Electronic Supporting Information

Design, Synthesis, Molecular docking and *In-vitro* anticancer activities of 1-(4-(benzamido)phenyl)-3-arylurea derivatives

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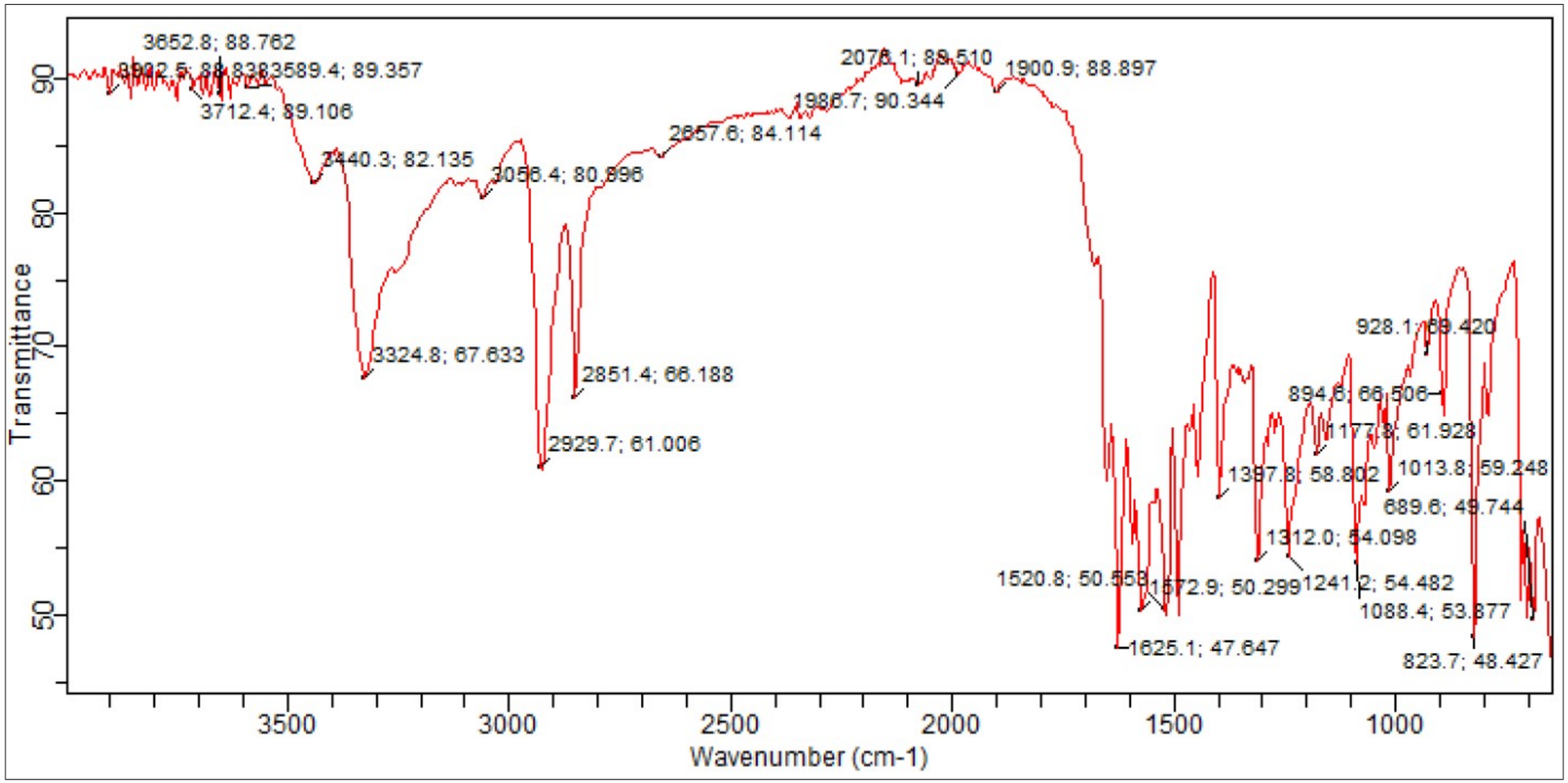
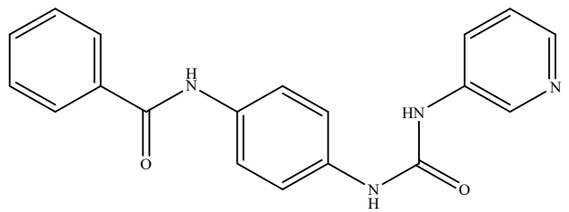


Figure S1. FTIR spectrum of compound 6a

Interpretation:

Structure	Functional Group	Standard Values	Observed Values
	N-H stretching	3350-3310	3324.8
	C-N stretching (Ar)	1342-1266	1241.2
	N-H bending	1650-1580	1520.8
	C=N stretching	1690-1640	1672.9
	C=O stretching (amide)	1690	1625.1
	aromatic C-H bending	900-700	823.7, 689.6, 894.6

