

## **Supporting Information**

### **Exploring Synthetic and Therapeutic Prospects of New Thiazoline Derivatives as Aldose Reductase (ALR2) Inhibitors**

Muhammad Tariq Shehzad,<sup>a\*</sup>, Aqeel Imran<sup>b†</sup>, Abdul Hameed<sup>c</sup>, Mariya al-Rashida<sup>c</sup>, Marium Bibi,<sup>d</sup> Maliha Uroos,<sup>e</sup> Asnuzilawati Asari,<sup>f</sup> Shafia Iftikhar,<sup>g</sup> Habsah Mohamad,<sup>h</sup> Muhammad Nawaz Tahir,<sup>i</sup> Zahid Shafiq,<sup>a\*</sup> and Jamshed Iqbal,<sup>b\*</sup>

<sup>a</sup> Institute of Chemical Sciences, Bahauddin Zakariya University, Multan 60800, Pakistan

<sup>b</sup> Centre for Advanced Drug Research, COMSATS University Islamabad, Abbottabad Campus, Abbottabad-22060, Pakistan

<sup>c</sup> Department of Chemistry, Forman Christian College (A Chartered University), Ferozepur Road, Lahore-54600, Pakistan

<sup>d</sup> Department of Biosciences, 90 and 100 Clifton, Shaheed Zulfikar Ali Bhutto Institute of Science and Technology, Block 5, Clifton, Karachi-75600, Pakistan

<sup>e</sup> Institute of Chemistry, University of The Punjab, Lahore-54590, Pakistan

<sup>f</sup> Faculty of Science and Marine Environment, Universiti Malaysia Terengganu, 21030 Kuala Nerus, Terengganu, Malaysia

<sup>g</sup> Department of Chemistry, University of Sahiwal, Sahiwal 57000, Pakistan

<sup>h</sup> Institute of Marine Biotechnology, Universiti Malaysia Terengganu, 21030 Kuala Nerus, Terengganu, Malaysia

<sup>i</sup> Department of Physics, University of Sargodha, Sargodha, Pakistan

†Both authors contributed equally

---

\*[zahidshafiq@bzu.edu.pk](mailto:zahidshafiq@bzu.edu.pk) (Z. Shafiq)

\*[drjamshed@ciit.net.pk](mailto:drjamshed@ciit.net.pk) / [jamshediqb@googlemail.com](mailto:jamshediqb@googlemail.com) (J. Iqbal).

## **Molecular Docking Studies.**

### **Protein selection ;**

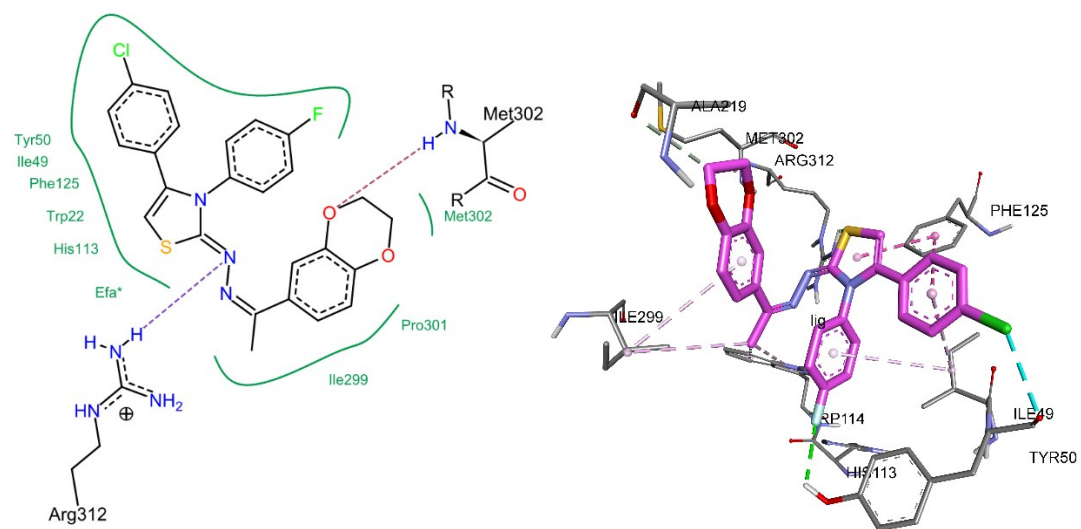
To perform docking analysis , crystalized protein structures were downloaded in PDB format. The crystal structures of porcine ALR1<sup>1</sup> and human ALR2<sup>2</sup> were downloaded from the Protein Data Bank [PDB ids: 3FX4 at 1.99 Å and 1US0 at 0.66 Å respectively]. The porcine and human ALR1 bears identical active site residues and approximately 97% sequence homology. The issues related downloaded crystallographic protein were resolved like removal of undesired co-crystal ligand and water molecules. The addition of hydrogen atoms and correct charges were assigned to protein structures.

### **Preparation of the ligands:**

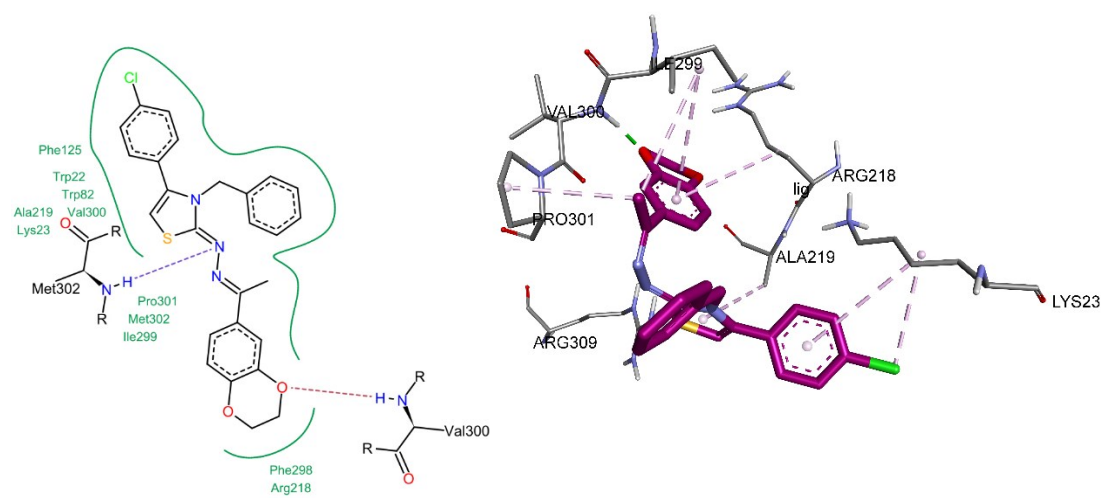
The structures for newly synthesized derivatives were developed by using builder tool of MOE software (version 2019). Initially, the charges were assigned to each atom and hydrogen atoms were added to all synthesized derivatives. Eventually, the energy minimization for each inhibitor's structure was performed via applying force field named MMFF94x along with RMS gradient of 0.001kcal/mol/Å<sup>2</sup>.

### **Docking studies:**

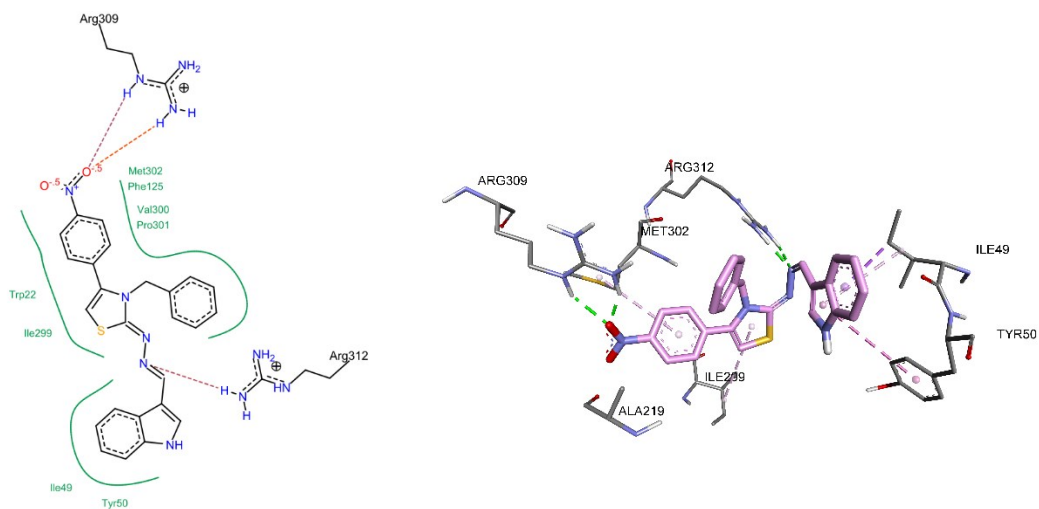
Docking studies for ALR1 and ALR2 were executed through automated molecular docking program LeadIT(2.3.2) using default parameters. While using LeadIT software first PDB protein structure is uploaded during new project execution then receptor preparation (3FX4 and 1US0) was carried out. The ligand structure was uploaded and docking study was initiated. LeadIt generated various docked poses. The hyde assessment for these docked pose was done and free binding energy was estimated. Those poses exhibited lowest free binding energy ( $\Delta G$ ), were chosen for further visualization of docked compound at the active site of enzyme. The exploration of putative 2D and 3D binding interaction of inhibitor with residues of active site of the enzyme was carried out by using Discovery studio visualizer (Discovery Studio Visualizer, 4.0).



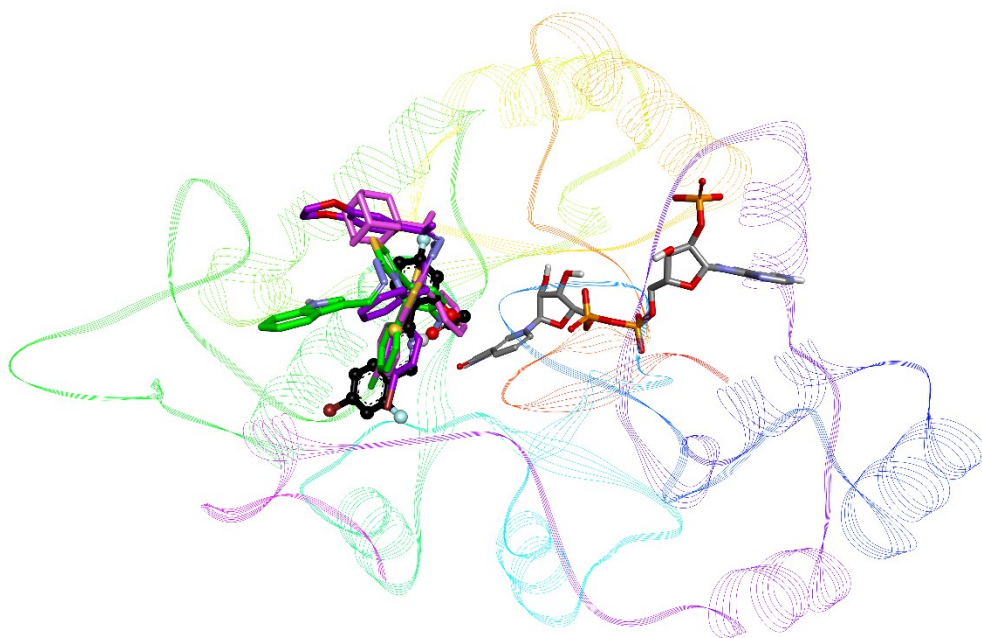
**Figure S1:** Docked conformation of ALR1 inhibitor **7h**.



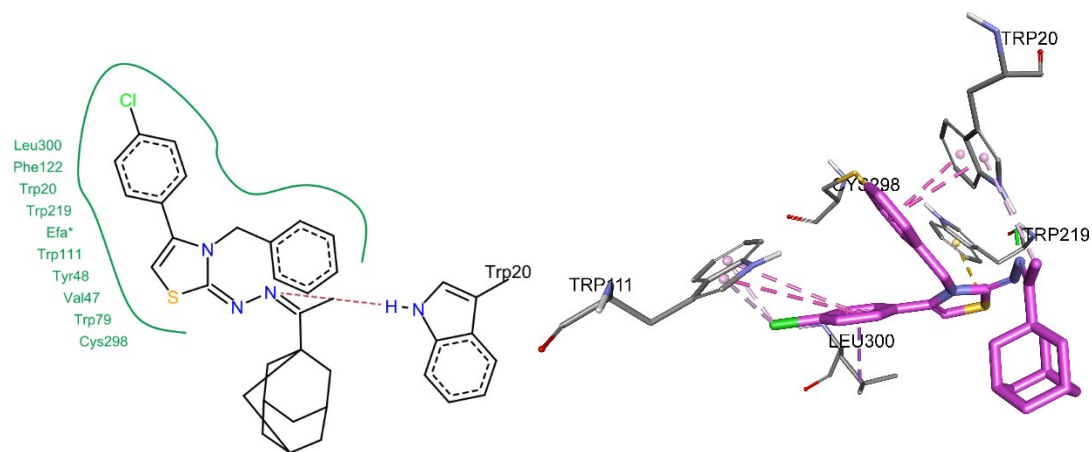
**Figure S2:** Docked conformation of ALR1 inhibitor **7i**.



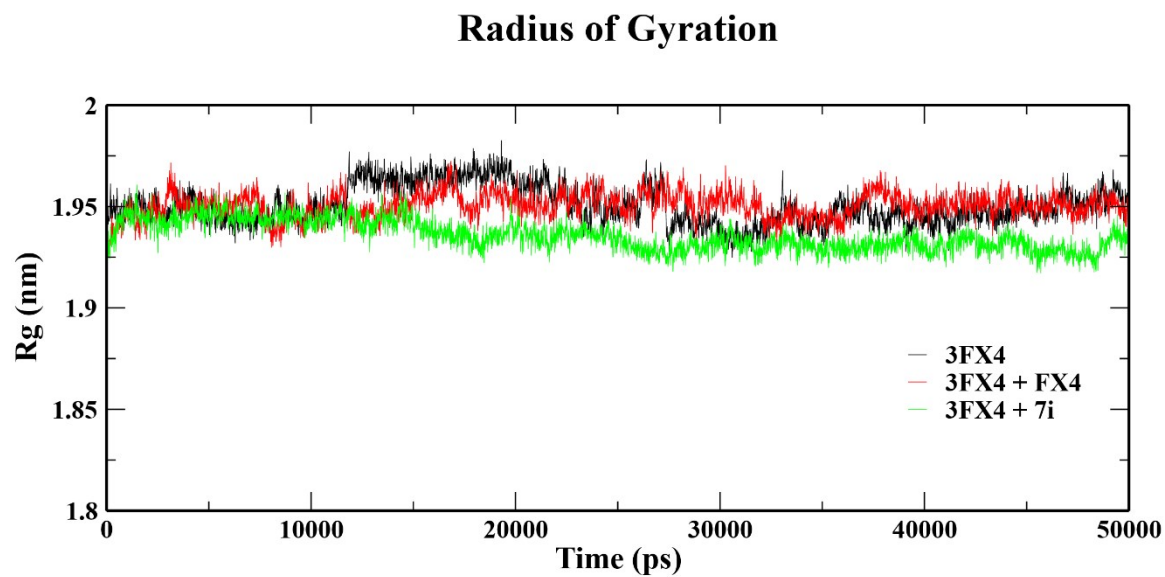
**Figure S3:** Docked conformation of ALR1 inhibitor **8e**.



**Figure S4:** Overlap of ALR2 inhibitors **6e** (pink), **7b** (purple) and **8e** (green) with the co-crystallized inhibitor LDT [2-[(4-bromo-2-fluorobenzyl)carbamothioyl]-5-fluorophenoxy]acetic acid (black), NADPH is shown in grey.

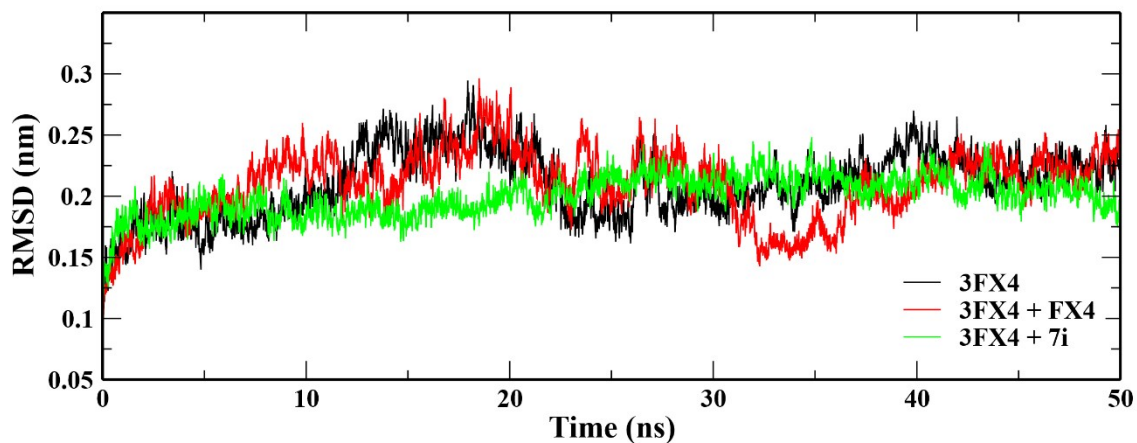


**Figure S5:** Docked conformation of ALR2 inhibitor **6e**.



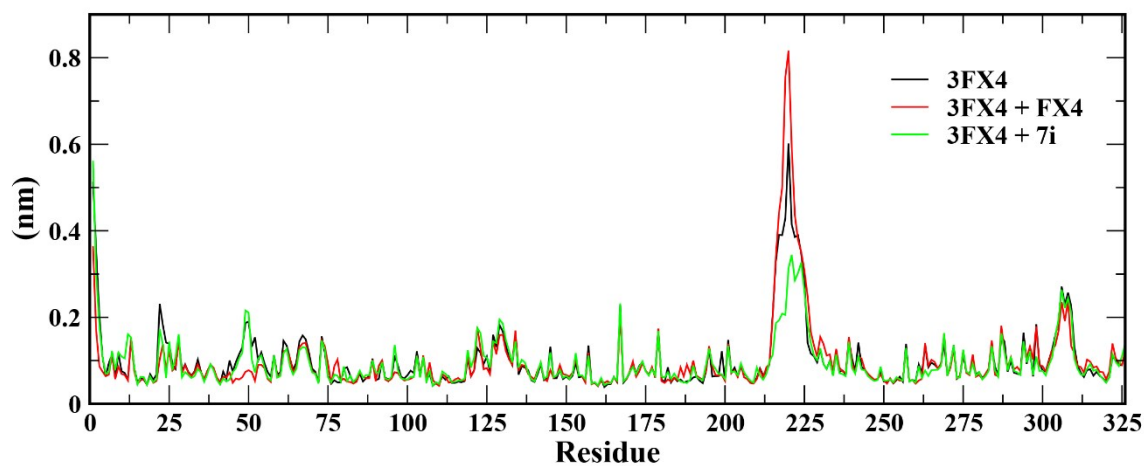
**Figure S6:** Radius of gyration (Rg) of 3FX4, protein plus cognate ligand (FX4) and protein plus selective compound (**7i**) during 50 ns MD-simulation run.

## RMSD



**Figure S7:** Root Mean Square Deviation (RMSD) of 3FX4, protein plus cognate ligand (FX4) and protein plus selective compound (7i) during 50 ns MD-simulation run.

## RMS Fluctuation



**Figure S8:** Root Mean Square Fluctuation (RMSF) of 3FX4, protein plus cognate ligand (FX4) and protein plus selective compound (7i) during 50 ns MD-simulation run.

**Table S1:** Binding free energies and non-bonded interactions of ALR1 (**7h**, **7i**, **8e**) and ALR2 (**6e**, **7b**, **8e**) inhibitors with their respective receptors.

