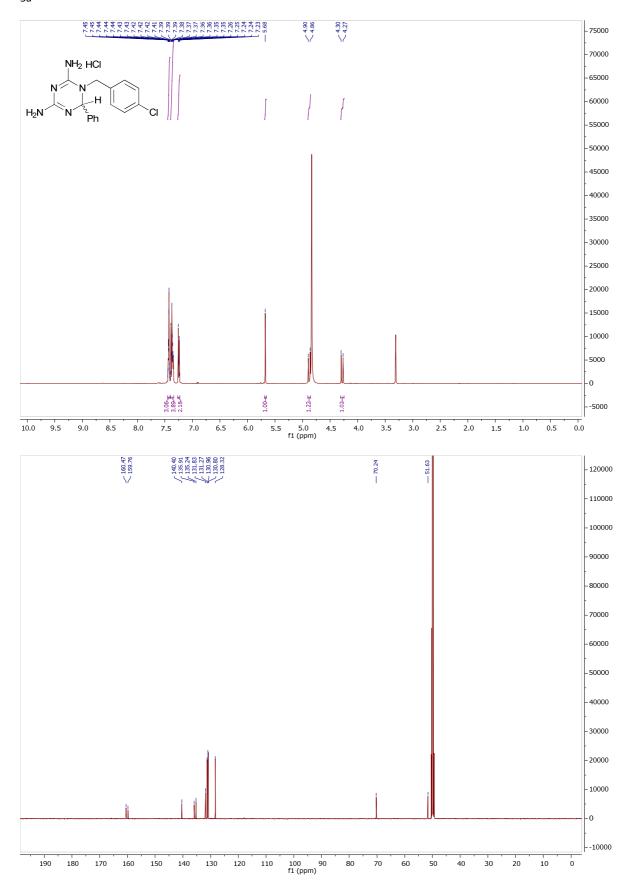
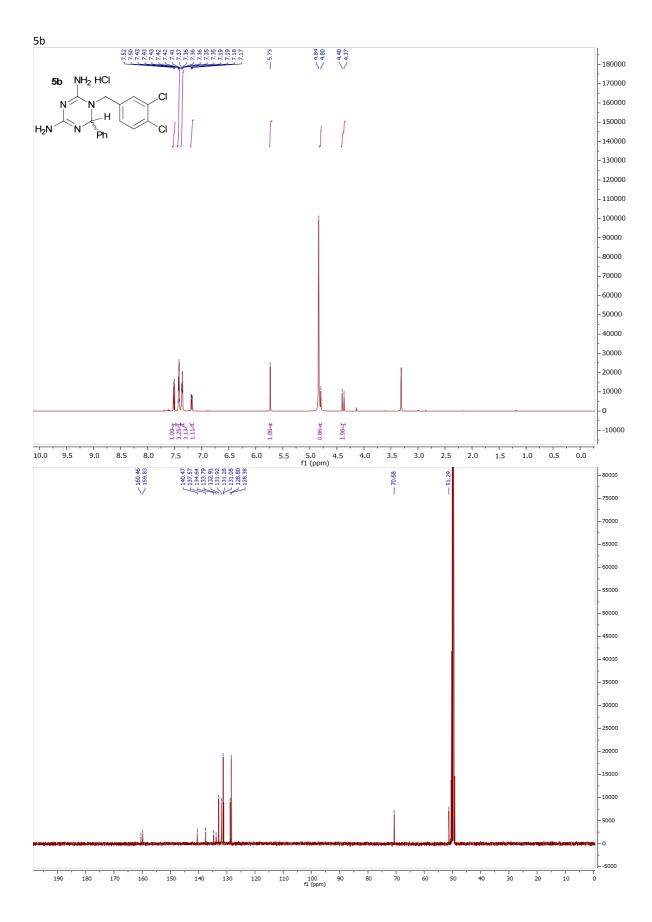
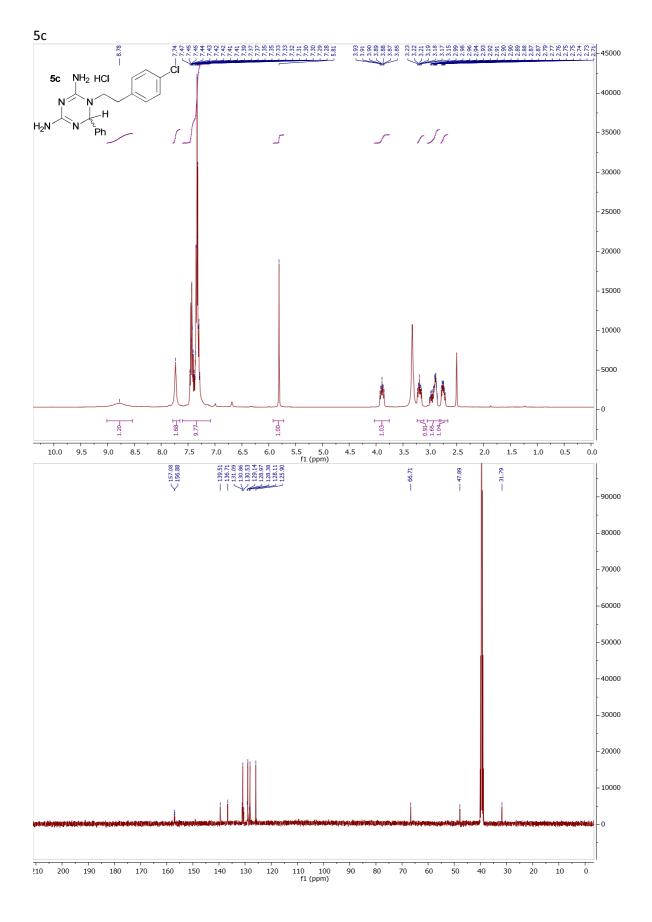
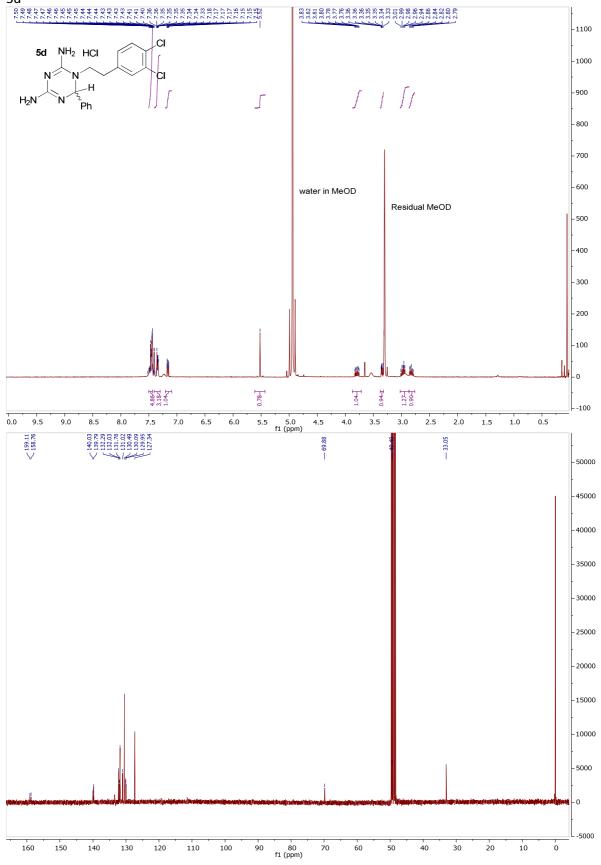
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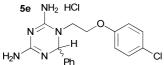
NMR spectra were run on either a Varian 200 MHz Gemini 2000 instrument, or on a 400 MHz Varian INOVA instrument. Chemical shifts (δ scale) are reported in parts per million (ppm) relative to the central peak of methanol, 49.00 ppm for ¹³C and 3.31 ppm for ¹H; chloroform, 77.16 ppm for ¹³C and 7.26 ppm for ¹H. Spectra are reported in the following order: multiplicity, approximate coupling constant (J value) in hertz (Hz), number of protons or carbons; signals were characterized as s (singlet), d (doublet), dd (doublet of doublets), ddd (doublet of doublets of doublets), t (triplet), dt (doublet of triplets), q (quartet), p (pentet), br s (broad signal) and m (multiplet). High resolution mass spectra were generated on a Waters SYNAPT G1 HDMS mass spectrometer operated in electrospray mode. Leucine enkephalin (50 pg/ml) was used as reference calibrant to obtain typical mass accuracies between 1 and 3 mDa. The mass spectrometer was operated in positive mode with a capillary voltage of 2 kV, the sampling cone at 30 V and the extraction cone at 4 V. The source temperature was 120 C and the desolvation temperature was set at 350 °C. Nitrogen gas was used as the nebulisation gas at a flow rate of 450 L/h. Purity of final compounds was determined by UPLC, using a Waters Acquity UPLC coupled in tandem to an UPDA detector (200-500 nm). All chemicals for UPLC-MS work were of ultra-pure LC MS grade and purchased from Fluka (Steinheim, Germany) while ultra-grade solvents were purchased from Honeywell (Burdick & Jackson, Muskegon, USA). The analytical column used was a Waters Acquity HSS C18, 150 x 2.1 mm (1.7 mm) equilibrated at 45 °C in a column heater. The mobile phase consisted of acetonitrile and ultra-pure water containing 0.1% formic acid (v/v). A linear gradient was used to ramp the mobile phase composition from 95% water to 10% water in 6 min. The runtime was 10 min per sample. The software used to control the hyphenated system and do all data manipulation was MassLynx 4.1 (SCN 704).

