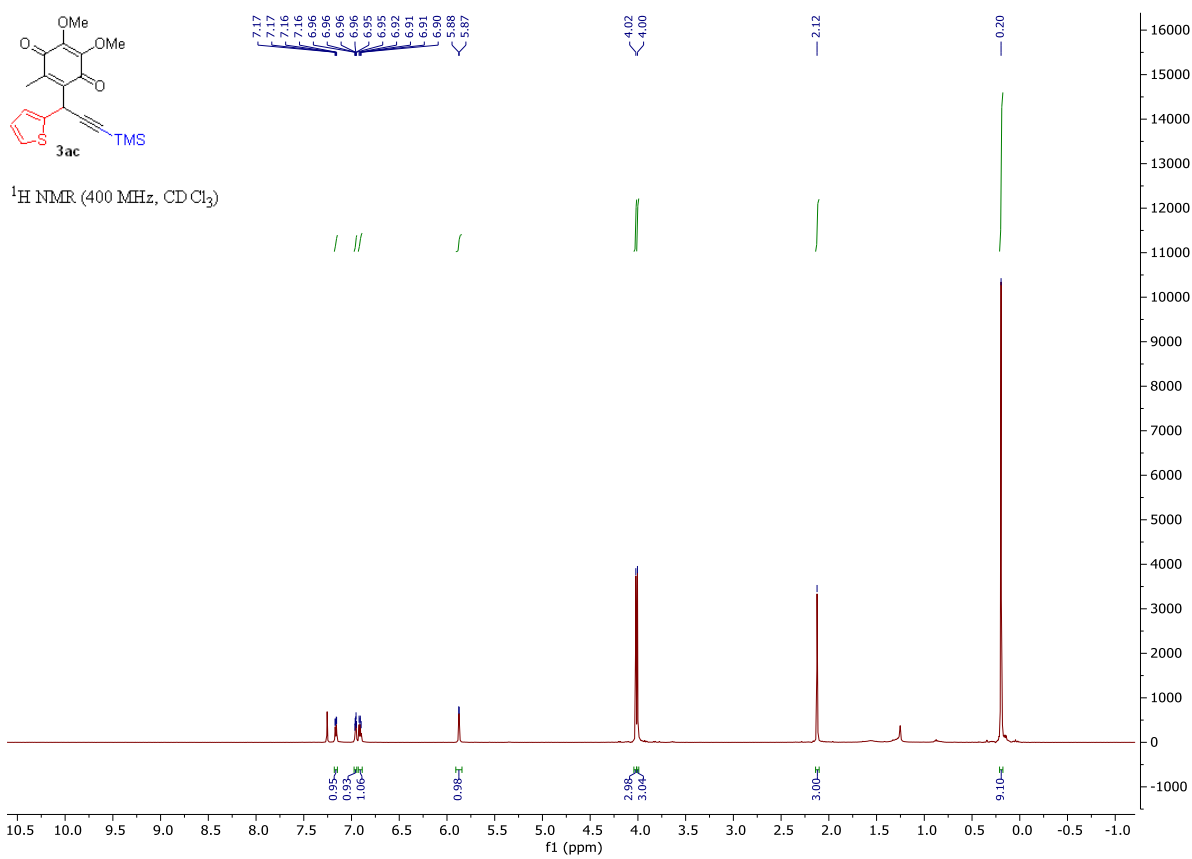
