

# Supplemental File

## For

**Exploring a novel of isatin-based Schiff bases as multi-target agents: design, synthesis, *in vitro* biological evaluation, and *in silico* ADMET analysis with molecular modeling simulations**

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Ahmed Ragab, Department of Chemistry, Faculty of Science (Boys), Al-Azhar University, Nasr City, Cairo 11884, Egypt.

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**Table S1:** Significant correlations among measurements of the different biological activities of isatin-based Schiff bases **2a**, **2b**, **3a-d**, **4**, **5a-c**, **7a**, and **7b**.

		Antioxidant Activity		Scavenging Activity		Inhibition (%)		Anti-arthritis activity	
		IRP	TAC	ABTS	DPPH	$\alpha$ -amylase	ACE	Proteinase Denaturation	Inhibition of Proteinase
Antioxidant Activity	IRP	-	0.000**	0.000**	-0.000**	0.000**	0.000**	0.000**	0.000**
	TAC	0.000**	-	0.000**	-0.000**	0.000**	0.000**	0.000**	0.000**
Scavenging Activity	ABTS	0.000**	0.000**	-	-0.000**	0.000**	0.000**	0.000**	0.000**
	DPPH	-0.000**	-0.000**	-0.000**	-	-0.000**	-0.000**	-0.000**	-0.000**
Inhibition (%)	$\alpha$ -amylase	0.000**	0.000**	0.000**	-0.000**	-	0.000**	0.000**	0.000**
	ACE	0.000**	0.000**	0.000**	-0.000**	0.000**	-	0.000**	0.000**
Anti-arthritis Activity	Proteinase Denaturation	0.000**	0.000**	0.000**	-0.000**	0.000**	0.000**	-	0.000**
	Inhibition of Proteinase	0.000**	0.000**	0.000**	-0.000**	0.000**	0.000**	0.000**	-

\*\* High significant correlation at P<0.01; Yellow cell indicates a negative correlation, Green cell indicates a positive correlation.

**Table S2:** Quantum chemical descriptors of the most active derivatives

Chemical descriptors	Most active compounds			
	3b	5a	5b	5c
Total Energy (Hartree)	-1332.63	-1541.58	-1273.73	-1313.04
Dipole moment (Debye)	3.82	4.79	4.98	4.56
E HOMO (eV)	-5.76	-5.76	-5.73	-5.69
E LUMO (eV)	-2.88	-2.35	-2.35	-2.33
$\Delta E$ (eV)	2.88	3.41	3.38	3.37
IP = - HOMO	5.756	5.76	5.73	5.69
EA = - LUMO	2.88	2.35	2.35	2.33
X (electronegativity)	4.32	4.05	4.04	4.01
$\eta$ (chemical hardness)	1.434	1.71	1.69	1.68
S (chemical softness)	0.696	0.586	0.59	0.59
$\mu$ (chemical potential)	-4.32	-4.05	-4.04	-4.01
$\omega$ (electrophilic index)	6.49	4.81	4.83	4.78

## Molecular docking simulation

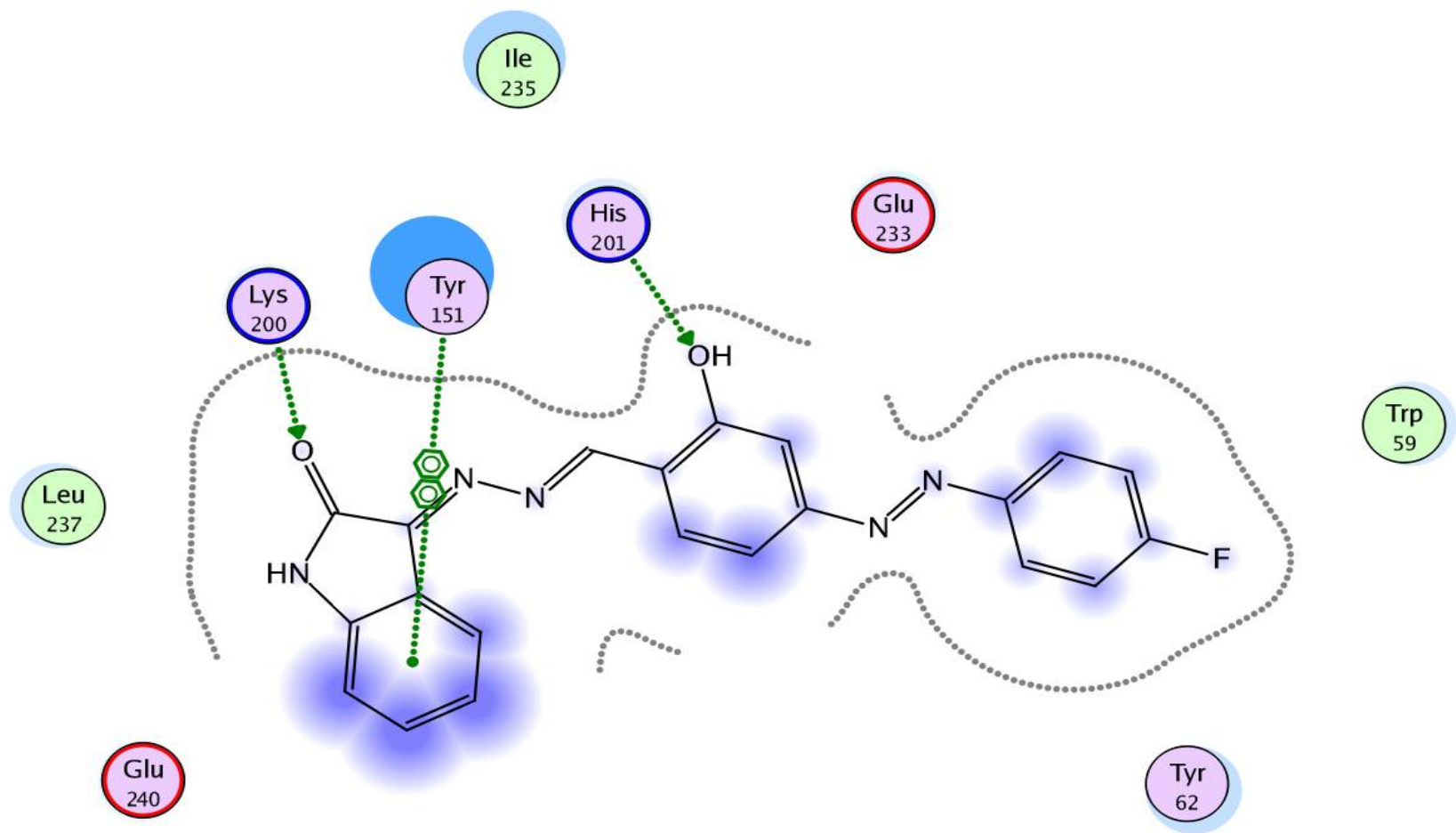
The docking simulation of the most active derivatives were performed inside the active site of  $\alpha$ -amylase (PDB: 2QV4) and acetylcholinesterase AChE (PDB: 4EY7) using Molecular Operating Environment (MOE). The docking score energy is represented by binding energy (S) with negative values. The structure of the tested derivatives was built using chembiodraw2014, and then exported to MOE, and all hydrogen atoms were added. Additionally, all the structures were minimized using forcefield MMFF94X and finally saved <sup>1-3</sup>. Moreover, all the proteins were downloaded from the protein data bank (<https://www.rcsb.org/>). For  $\alpha$ -amylase (PDB: 2QV4), the protein contained only one selected chain, and all water molecules were removed as described <sup>4,5</sup>. The hydrogen atom was added, and the protein with a co-crystallized ligand was exposed to minimize the energy using forcefield MMFF94X with a gradient of 0.05 Kcal/mol. Then the validation process was performed inside the active site where the co-crystallized ligand (acarbose) displayed binding energy S = -32.53 Kcal/mol and RMSD value of 1.13 Å. The co-crystallized ligand (acarbose) could form through two hydrogen bonds sidechain acceptors (His201 and Arg195), four hydrogen bonds sidechain donor (Glu233, His299, and Asp300), and one hydrogen bond backbone donor (Ala106). On the other hand, for acetylcholinesterase AChE (PDB: 4EY7), chain b was selected. The active site was generated according to a standard protocol where the co-crystallized ligand (Donepezil) was redocked as described <sup>6,7</sup>. It demonstrated binding energy S = -32.42 Kcal/mol with RMSD = 0.714 Å through two arene-arene " $\pi$ - $\pi$ " interactions between the residues Trp86 and Trp286 with phenyl of *N*-benzylidene and phenyl of 1*H*-inden-1-one derivative, respectively. Besides, the arene-cation " $\pi$ -cation" interaction between the residue amino acid (Tyr337) and NH of piperidinyl moiety and hydrophobic interaction that appears on the two methoxy groups

## References:

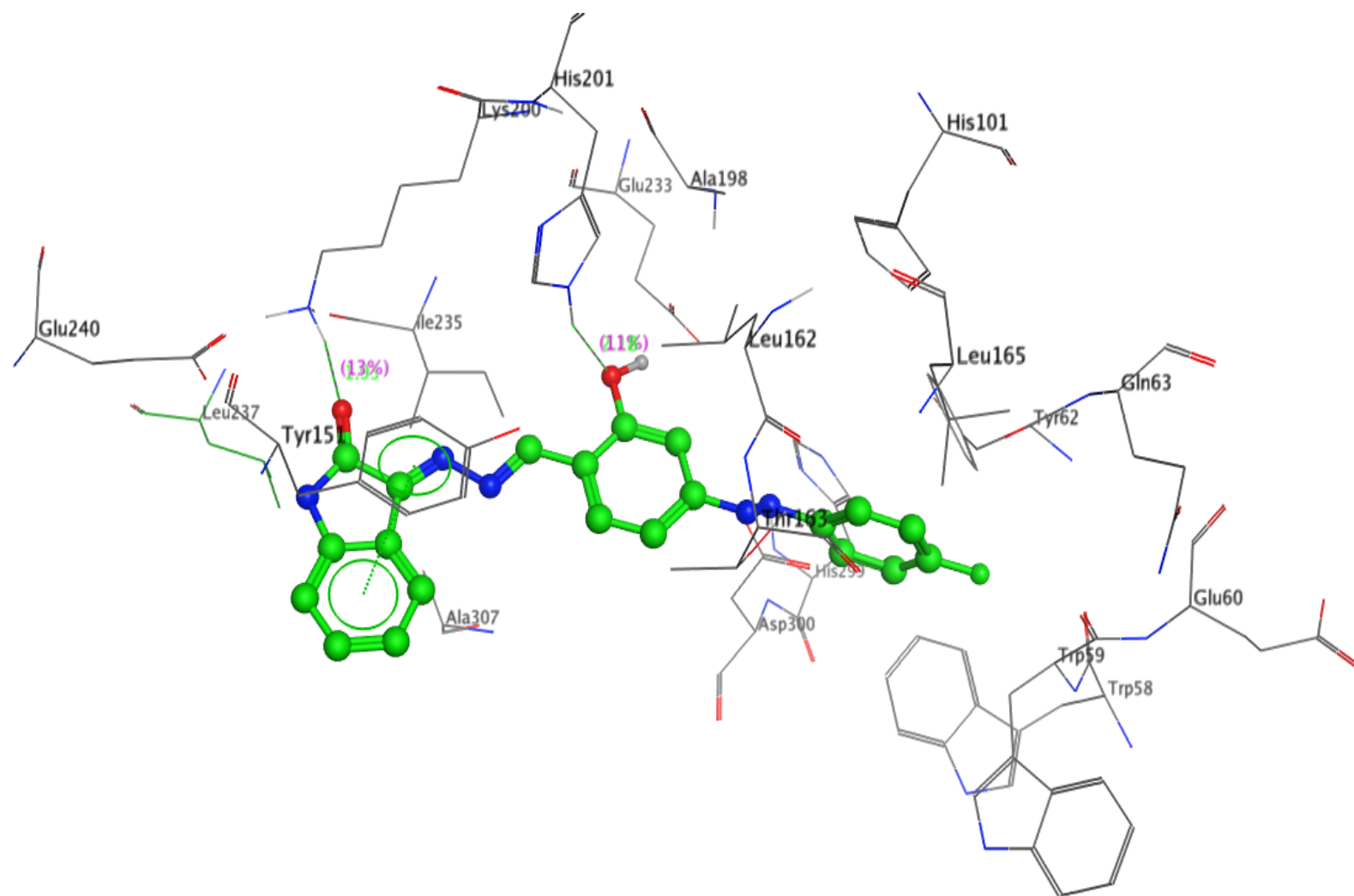
- 1 M. Eldeeb, E. F. Sanad, A. Ragab, Y. A. Ammar, K. Mahmoud, M. M. Ali and N. M. Hamdy, *biomedicines*, , DOI:<https://doi.org/10.3390/biomedicines10030722>.
- 2 S. A. El-Kalyoubi, A. Ragab, O. A. Abu Ali, Y. A. Ammar, M. G. Seadawy, A. Ahmed and E. A. Fayed, *Pharmaceuticals*, ,

DOI:10.3390/ph15030376.

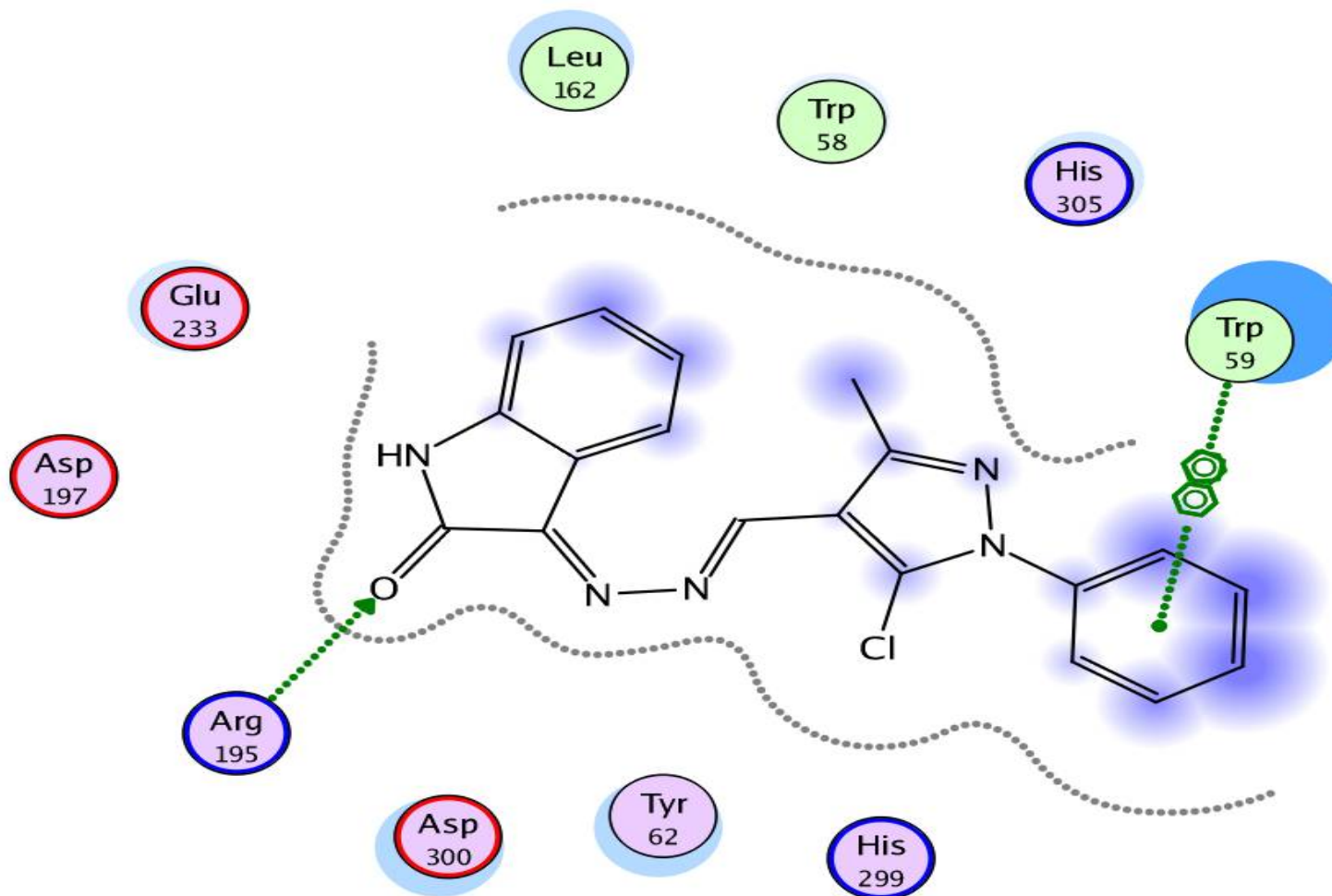
- 3 H. Ali Mohamed, Y. A. Ammar, G. A.m. Elhagali, H. A. Eyada, D. S. Aboul-Magd and A. Ragab, *ACS Omega*, 2022, **7**, 4970–4990.
- 4 M. Y. Sameeh, M. M. Khowdiary, H. S. Nassar, M. M. Abdelall, H. H. Amer, A. Hamed and A. A. Elhenawy, *Mol.* , 2022, 27.
- 5 P. Kumar, M. Duhan, K. Kadyan, J. Sindhu, S. Kumar and H. Sharma, *Medchemcomm*, 2017, **8**, 1468–1476.
- 6 A. Kamalı, R. Çakmak and M. Boğa, *J. Chinese Chem. Soc.*, 2022, **69**, 731–743.
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2D structure of compound **3b** inside the active site of  $\alpha$ -amylase (PDB: 2QV4)

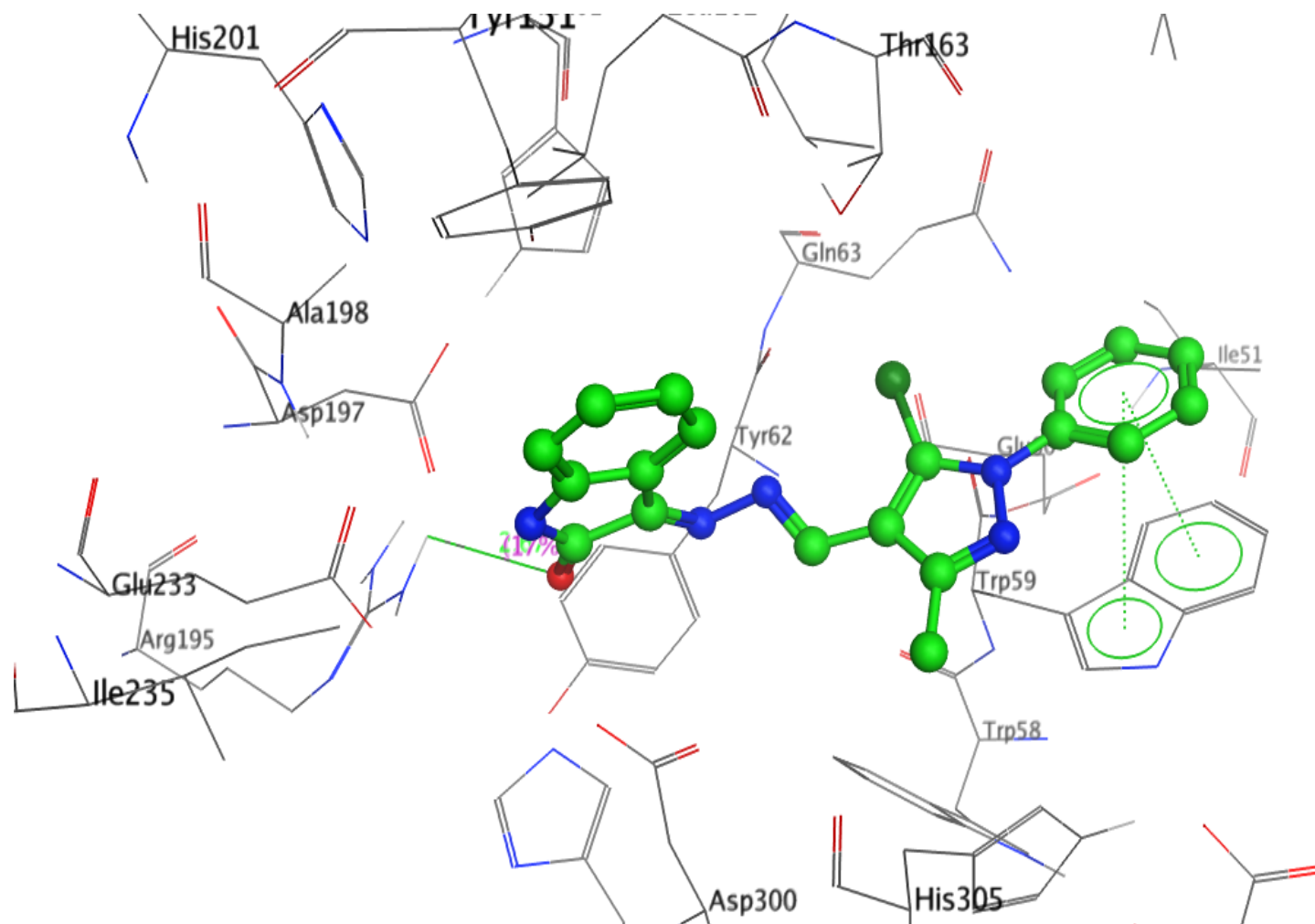


3D structure of compound **3b** inside the active site of  $\alpha$ -amylase (PDB: 2QV4)