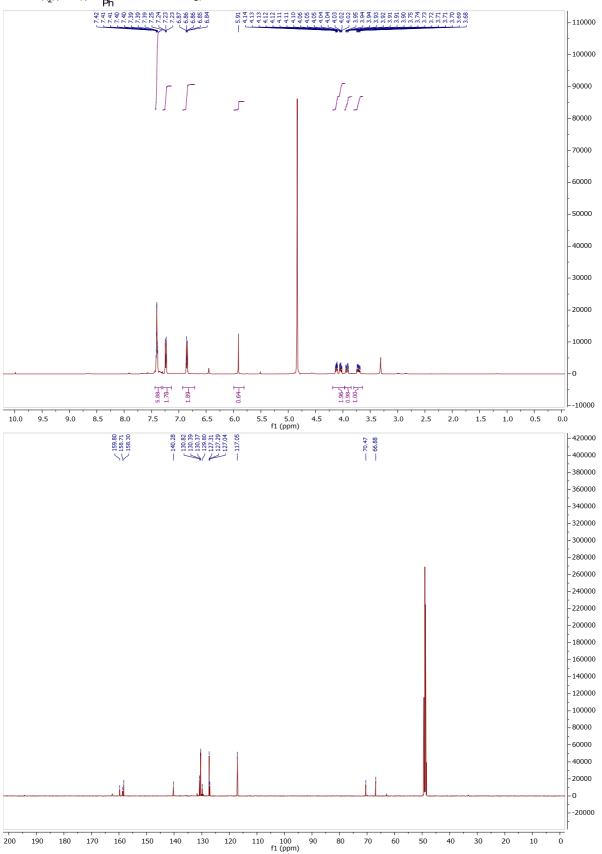


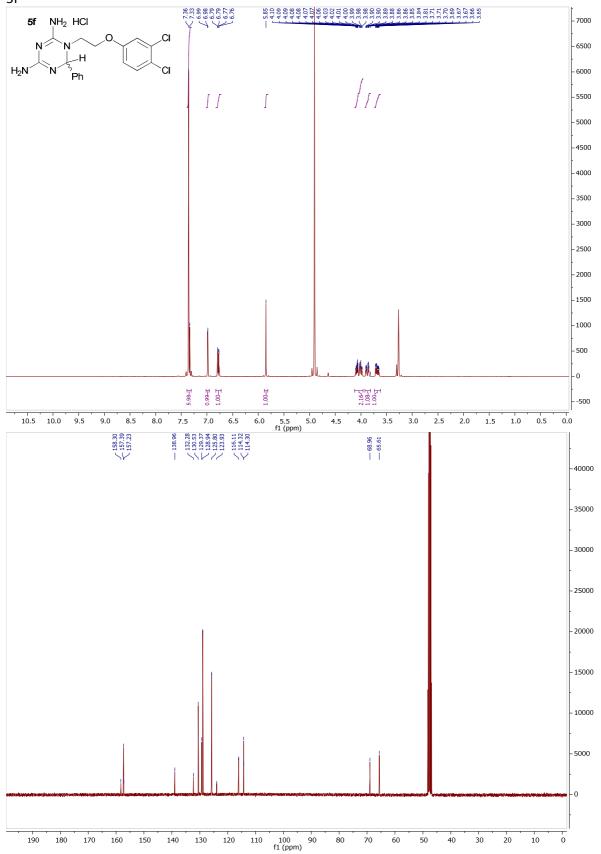


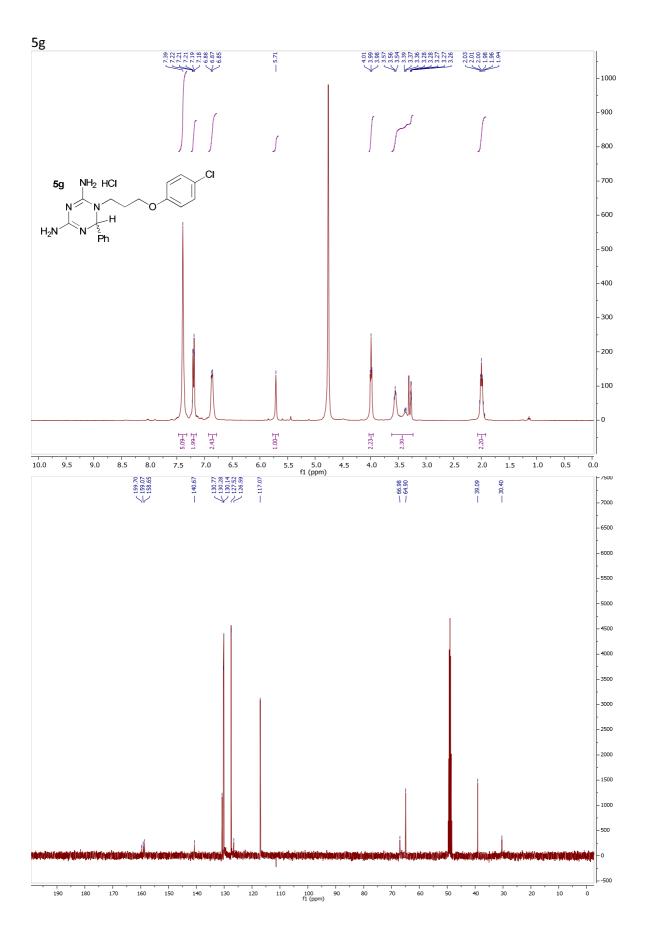


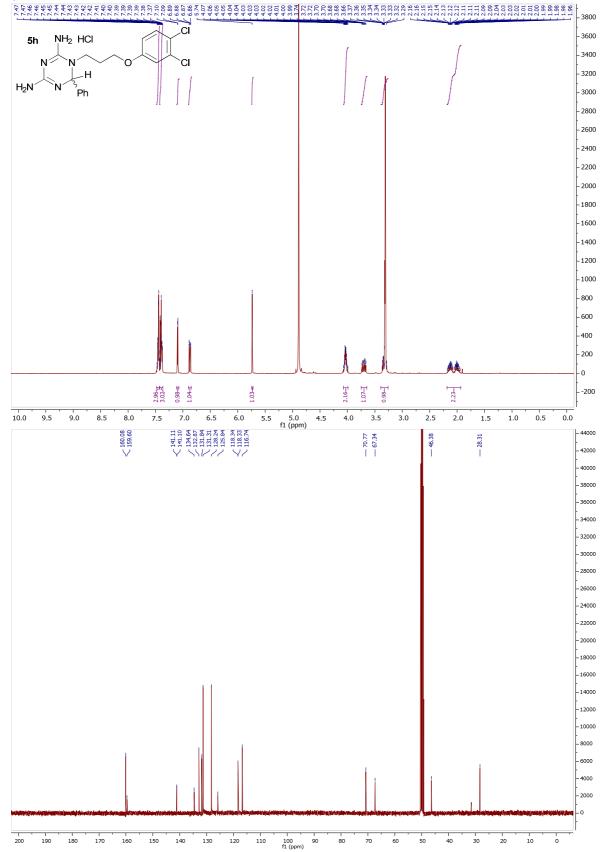