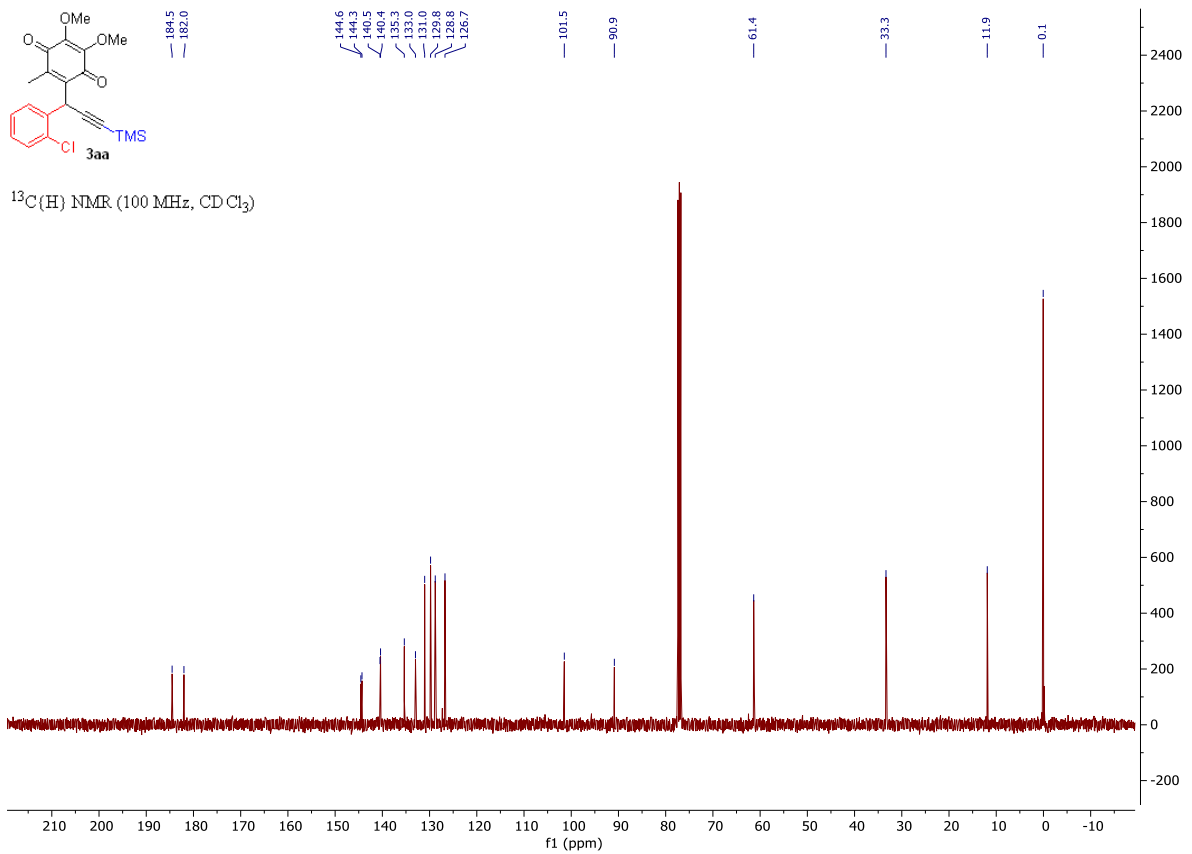