Ligand	Binding Free Energy (kJ/mol)	Hydrophobic Interactions	Hydrogen bond interactions	Hydrogen bond distance (Å)	Other interactions and distance (Å)
<b>ALR1 Inhibitors</b>					
<b>7h</b>	-17	Phe125 (pi-pi stacked), Ile299 (alkyl, pi-alkyl), Ile49 (pi-alkyl), Trp114 (pi-alkyl)	Tyr50 (H-Donor towards F), Met302 (H-Donor), Arg312 (H-Donor)	2.56, 2.15, 2.30	Tyr50 (Halogen bond acceptor) (3.02)
<b>7i</b>	-19	Ile299 (alkyl, pi-alkyl), Pro301 (alkyl), Lys23 (alkyl, pi-alkyl), Ala219 (pi-alkyl), Arg218 (pi-alkyl)	Val300 (H-Donor), Arg302 (H-Donor)	1.73, 2.01	–
<b>8e</b>	-18	Ile49 (pi-sigma, pi-alkyl), Tyr50 (pi-pi stacked), Ile299 (pi-alkyl), Met302 (pi-alkyl)	Arg309 (H-Donor), Arg312 (H-Donor)	2.17 and 1.78, 1.89 and 2.66	–
<b>ALR2 Inhibitors</b>					
<b>6e</b>	-15	Leu300 (pi-sigma), Trp20 (pi-pi stacked, pi-alkyl), Trp111 (pi-stacked, pi-alkyl)	Trp20 (H-Donor)	1.89	Trp219 (pi-sulfur) (4.12), Cys298 (pi-sulfur) (4.61)
<b>7b</b>	-16	Trp111 (pi-pi stacked, pi-alkyl), Trp20 (pi-pi T-shaped), Pro218 (alkyl), Leu300 (pi-alkyl), Val47 (pi-alkyl)	Trp20 (H-Donor)	1.99, 2.12	Tyr48 (pi-sulfur) (4.89)
<b>8e</b>	-16	Leu300 (pi-sigma, pi-	Tyr48 (H-Donor),	2.30, 1.56	Lys77 (electrostatic,

		alkyl), Phe122 (pi-pi T-shaped), Trp20 (pi-pi T-shaped), Val47 (pi-alkyl)	Trp111 (H-Donor)		attractive charge) (5.42), Trp20 (electrostatic, pi-anion) (4.89)
--	--	---	------------------	--	---



## **Bioactivity Protocol**

### **Enzyme extraction and determination of enzyme activities**

#### **Extraction of aldehyde reductase (ALR1):**

Kidneys were removed from the calf soon after slaughtering and dissolved in 3 volume of 10 mM sodium phosphate buffer, pH 7.2, containing 0.25M sucrose, 2.0 mM EDTA dipotassium salt and 2.5 mM  $\beta$ -mercaptoethanols. Centrifuged the homogenate at 12,000 x g at 0-4 0C for 30 minutes. The precipitate was discarded as it contains insoluble lipids. Collected supernatant layer was subjected to 40% ammonium sulfate saturation to isolate ALR1. This 40% saturated liquid is centrifuged at 12,000 x g at 0-4 0C for 30 minutes. Again precipitate was discarded and supernatant was subjected to 50% saturation with ammonium sulphate salt. Then the same procedure was repeated with this and in the last step powdered ammonium sulphate was added to increase the saturation upto 75%. Centrifuged the supernatant at 12,000 x g for 30 min, causing the precipitation of ALR1. Now precipitated material is collected and supernatant was discarded. The precipitated material containing ALR1 was redissolved in 10 mM sodium phosphate buffer, pH 7.2, containing 2.0 mM EDTA dipotassium salt and 2.0 mM  $\beta$ -mercaptoethanol and then dialyzed over night using the same buffer. The dialyzed material containing ALR1 was aliquoted and stored at -80 0C before use<sup>3</sup>

#### **Extraction of Aldose reductase (ALR2):**

Isolation of ALR2 was done as described in (Hayman and Kinoshita 1965) by minor modification. Briefly, ALR2 was isolated from calf lenses. The lenses were removed from the eyes immediately after slaughtering and were frozen until use. Lenses (100-200g) were homogenized in 3 volumes of cold distilled water and then homogenate was centrifuged at 10,000 x g for 15 minutes to remove insoluble material. Precipitated material was discarded as it contained lipids. Supernatant layer was separated and ammonium sulphate salt was added to make the saturation upto 40%. It was centrifuged at 10,000 x g for 15 min, again precipitate was discarded. Additional inert protein was removed by increasing the concentration of ammonium sulfate upto 50%. Pure ALR2 was precipitated by addition of powdered ammonium sulfate to 75% saturation. After centrifugation, supernatant was discarded and redissolved the precipitated enzyme in 50 mM NaCl and dialyzed over night against 4 liters 50 mM NaCl. The volume of the suspension was recorded and the sample was dialyzed overnight against 50 mM NaCl (double replacement of dialysis solution). After

dialysis, the volume of the sample was recorded and treated to liquid nitrogen then samples were stored in 1 mL aliquots in eppendorf tubes in deep freezer at -80 °C for the determination of the total protein, enzyme activity and inhibition studies<sup>4</sup>.

### **Determination Enzymatic activity for ALR1 and ALR2.**

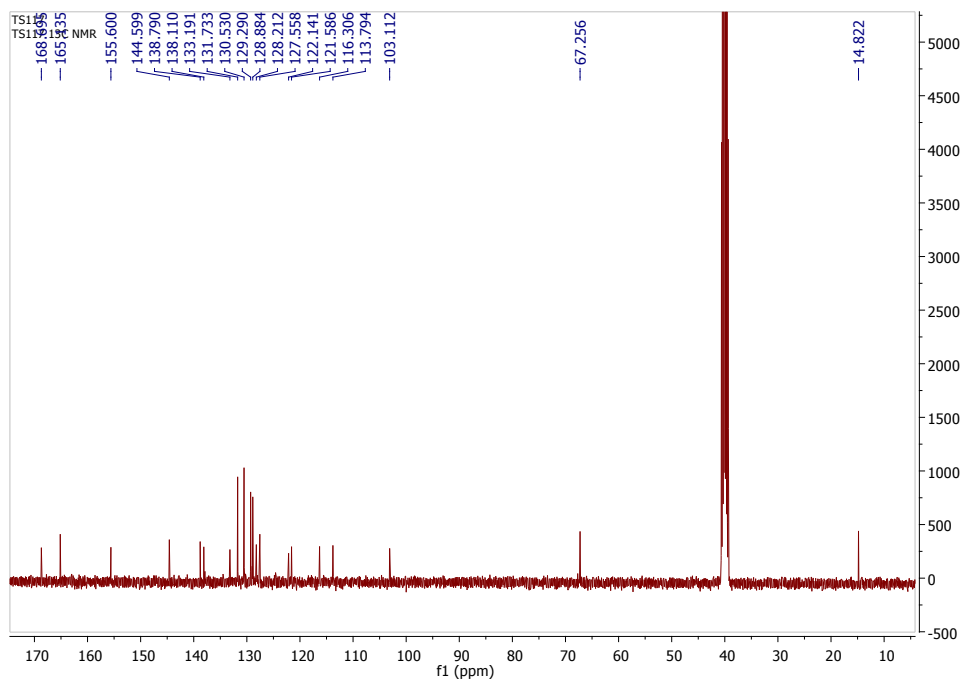
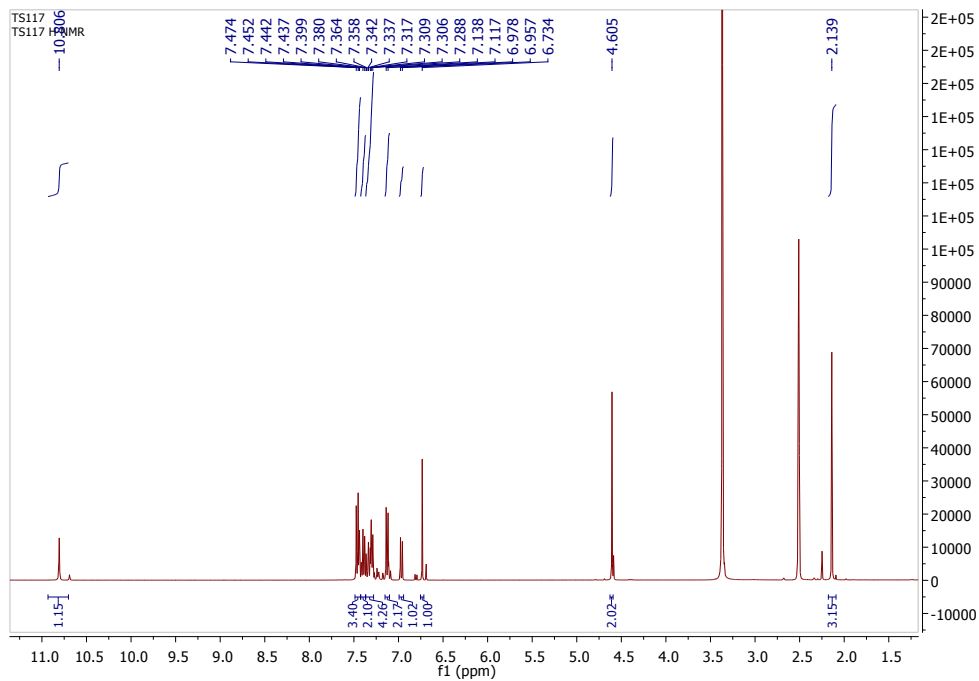
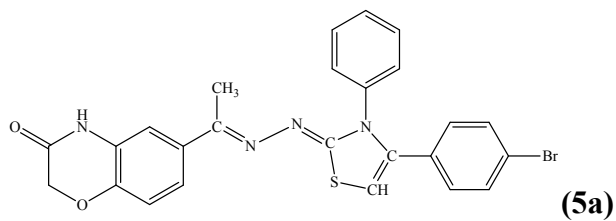
The activity of ALR2 and ALR1 was assayed by using FLUOstar® Omega micro plate reader (BMG LABTECH) by measuring absorbance at 340 nm and decrease in absorbance of NADPH was associated with enzymatic activity. To calculate the inhibitory activity for ALR2, DL-glyceraldehyde was used as substrate whereas inhibitory activity of ALR1 was estimated with sodium -D-glucuronate as a substrate. Newly synthesized compounds were dissolved in DMSO and final concentration of DMSO was kept 0.1% in all incubations. The reaction mixture (total assay volume 100µL) was composed of 20µL of phosphate buffer (100mM), 10µL of test compound (1mM), 30µL of enzyme (partially purified) and 20µL(0.1mM) of substrate. The reaction mixture was pre incubated for 5minutes, then enzymatic reaction was initiated by the addition of cofactor NADPH (0.1mM). Pre-read was taken at 0 minute and again the mixture was incubated at 30°C for 20 minutes. Then after-read was taken and change in absorbance was noted<sup>5</sup>. In the assay valproic acid and sorbinil was used as standard inhibitor for ALR1 and ALR2, respectively. All enzymatic reactions were performed in triplicate and percent inhibition was calculated and IC<sub>50</sub> values were calculated through non-linear regression analysis via using GraphPad Prism version 8.

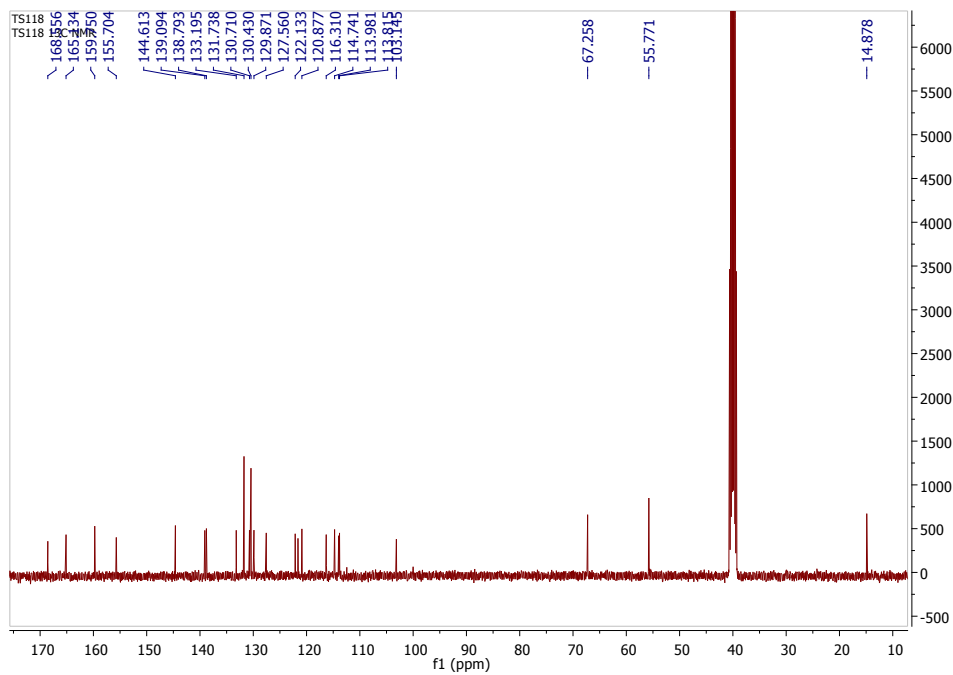
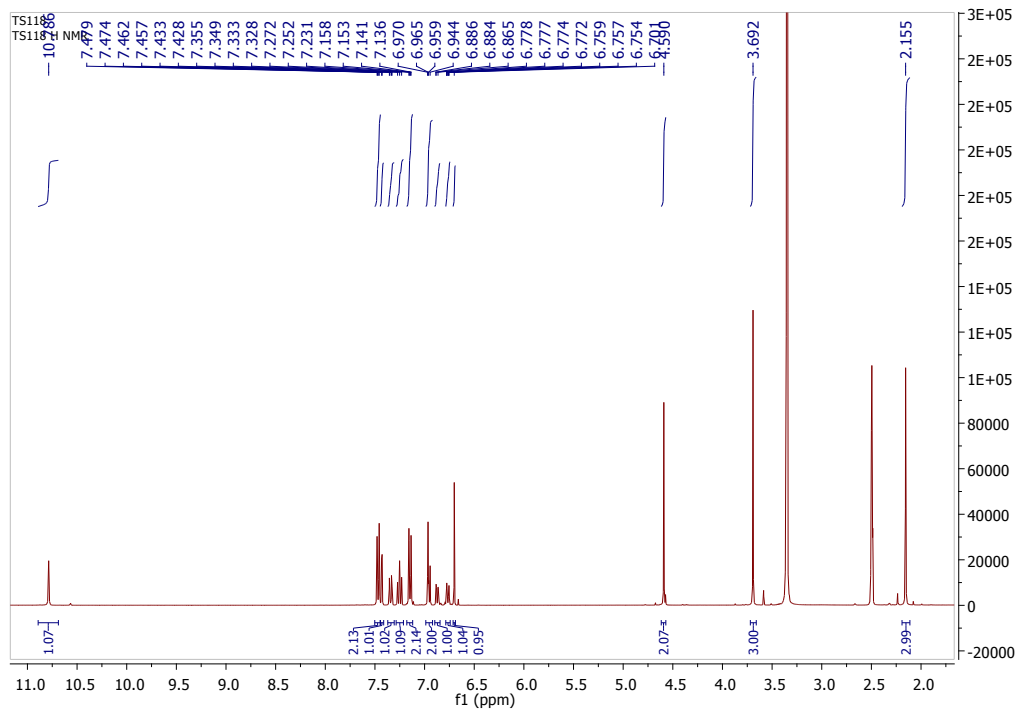
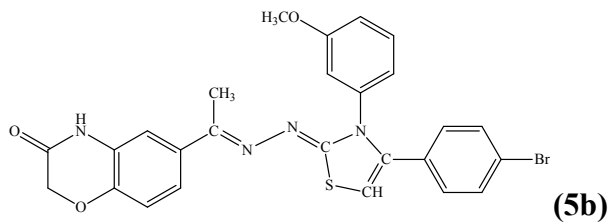
### **References:**

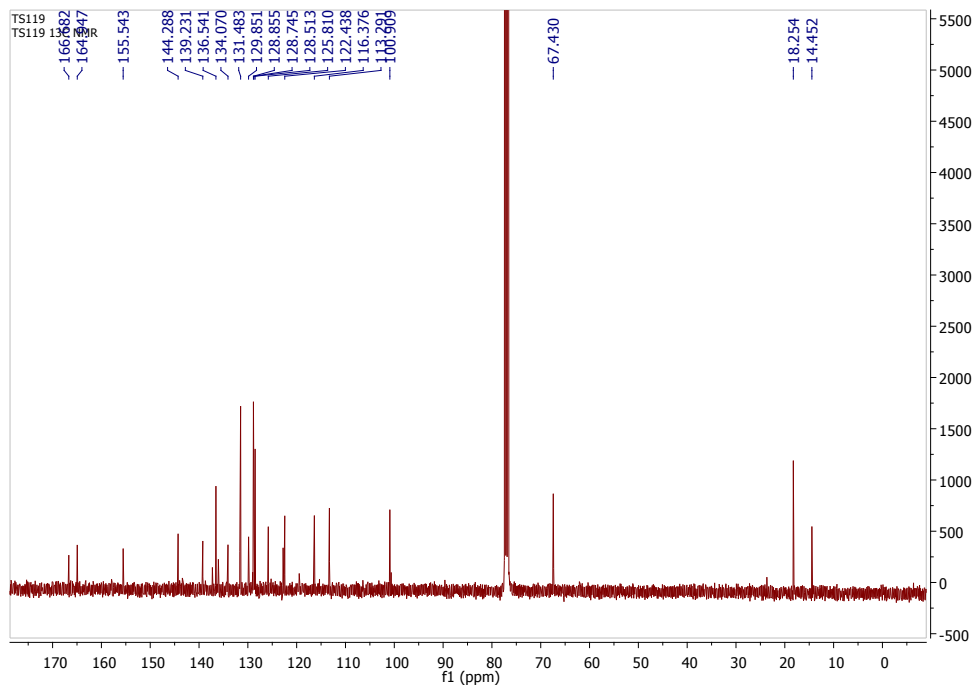
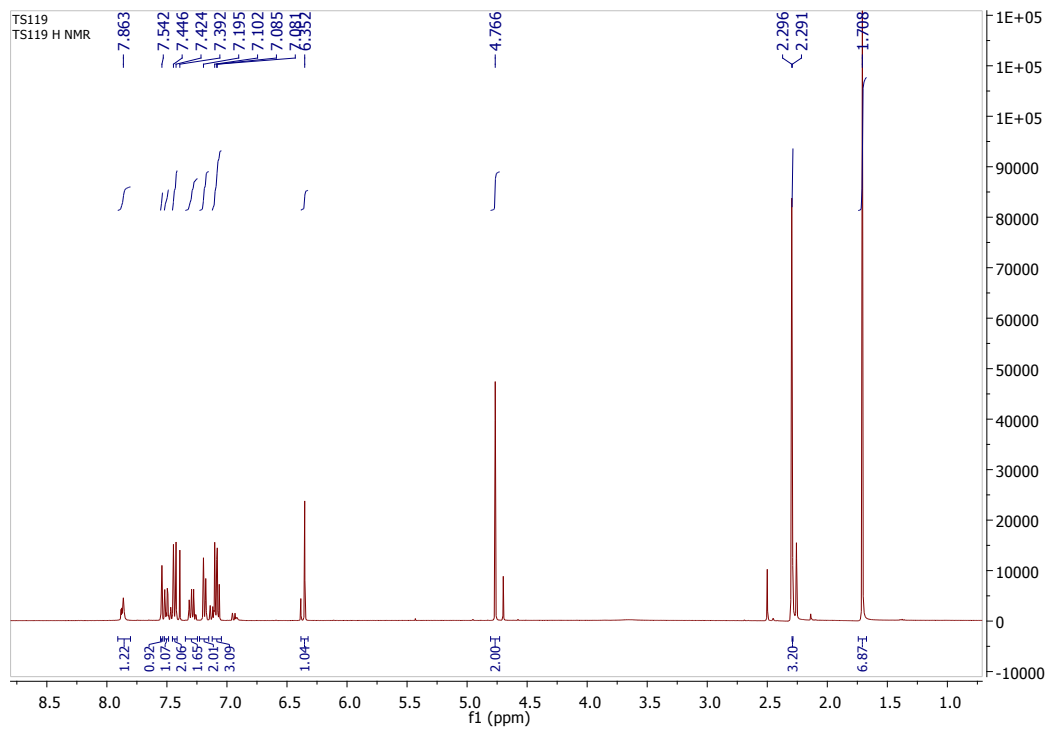
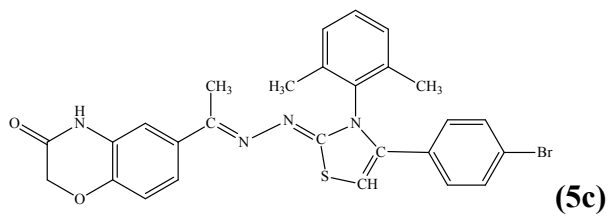
1. V. Carbone and O. El-Kabbani, *RSCB Protein Databank. PDB ID: 3FX4*, 2009.
2. E. I. Howard, R. Sanishvili, R. Cachau, A. Mitschler, B. Chevrier, P. Barth, V. Lamour, M. Van Zandt, E. Sibley and C. Bon, *Proteins: Structure, Function, and Bioinformatics*, 2004, **55**, 792-804.
3. W. H. Ward, C. M. Sennitt, H. Ross, A. Dingle, D. Timms, D. J. Mirrlees and D. P. Tuffin, *Biochemical pharmacology*, 1990, **39**, 337-346.
4. P. F. Kador, J. Kinoshita, D. Brittain, D. Mirrlees, C. Sennitt and D. Stribling, *Biochemical Journal*, 1986, **240**, 233-237.
5. F. Da Settimo, G. Primofiore, A. Da Settimo, C. La Motta, S. Taliani, F. Simorini, E. Novellino, G. Greco, A. Lavecchia and E. Boldrini, *Journal of medicinal chemistry*, 2001, **44**, 4359-4369.