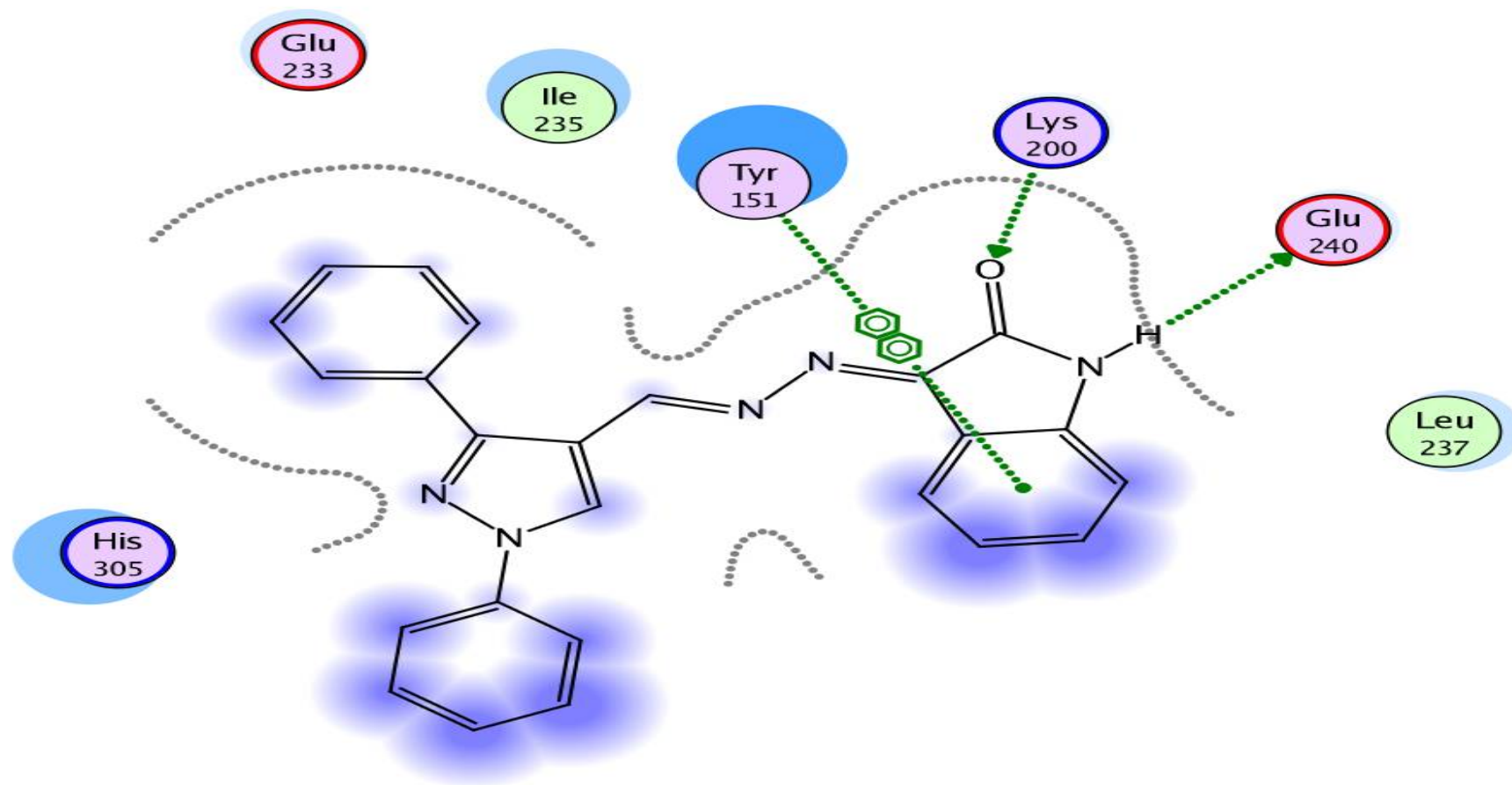


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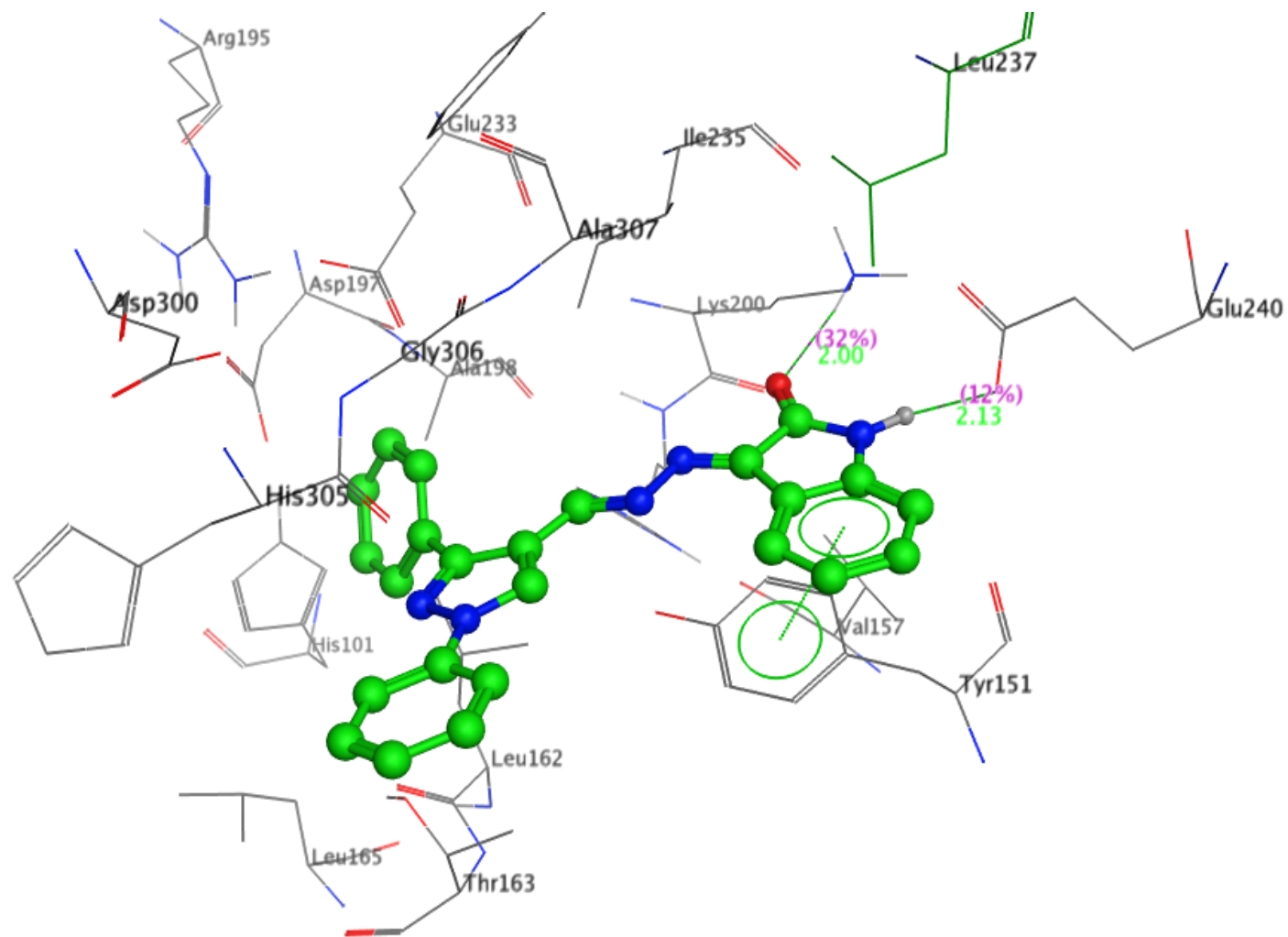




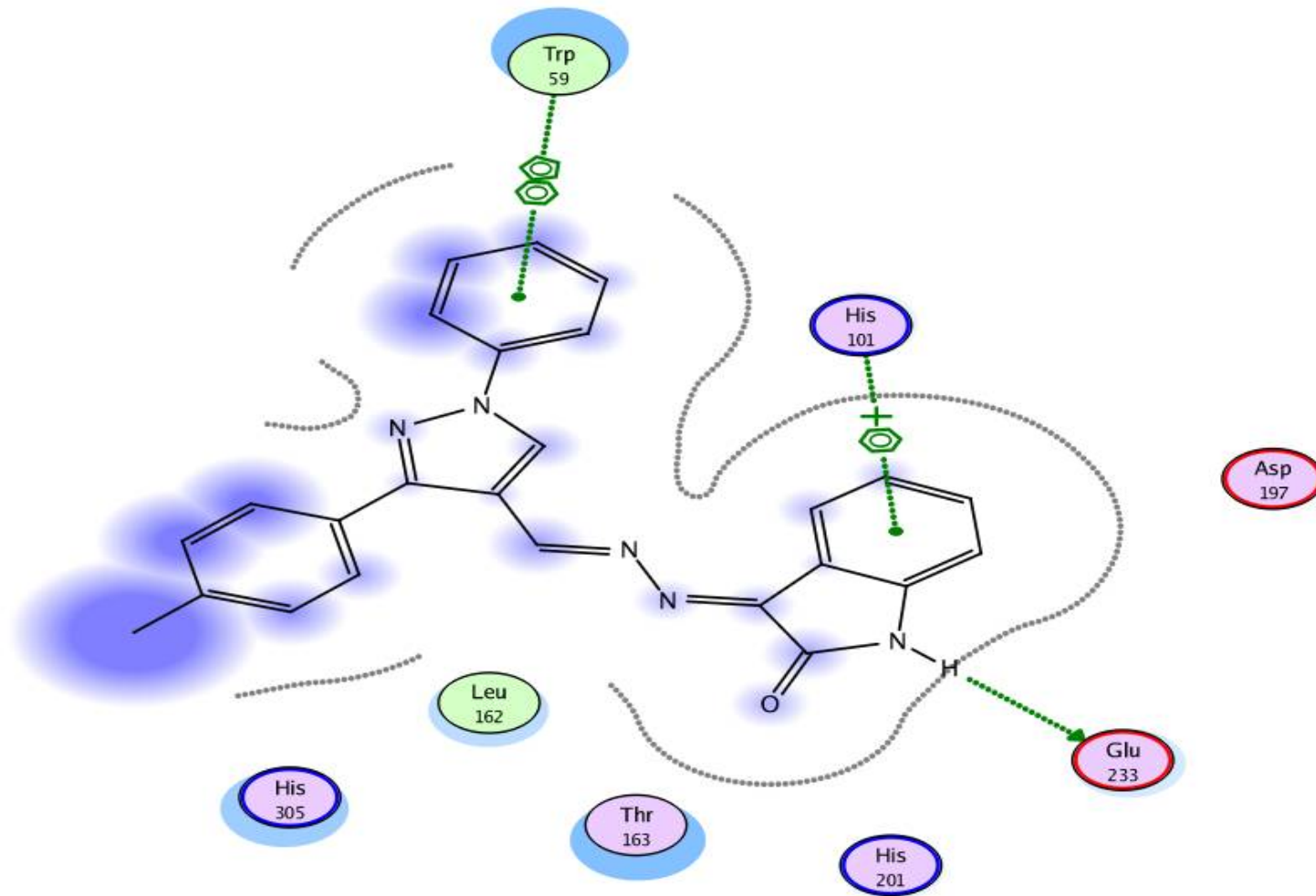
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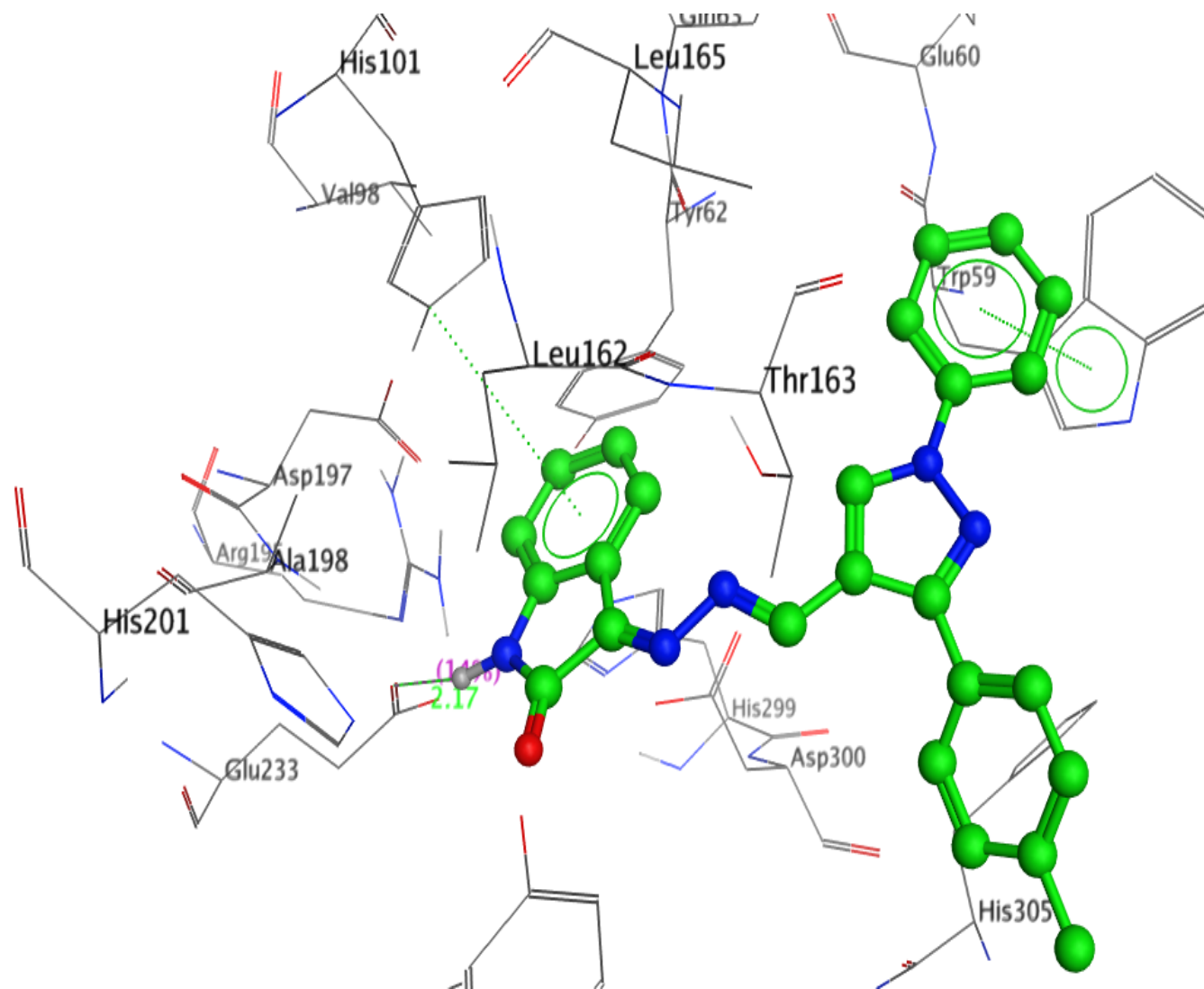
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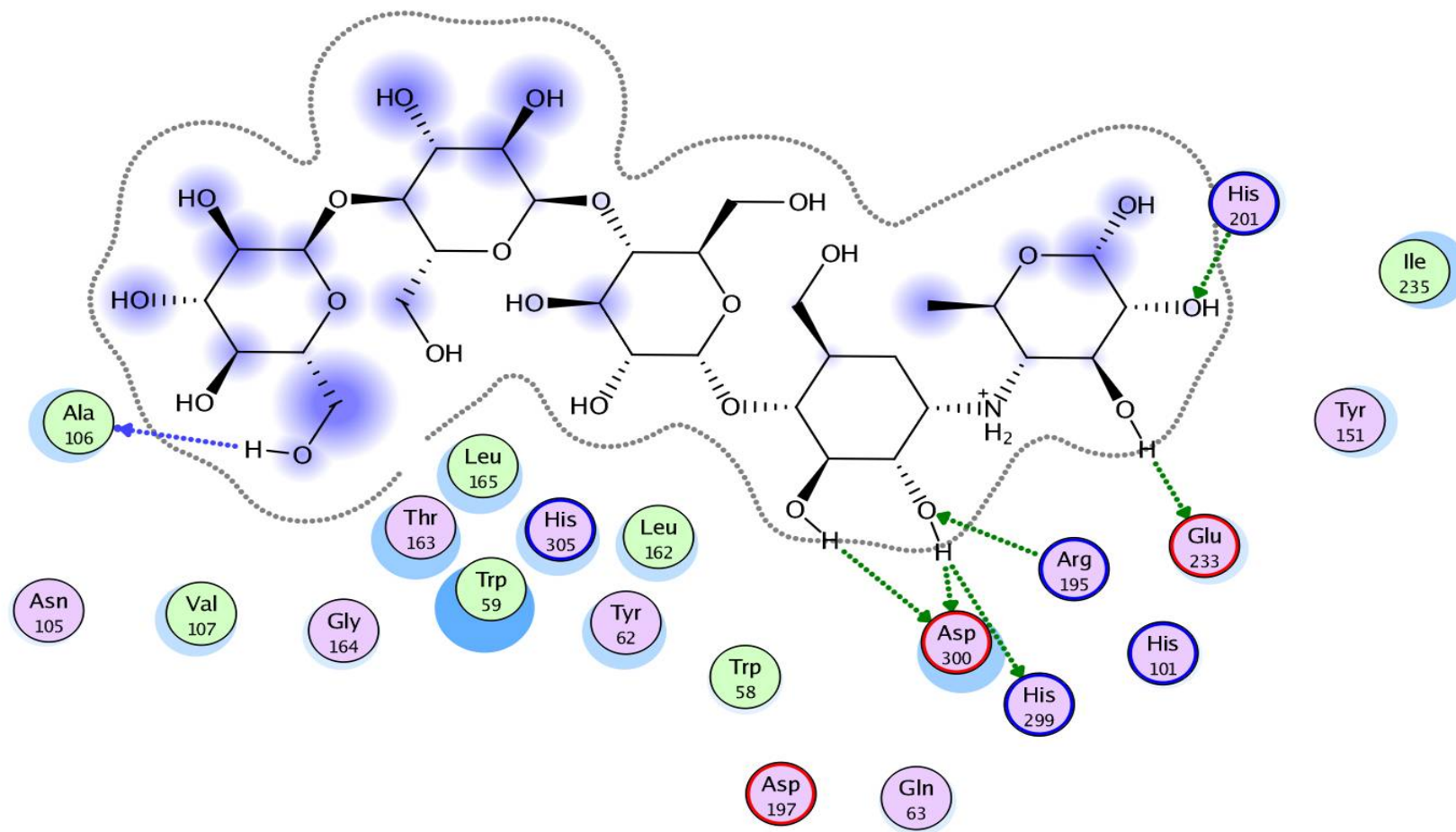
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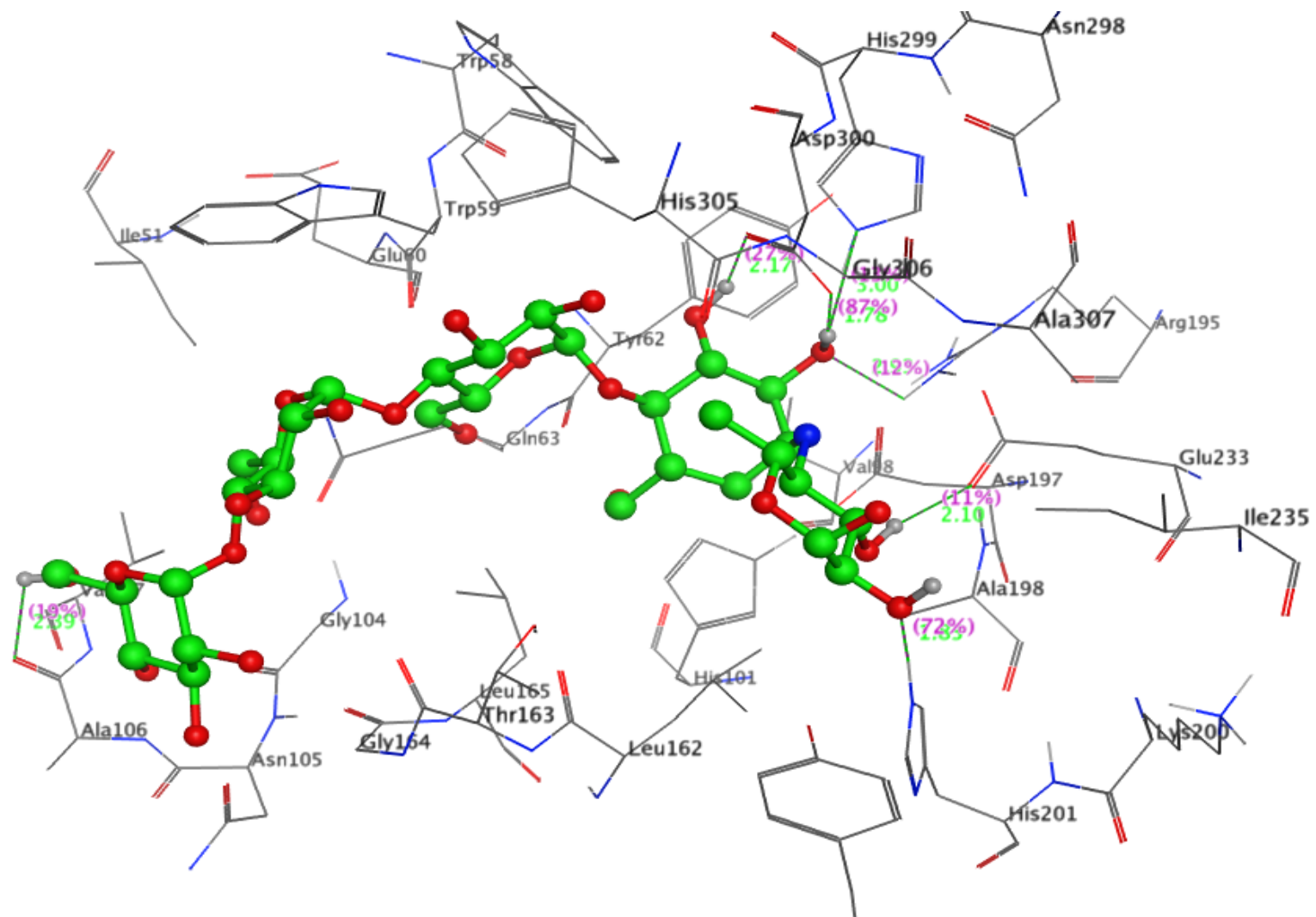
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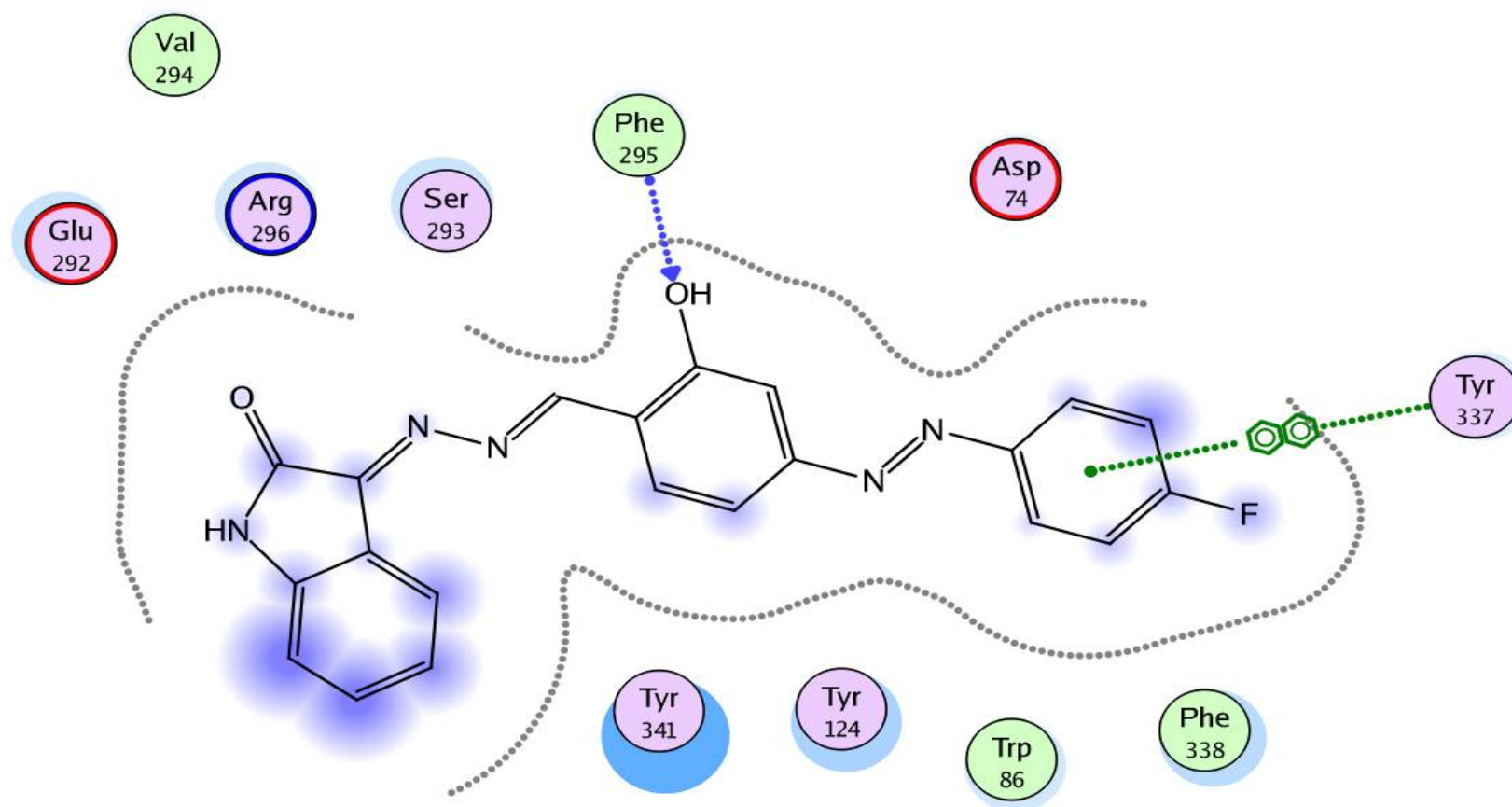
3D structure of compound **5c** inside the active site of  $\alpha$ -amylase (PDB: 2QV4)