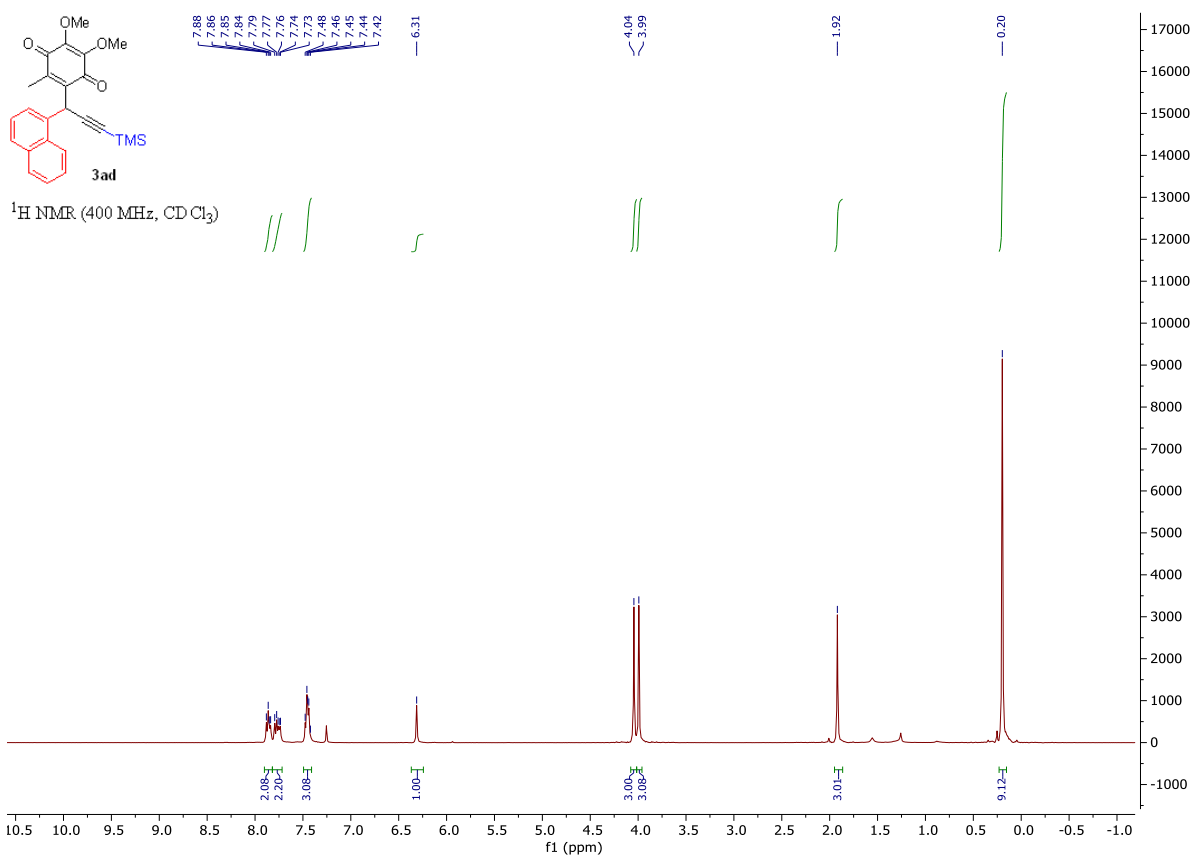
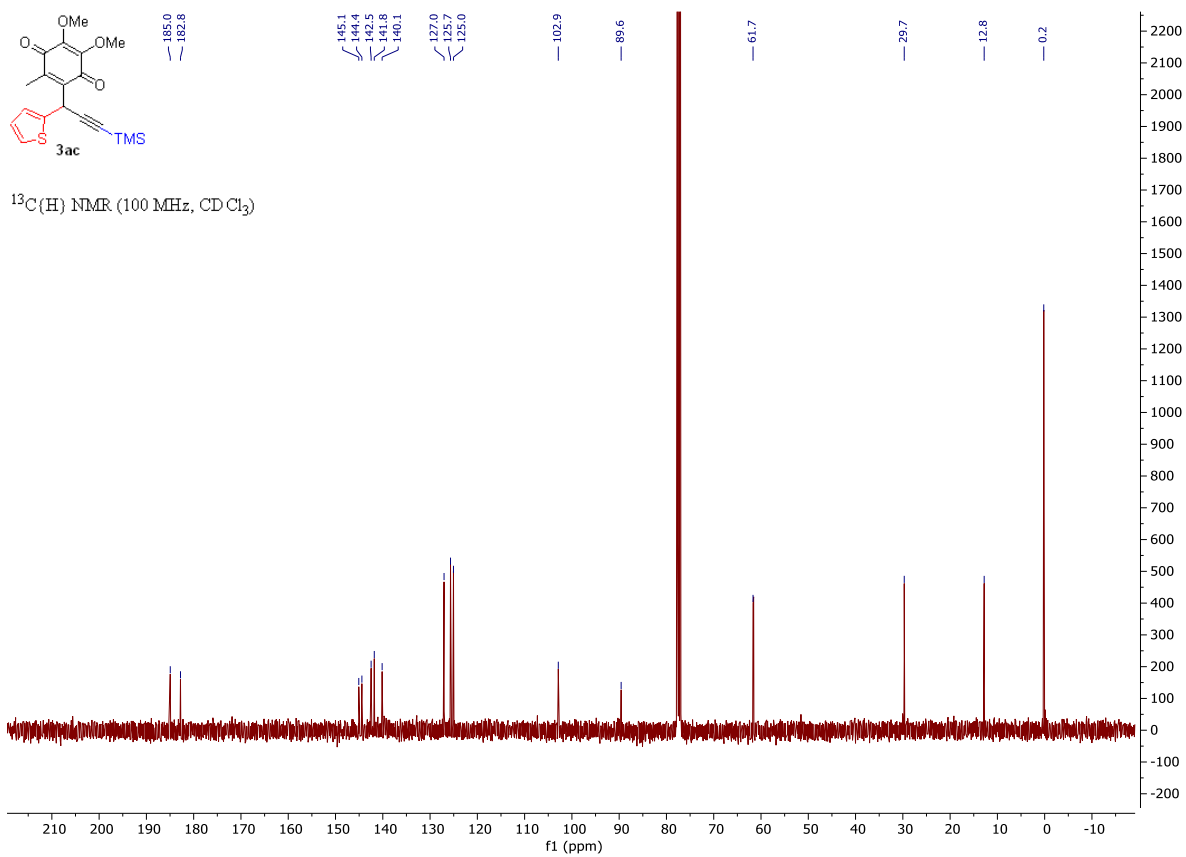


