

SUPPORTING INFORMATION

Design, Synthesis, Biological Evaluation, and In Silico Studies of Novel 1,3-Thiazole Derivatives

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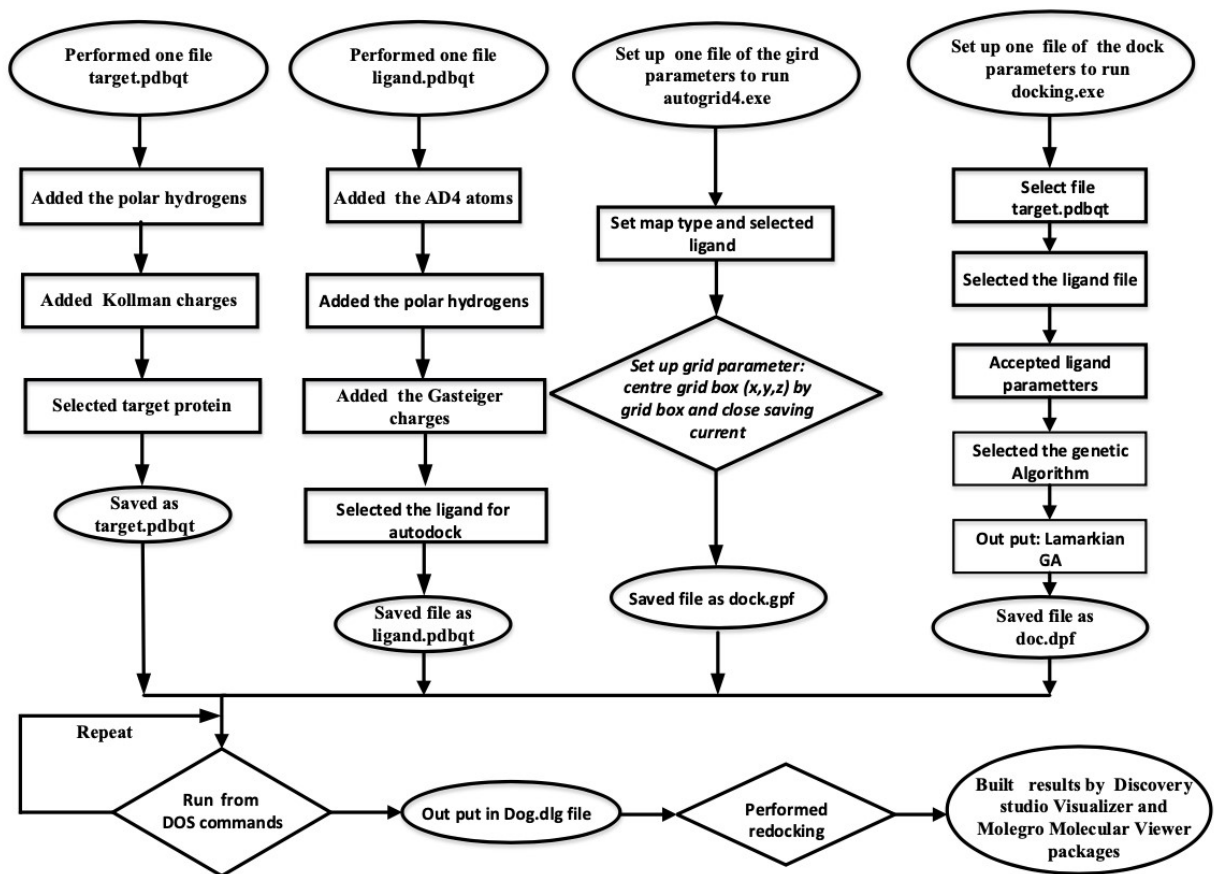
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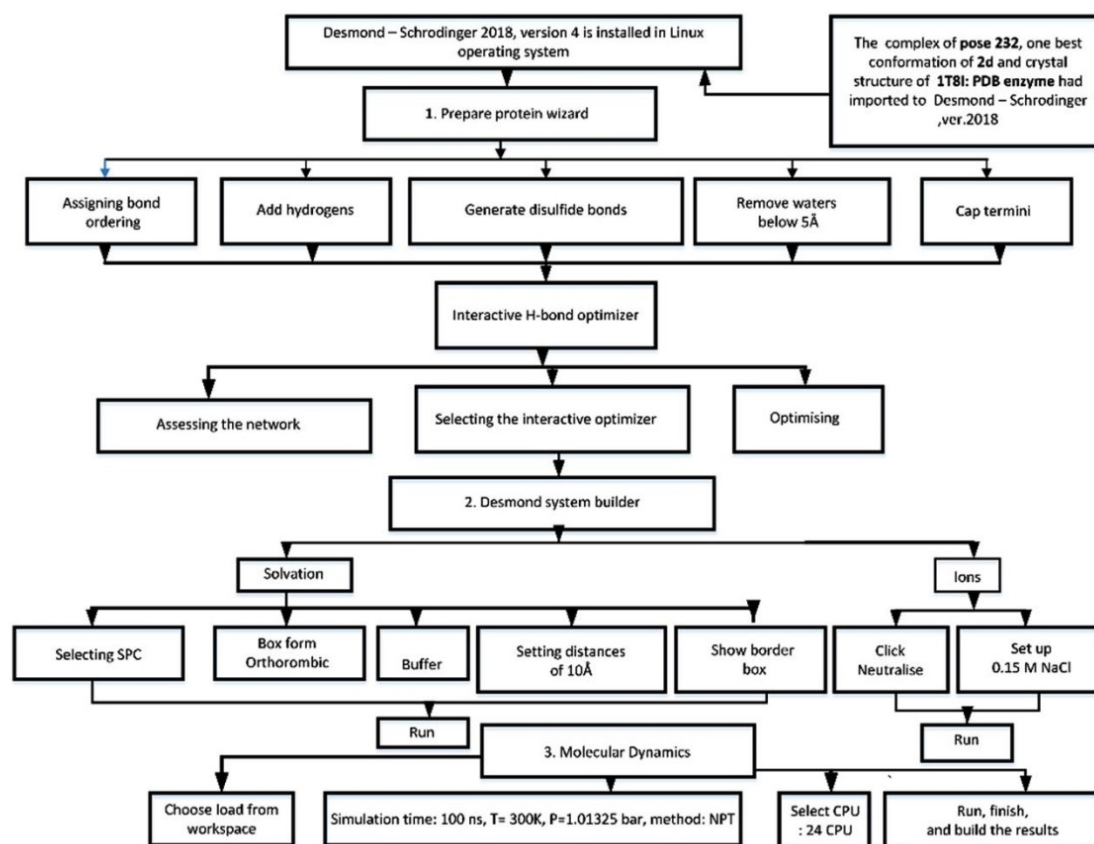
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The Supporting Information file contains spectral characteristics, drug-likeness assessments, and molecular dynamics (MD) simulations, which reinforce the results and interpretations discussed in the main text. Schemes S1–S2 illustrate the docking interactions between the ligands and the receptor, as well as the MD simulation process of compound **4l** (pose 612) with the 4J5T enzyme. Figs. S1 to S82 provide the FT-IR, ¹H NMR, ¹³C NMR, and HR-MS spectral data of compounds **1**, **2**, **3**, and **4a** to **4q**, confirming their structures. Tables S1–S8 present the ADMET (absorption, distribution, metabolism, excretion, and toxicity) profiles, demonstrating the drug-likeness and potential safety of the compounds. Figs S83–S96 provide the *in vitro* antibacterial and antifungal profiles of the synthesised compounds and reference drugs, comprising agar plate assays and minimum inhibitory concentration (MIC) measurements. Figs S97–S102 present the molecular dynamics (MD) simulation results for the **4l**–4J5T complex, illustrating its conformational stability, hydrogen-bonding interactions, and binding behaviour throughout the 100 ns trajectory.

- **Scheme S1.** Framework of docking between ligand and receptor.
- **Scheme S2.** MD simulation of **4l** (pose 612) with 4J5T enzyme.
- **Figs.S1-S82.** FT-IR, ¹H-NMR, ¹³C-NMR, HR-MS spectra of compounds (**1**, **2**, **3**, **4a–4q**).
- **Table S1.** Physicochemical properties of compound **4l**.
- **Table S2.** Medicinal chemistry descriptors of compound **4l**.
- **Table S3.** Absorption properties of compound **4l**.
- **Table S4.** Distribution properties of compound **4l**.
- **Table S5.** Metabolism properties of compound **4l**.
- **Table S6.** Excretion properties of compound **4l**.
- **Table S7.** Toxicity profiles of compound **4l**.
- **Table S8.** Toxicophoric alerts of compound **4l**.
- **Figs. S83-S96.** Supplements on the inhibitory potential *in vitro* bioactivity of compounds and positive controls
- **Figs. S97-S102.** Result MD of **4l**–4J5T complex



Scheme S1. The overarching framework of docking between a ligand and a receptor/compound is illustrated by an enzyme or the crystalline structure of an enzyme, such as 1T8I, 4WCU, and 4J5T.



Scheme S2. Procedure to simulate complex pose 612 or compound 4l and the crystal structure of 4J5T enzyme by NPT method via Desmond software, version 2018, in Linux OS.

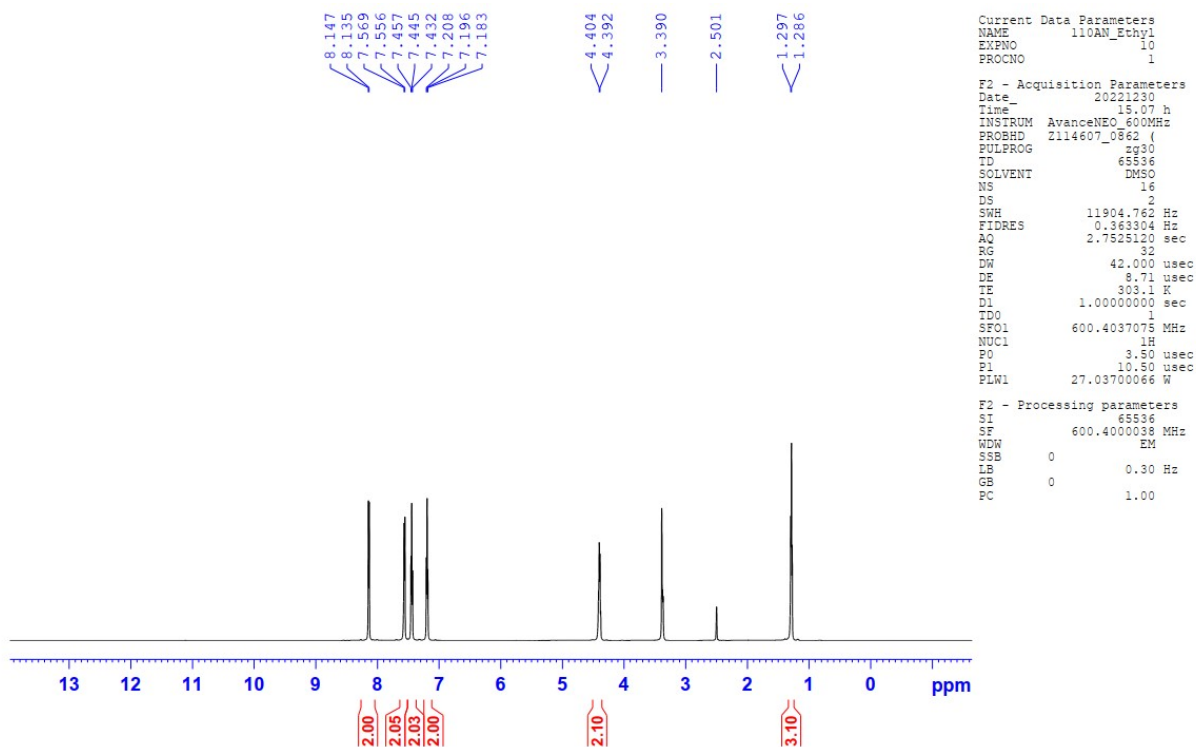


Fig. S 1. ¹H-NMR spectrum of compound 1.

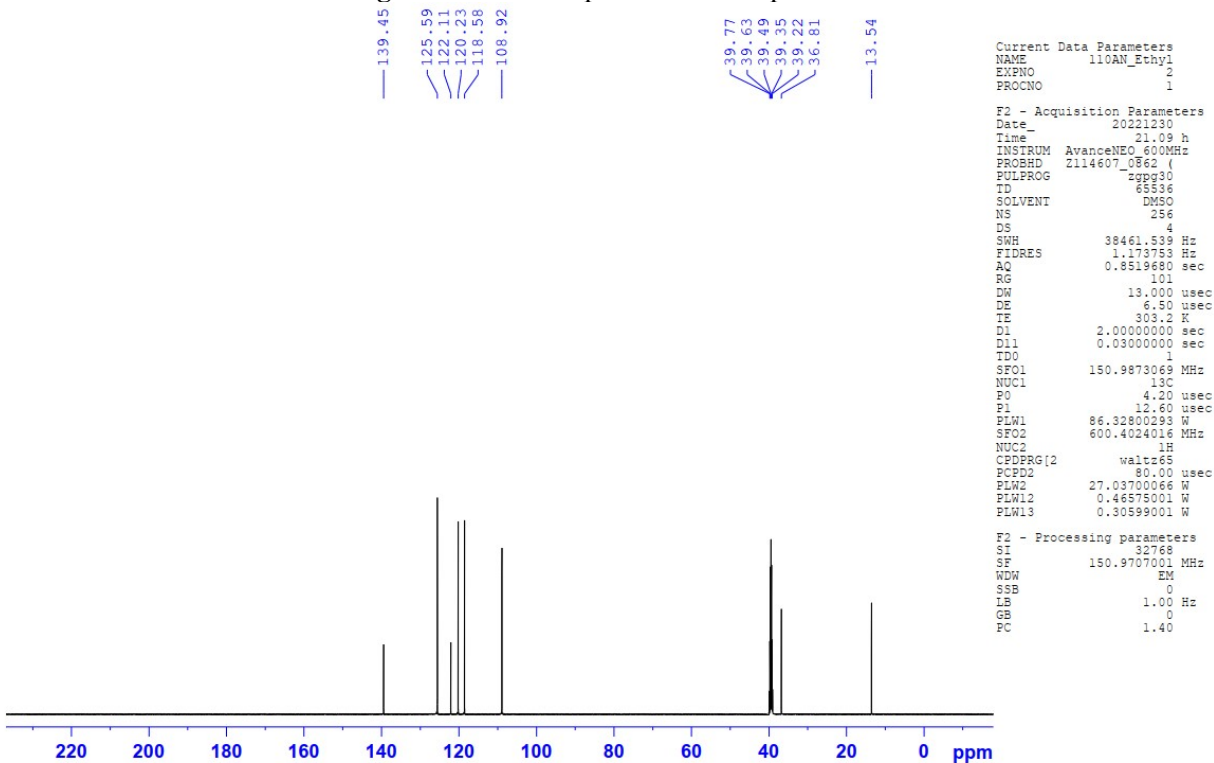


Fig. S 2. ¹³C-NMR spectrum of compound 1.

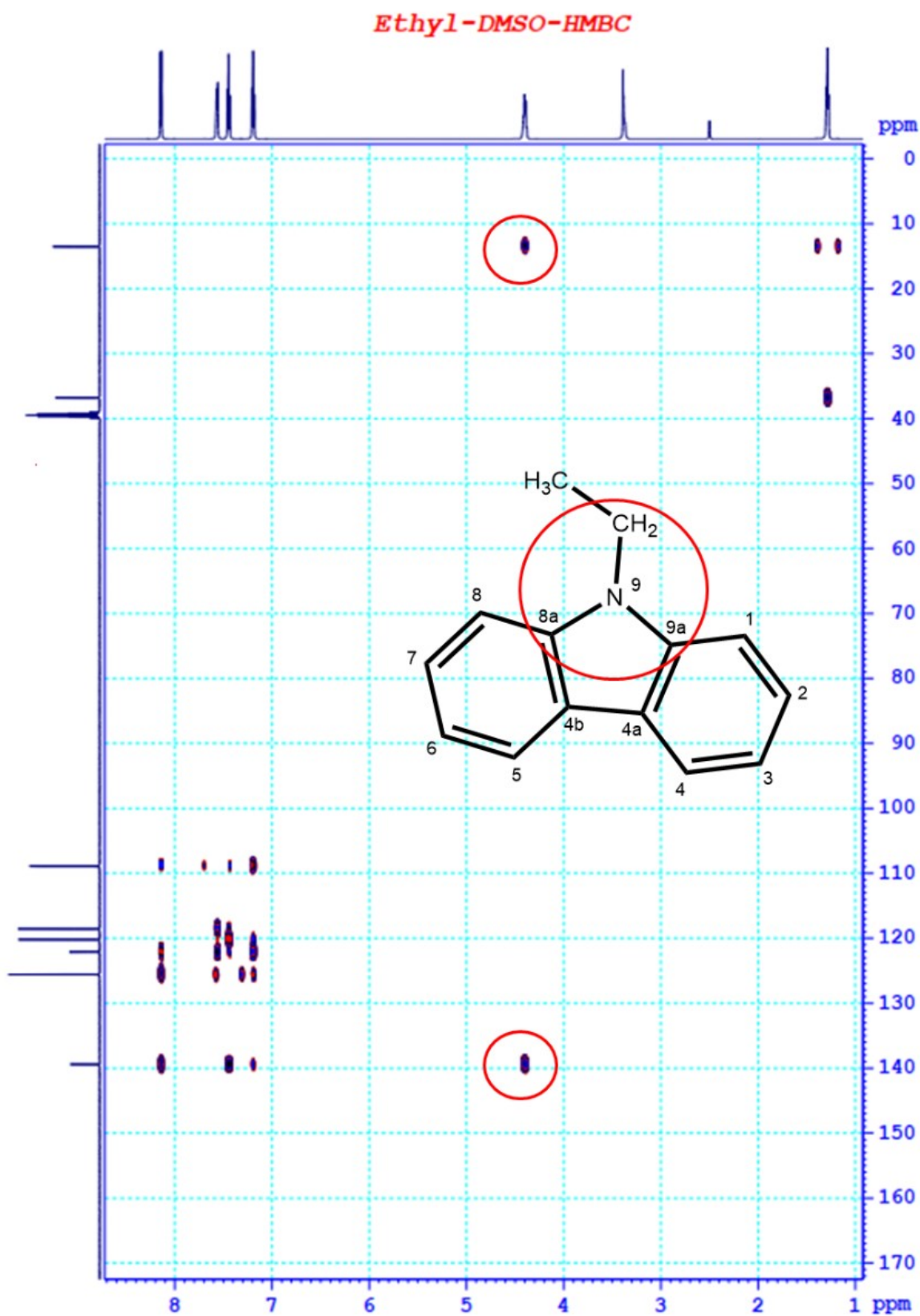


Fig. S 3. HMBC spectrum of compound 1.

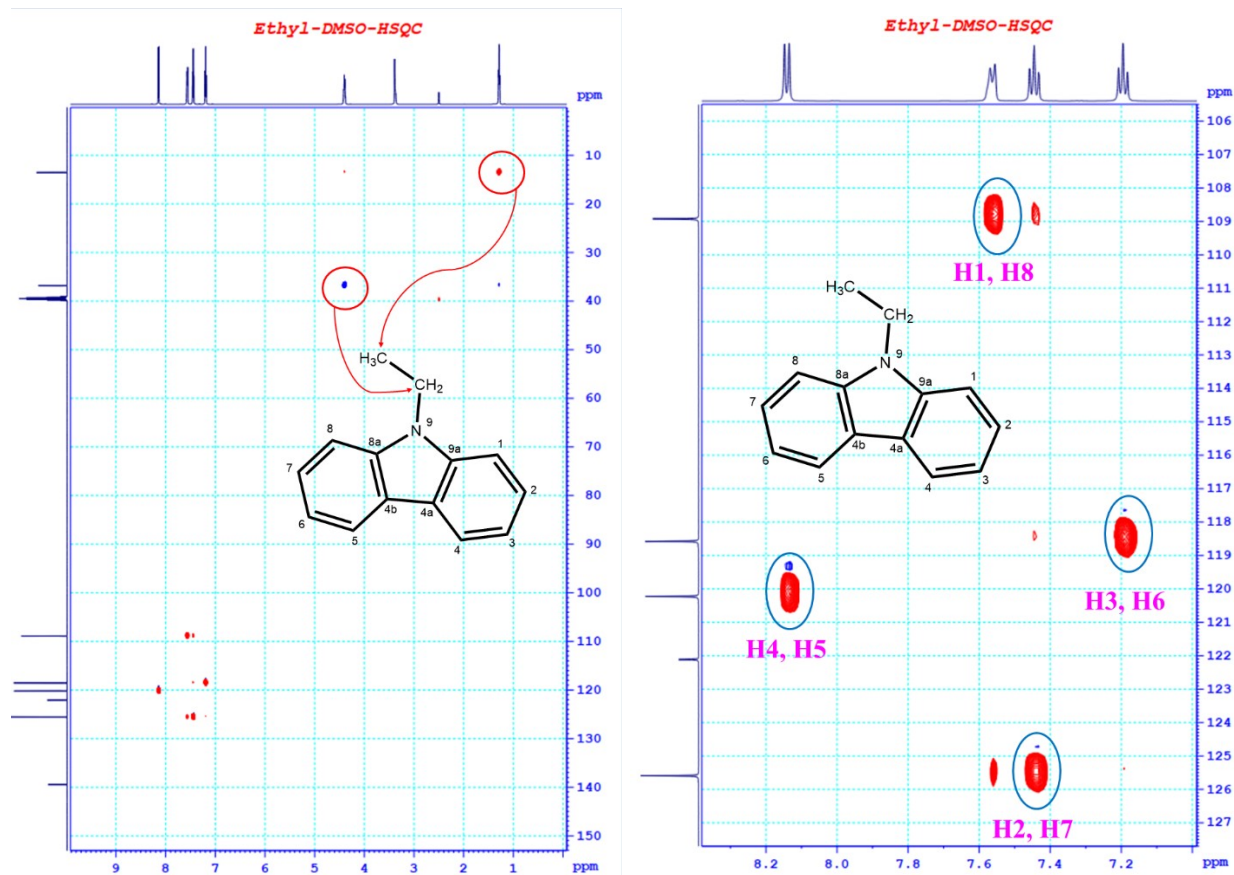


Fig. S 4. HSQC spectrum of compound 1.

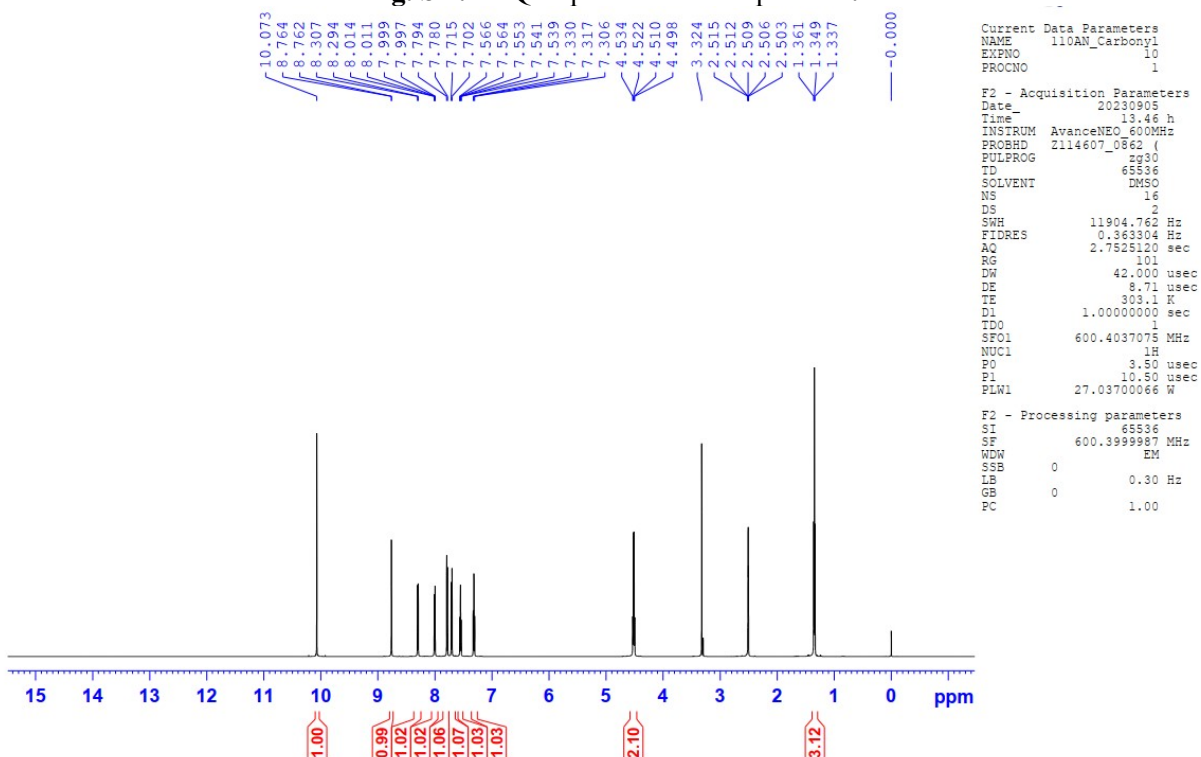


Fig. S 5. ¹H-NMR spectrum of compound 2.

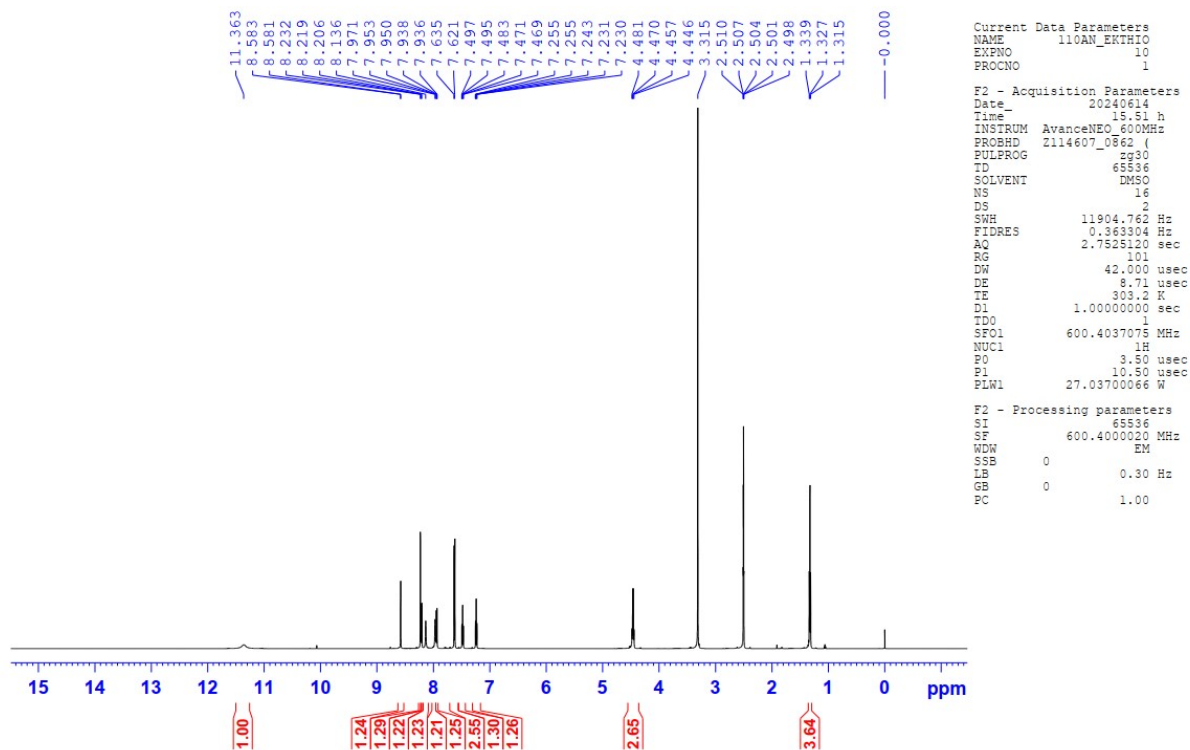


Fig. S 6. ¹H-NMR spectrum of compound 3.

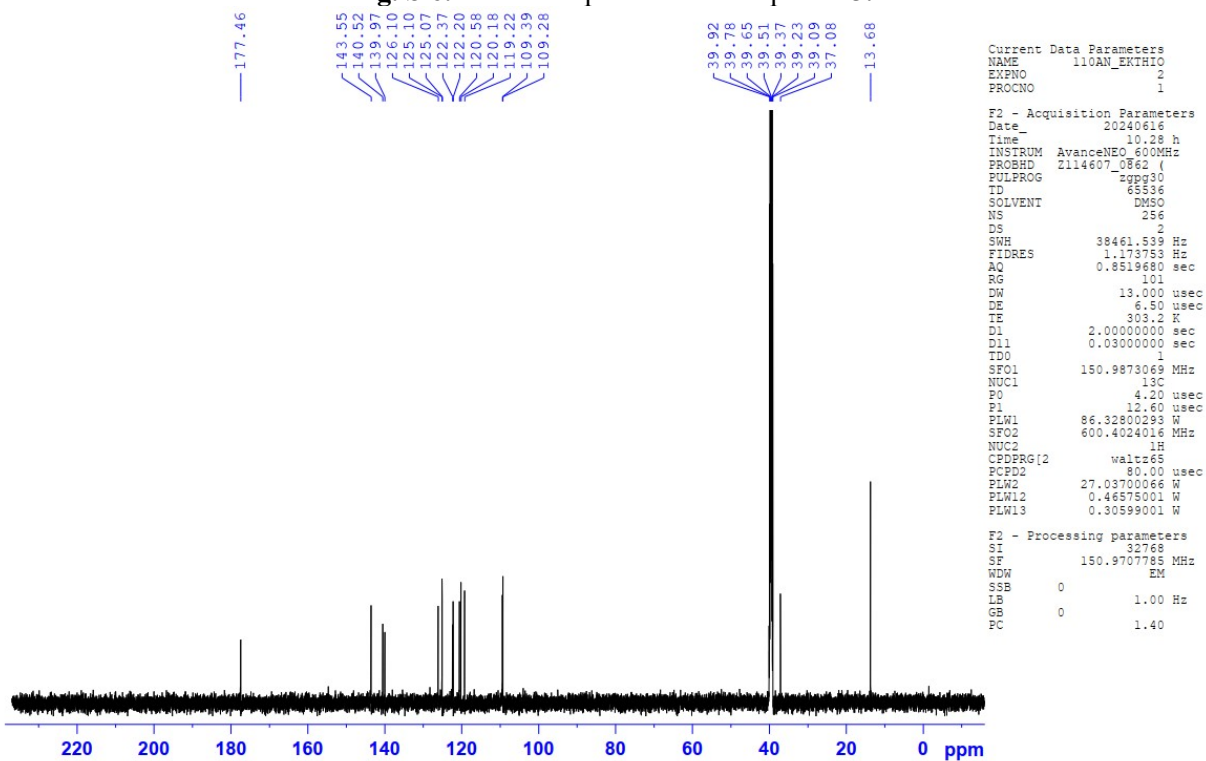


Fig. S 7. ¹³C-NMR spectrum of compound 3.

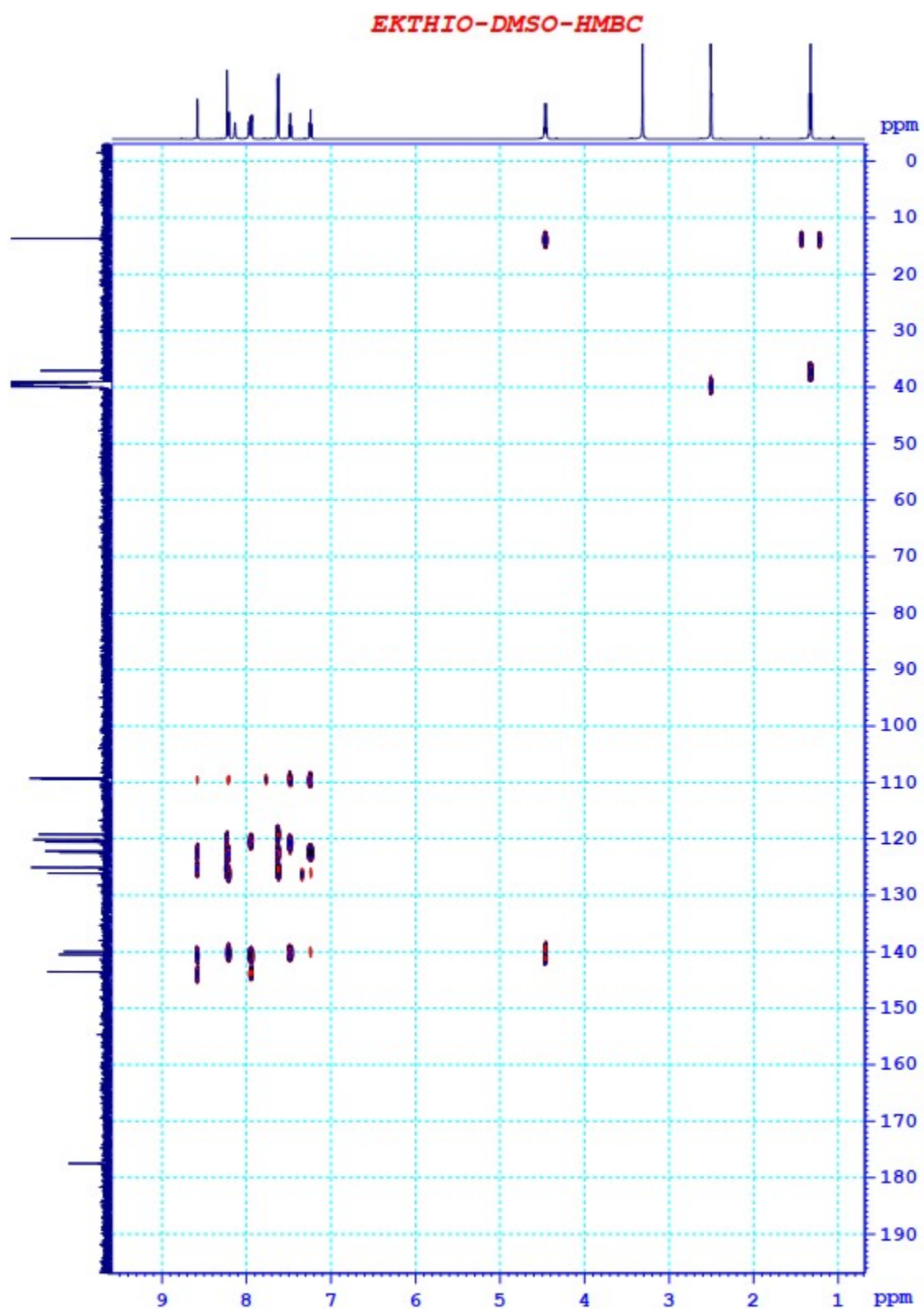


Fig. S 8. HMBC spectrum of compound 3.