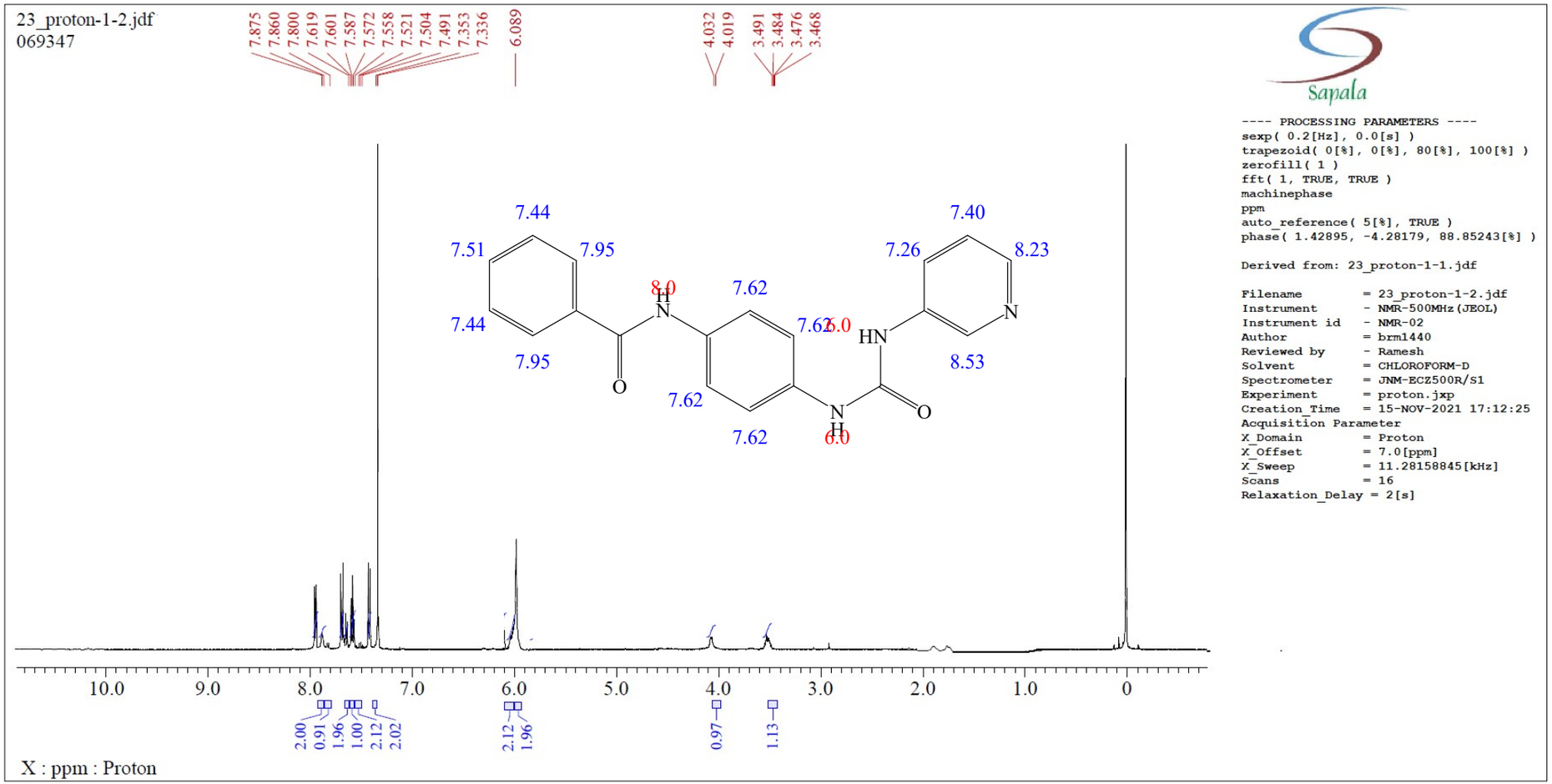


Figure S2. ^{1}HNMR spectrum of compound 6a

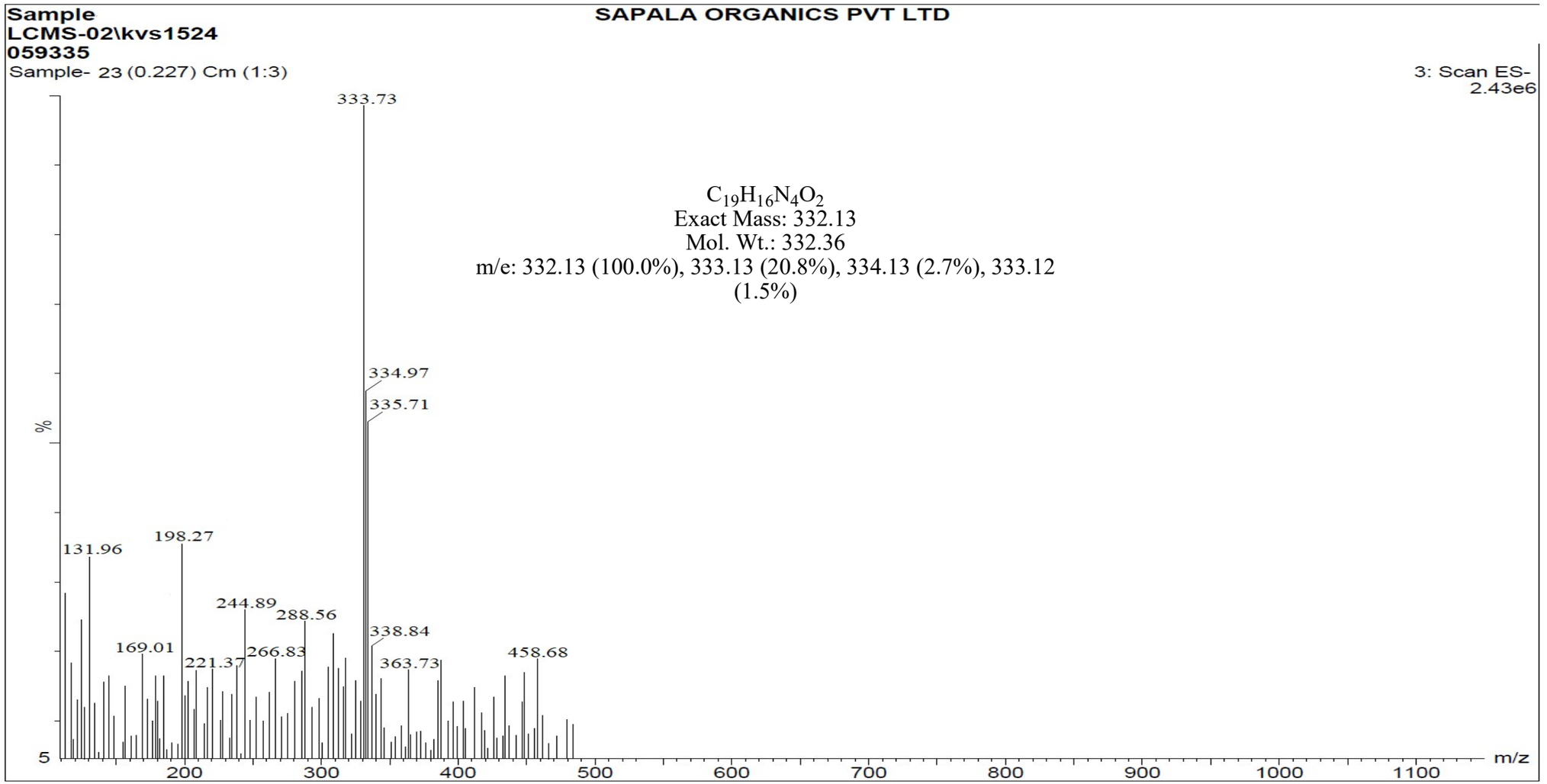


Figure S3. Mass spectrum of compound 6a

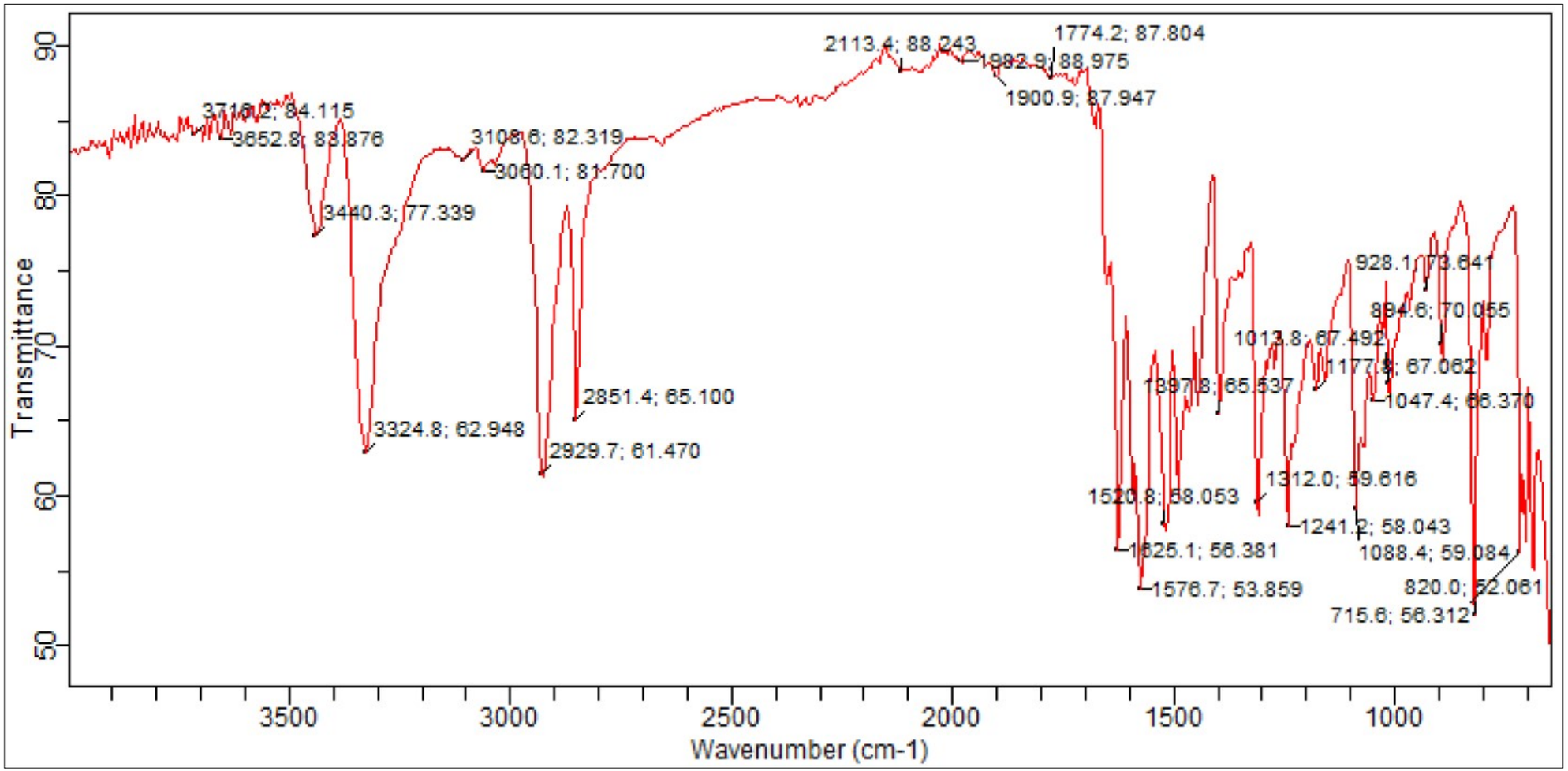
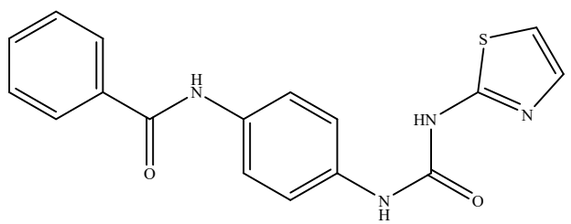


Figure S4. FTIR spectrum of compound 6b

Interpretation:

Structure	Functional Group	Standard Values	Observed Values
	N-H stretching	3350-3310	3324.8
	C-N stretching (Ar)	1342-1266	1312.0
	N-H bending	1650-1580	1576.7
	C=N stretching	1690-1640	1672.9
	C=O stretching (amide)	1690	1625.1
	aromatic C-H bending	900-700	820.0, 715.6, 894.6