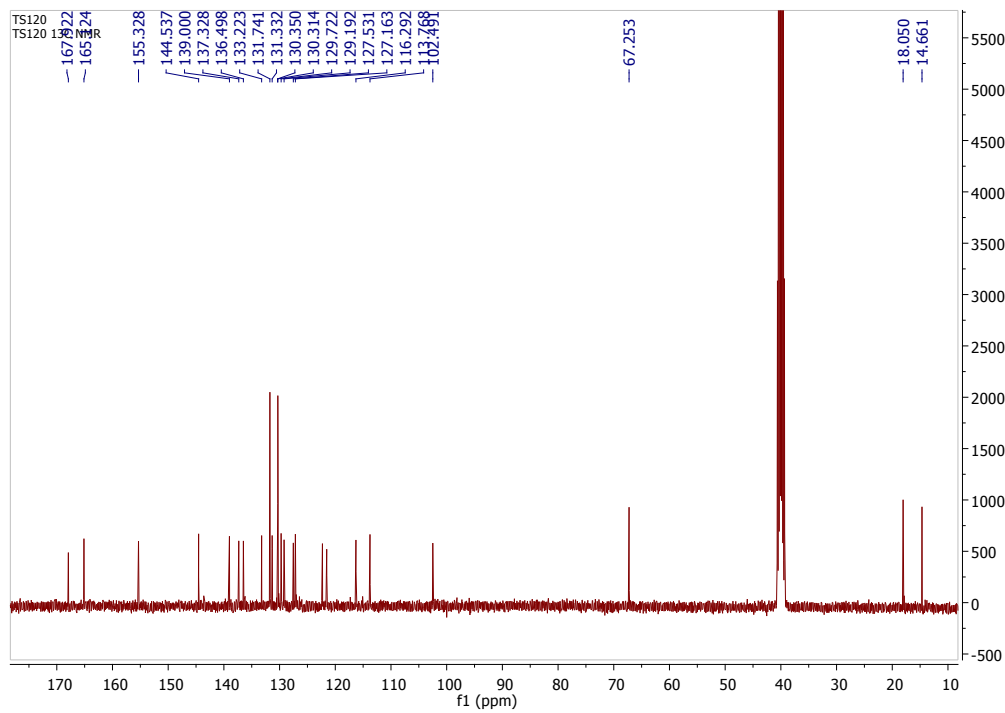
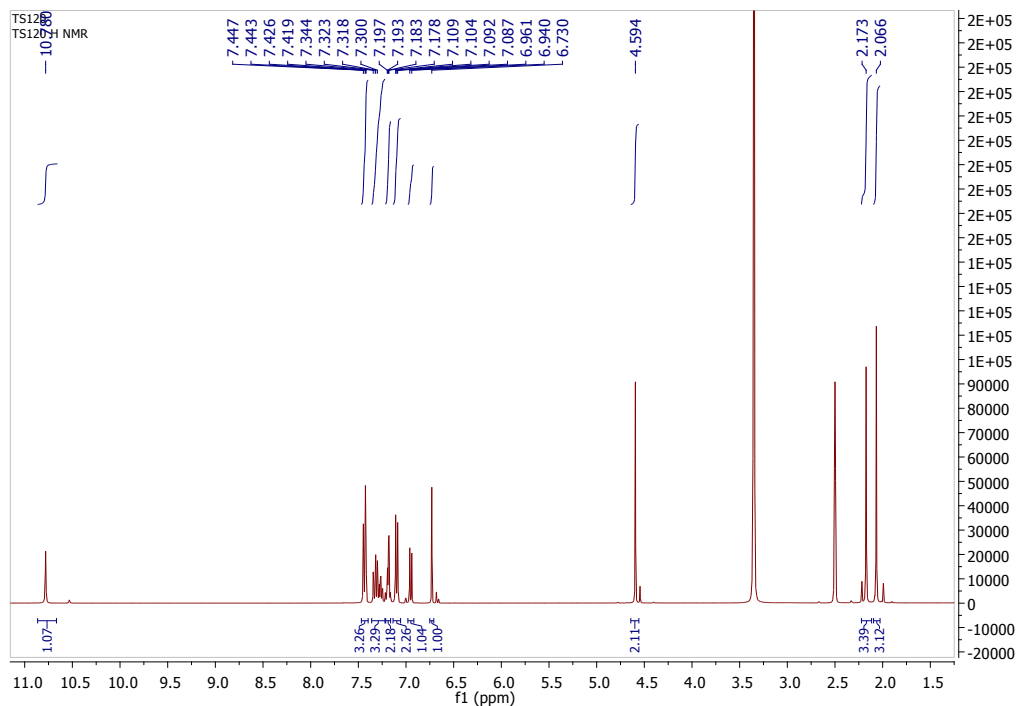
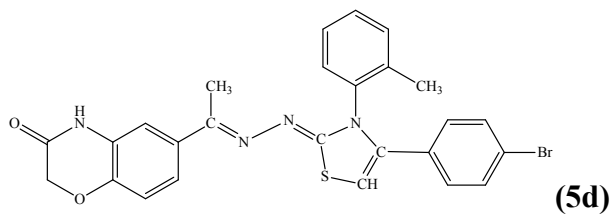


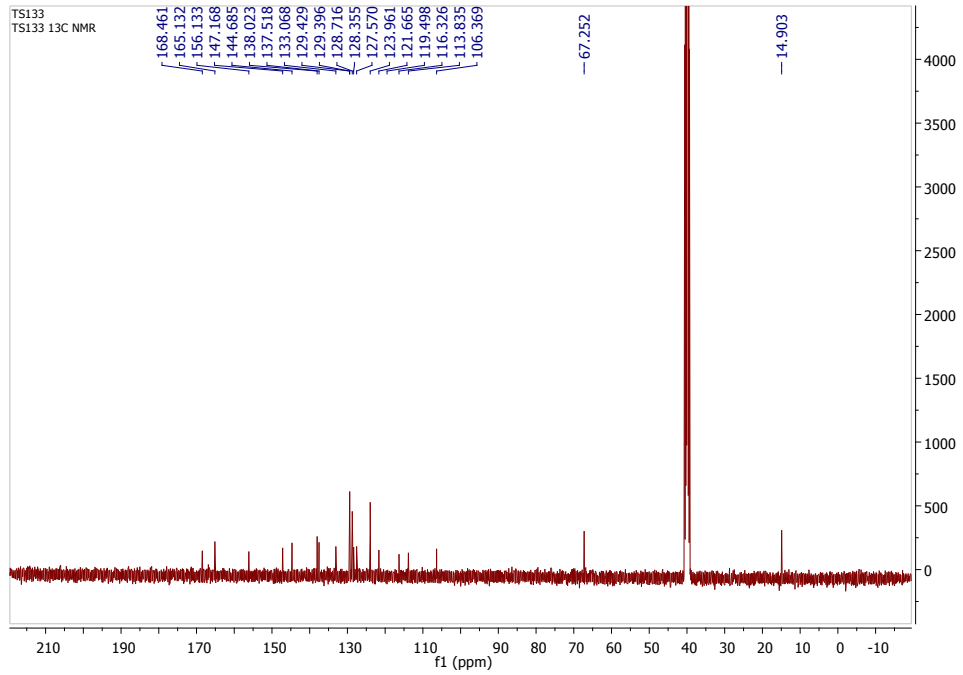
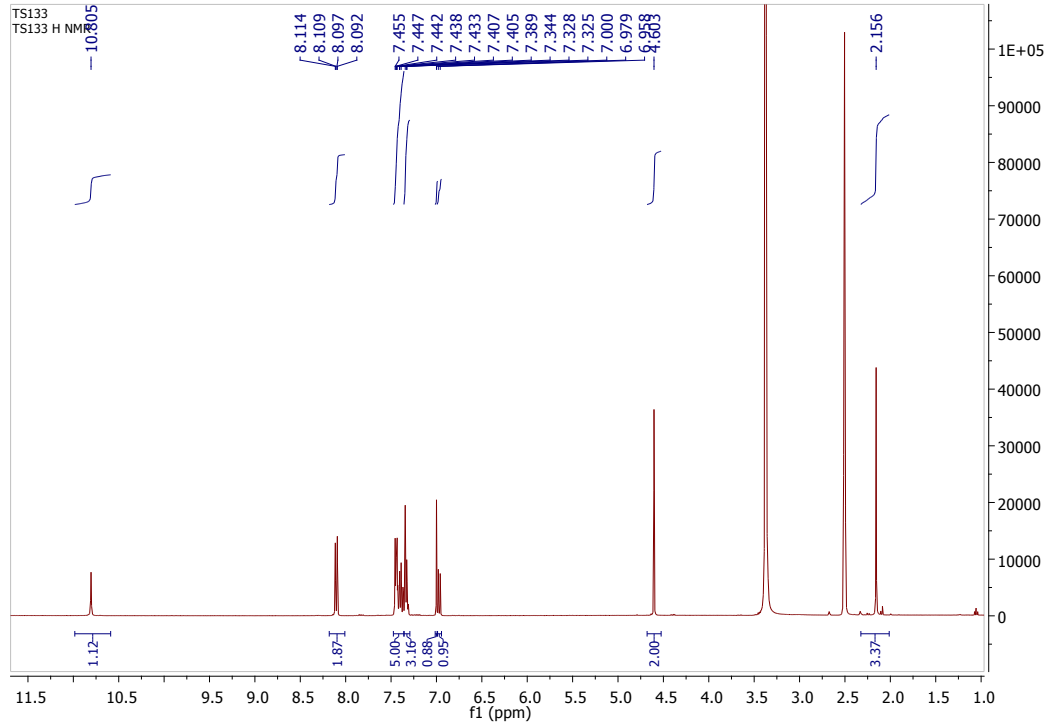
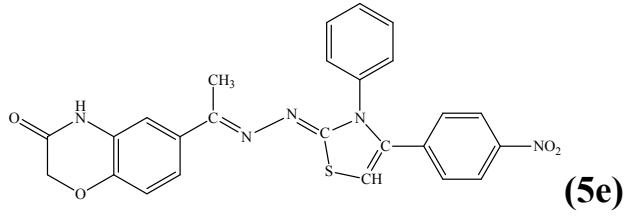
# <sup>1</sup>H NMR & <sup>13</sup>C Spectra



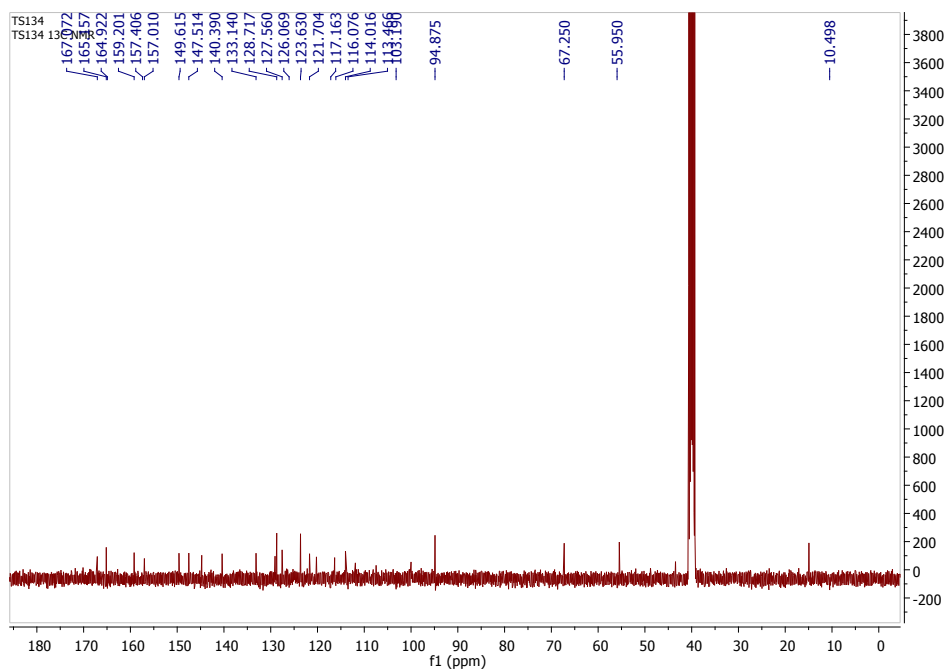
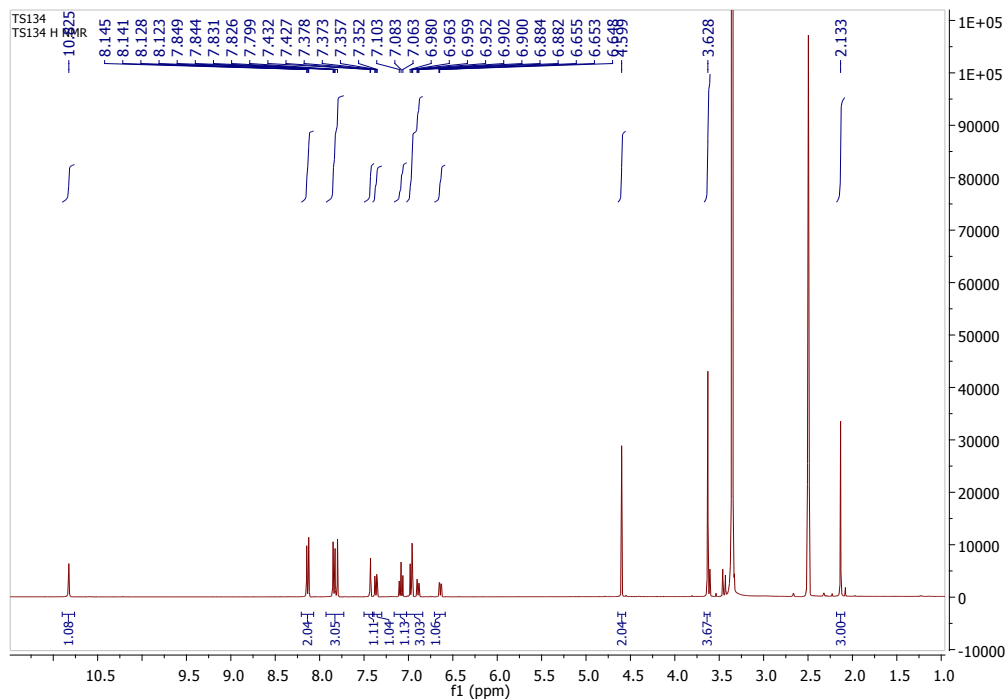
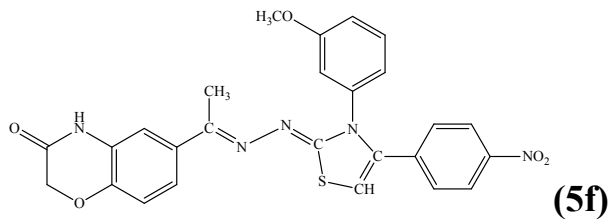


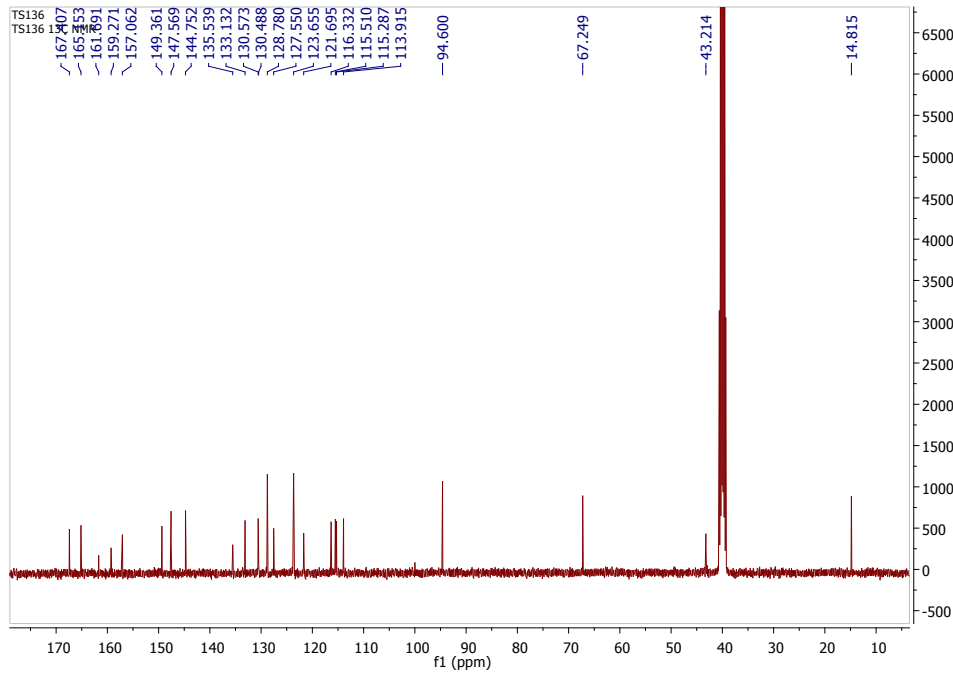
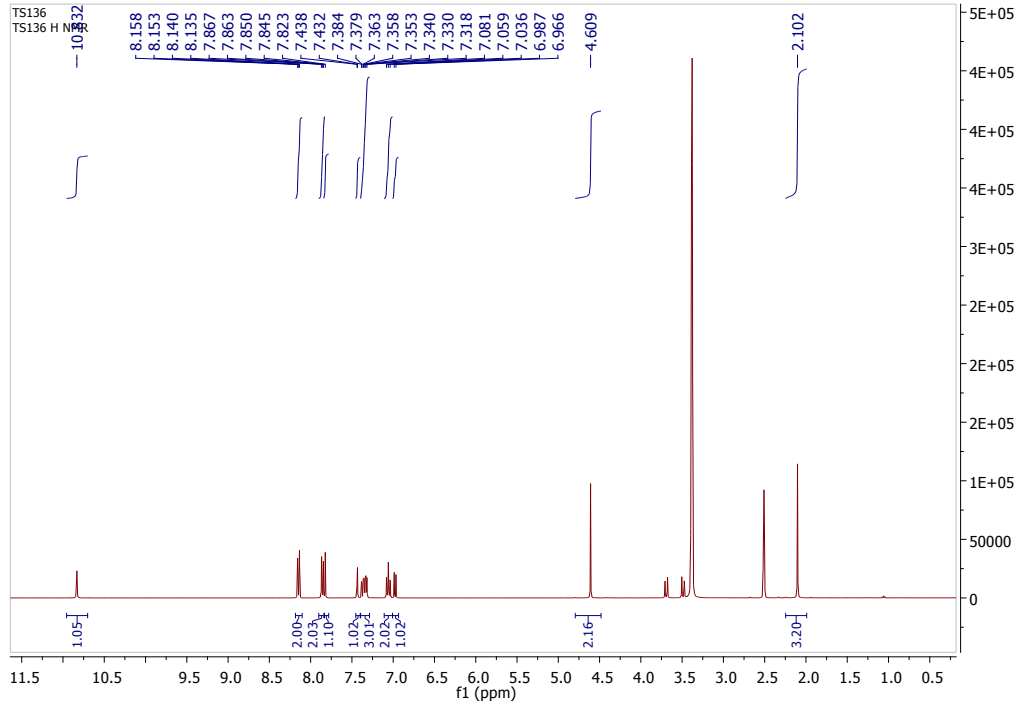
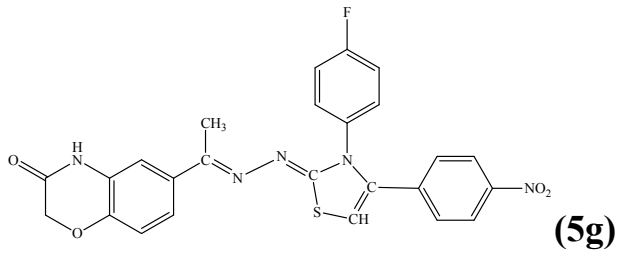