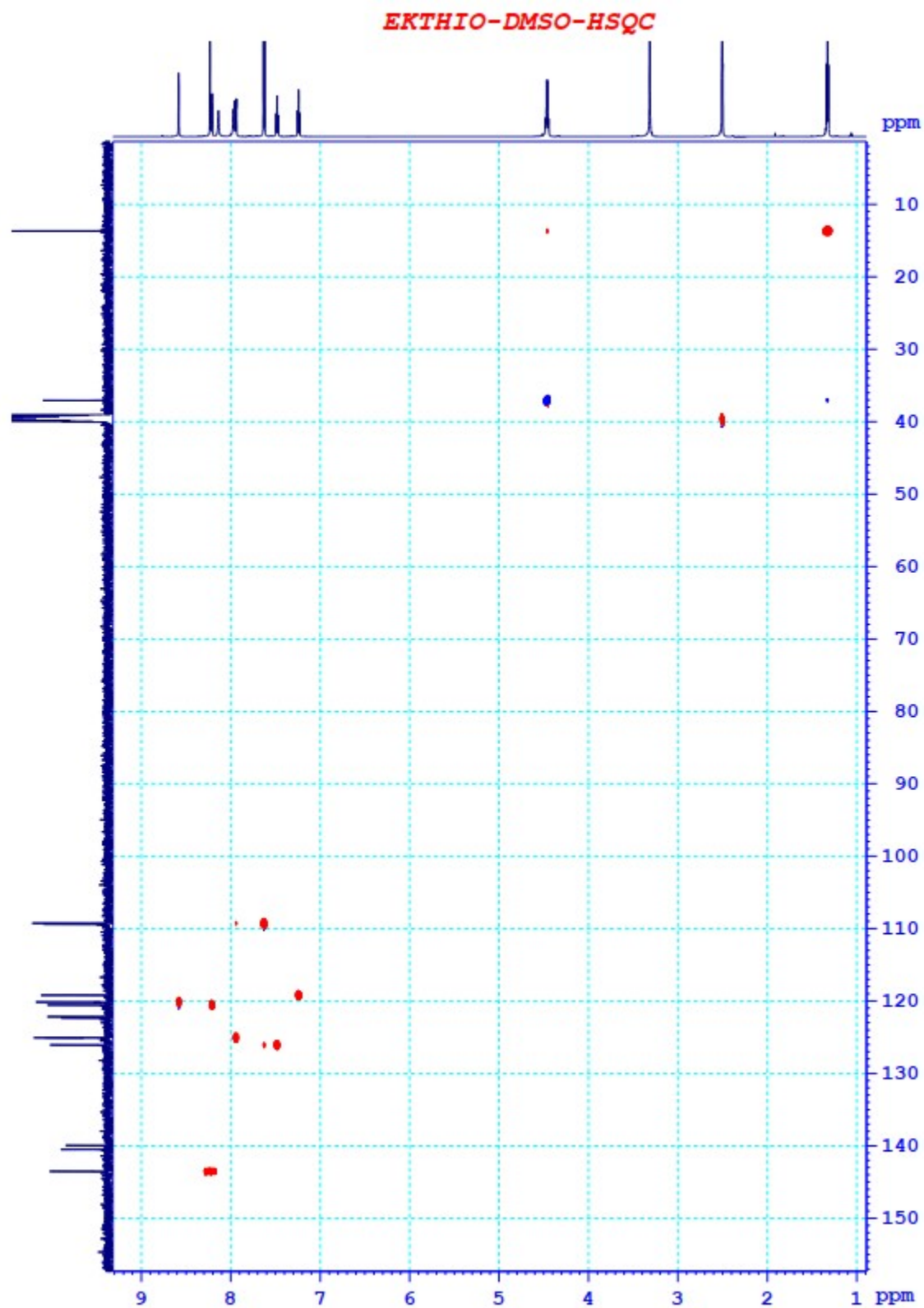


Fig. S 9. HSQC spectrum of compound 3.

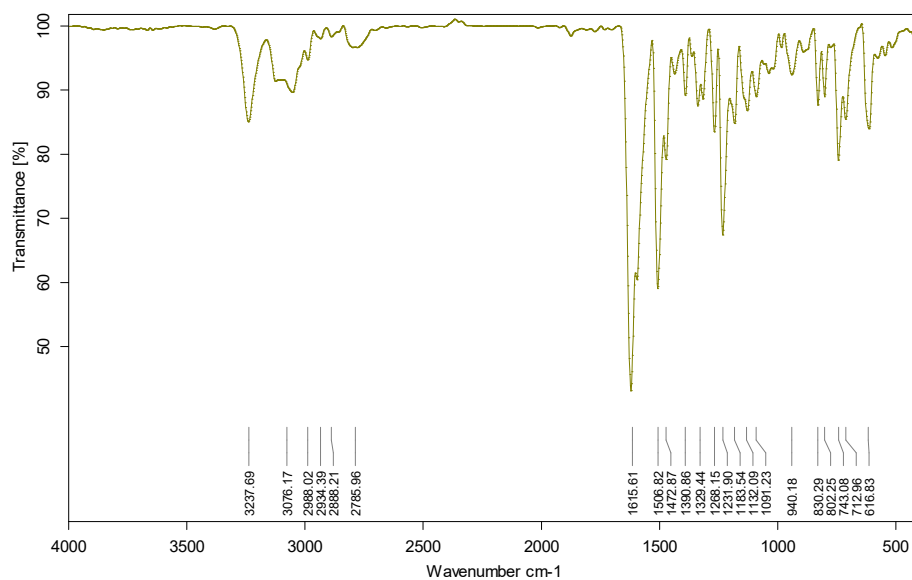


Fig. S 10. FT-IR spectrum of compound 4a.

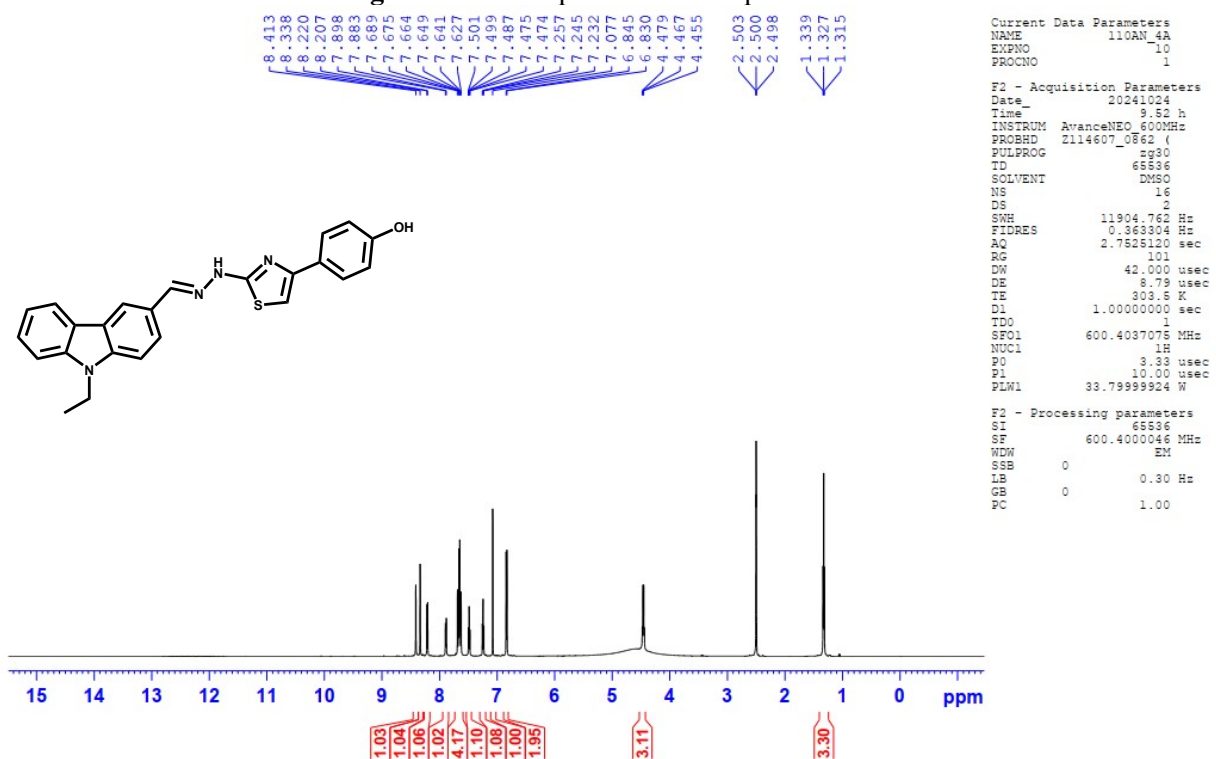


Fig. S 11. ¹H-NMR spectrum of compound 4a.

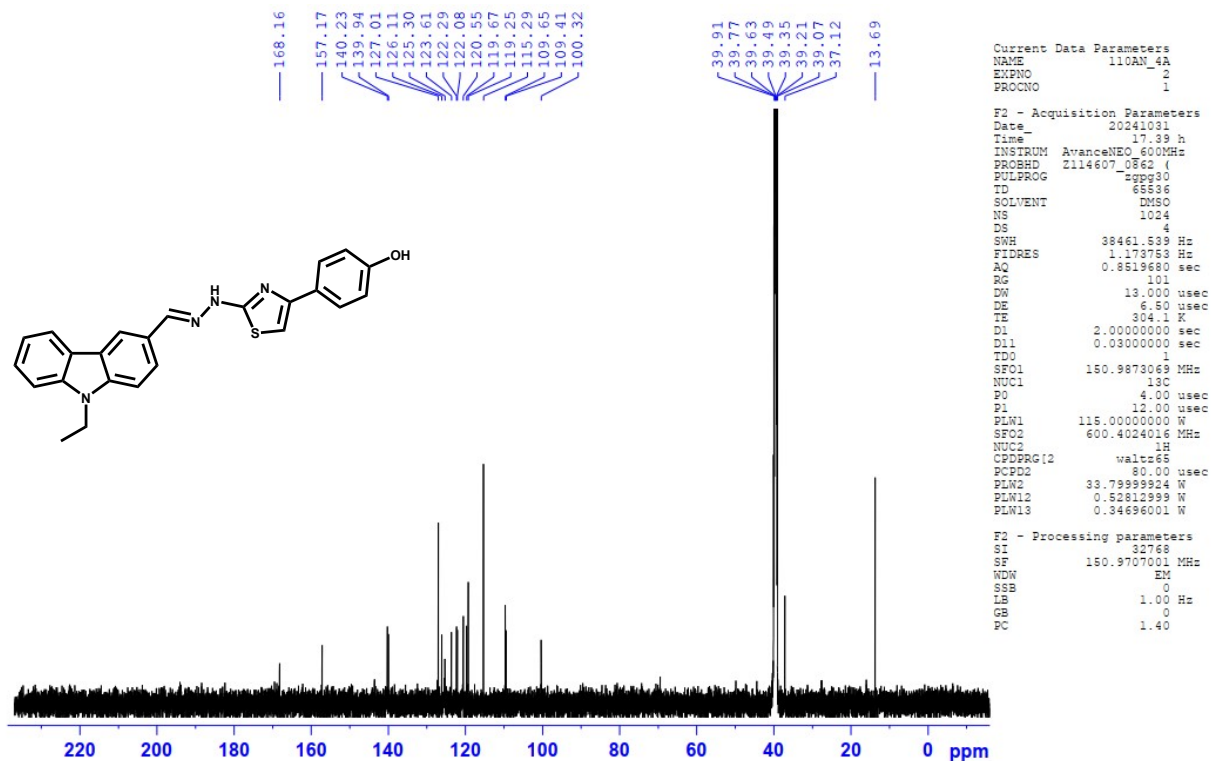


Fig. S 12. ¹³C-NMR spectrum of compound 4a.

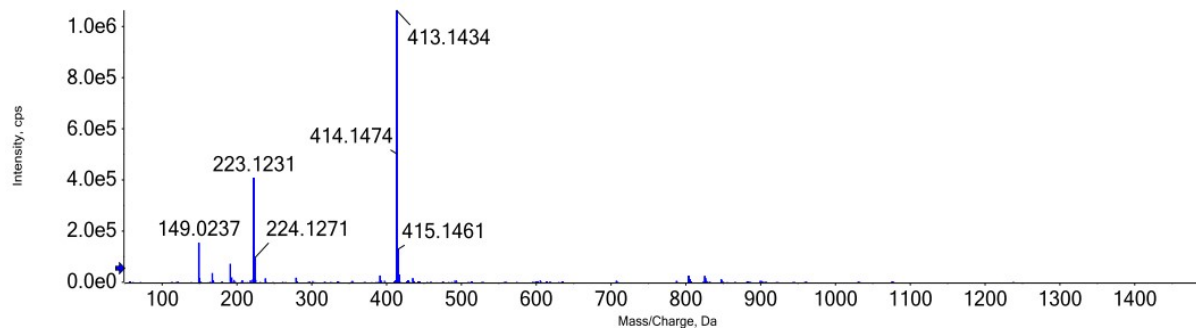


Fig. S 13. HR-MS spectrum of compound 4a.

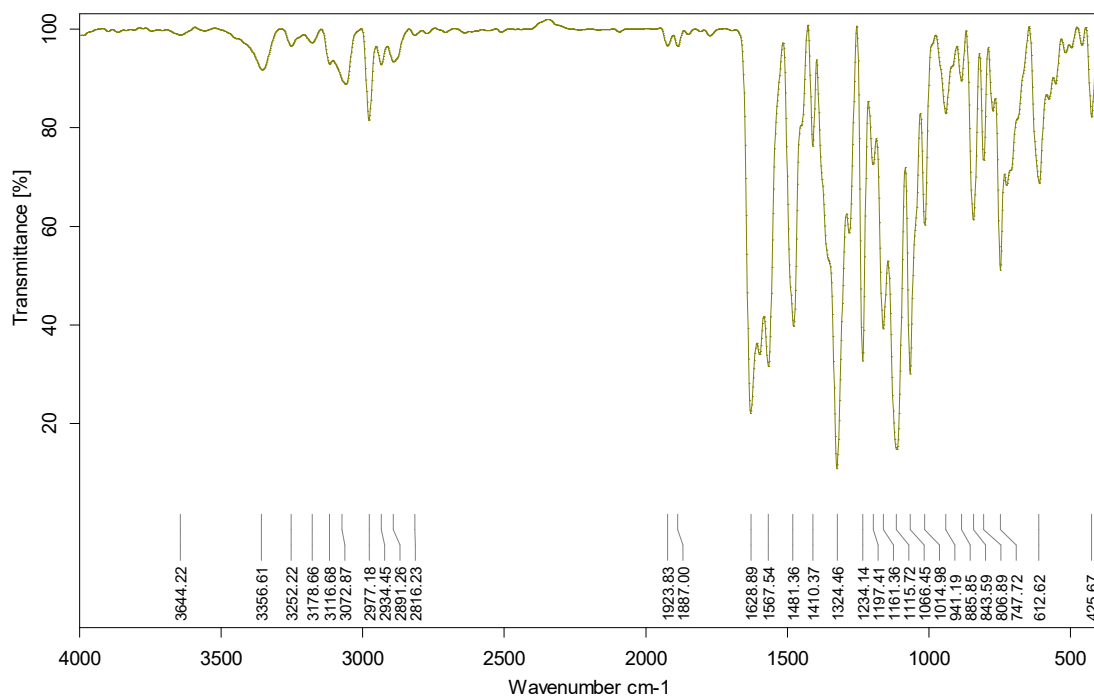


Fig. S 14. FT-IR spectrum of compound 4b.

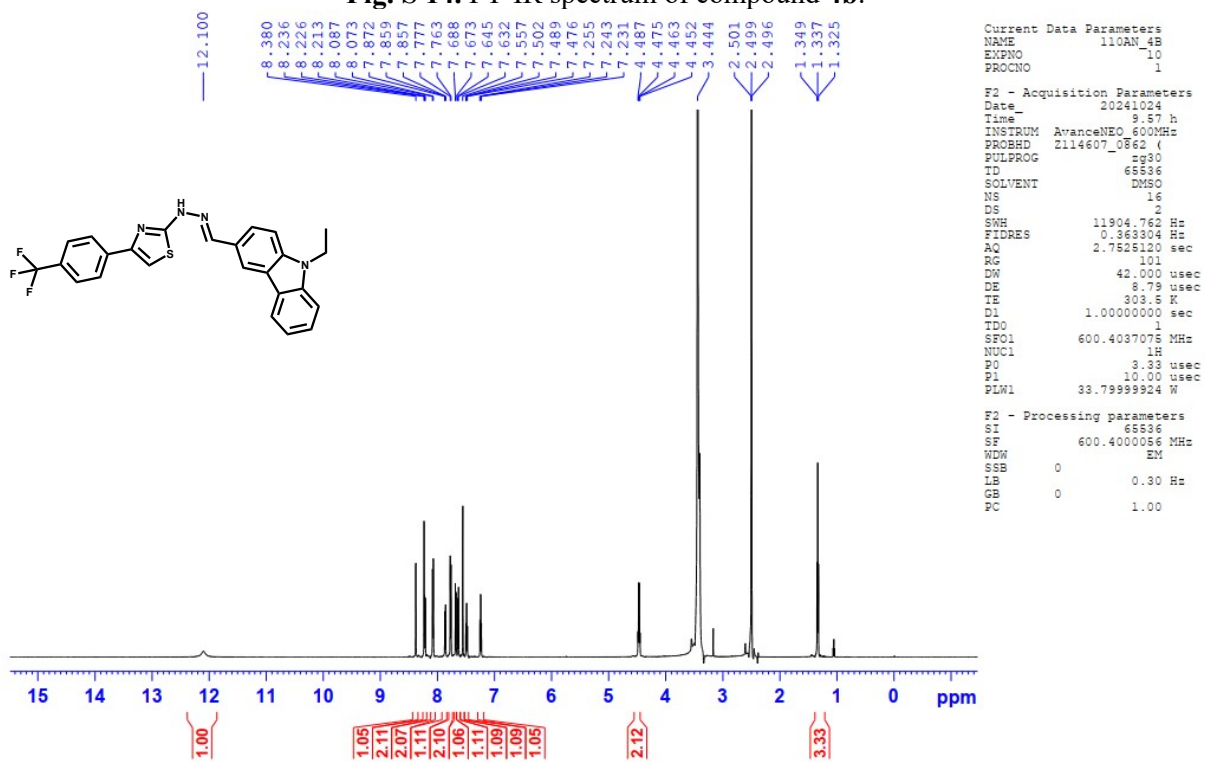


Fig. S 15. ¹H-NMR spectrum of compound 4b.

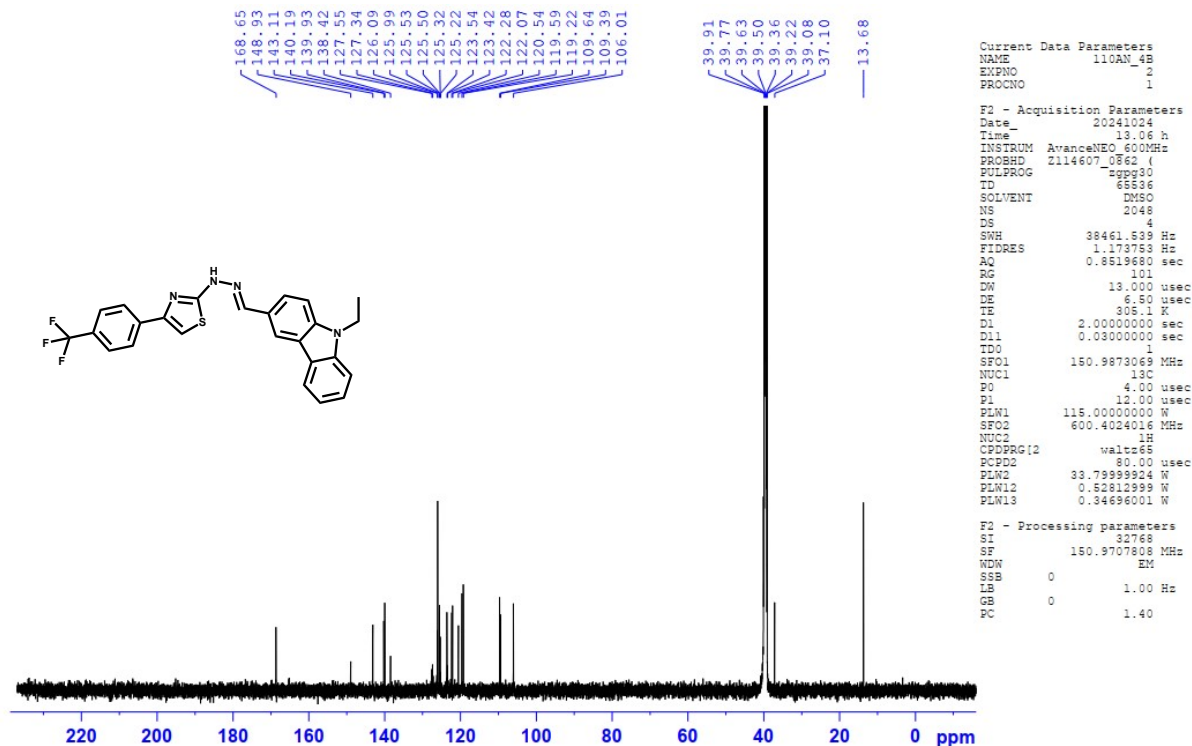


Fig. S 16. ^{13}C -NMR spectrum of compound 4b.

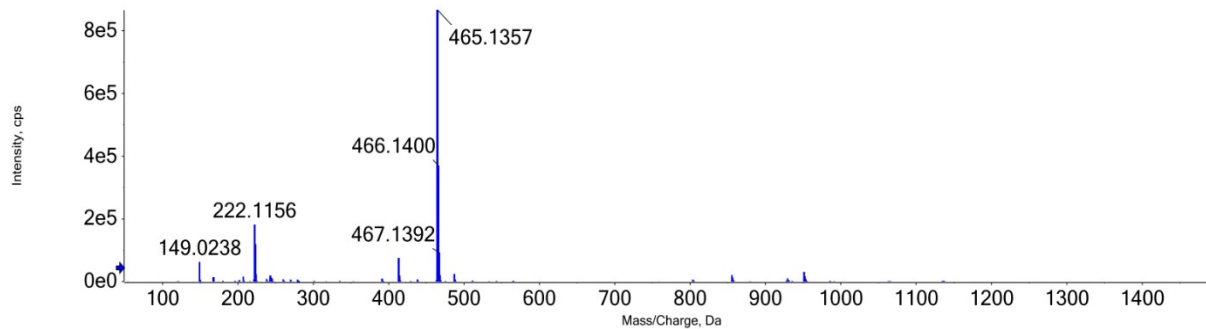


Fig. S 17. HR-MS spectrum of compound 4b.

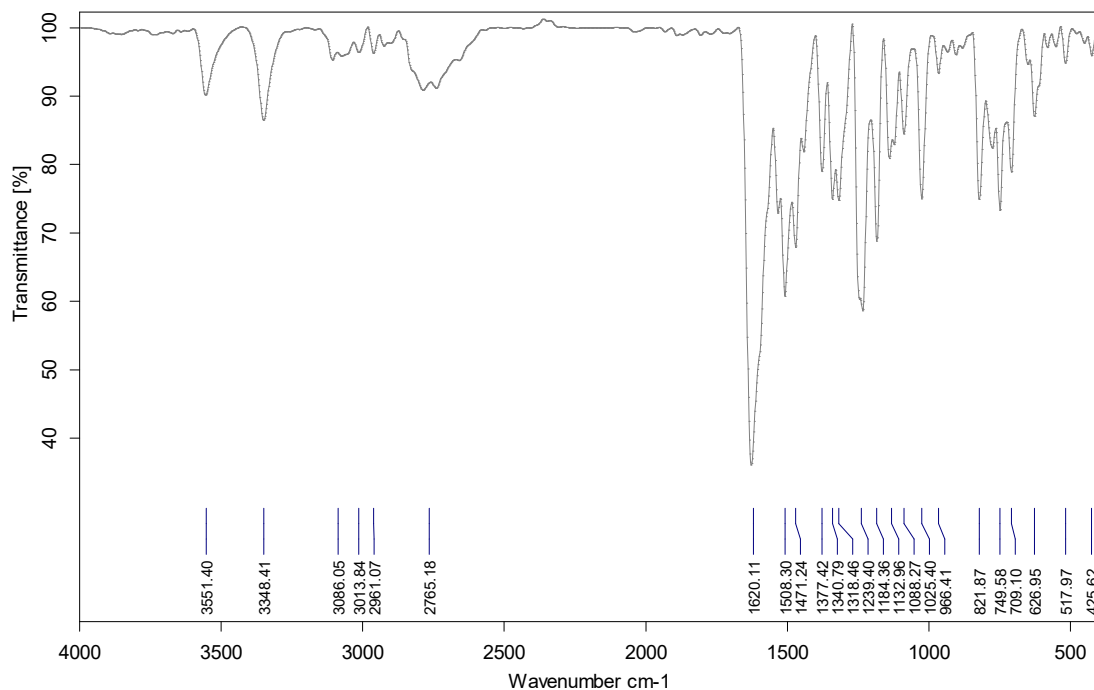


Fig. S 18. FT-IR spectrum of compound 4c.

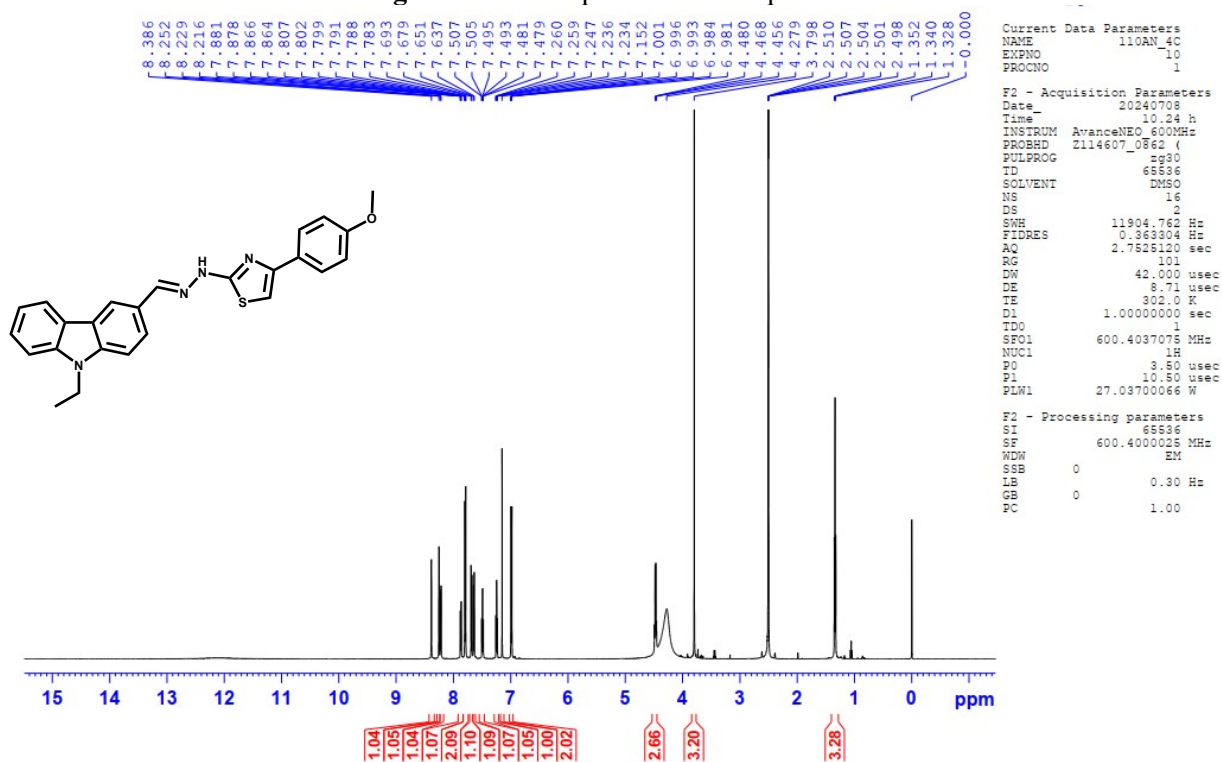


Fig. S 19. ¹H-NMR spectrum of compound 4c.

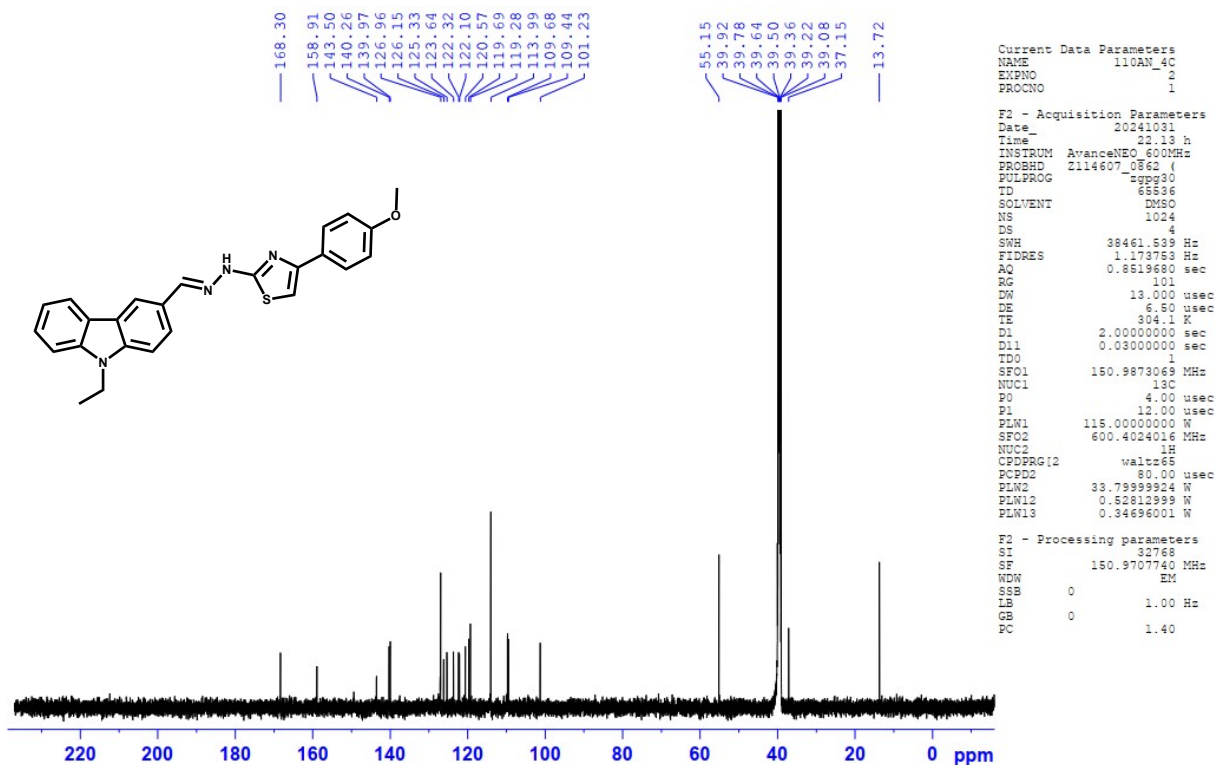


Fig. S 20. ¹³C-NMR spectrum of compound 4c.

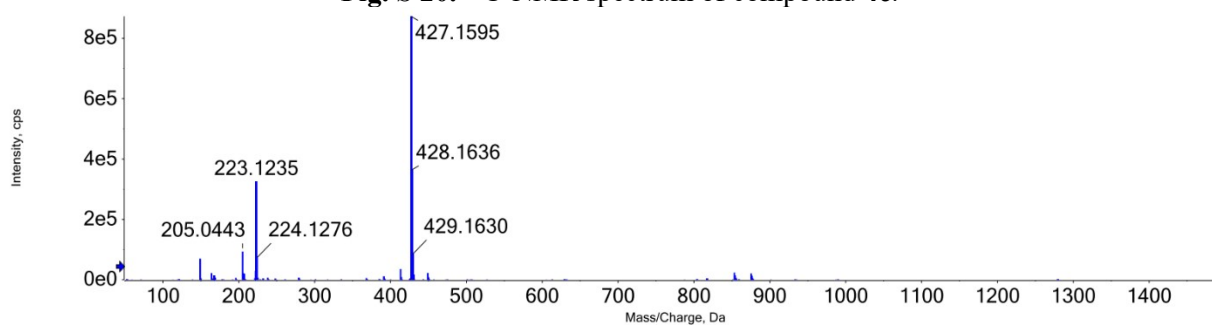


Fig. S 21. HR-MS spectrum of compound 4c.

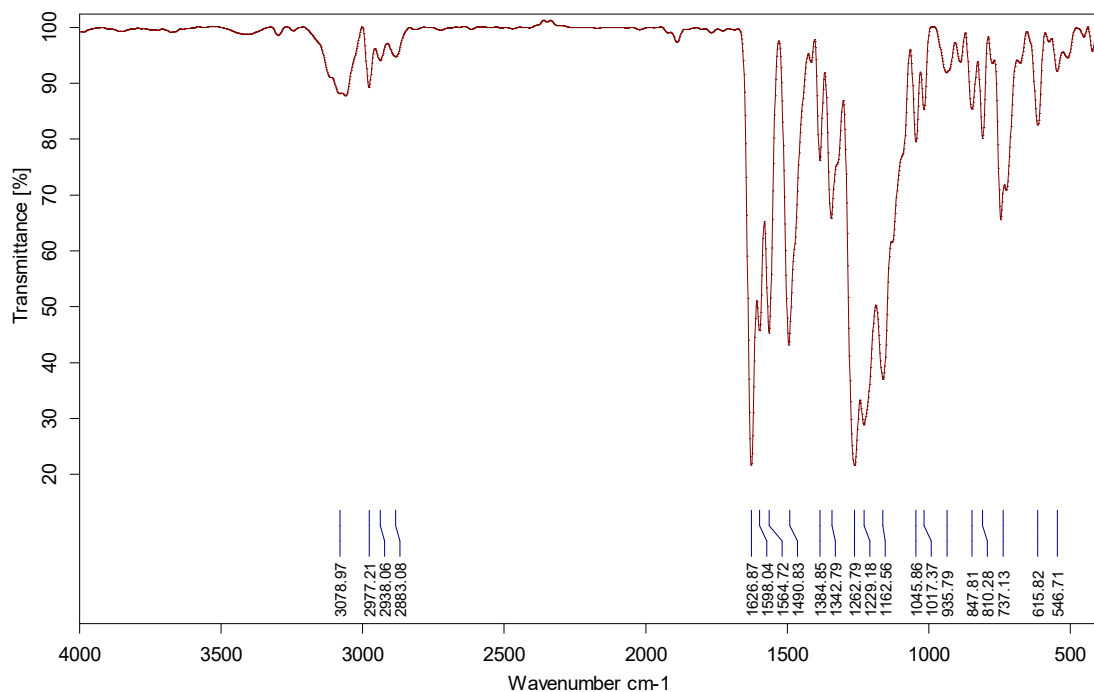


Fig. S 22. FT-IR spectrum of compound 4d.