2D structure of compound **co-crystallized ligand** inside the active site of  $\alpha$ -amylase (PDB: 2QV4)

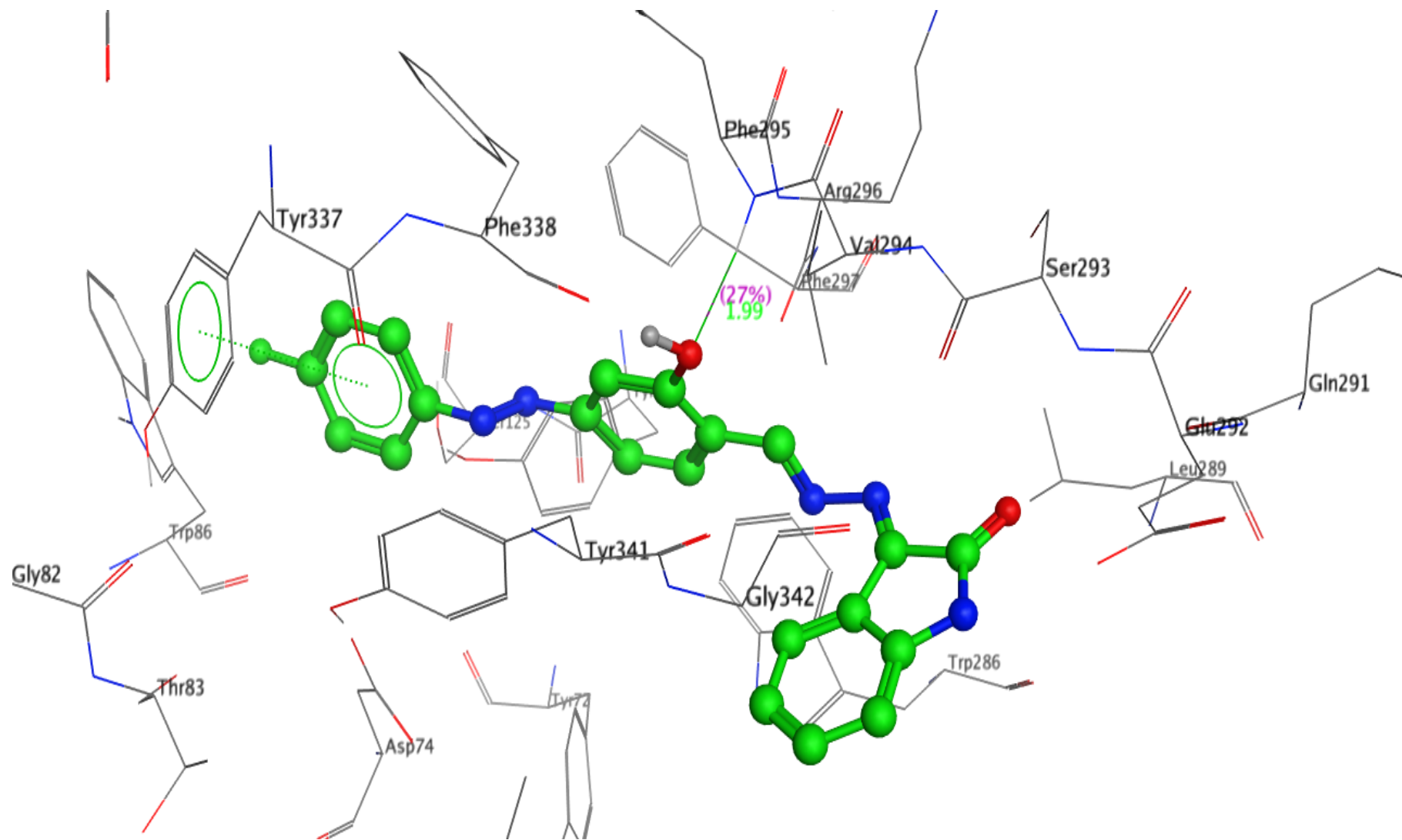


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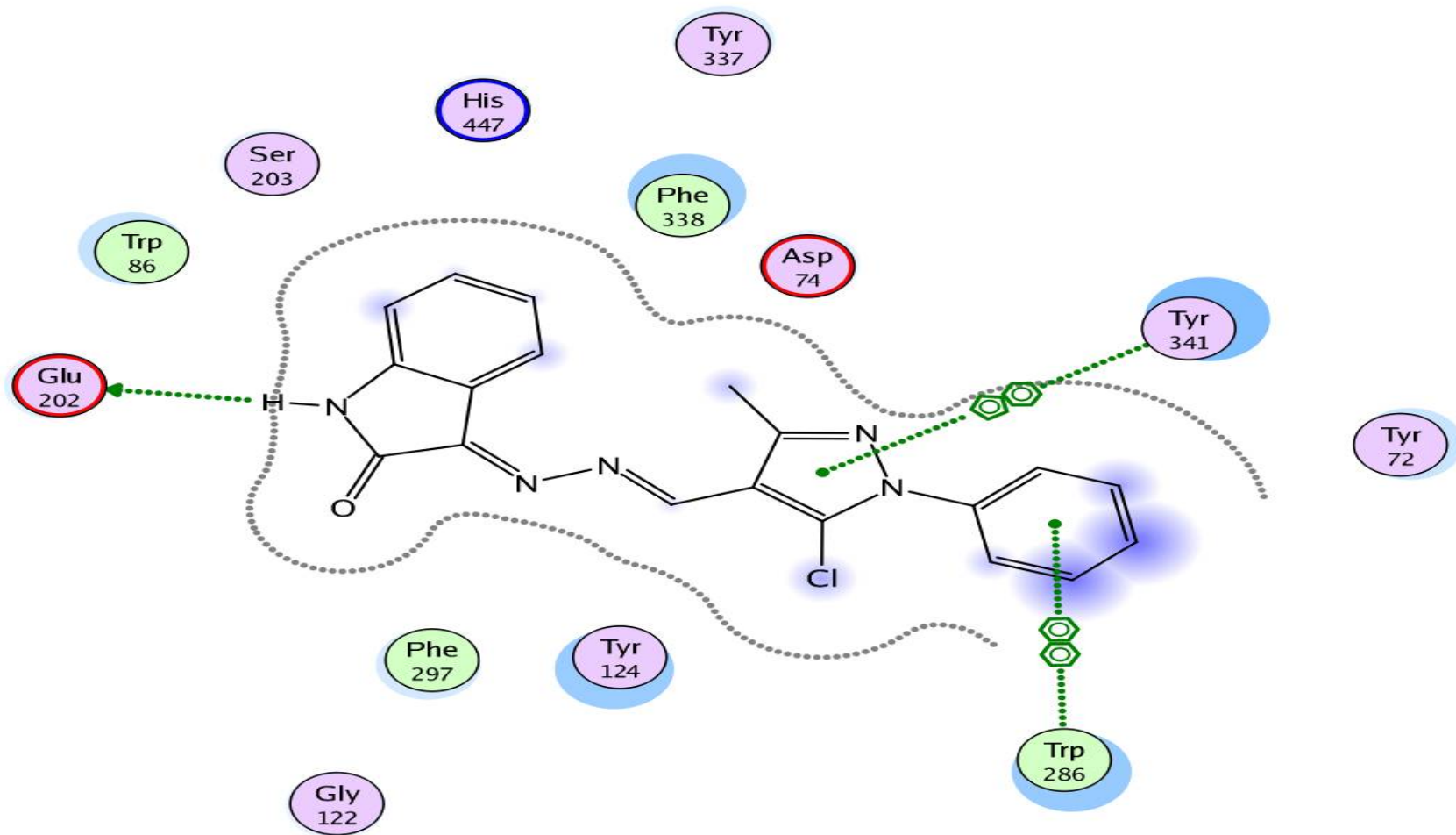


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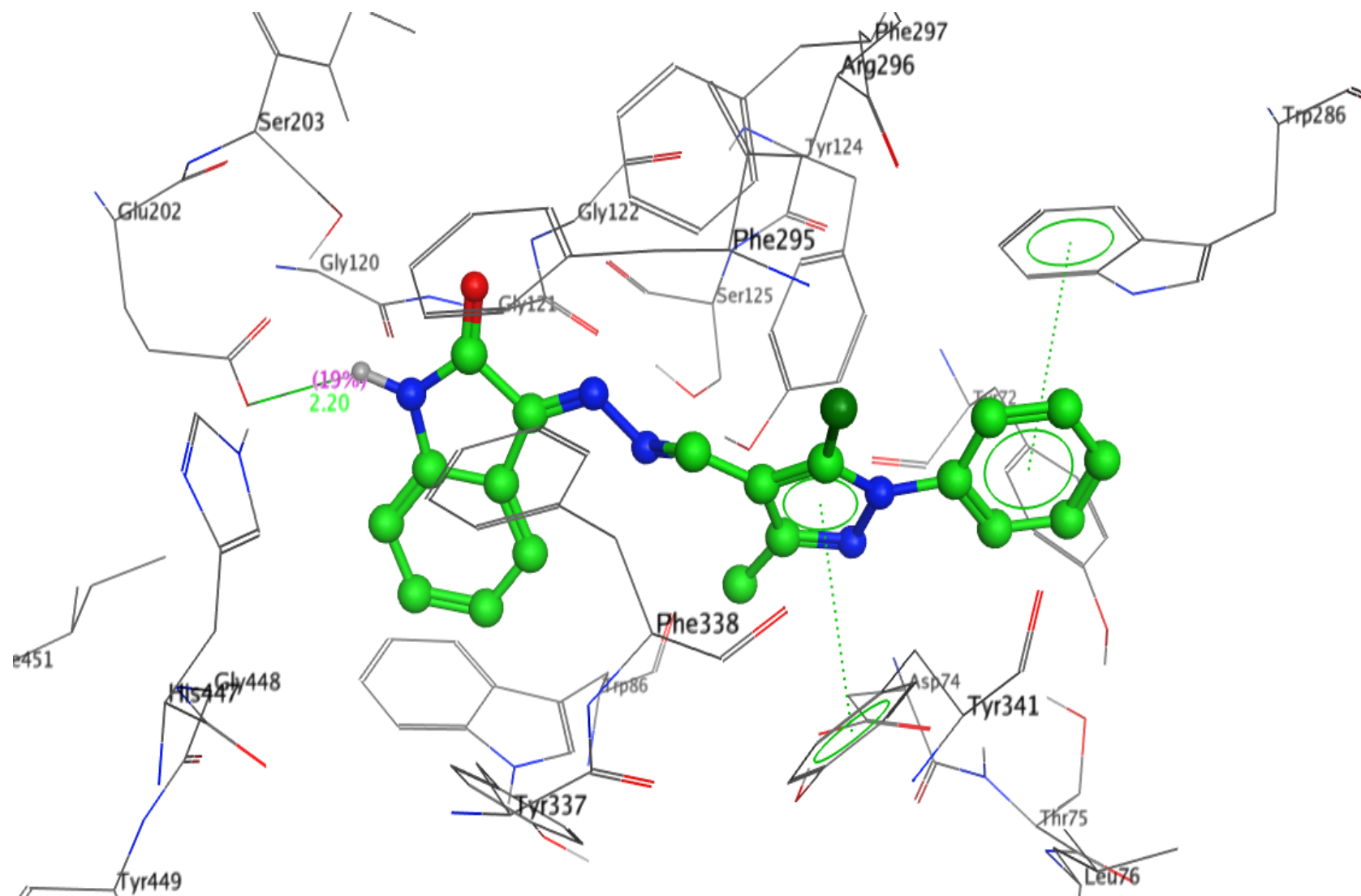