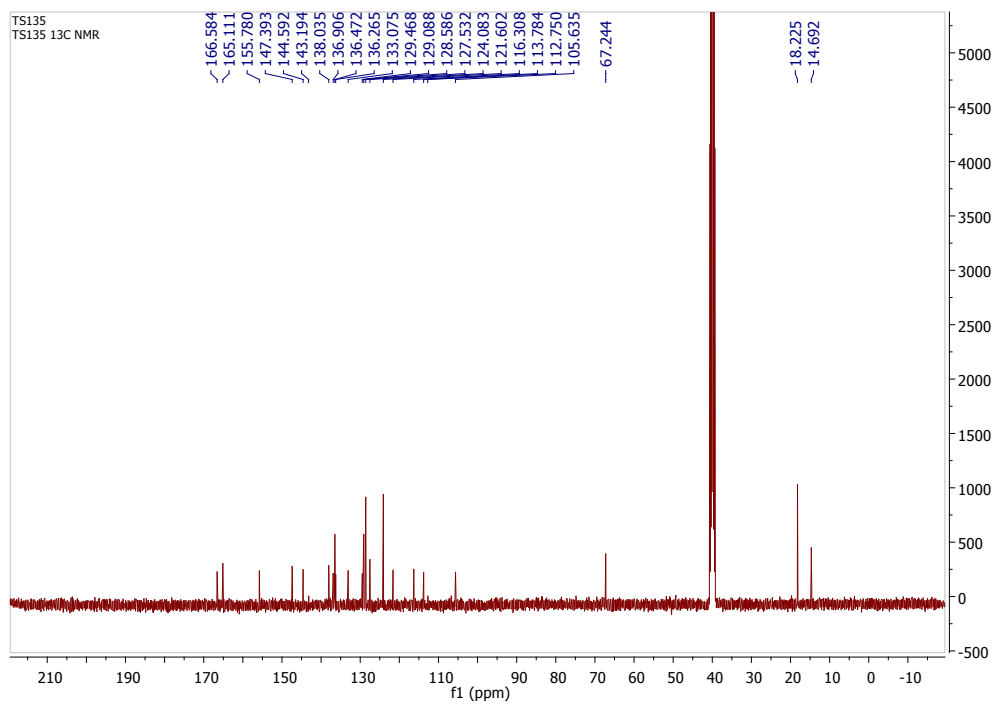
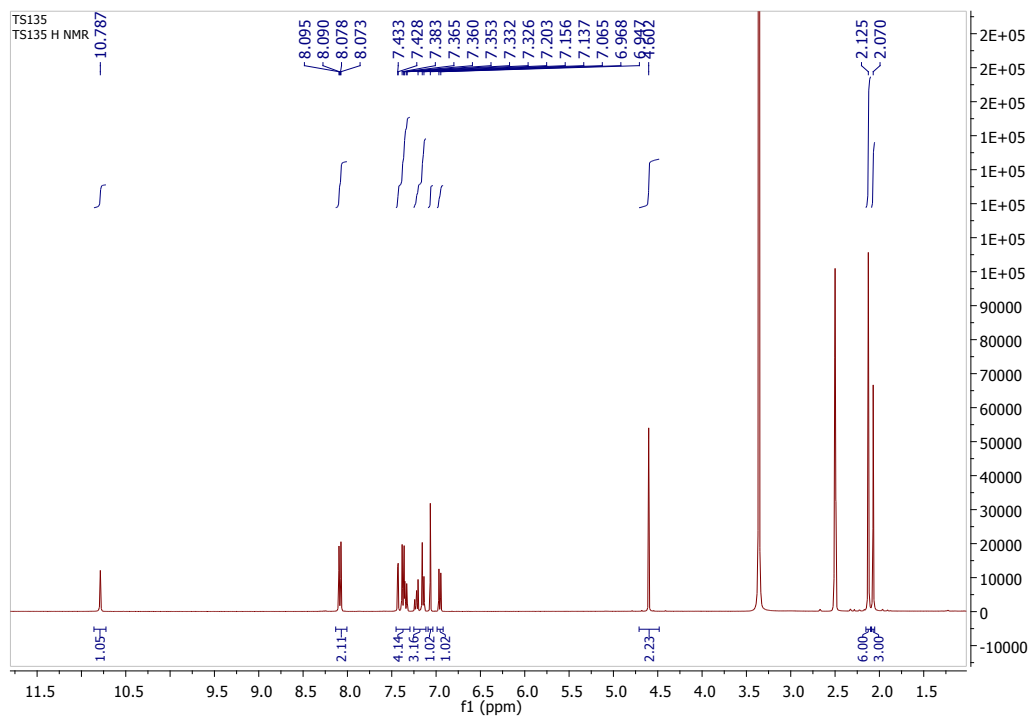
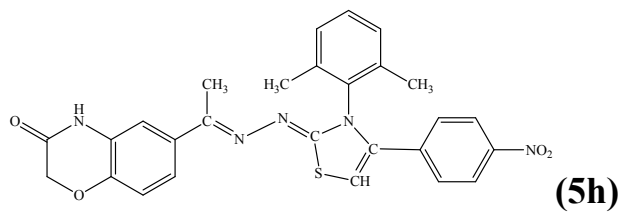


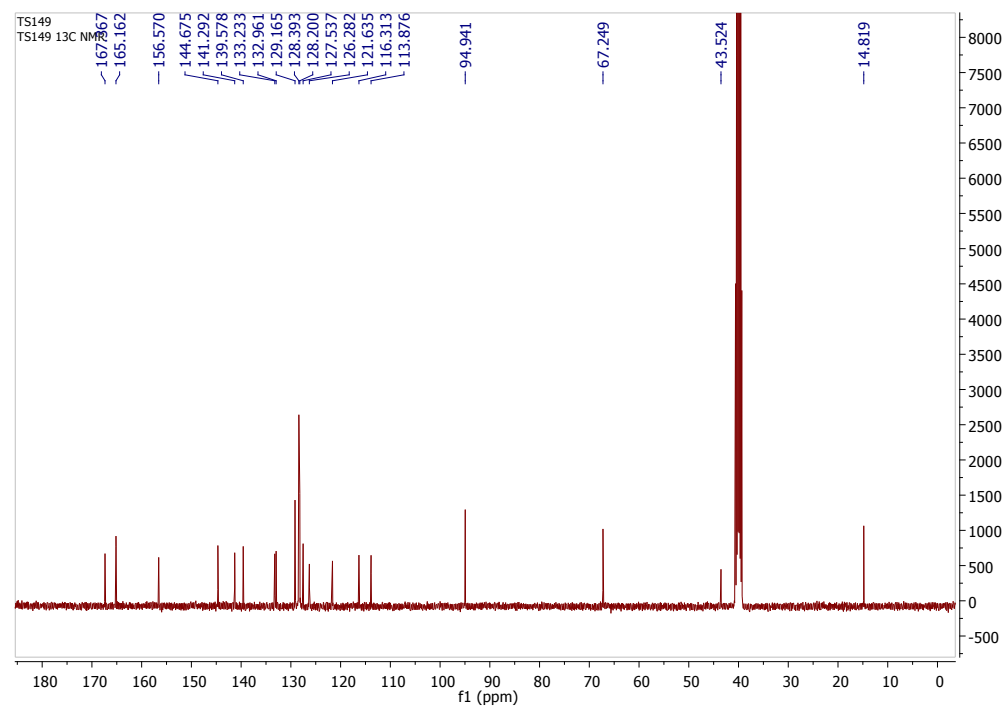
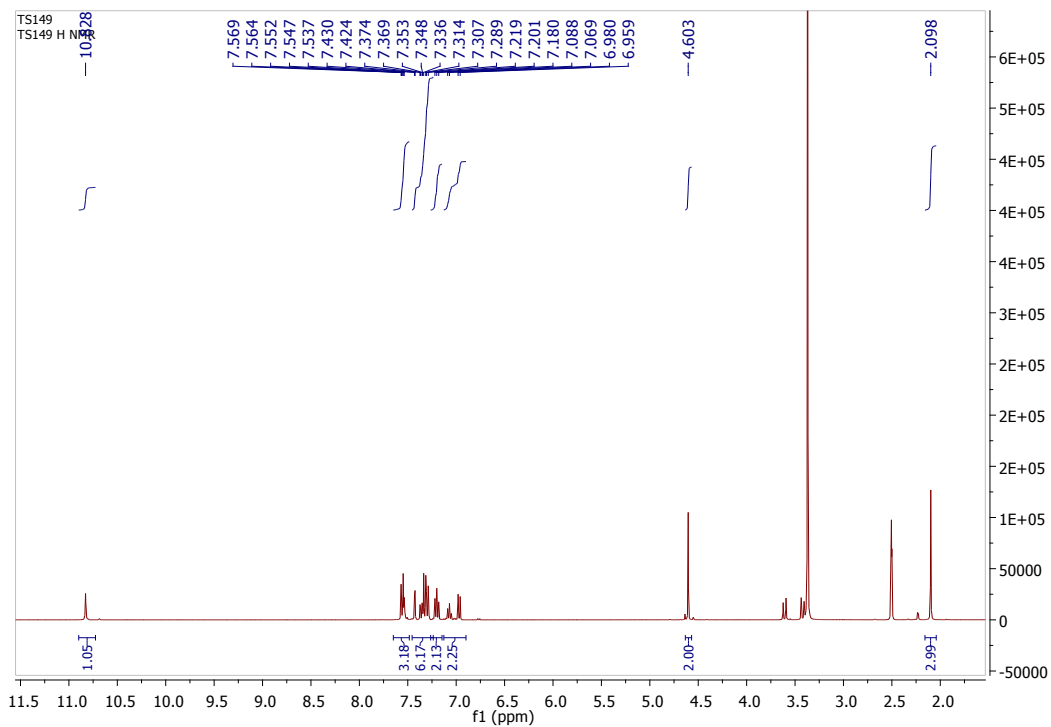
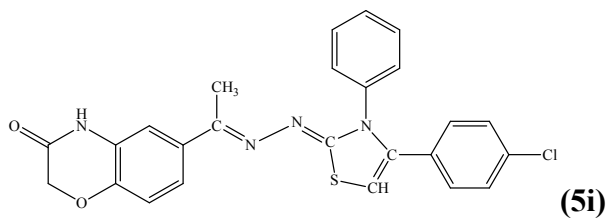


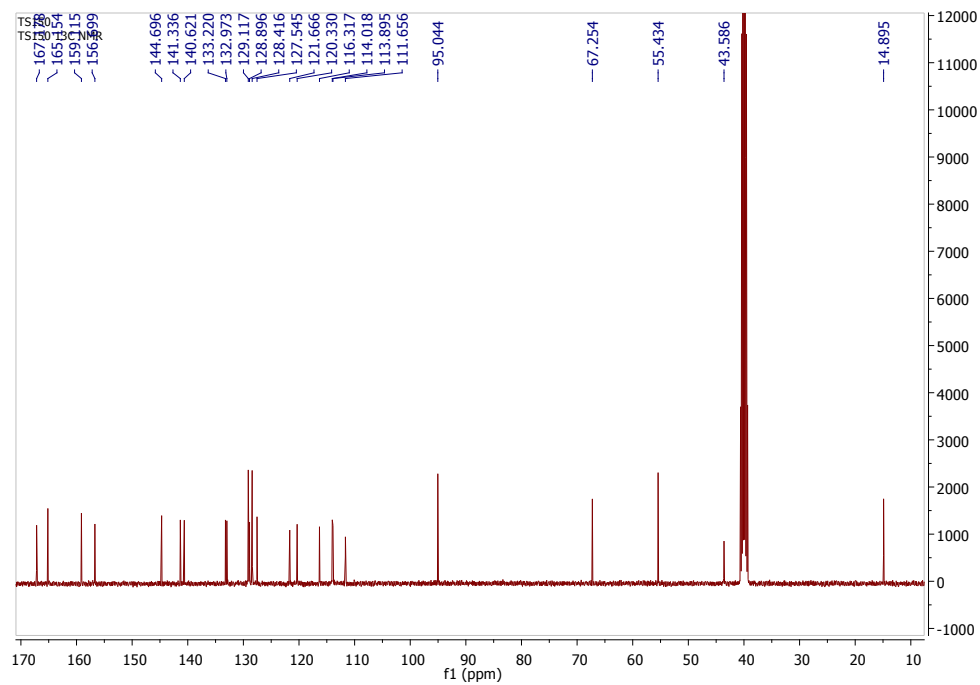
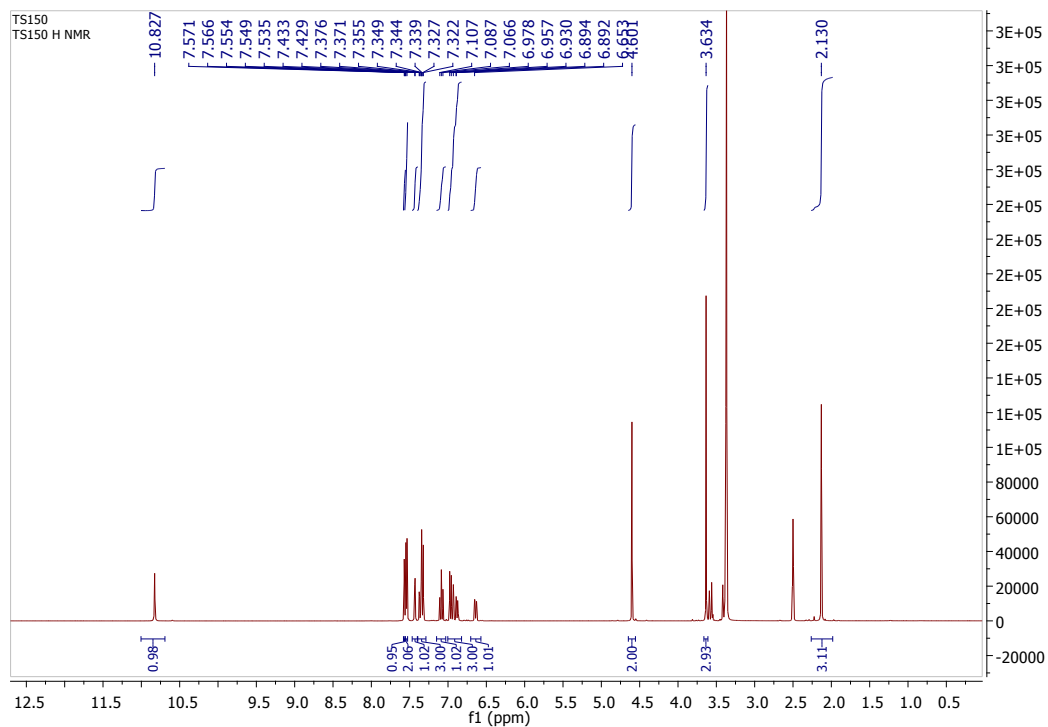
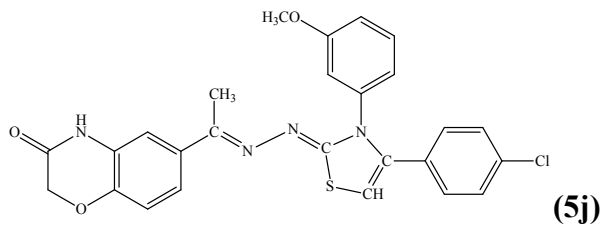


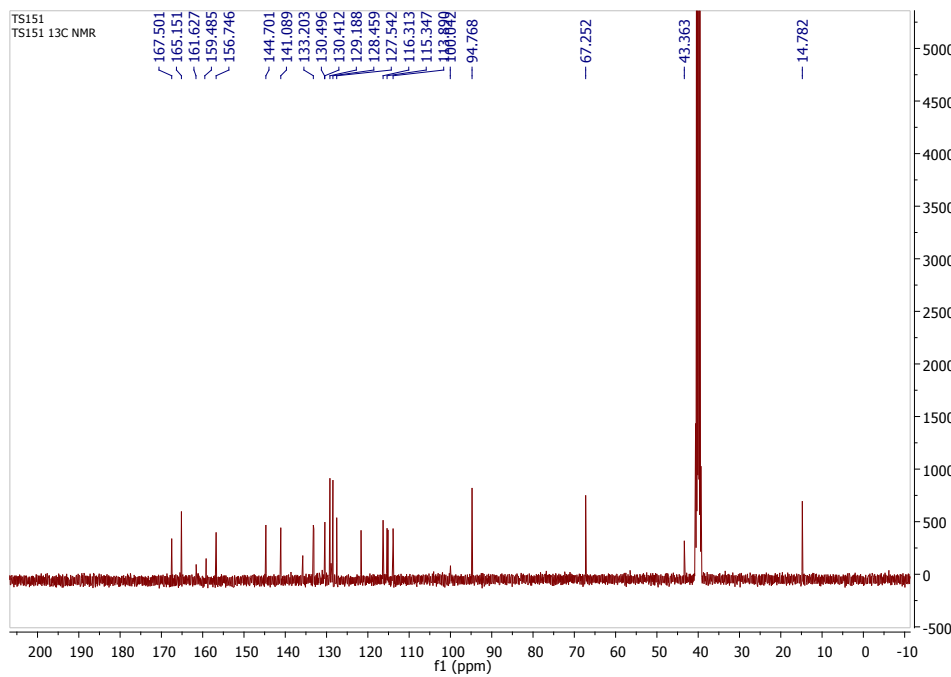
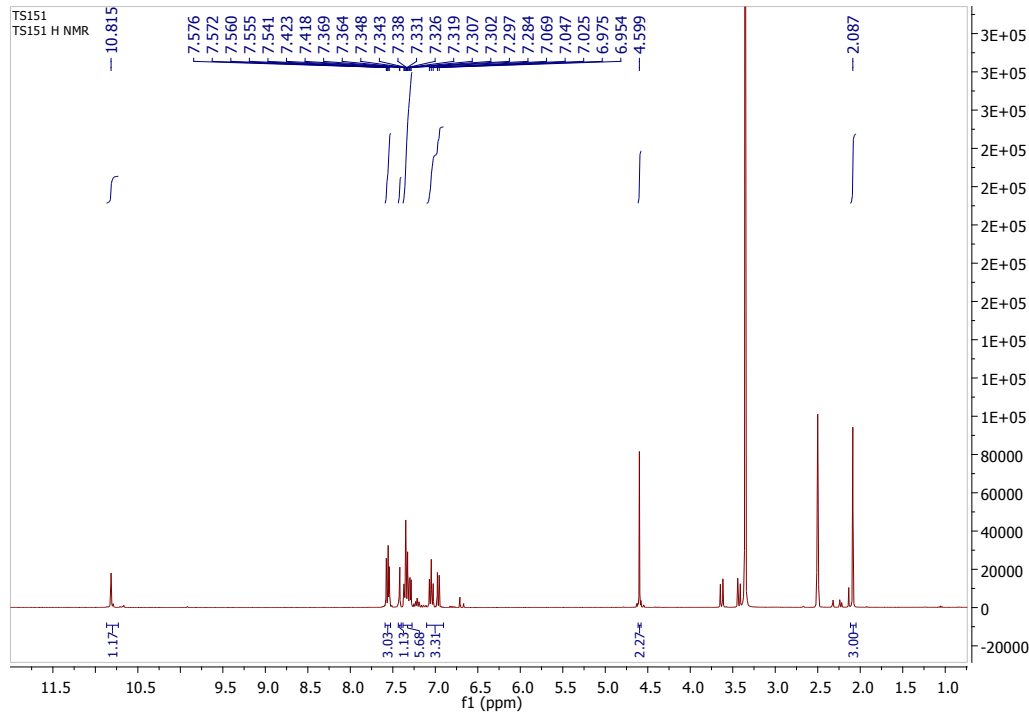
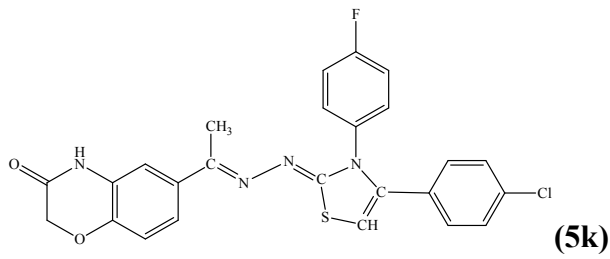