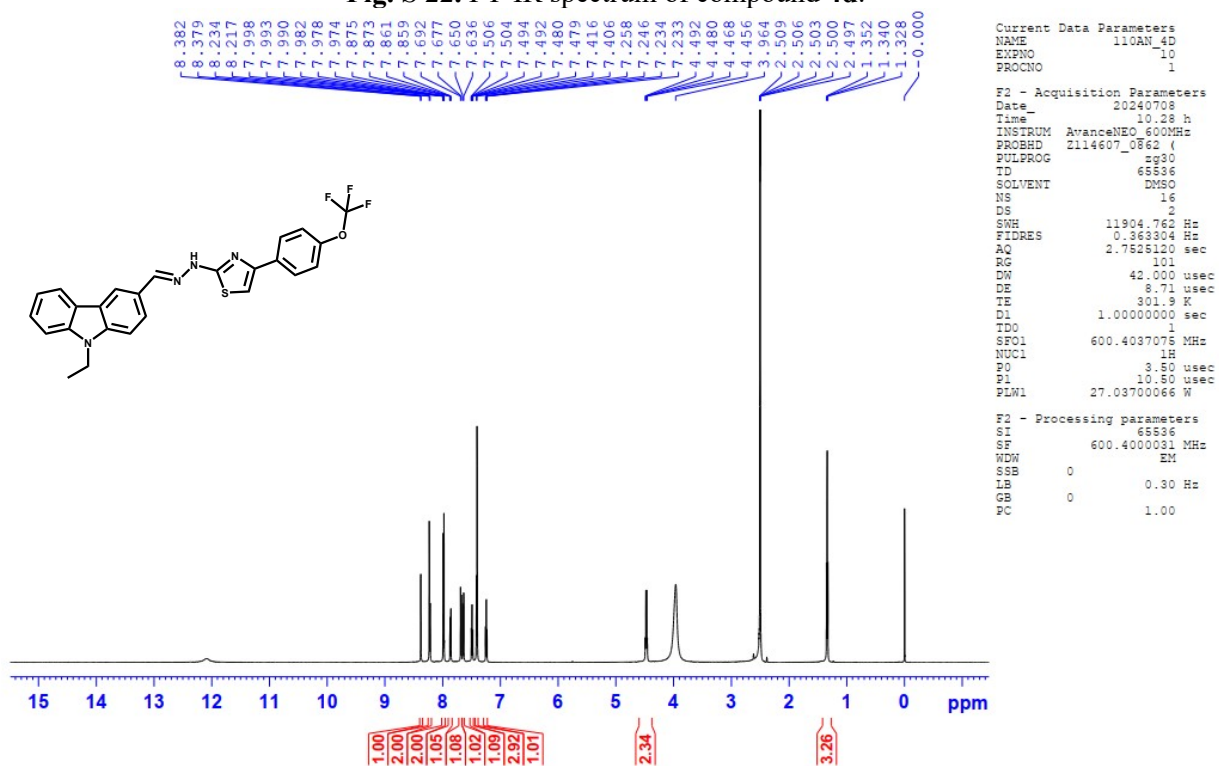


Fig. S 23. ¹H-NMR spectrum of compound 4d.

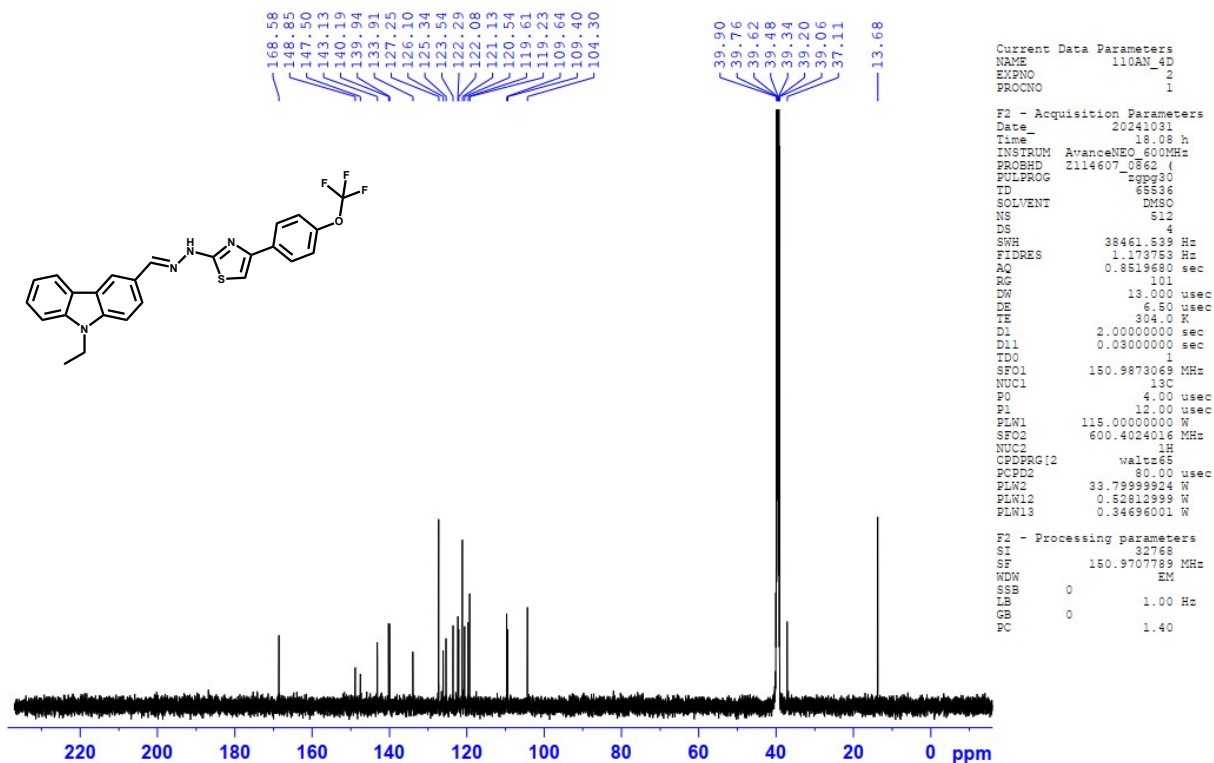


Fig. S 24. ¹³C-NMR spectrum of compound 4d.

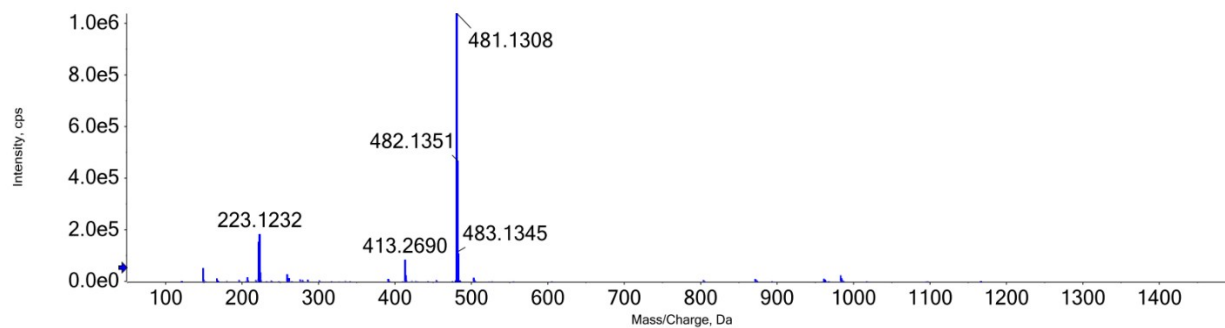


Fig. S 25. HR-MS spectrum of compound 4d.

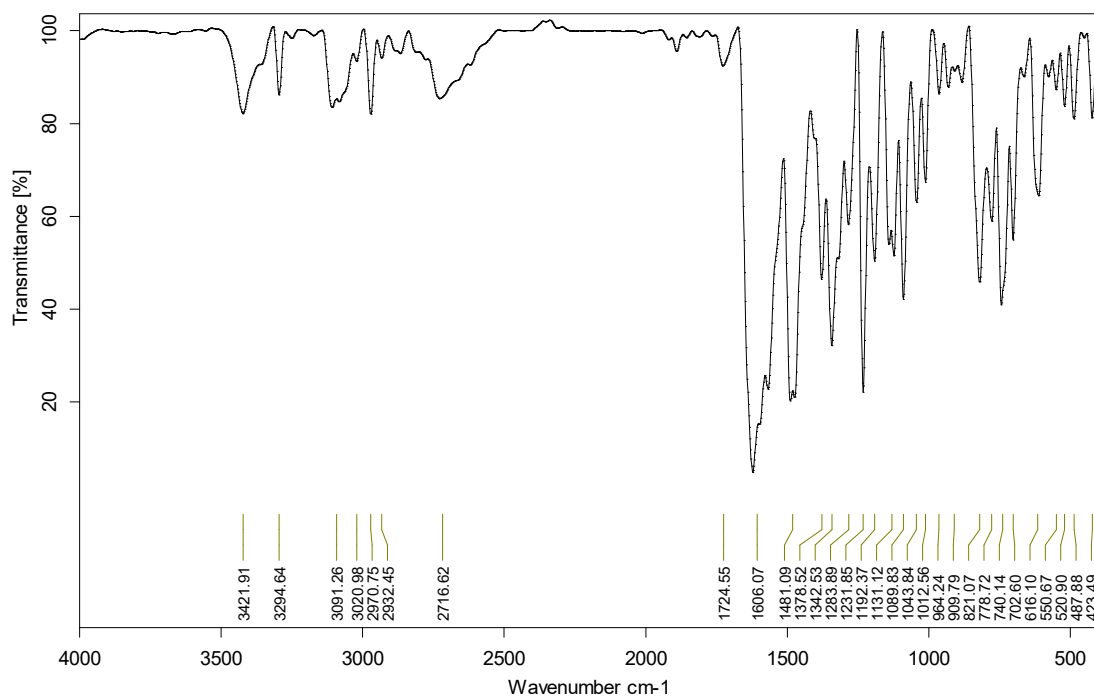


Fig. S 26. FT-IR spectrum of compound 4e.

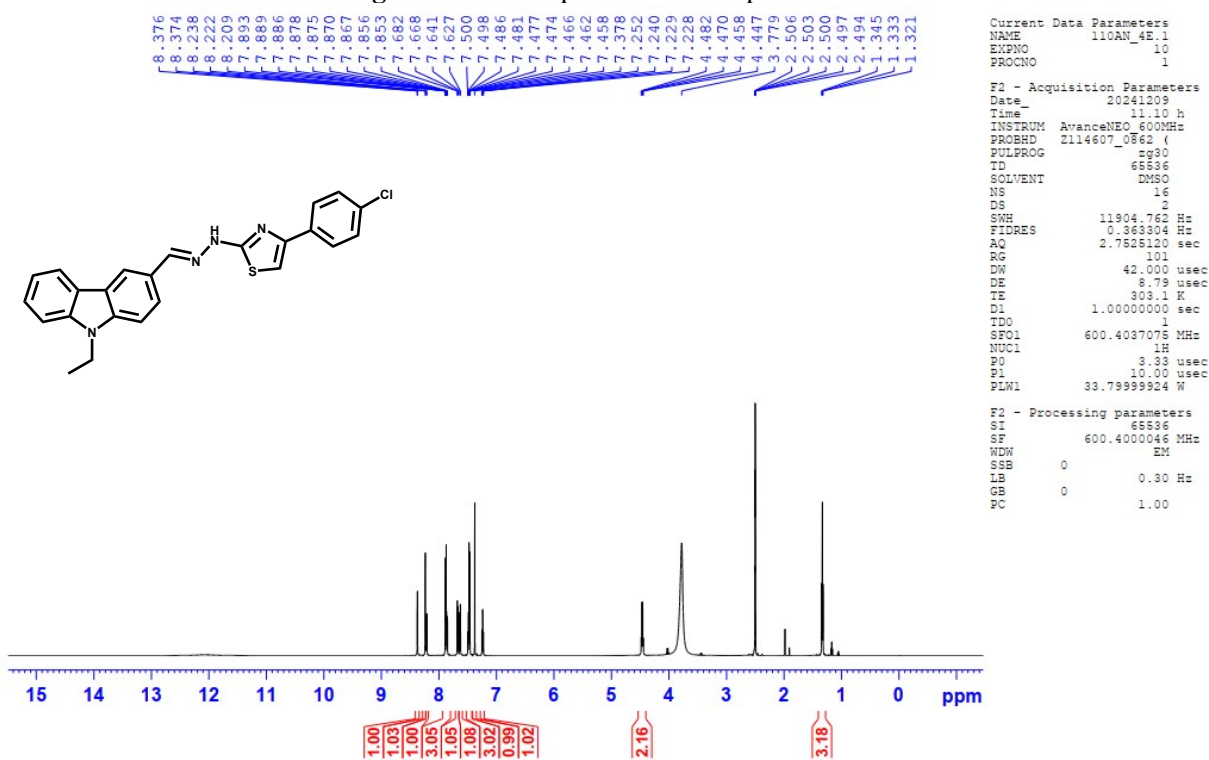


Fig. S 27. ¹H-NMR spectrum of compound 4e.

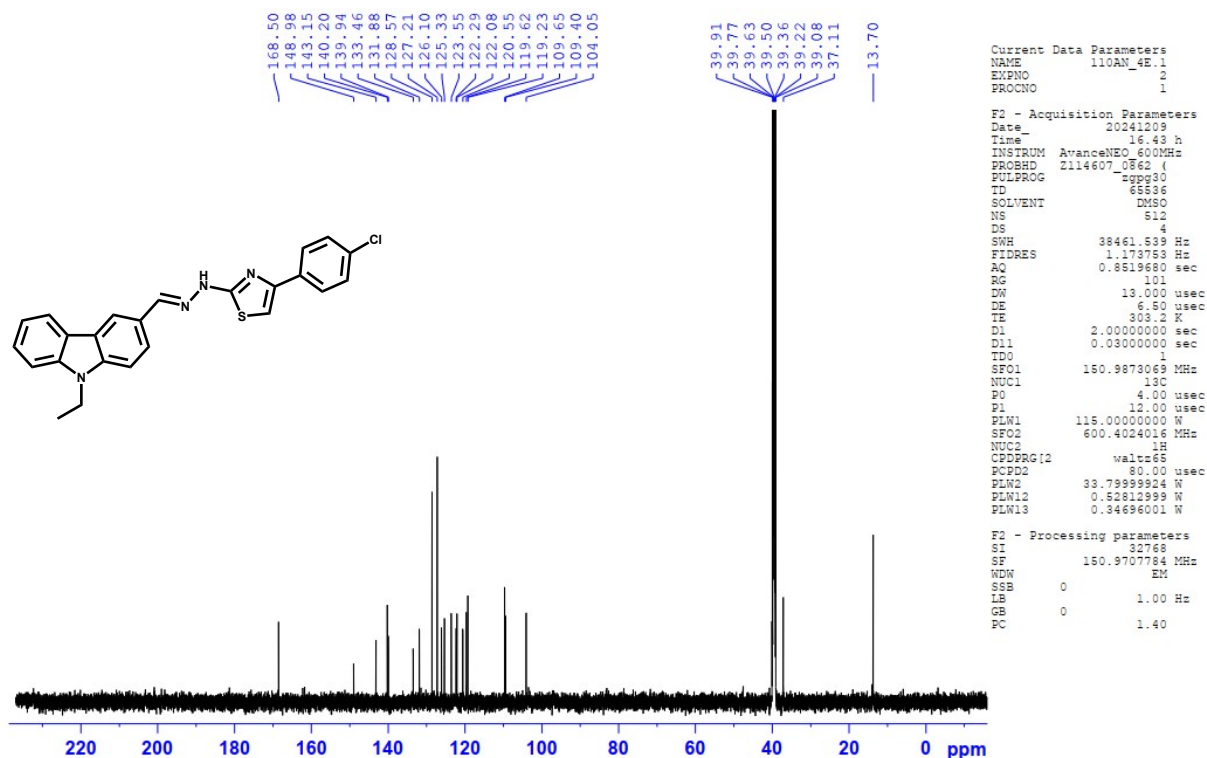


Fig. S 28. ^{13}C -NMR spectrum of compound 4e.

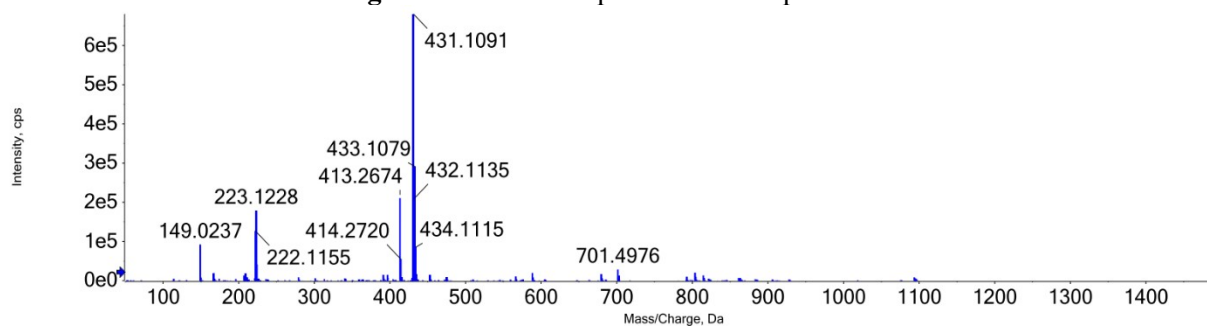


Fig. S 29. HR-MS spectrum of compound 4e.

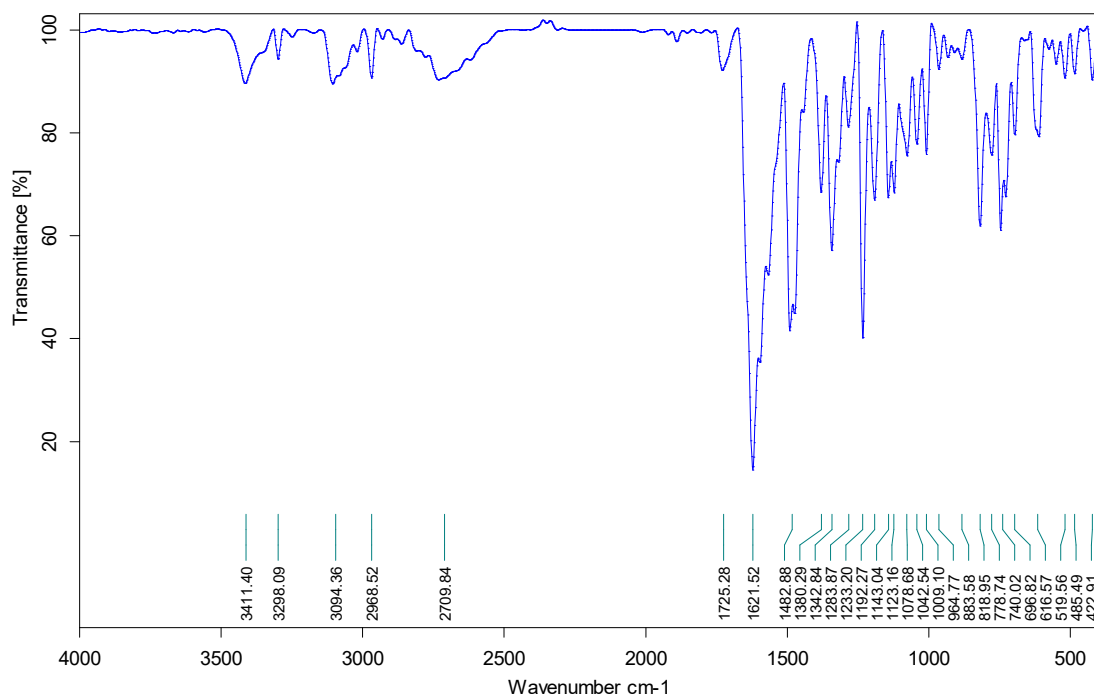


Fig. S 30. FT-IR spectrum of compound 4f.

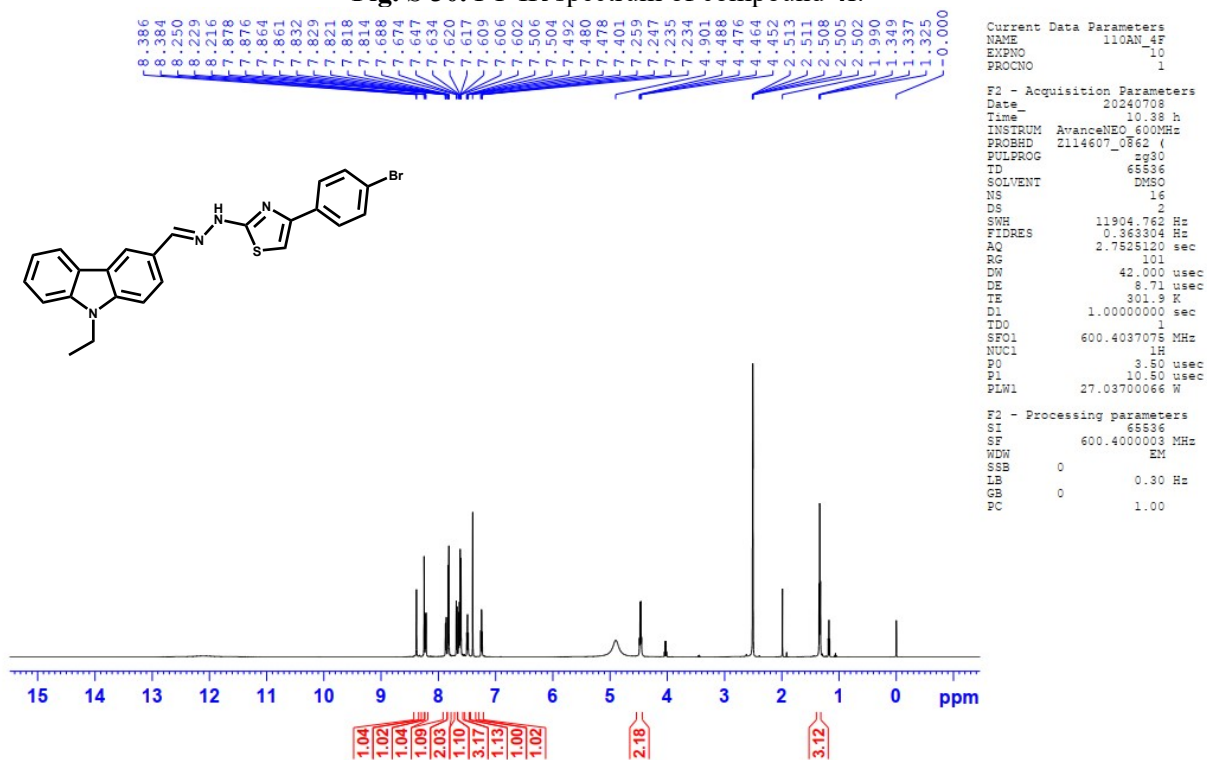


Fig. S 31. ¹H-NMR spectrum of compound 4f.

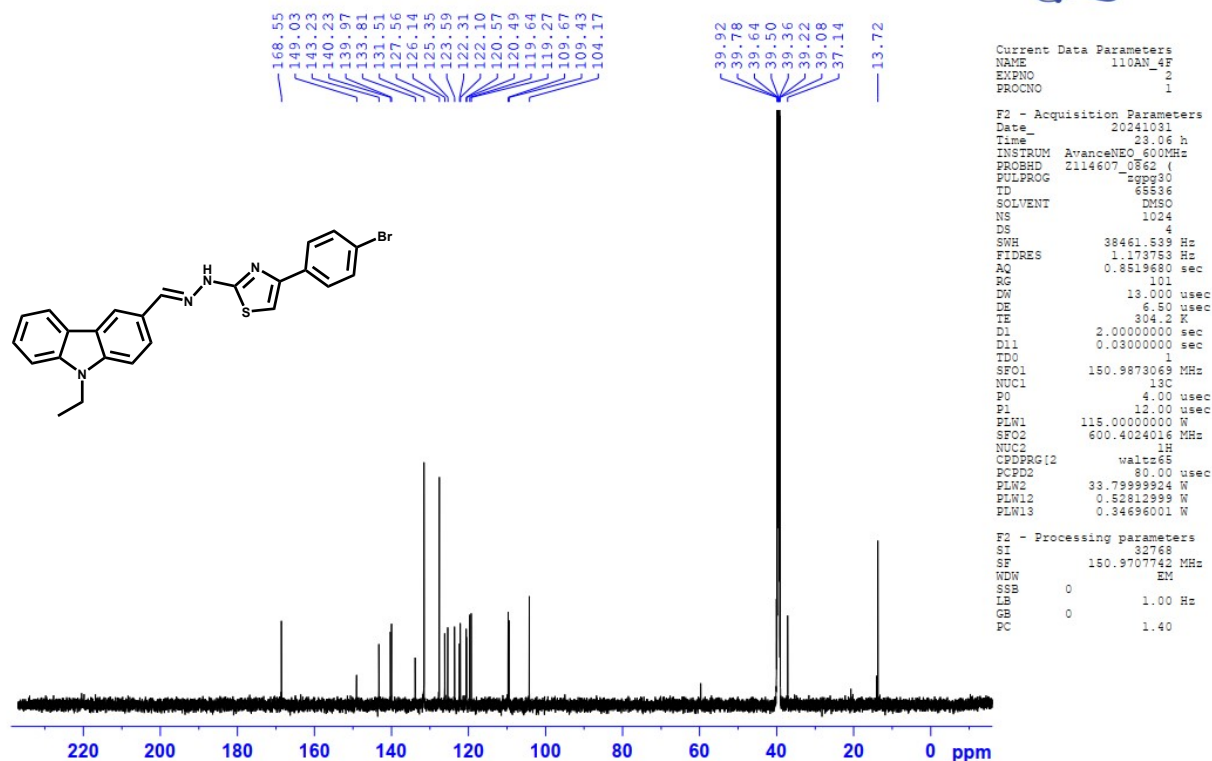


Fig. S 32. ¹³C-NMR spectrum of compound 4f.

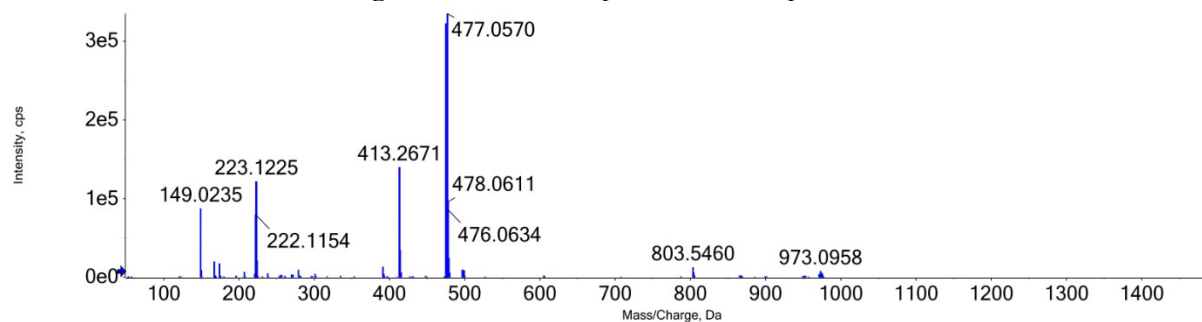


Fig. S 33. HR-MS spectrum of compound 4f.

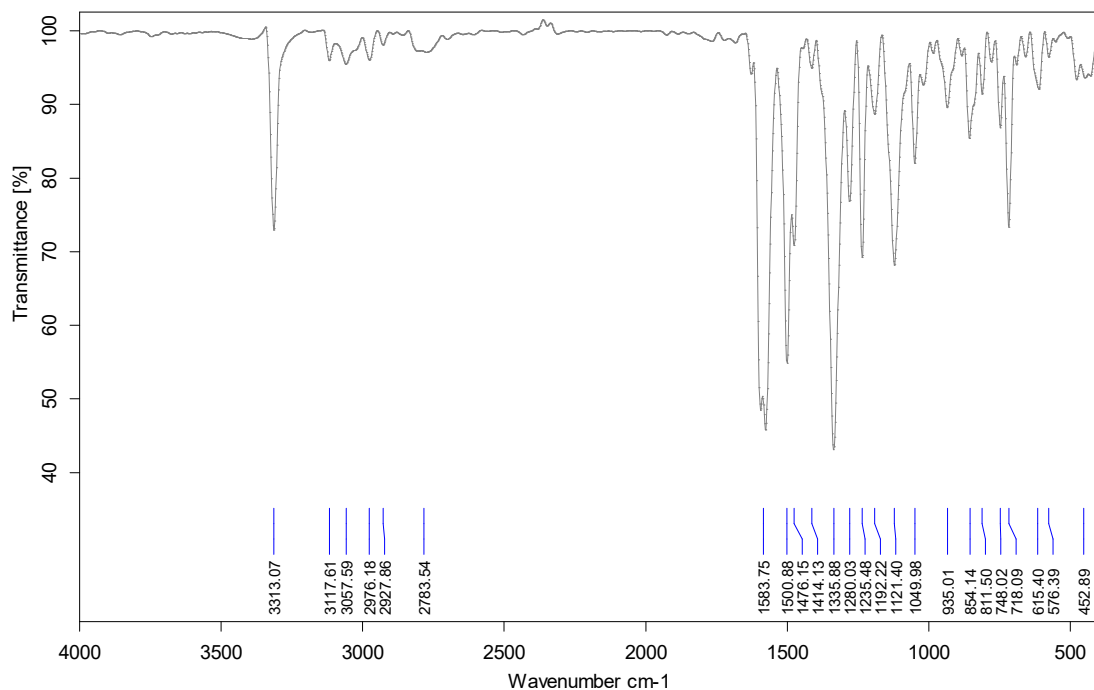


Fig. S 34. FT-IR spectrum of compound **4g**.

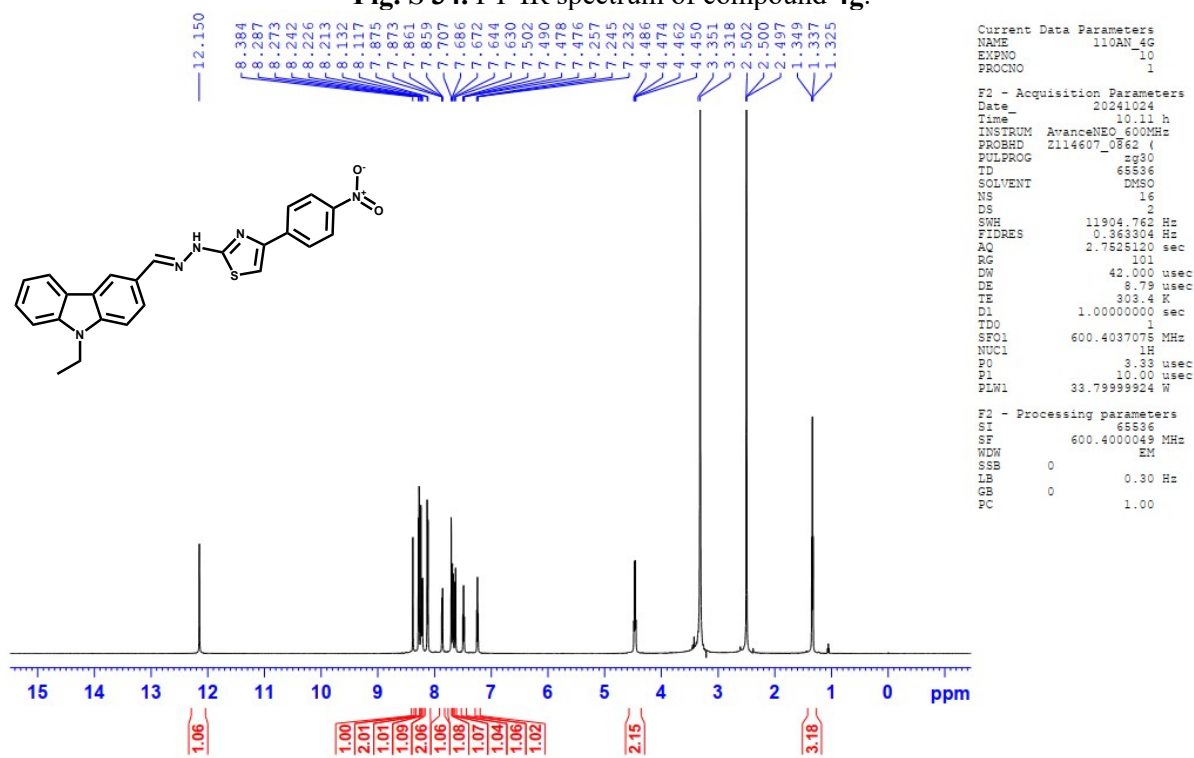


Fig. S 35. ¹H-NMR spectrum of compound **4g**.

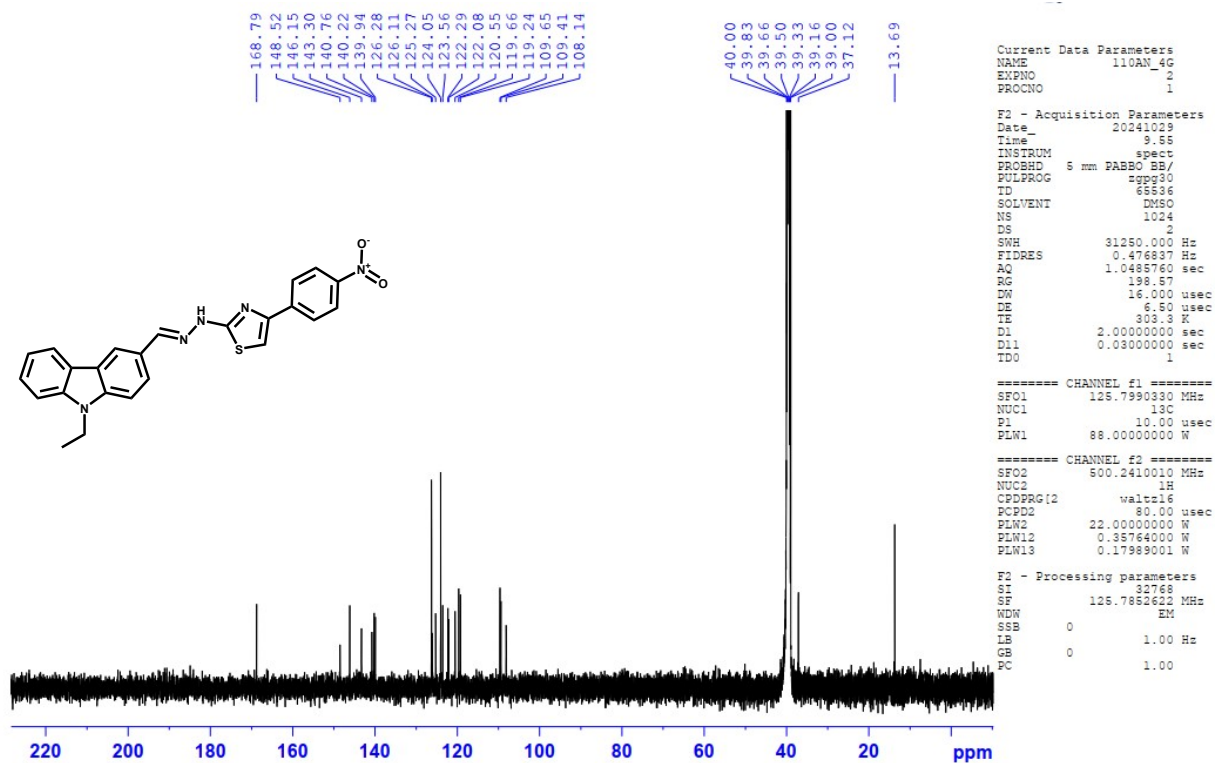


Fig. S 36. ¹³C-NMR spectrum of compound 4g.

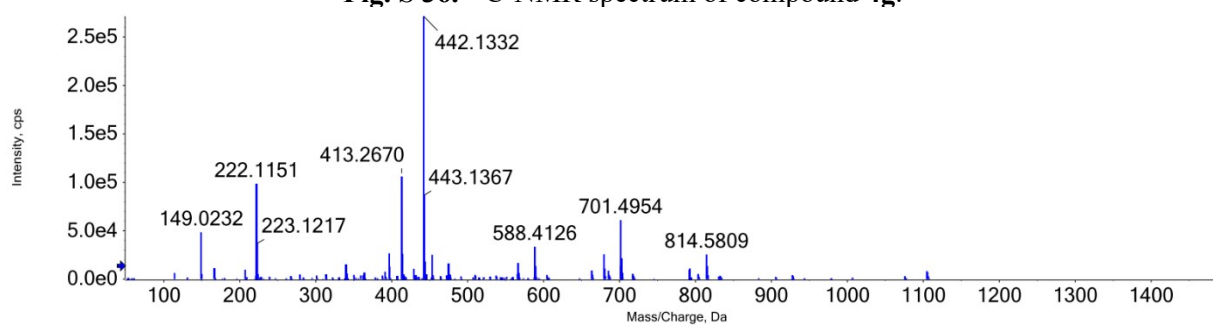


Fig. S 37. HR-MS spectrum of compound 4g.