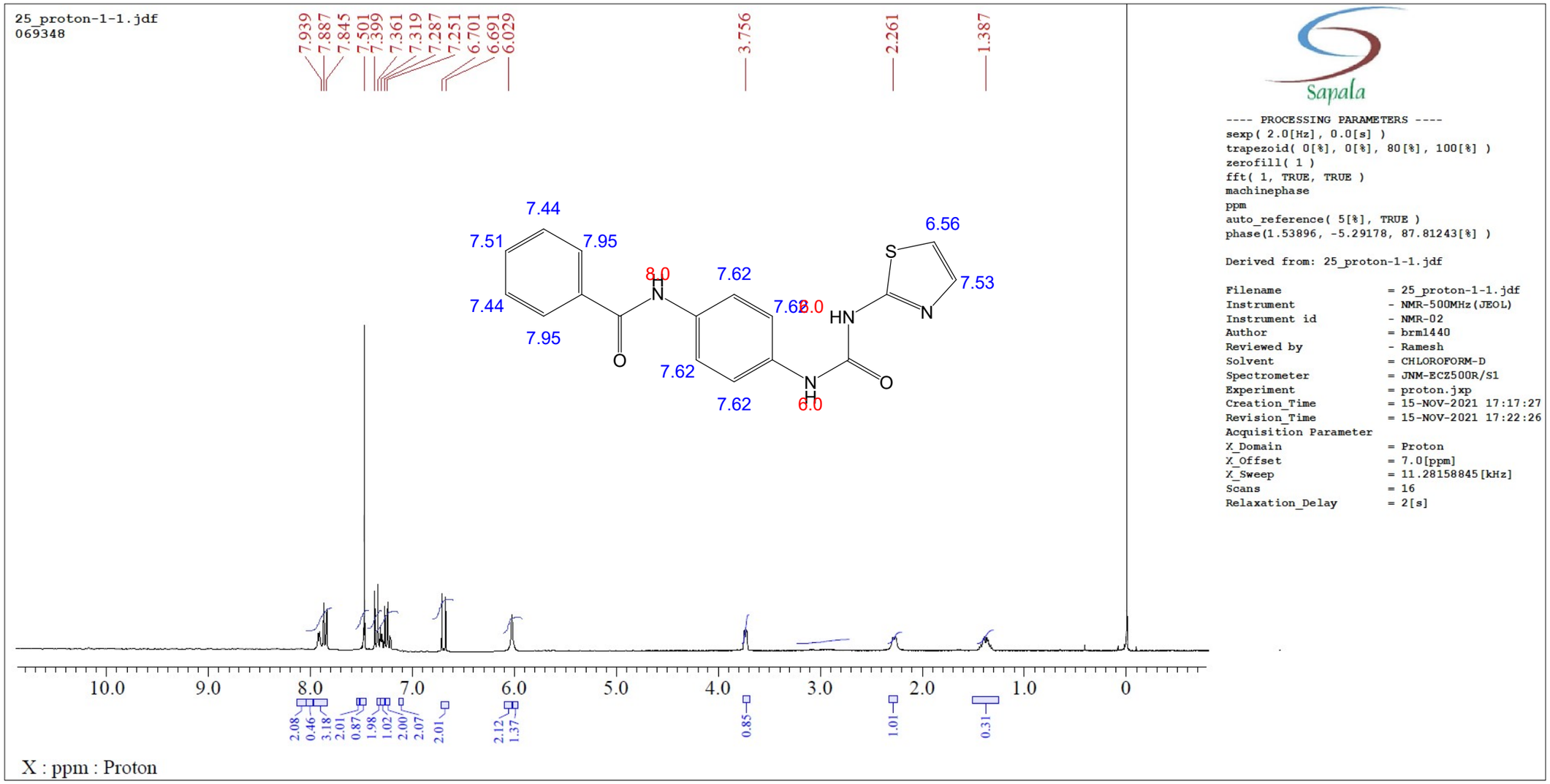


Figure S5. ^{1}HNMR spectrum of compound 6b

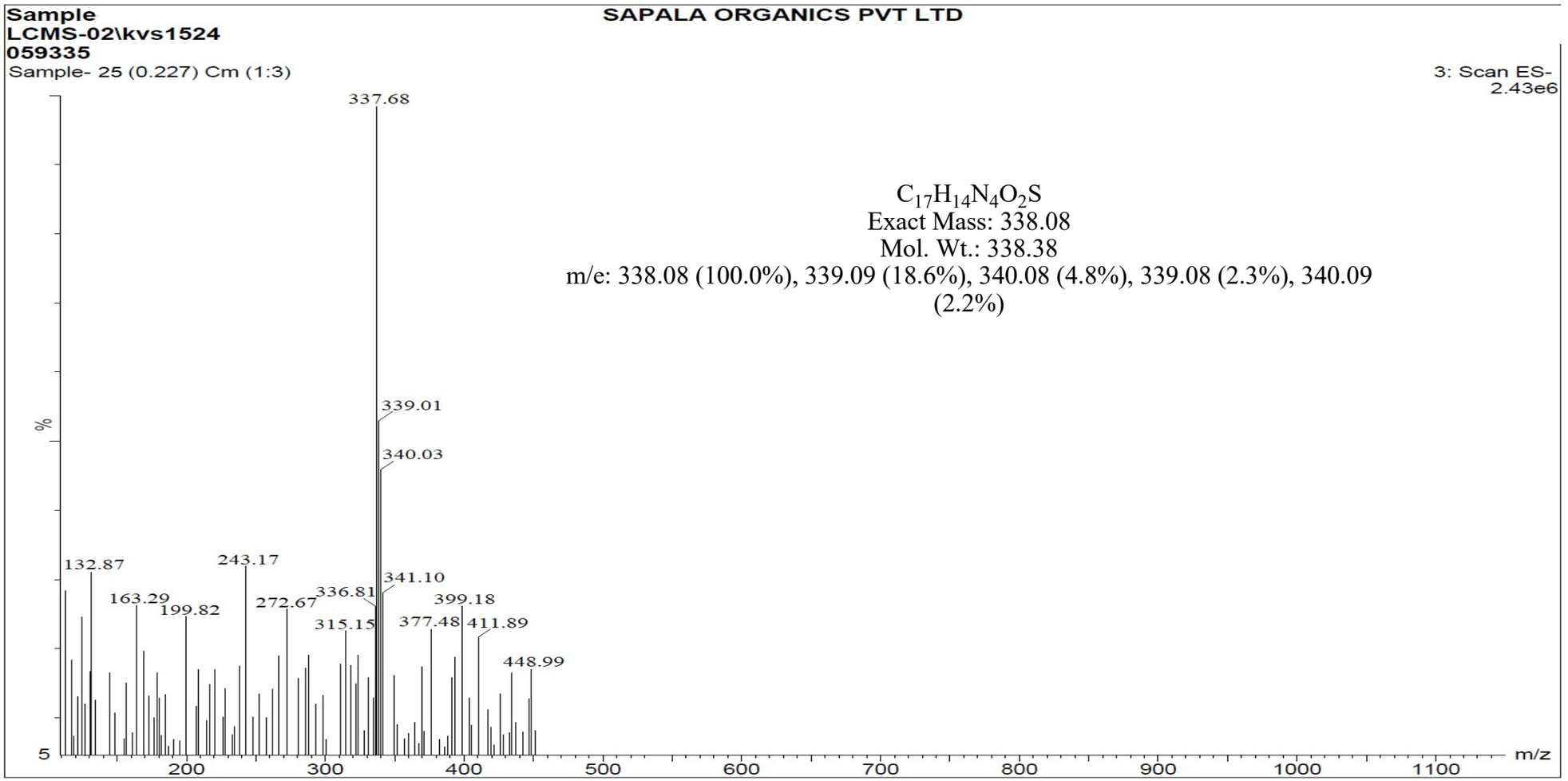


Figure S6. Mass spectrum of compound 6b

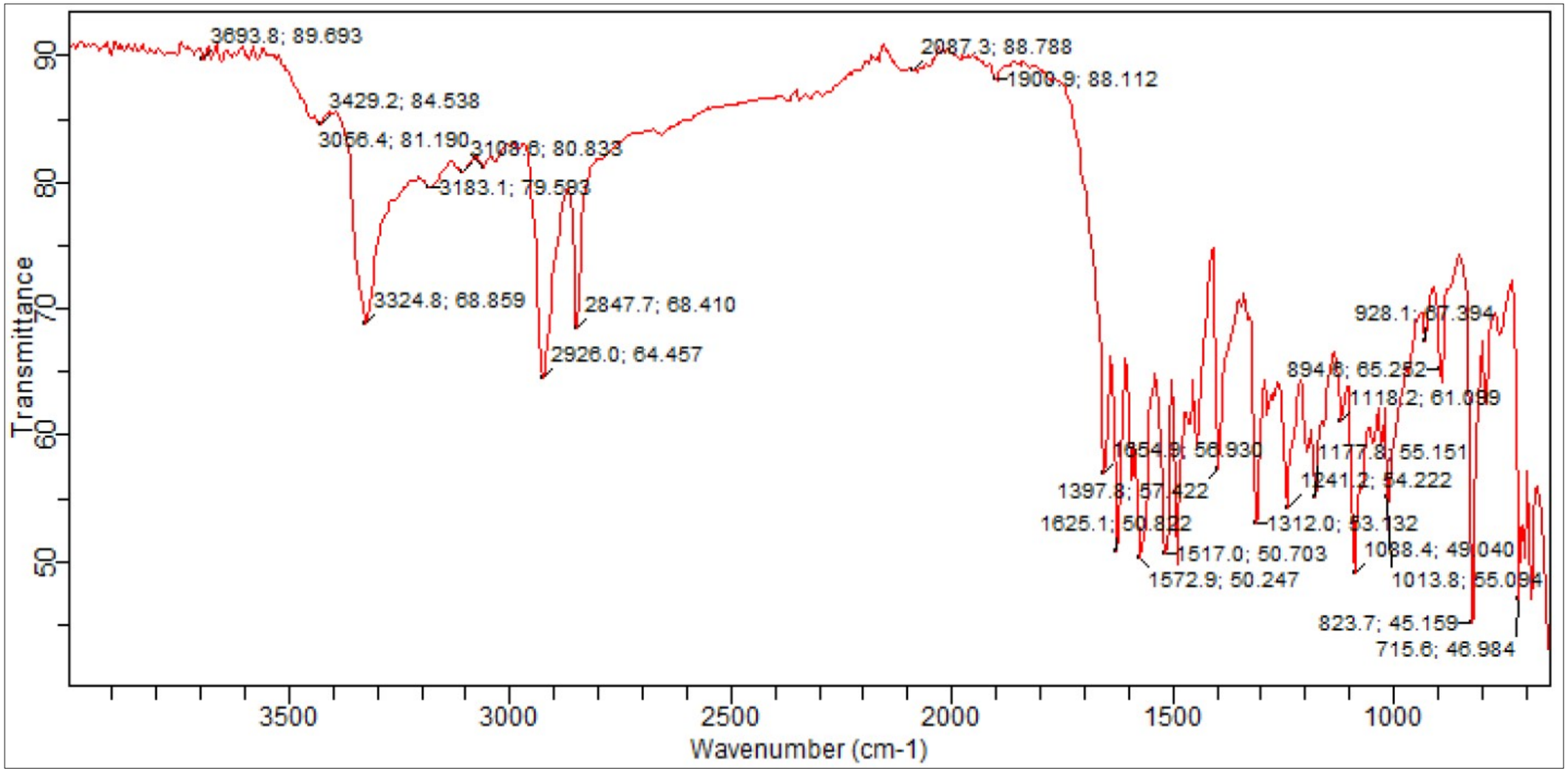
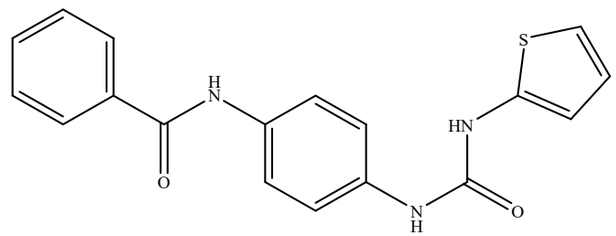


Figure S7. FTIR spectrum of compound 6c

Interpretation:

Structure	Functional Group	Standard Values	Observed Values
	N-H stretching	3350-3310	3324.8
	C-N stretching (Ar)	1342-1266	1312.0
	N-H bending	1650-1580	1572.9
	C=N stretching	1690-1640	1654.9
	C=O stretching (amide)	1690	1625.1
	aromatic C-H bending	900-700	823.7, 894.6,715.6