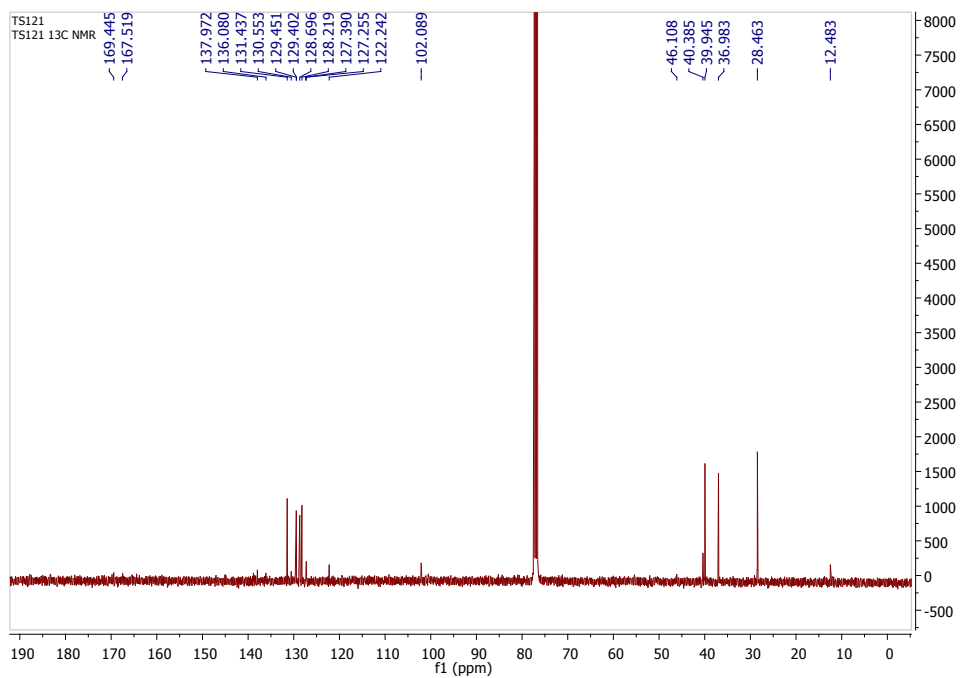
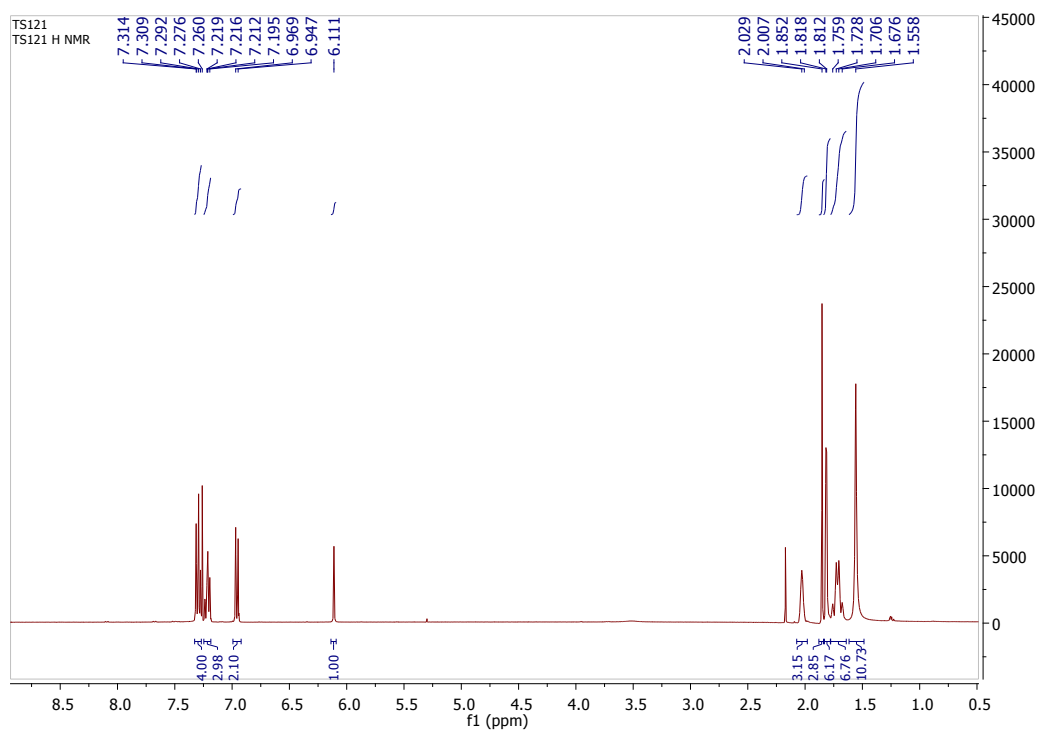
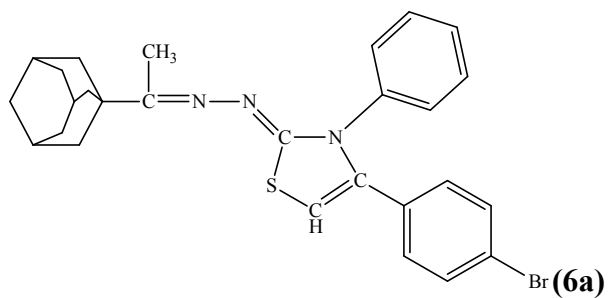


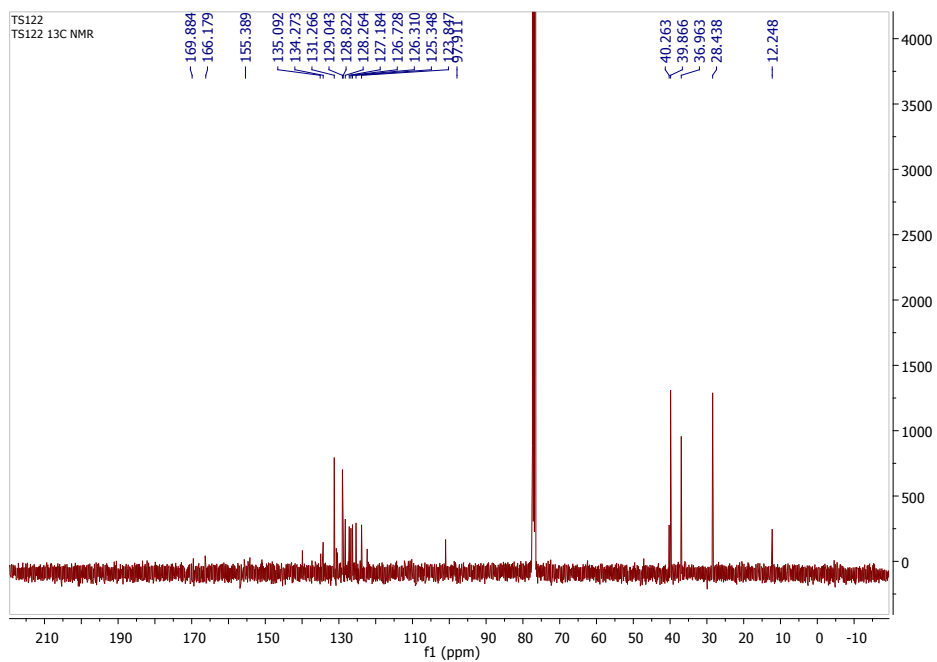
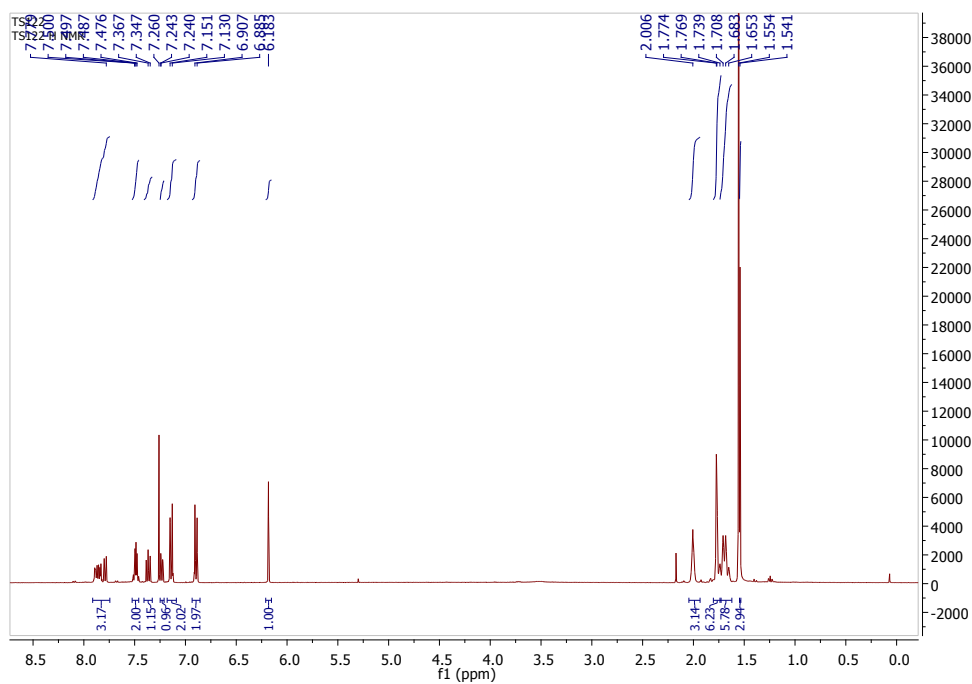
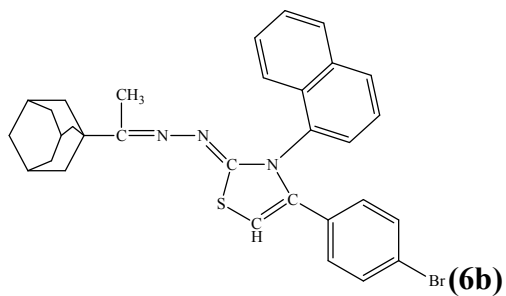




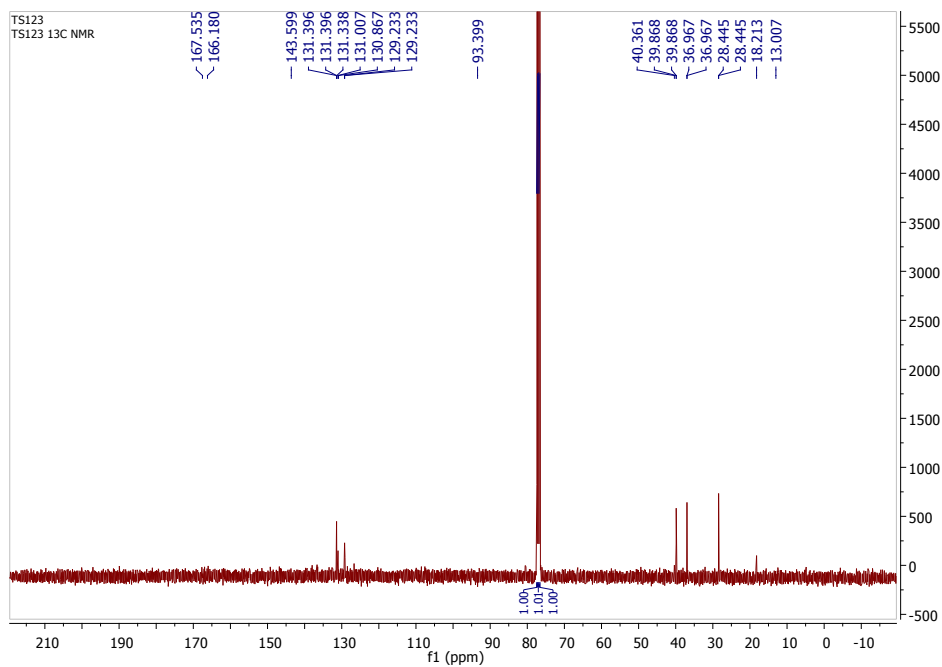
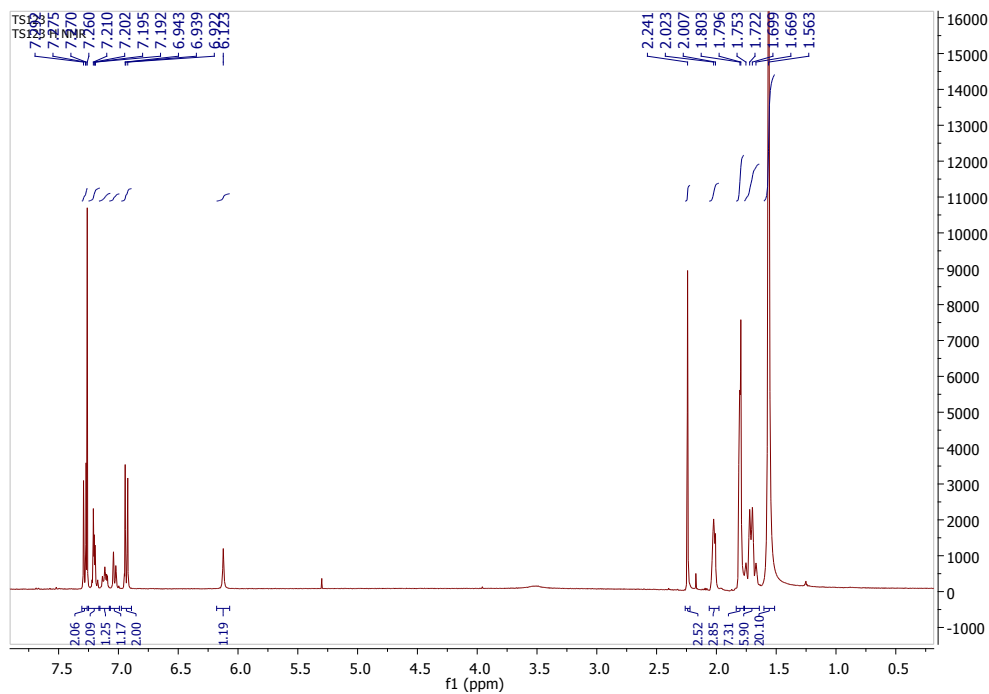
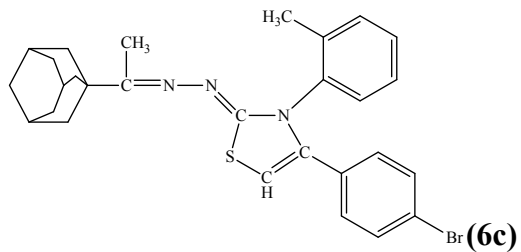


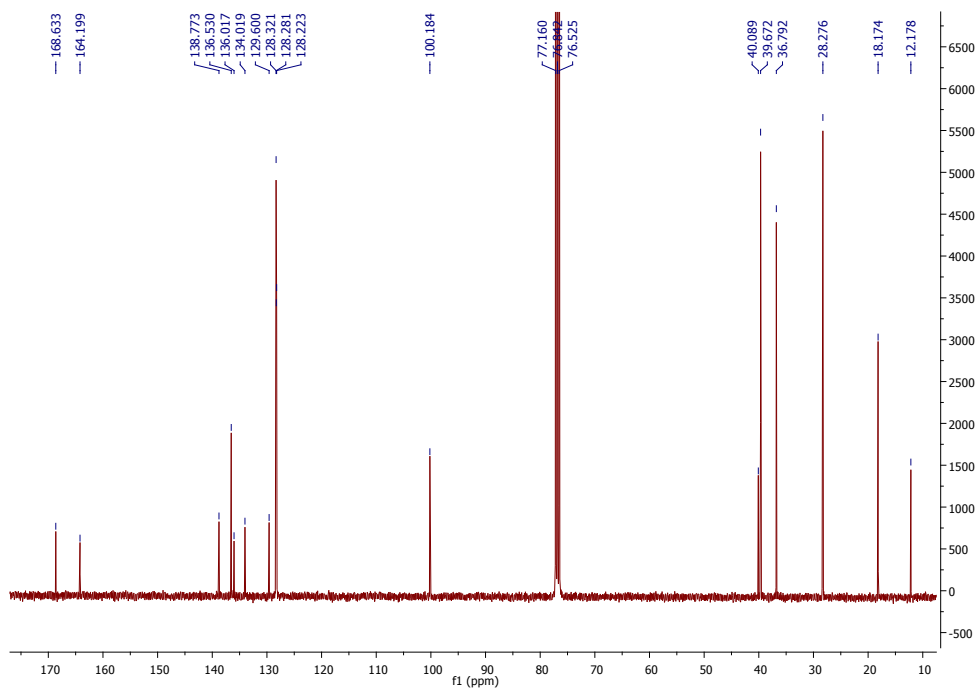
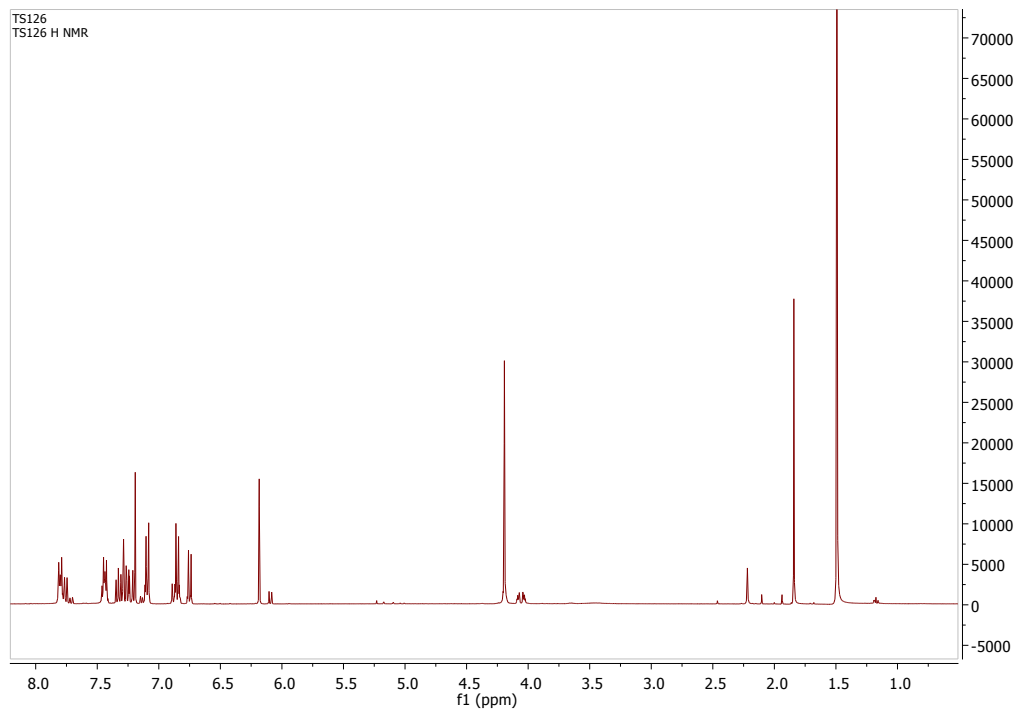
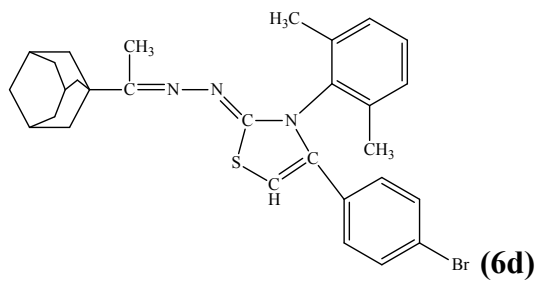