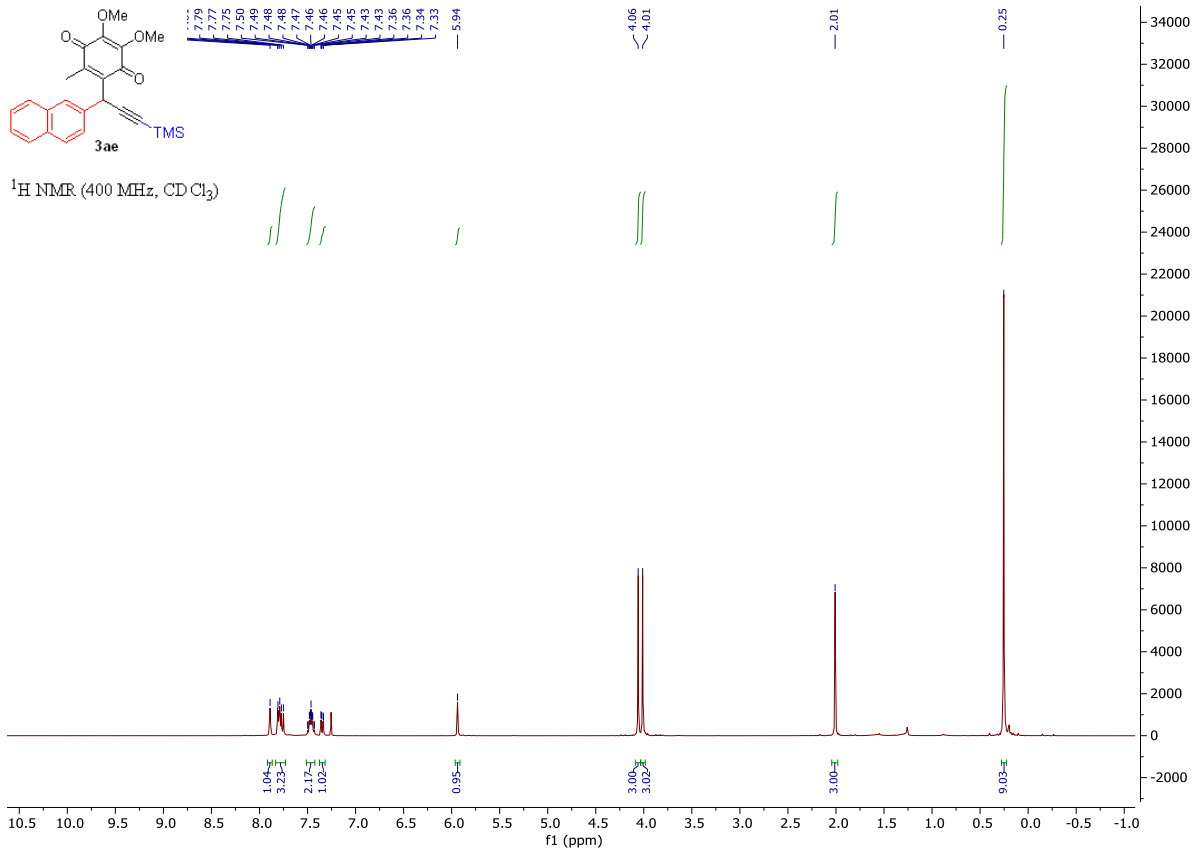
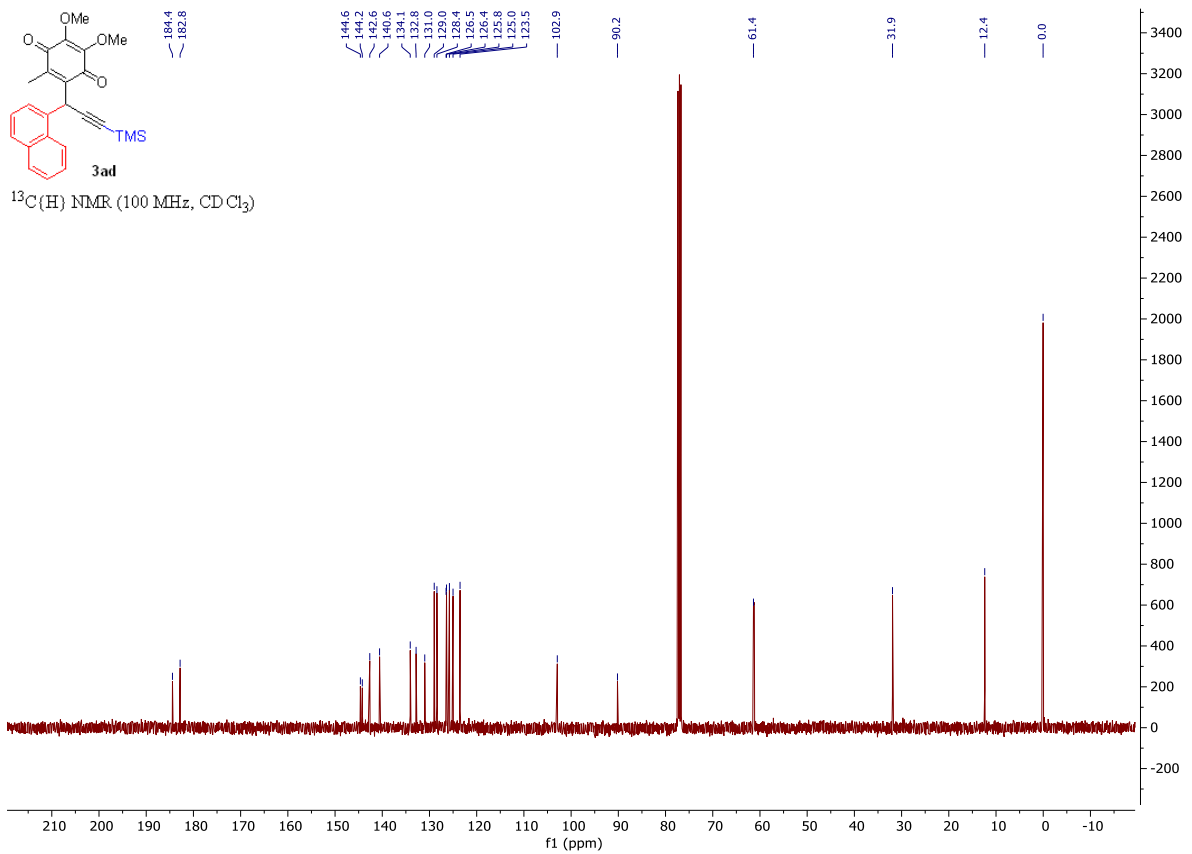