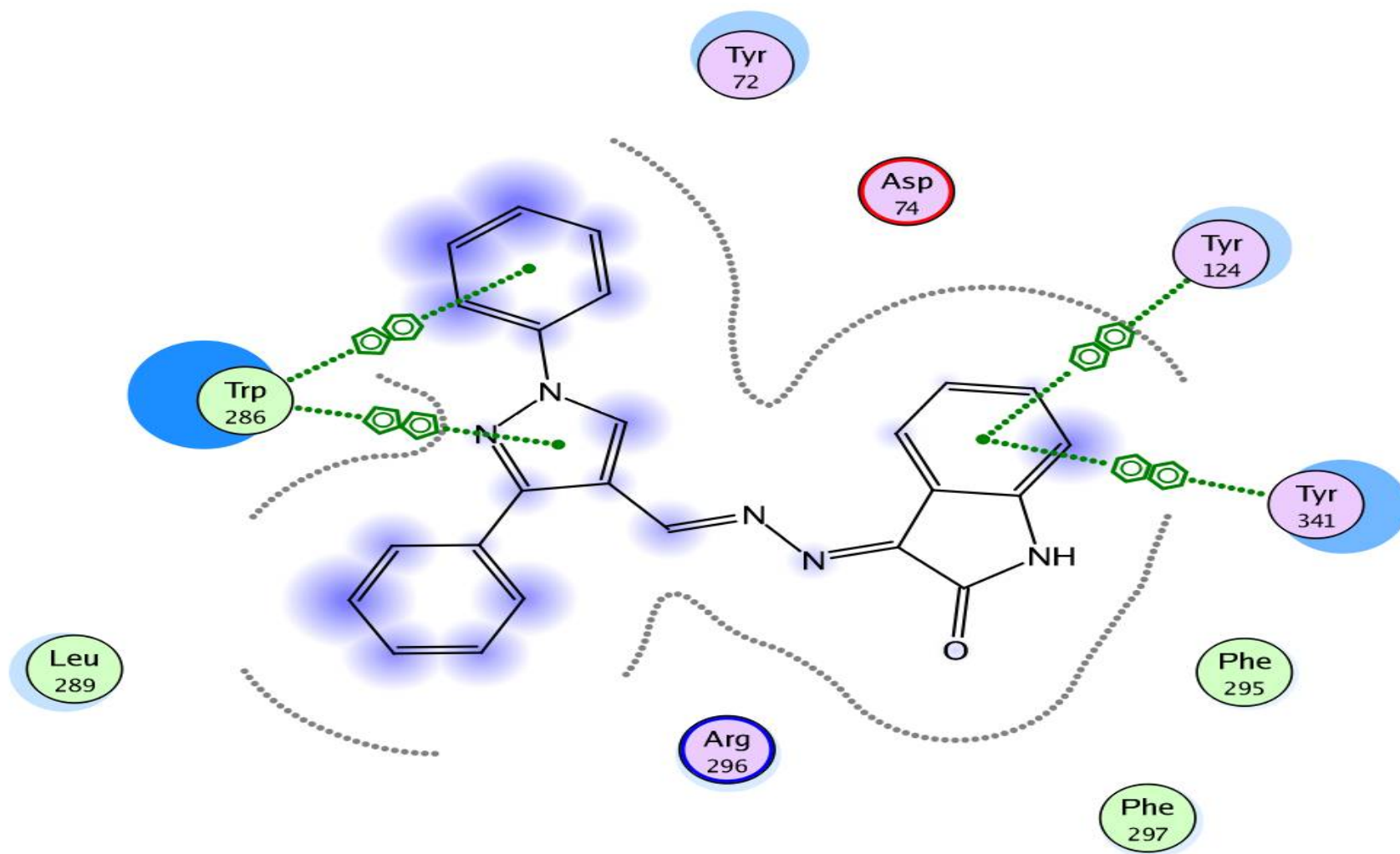
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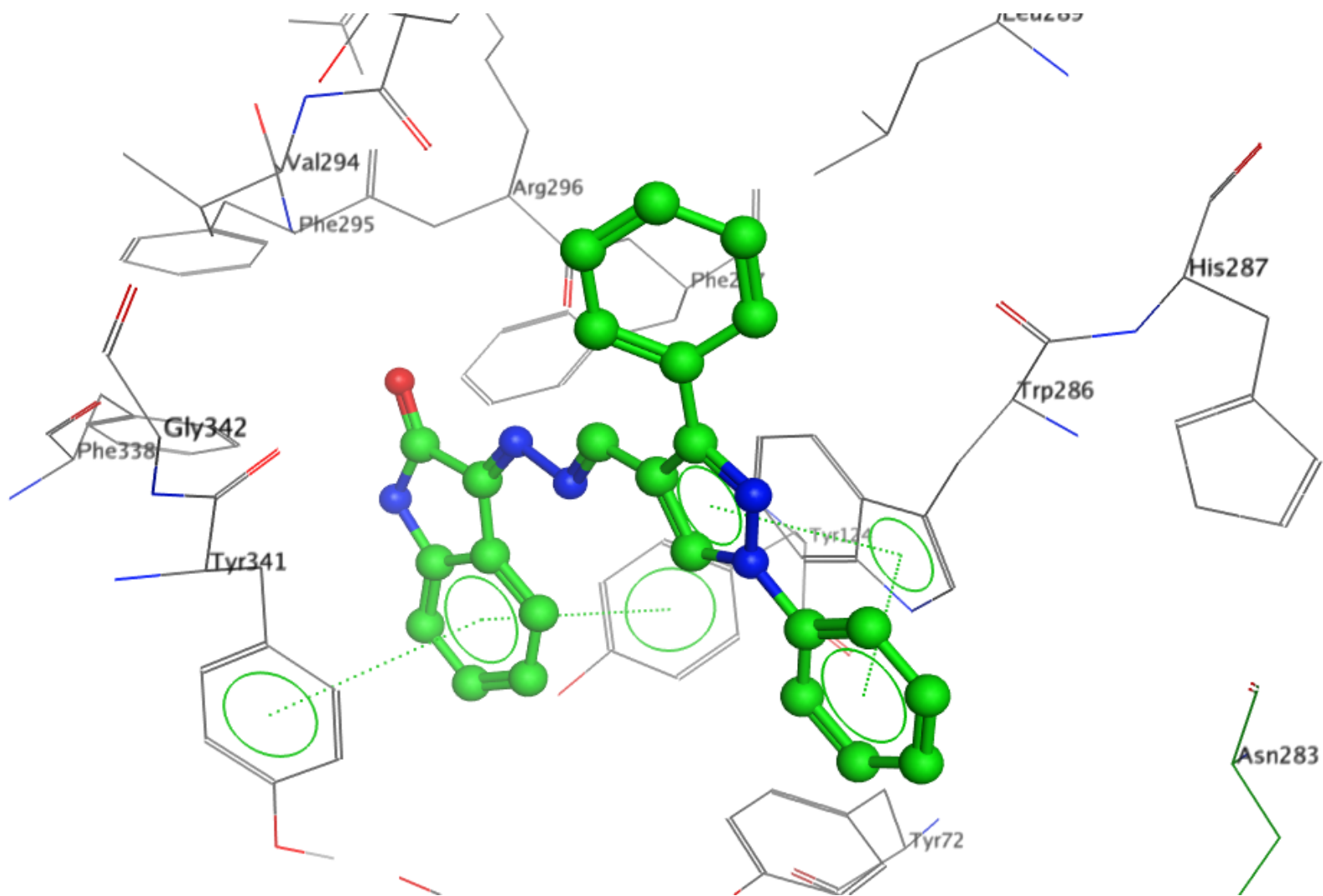
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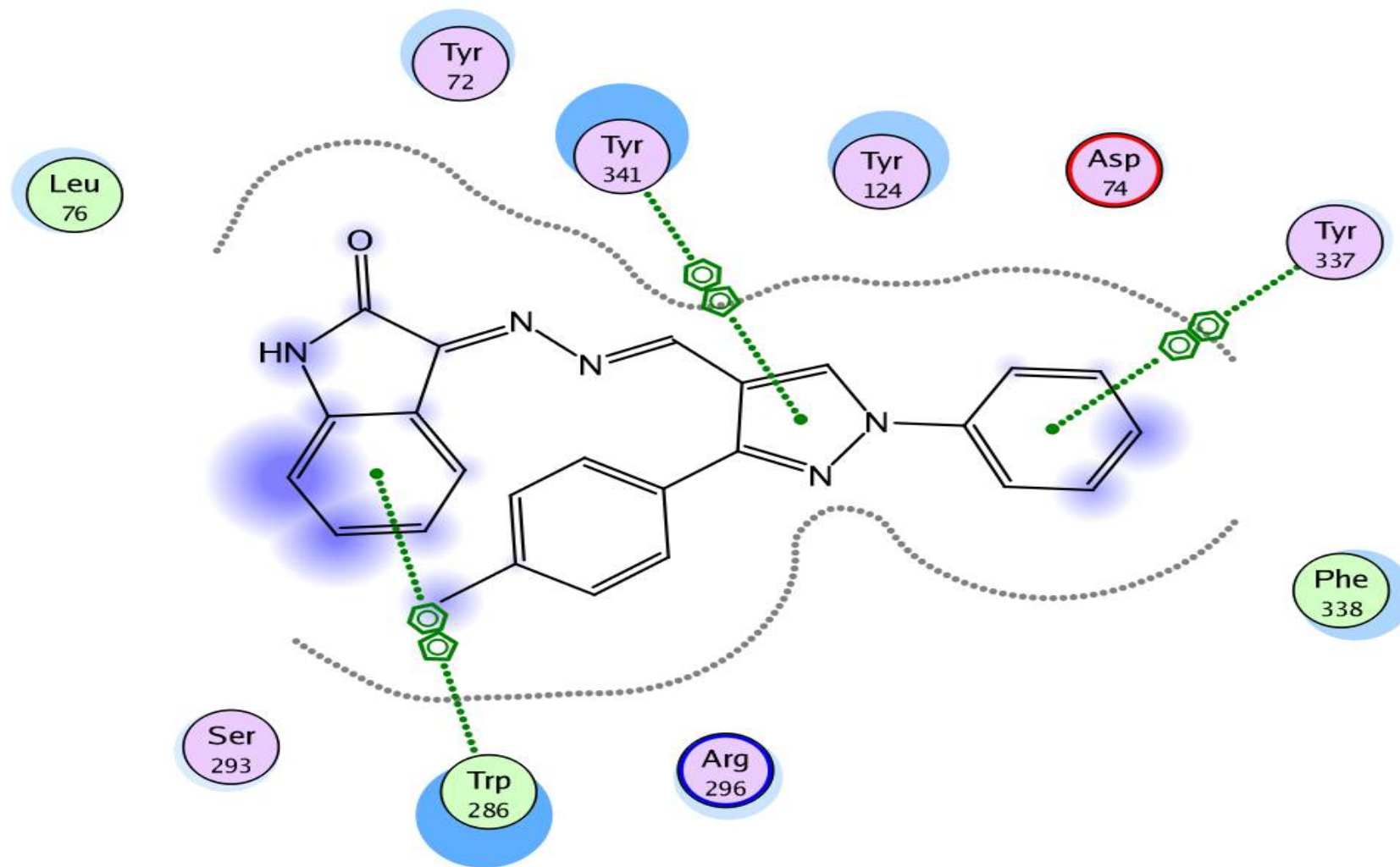
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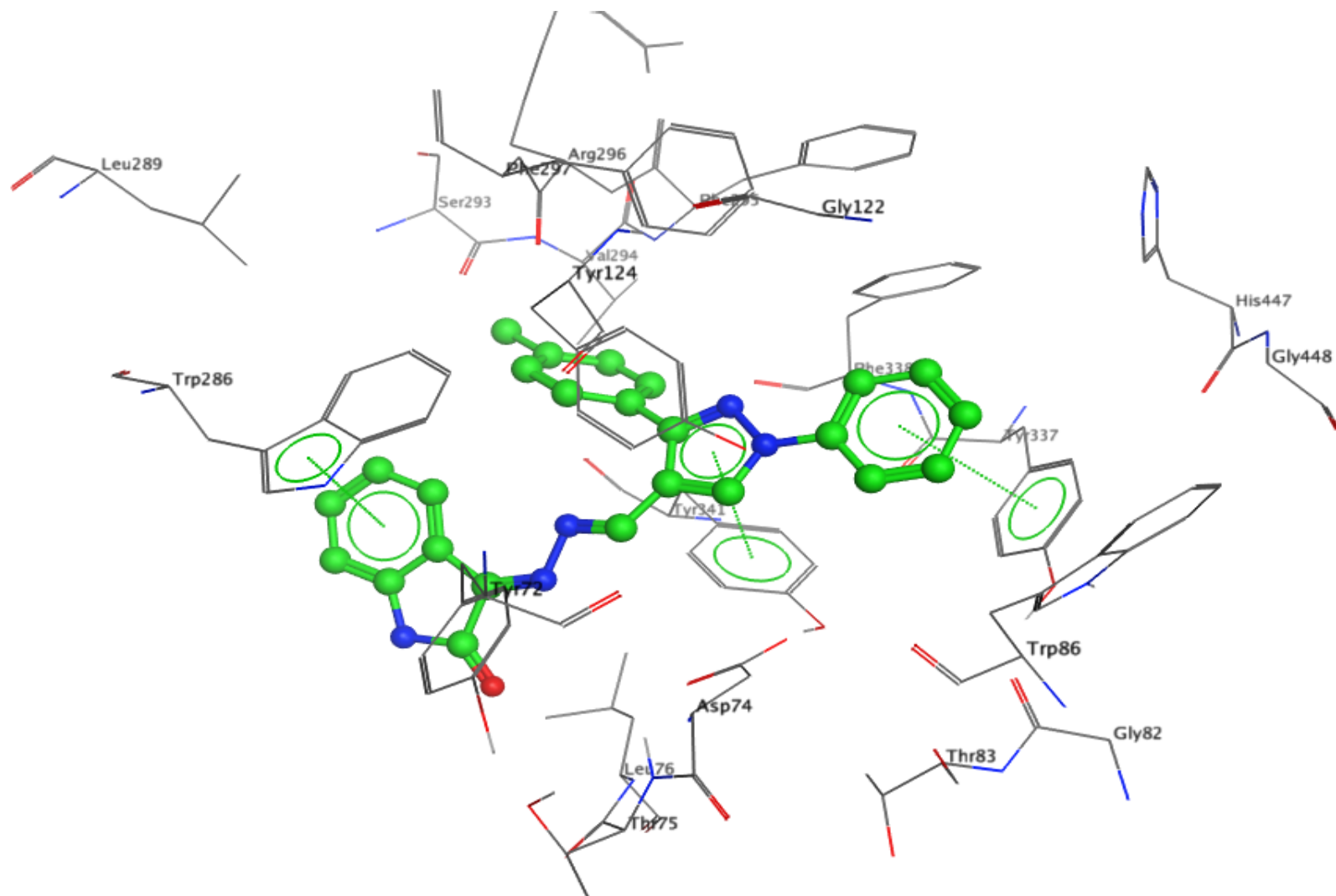
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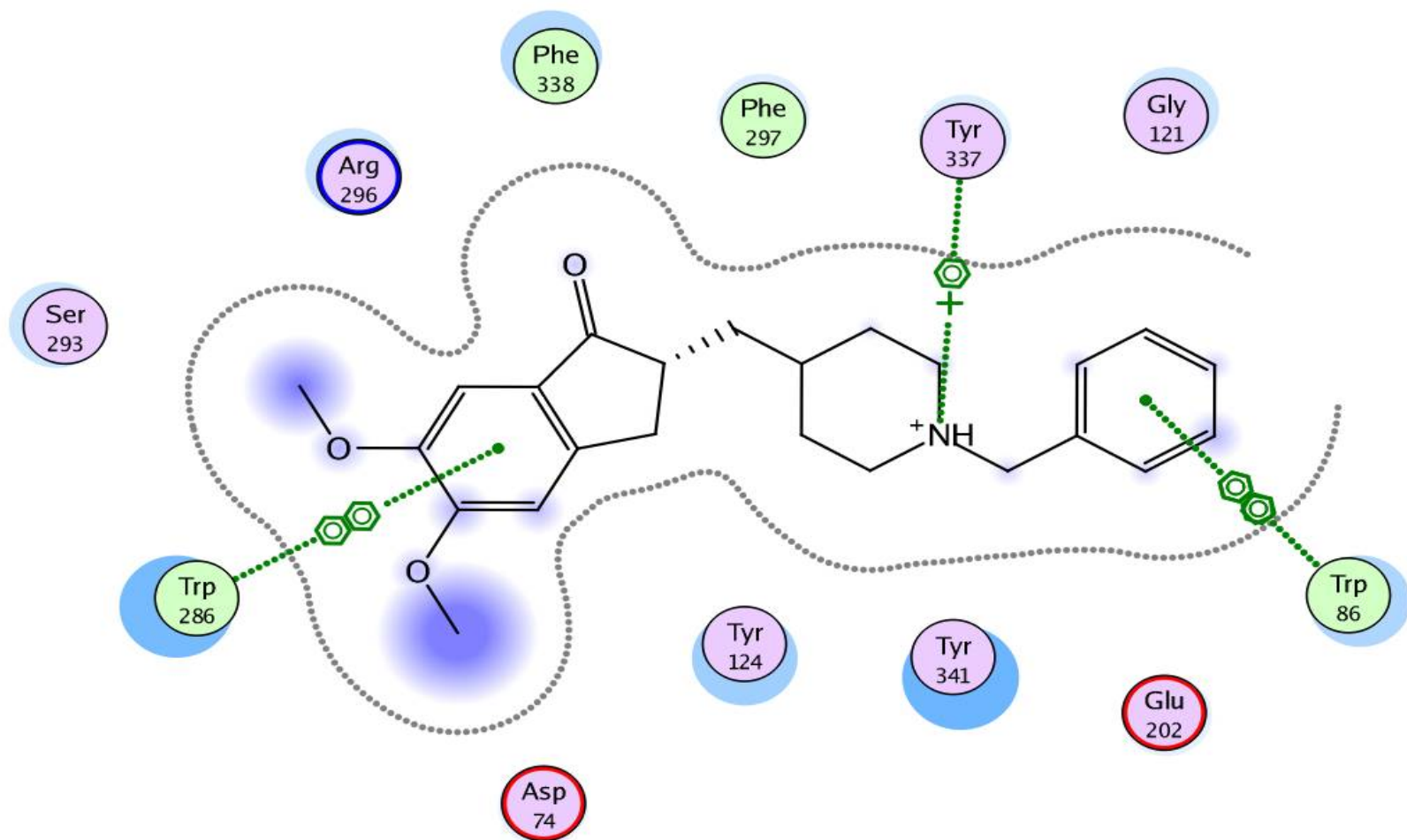
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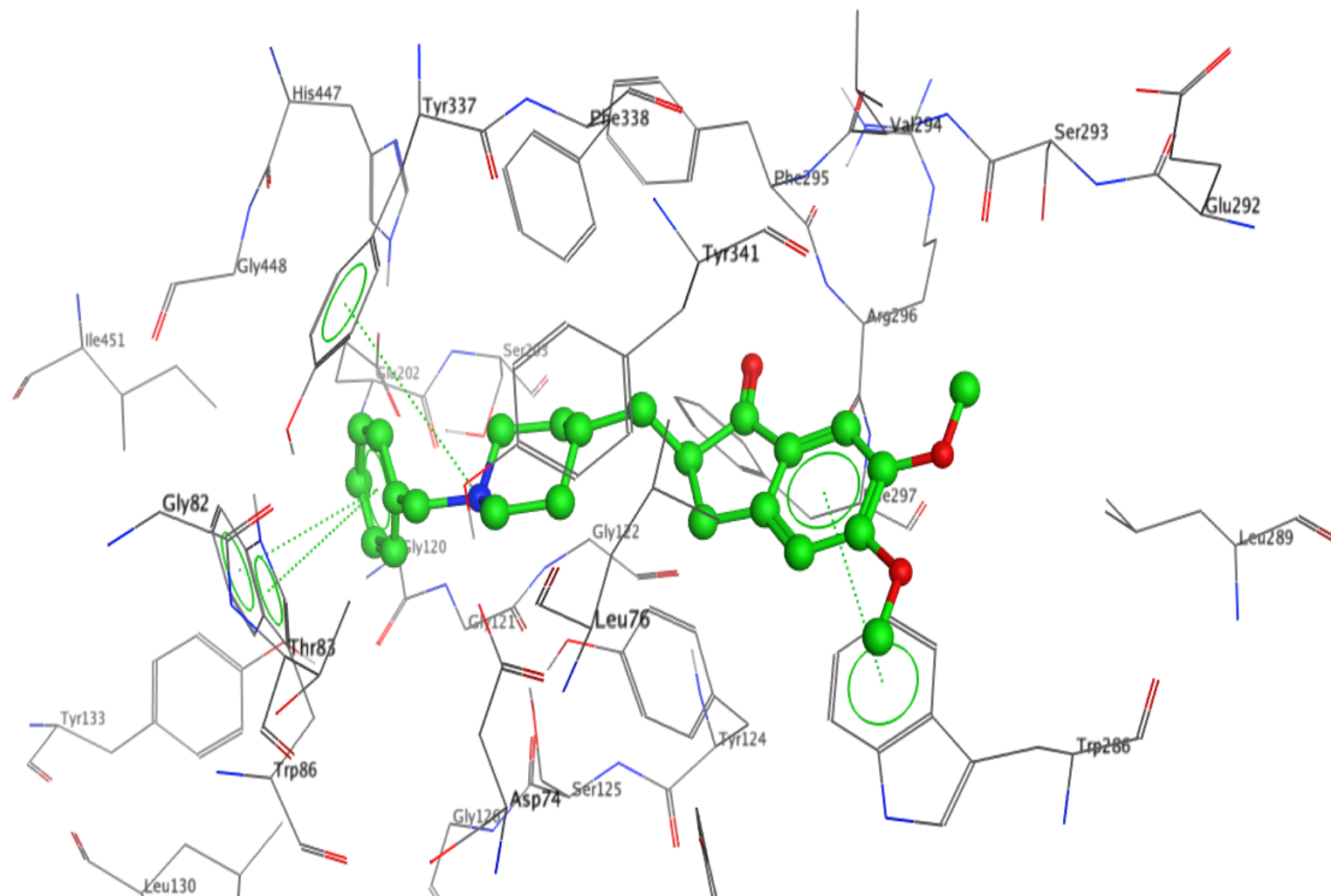


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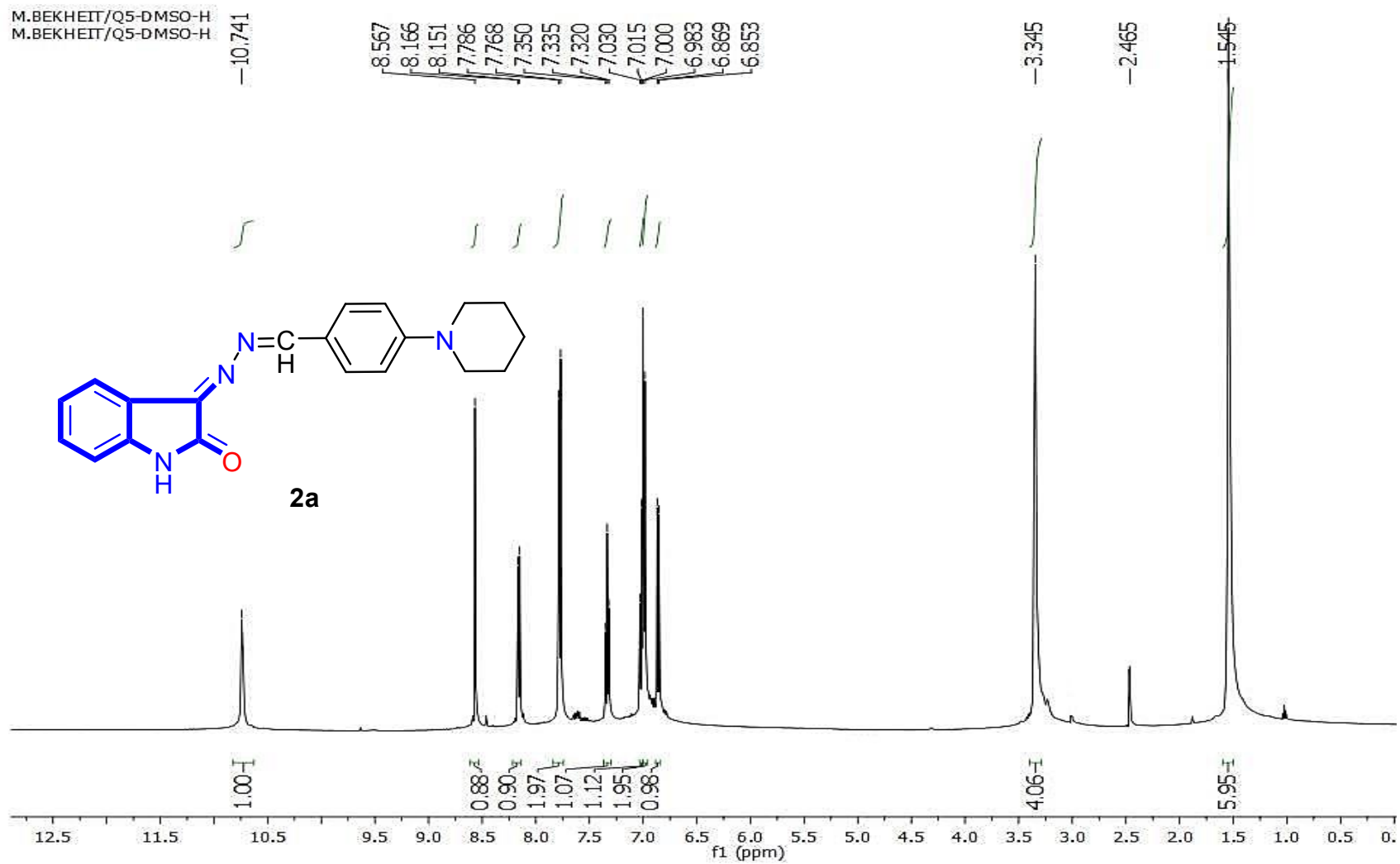


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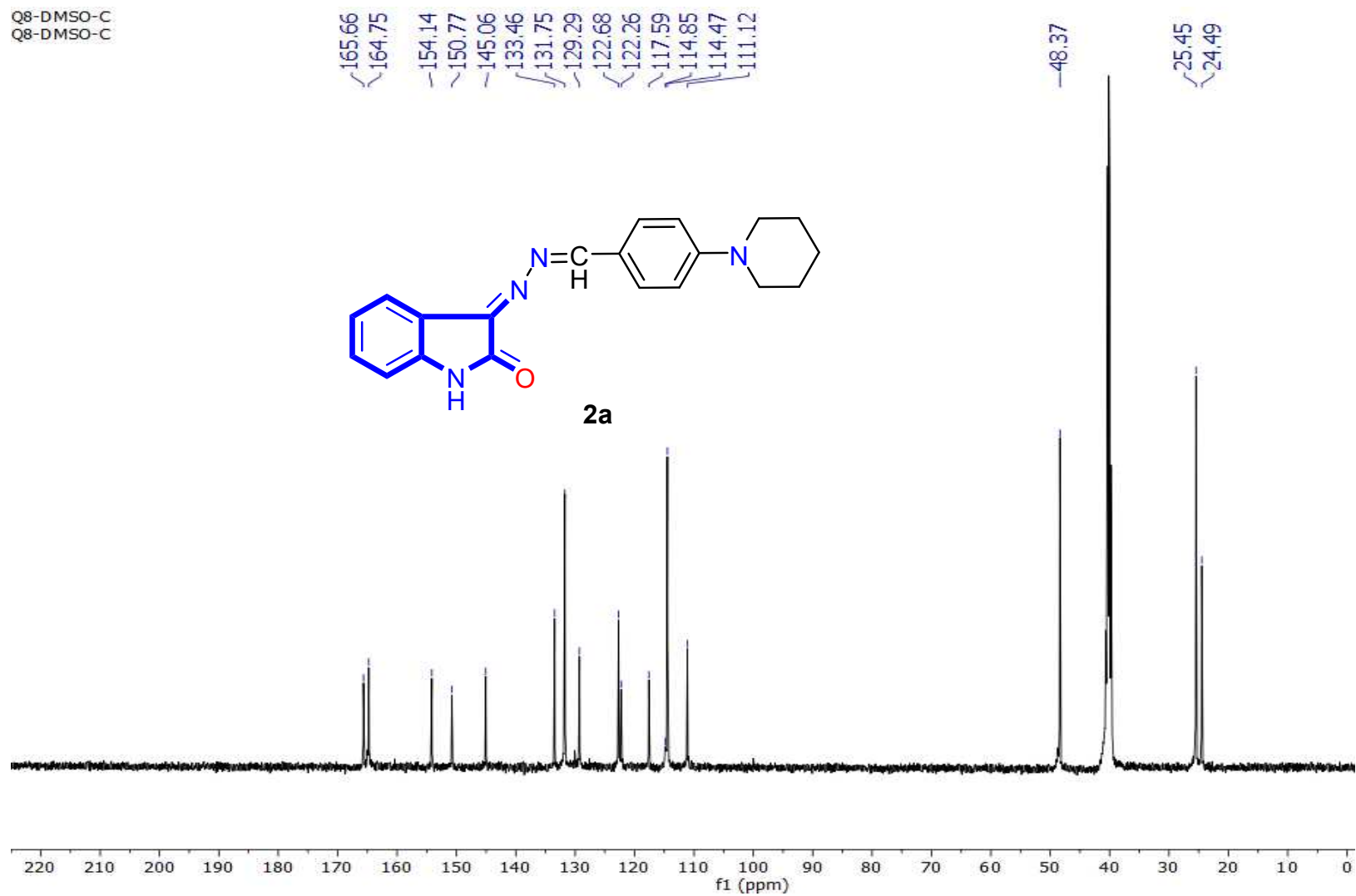


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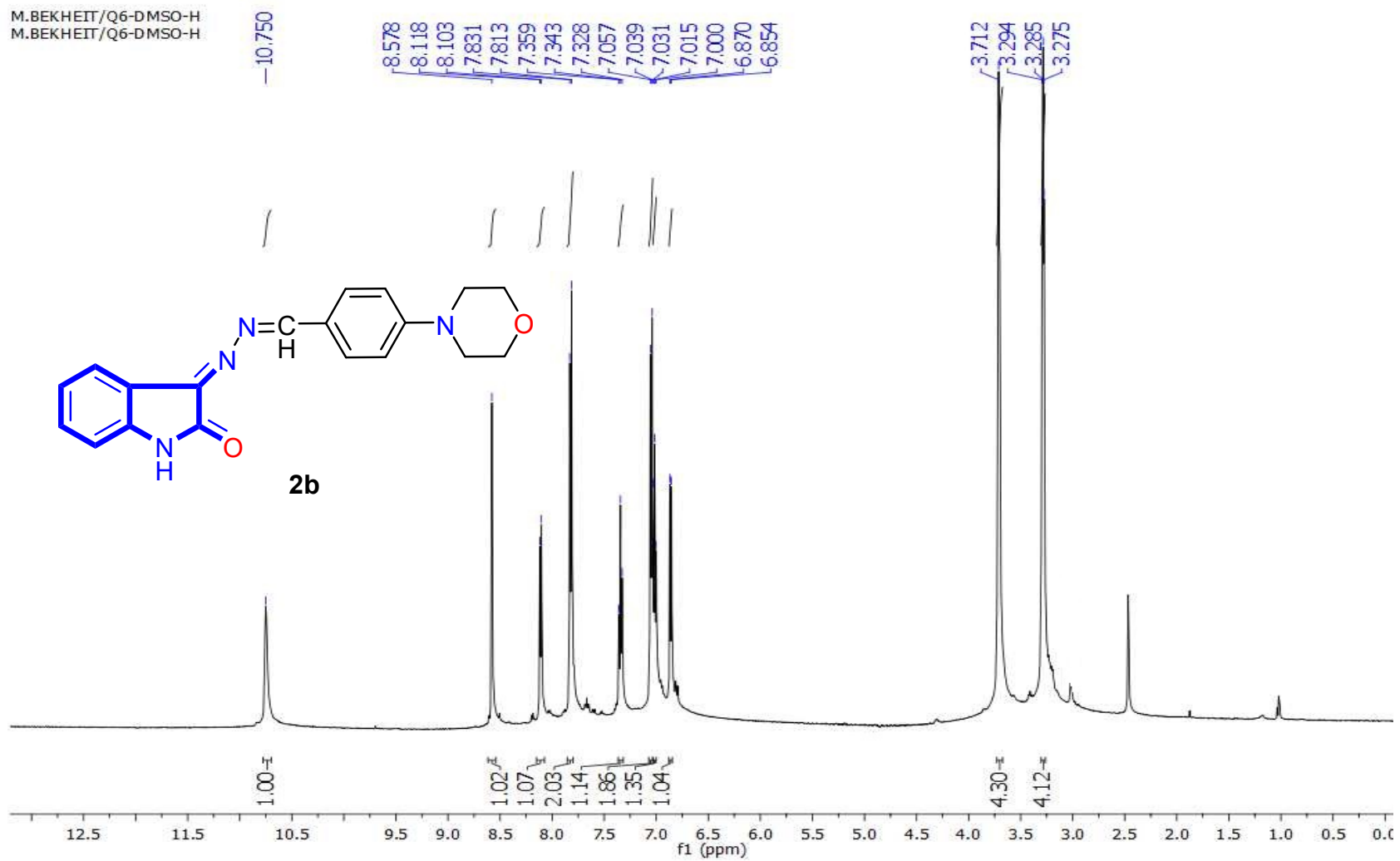