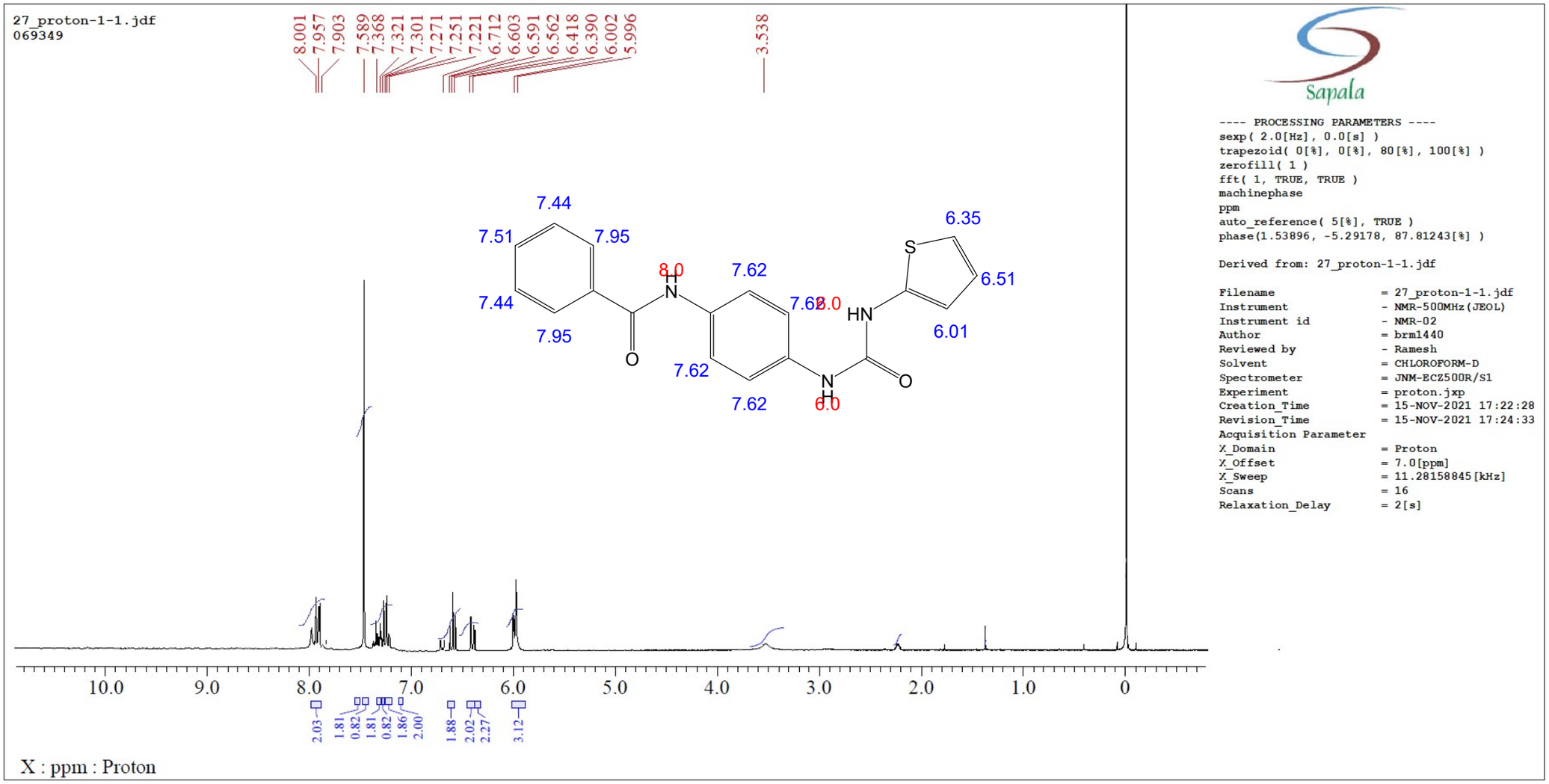


Figure S8. ^{1}HNMR spectrum of compound 6c

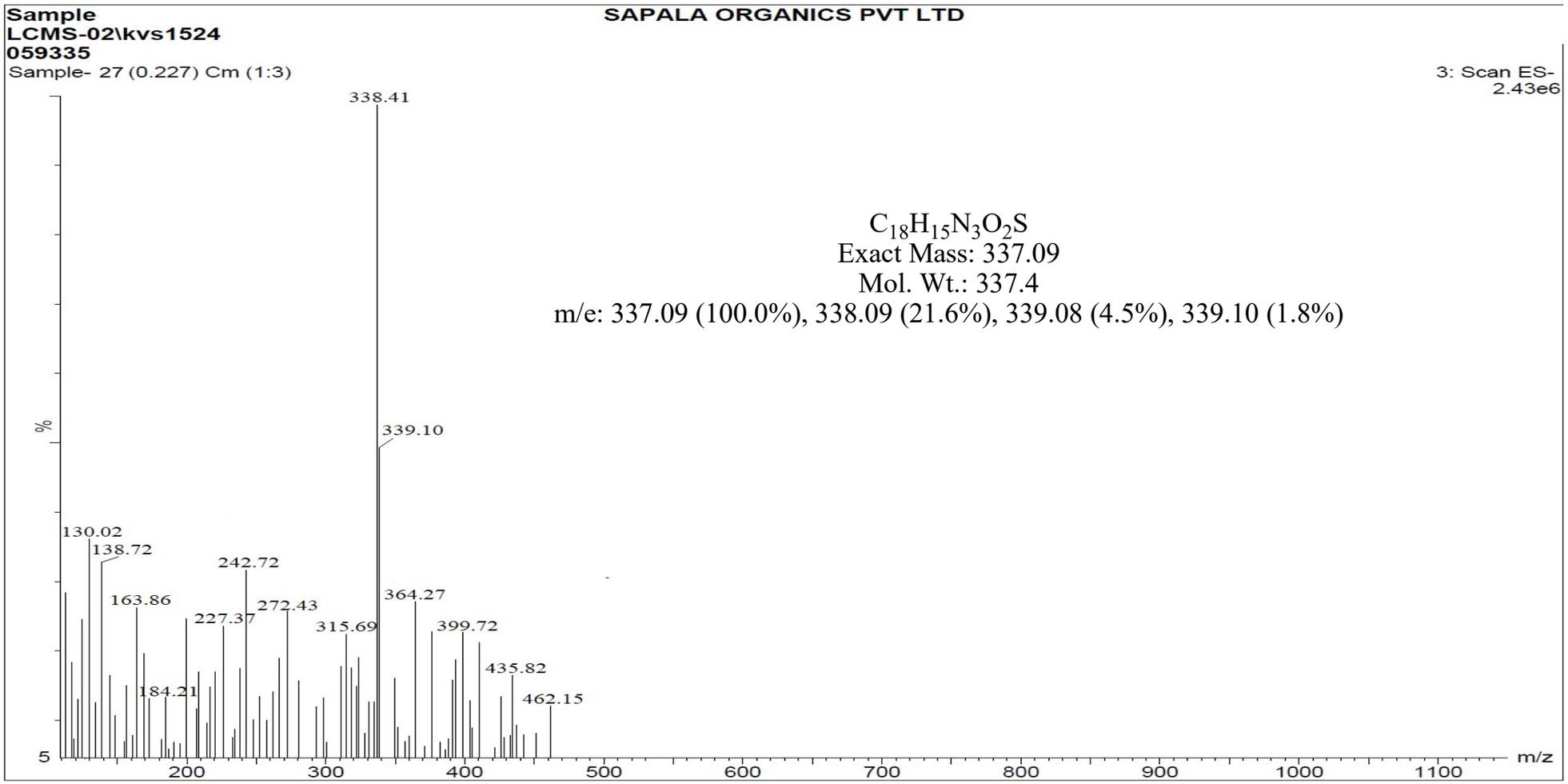


Figure S9. Mass spectrum of compound 6c

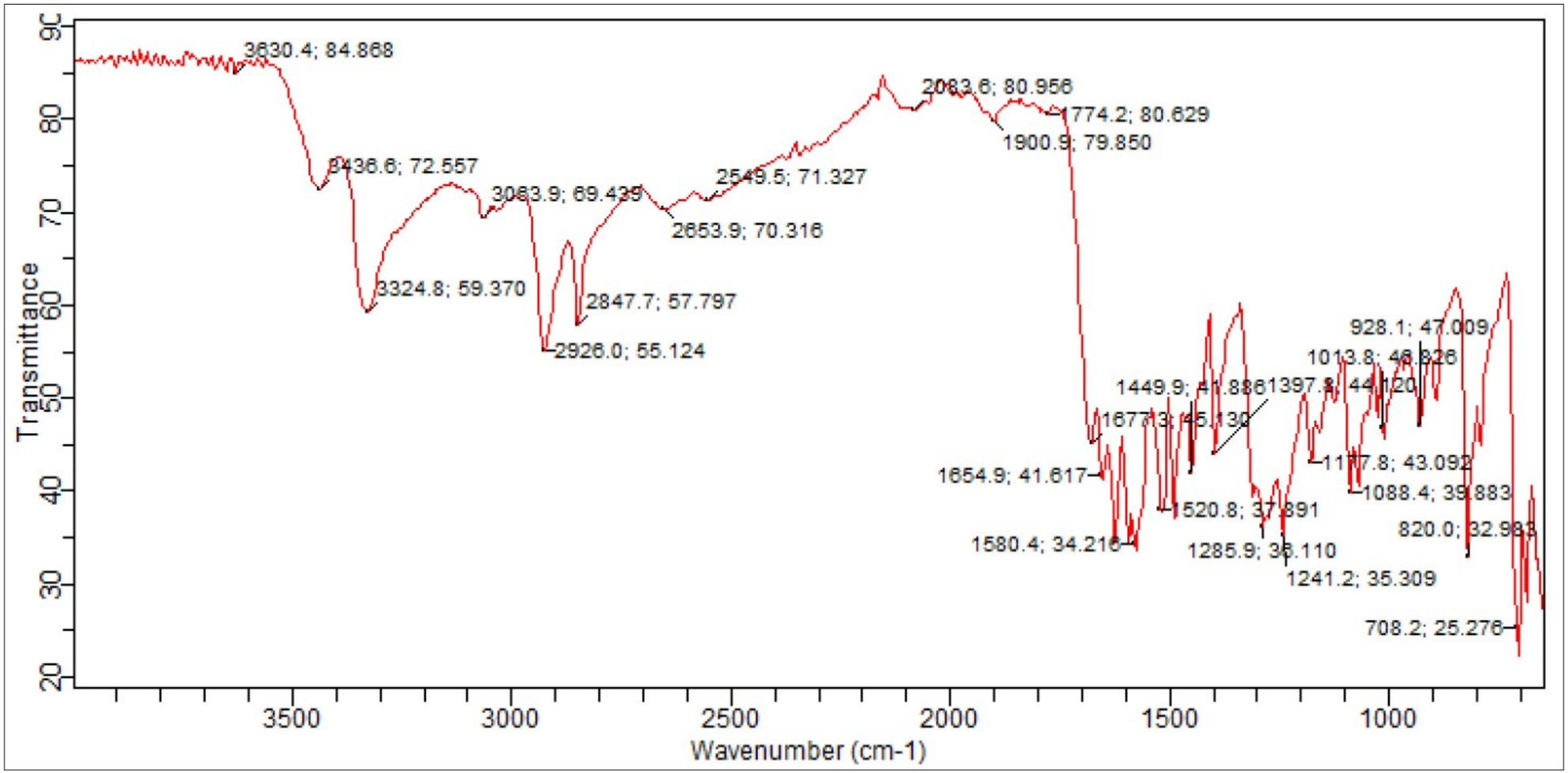
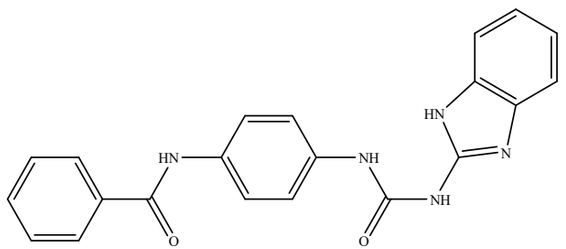


Figure S10. FTIR spectrum of compound 6d

Interpretation:

Structure	Functional Group	Standard Values	Observed Values
	N-H stretching	3350-3310	3324.8
	C-N stretching (Ar)	1342-1266	1285.9
	N-H bending	1650-1580	1580.4
	C=N stretching	1690-1640	1677.3
	C=O stretching (amide)	1690	1625.1
	aromatic C-H bending	900-700	820.0, 708.2, 894.6