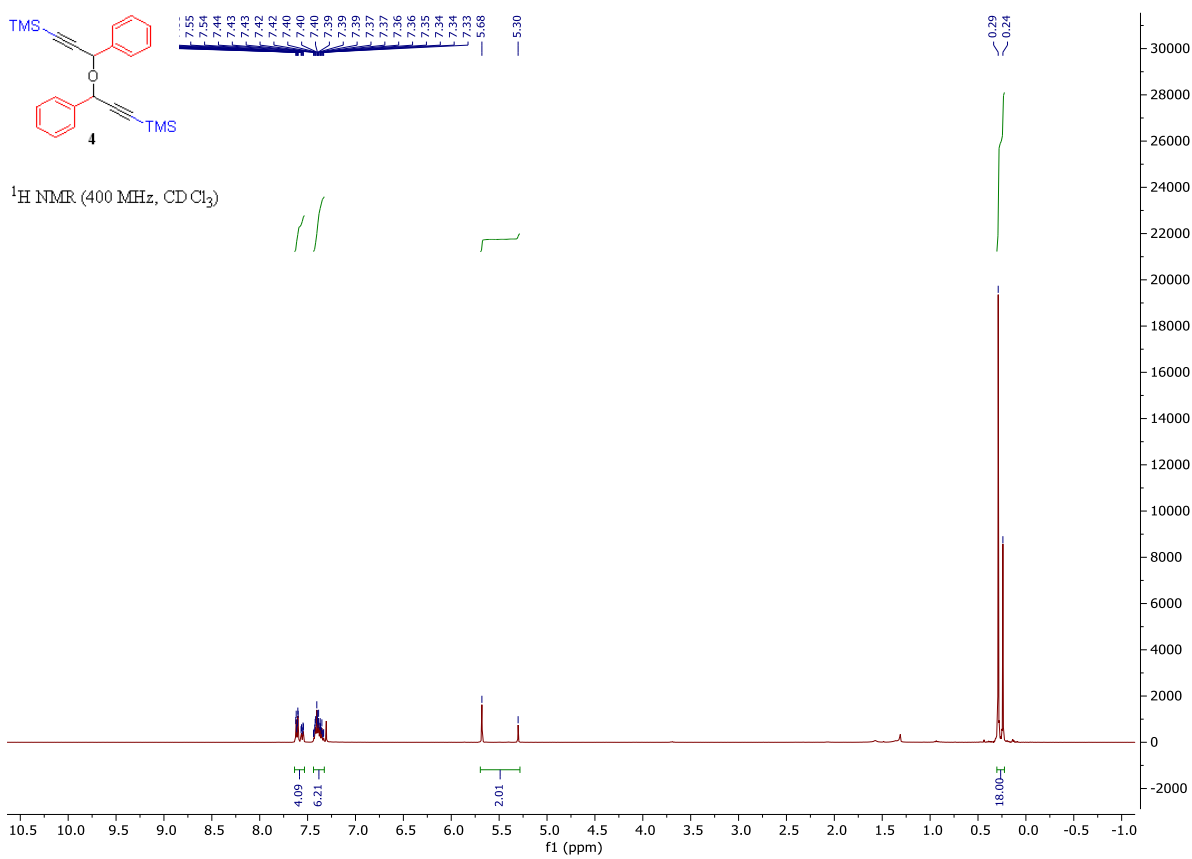
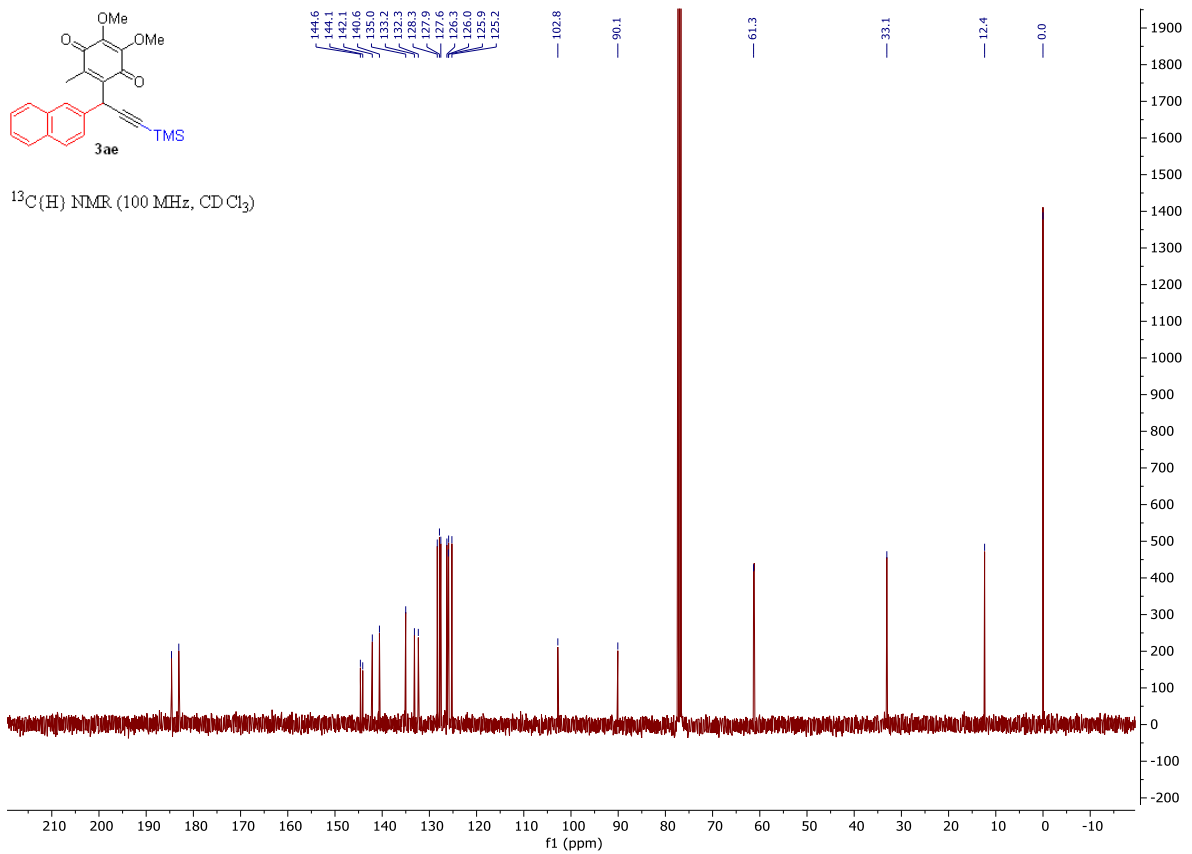