The  $^1\text{H}$  NMR spectrum of **2a**

Q8-DMSO-C  
Q8-DMSO-C

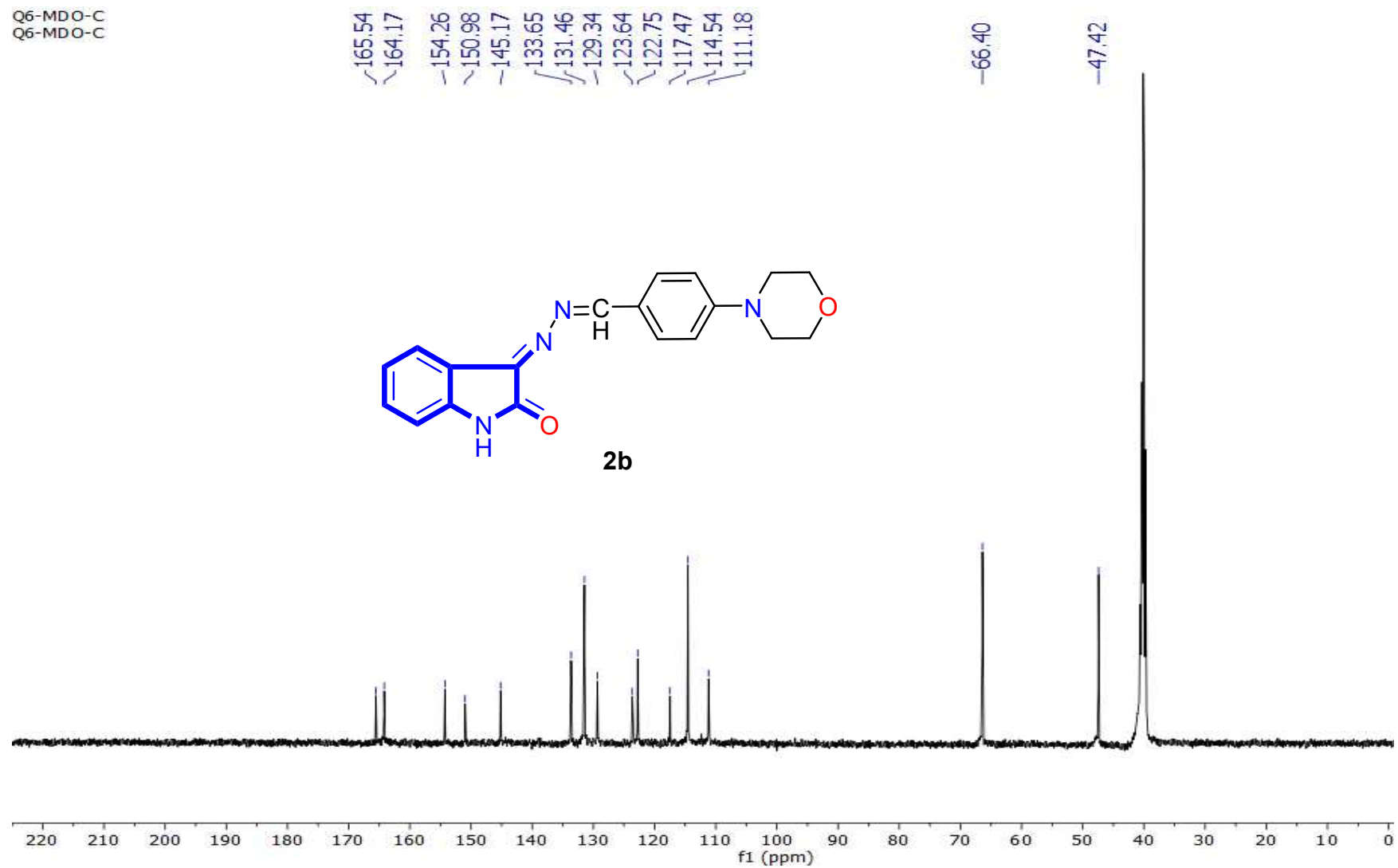


The  $^{13}\text{C}$  NMR spectrum of **2a**



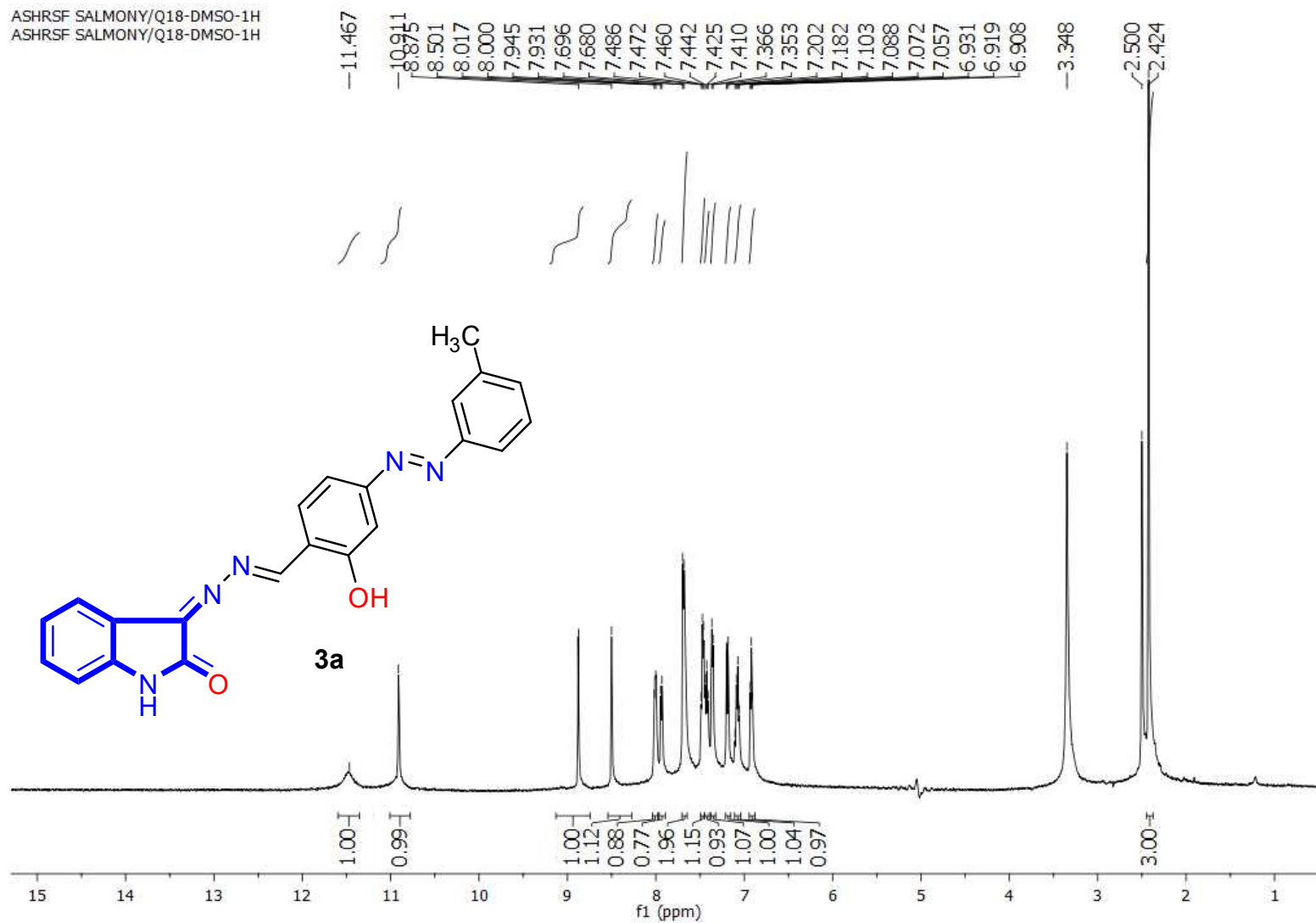
The  $^1\text{H}$  NMR spectrum of **2b**

Q6-MDO-C  
Q6-MDO-C



The  $^{13}\text{C}$  NMR spectrum of **2b**

ASHRSF SALMONY/Q18-DMSO-1H  
ASHRSF SALMONY/Q18-DMSO-1H

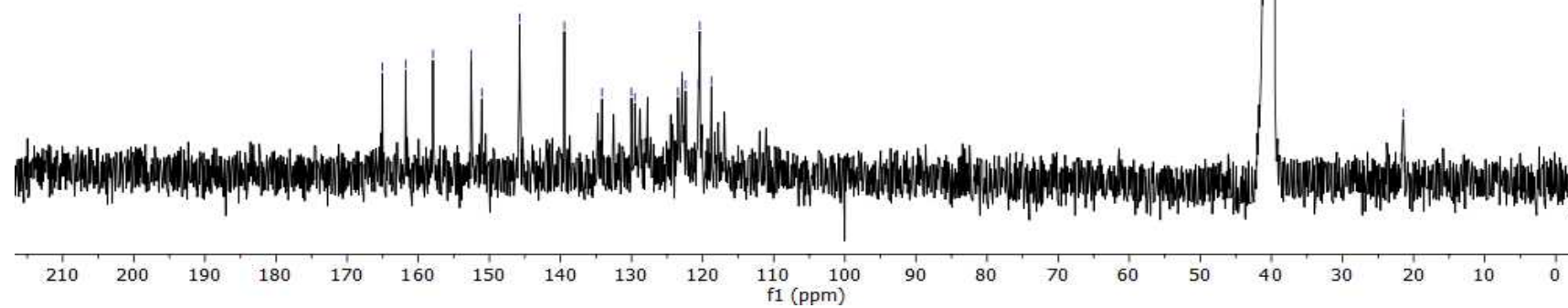
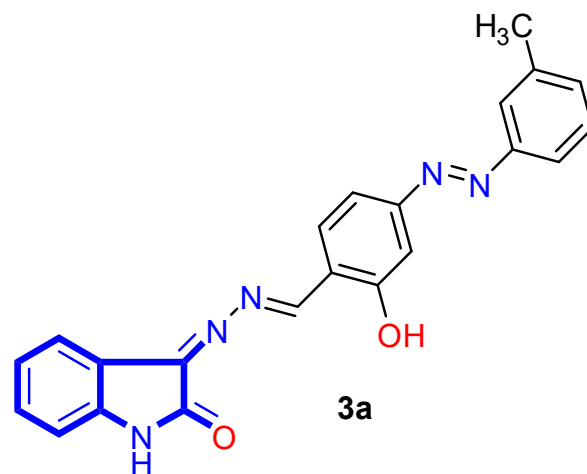


The <sup>1</sup>H NMR spectrum of 3a

Q18-DMSO-13C  
Q18-DMSO-13C

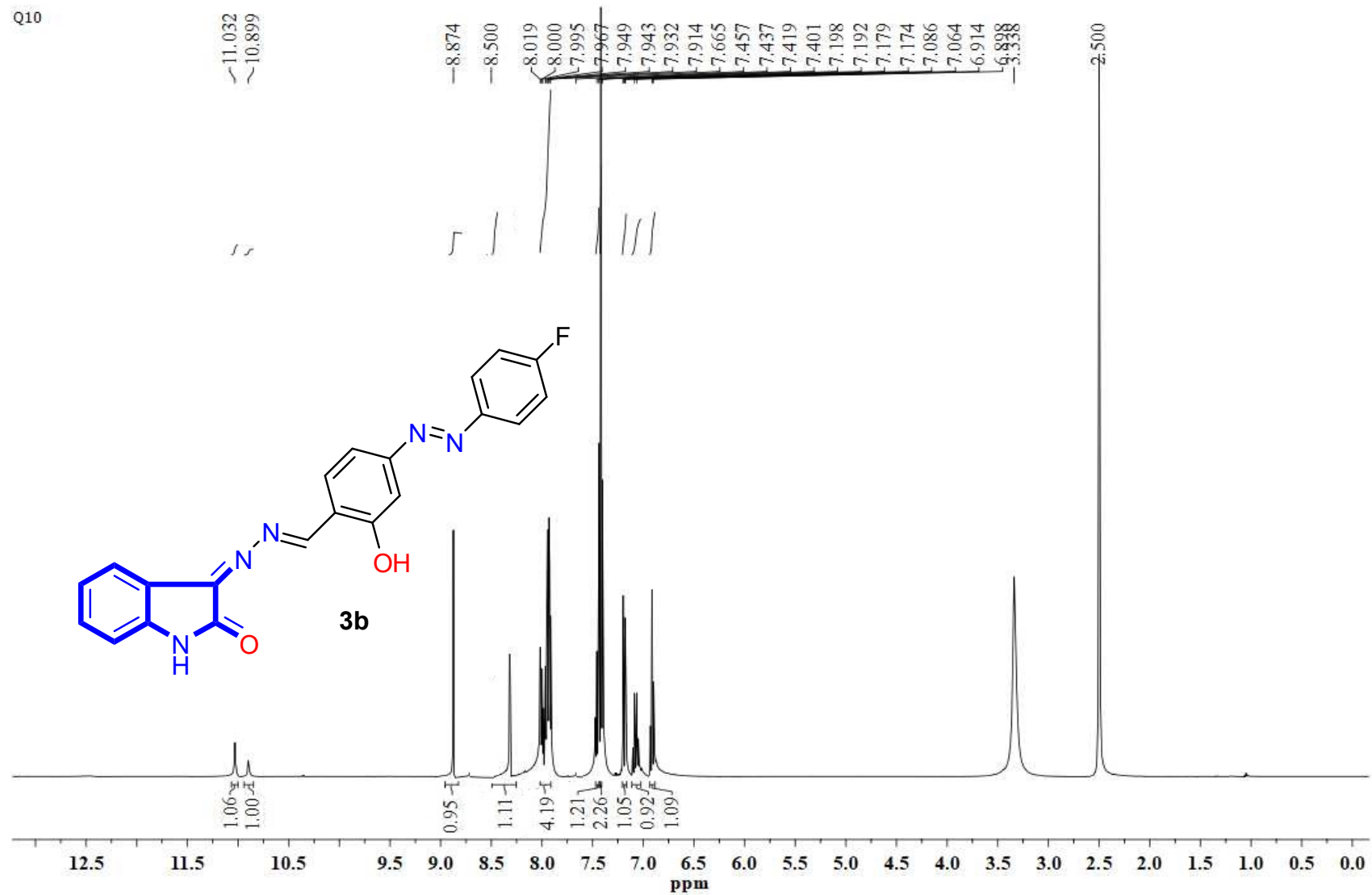
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157.93  
152.56  
151.06  
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139.46  
134.17  
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122.90  
122.39  
120.56  
120.40  
118.77