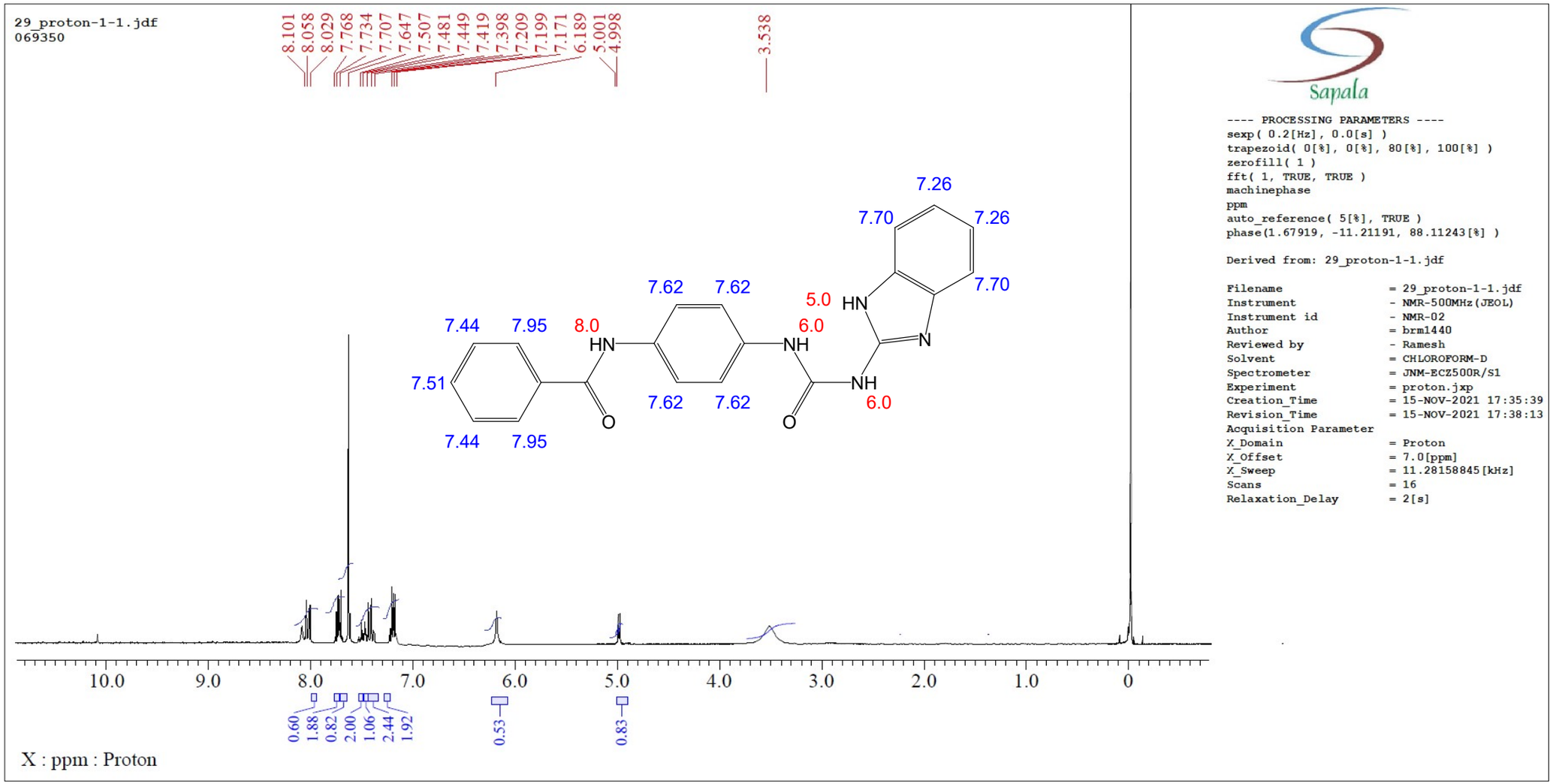


Figure S11. ^{1}HNMR spectrum of compound 6d

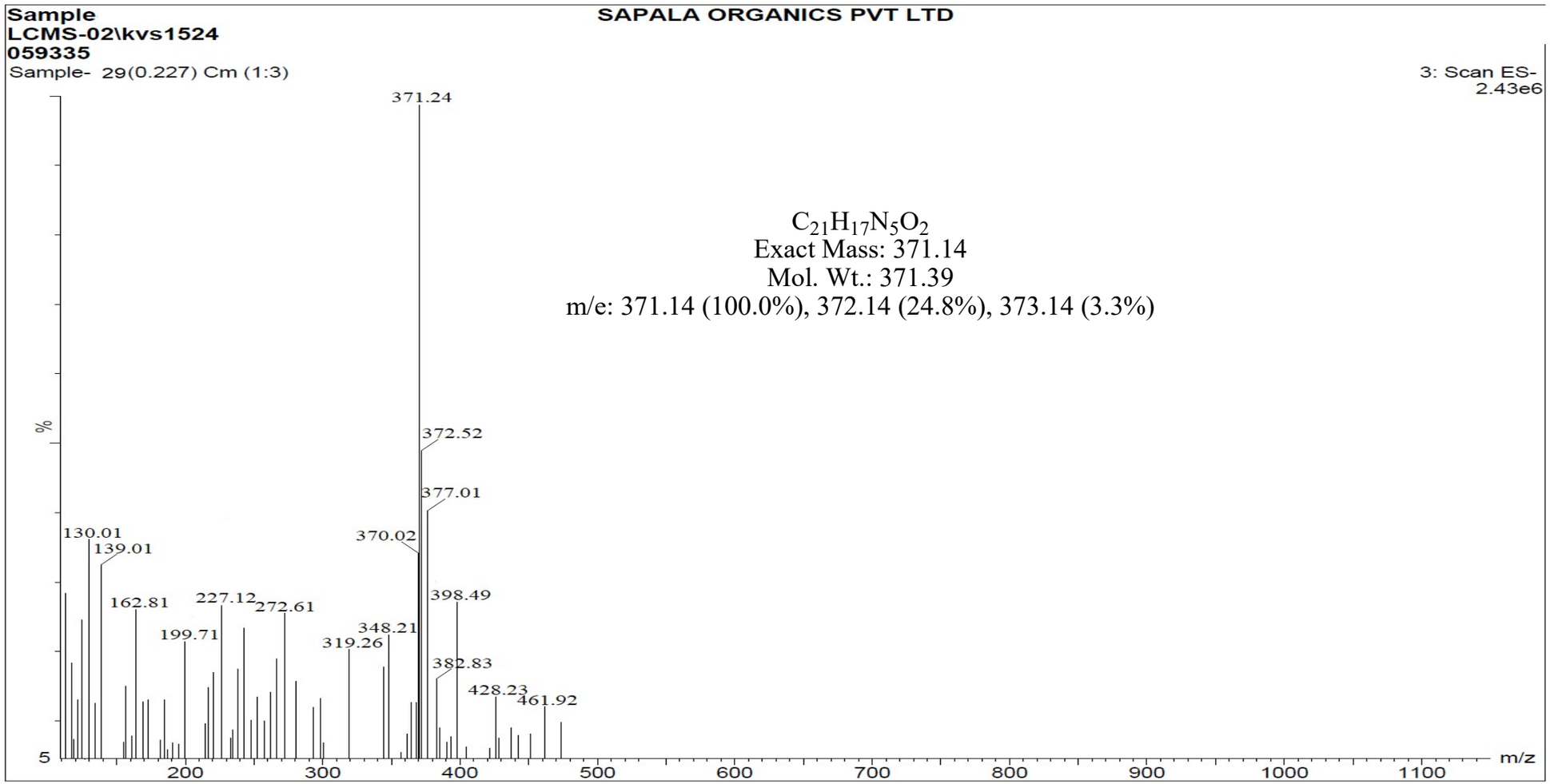


Figure S12. Mass spectrum of compound 6d

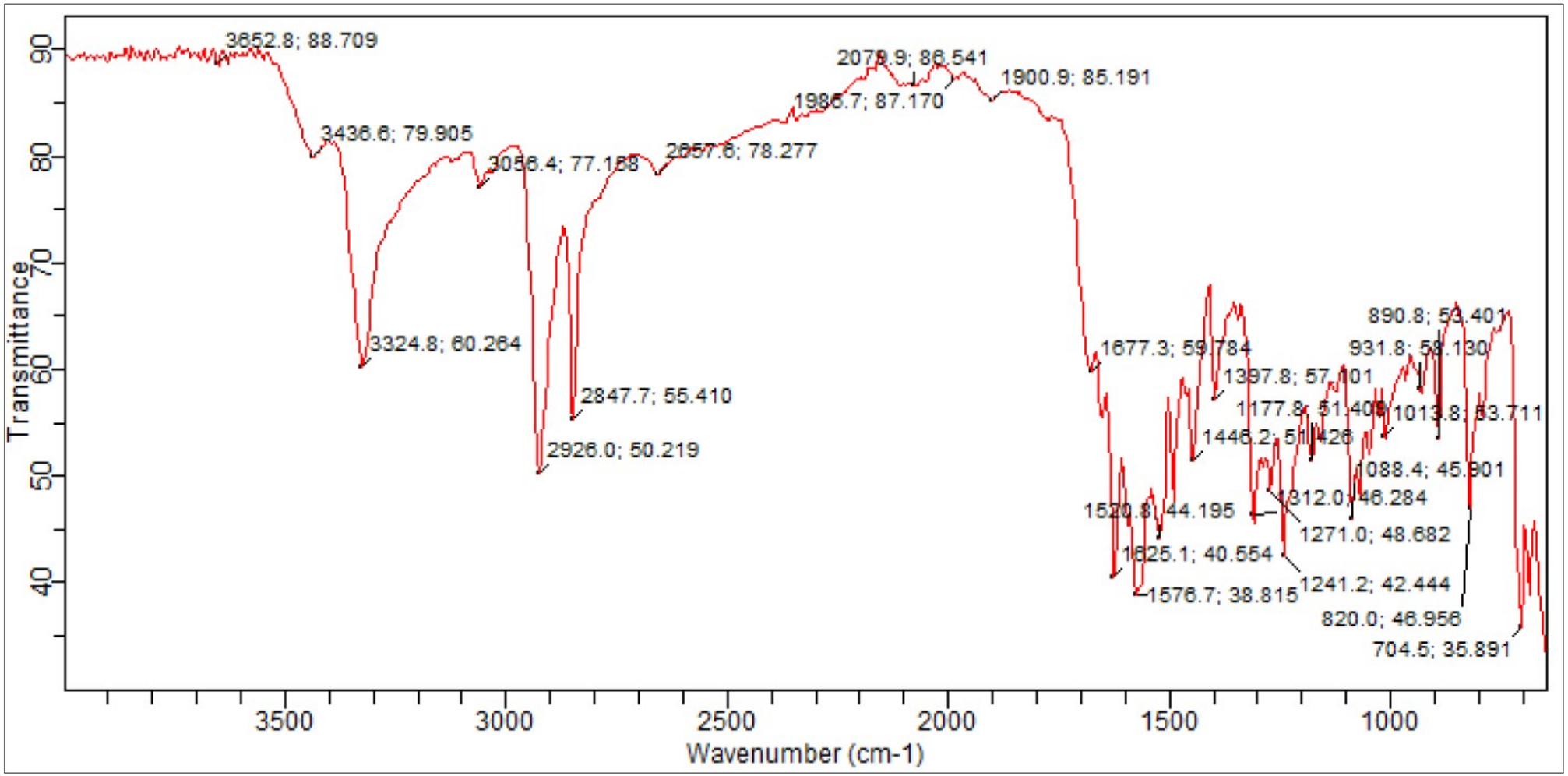
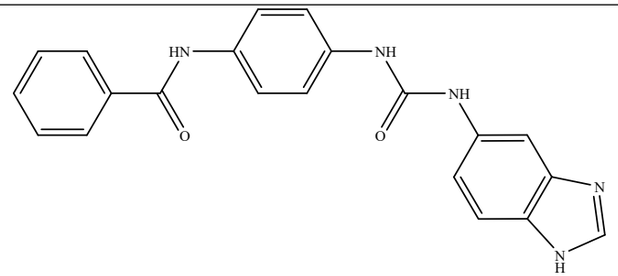


Figure S13. FTIR spectrum of compound 6e

Interpretation:

Structure	Functional Group	Standard Values	Observed Values
	N-H stretching	3350-3310	3324.8
	C-N stretching (Ar)	1342-1266	1312.0
	N-H bending	1650-1580	1576.7
	C=N stretching	1690-1640	1677.3
	C=O stretching (amide)	1690	1625.1
	aromatic C-H bending	900-700	820.0, 704.5, 894.6

^{1}H NMR:

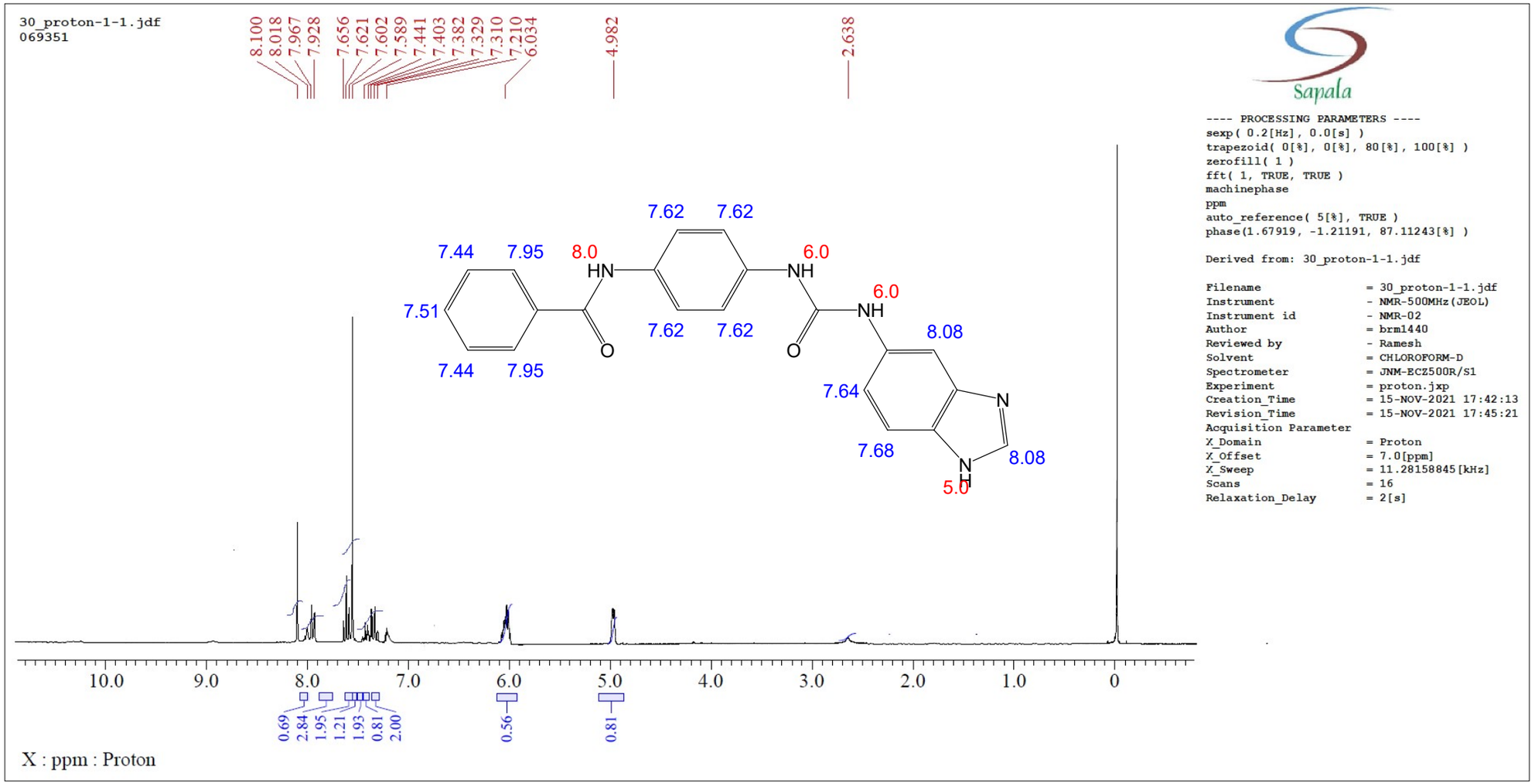


Figure S14. ^{1}HNMR spectrum of compound 6e

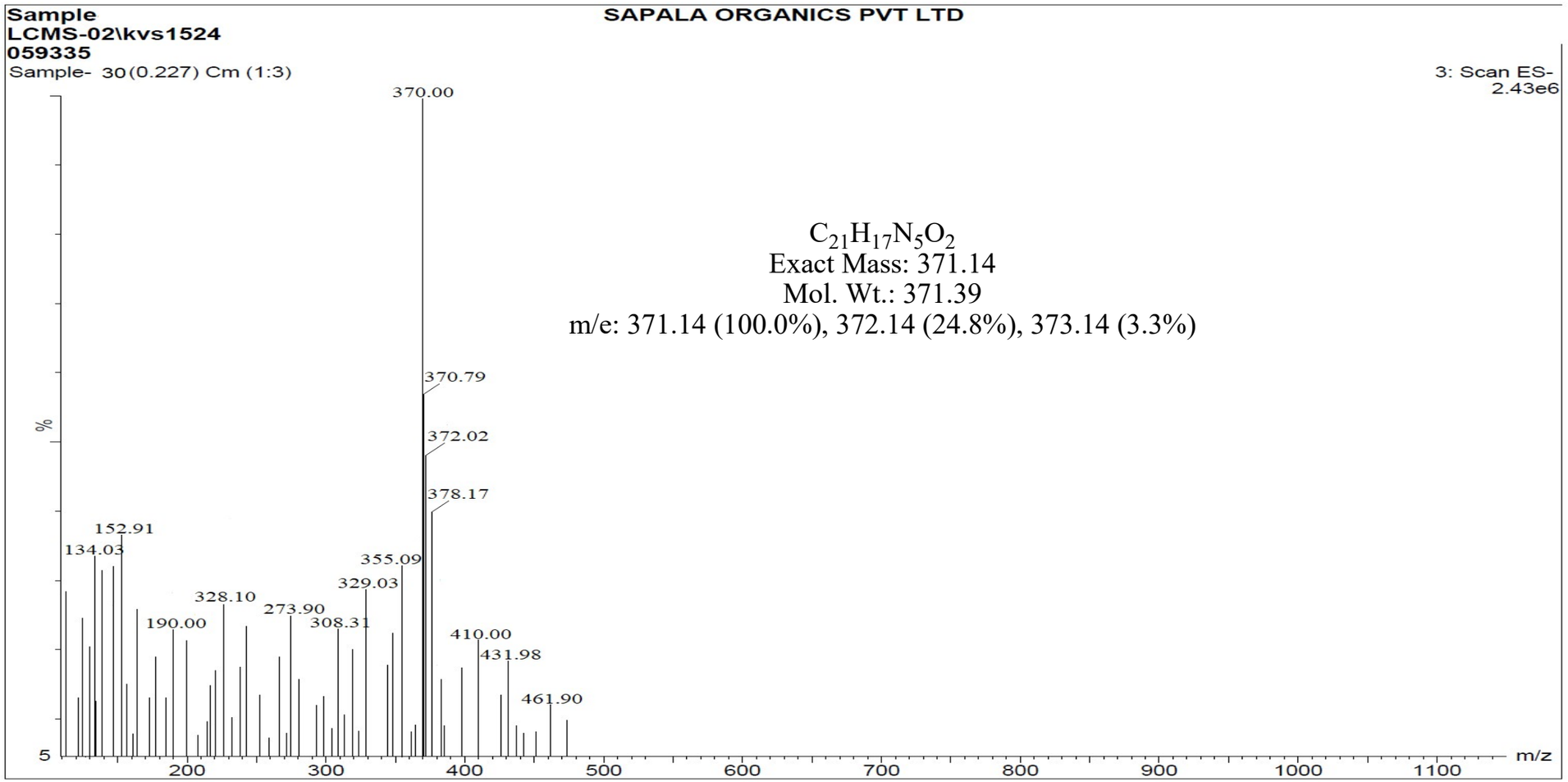


Figure S15. Mass spectrum of compound 6e

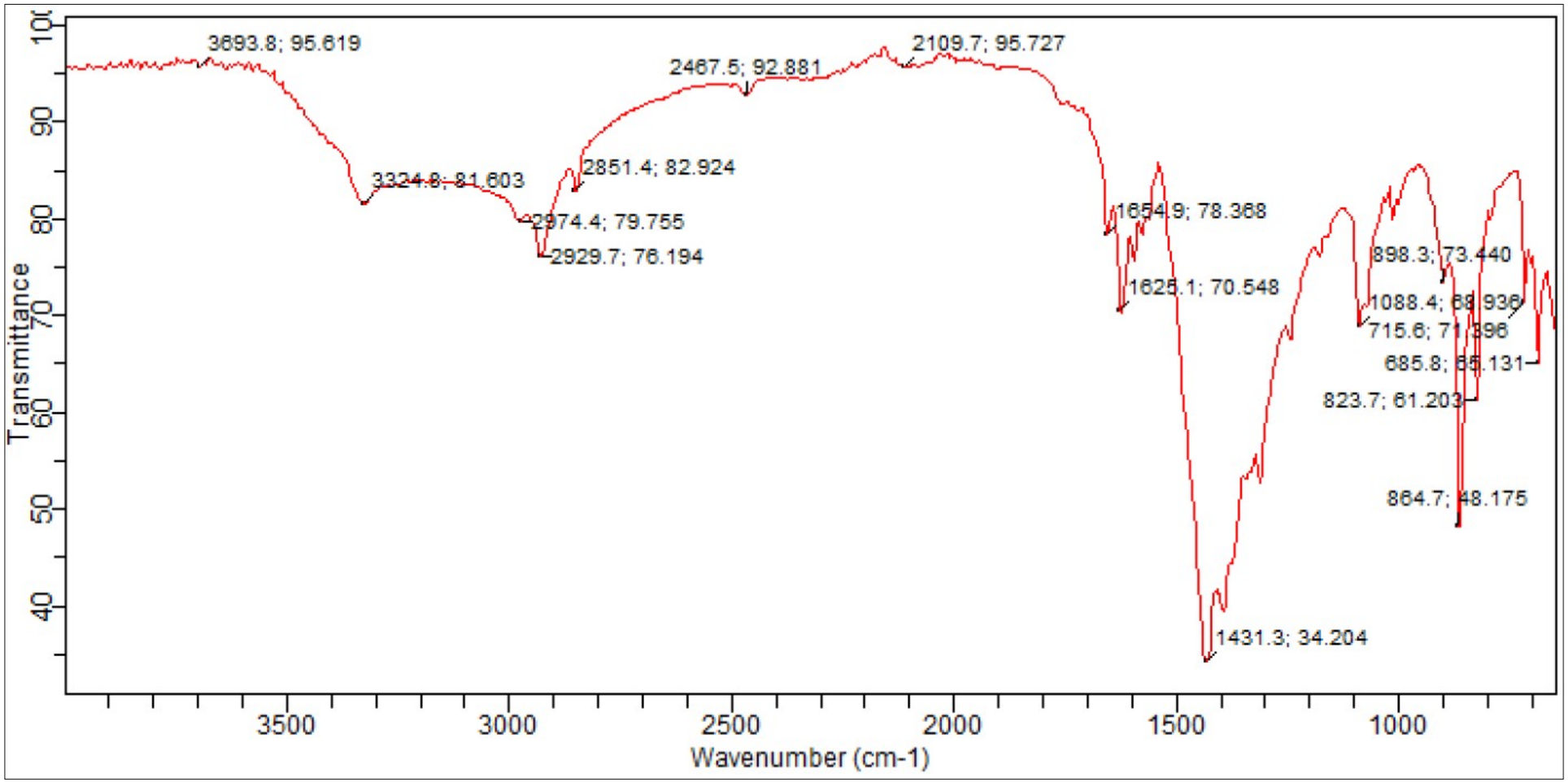
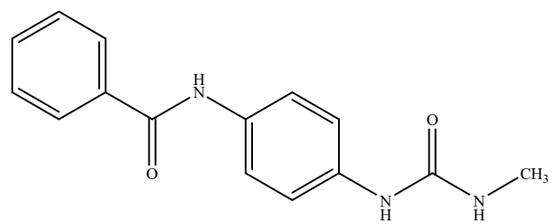


Figure S16. FTIR spectrum of compound 6f

Interpretation:

Structure	Functional Group	Standard Values	Observed Values
	N-H stretching	3350-3310	3324.8
	C-N stretching (Ar)	1342-1266	1312.0
	N-H bending	1650-1580	1576.7
	C=N stretching	1690-1640	1672.9
	C=O stretching (amide)	1690	1625.1
	aromatic C-H bending	900-700	823.7, 715.6, 894.6