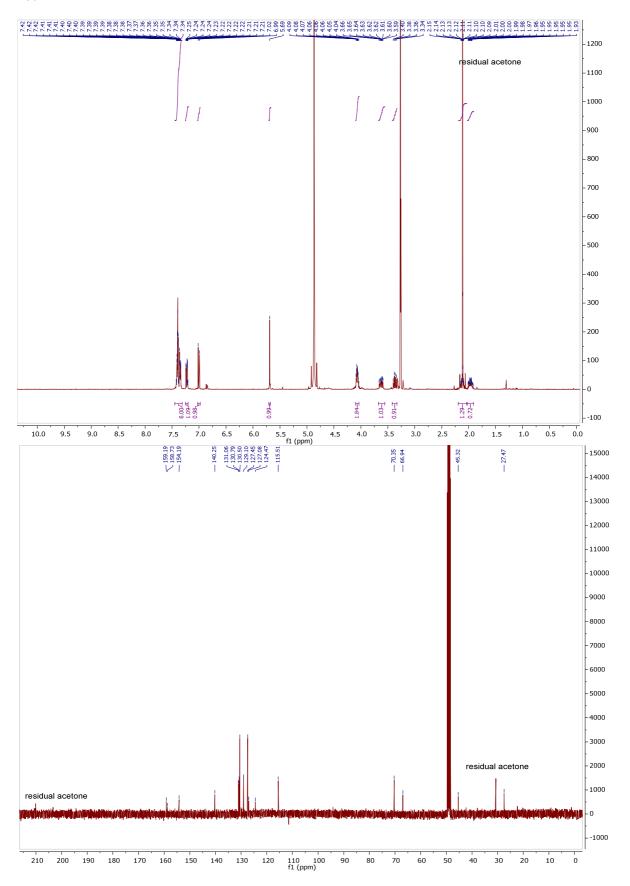


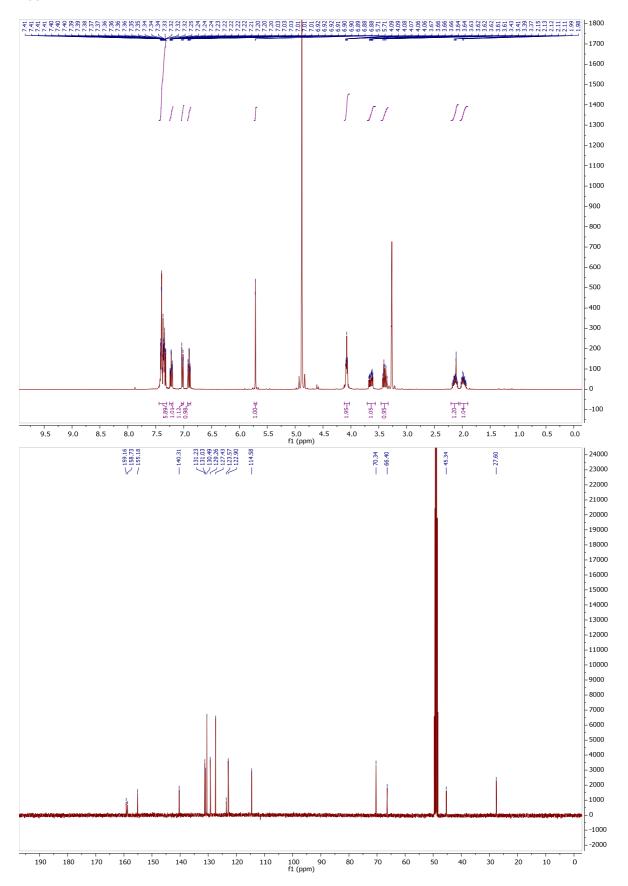


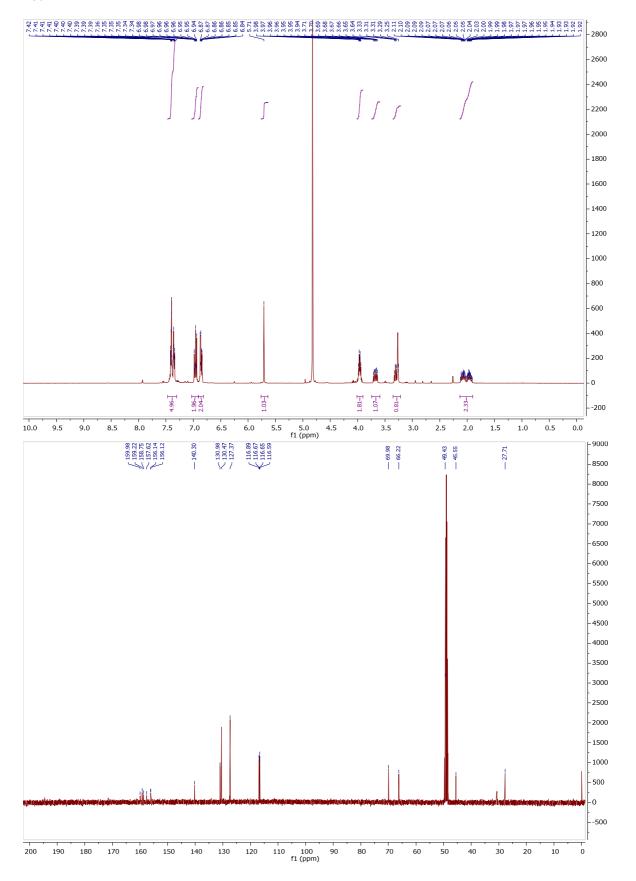


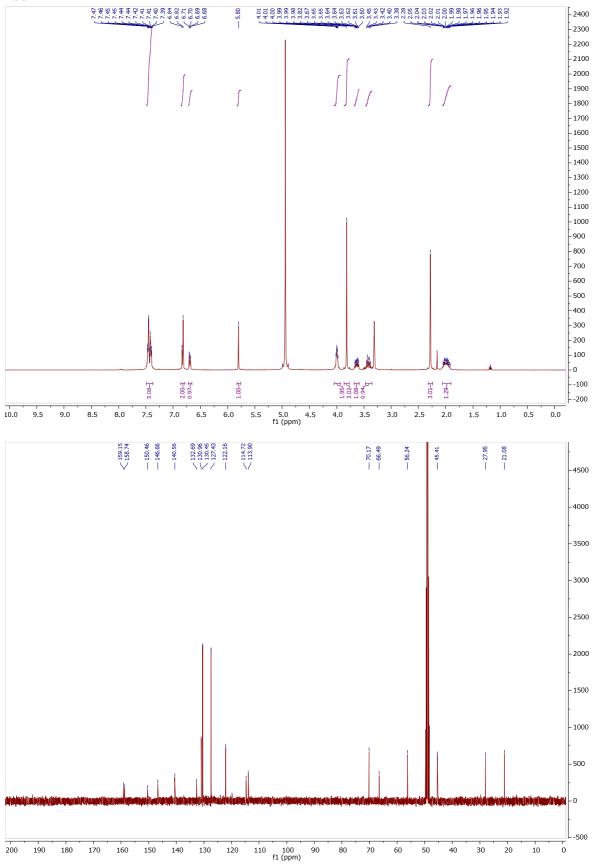