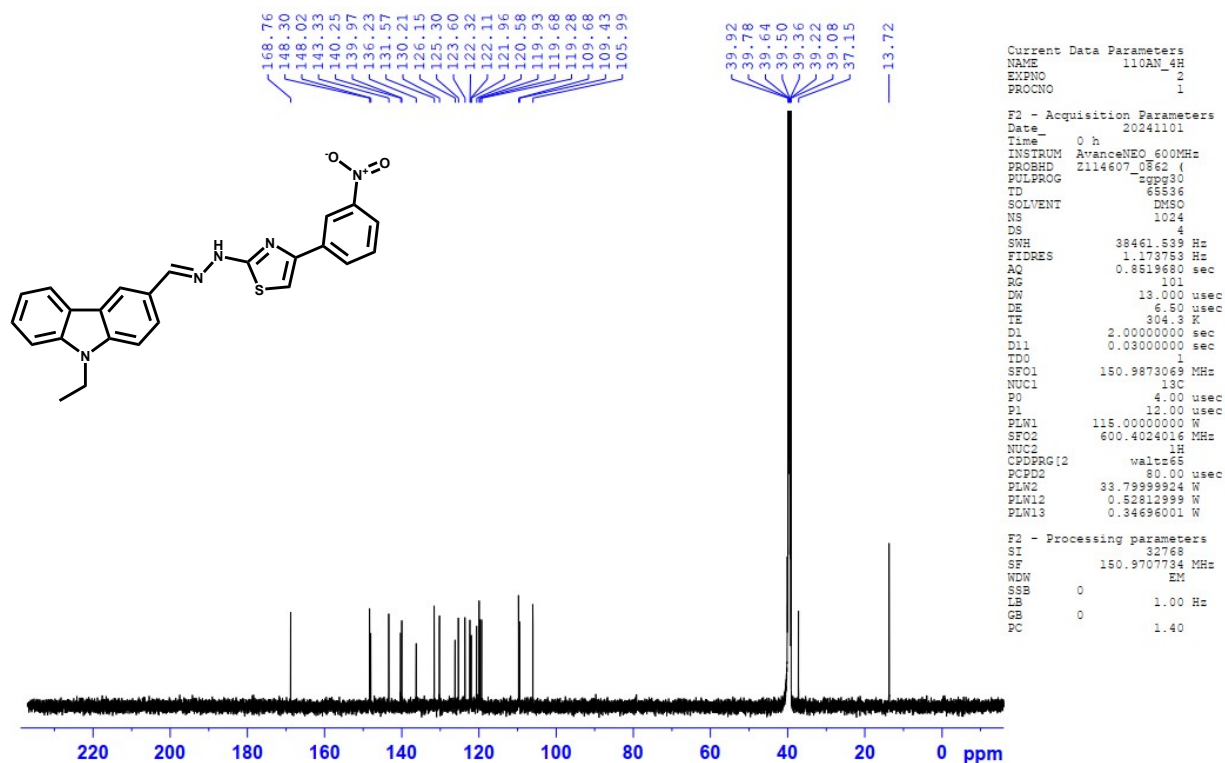


Fig. S 40. ¹³C-NMR spectrum of compound 4h.

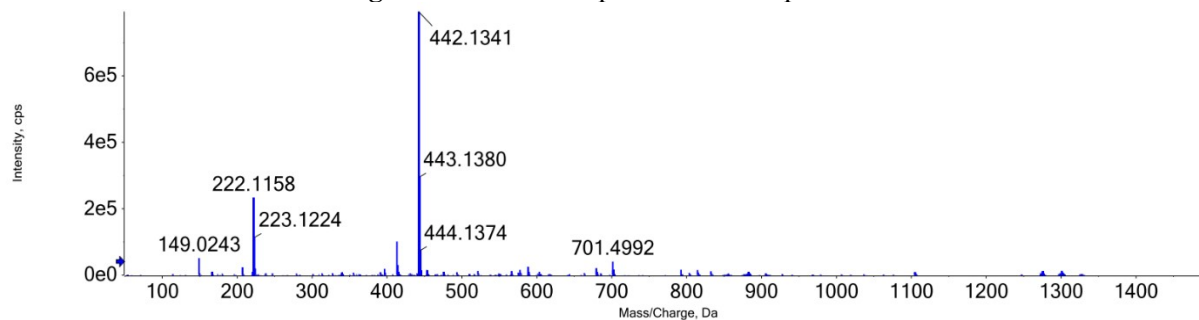


Fig. S 41. HR-MS spectrum of compound 4h.

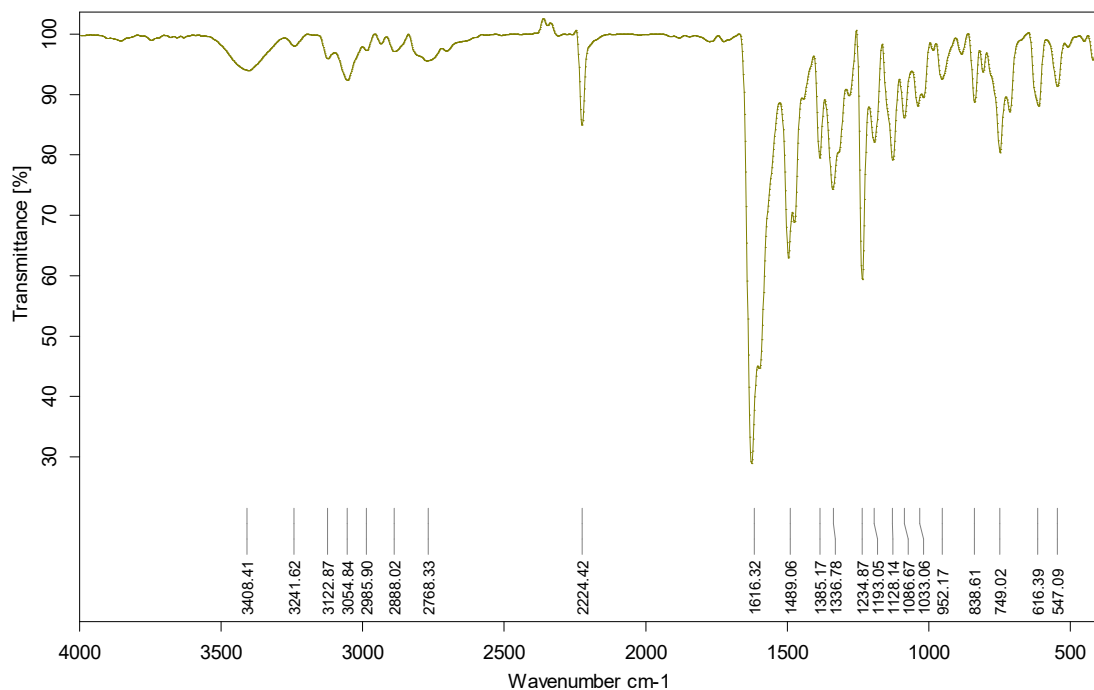


Fig. S 42. FT-IR spectrum of compound 4i.

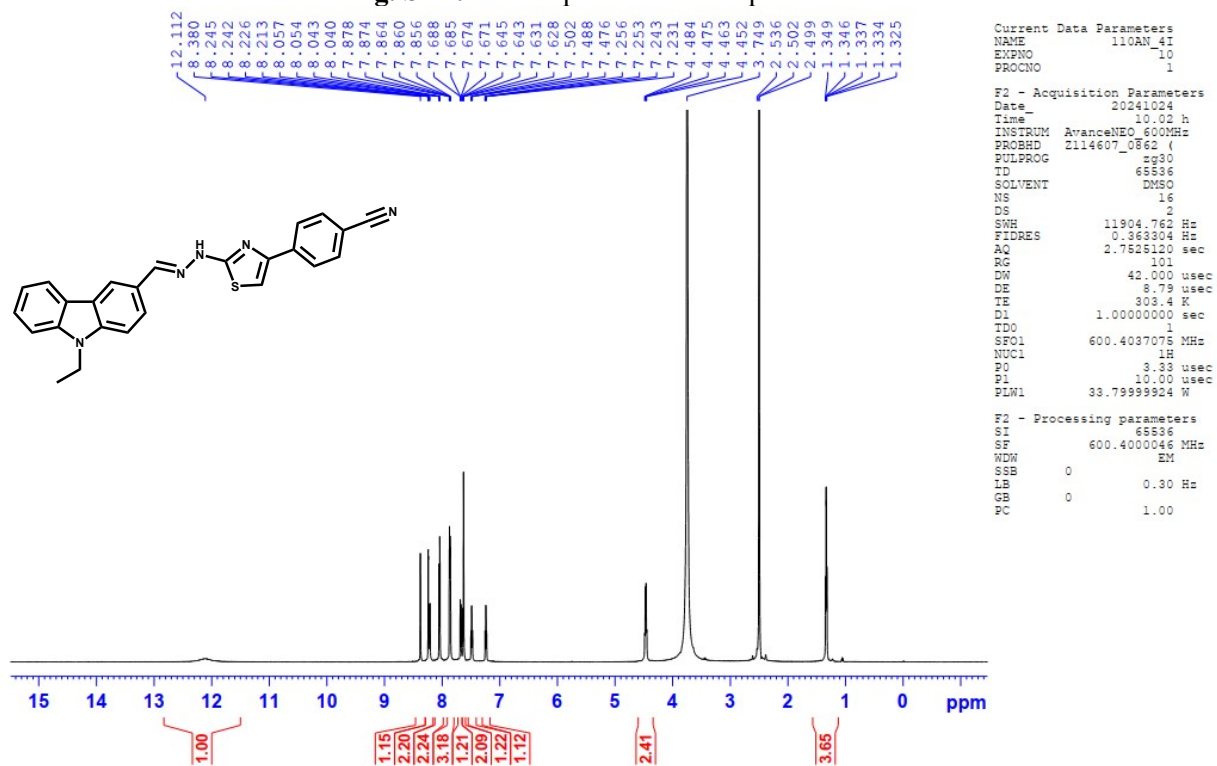


Fig. S 43. ¹H-NMR spectrum of compound 4i.

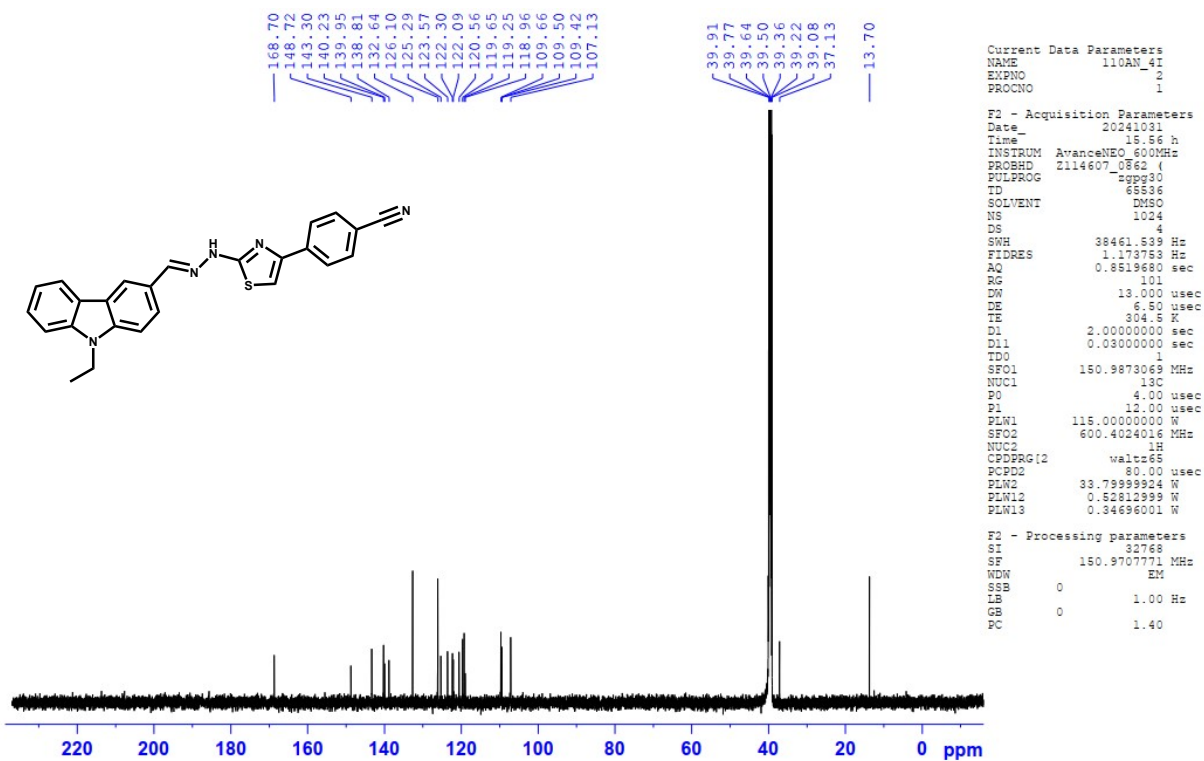


Fig. S 44. ¹³C-NMR spectrum of compound 4i.

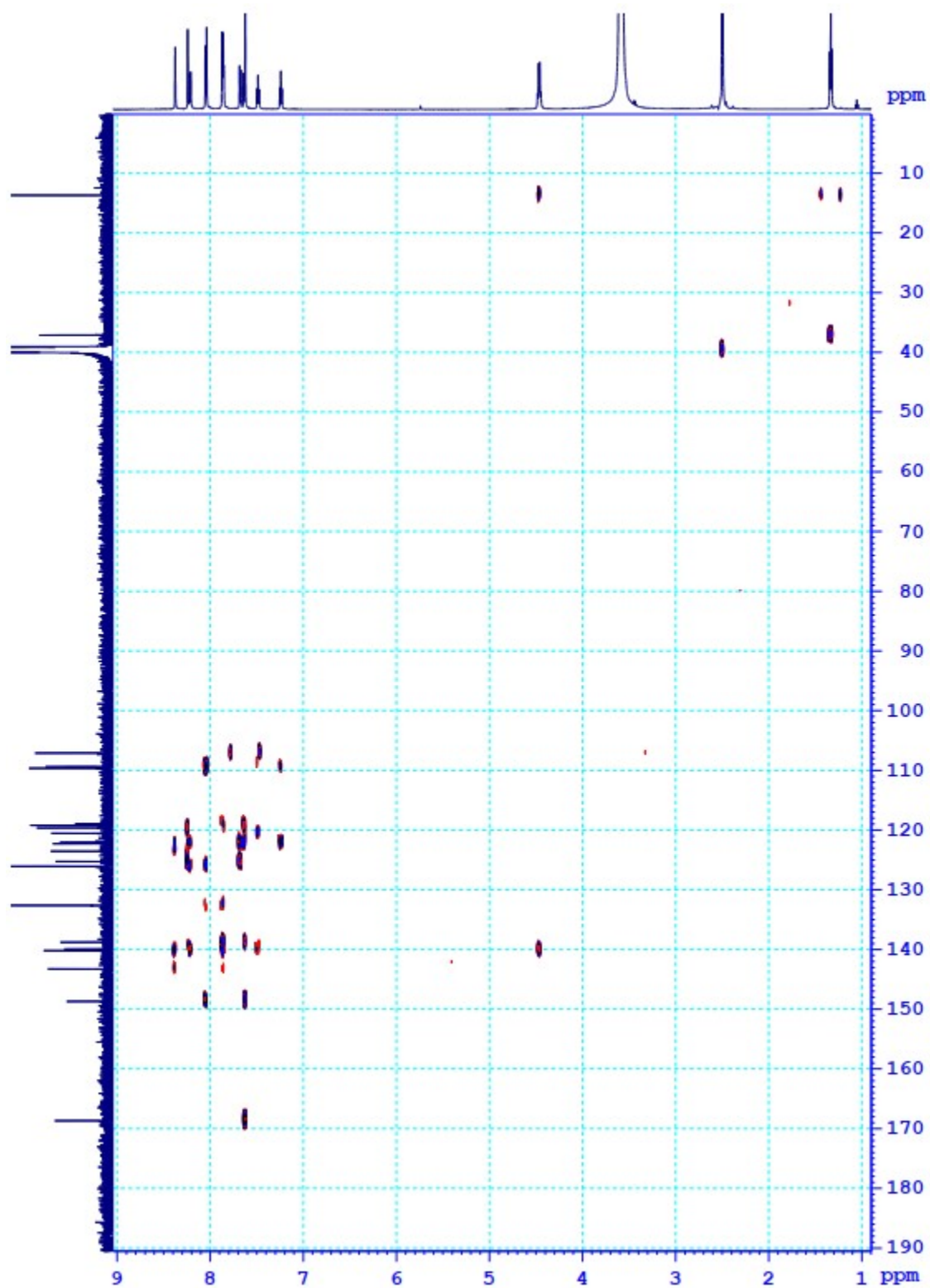


Fig. S 45. HMBC spectrum of compound 4i.

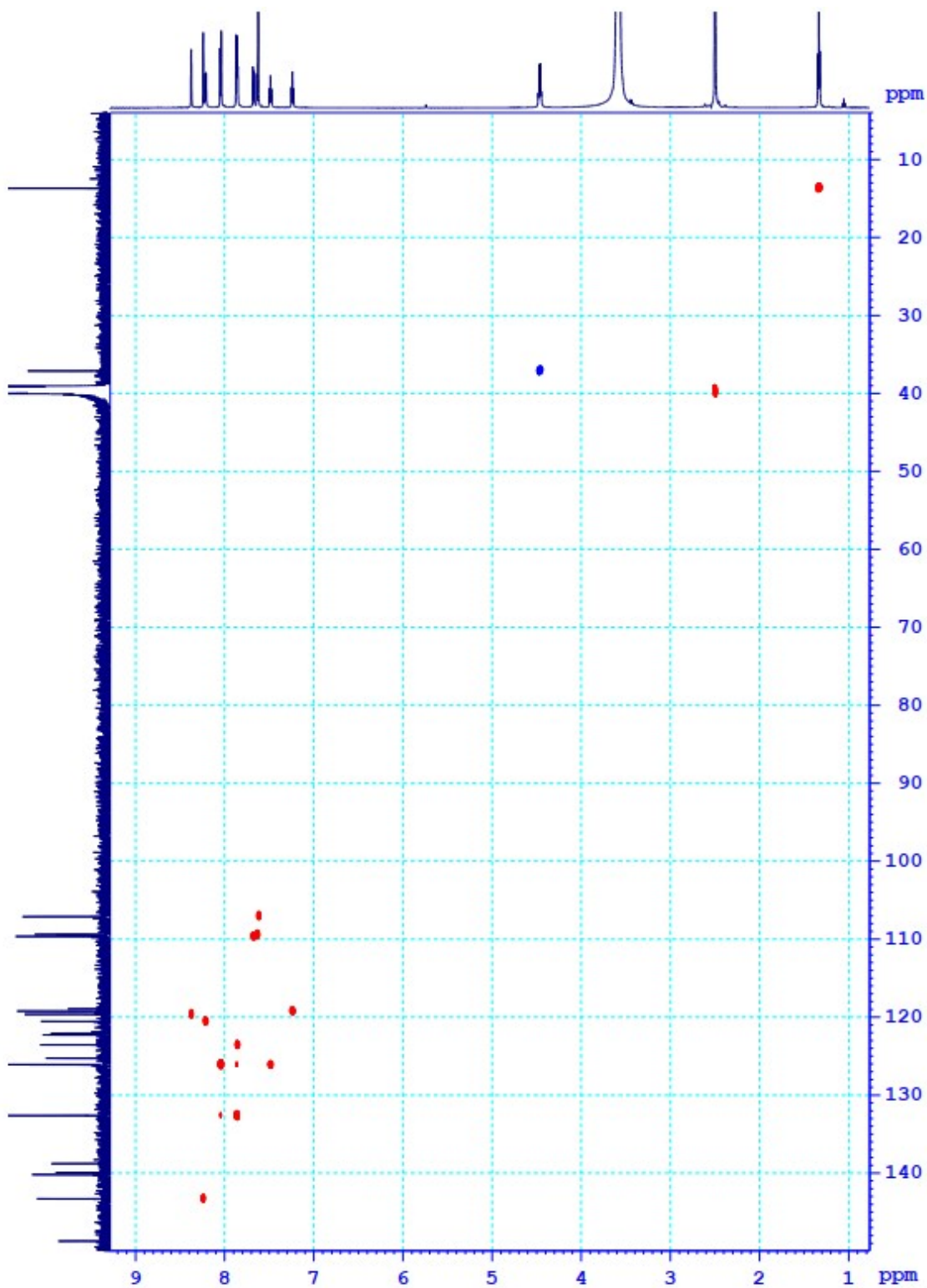


Fig. S 46. HSQC spectrum of compound 4i.

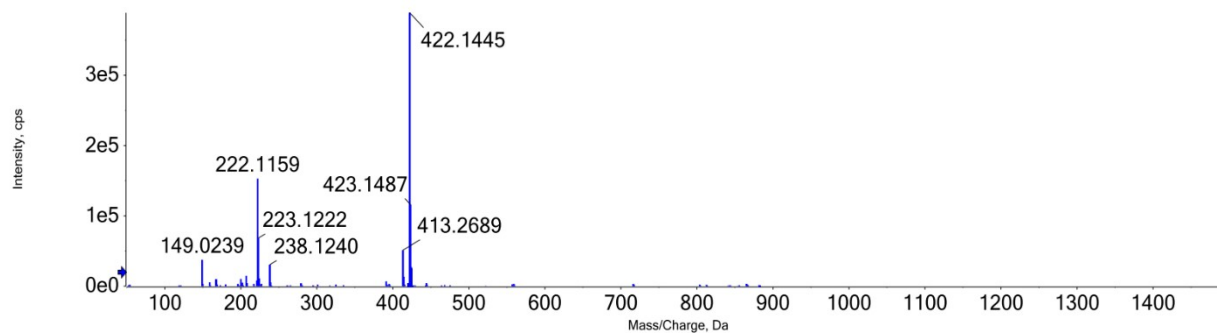


Fig. S 47. HR-MS spectrum of compound **4i**.

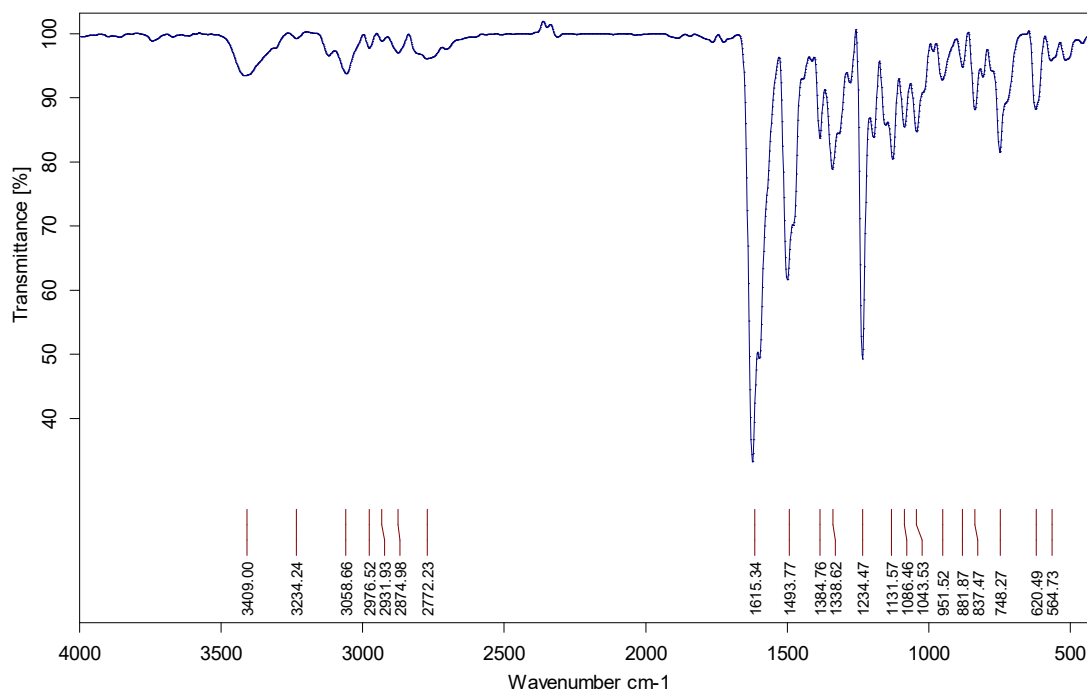


Fig. S 48. FT-IR spectrum of compound **4j**.

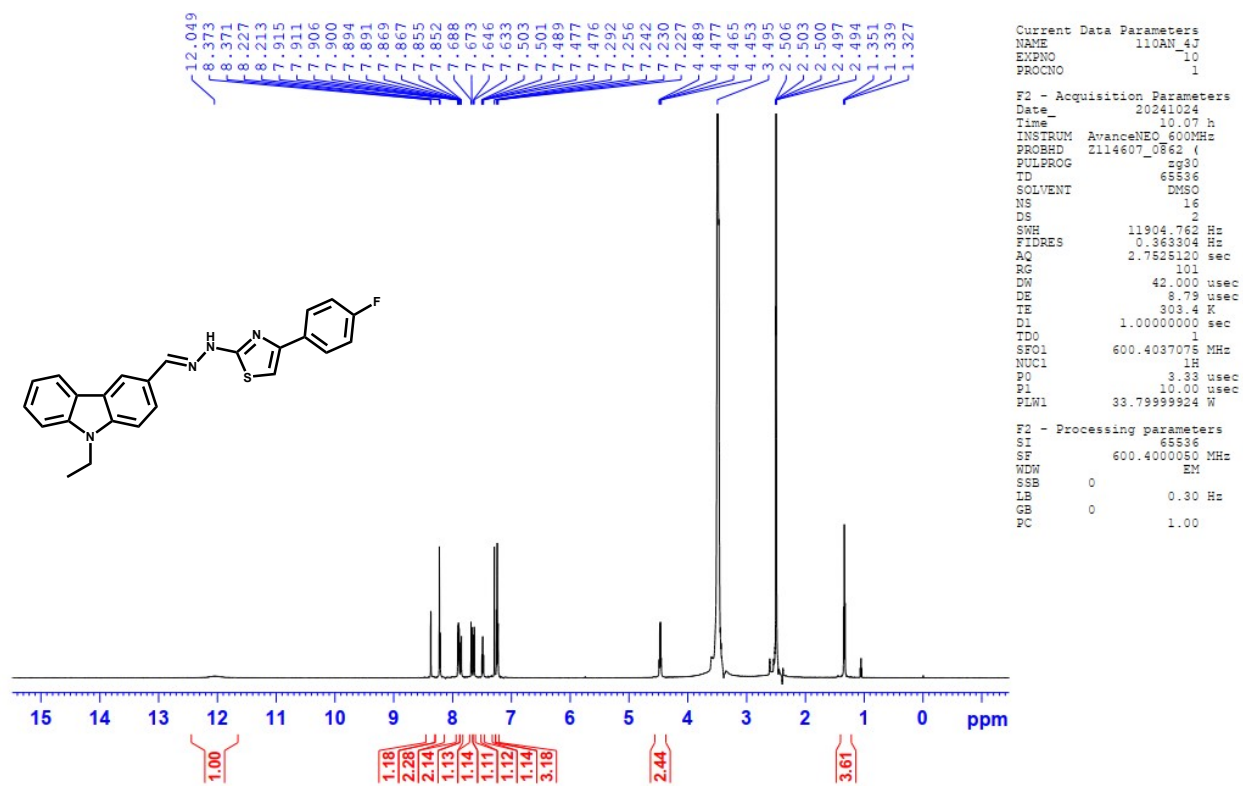


Fig. S 49. ¹H-NMR spectrum of compound 4j.

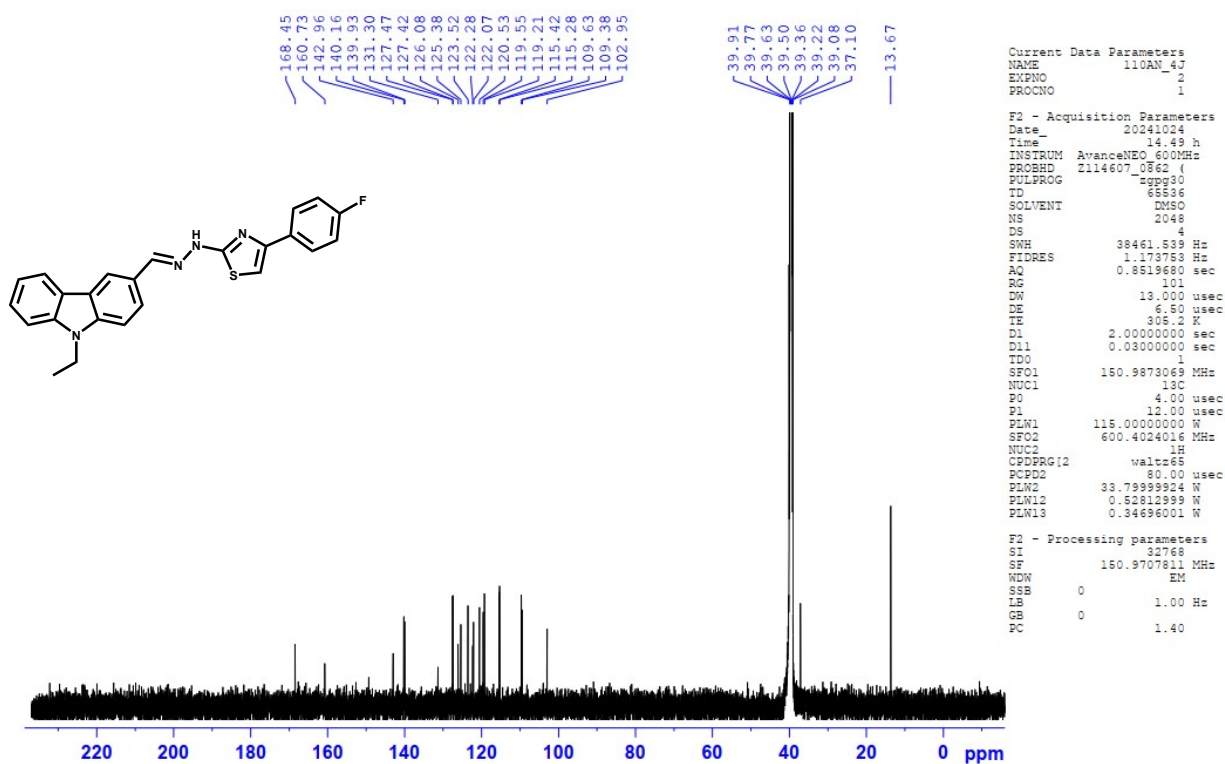


Fig. S 50. ¹³C-NMR spectrum of compound 4j.

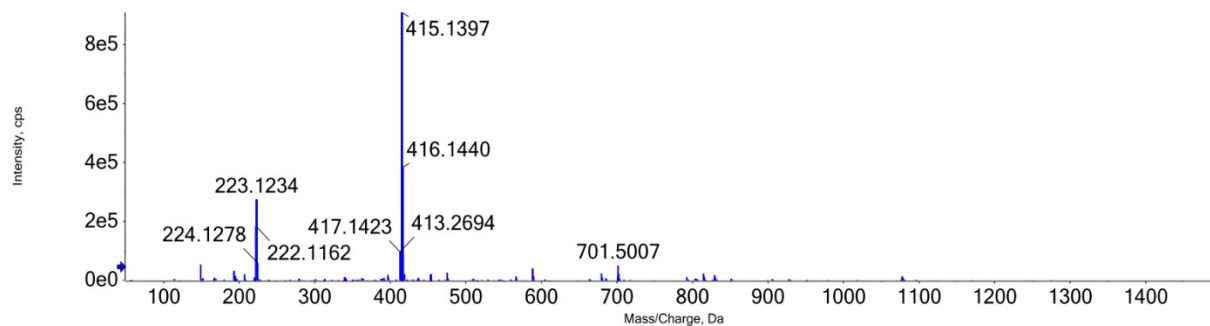


Fig. S 51. HR-MS spectrum of compound **4j**.

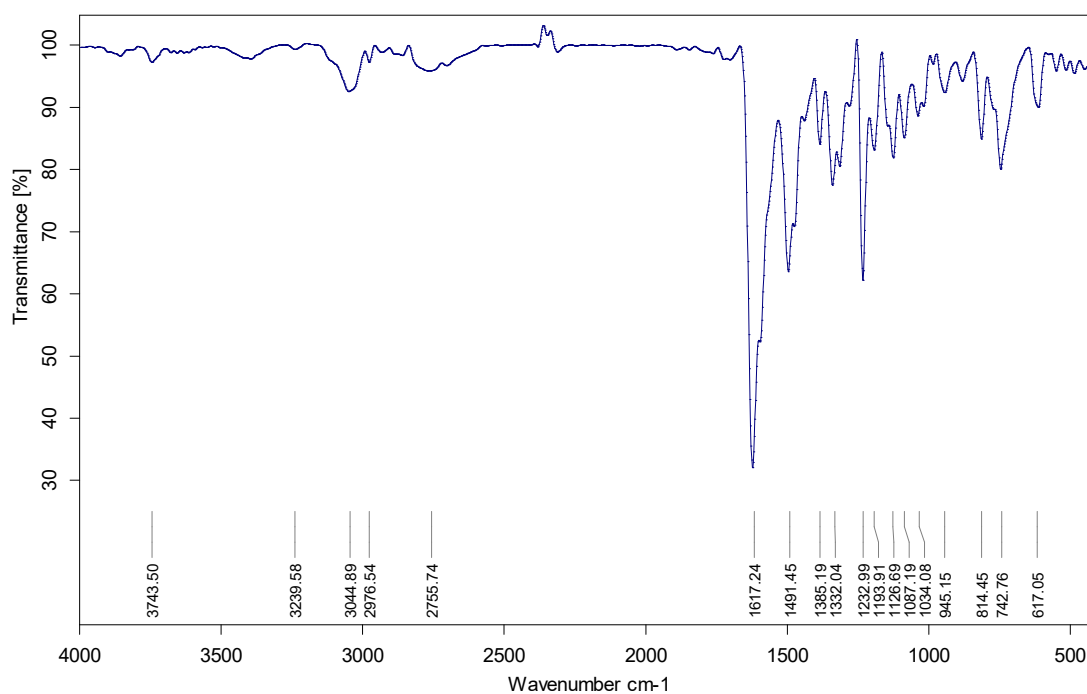


Fig. S 52. FT-IR spectrum of compound **4k**.