2. Mechanistic studies – LCMS analysis of raw reaction mixture

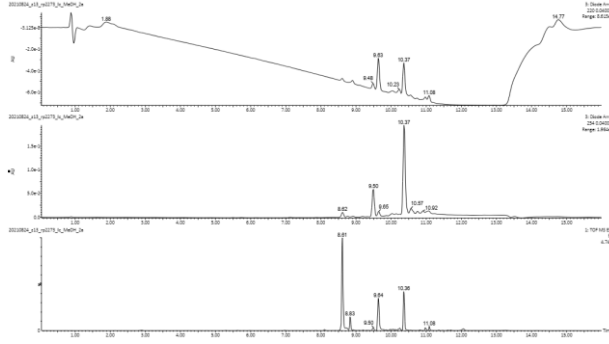


Fig. 1 UV chromatograms (λ=220 nm – top, λ=254 nm – middle) and Base Peak chromatogram – bottom for sample: QAT-163

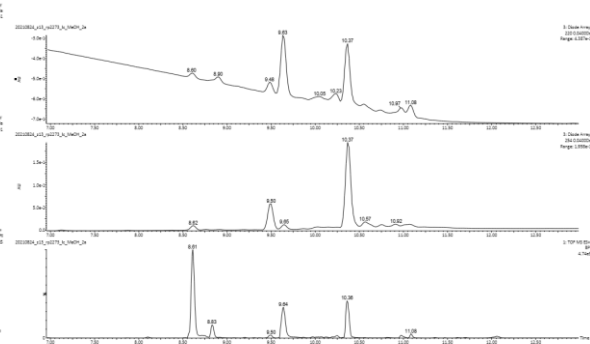


Fig. 2 Close-ups of UV chromatograms (λ=220 nm – top, λ=254 nm – middle) and Base Peak chromatogram – bottom for sample: QAT-163

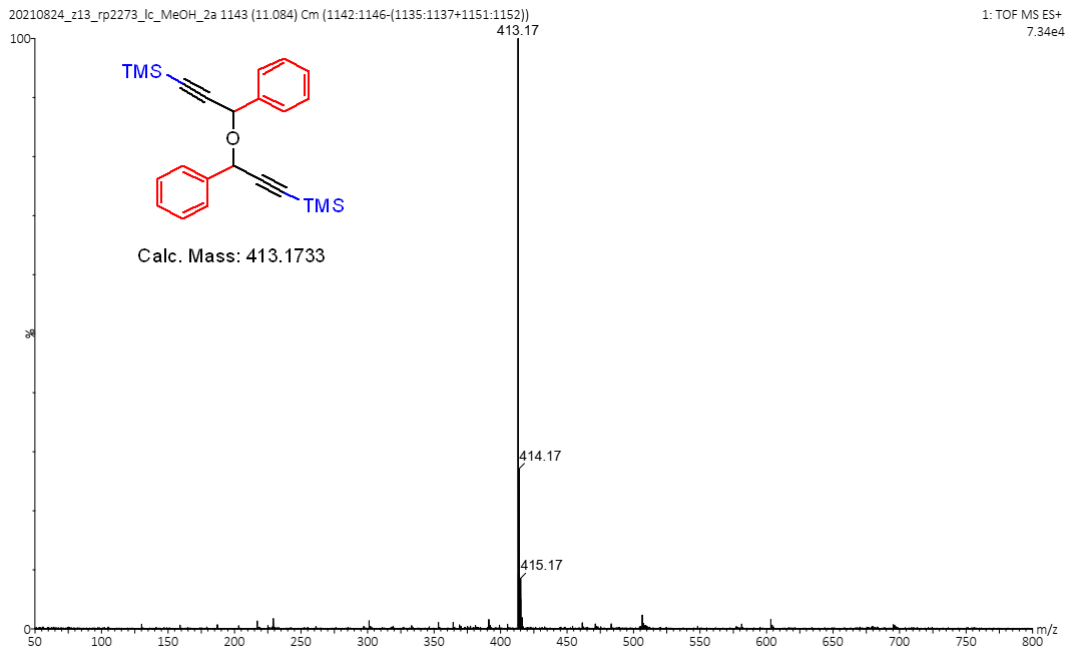
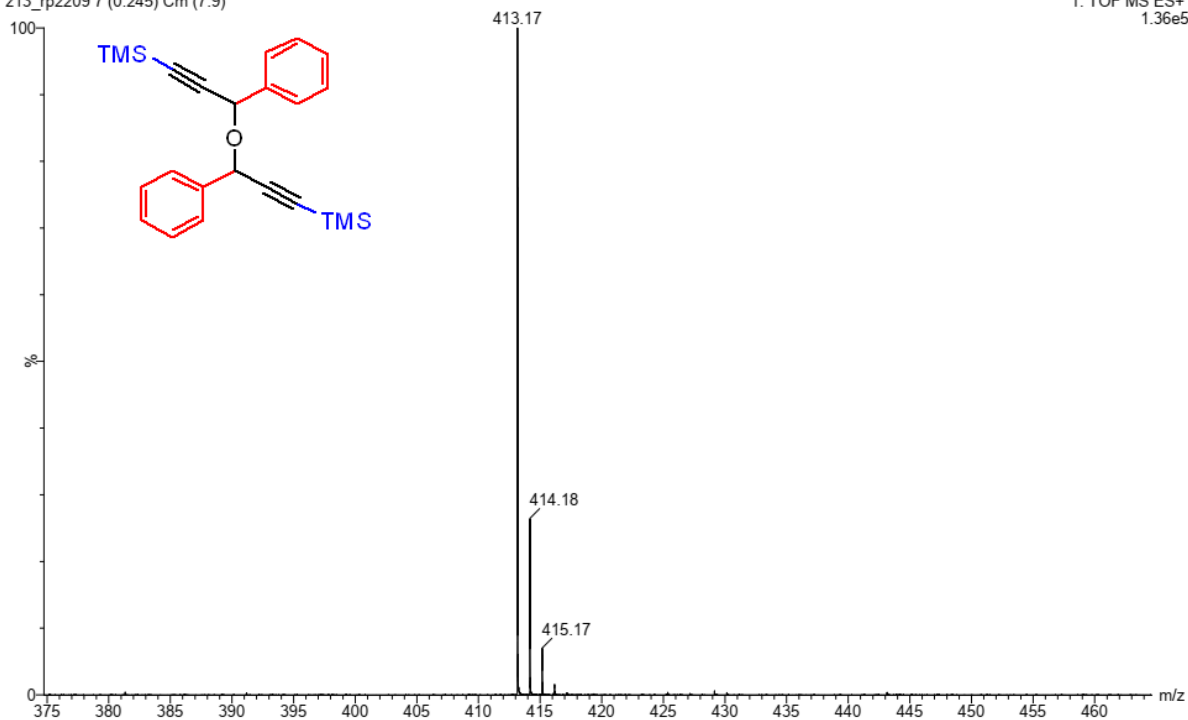