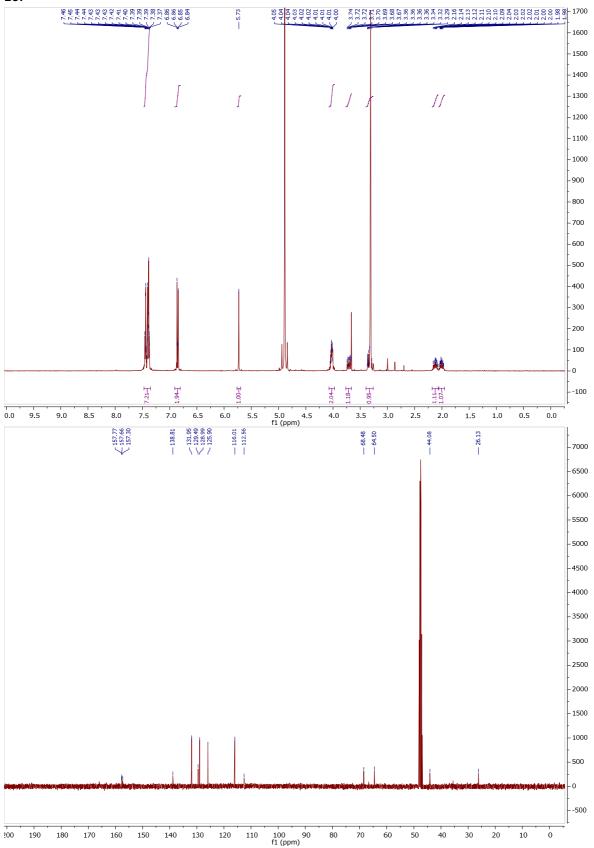




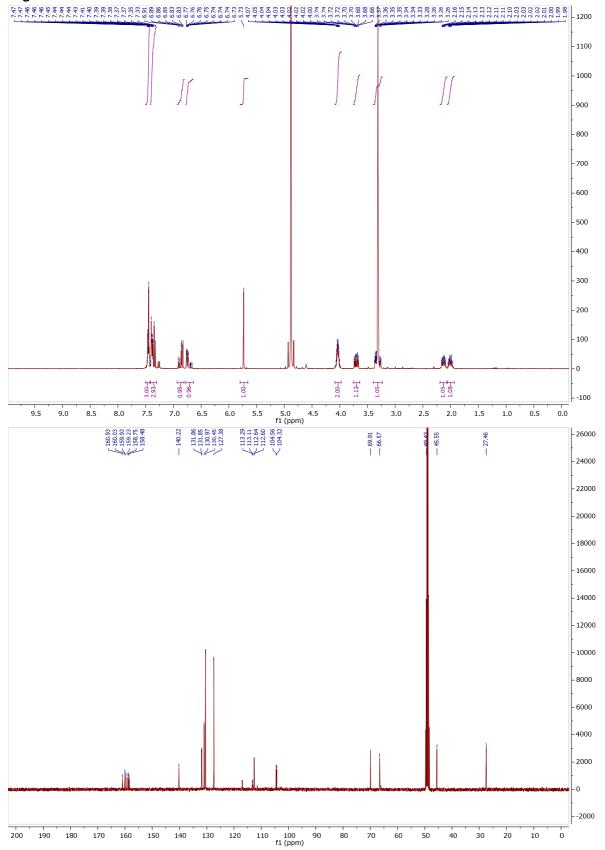


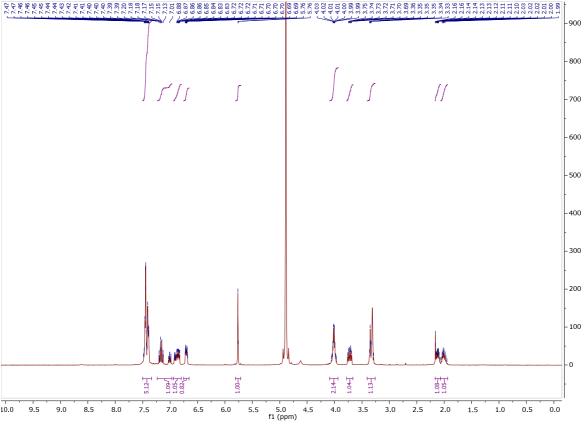


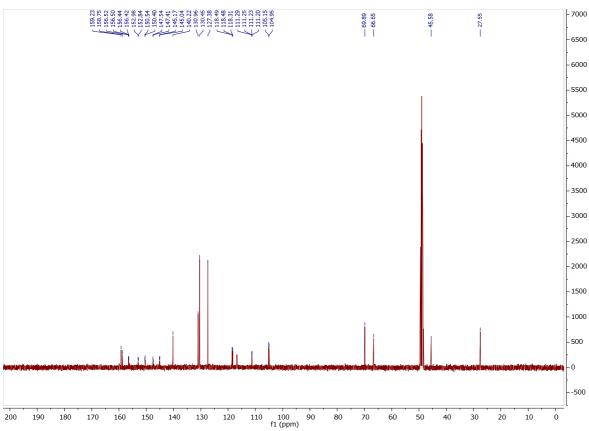