-21.41



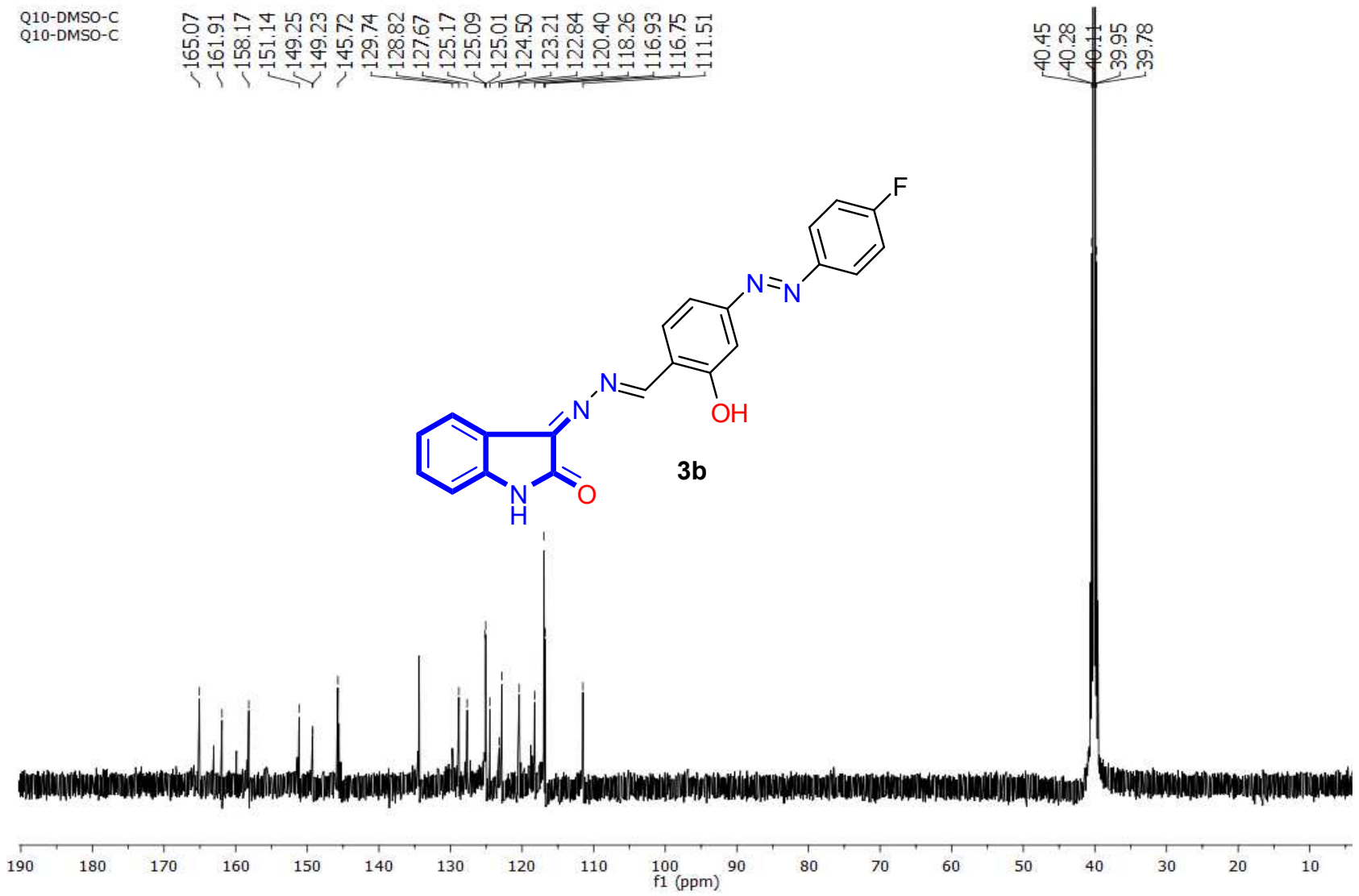
The <sup>13</sup>C NMR spectrum of 3a

Q10

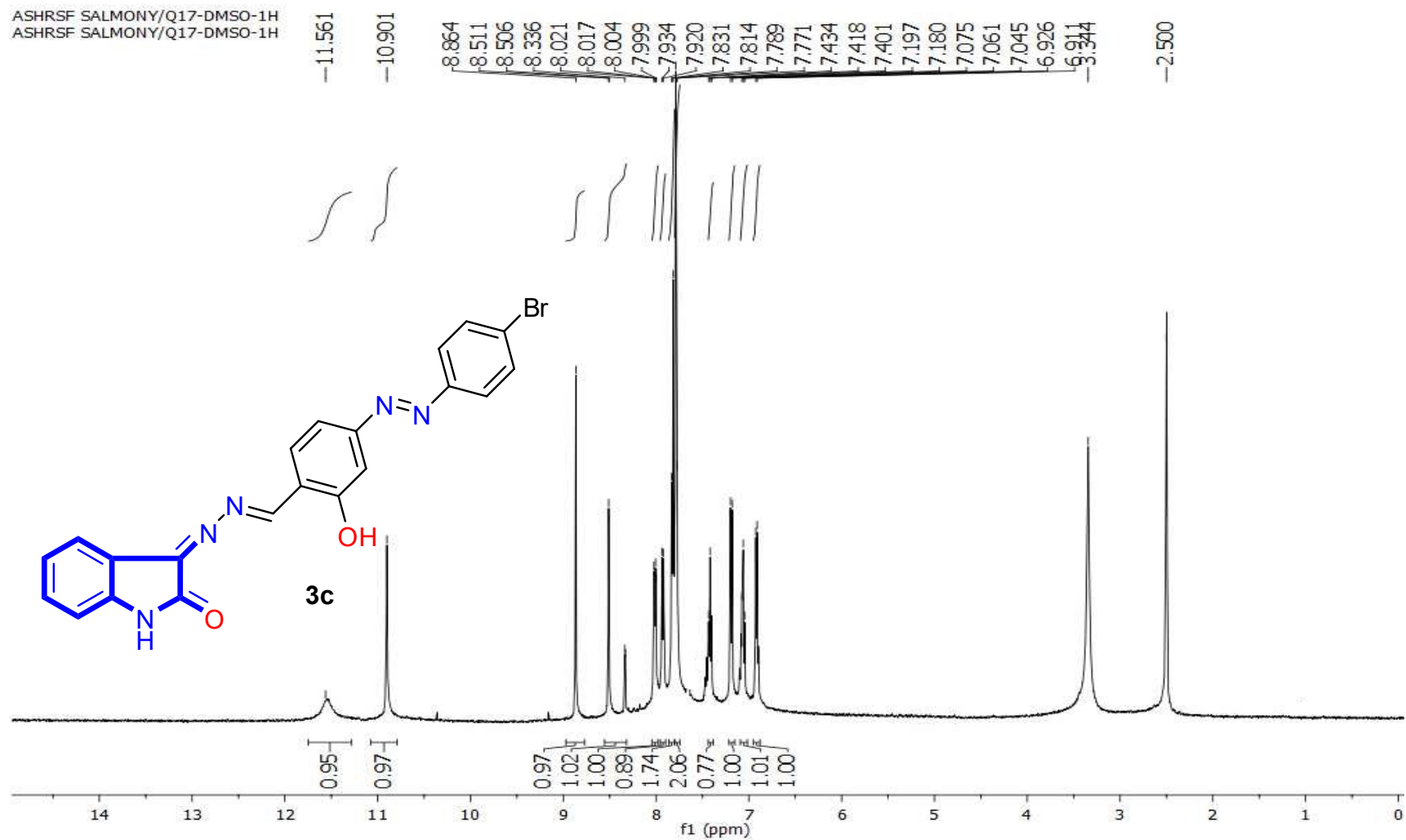


The <sup>1</sup>H NMR spectrum of **3b**





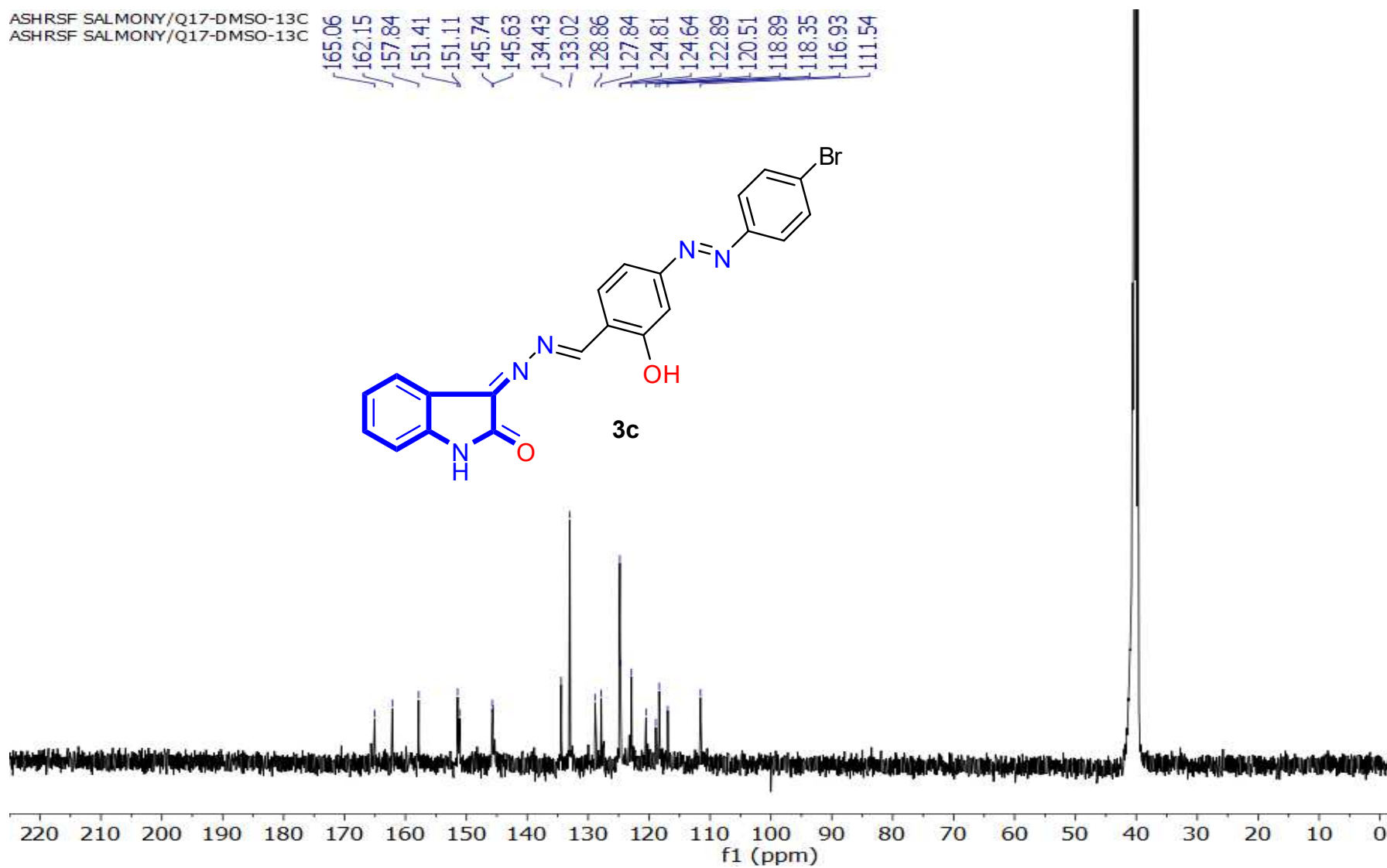
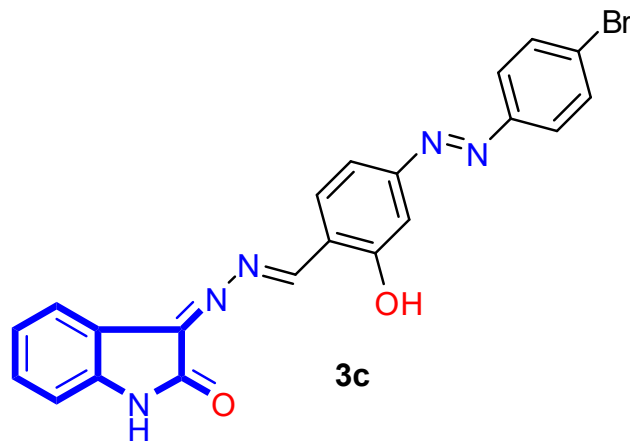
The  $^{13}\text{C}$  NMR spectrum of **3b**



The  $^1\text{H}$  NMR spectrum of **3c**

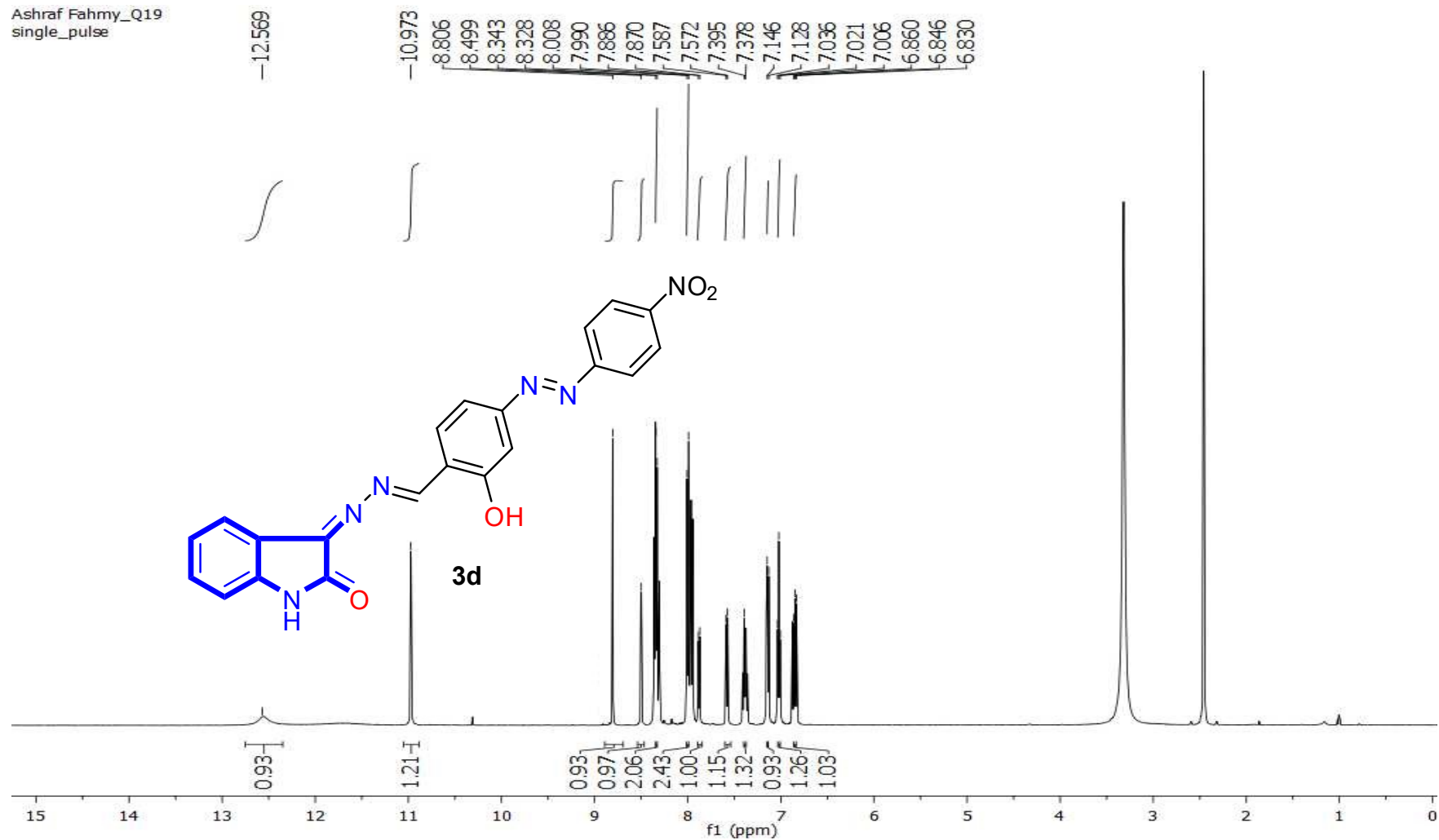
ASHRSF SALMONY/Q17-DMSO-13C  
ASHRSF SALMONY/Q17-DMSO-13C

165.06  
162.15  
157.84  
151.41  
151.11  
145.74  
145.63  
134.43  
133.02  
128.86  
127.84  
124.81  
124.64  
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120.51  
118.89  
118.35  
116.93  
111.54



The <sup>13</sup>C NMR spectrum of **3c**

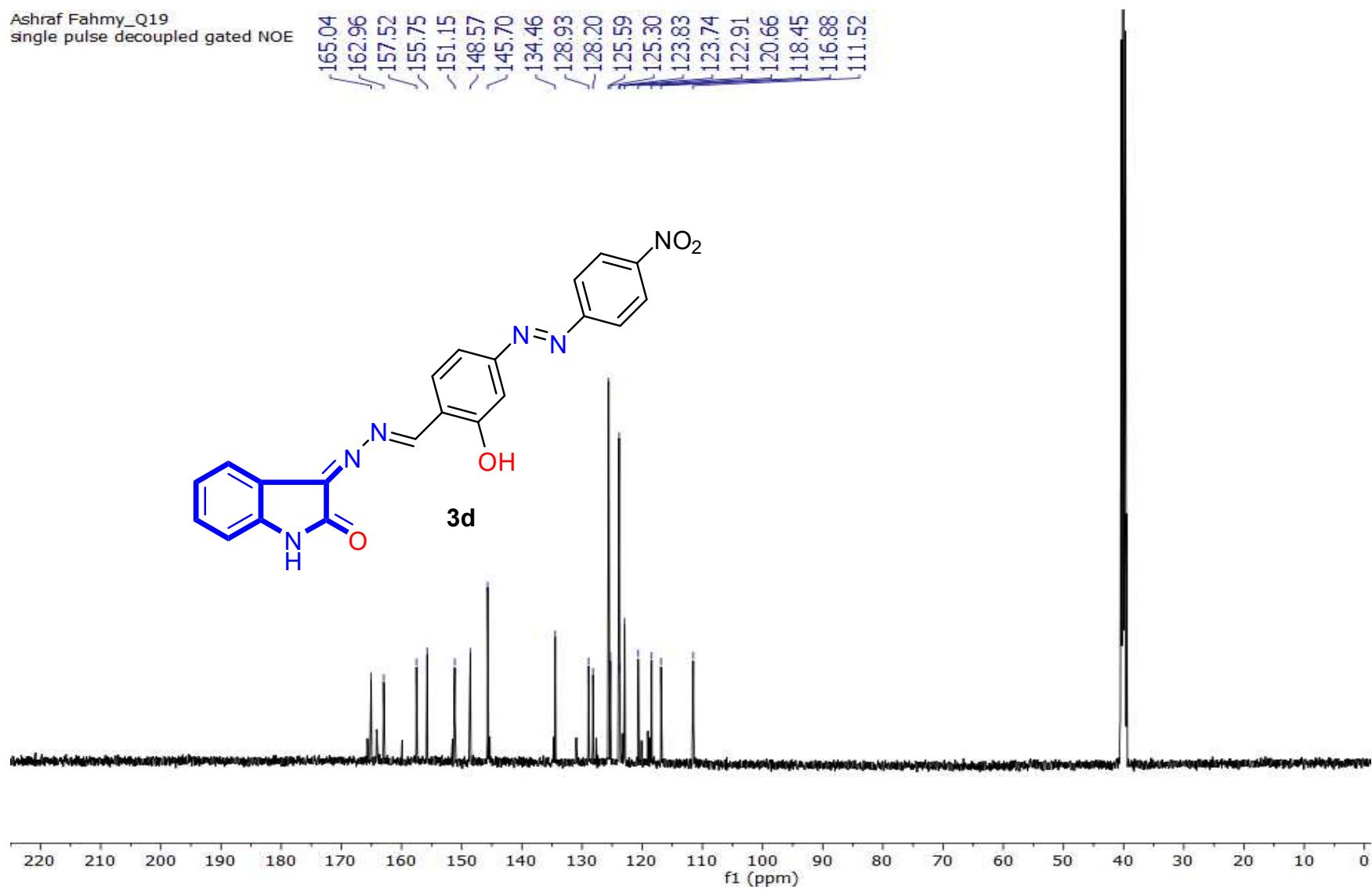
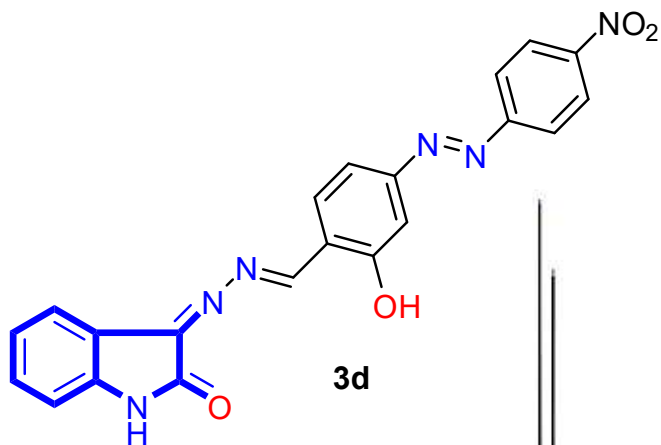
Ashraf Fahmy\_Q19  
single\_pulse



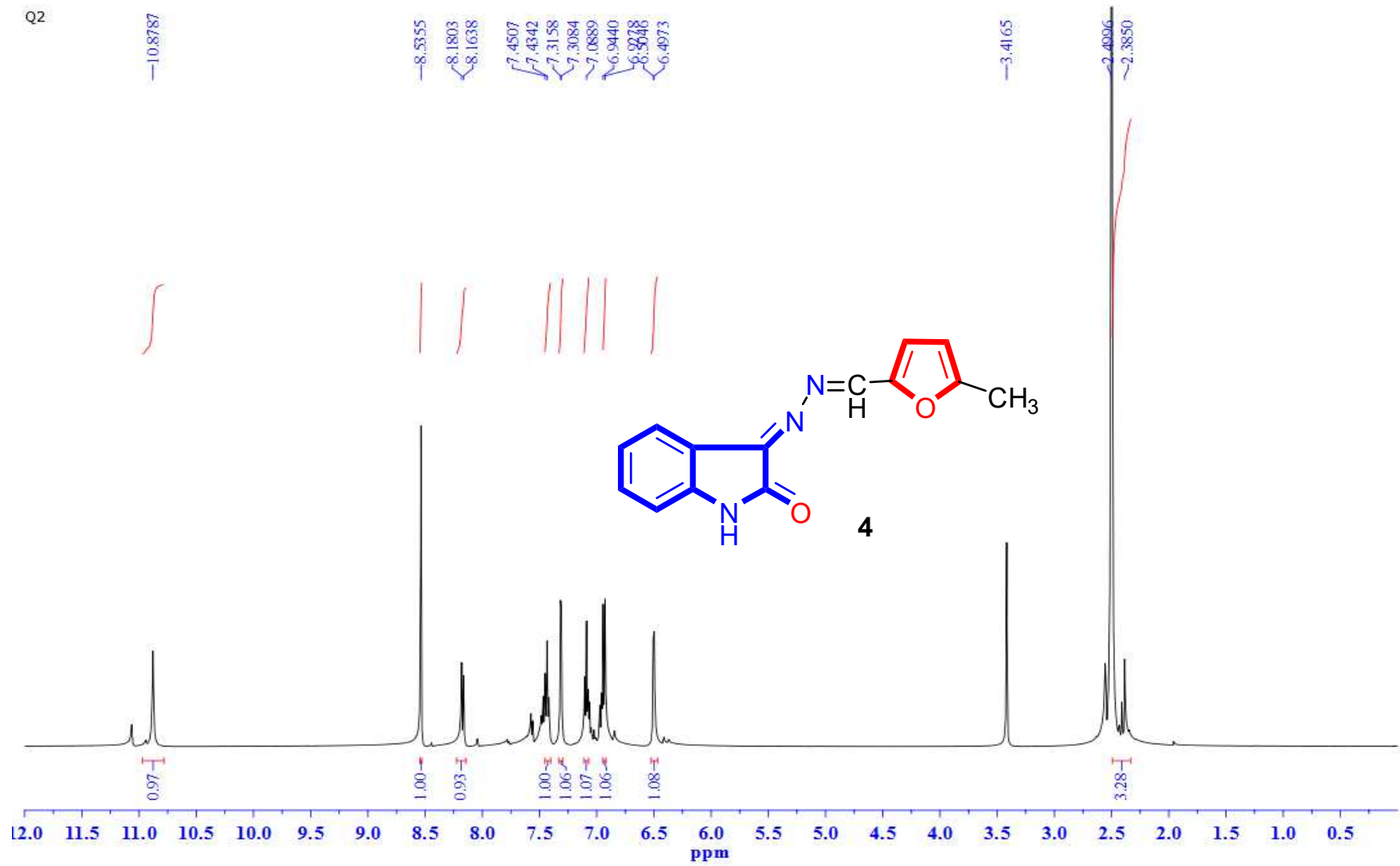
The <sup>1</sup>H NMR spectrum of **3d**

Ashraf Fahmy\_Q19  
single pulse decoupled gated NOE

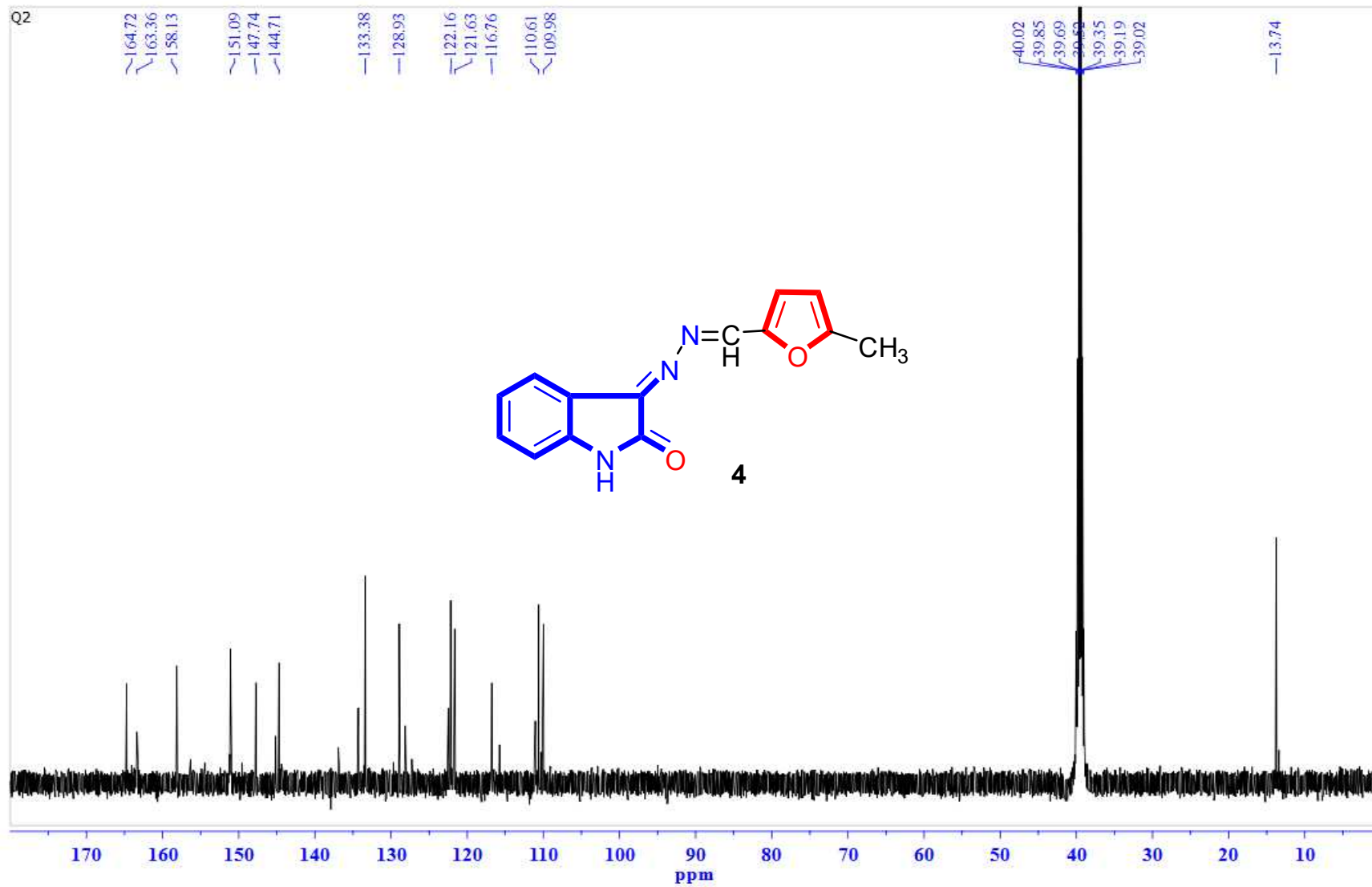
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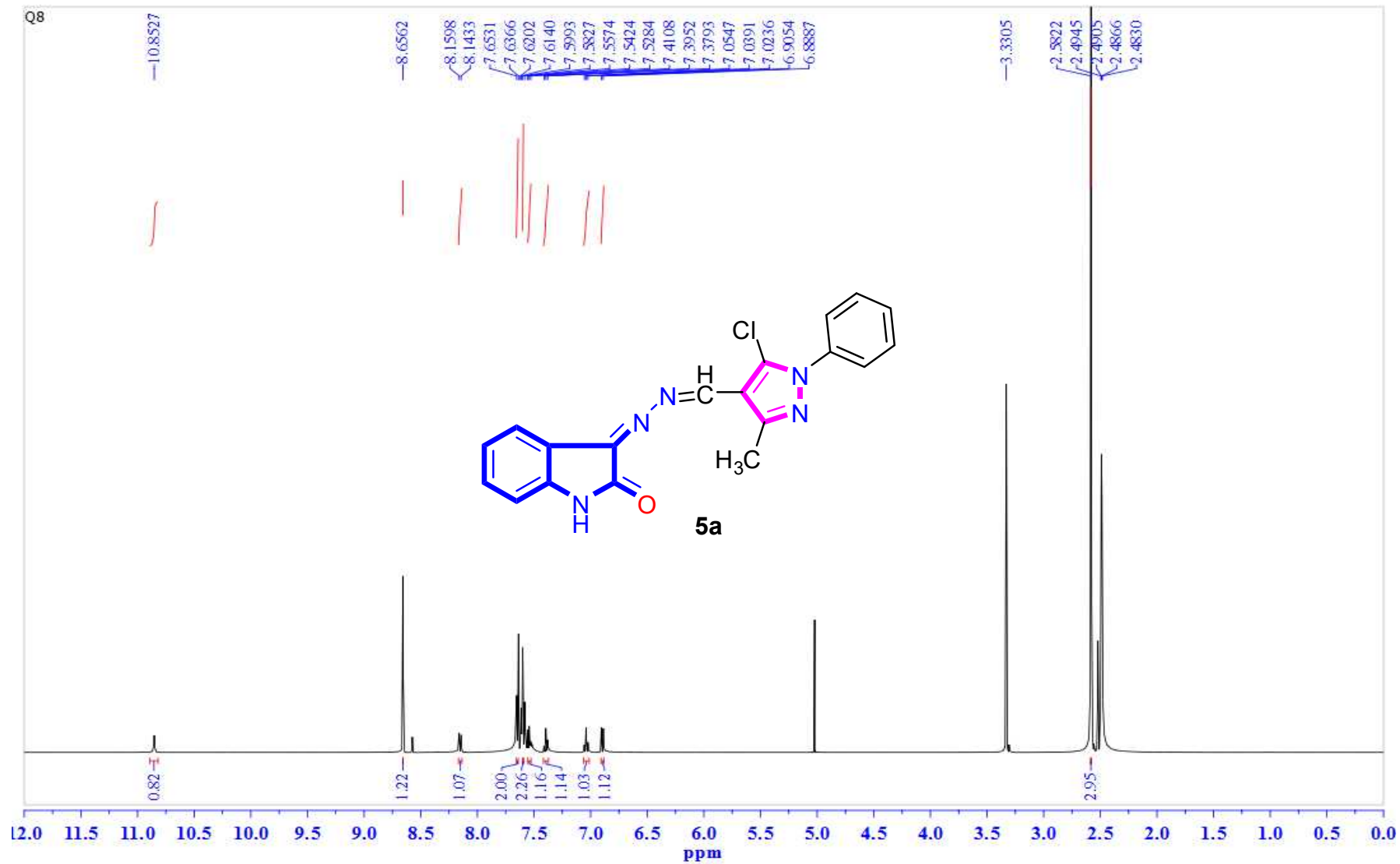
The <sup>13</sup>C NMR spectrum of **3d**