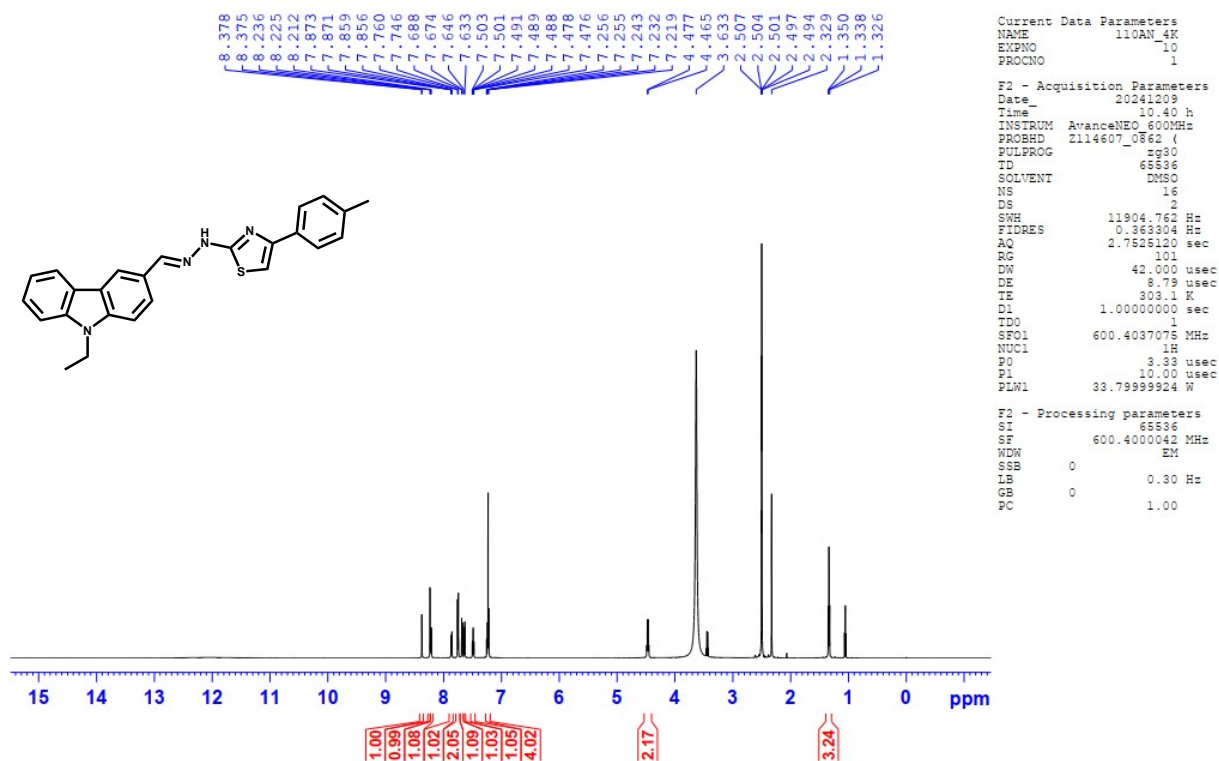


Fig. S 53. ¹H-NMR spectrum of compound 4k.

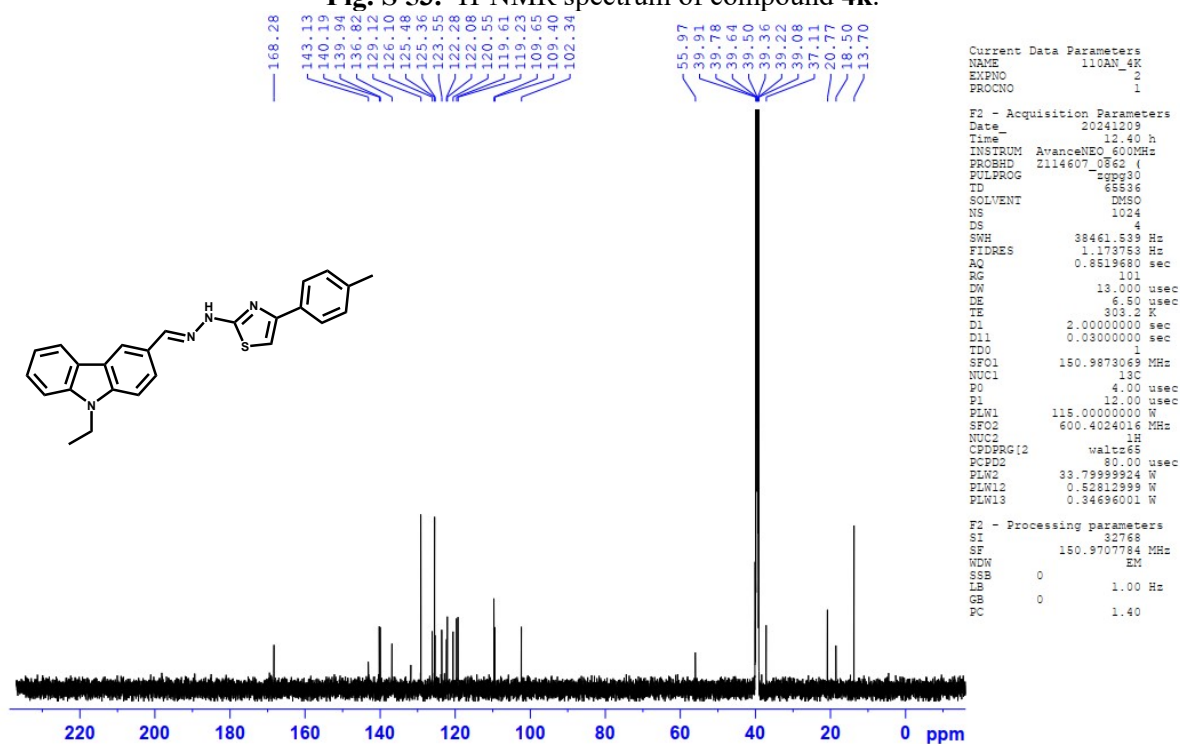


Fig. S 54. ¹³C-NMR spectrum of compound 4k.

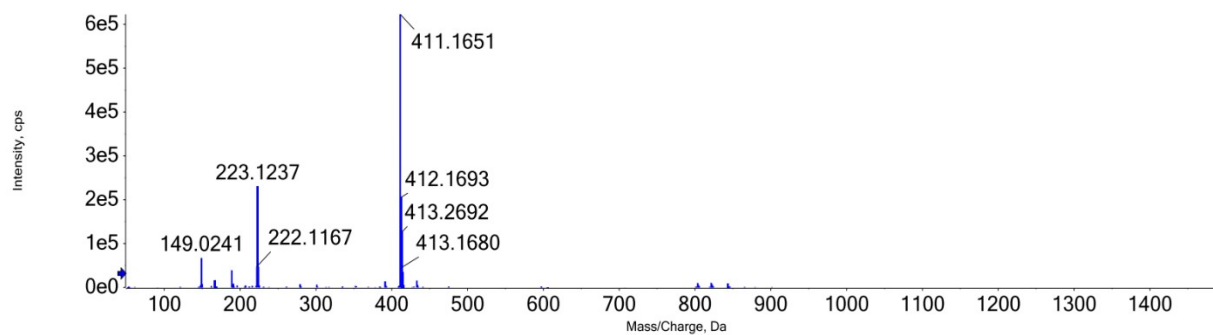


Fig. S 55. HR-MS spectrum of compound **4k**.

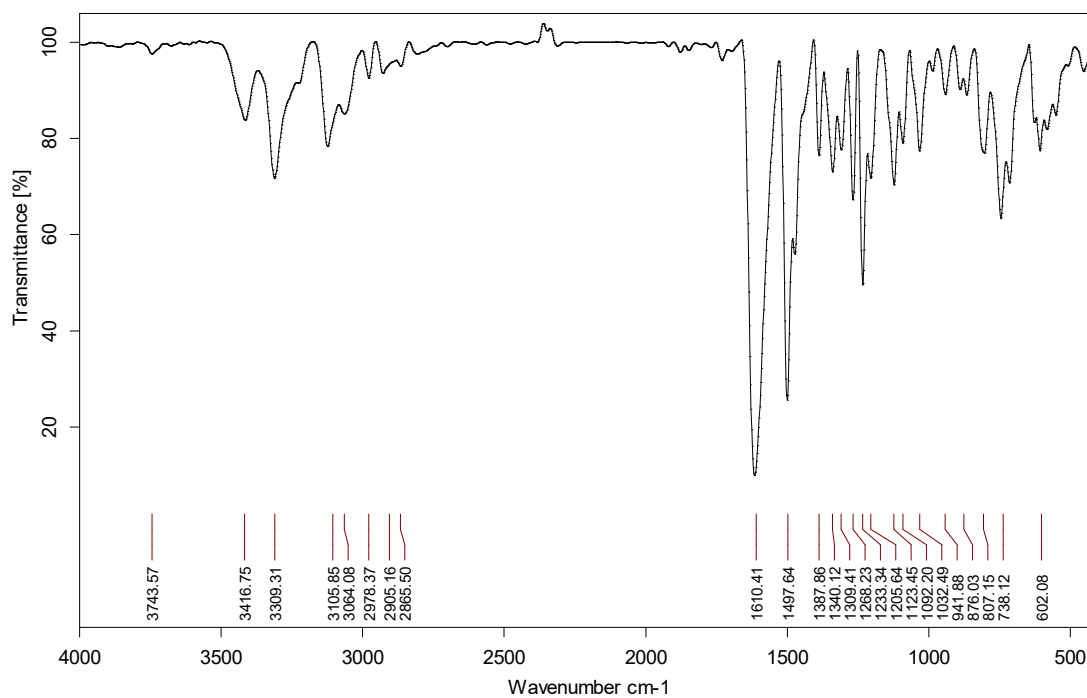


Fig. S 56. FT-IR spectrum of compound **4l**.

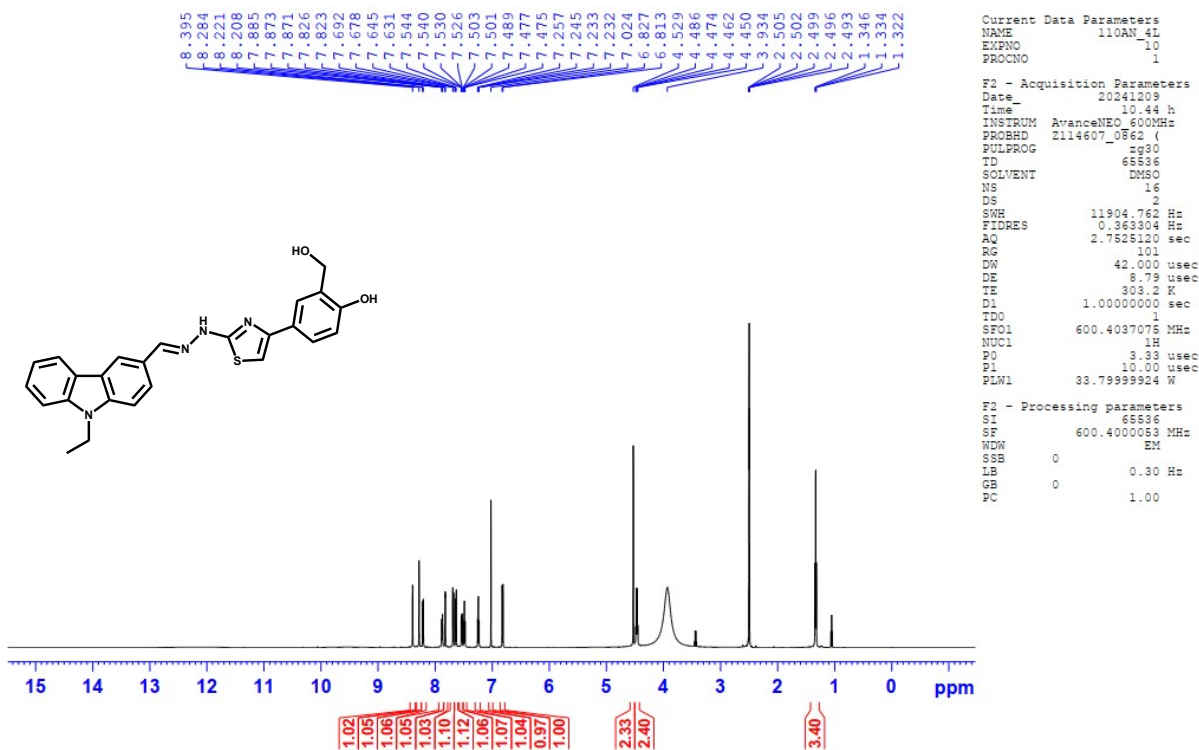


Fig. S 57. ¹H-NMR spectrum of compound 4l.

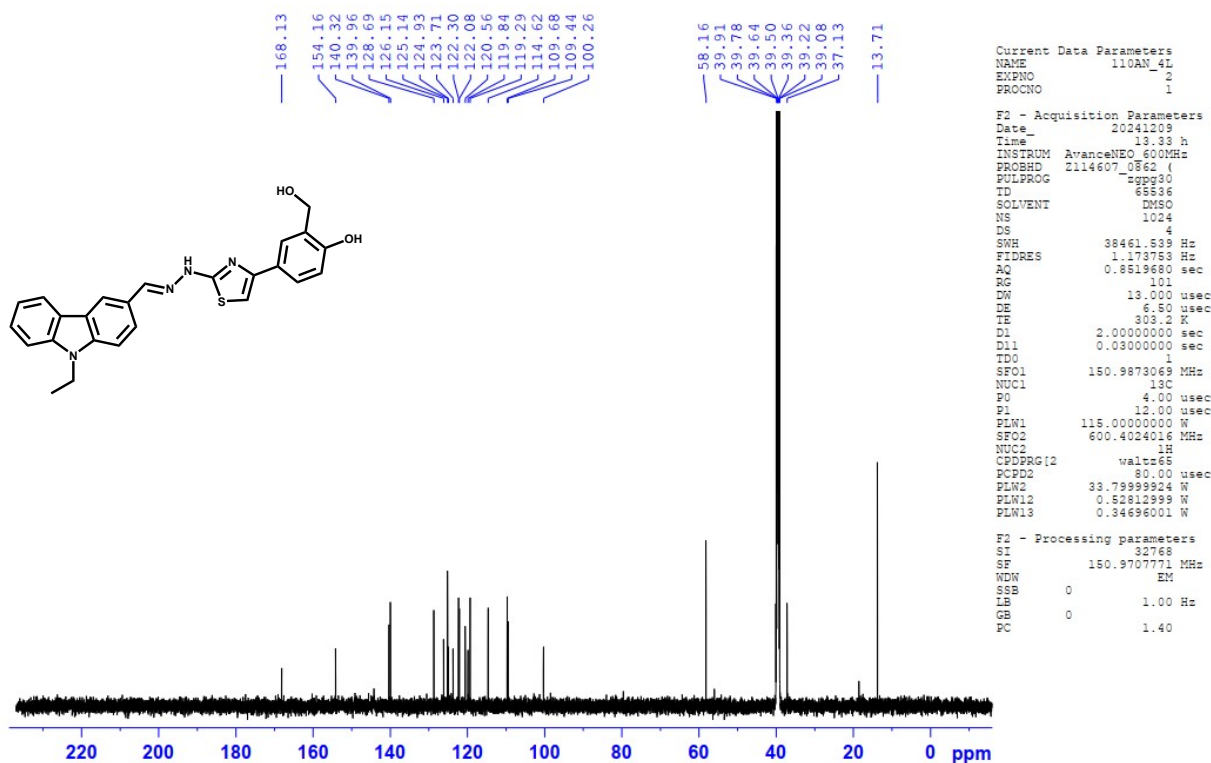


Fig. S 58. ¹³C-NMR spectrum of compound 4l.

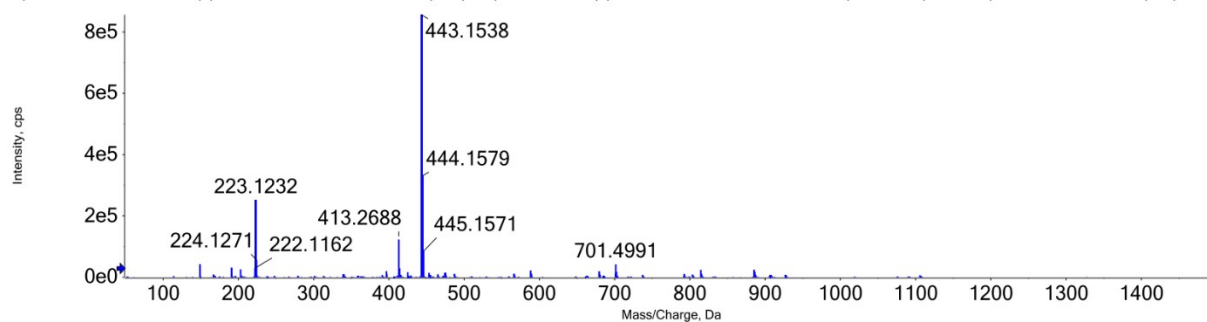


Fig. S 59. HR-MS spectrum of compound **4l**.

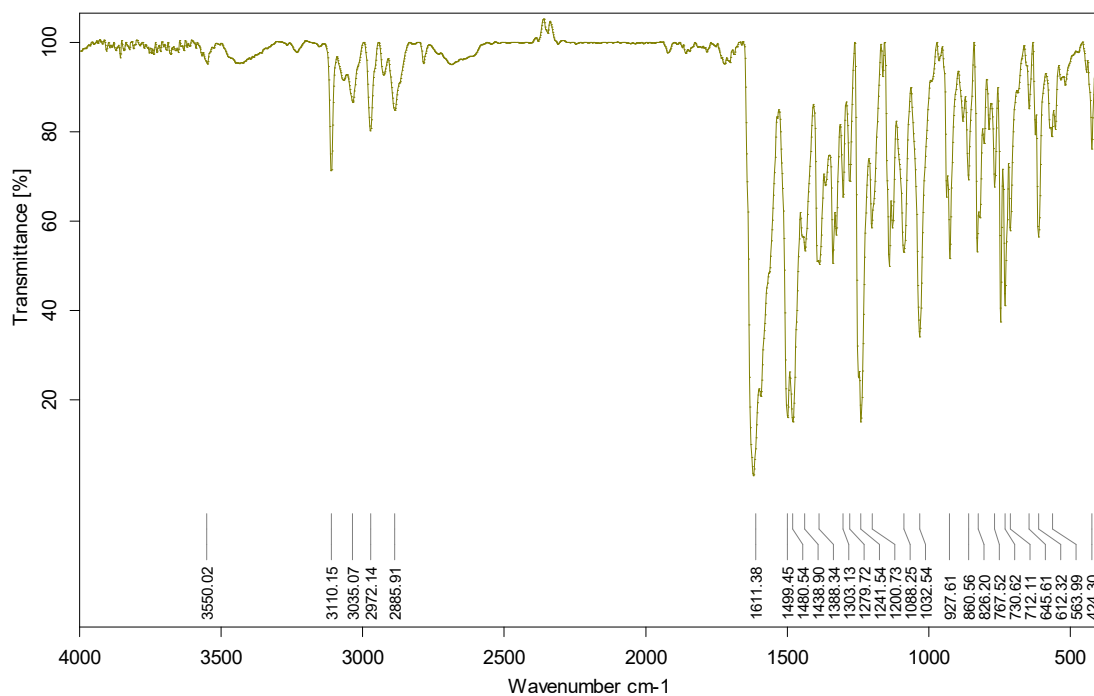


Fig. S 60. FT-IR spectrum of compound **4m**.

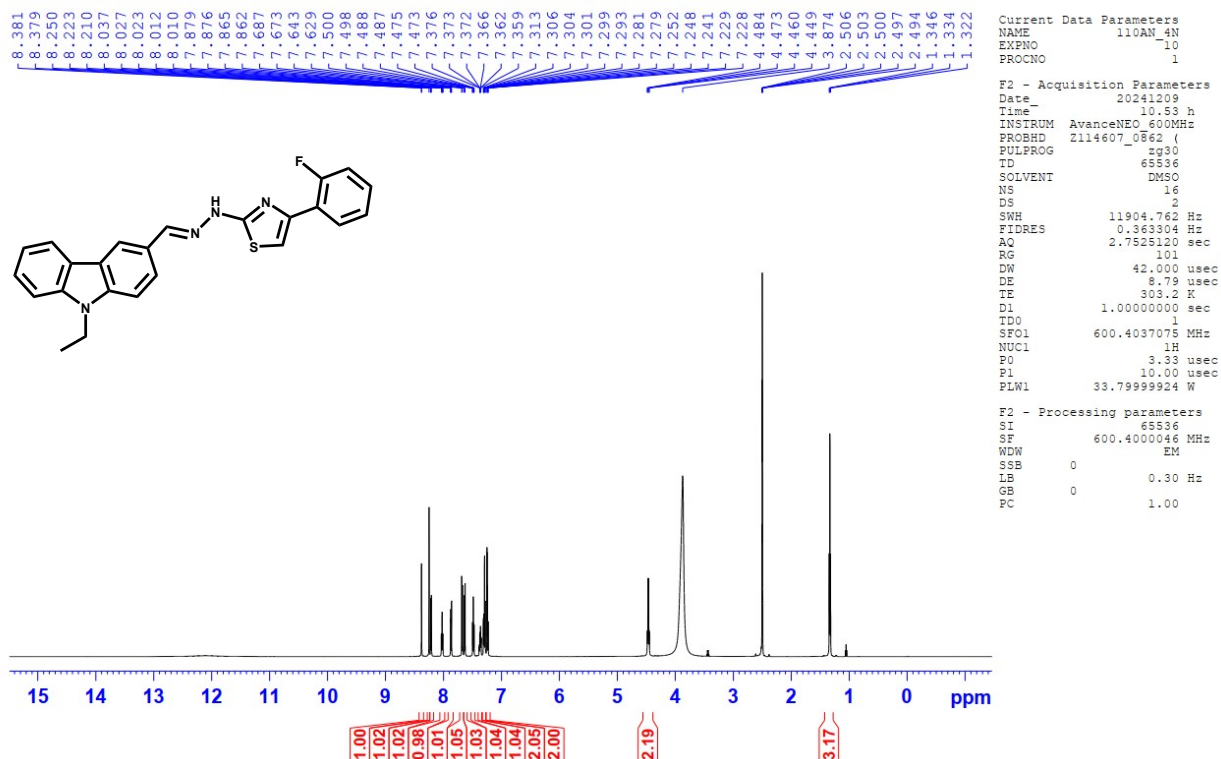


Fig. S 61. ¹H-NMR spectrum of compound 4m.

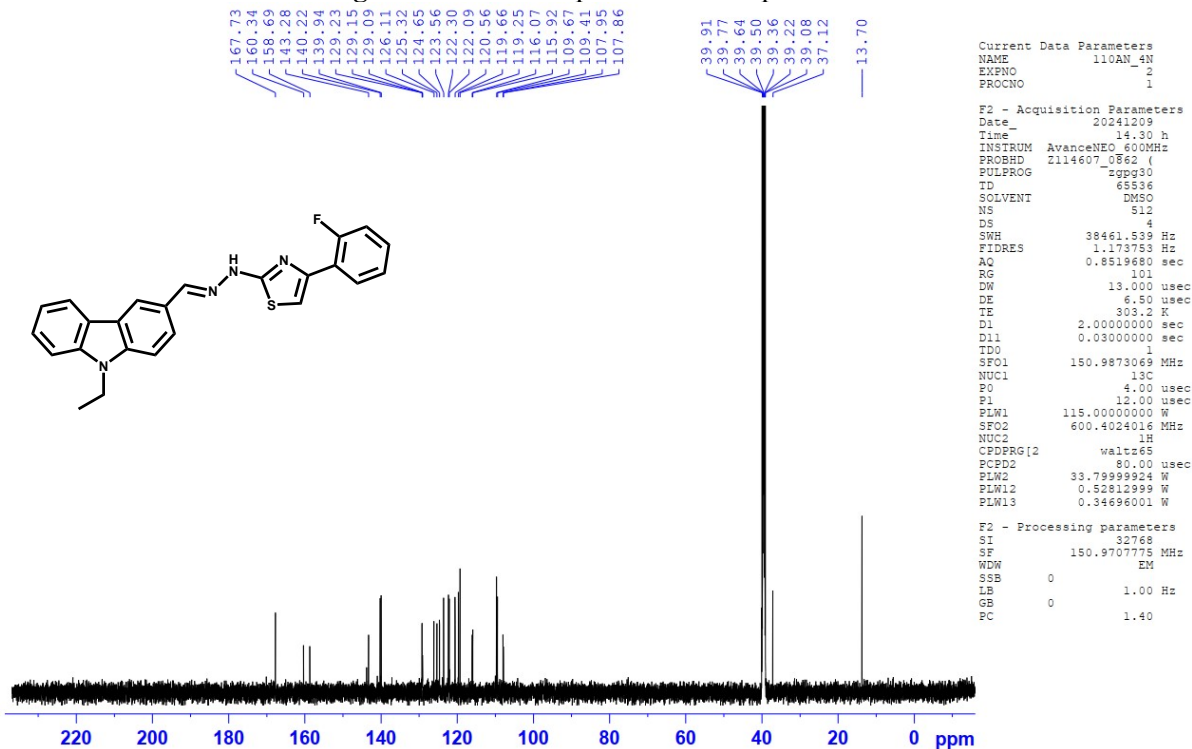


Fig. S 62. ¹³C-NMR spectrum of compound 4m.

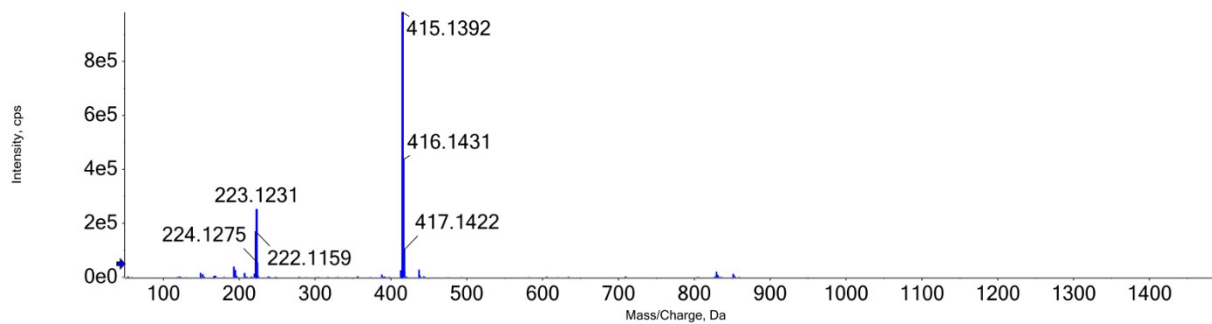


Fig. S 63. HR-MS spectrum of compound **4m**.

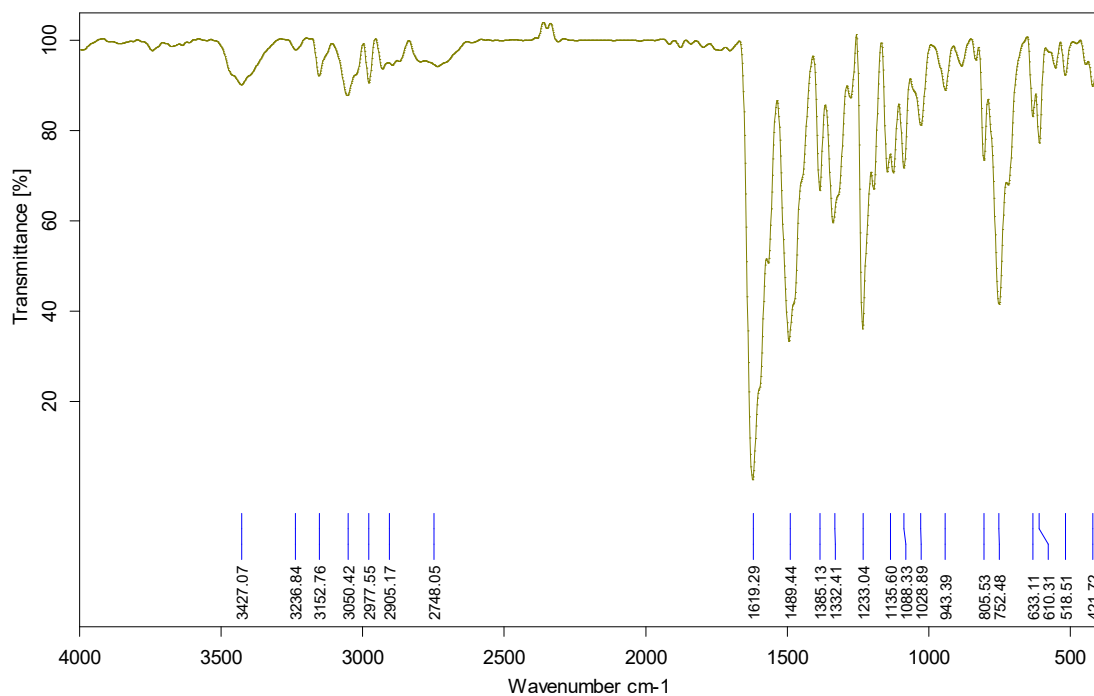


Fig. S 64. FT-IR spectrum of compound **4n**.

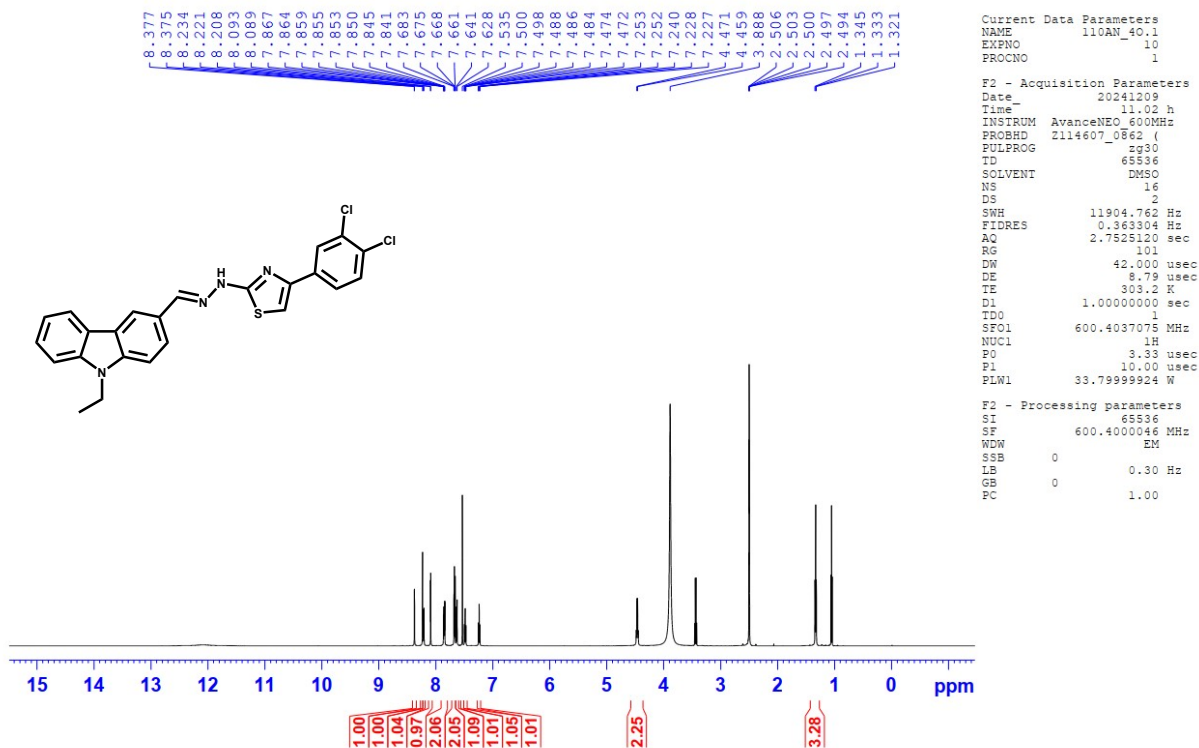


Fig. S 65. ¹H-NMR spectrum of compound 4n.

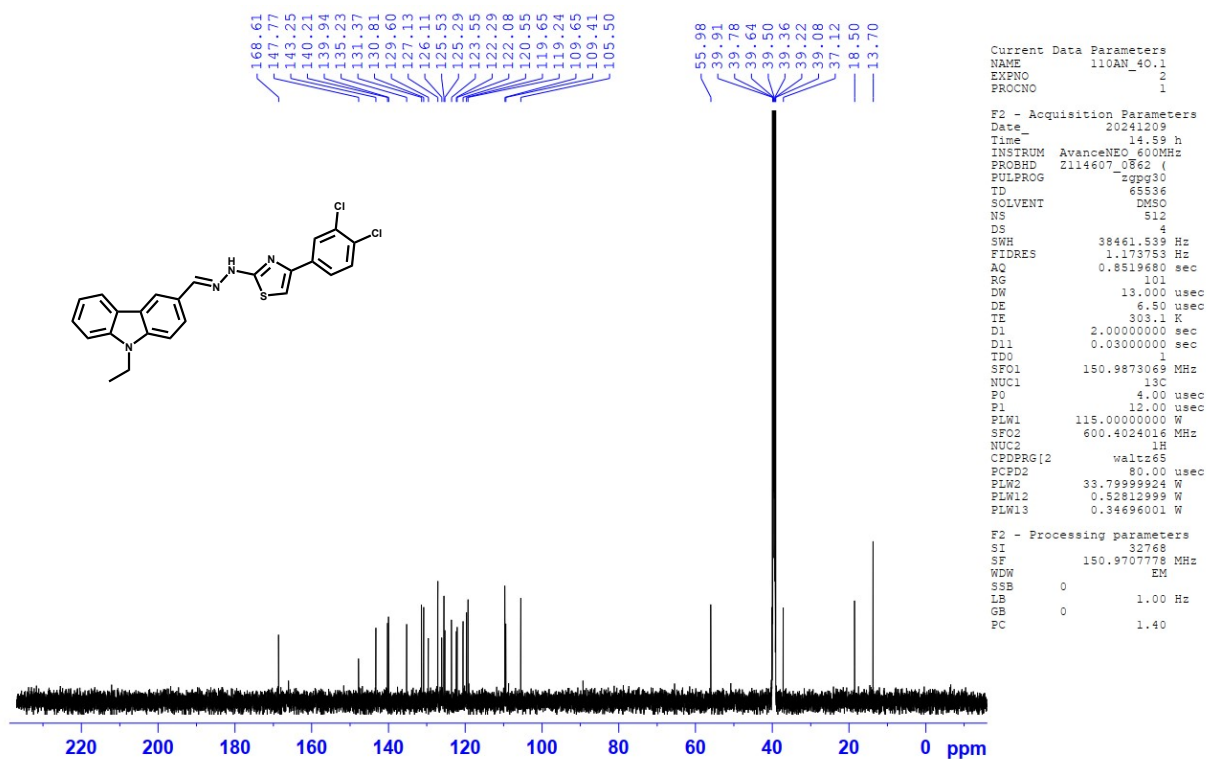


Fig. S 66. ¹³C-NMR spectrum of compound 4n.

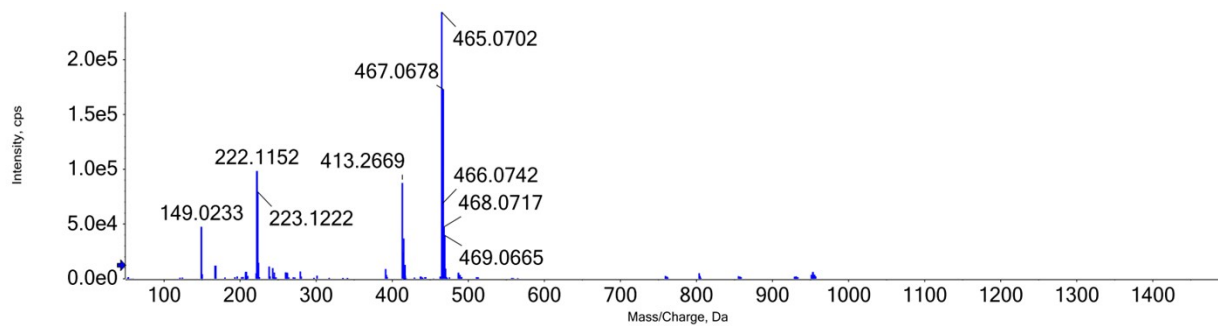


Fig. S 67. HR-MS spectrum of compound **4n**.