Fig.11 MS spectrum of the rt=11.08 peak

| Experimental Instrument Parameters - MS | QAT-163 | Experimental Instrument Parameters - LC | QAT-163 | | | |
|---|---------|---|---------------------------|----|-----|-------|
| Polarity | ESI + | Solvent A | 0.1% formic acid in water | | | |
| Capillary Voltage (kV) | 3.00 | Solvent B | Methanol | | | |
| Source temp. [C] | 120.0 | Run time | 16.00 min | | | |
| Sampling Cone | 60.0 | Flow rate | 0.30 ml/min | | | |
| Source Offset | 50.0 | Gradient table | time [min] | %A | %B | Curve |
| Source Gas Flow (mL/min) | 0.00 | | 0.00 | 95 | 5 | - |
| Desolvation temp. [C] | 250.0 | | 0.50 | 95 | 5 | 6 |
| Cone Gas [L/h] | 100.0 | | 10.00 | 0 | 100 | 6 |
| Desolvation Gas Flow [L/h] | 700.0 | | 12.00 | 0 | 100 | 6 |
| Nebuliser Gas Flow[bar] | 4.5 | | 13.00 | 95 | 5 | 6 |
| | | | 16.00 | 95 | 5 | 6 |



Single Mass Analysis

Tolerance = 3.0 mDa / DBE: min = -1.5, max = 100.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 3

Monoisotopic Mass, Even Electron Ions

20 formula(e) evaluated with 2 results within limits (all results (up to 1000) for each mass)

Elements Used:

C: 0-100

H: 0-200

O: 0-1

Na: 0-1

Si: 2-2

| Mass | Calc. Mass | mDa | PPM | DBE | Formula | i-FIT | i-FIT Norm | Fit Conf % | C | H | O | Na | Si |
|----------|------------|------|------|------|--|-------|------------|------------|----|----|---|----|----|
| 413.1740 | 413.1733 | 0.7 | 1.7 | 11.5 | C ₂₄ H ₃₀ O Na Si ₂ | 755.1 | 0.044 | 95.65 | 24 | 30 | 1 | 1 | 2 |
| | 413.1757 | -1.7 | -4.1 | 14.5 | C ₂₆ H ₂₉ O Si ₂ | 758.2 | 3.136 | 4.35 | 26 | 29 | 1 | | 2 |