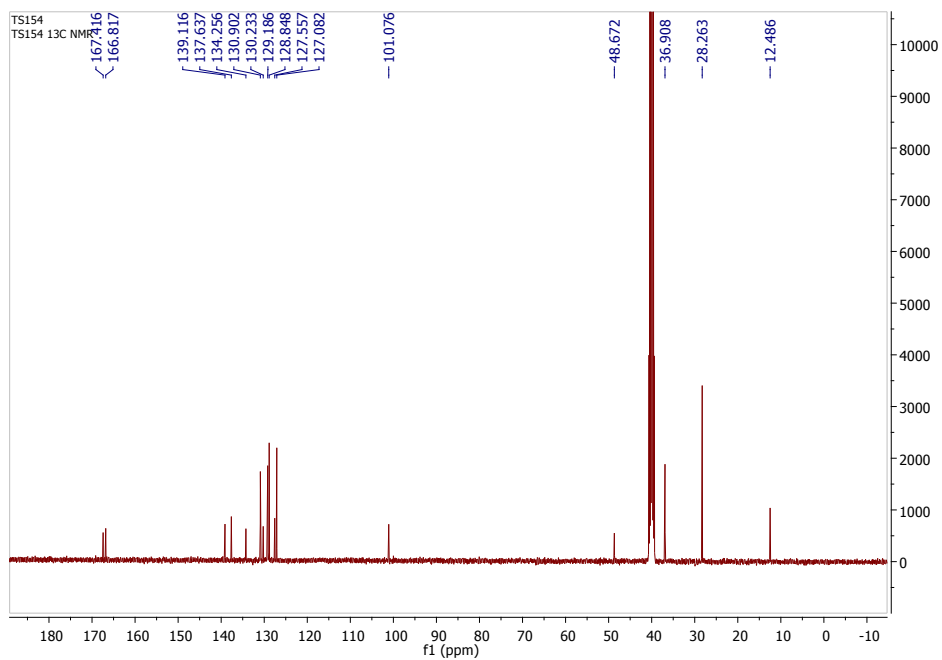
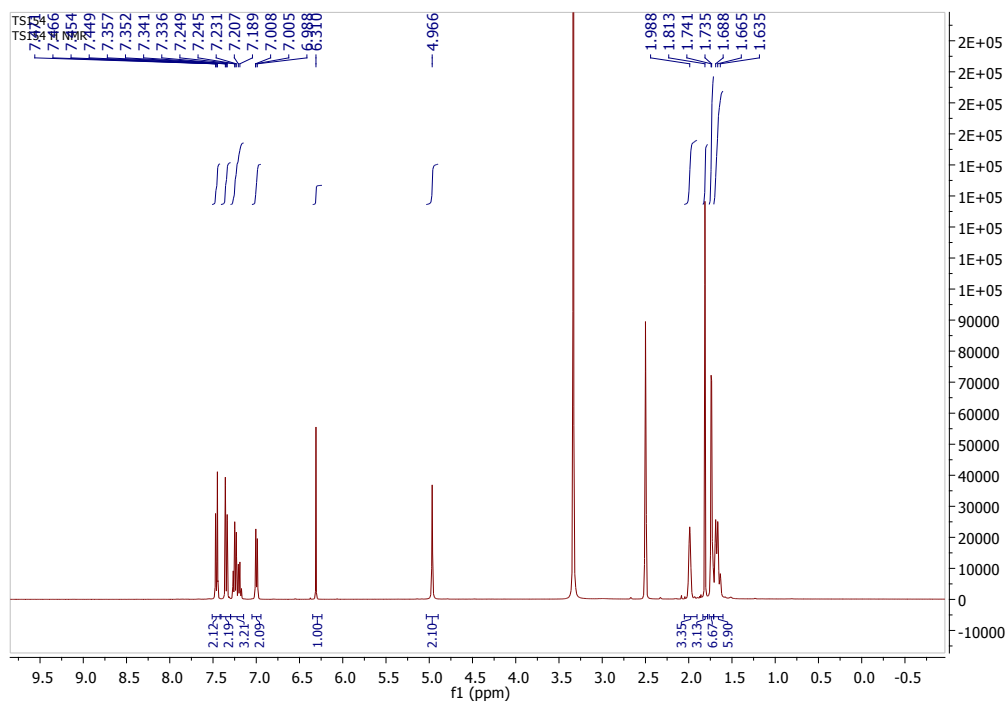
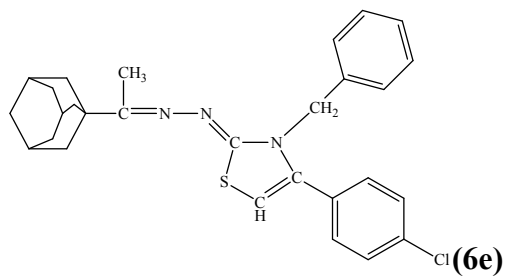


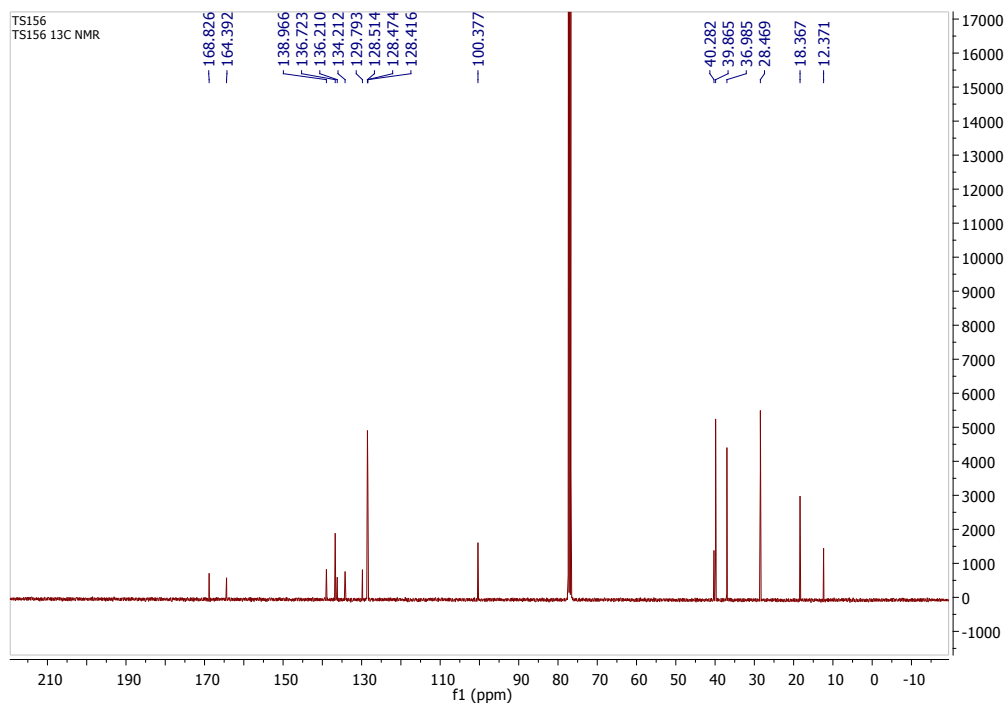
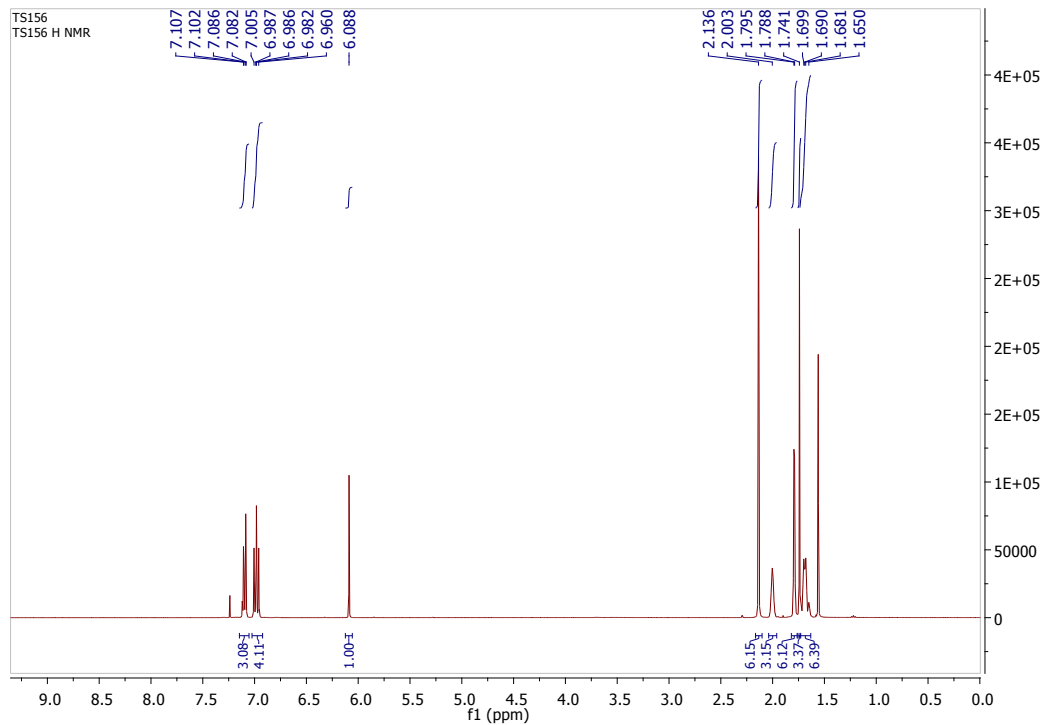
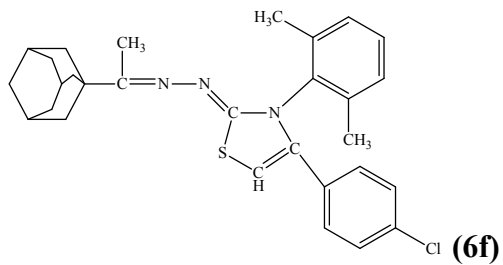


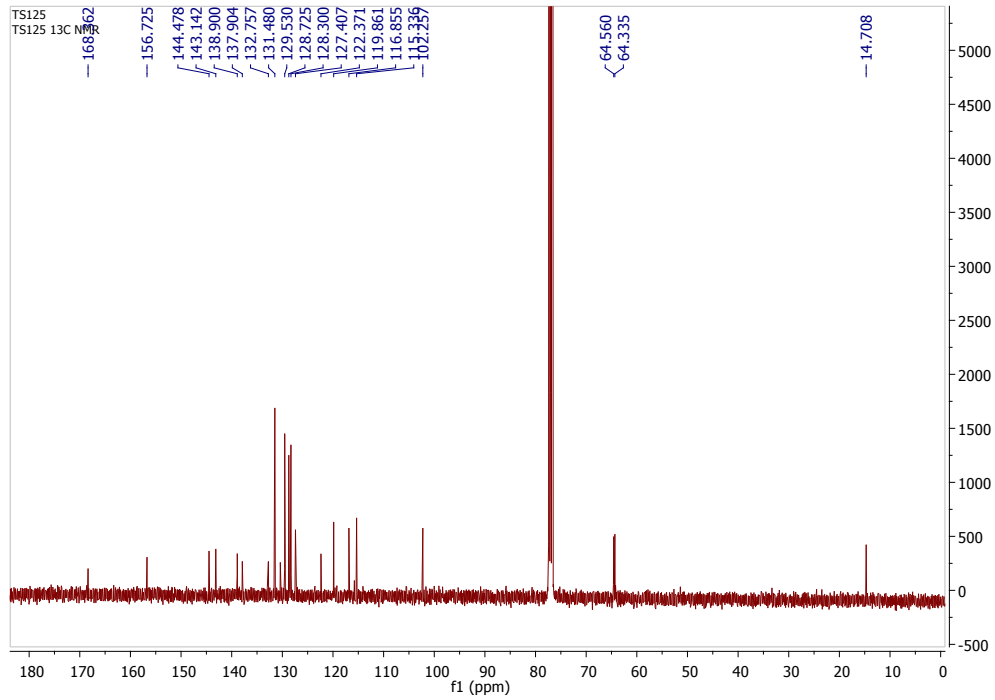
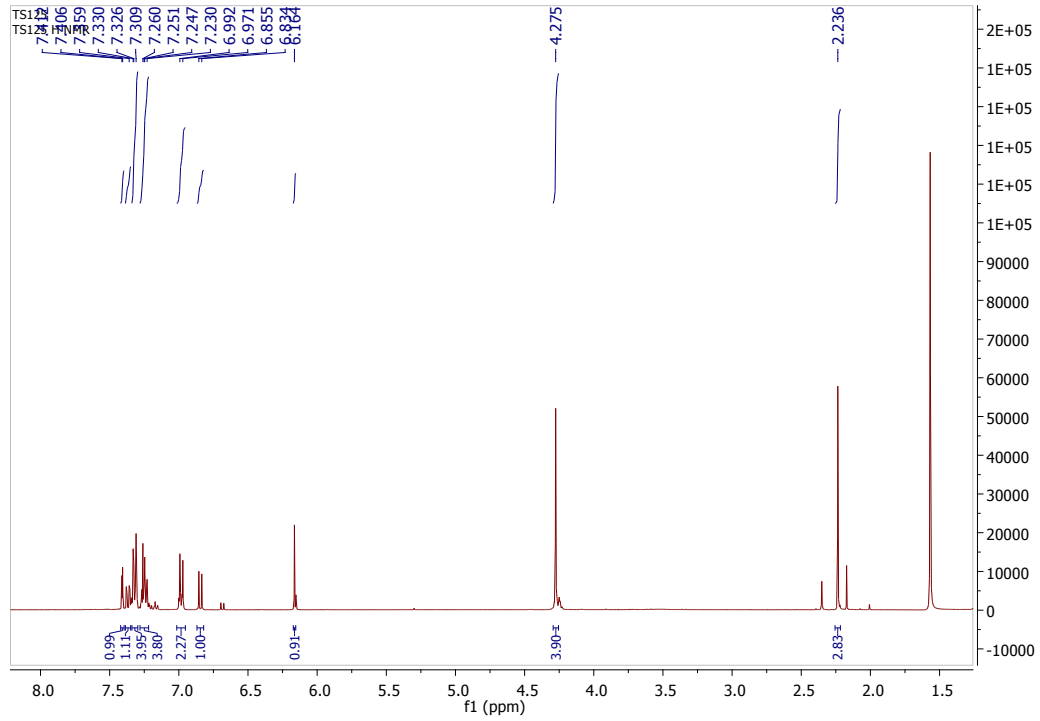
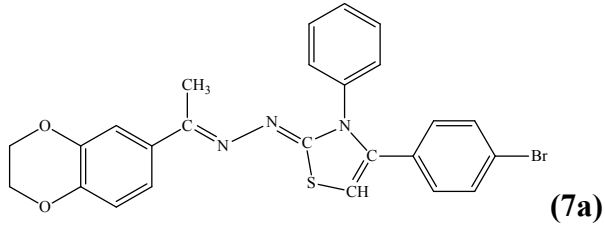


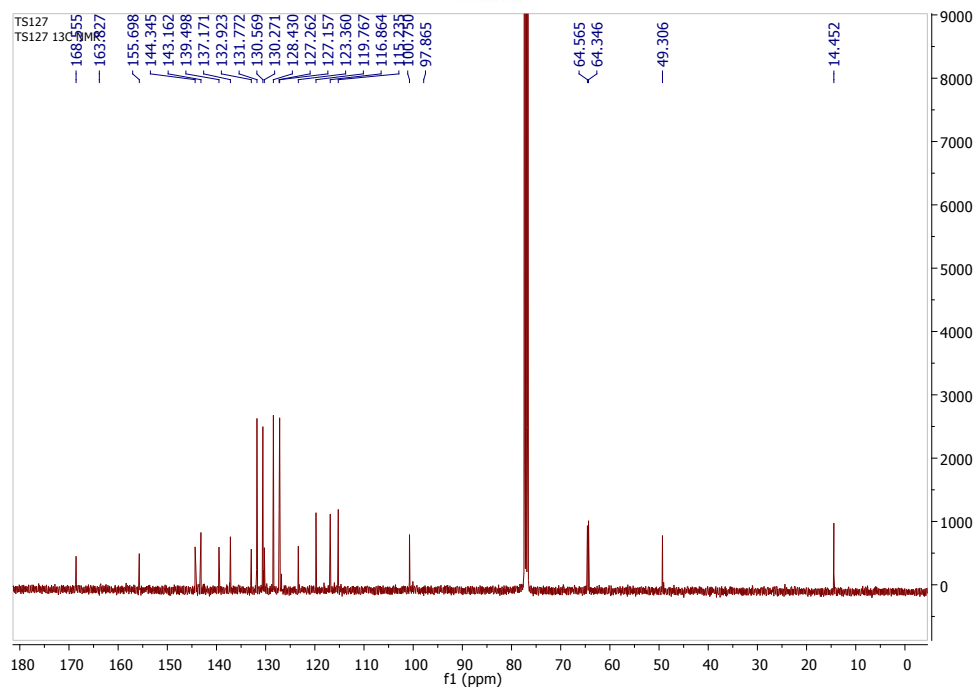
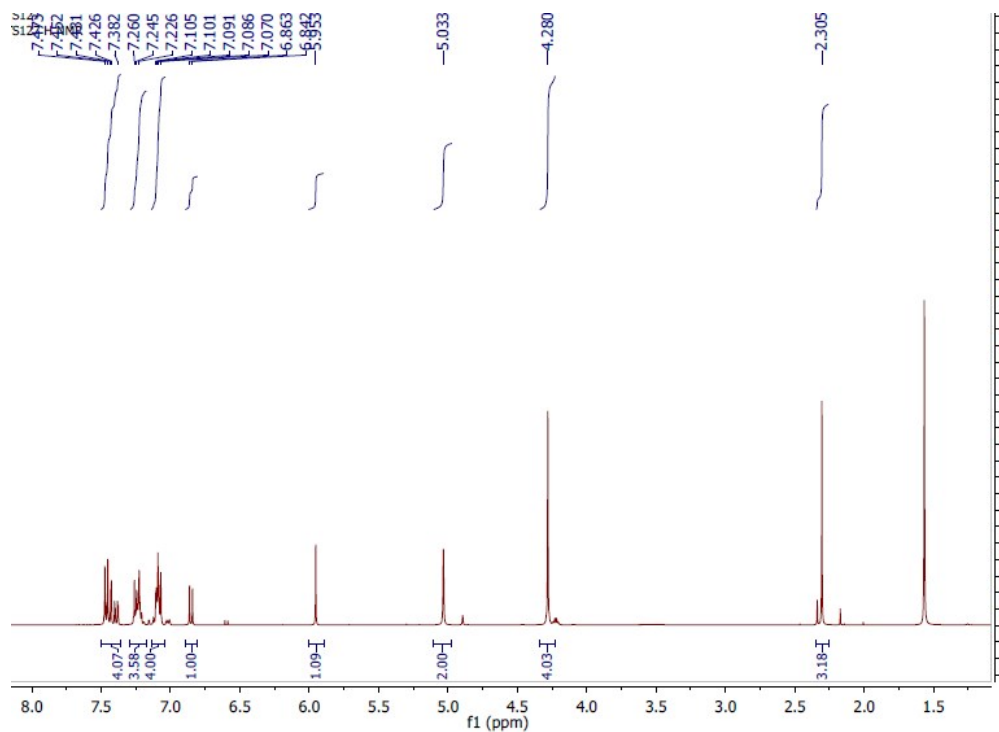
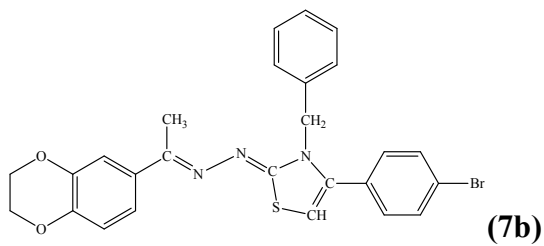