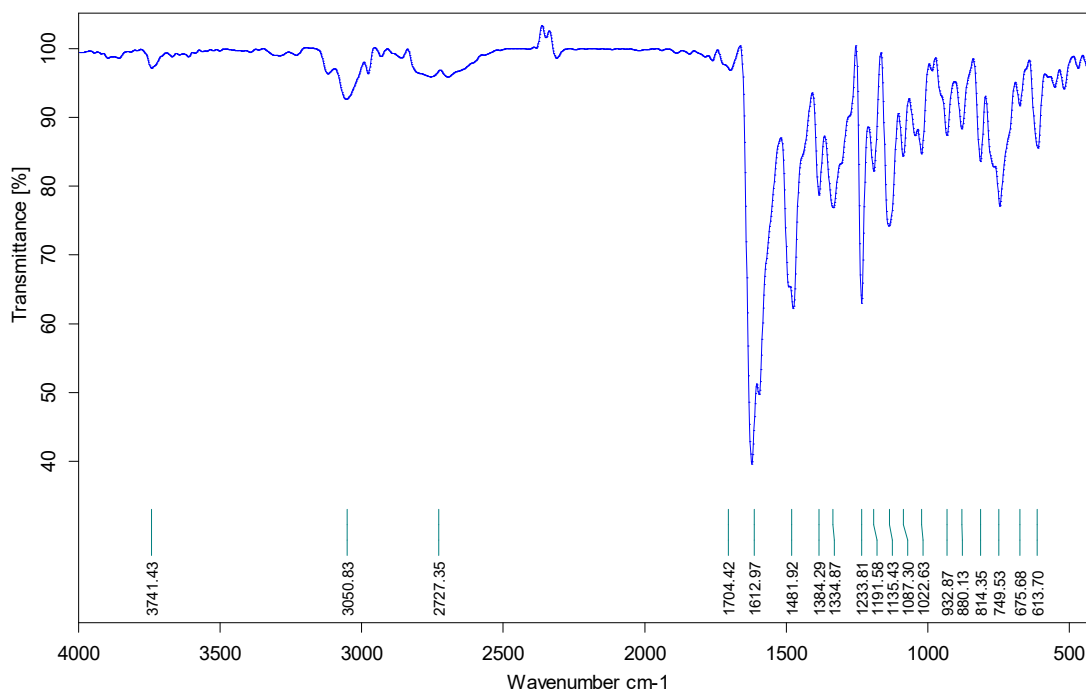


Fig. S 68. FT-IR spectrum of compound **4o**.

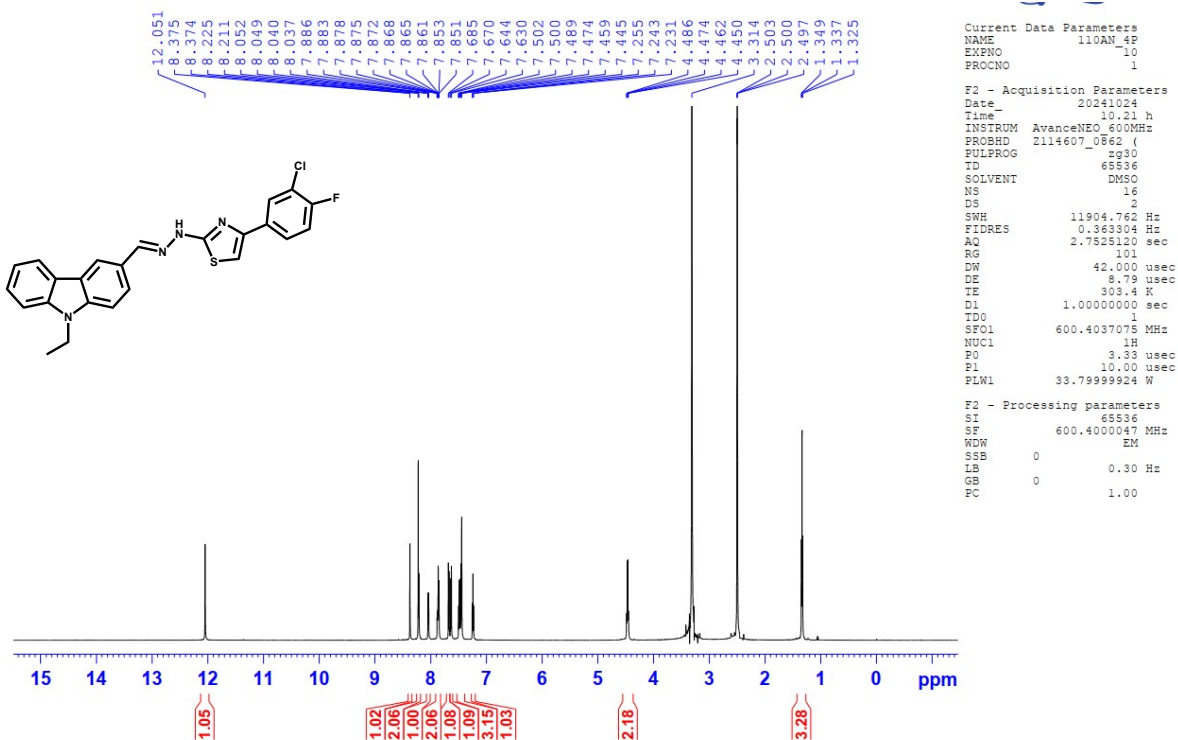


Fig. S 69. ¹H-NMR spectrum of compound 4o.

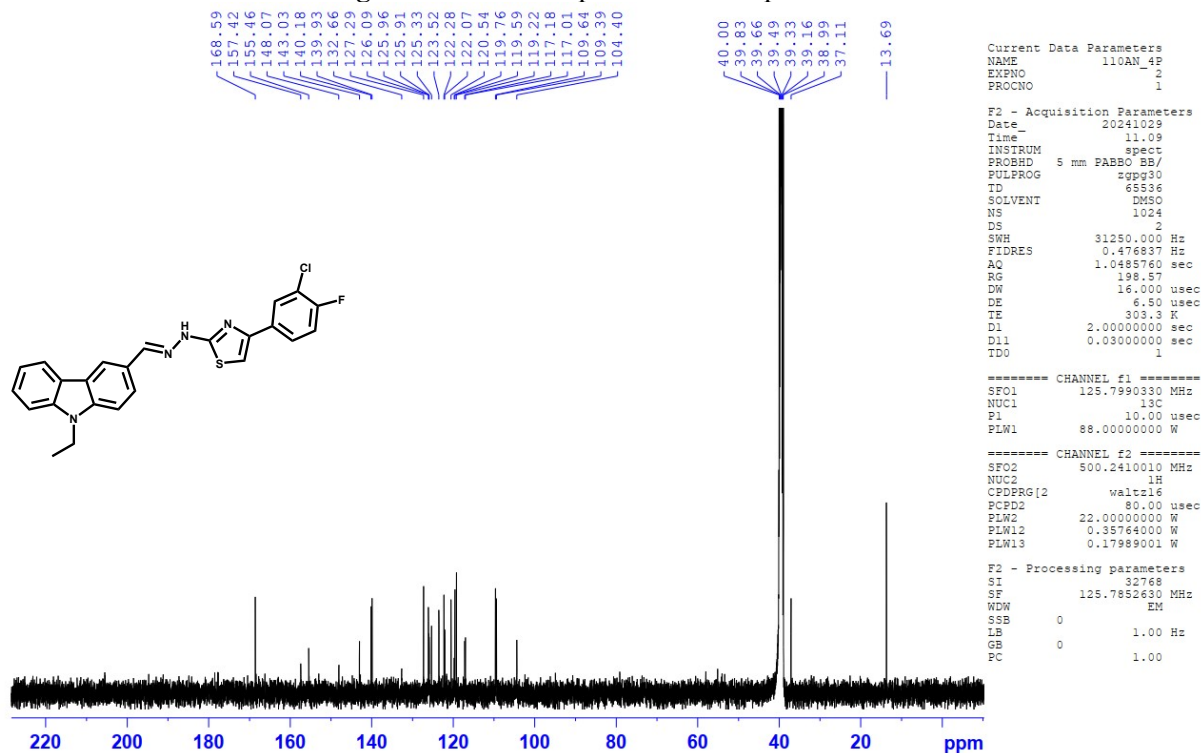


Fig. S 70. ¹³C-NMR spectrum of compound 4o.

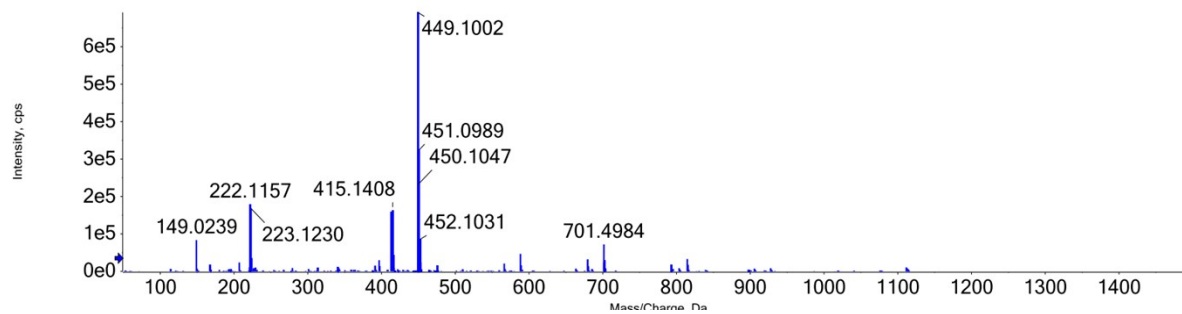


Fig. S 71. HR-MS spectrum of compound **4o**.

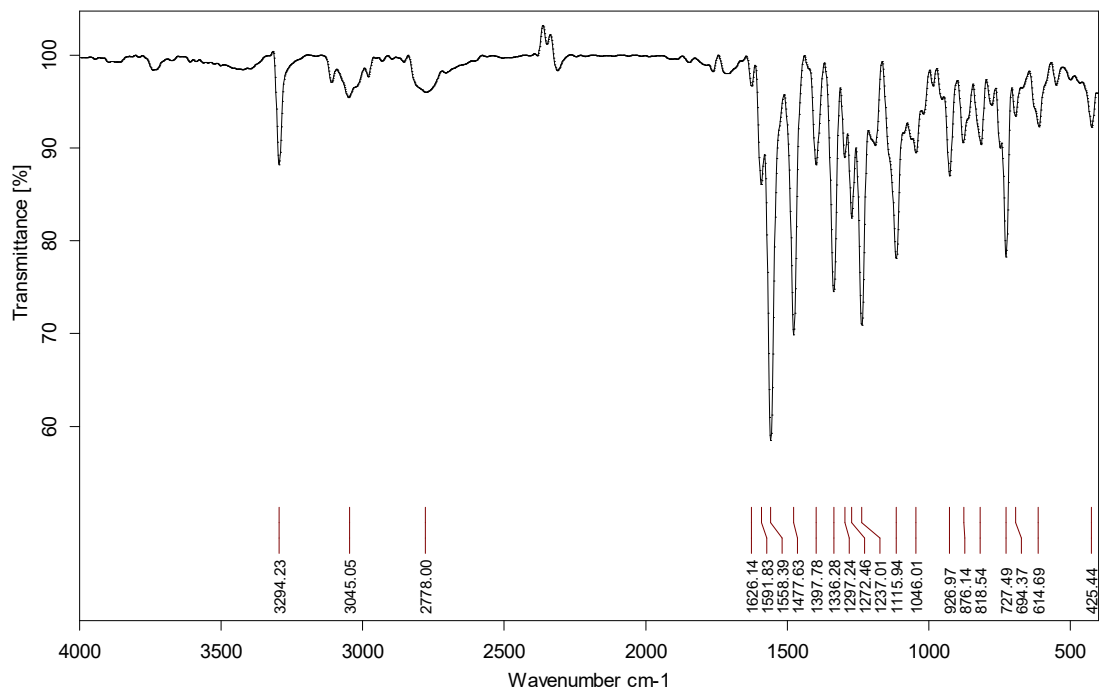


Fig. S 72. FT-IR spectrum of compound **4p**.

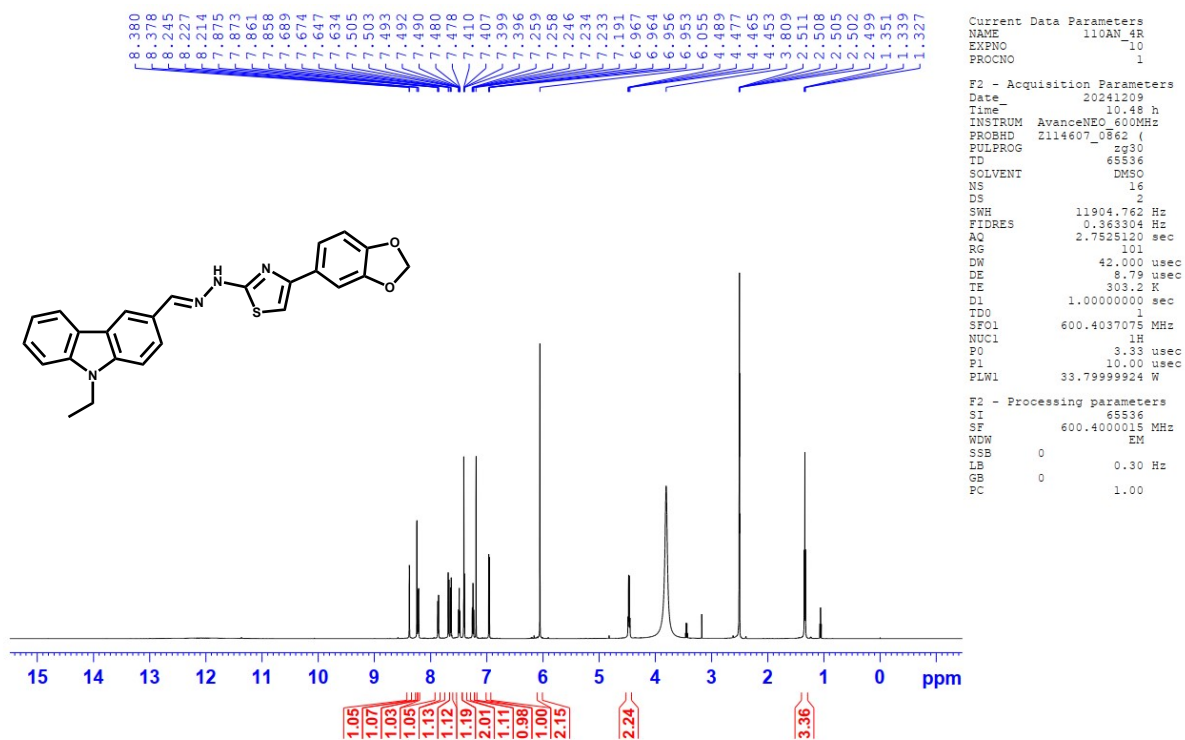


Fig. S 73. ¹H-NMR spectrum of compound 4p.

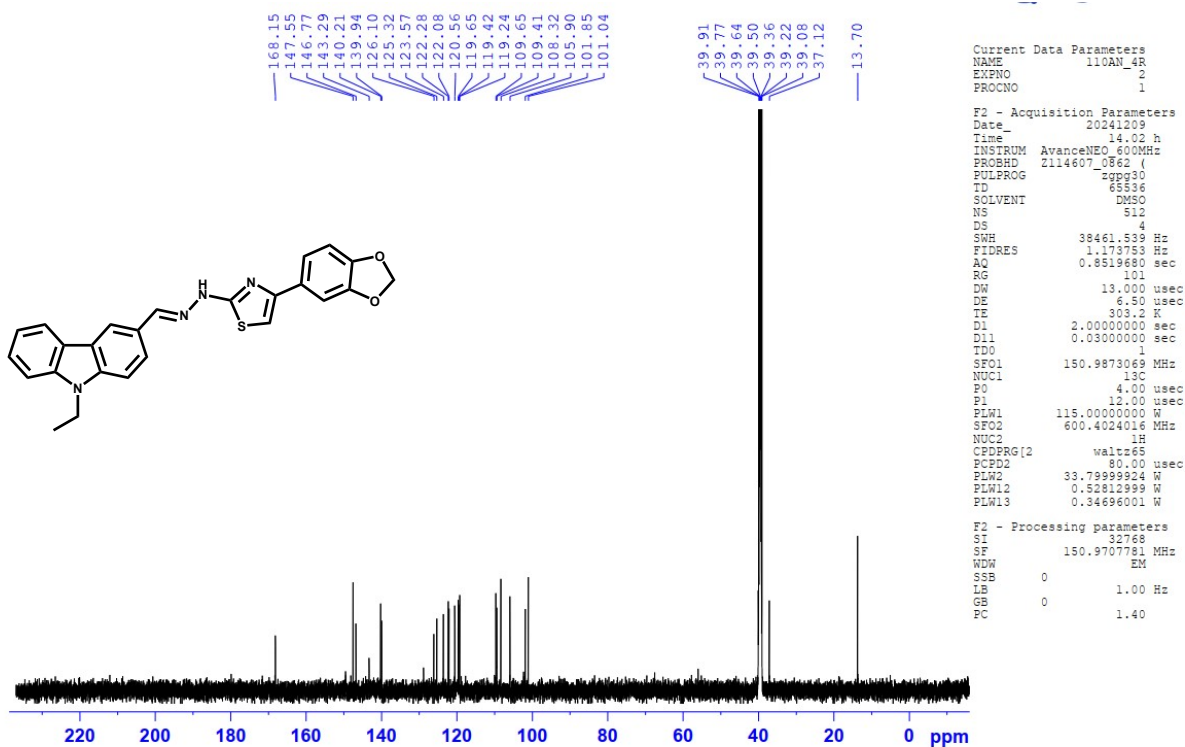


Fig. S 74. ¹³C-NMR spectrum of compound 4p.

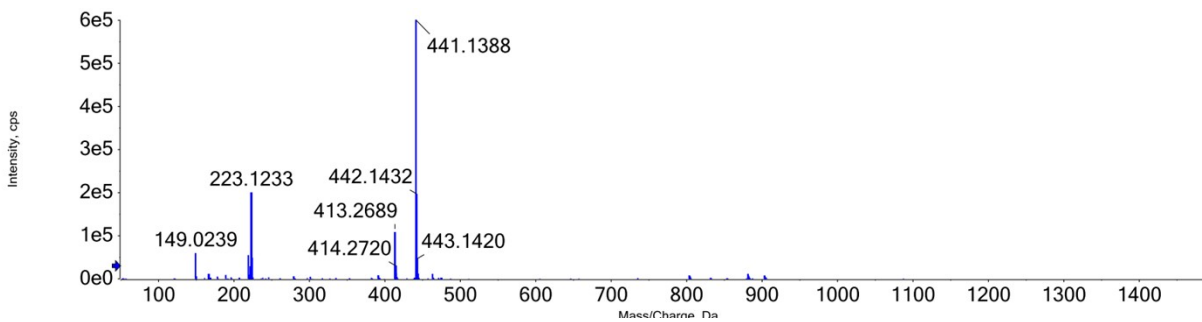


Fig. S 75. HR-MS spectrum of compound **4p**.

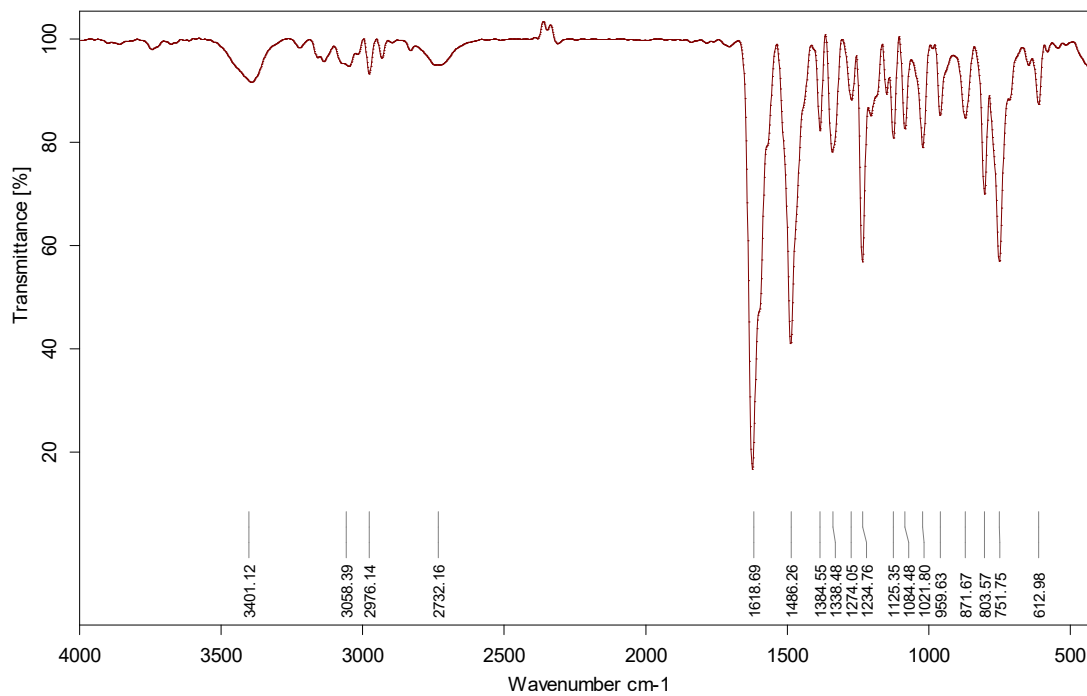


Fig. S 76. FT-IR spectrum of compound **4q**.

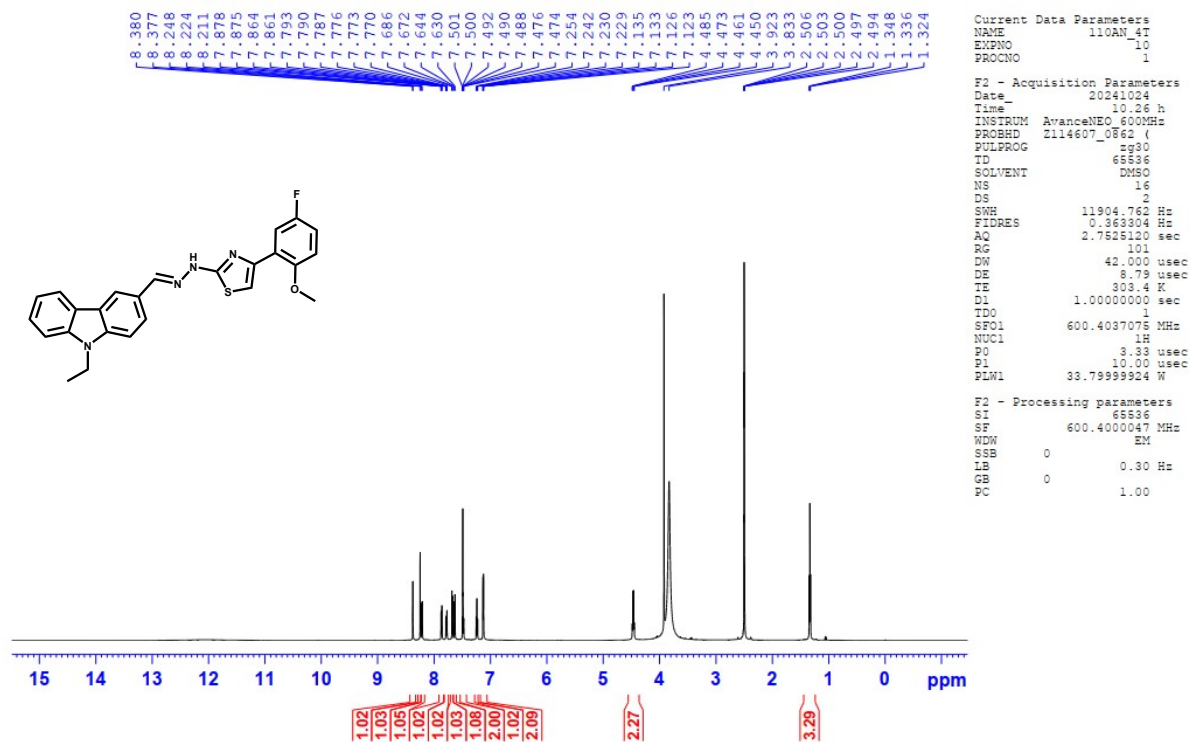


Fig. S 77. ¹H-NMR spectrum of compound 4q.

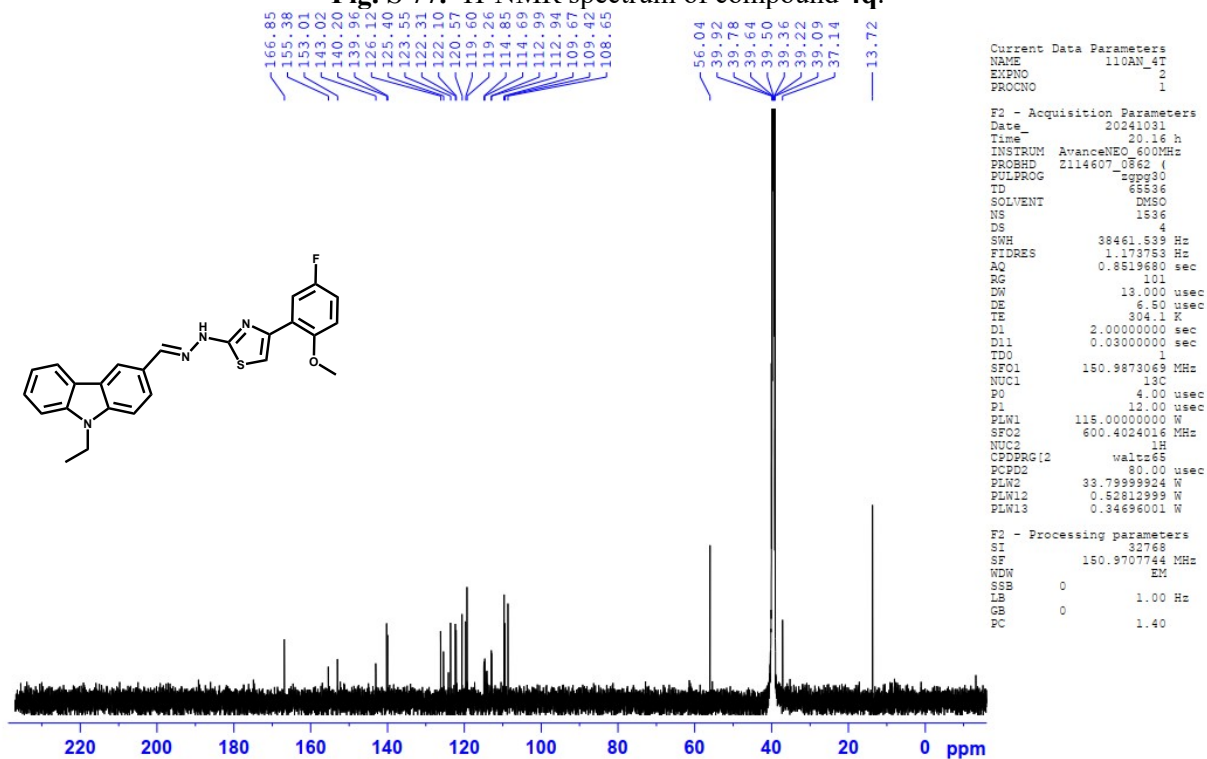


Fig. S 78. ¹³C-NMR spectrum of compound 4q.

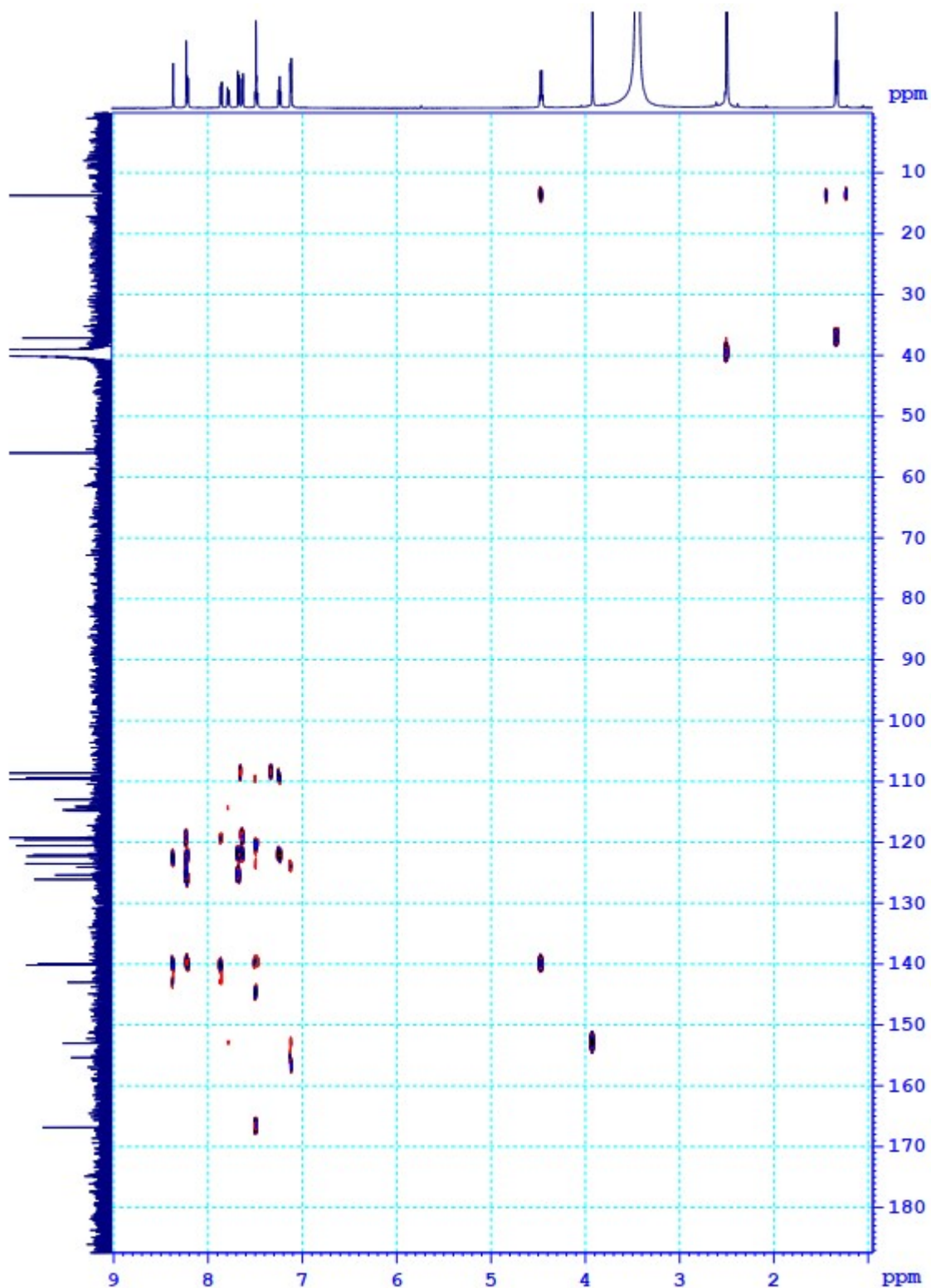


Fig. S 79. HMBC spectrum of compound **4q**.

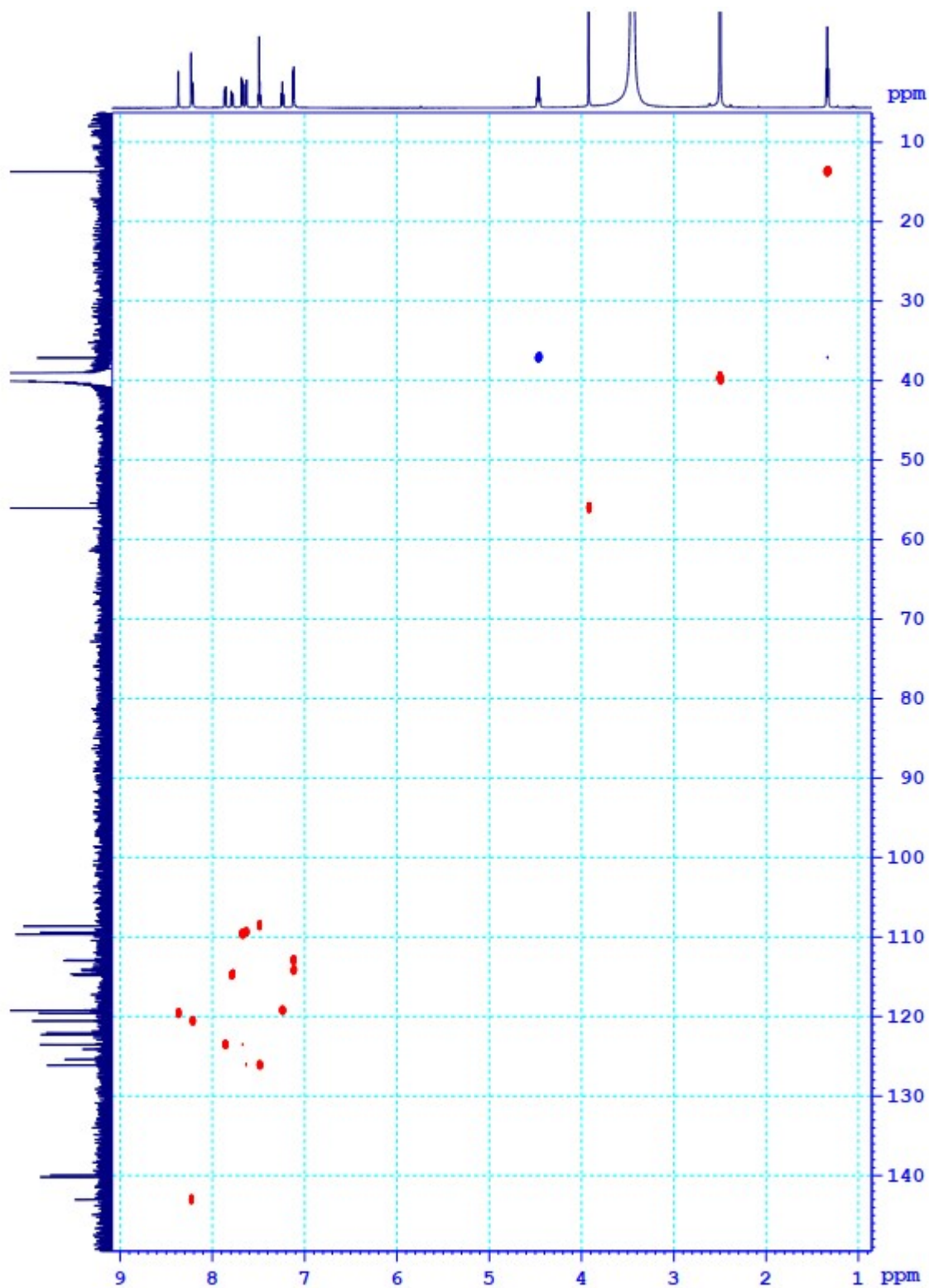


Fig. S 80. HSQC spectrum of compound 4q.

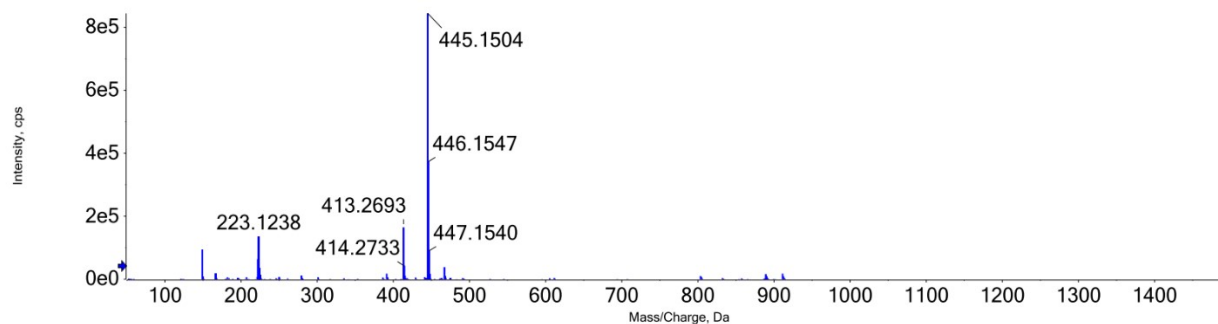


Fig. S 81. HR-MS spectrum of compound **4q**.