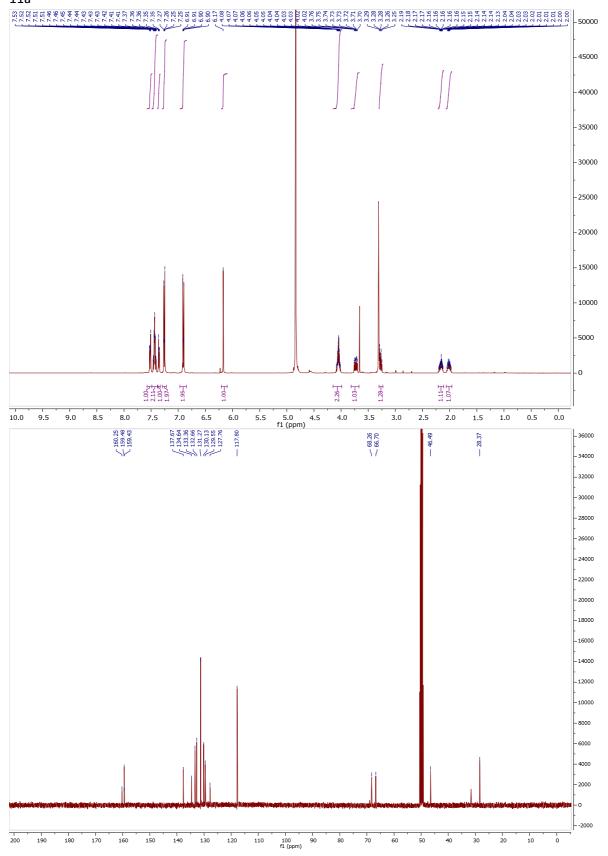


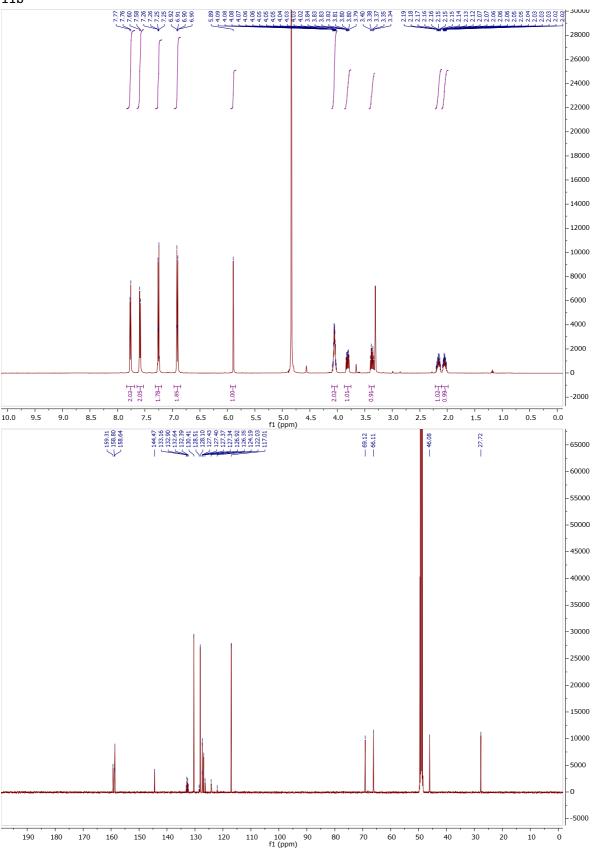


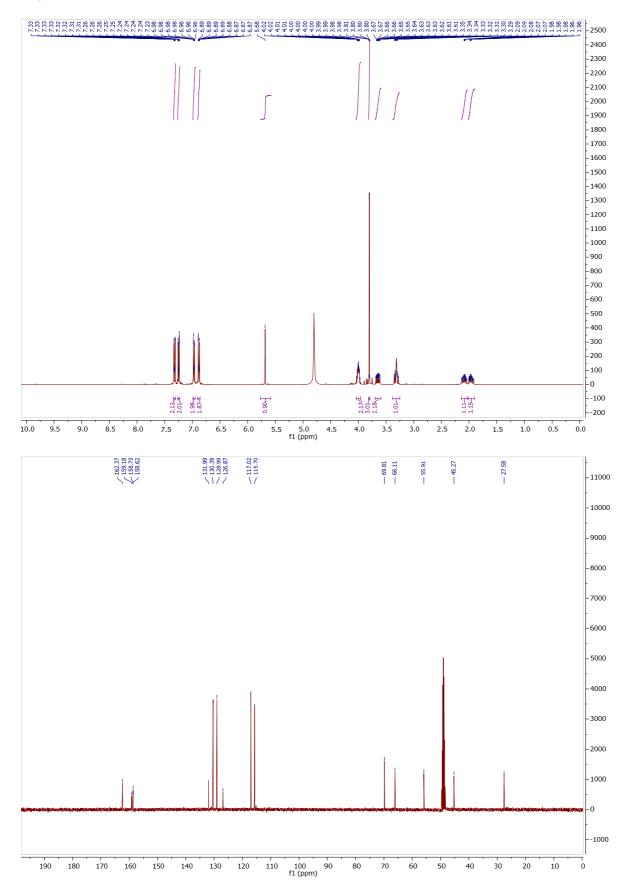


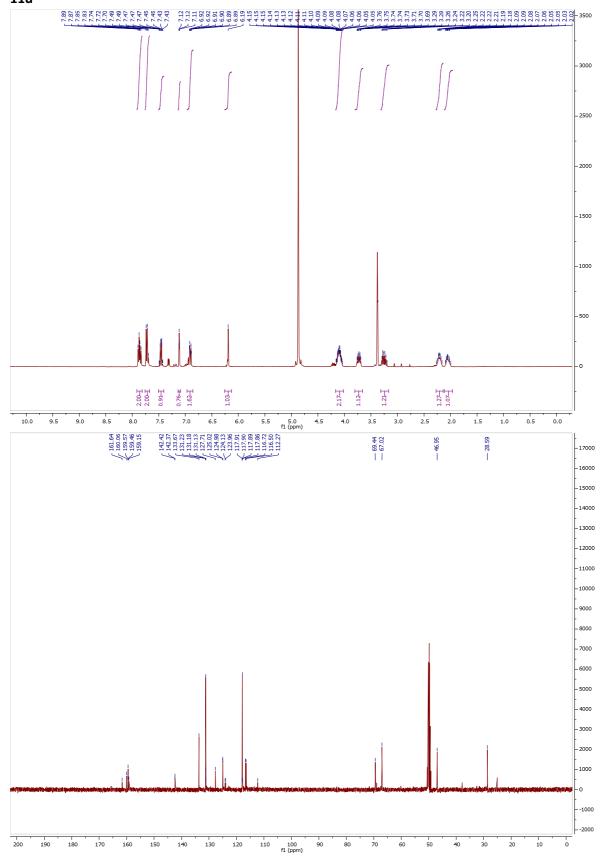