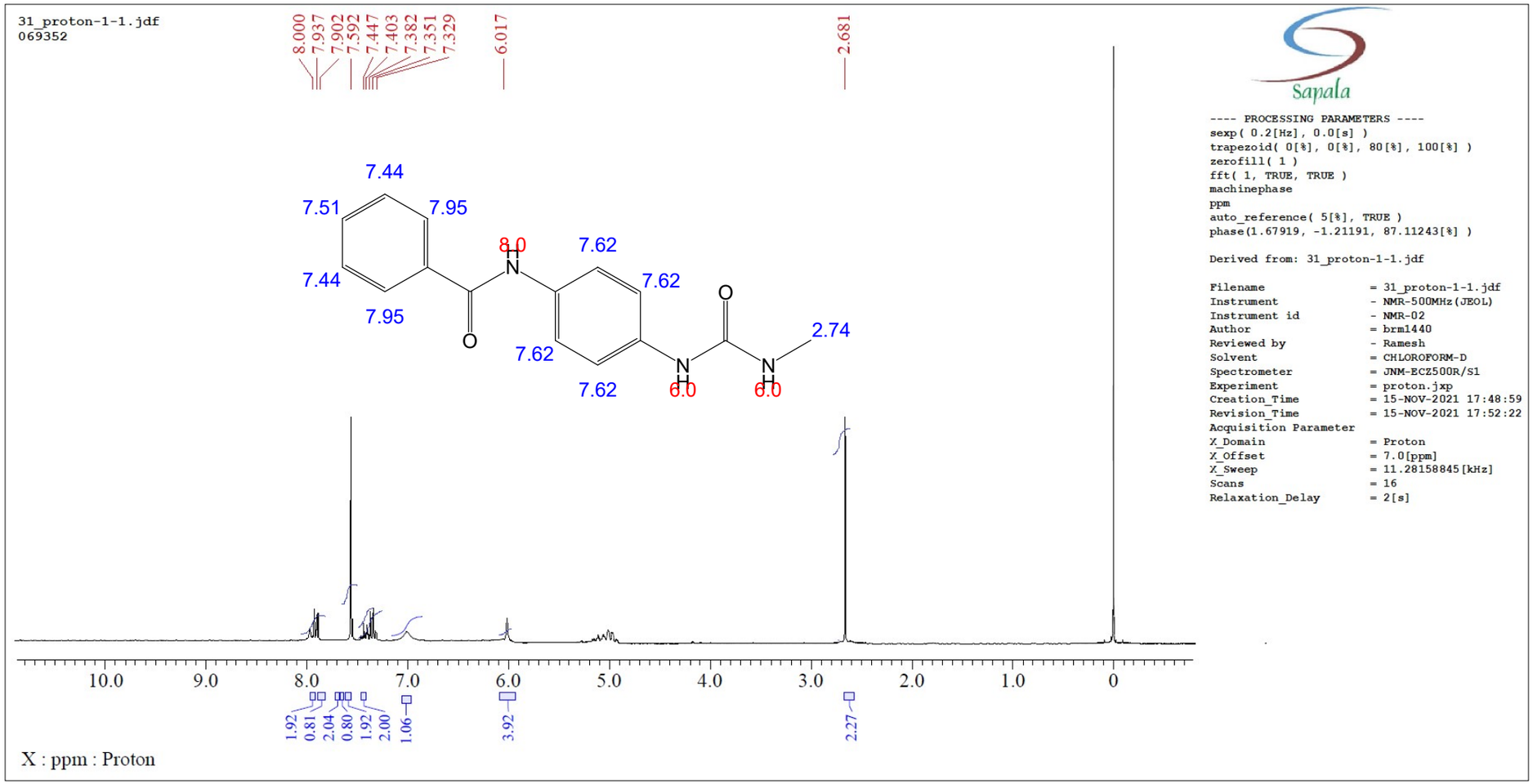


Figure S17. ^{1}HNMR spectrum of compound 6f

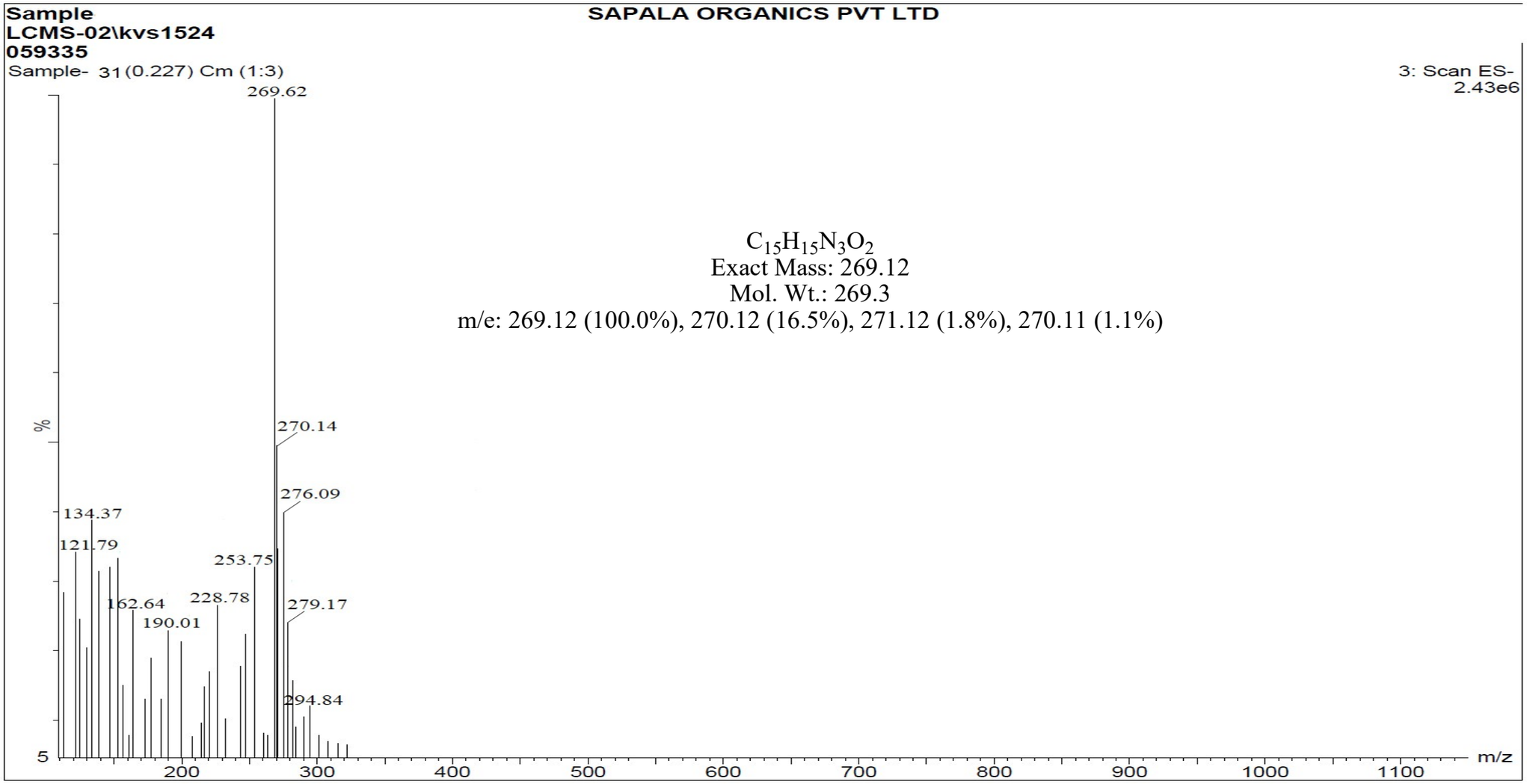


Figure S18. Mass spectrum of compound 6f

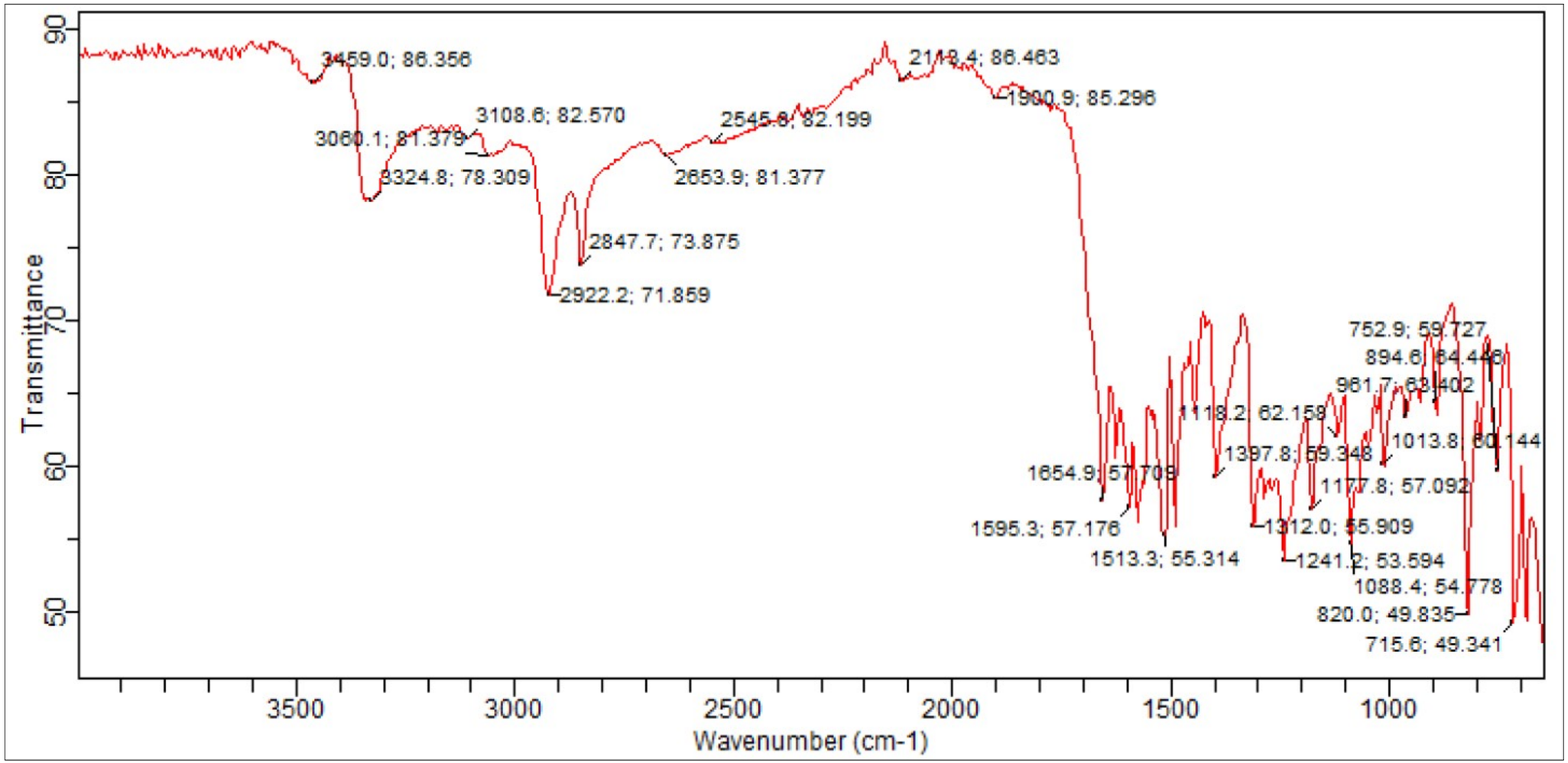
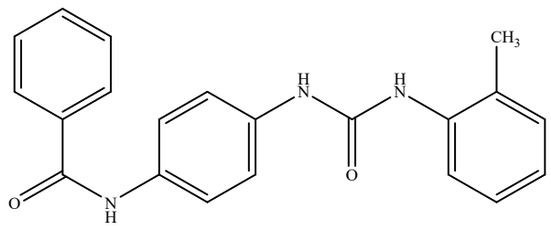


Figure S19. FTIR spectrum of compound 6g

Interpretation:

Structure	Functional Group	Standard Values	Observed Values
	N-H stretching	3350-3310	3324.8
	C-N stretching (Ar)	1342-1266	1312.0
	N-H bending	1650-1580	1576.7
	C=N stretching	1690-1640	1654.9
	C=O stretching (amide)	1690	1625.1
	aromatic C-H bending	900-700	820.0, 715.6, 894.6