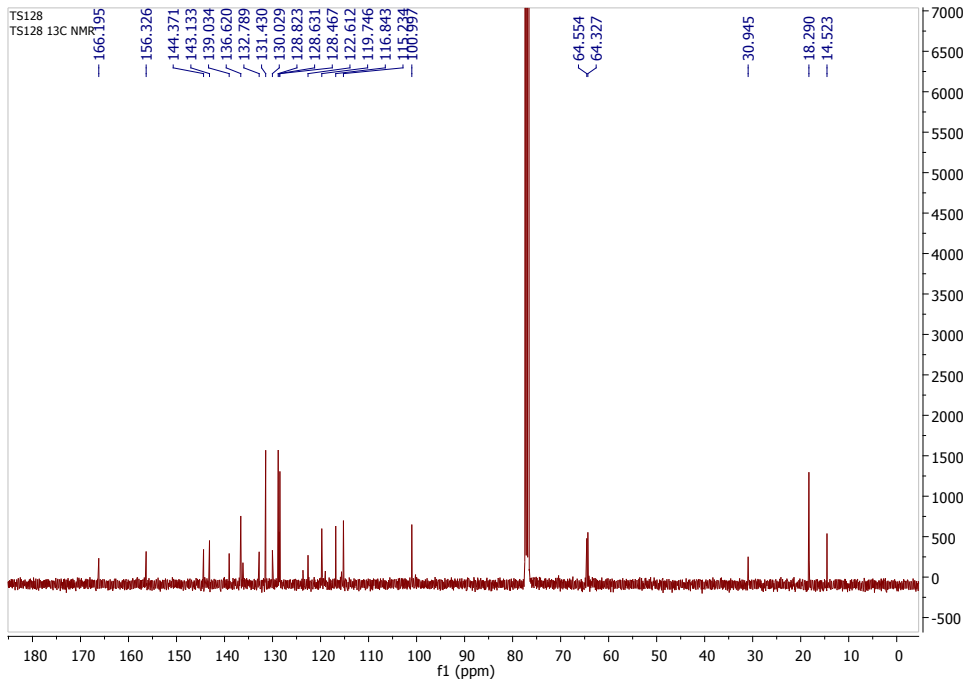
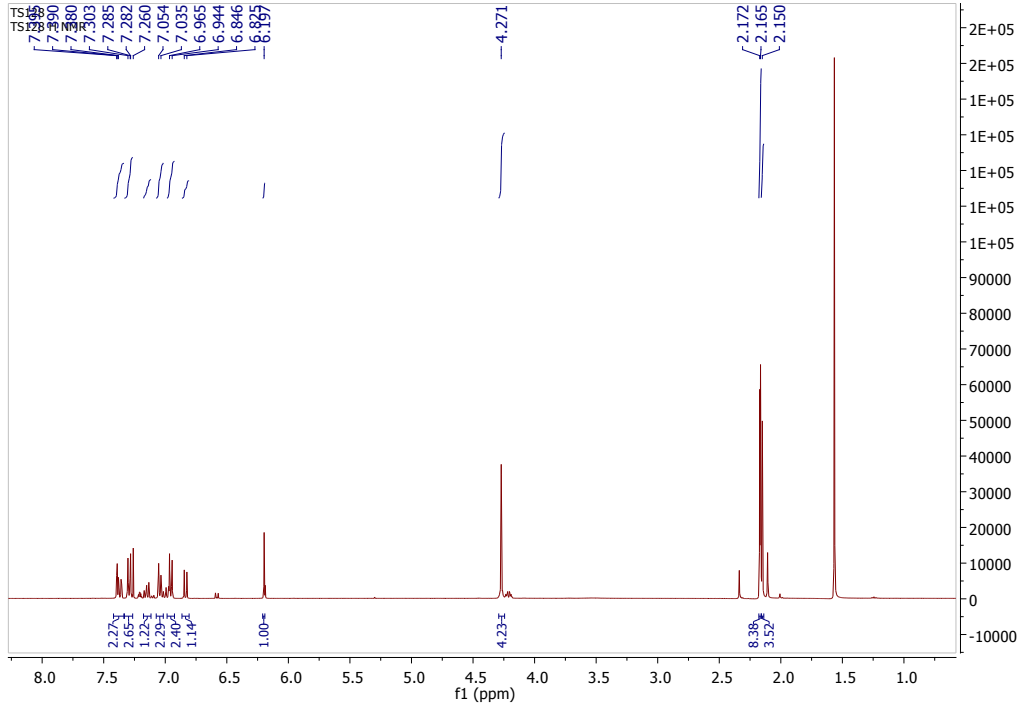
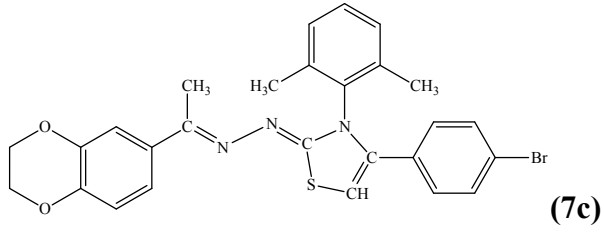


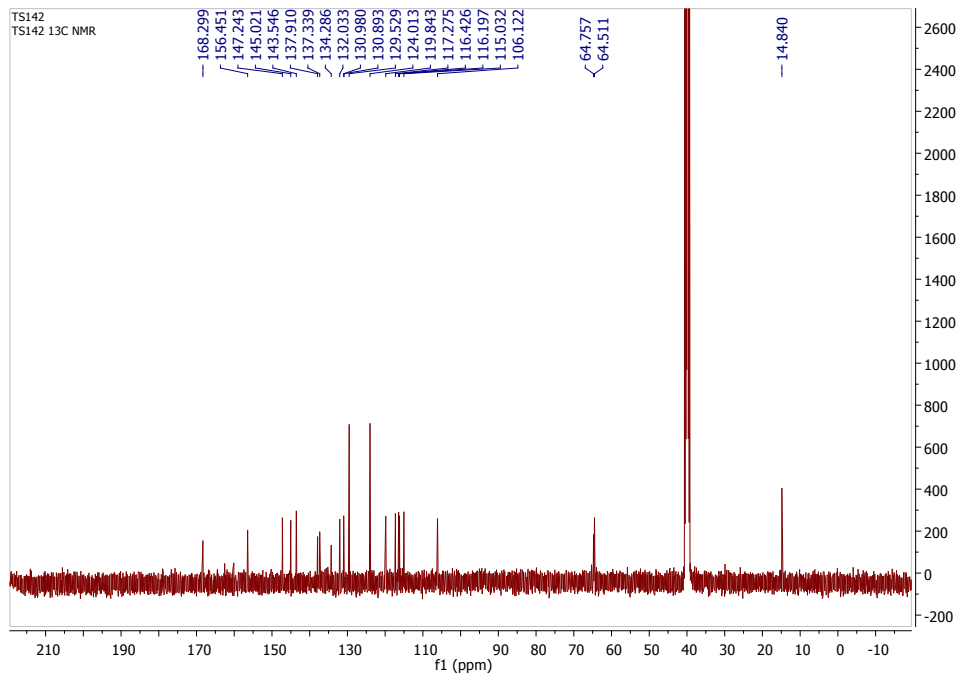
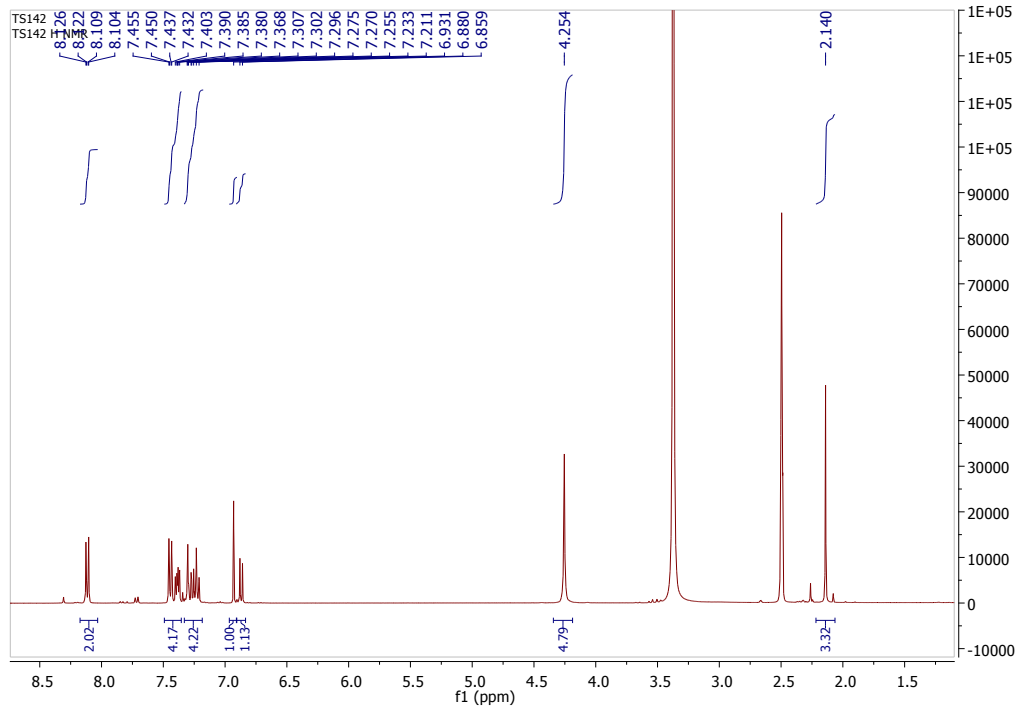
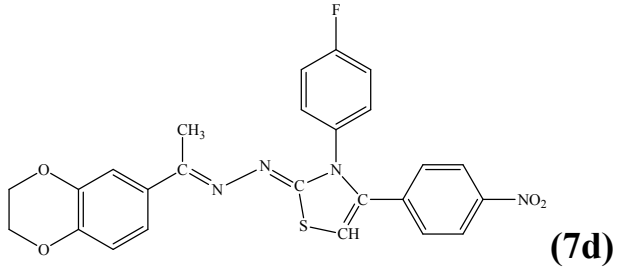




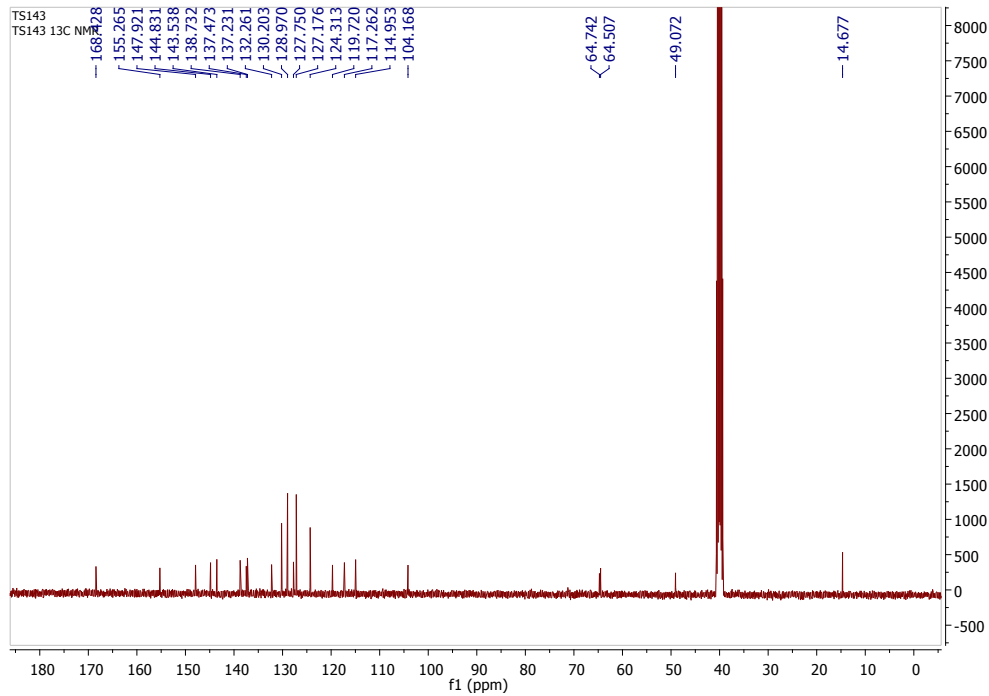
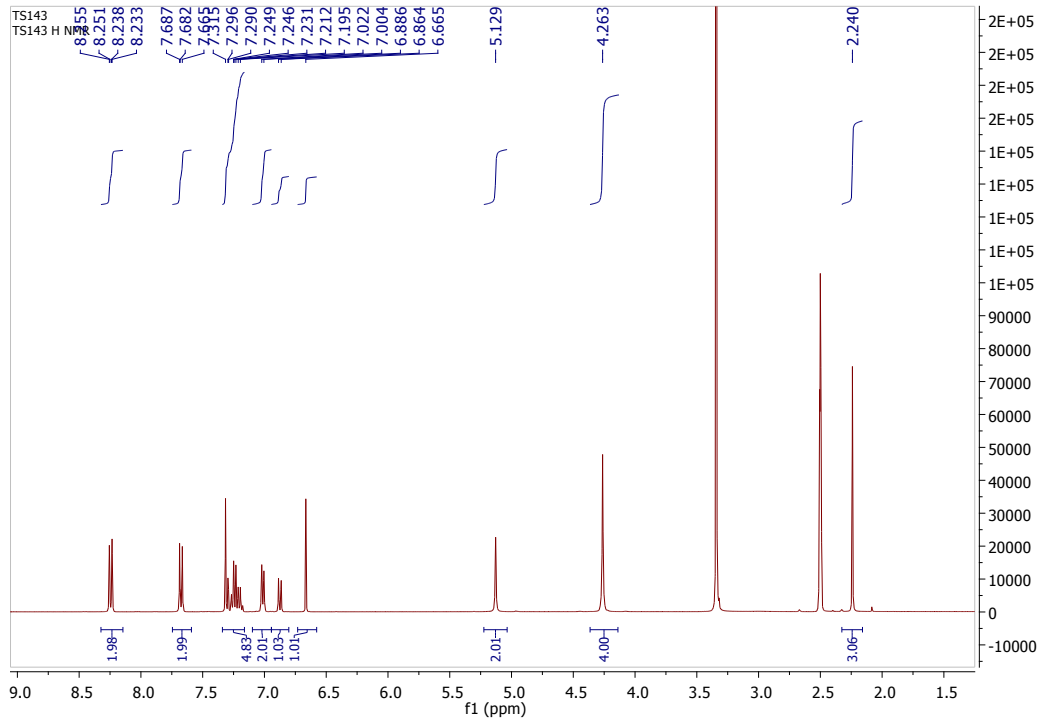
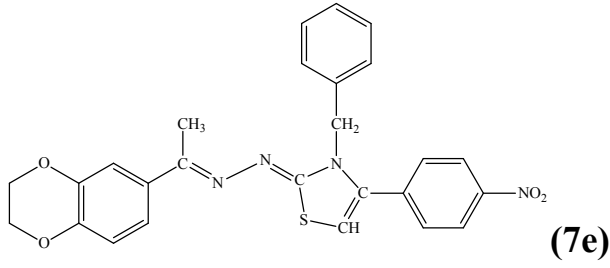


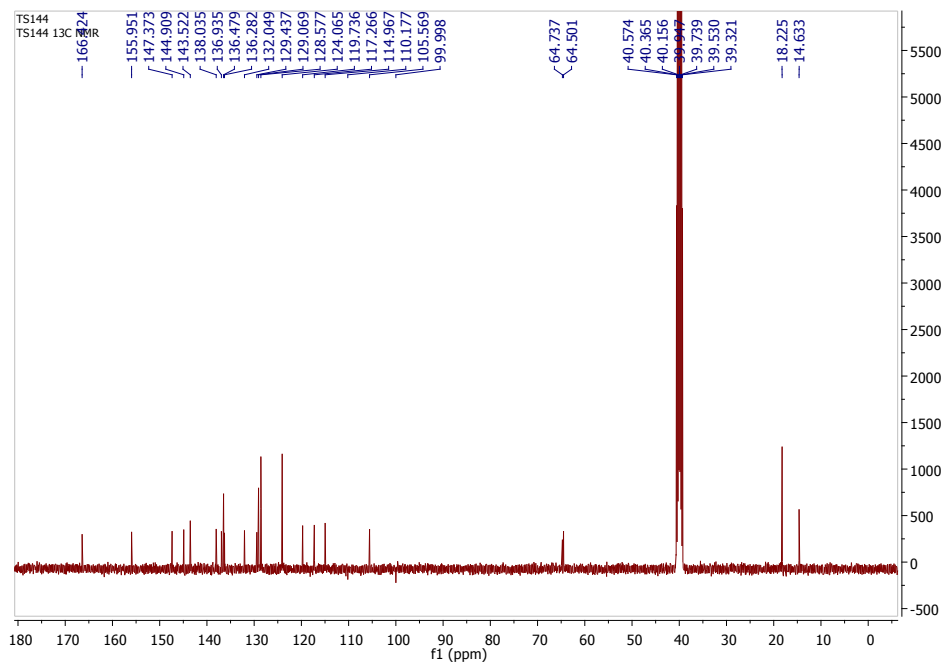
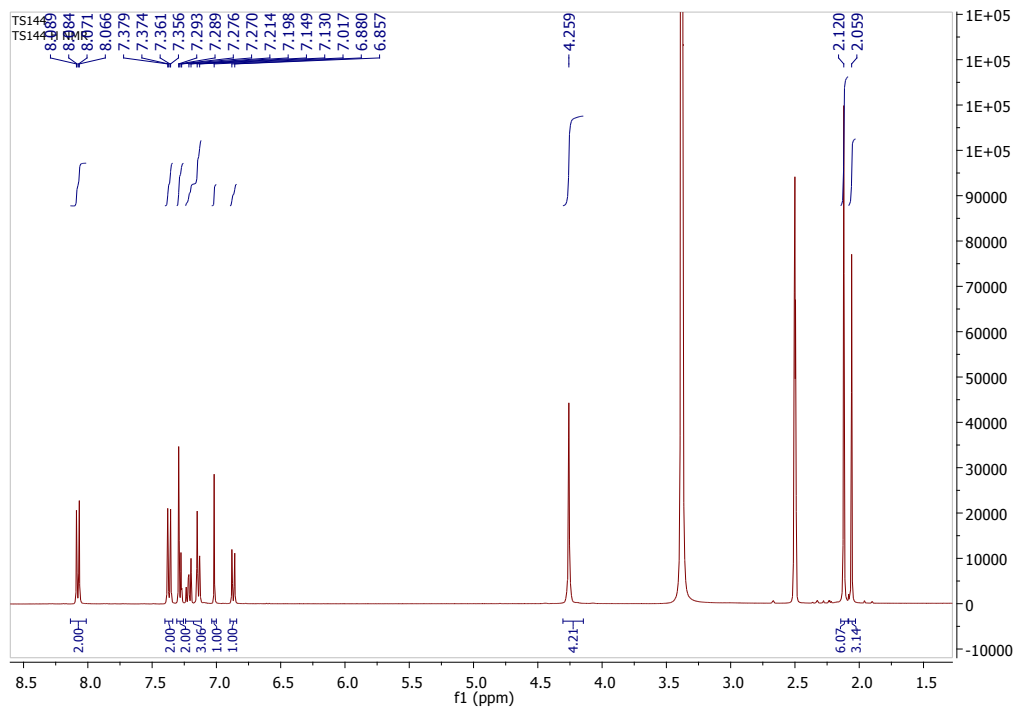
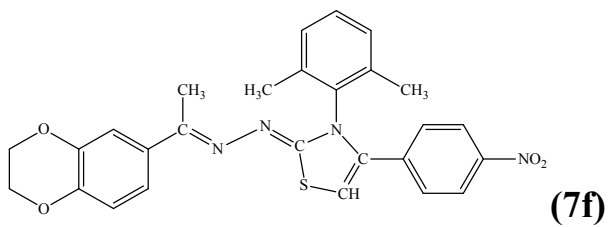