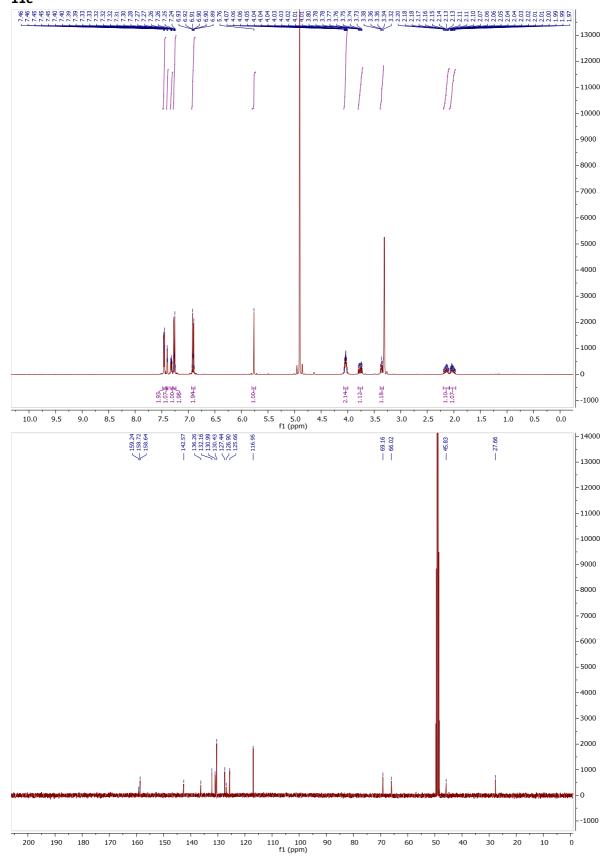


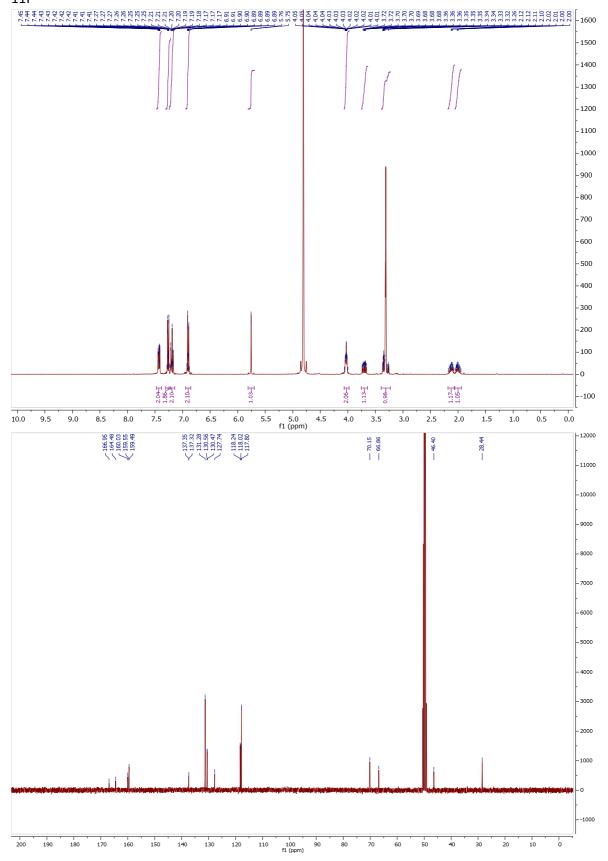




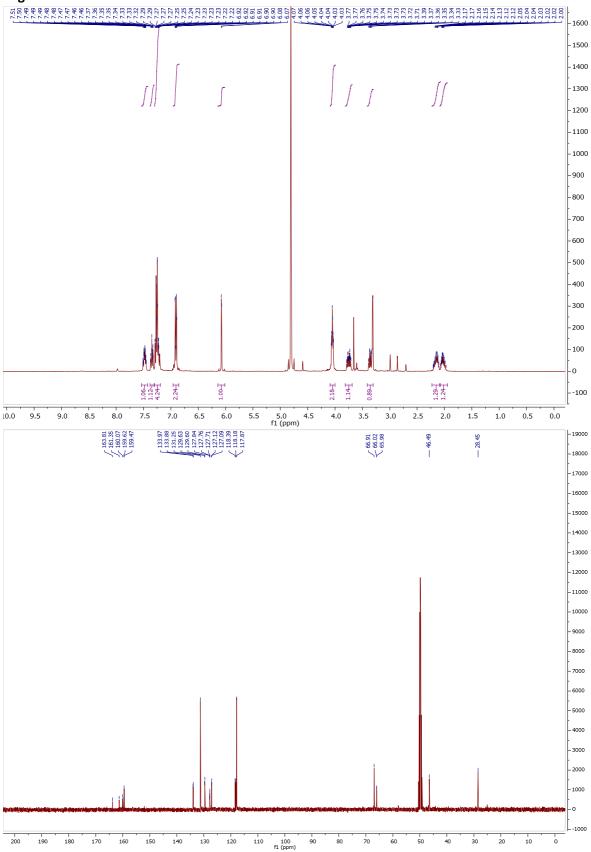


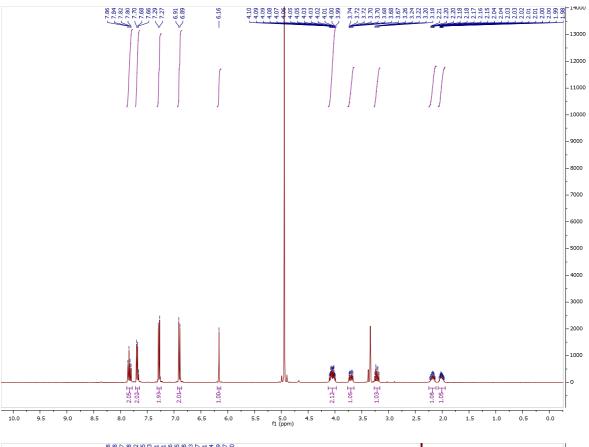