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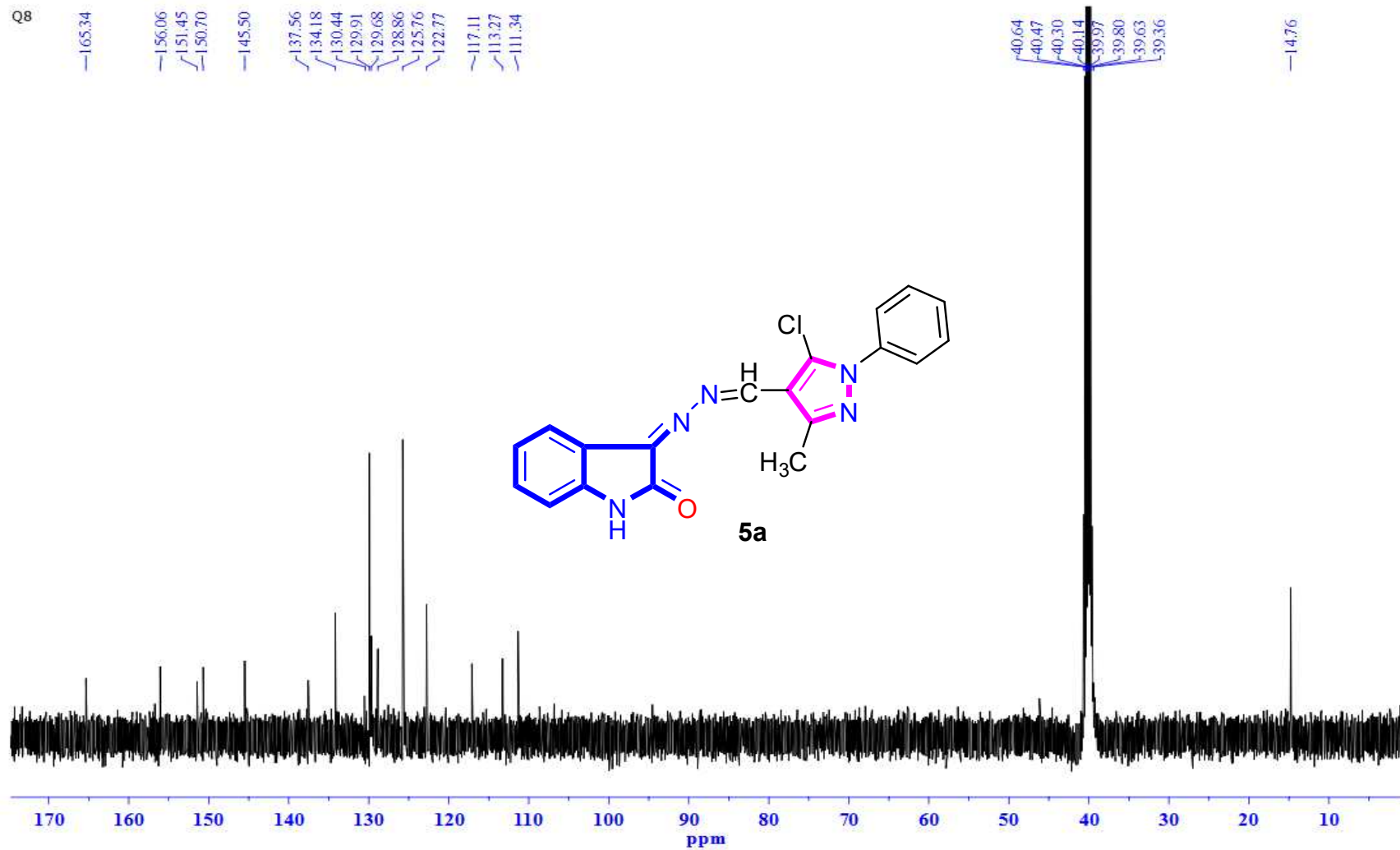


The  $^{13}\text{C}$  NMR spectrum of 4



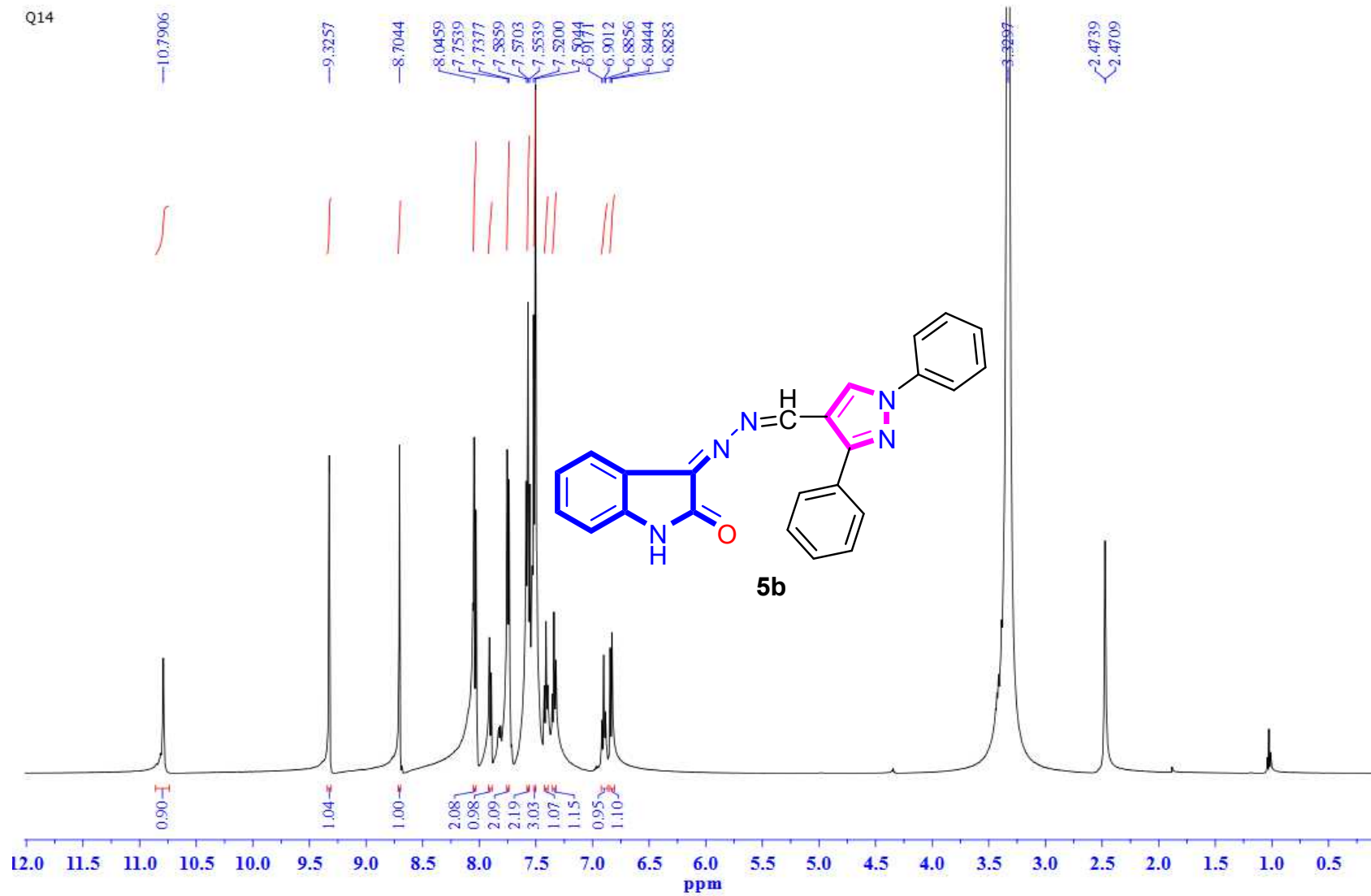
The <sup>1</sup>H NMR spectrum of **5a**