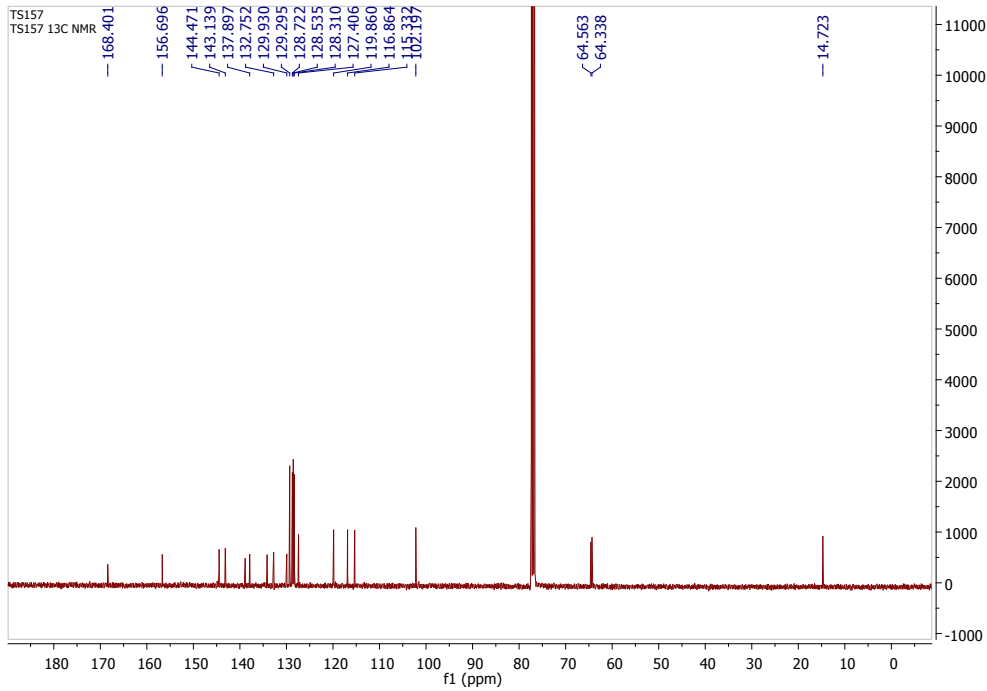
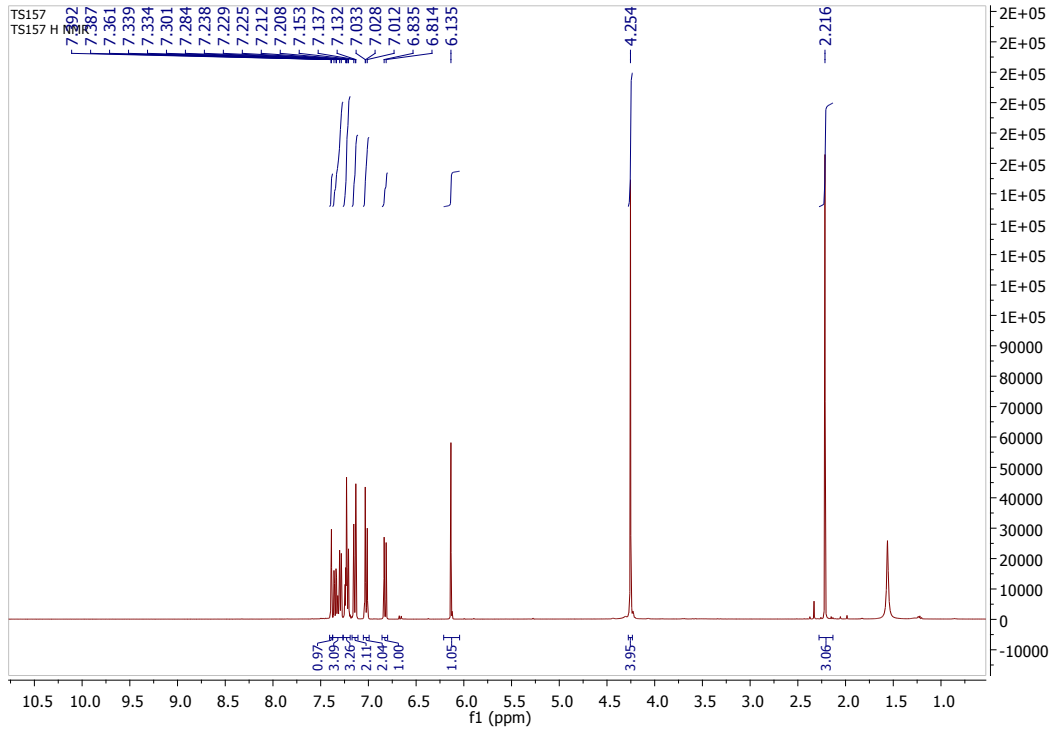
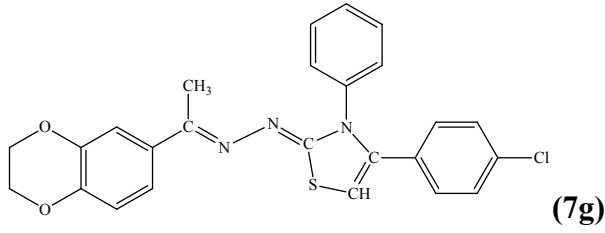


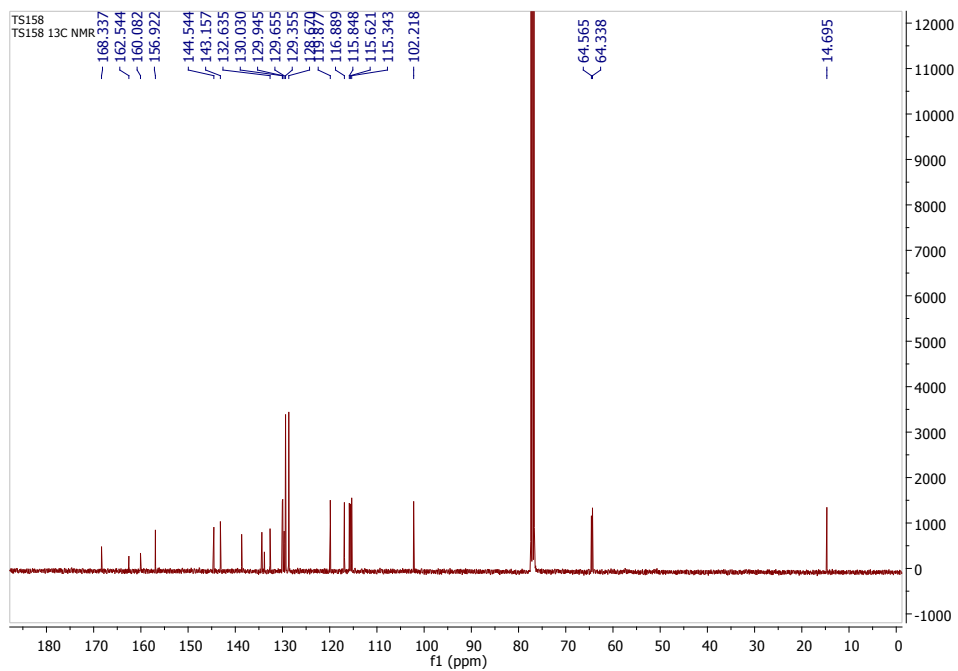
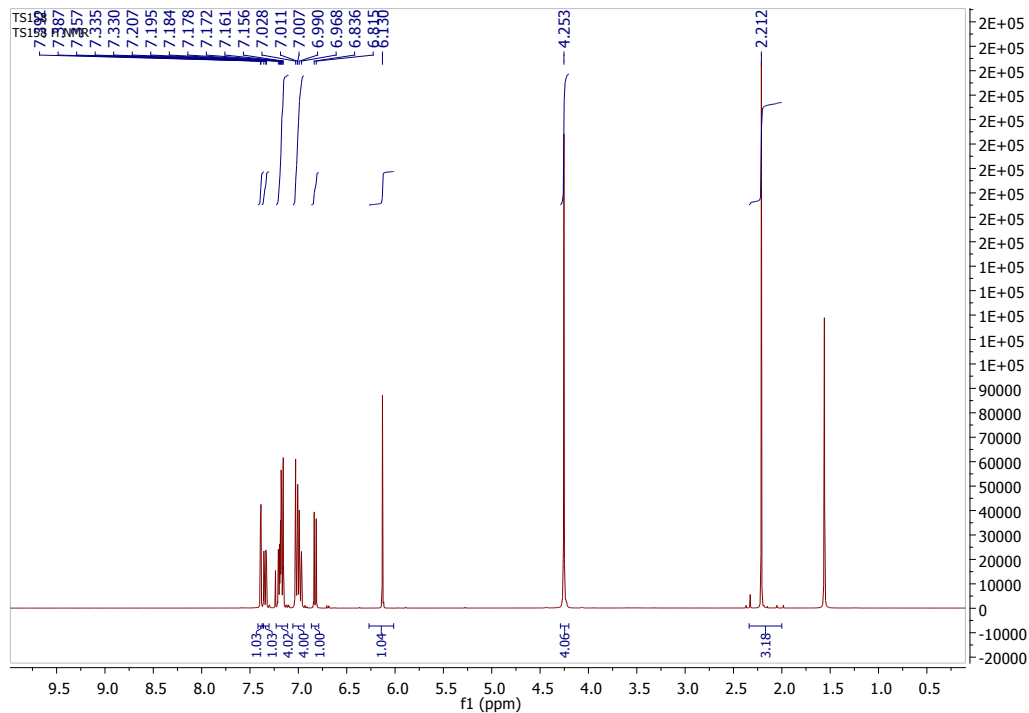
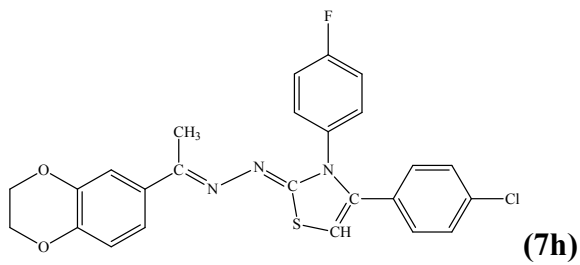


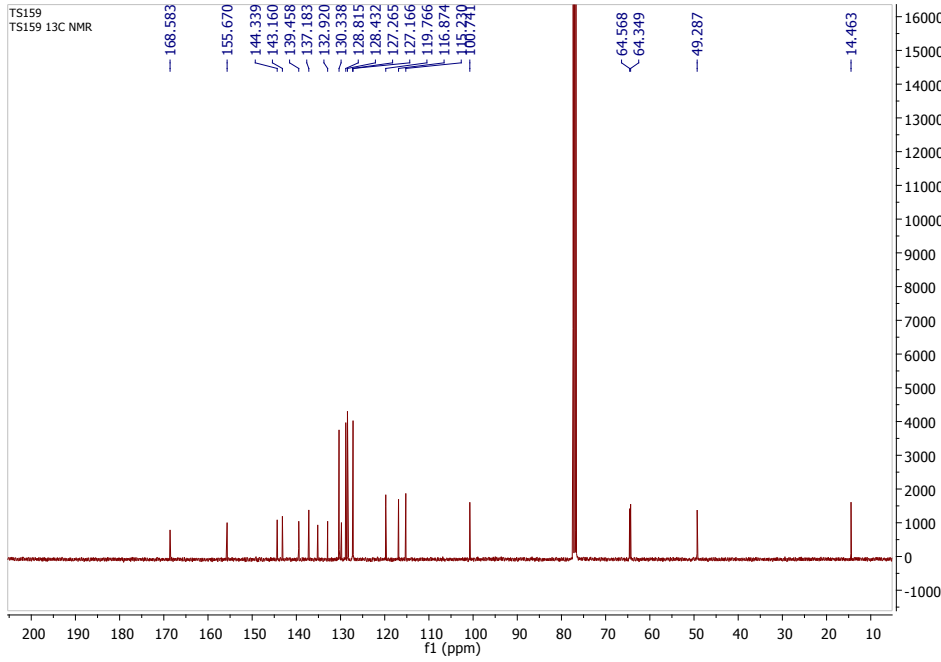
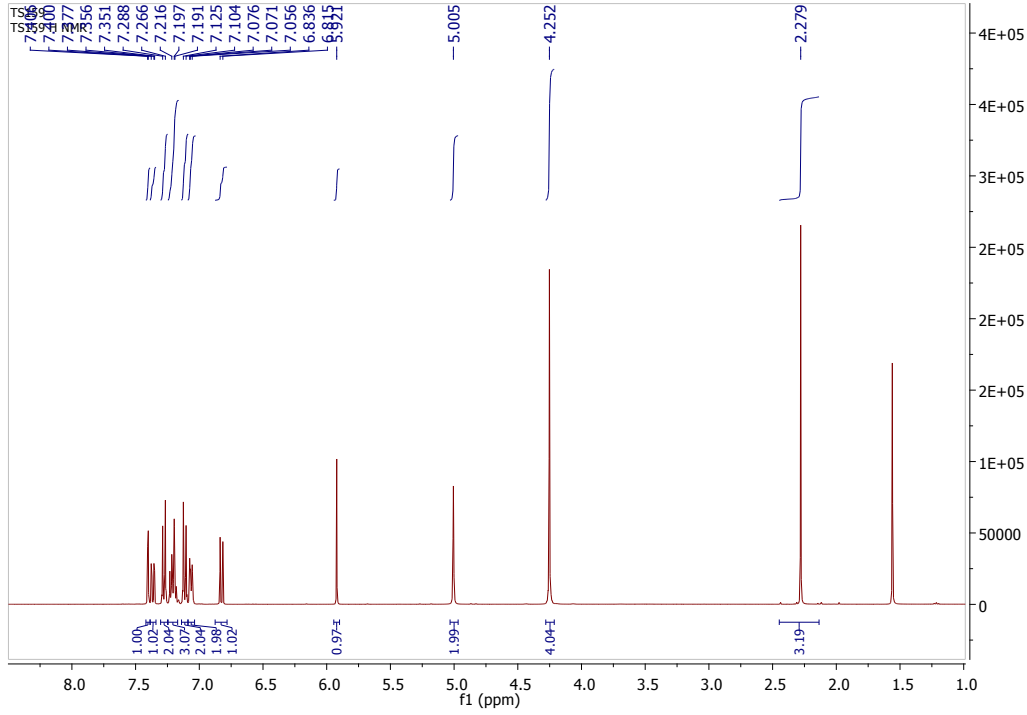
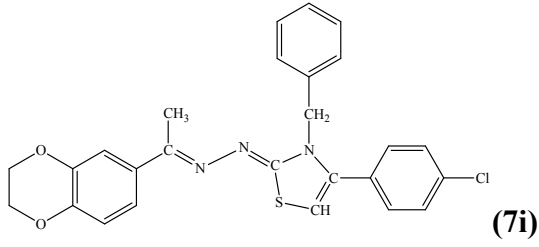


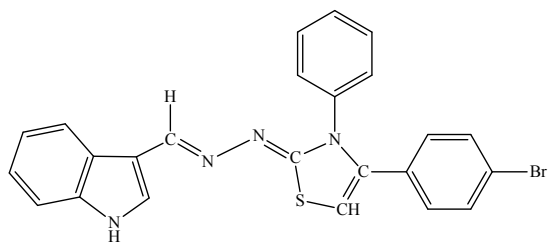




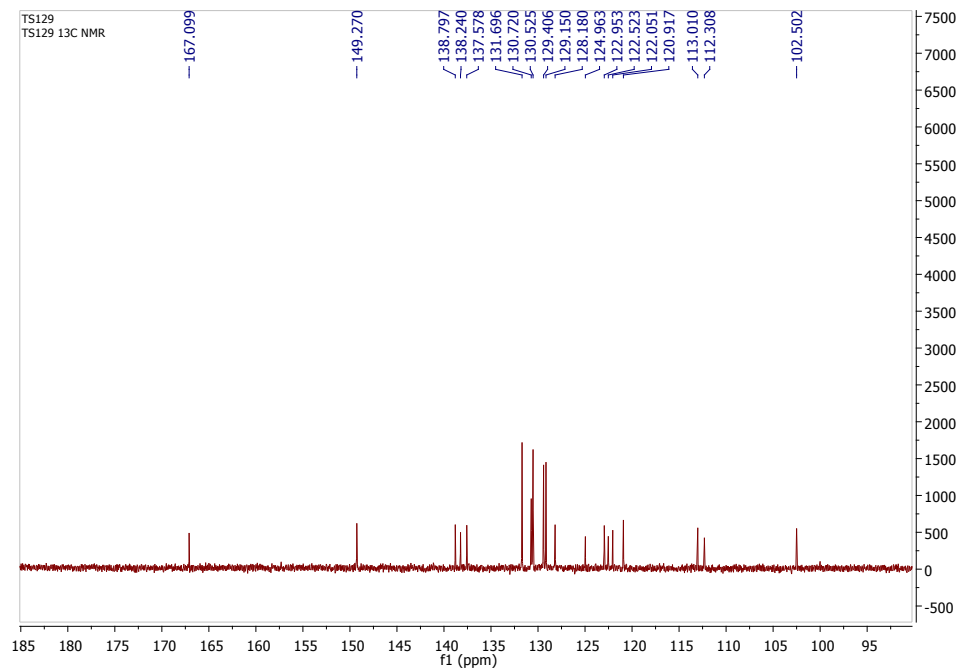
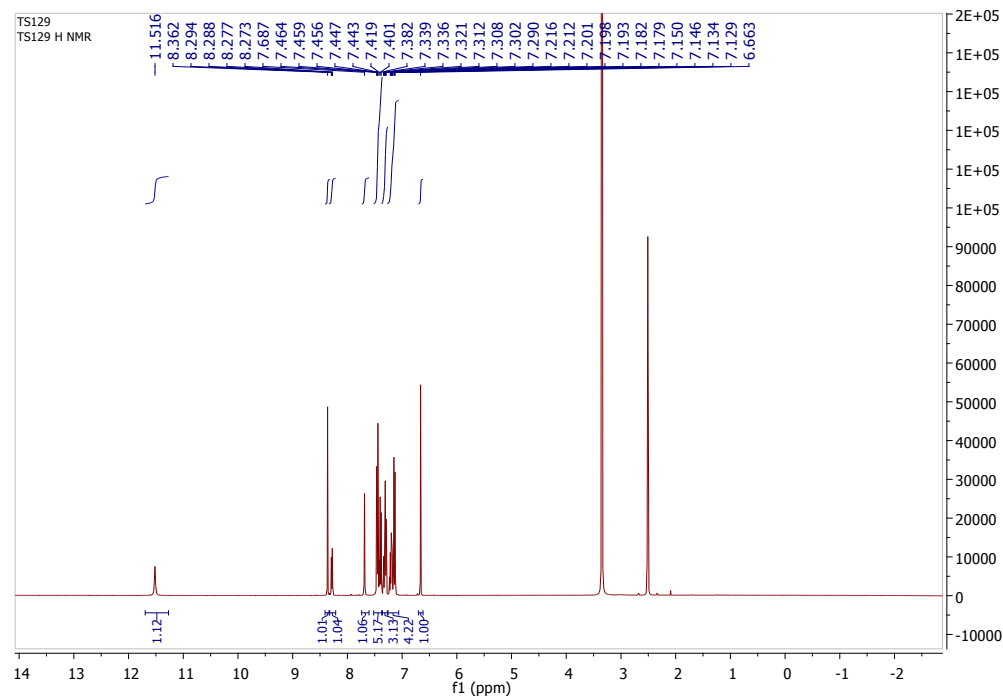


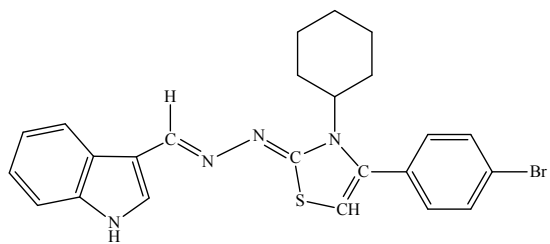






(8a)





(8b)