Escherichia coli ATCC 8739

(+) : Chloramphenicol
(-) : DMSO

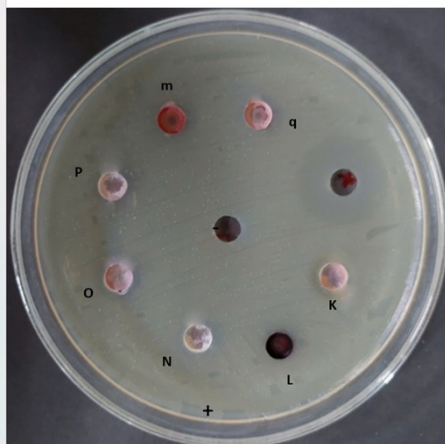


Fig. S 82. Antibacterial activity of compounds against *E. coli* on agar plates

Staphylococcus aureus ATCC 6538

(+) : Chloramphenicol
(-) : DMSO

4

Staphylococcus aureus ATCC 6538

(+) : Chloramphenicol
(-) : DMSO



Fig. S 83. Antibacterial activity of compounds against *S. aureus* on agar plates

Salmonella typhimurium ATCC 14028

(+) : Chloramphenicol
(-) : DMSO

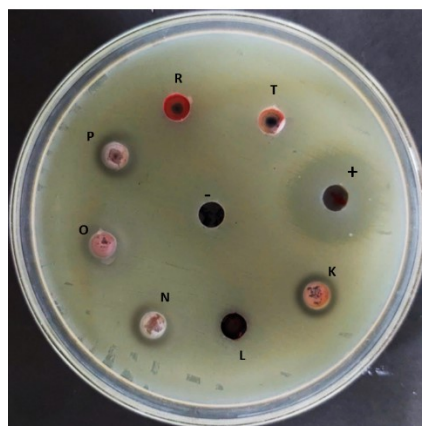


Fig. S 84. Antibacterial activity of compounds against *S.typhimurium* on agar plates

Candida albicans ATCC 10231

(+) : Nystatin
(-) : DMSO

4

Candida albicans ATCC 10231

(+) : Nystatin
(-) : DMSO



Fig. S 85. Antibacterial activity of compounds against *C.albicans* on agar plates

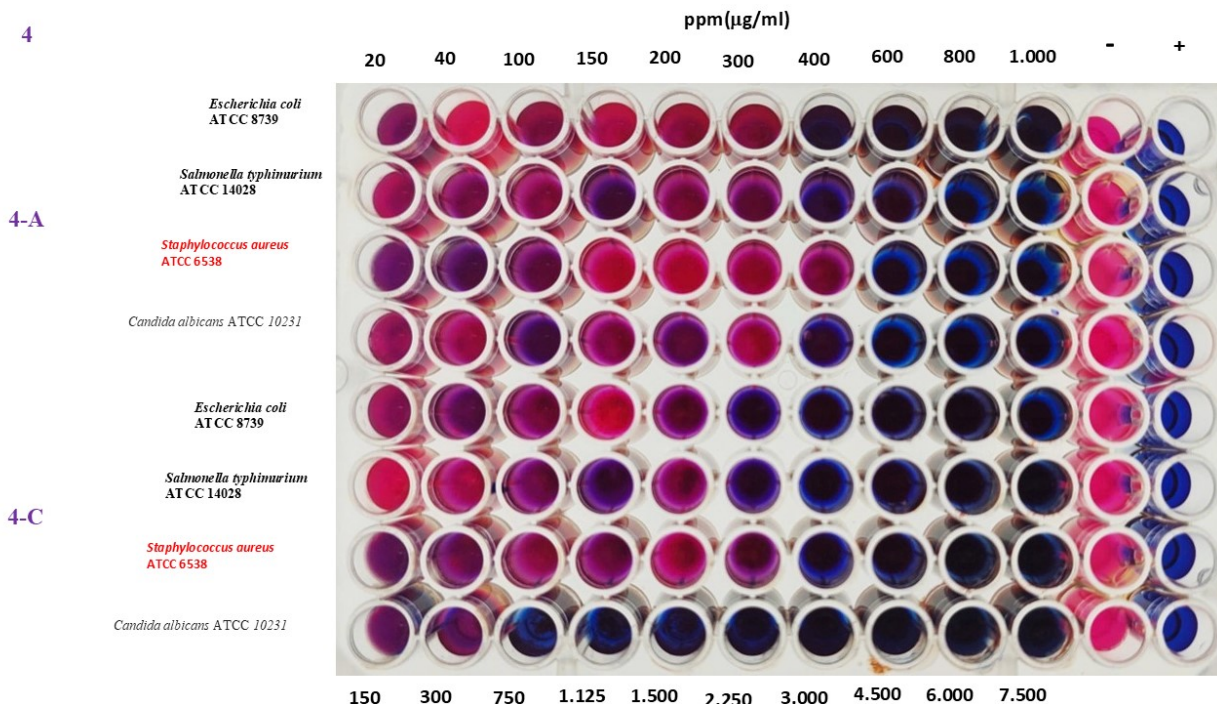


Fig. S 86. Antibacterial MIC measurement test of compounds **4a** and **4c**

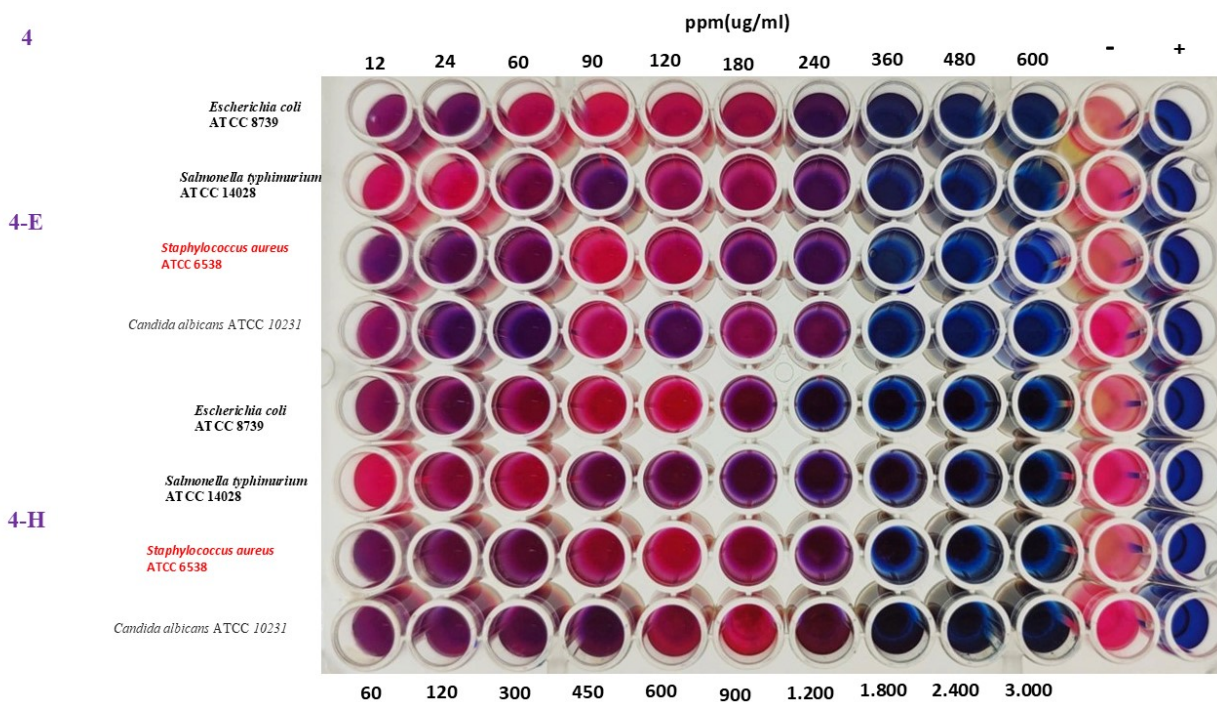


Fig. S 87. Antibacterial MIC measurement test of compounds **4e** and **4h**

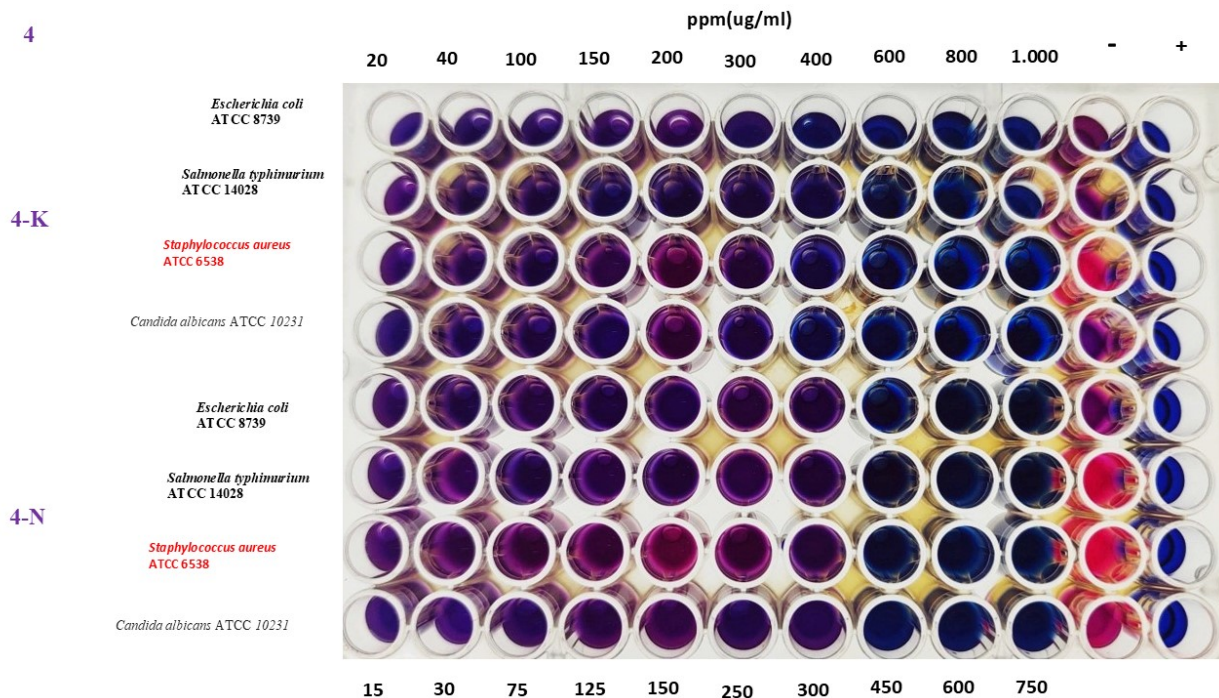


Fig. S 88. Antibacterial MIC measurement test of compounds **4k** and **4n**

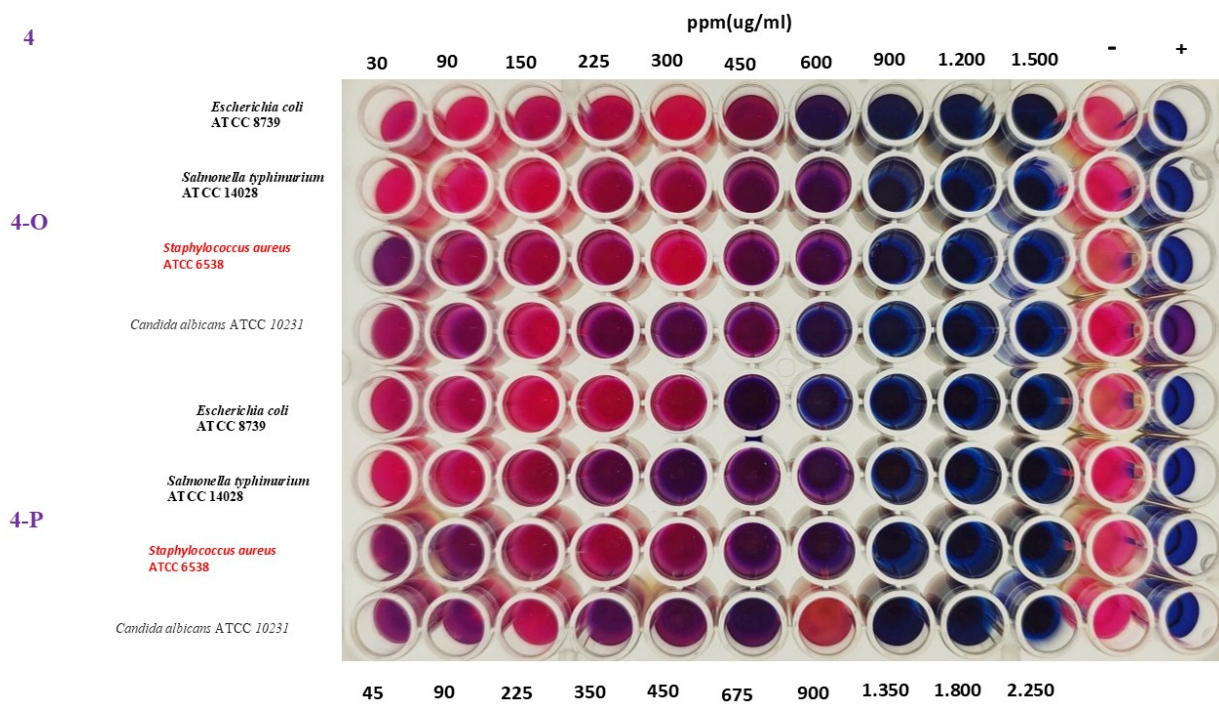


Fig. S 89. Antibacterial MIC measurement test of compounds **4o** and **4p**

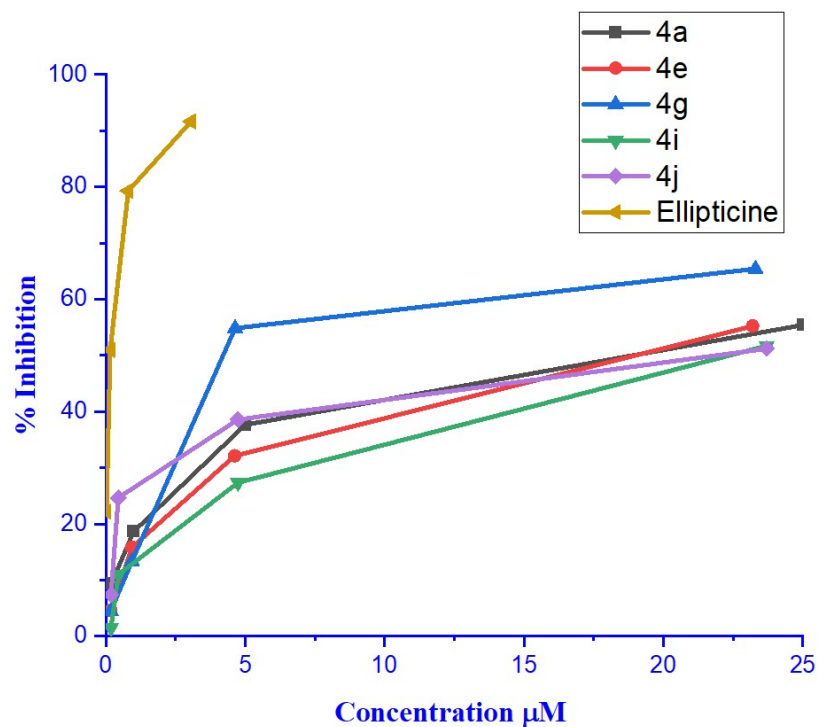


Fig. S 90. Inhibitory effects of active compounds and Ellipticine on cancer cells with MCF-7

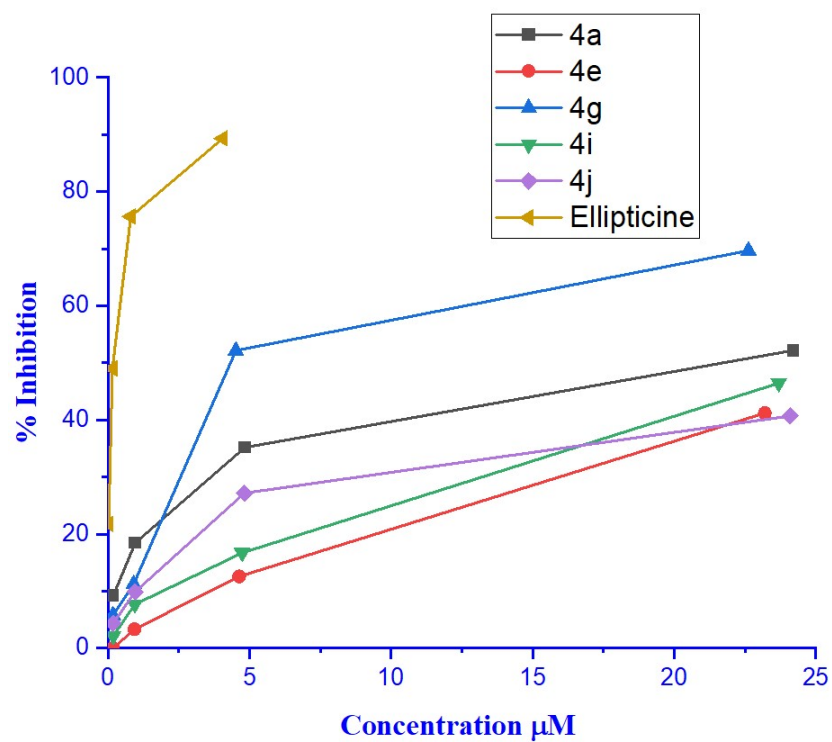


Fig. S 91. Inhibitory effects of active compounds and Ellipticine on cancer cells with A549

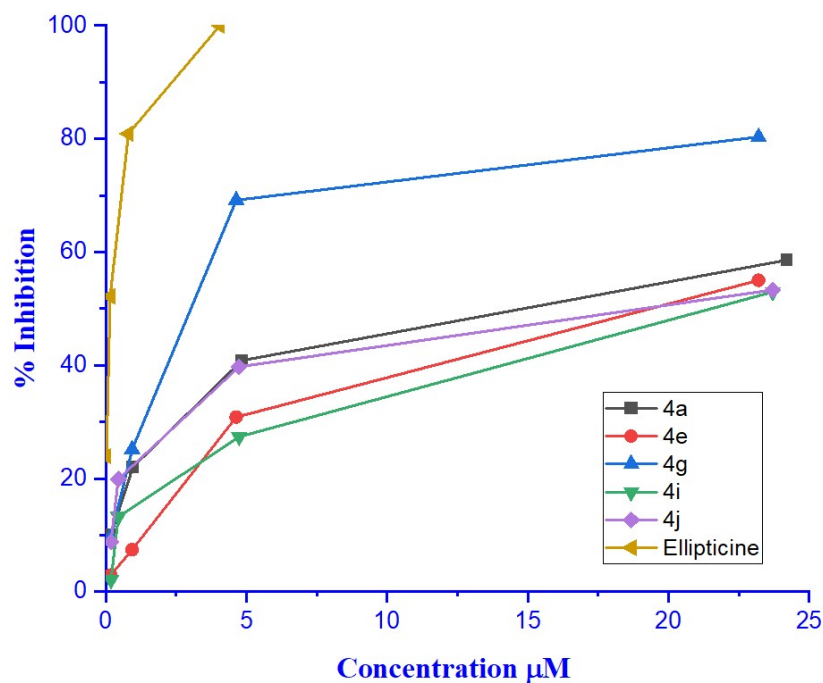


Fig. S 92. Inhibitory effects of active compounds and Ellipticine on cancer cells with HepG2

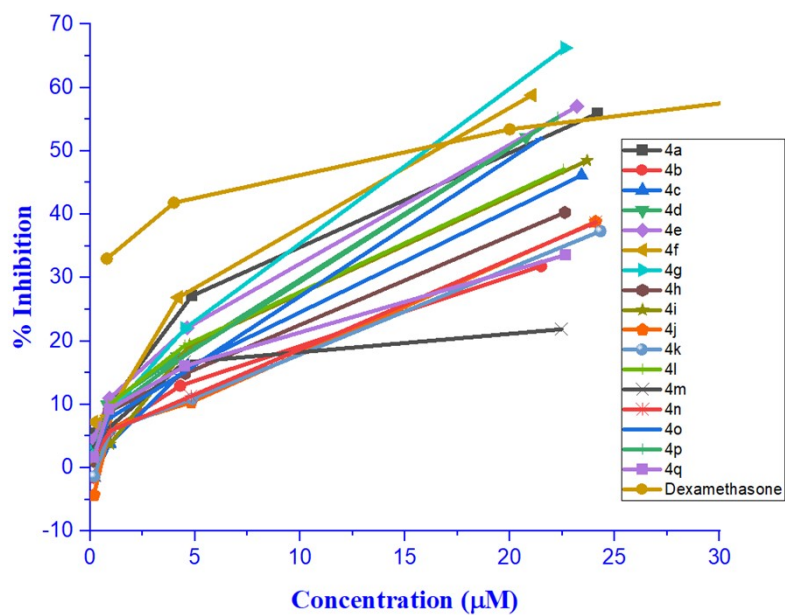


Fig. S 93. Anti-inflammatory inhibitory ability of active compounds and Dexamethasone.

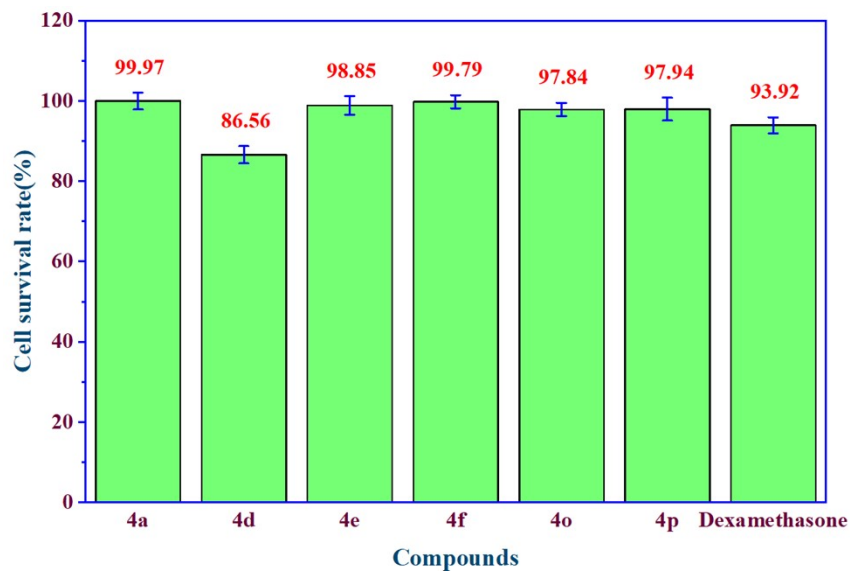


Fig. S 94. The cell viability rate at the maximum concentration in the anti-inflammatory chemical analysis of compounds attained the IC₅₀.

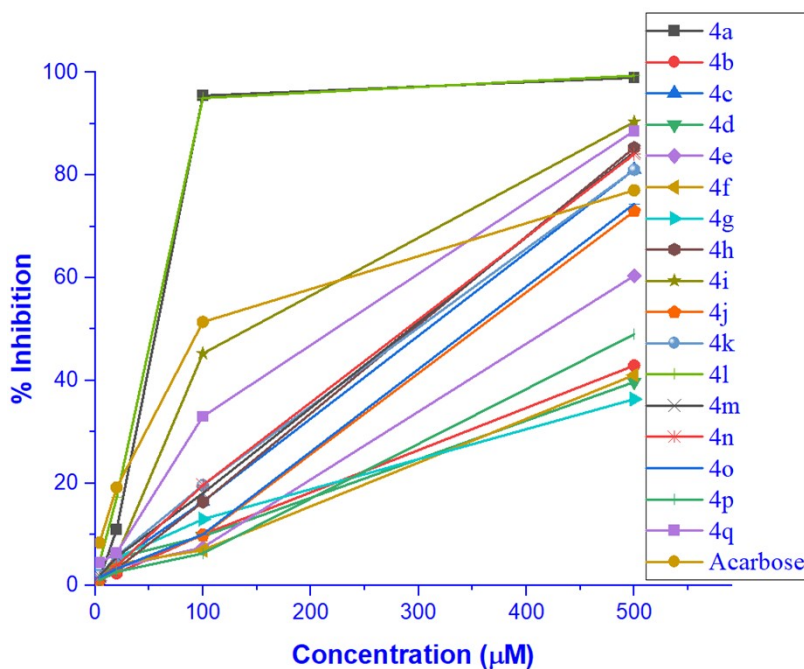


Fig. S 95. Inhibitory ability of the glucosidase enzymes of active compounds and Arcarbose

Table S1. Physicochemical Chemistry of the compound **4l**

<i>Property</i>	<i>Value</i>	<i>Comment</i>
LogS	-7.57	Log of aqueous solubility (log mol/L); Optimal: -4 to 0.5
LogD	4.43	LogP at physiological pH 7.4; Optimal: 1–3
LogP	5.89	Octanol/water partition coefficient; Optimal ≤ 5
TPSA	98.34	Topological Polar Surface Area; Optimal: 0–140 Å ²
MW	474.53	Molecular weight; Optimal: 100–600 Da

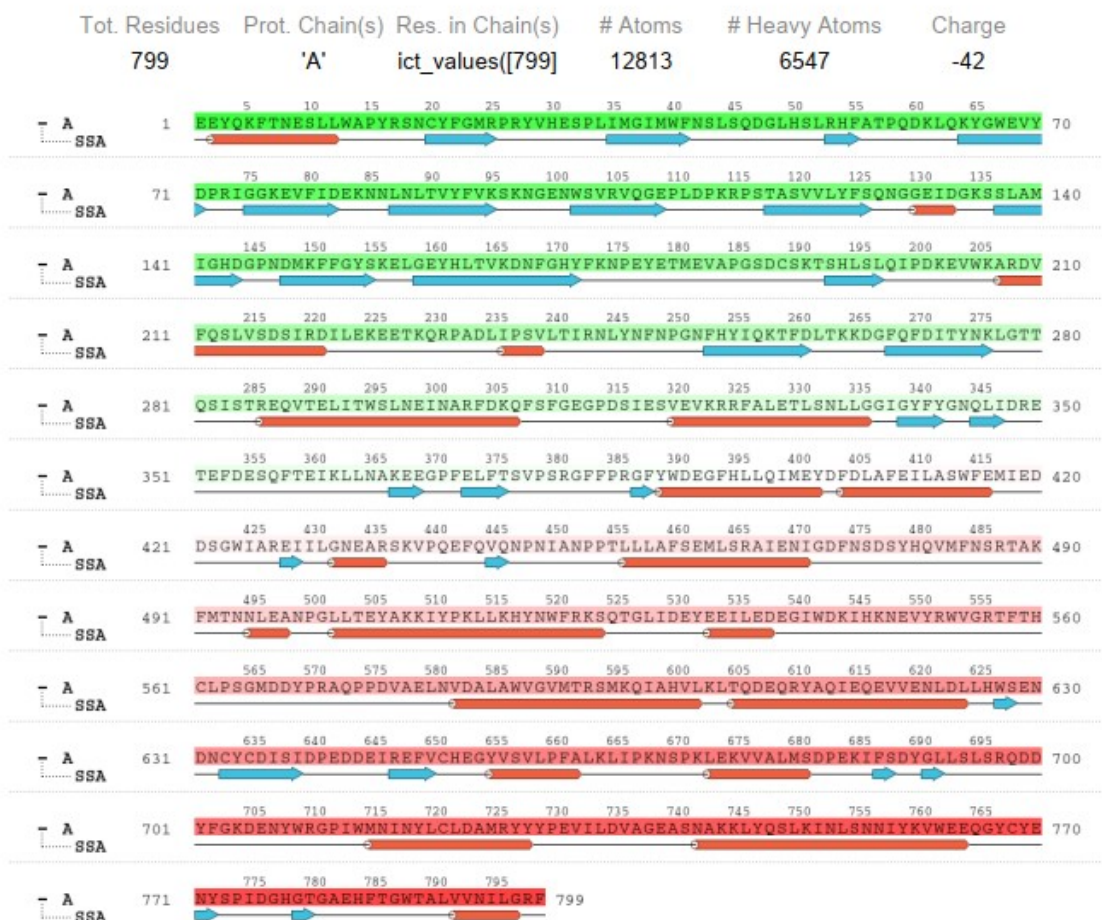
<i>Property</i>	<i>Value</i>	<i>Comment</i>
nHA	7	Number of hydrogen bond acceptors; Optimal: 0–12
nHD	2	Number of hydrogen bond donors; Optimal: 0–7
nRot	5	Number of rotatable bonds; Optimal: 0–11
nRing	4	Number of rings; Optimal: 0–6
Density	1.12	Density = MW/Volume
Table S2. Medical Chemistry of compound 4I		
<i>Property</i>	<i>Value</i>	<i>Comment</i>
QED	0.661	Quantitative Estimate of Drug-likeness; Attractive: >0.67
SAscore	3.15	Synthetic accessibility score; SAscore <6 = easy to synthesize
Fsp ³	0.22	Fraction of sp ³ hybridized carbons; Fsp ³ ≥ 0.42 considered suitable
MCE-18	26.0	Medicinal chemistry evolution index; MCE-18 ≥ 45 considered suitable
NP-likeness	-1.10	Natural product-likeness score; Range: -5 to +5
Lipinski rule	Accepted	MW ≤ 500; logP ≤ 5; H-acc ≤ 10; H-don ≤ 5
Pfizer rule	Accepted	logP > 3; TPSA < 75; Compounds exceeding limits are likely toxic
GSK rule	Rejected	MW ≤ 400; logP ≤ 4; Compound does not satisfy GSK criteria
Golden Triangle	Accepted	200 ≤ MW ≤ 500; -2 ≤ logD ≤ 5; Favorable ADMET profile expected
Table S3. Absorption properties of compound 4I		
<i>Property</i>	<i>Value</i>	<i>Comment</i>
Caco-2-permeability	-4.97	Optimal: > -5.15 log unit
Pgp-inhibitor	0.137	Category 1: inhibitor; Category 0: non-inhibitor; Probability of being an inhibitor
Pgp-substrate	0.001	Category 1: substrate; Category 0: non-substrate; Very low probability
HIA	0.013	Human intestinal absorption; Optimal: > 0.3
F(20%)	0.968	Fraction absorbed ≥ 20%; high absorption probability
F(30%)	1.000	Fraction absorbed ≥ 30%; excellent absorption
Table S4. Distribution properties of compound 4I		
<i>Property</i>	<i>Value</i>	<i>Comment</i>
PPB	98.7%	Plasma protein binding; Optimal < 90%; high binding may

<i>Property</i>	<i>Value</i>	<i>Comment</i>
		reduce free drug level
VD	0.38	Volume of distribution (L/kg); Optimal range: 0.04–20
BBB penetration	0.152	Probability of crossing the blood–brain barrier
Fu	1.4%	Fraction unbound in plasma; Low: <5%; indicates strong plasma binding
Table S5. Metabolism properties of compound 4I		
<i>Property</i>	<i>Value</i>	<i>Comment</i>
CYP1A2 inhibitor	0.824	Category 1: inhibitor; compound may inhibit CYP1A2
CYP2C19 inhibitor	0.334	Category 1: inhibitor; moderate probability
CYP2C9 inhibitor	0.476	Category 1: inhibitor; possible CYP2C9 inhibition
CYP2D6 inhibitor	0.201	Category 0: non-inhibitor; unlikely to inhibit CYP2D6
CYP3A4 inhibitor	0.547	Category 1: inhibitor; potential CYP3A4 inhibition
CYP1A2 substrate	0.198	Category 0: non-substrate; unlikely to be metabolized by CYP1A2
CYP2C9 substrate	0.741	Category 1: substrate; likely to be metabolized by CYP2C9
CYP2D6 substrate	0.835	Category 1: substrate; likely to be metabolized by CYP2D6
CYP3A4 substrate	0.118	Category 0: non-substrate; not a substrate for CYP3A4
Table S6. Excretion properties of compound 4I		
<i>Property</i>	<i>Value</i>	<i>Comment</i>
CL	4.86	Clearance rate (mL/min/kg); Low: <5
T _{1/2}	0.69	Probability of long half-life; 0.5–1 indicates moderate half-life potential
Table S7. Toxicity properties of compound 4I		
<i>Property</i>	<i>Value</i>	<i>Comment</i>
hERG blocker	0.062	Probability of cardiotoxicity; <0.3 = safe
H-HT	0.926	Human hepatotoxicity: high probability of liver toxicity
DILI	0.811	Drug-induced liver injury; compound at risk of liver toxicity
AMES toxicity	0.045	Ames mutagenicity test; non-mutagenic
FDAMDD	0.054	Maximum recommended daily dose (FDA); safe
Skin sensitization	0.489	Probability of skin sensitization: moderate
Carcinogenicity	0.567	Probability of carcinogenicity: moderate
Eye irritation	0.031	Probability of eye irritation: low
Respiratory	0.098	Probability of respiratory toxicity: low

<i>Property</i>	<i>Value</i>	<i>Comment</i>
Table S8. Toxicophoric alerts of compound 4l		
<i>Property</i>	<i>Value</i>	<i>Comment</i>
Acute toxicity rule	0 alerts	No structural alerts for acute oral toxicity
Genotoxic carcinogenicity rule	2 alerts	Two substructures associated with genotoxic carcinogenicity
Skin sensitization rule	1 alerts	One structural alert for potential skin irritation
Aquatic toxicity rule	0 alerts	No alerts for aquatic toxicity
Non-biodegradable rule	0 alerts	Biodegradable; no non-biodegradability alerts detected

CPU #	Job Type	Ensemble	Temp. [K]	Sim. Time [ns]	# Atoms	# Waters	Charge
1	mdsim	NPT	300.0	100.102	63649	16882	0

Protein Information



Ligand Information

SMILES c1cccc(c1c23)n(CC)c2ccc(c3)/C=N/N=c([nH]4)sc4-c(c5)ccc(O)c5CO

Fig. S 96. Information protein 4J5T and ligand (pose 612 of compound **4I**)