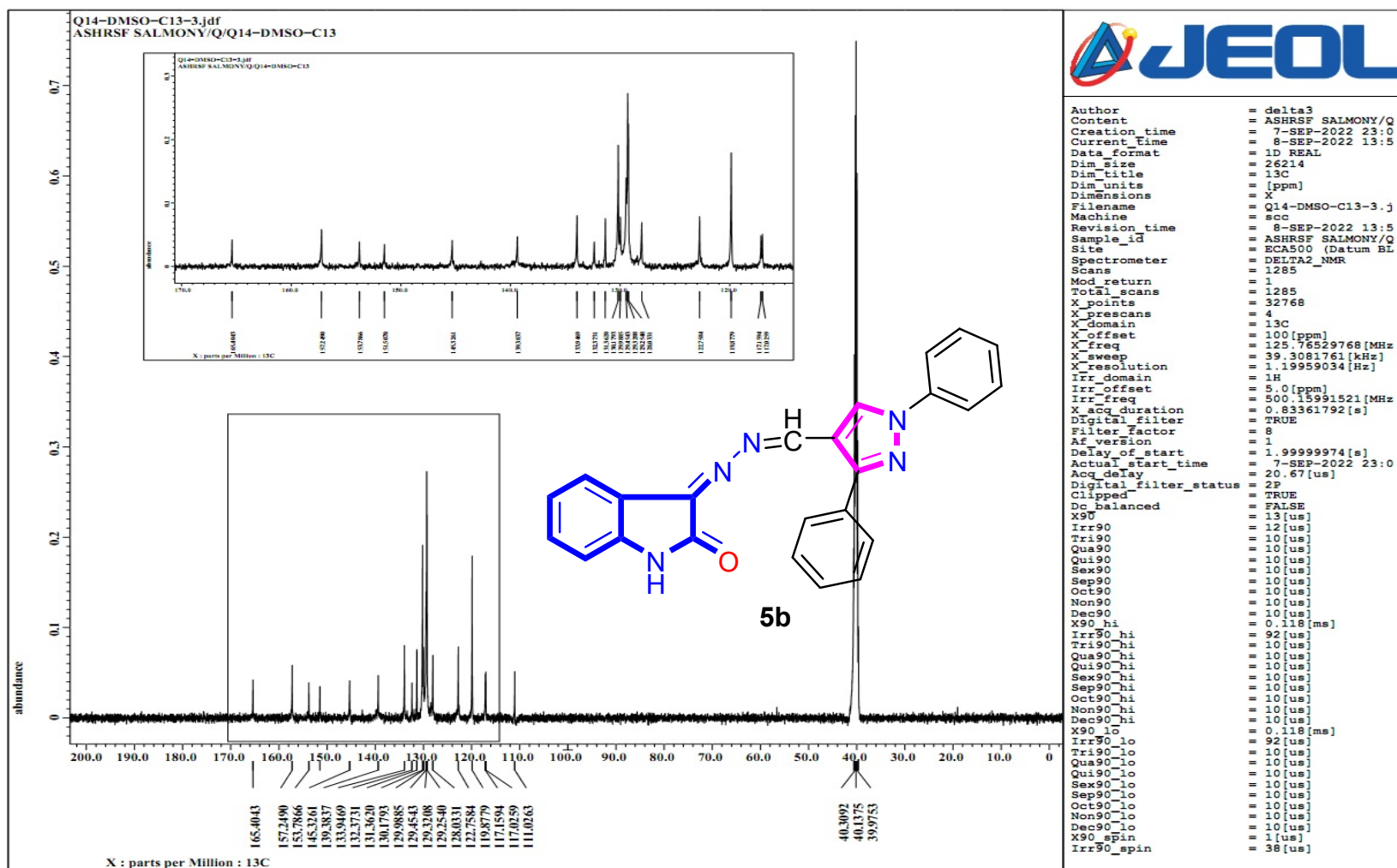


The <sup>13</sup>C NMR spectrum of **5a**

Q14

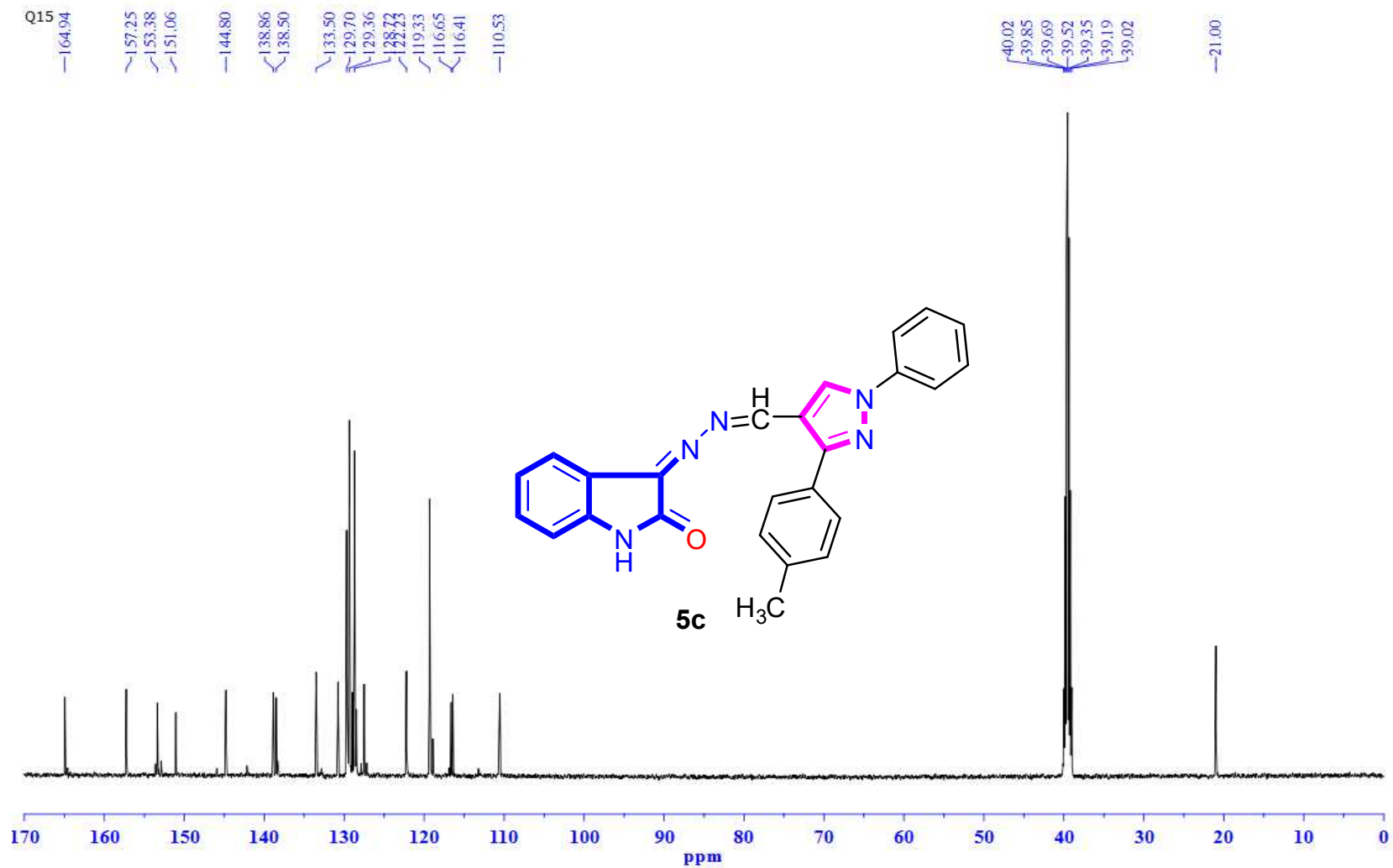


The  $^1\text{H}$  NMR spectrum of **5b**

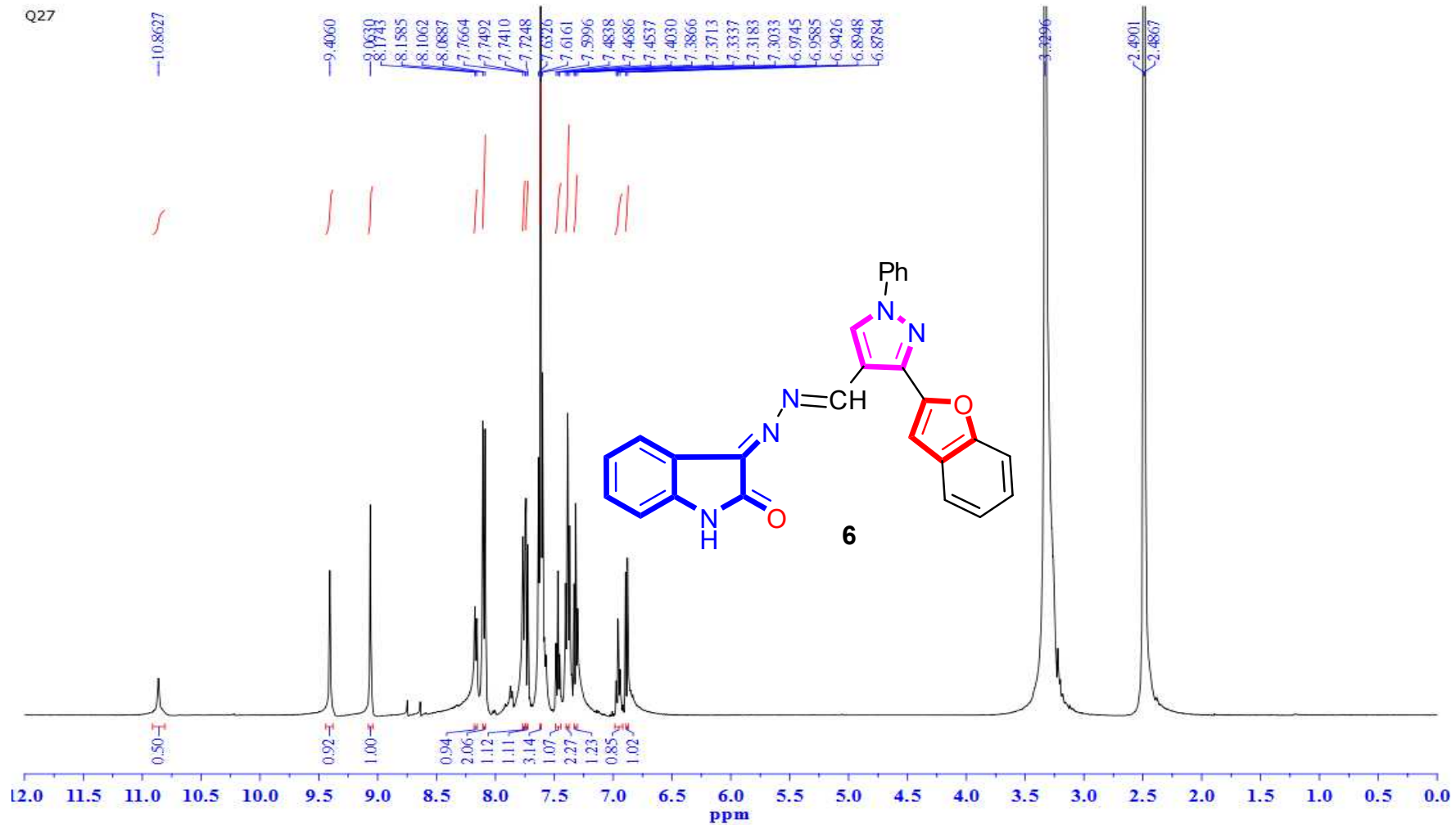


The  $^{13}\text{C}$  NMR spectrum of **5b**

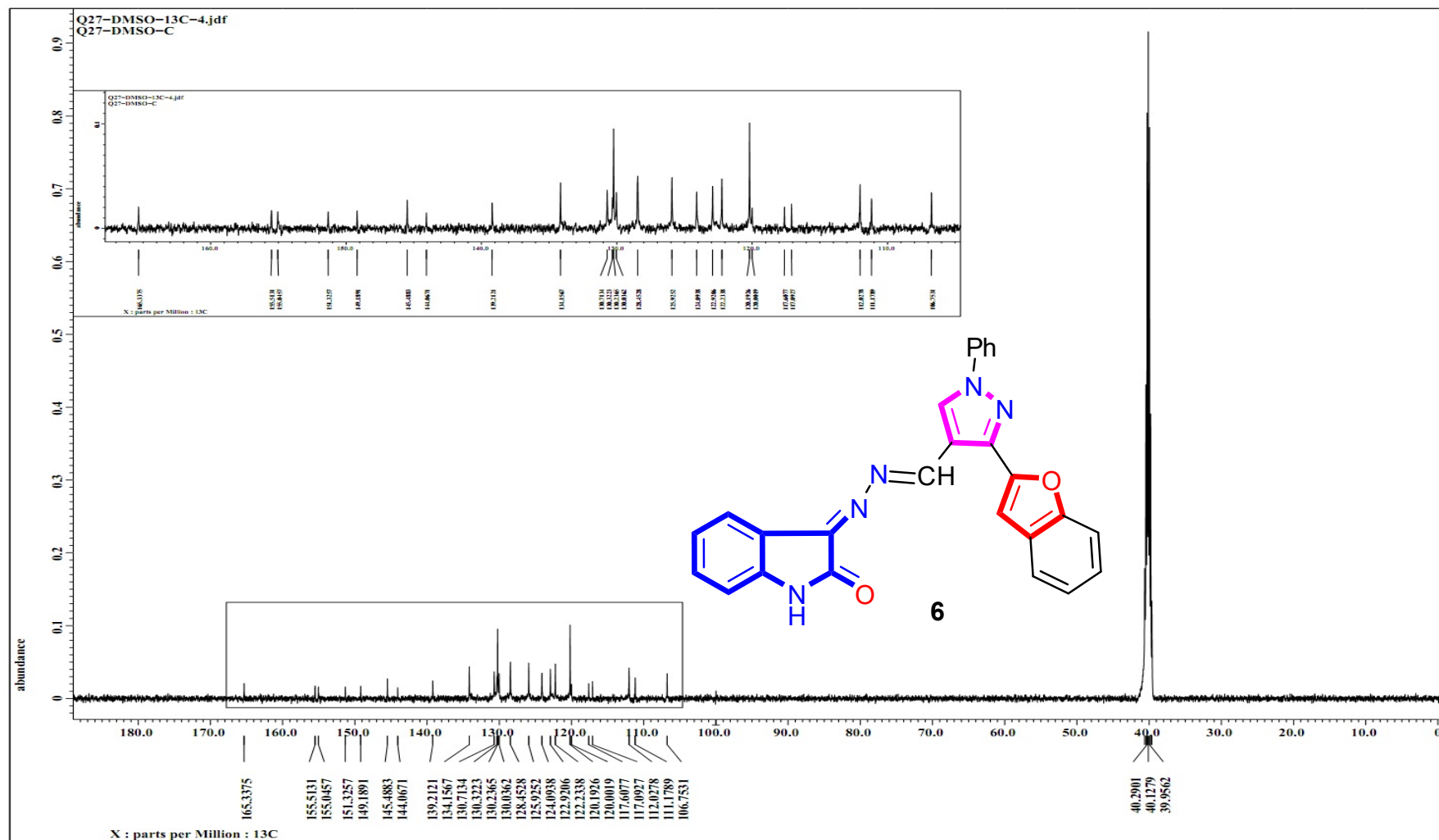




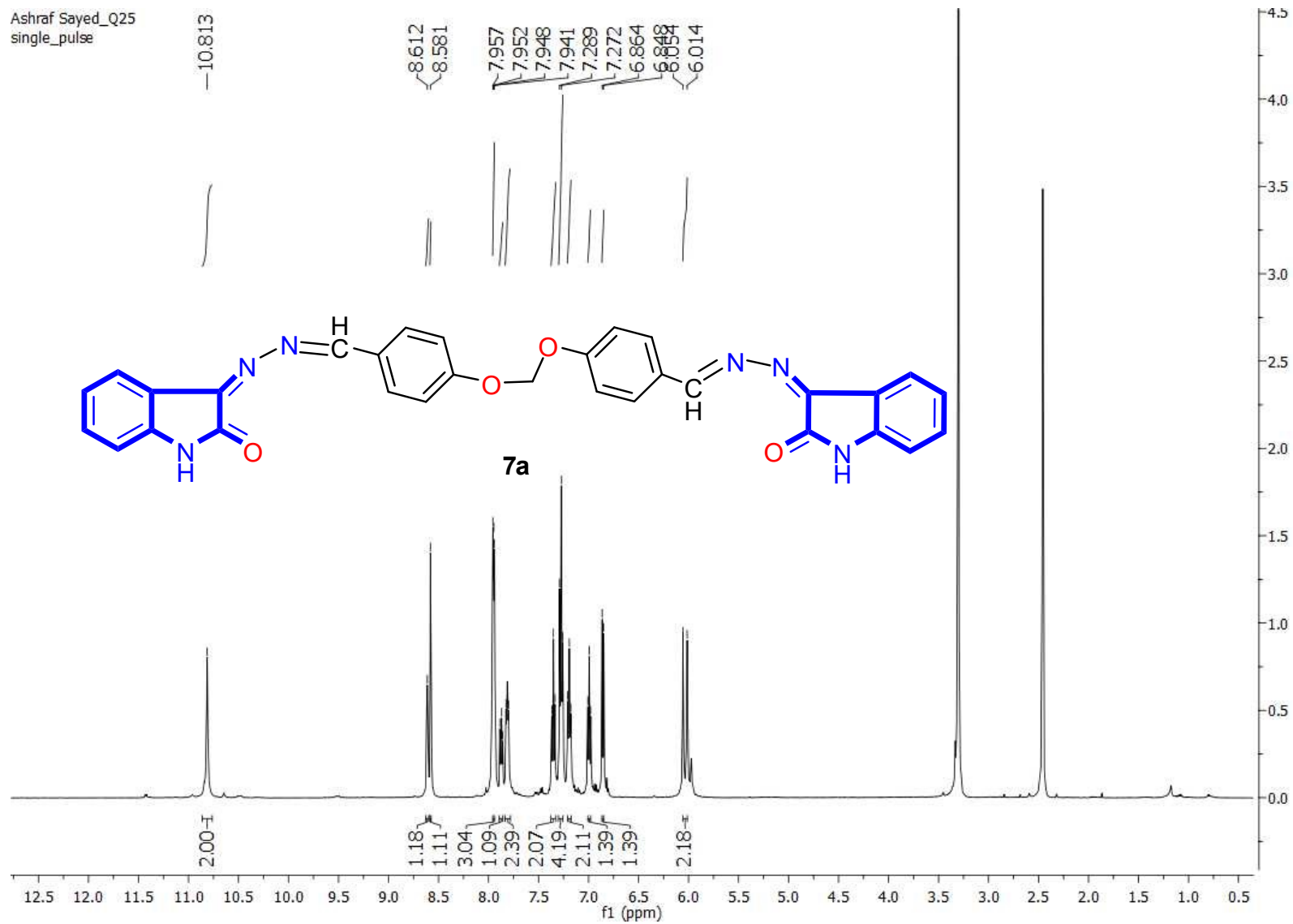
The <sup>13</sup>C NMR spectrum of **5c**



The  $^1\text{H}$  NMR spectrum of **6**



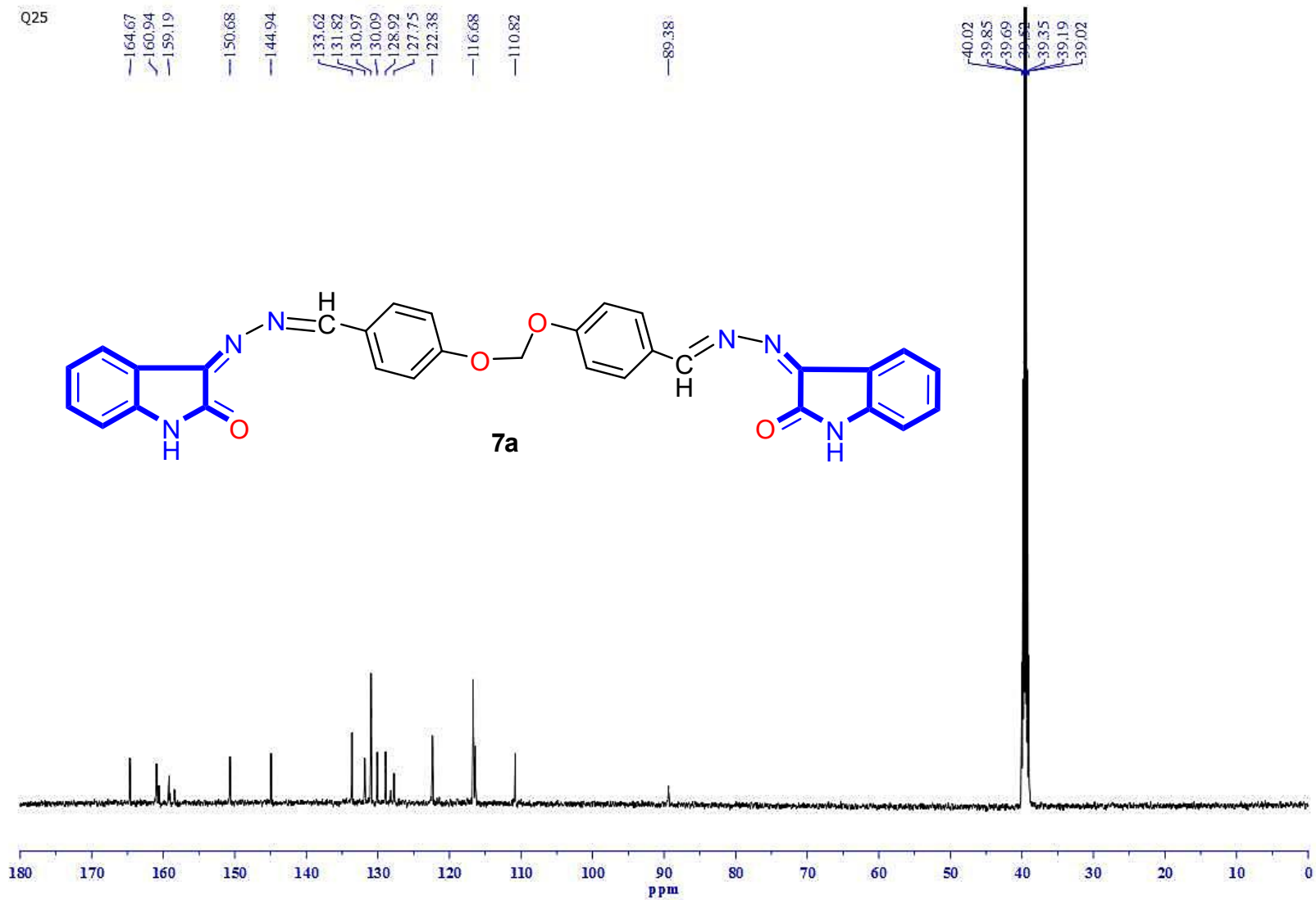
The  $^{13}\text{C}$  NMR spectrum of 6



The  $^1\text{H}$  NMR spectrum of **7a**

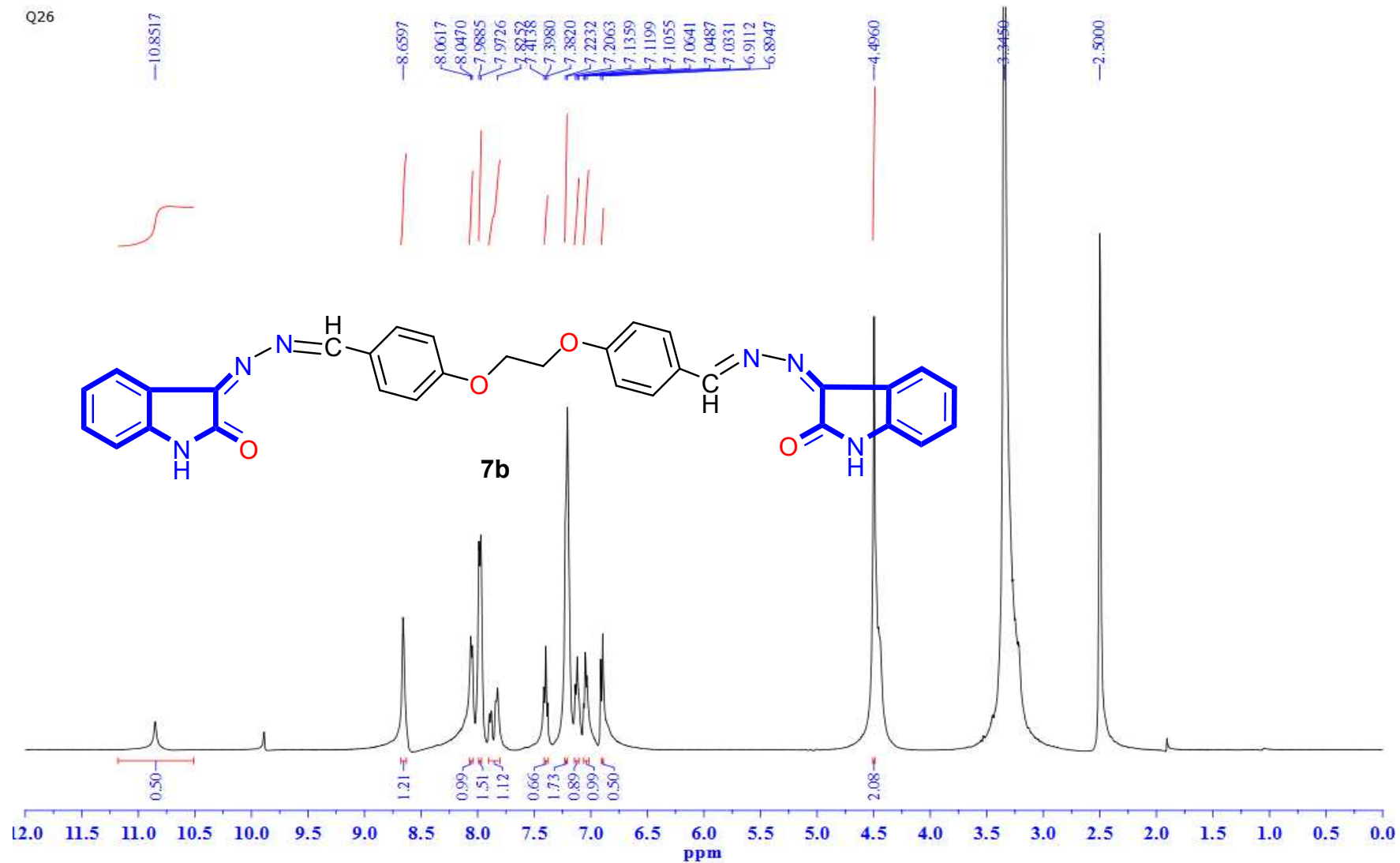


Q25



The  $^{13}\text{C}$  NMR spectrum of **7a**

Q26



The  $^1\text{H}$  NMR spectrum of **7b**

## **In vitro biological activities**

### **Antioxidant activity**

#### **Total antioxidant capacity**

Total antioxidant capacity (TAC) was determined by evaluating the green phosphate/Mo<sup>5+</sup> complex at wavelength 695 nm using the method described by Prieto *et al.* It was expressed as mg gallic acid equivalent per gram dry weight. Briefly, 0.1 ml of the extract was combined with 1 ml of reagent solution (0.3 N sulfuric acid, 28 mM sodium phosphate and 4 mM ammonium molybdate). The tubes were capped and incubated in a boiling water bath for 90 min. Then, the samples were cooled to room temperature and the absorbance was measured at wave length 695 nm against blank containing methanol (80%) instead of extract. Antioxidant capacity was expressed as mg gallic acid equivalent per gram dry weight.

#### **Iron-reducing power**

Total iron-reducing power was assessed using the method suggested by Oyaizu as  $\mu\text{g/mL}$ . A high absorbance of the reaction mixture at 700 nm indicates a higher reducing power. In brief, 1ml of the extract (1mg/ml) was mixed with 1ml of 200 mM of sodium phosphate buffer (pH 6.6) and 1ml of 1% potassium ferricyanide. Consequently, the mixture was incubated at 50 °C for 20 min. followed by adding 1ml of trichloroacetic acid (10% w/v). The mixture was centrifuged at 2000 rpm for 10 min. The upper layer solution (2.5 ml) was mixed with 2.5 ml of double deionised water and 1ml of freshly prepared ferric chloride solution (0.1%). The absorbance was measured at 700 nm against blank prepared without adding extract. Various concentrations of ascorbic acid were used as standard. A high absorbance of the reaction mixture at 700 nm indicates a higher reducing power.

#### **DPPH radical-scavenging activity**

The scavenging activity against 1, 1-diphenyl-2-picryl-hydrazyl (DPPH) radical was assayed by calculating the median inhibitory concentration (IC<sub>50</sub>) according to the method suggested. The substance (antioxidant) that can donate a hydrogen atom to solution containing DPPH- can

reduce the stable free radical and change the color of solution from violet to pale yellow. Non reacted DPPH- radical form was quantified by measuring intensity of a light-purple colored DPPH methanol solution in the visible range at 518 nm against blank solution by spectroscopic method.

Then, the inhibition % was plotted against concentration, and from the graph IC<sub>50</sub> was calculated.

Percent inhibition of the DPPH free radical was calculated by the following equation:

The DPPH radical scavenging activity %:

$$(\text{Control OD} - \text{sample OD}/\text{control OD}) \times 100$$

Serial concentrations spanning from 0.78 till 100 µg/mL were prepared from different samples. Two milliliter of DPPH solution (100 µM) in ethanol was mixed with 2 mL of sample (100µg/mL). The effective test concentrations of DPPH and the sample were 50µM and 50µg/mL, respectively. The reaction mixture of different dilutions, for different concentrations, was vortexed thoroughly then incubated in the dark at room temperature for 30 min. Thereafter, the absorbance was measured spectrophotometrically at 518 nm against blank (ethanol). For control, 2 mL of ethanol was added instead of sample and run simultaneously with the test. Ascorbic acid was used as positive control.

#### **ABTS radical scavenging assay**

The 2, 2'-azinobis-(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) assay was carried out to determine the percent of the ABTS radical inhibition (%) according to the method modified by Arnao *et al* using ascorbic acid as standard. The stock solutions were consisting of ABTS solution (7 mM) and potassium persulfate solution (2.4 mM). Then, the working solution was prepared by mixing the two stock solutions in equal quantities and allowing them to react at room temperature in dark place for 14 h. The solution was then diluted by mixing 1 ml ABTS solution with 60 ml methanol to obtain an absorbance of  $0.706 \pm 0.01$  units at 734 nm using a spectrophotometer. Fresh ABTS solution was

prepared for each assay. The extracts (1 ml) were allowed to react with 1 ml of the ABTS solution and the absorbance was taken at 734 nm after 7 min using a spectrophotometer. The ABTS scavenging capacity of the extract was compared with that of ascorbic acid

#### **Anti-diabetic activity ( $\alpha$ -amylase inhibitory assay)**

The anti-diabetic activity was assayed by  $\alpha$ -amylase inhibitory assay according to the 3,5-dinitrosalicylic acid (DNSA) method for calculating the percentage of  $\alpha$ -amylase inhibition (%) using Acarbose as a standard drug. In brief, 0.5 ml of test solution was mixed with 0.5 ml of  $\alpha$ -amylase solution (0.5 mg/ml) with buffer ( $\text{Na}_2\text{HPO}_4/\text{NaH}_2\text{PO}_4$  (0.02 M), NaCl (0.006 M) at pH 6.9) to give concentrations ranging from 25 to 800  $\mu\text{g}/\text{mL}$ . The mixture was incubated at room temperature for 10 min and 200  $\mu\text{L}$  of the starch solution (1% in water (w/v) buffer ( $\text{Na}_2\text{HPO}_4/\text{NaH}_2\text{PO}_4$  (0.02 M), NaCl (0.006 M) at pH 6.9)) was added. The reaction was terminated by adding 200  $\mu\text{L}$  DNSA (coloring) reagent (12 g of sodium potassium tartrate tetrahydrate in 8.0 mL of 2 M NaOH and 20 mL of 96 mM of DNSA solution). At this time, the test tubes were placed in a boiling water bath (100  $^\circ\text{C}$ ) for 10 min and the mixture was cooled to ambient temperature and was diluted with 5 mL of distilled water, and the absorbance was measured at 540 nm using a UV-Visible spectrophotometer.

The blank with 100% enzyme activity was prepared by replacing the plant extract with 200  $\mu\text{L}$  of the buffer. A blank reaction was similarly prepared using the plant extract at each concentration in the absence of the enzyme solution. A positive control sample was prepared using acarbose and the reaction was performed similarly to the reaction with plant extract as mentioned above. Absorbance of blank (buffer instead of analyte and amylase solution) and control (buffer instead of extract) samples were also determined. Acarbose was used as standard drug. Percentage of  $\alpha$ -amylase inhibition was calculated using the following equation: The  $\alpha$ -amylase activity inhibition %:

$$\frac{[(\mathbf{Ab}_{\text{control}} - \mathbf{Abc}_{\text{blank}}) - (\mathbf{Ab}_{\text{sample}} - \mathbf{Abs}_{\text{blank}})]}{(\mathbf{Ab}_{\text{control}} - \mathbf{Abc}_{\text{blank}})} \times 100$$

Where,  $\mathbf{Ab}_{\text{control}}$ : absorbance of control;  $\mathbf{Abc}_{\text{blank}}$ : absorbance of control blank;  $\mathbf{Ab}_{\text{sample}}$ : absorbance of sample; and  $\mathbf{Abs}_{\text{blank}}$ : absorbance of sample blank.

### **Anti-Alzheimer activity (acetylcholinesterase (AChE) enzyme inhibition)**

The anti-Alzheimer activity was measured by calculating the percentage of acetylcholinesterase (AChE) enzyme inhibition (%) according to Ellman's method. The tested compounds were dissolved in a 0.1 M phosphate buffer, pH 8. To a flat bottom 96-well plate, typical run consisted of, 5  $\mu$ l of Acetylthiocholine (ATCh) (0.5 mM), 5  $\mu$ l of 5, 5'-dithiobis-2-nitrobenzoic acid (DTNB) (0.03 mM) and 5  $\mu$ l of the tested samples solution at the different concentrations evaluated, which were mixed and incubated for 10 min at 30 °C. Then, 5  $\mu$ l of AChE (0.3 U/ml) solution was added to the initial mixture to start the reaction and then absorbance was determined at 412 nm. A control run contained all the aforementioned constituents with exception of the test extract. All experiments were performed in triplicates. The concentration of the tested extract that inhibited the hydrolysis of substrate ATCh was determined by linear regression analysis.

### **Anti-arthritic activity**

#### **Protein denaturation**

The percentage of protein denaturation inhibition was calculated according to the method suggested by Lavanya *et al* and modified by Soni and Sureshkumar. All results were compared with the standard (diclofenac sodium) that was prepared according to the method described. The control represents 100% protein denaturation. The test control solution (0.5 ml) consists of 0.45 ml of bovine serum albumin (5% w/v aqueous solution) and 0.05 ml of distilled water. The product control (0.5 ml) consists of 0.45 ml of distilled water and 0.05 ml of the test solution. The standard solution (0.5 ml) consists of 0.45ml of bovine serum albumin (5% w/v aqueous solution) and 0.05 ml of diclofenac sodium. Various concentrations (100, 150, 200 mgml<sup>-1</sup>) of test solution and diclofenac sodium (standard) were taken. All the above solutions were adjusted to pH 6.3 using 1 N HCl. The samples were incubated at 37 °C for 20 min and the temperature was increased to maintain the samples at 57 °C for 3 min. After being cooled, 2.5 ml of phosphate buffer was added to the above prepared solutions. The absorbance was measured using a UV-Visible spectrophotometer at 416 nm. The control represents 100% protein denaturation. The results were compared with diclofenac sodium. The percentage inhibition of protein denaturation can be calculated.

### **Proteinase inhibitory activity**

This assay was carried out by calculating the percentage of the proteinase inhibitory activity was according to the method suggested. The test was performed according to the modified method of Oyedapo and Famurewa. The reaction mixture (2 ml) contained 0.06 mg trypsin, 1 ml of 20 mM Tris HCl buffer (pH 7.4) and 1 ml of the test sample of different concentrations. The mixture was incubated at 37 °C for 5 min and then 1 ml of 0.8% (w/v) casein was added. The mixture was incubated for an additional 20 min. 2 ml of 70% perchloric acid was added to terminate the reaction. The cloudy suspension was centrifuged and the absorbance of the supernatant was measured at 210 nm against buffer as the blank. The experiment was performed in triplicate to confirm the reproducibility of the result. The percentage inhibition of proteinase inhibitory activity was calculated.