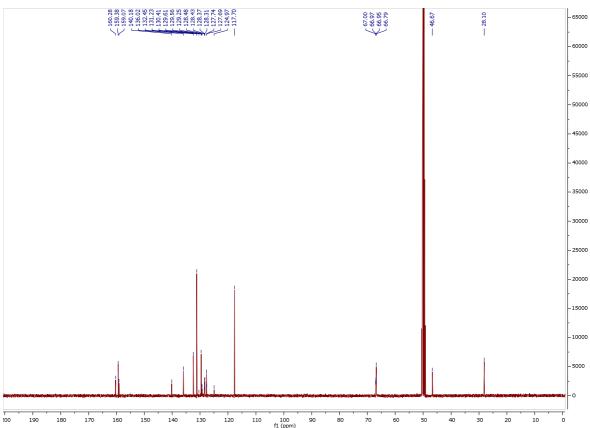


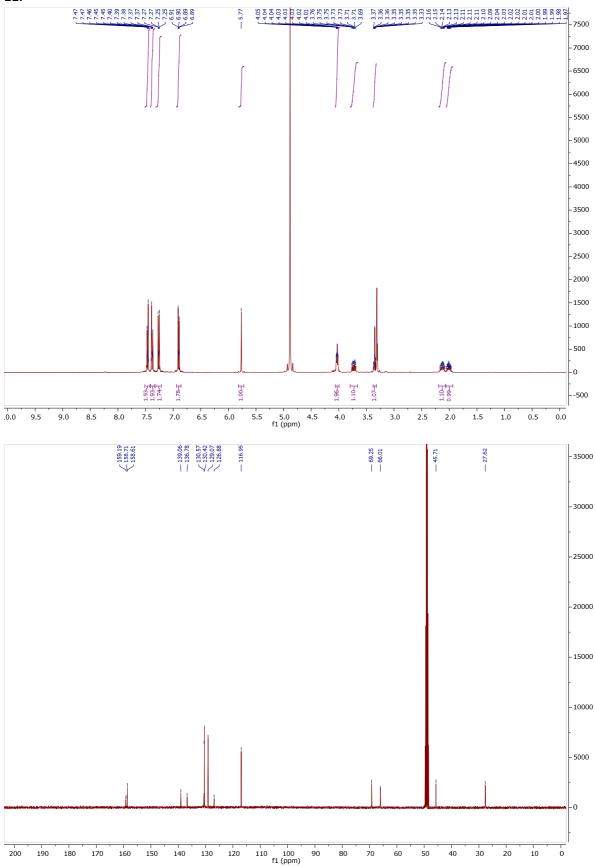


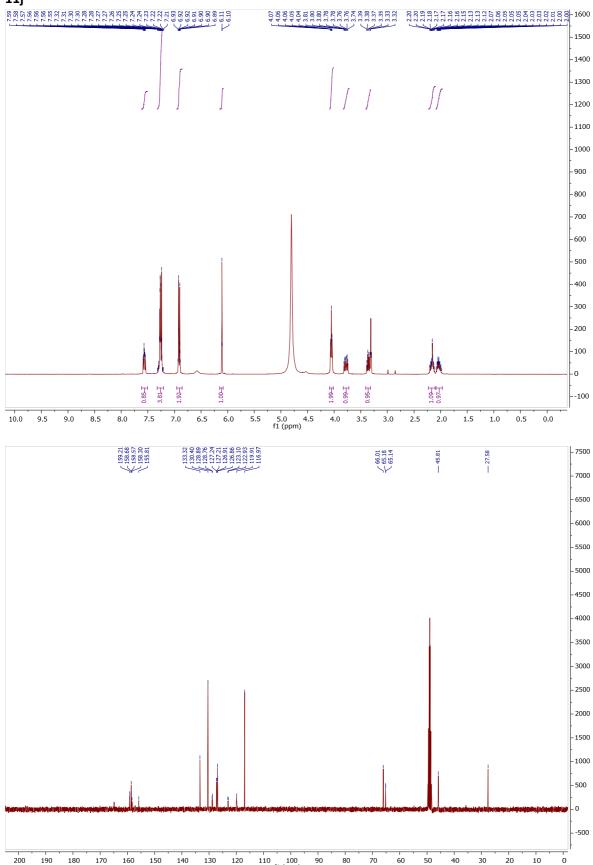










110 100 f1 (ppm)