Ligand Properties

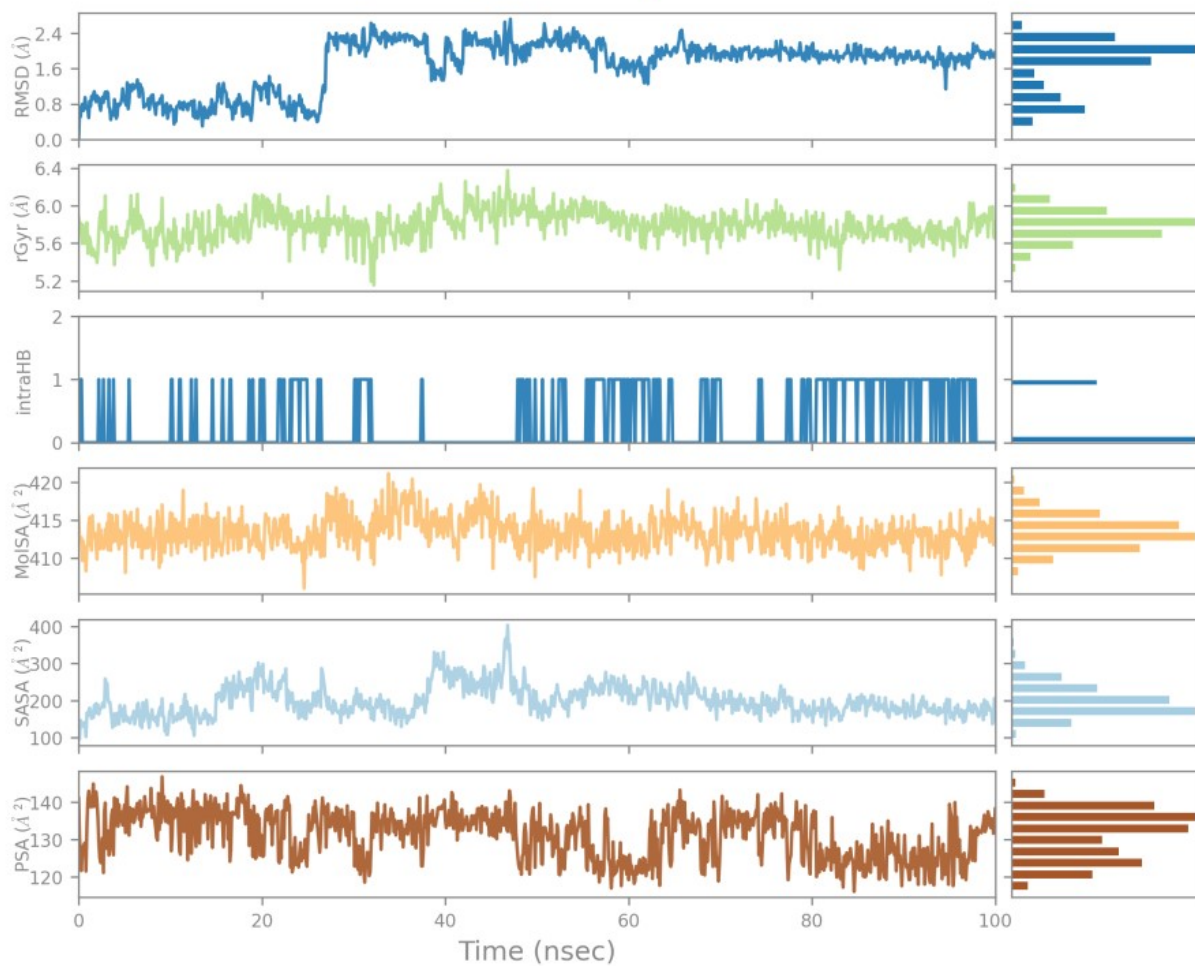


Fig. S 97. Ligand (pose 612 of compound **4l**) properties

Ligand Torsion Profile

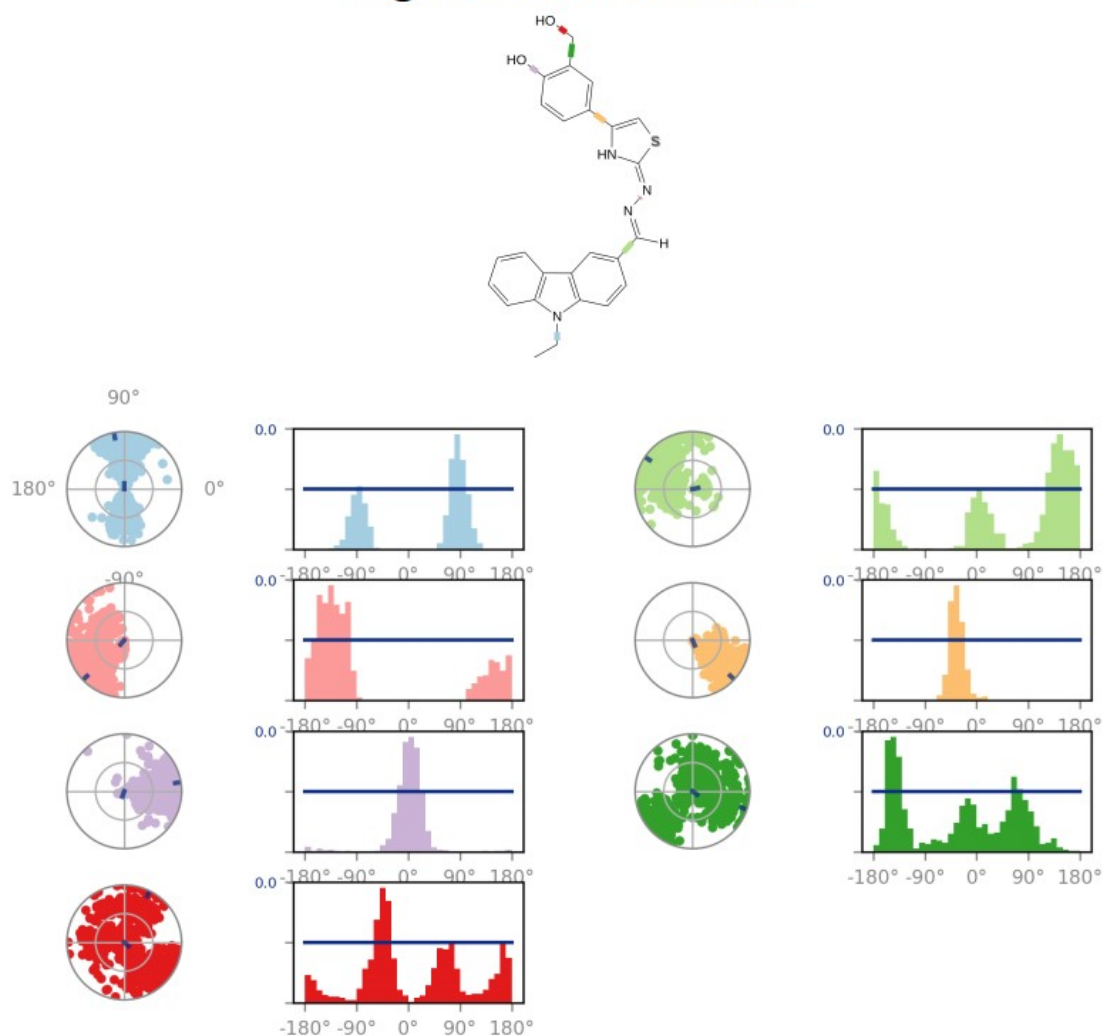


Fig. S 98. Ligand (pose 612 of compound 4l) Torsion Profile

Protein Secondary Structure

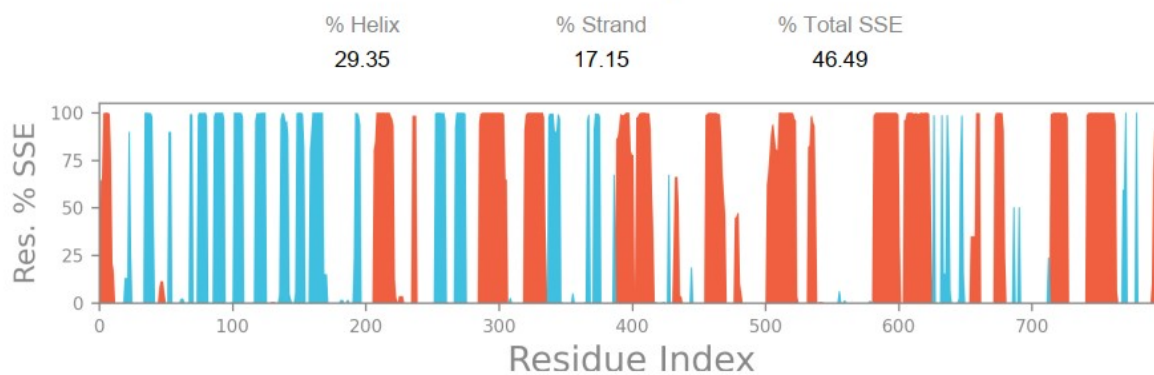


Fig. S 99. Protein (4J5T) Secondary Structure

Protein-Ligand Contacts (cont.)

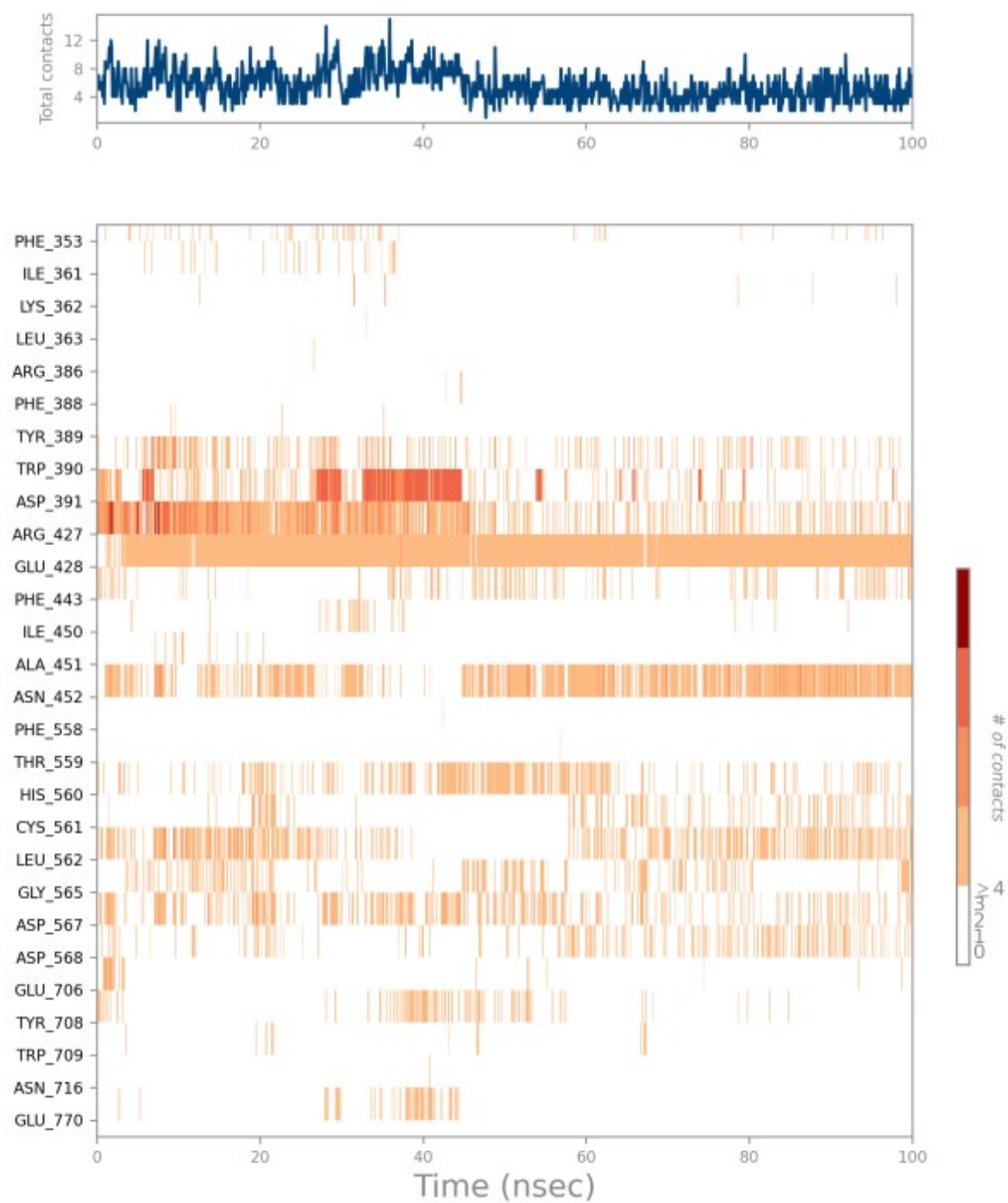


Fig. S 100. Protein – Ligand contact

Ligand RMSF

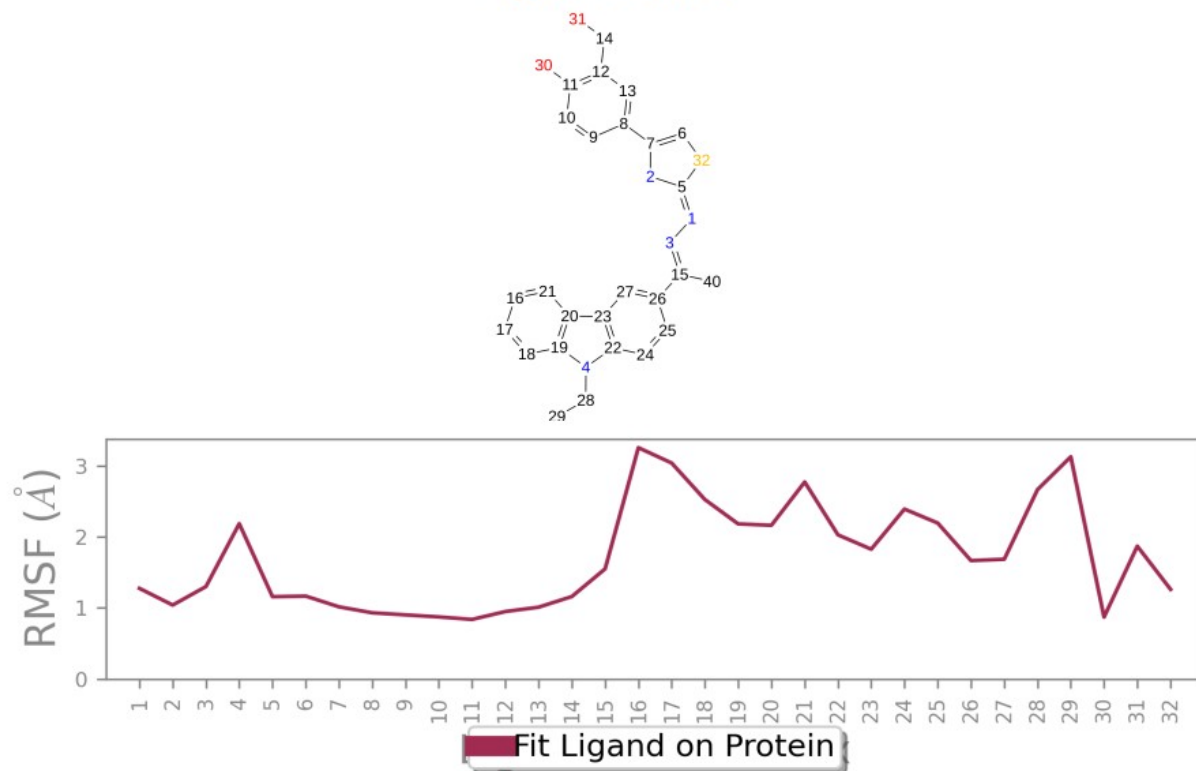


Fig. S 101. RMSF Ligand (pose 612 of compound 4l)

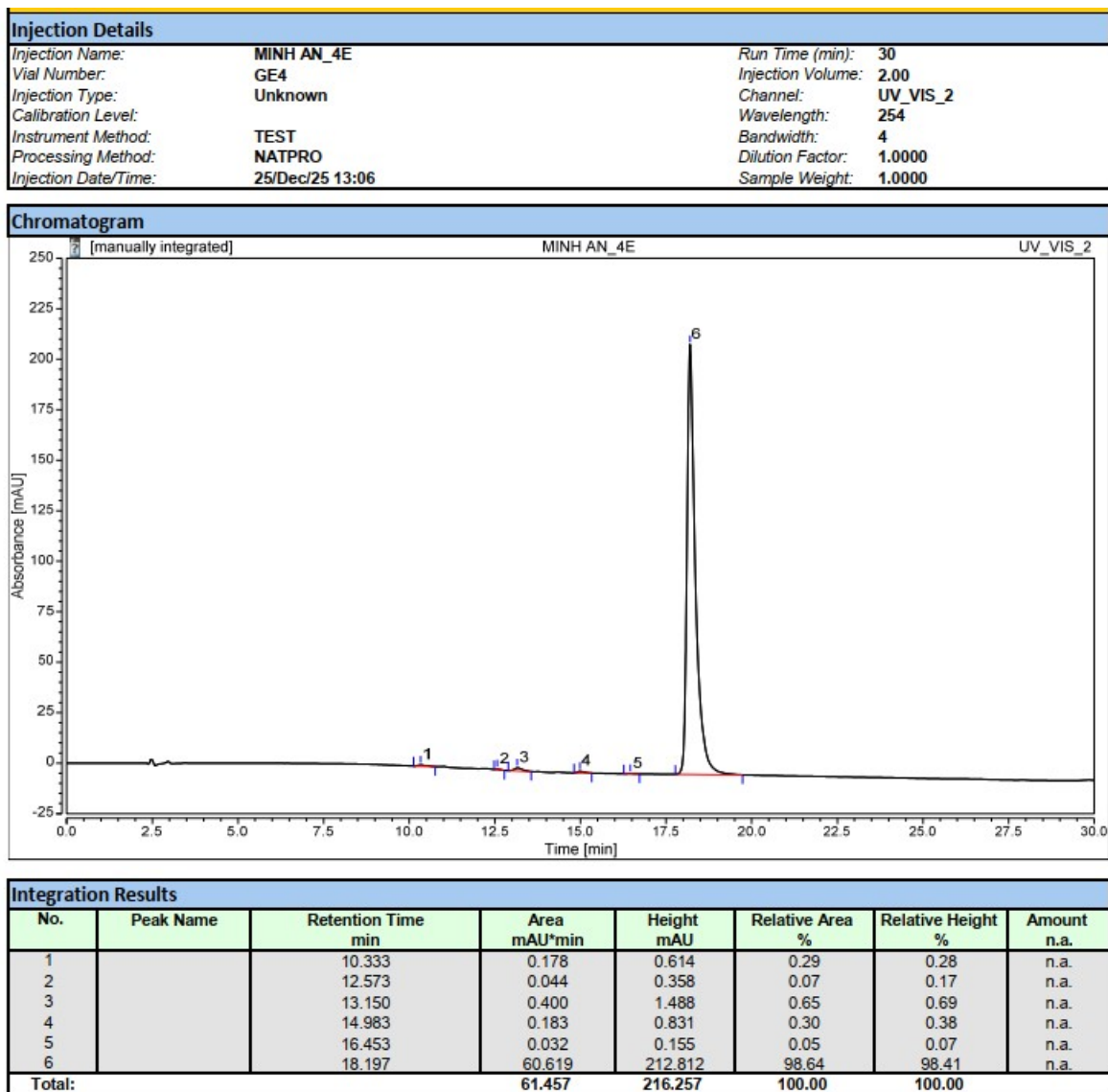
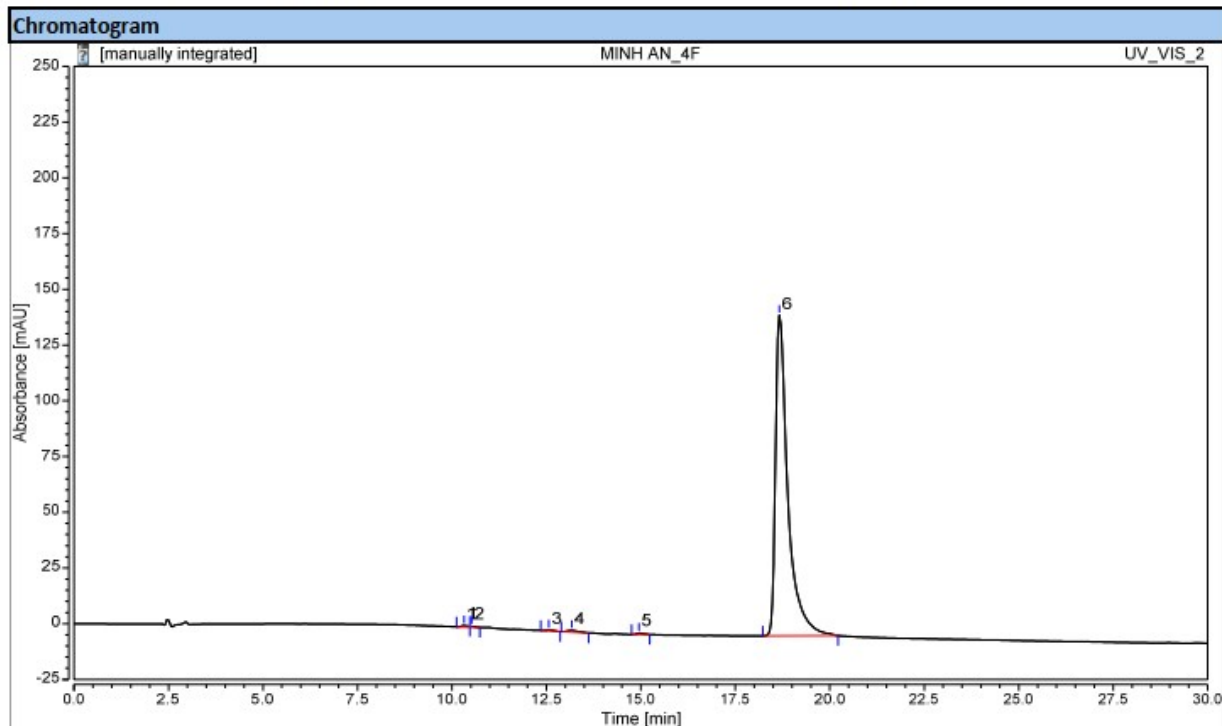


Fig. S102. HPLC of compound 4e.

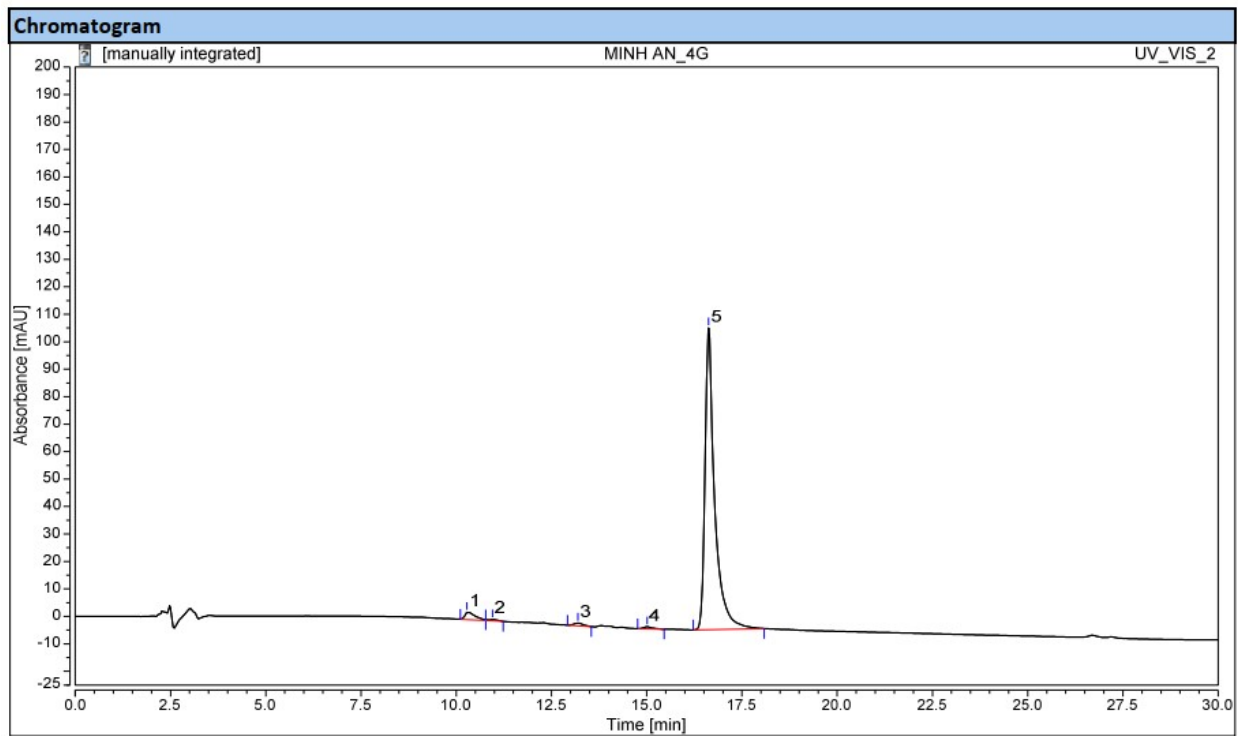
Injection Details			
Injection Name:	MINH AN_4F	Run Time (min):	30
Vial Number:	GE3	Injection Volume:	2.00
Injection Type:	Unknown	Channel:	UV_VIS_2
Calibration Level:		Wavelength:	254
Instrument Method:	TEST	Bandwidth:	4
Processing Method:	NATPRO	Dilution Factor:	1.0000
Injection Date/Time:	25/Dec/25 12:29	Sample Weight:	1.0000



Integration Results							
No.	Peak Name	Retention Time min	Area mAU*min	Height mAU	Relative Area %	Relative Height %	Amount n.a.
1		10.320	0.134	0.648	0.24	0.44	n.a.
2		10.523	0.067	0.421	0.12	0.29	n.a.
3		12.563	0.118	0.558	0.21	0.38	n.a.
4		13.170	0.283	0.804	0.51	0.55	n.a.
5		14.947	0.138	0.674	0.25	0.46	n.a.
6		18.667	54.610	143.890	98.66	97.89	n.a.
Total:			55.350	146.993	100.00	100.00	

Fig. S103. HPLC of compound **4f**.

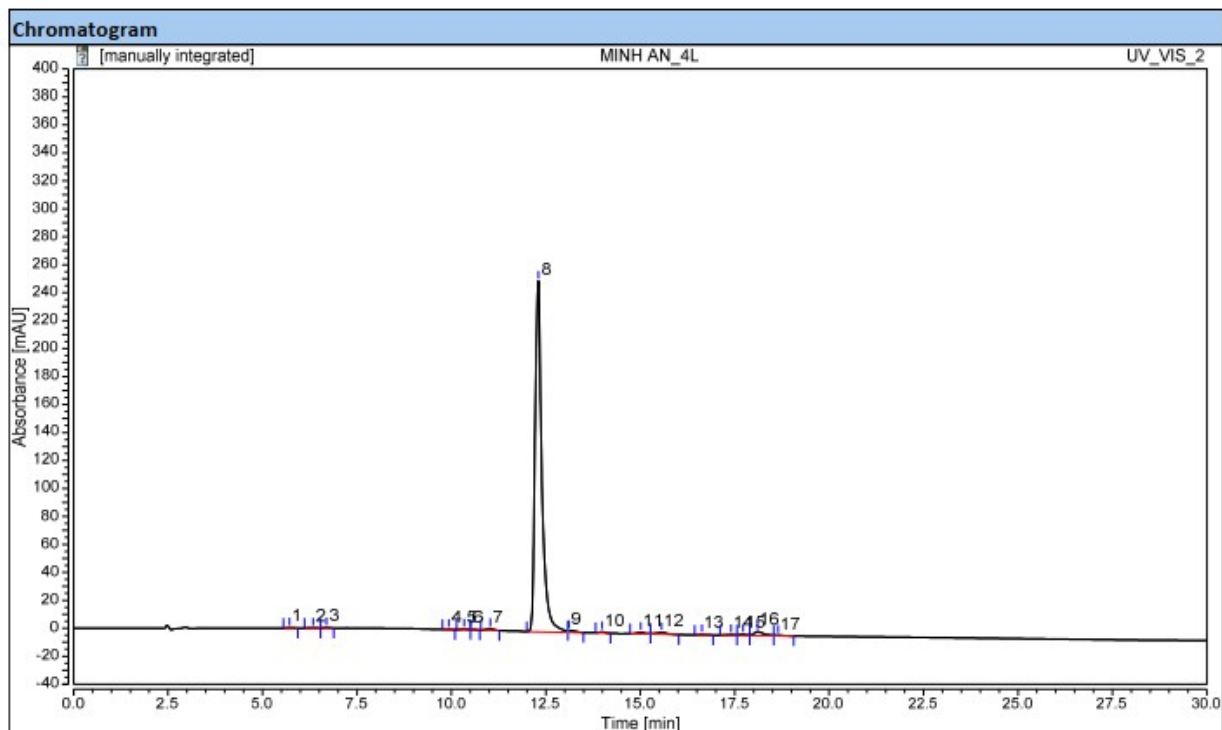
Injection Details			
Injection Name:	MINH AN_4G	Run Time (min):	30
Vial Number:	GE5	Injection Volume:	2.00
Injection Type:	Unknown	Channel:	UV_VIS_2
Calibration Level:		Wavelength:	254
Instrument Method:	TEST	Bandwidth:	4
Processing Method:	NATPRO	Dilution Factor:	1.0000
Injection Date/Time:	25/Dec/25 15:38	Sample Weight:	1.0000



Integration Results							
No.	Peak Name	Retention Time min	Area mAU*min	Height mAU	Relative Area %	Relative Height %	Amount n.a.
1		10.280	0.856	2.612	2.54	2.28	n.a.
2		10.953	0.130	0.416	0.39	0.36	n.a.
3		13.197	0.278	0.959	0.82	0.84	n.a.
4		15.010	0.205	0.794	0.61	0.69	n.a.
5		16.627	32.266	109.886	95.64	95.83	n.a.
Total:			33.736	114.667	100.00	100.00	

Fig. S104. HPLC of compound 4g.

Injection Details			
Injection Name:	MINH AN_4L	Run Time (min):	30
Vial Number:	GE2	Injection Volume:	2.00
Injection Type:	Unknown	Channel:	UV_VIS_2
Calibration Level:		Wavelength:	254
Instrument Method:	TEST	Bandwidth:	4
Processing Method:	NATPRO	Dilution Factor:	1.0000
Injection Date/Time:	25/Dec/25 14:22	Sample Weight:	1.0000

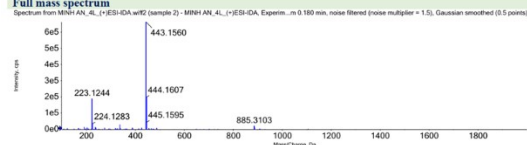


Integration Results							
No.	Peak Name	Retention Time min	Area mAU*min	Height mAU	Relative Area %	Relative Height %	Amount n.a.
1		5.713	0.027	0.184	0.05	0.07	n.a.
2		6.340	0.029	0.124	0.05	0.05	n.a.
3		6.690	0.059	0.409	0.11	0.16	n.a.
4		9.930	0.037	0.232	0.07	0.09	n.a.
5		10.340	0.117	0.562	0.21	0.21	n.a.
6		10.510	0.044	0.235	0.08	0.09	n.a.
7		11.030	0.269	1.320	0.49	0.50	n.a.
8		12.300	52.316	250.875	94.37	95.15	n.a.
9		13.113	0.306	1.310	0.55	0.50	n.a.
10		13.990	0.150	0.879	0.27	0.33	n.a.
11		15.010	0.289	1.158	0.52	0.44	n.a.
12		15.563	0.454	1.327	0.82	0.50	n.a.
13		16.630	0.070	0.357	0.13	0.14	n.a.
14		17.403	0.104	0.476	0.19	0.18	n.a.
15		17.723	0.181	0.843	0.33	0.32	n.a.
16		18.107	0.868	2.916	1.57	1.11	n.a.
17		18.650	0.116	0.450	0.21	0.17	n.a.
Total:			55.434	263.656	100.00	100.00	

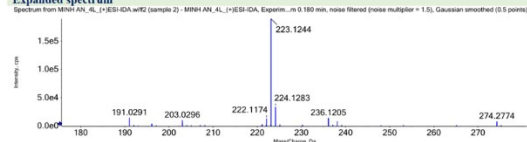
Fig. S105. HPLC of compound 4l.

Injection details			
Sample name	4L	Vial position	50
Sample file name	SR_wi02-MINH AN	Inject volume	2.00
Acquisition date	24/12/2025 01:10:35 PM	Acquisition method	ESI_POS_SCAN_IDA
Operator	CB21261708	Instrument name	X500g QTOF

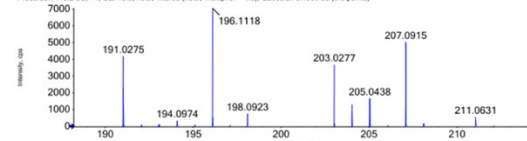
Full mass spectrum



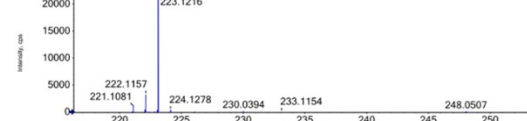
Expanded spectrum



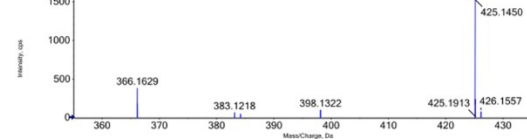
Spectrum from MINH AN_4L_1(+ESI-IDA.wi02 (sample 2) - MINH AN_4L_1(+ESI-IDA, Experiment 9, 0.159 min, noise filtered (noise multiplier = 1.5), Gaussian smoothed (0.5 points)



Spectrum from MINH AN_4L_1(+ESI-IDA.wi02 (sample 2) - MINH AN_4L_1(+ESI-IDA, Experiment 9, 0.159 min, noise filtered (noise multiplier = 1.5), Gaussian smoothed (0.5 points)

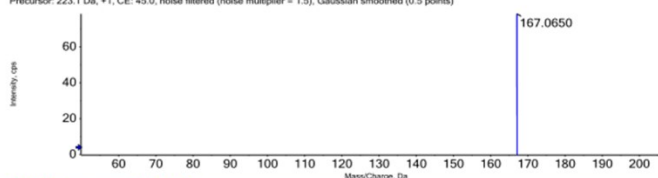


Spectrum from MINH AN_4L_1(+ESI-IDA.wi02 (sample 2) - MINH AN_4L_1(+ESI-IDA, Experiment 9, 0.159 min, noise filtered (noise multiplier = 1.5), Gaussian smoothed (0.5 points)



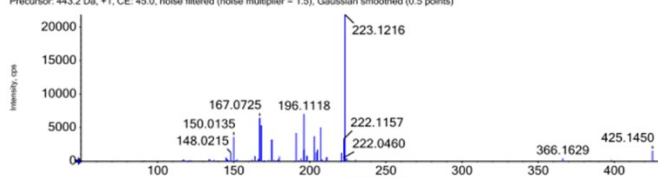
MS/MS spectrum of 223.1244

Spectrum from MINH AN_4L_1(+ESI-IDA.wi02 (sample 2) - MINH AN_4L_1(+ESI-IDA, Experiment 9, 0.159 min, noise filtered (noise multiplier = 1.5), Gaussian smoothed (0.5 points)

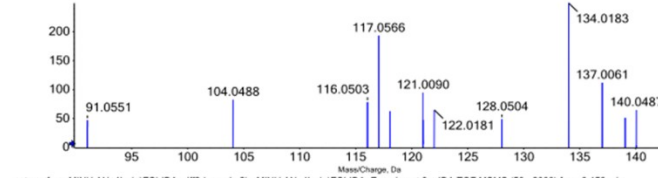


MS/MS spectrum of 443.1560

Spectrum from MINH AN_4L_1(+ESI-IDA.wi02 (sample 2) - MINH AN_4L_1(+ESI-IDA, Experiment 9, 0.159 min, noise filtered (noise multiplier = 1.5), Gaussian smoothed (0.5 points)



Spectrum from MINH AN_4L_1(+ESI-IDA.wi02 (sample 2) - MINH AN_4L_1(+ESI-IDA, Experiment 9, 0.159 min, noise filtered (noise multiplier = 1.5), Gaussian smoothed (0.5 points)



Spectrum from MINH AN_4L_1(+ESI-IDA.wi02 (sample 2) - MINH AN_4L_1(+ESI-IDA, Experiment 9, 0.159 min, noise filtered (noise multiplier = 1.5), Gaussian smoothed (0.5 points)

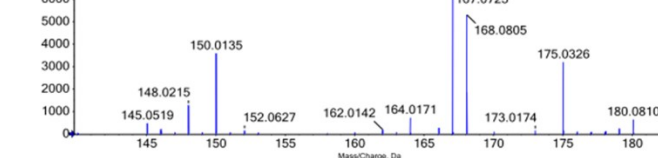


Fig. S106. MS/MS of compound 4L.