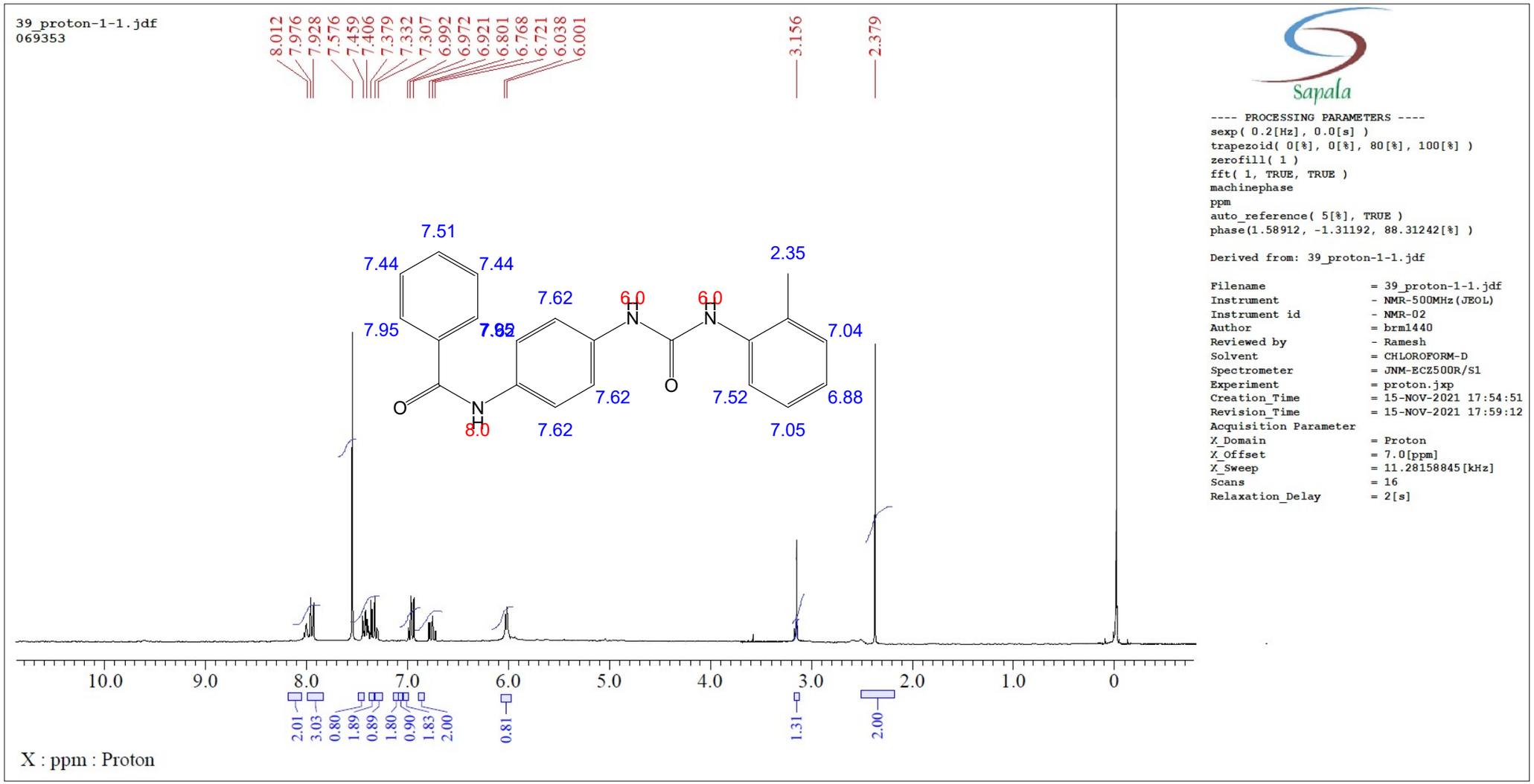


Figure S20. ^{1}HNMR spectrum of compound 6g

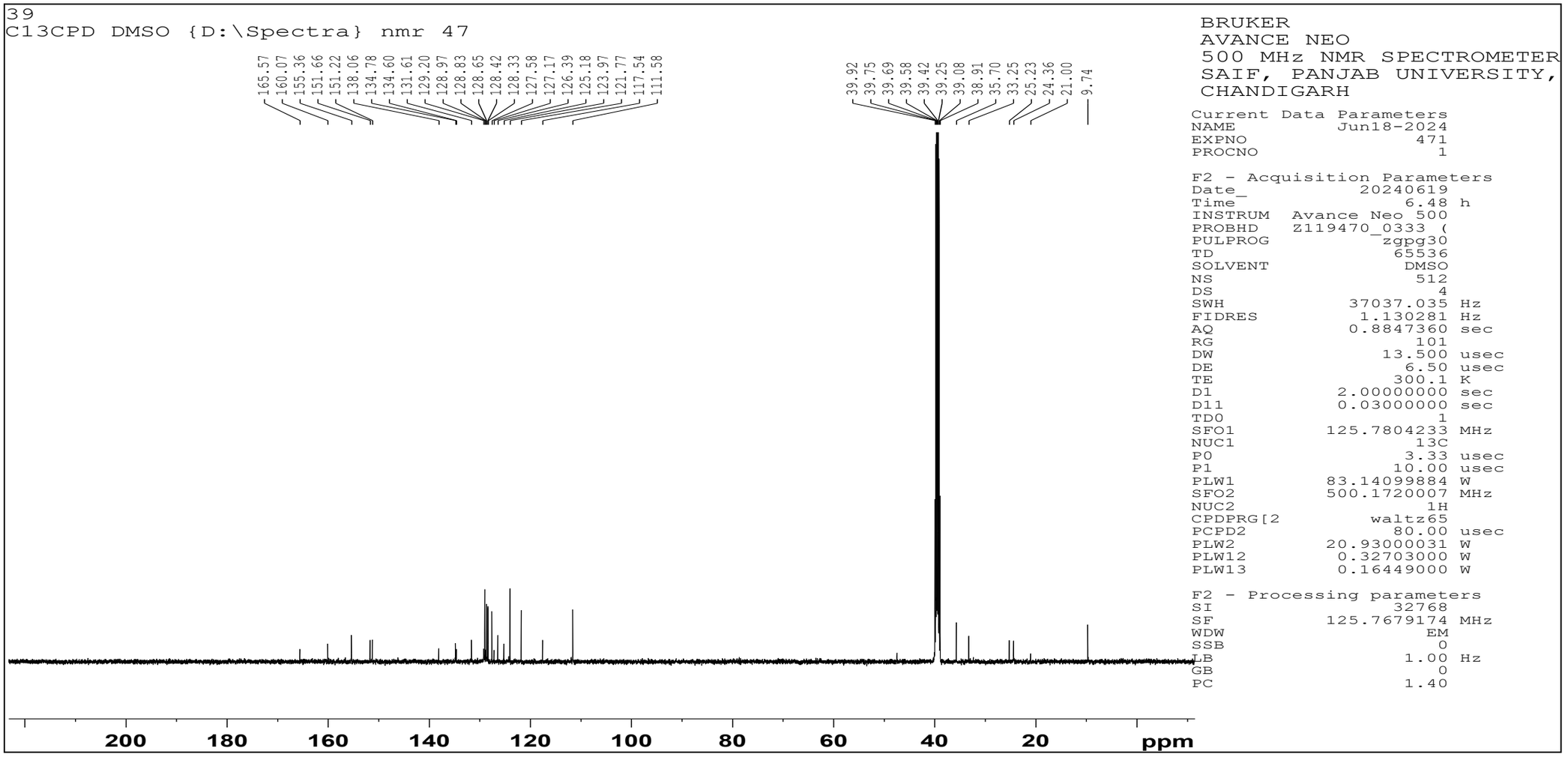


Figure S21. ^{13}C NMR spectrum of compound 6g

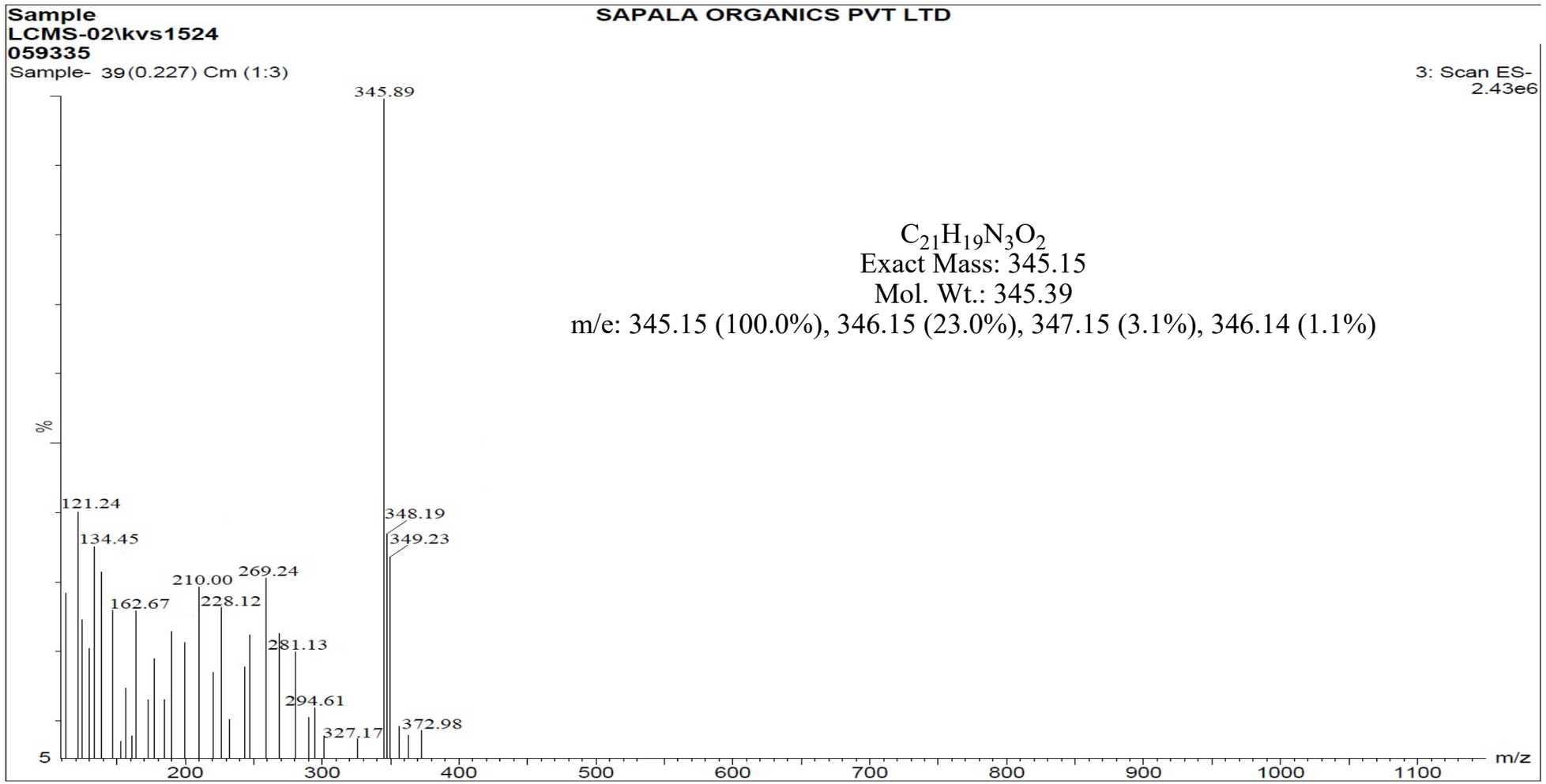
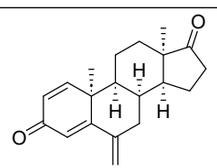


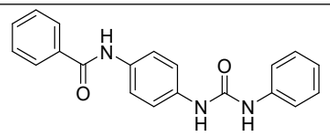
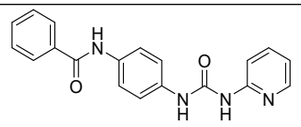
Figure S22. Mass spectrum of compound 6g

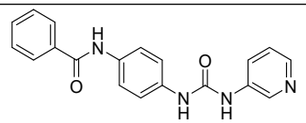
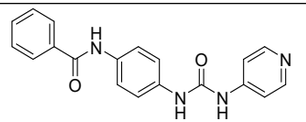
Supporting Information

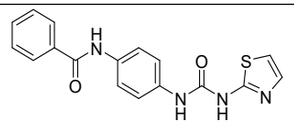
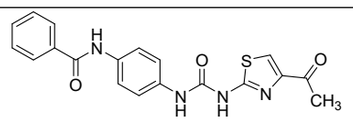
Contents

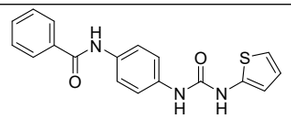
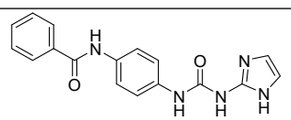
Table D1. The docking scores of native ligand and novel derivatives with aromatase enzyme

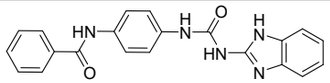
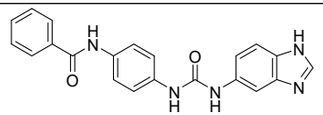
Compound Code		**Ligand Energy (kcal/mol)**	**Binding energy (kcal/mol)**	**rmsd/ub**	**rmsd/lb**
Native Ligand		1113.62	-8.9	0	0
			-8.8	3.765	2.54
			-8.8	6.864	1.751
			-8.7	5.027	3.134
			-8.7	6.537	1.282
			-8.7	6.557	1.519
			-8.2	7.204	4.375
			-7.8	6.447	2.492

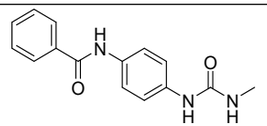
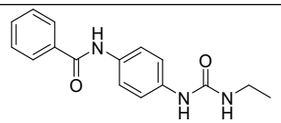
			-7.6	18.619	16.842
D1.		250.47	-8.4	0	0
			-8.3	2.304	1.876
			-7.8	10.72	1.767
			-7.4	19.8	18.345
			-7.1	24.381	18.503
			-7	22.241	18.557
			-6.7	24.457	22.368
			-6.7	25.452	19.957
			-6.6	24.166	20.094
D2.		277.44	-8.4	0	0
			-8.2	10.689	1.336
			-8.2	10.814	1.941
			-8.1	2.303	1.633
			-7.3	21.399	18.674
			-7.2	18.727	16.332
			-7.1	24.172	18.663

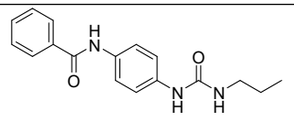
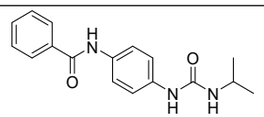
			-6.9	22.569	19.257
			-6.9	26.972	22.353
D3.		287.84	-8.2	0	0
			-7.2	22.603	18.82
			-7.2	20.674	19.006
			-7.1	21.194	19.308
			-7.1	20.902	19.717
			-6.9	21.297	20.229
			-6.8	24.83	19.862
			-6.7	23.984	19.451
			-6.6	21.957	20.155
D4.		275.03	-8	0	0
			-7.9	10.801	2.172
			-7.9	19.154	13.894
			-7.8	2.333	2.109
			-7.2	10.711	1.722
			-7.2	20.74	19.516

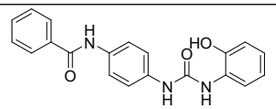
			-7.1	20.906	19.589
			-7.1	6.461	5.216
			-7	22.74	19.232
D5.		458.41	-8	0	0
			-7.7	10.566	3.42
			-7.3	19.374	14.45
			-7.3	19.355	16.393
			-7	20.809	19.544
			-7	16.296	14.836
			-6.8	25.115	22.859
			-6.8	22.589	19.141
			-6.7	20.96	19.247
D6.		575.4	-7.2	0	0
			-7.1	12.602	4.131
			-7	40.393	39.872
			-7	29.199	27.281
			-6.9	40.584	39.852

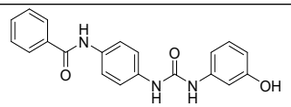
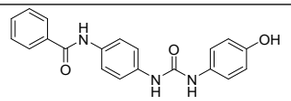
			-6.9	19.892	17.711
			-6.9	8.695	5.519
			-6.8	7.773	4.861
			-6.7	22.856	20.769
D7.		402.26	-8.1	0	0
			-7.9	2.286	2.102
			-7.7	10.592	3.314
			-7.3	10.346	2.939
			-7.2	20.58	19.428
			-7.1	20.378	18.959
			-6.5	23.688	19.474
			-6.5	20.759	18.756
			-6.4	25.548	23.804
D8.		420.02	-8.3	0	0
			-8.2	10.24	1.61
			-7.6	19.302	14.387
			-7.5	20.366	18.943

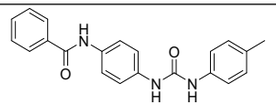
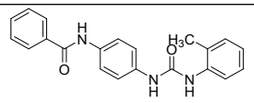
			-7.5	10.411	2.324
			-7.1	21.3	19.535
			-7.1	20.766	19.352
			-7.1	20.834	18.352
			-7	20.292	17.322
D9.		514.81	-7.9	0	0
			-7.7	26.911	22.644
			-7.6	20.553	18.832
			-7.6	18.179	14.673
			-7.5	37.06	32.877
			-7.5	32.162	30.301
			-7.3	20.07	16.226
			-7.3	24.679	22.528
			-7.2	18.587	14.365
D10.		528.5	-7.9	0	0
			-7.7	22.503	19.843
			-7.6	23.813	19.079

			-7.5	12.06	2.386
			-7.5	30.251	28.76
			-7.5	15.595	14.786
			-7.4	26.682	24.898
			-7.2	26.249	23.68
			-7.2	41.226	39.692
D11.		175.12	-7.8	0	0
			-7.5	9.553	5.698
			-7.5	8.72	4.79
			-7.4	6.825	6.016
			-7.2	24.659	22.792
			-7.1	5.347	4.766
			-7	5.778	4.846
			-6.9	8.952	4.601
			-6.9	14.612	12.003
D12.		174.28	-7.4	0	0
			-7.1	2.761	2.007

			-7	2.33	1.699
			-7	9.584	2.255
			-6.9	2.581	2.11
			-6.8	19.439	18.763
			-6.6	16.176	14.997
			-6.4	20.52	19.093
			-6.3	3.159	2.862
D13.		172.5	-6.4	0	0
			-6.4	24.434	19.909
			-6.3	10.324	4.165
			-6.1	28.169	26.124
			-6	22.707	18.682
			-6	9.638	1.426
			-5.9	20.669	18.877
			-5.9	17.591	15.4
			-5.8	50.408	49.202
D14.		177.15	-7.9	0	0

			-7.2	9.686	1.948
			-7.1	9.38	1.245
			-6.7	19.059	14.96
			-6.7	1.908	1.656
			-6.7	9.46	1.856
			-6.6	19.667	18.187
			-6.3	22.288	18.368
			-6.1	2.904	1.93
D15.		274.78	-7.9	0	0
			-7.9	15.961	13.92
			-7.2	39.269	33.961
			-7.1	37.415	31.546
			-7.1	32.608	30.701
			-7.1	41.767	37.631
			-7	37.195	32.464
			-6.7	38.521	34.046
			-6.6	29.459	24.572

D16.		284.12	-8.6	0	0
			-8.4	10.979	1.642
			-8.2	2.275	1.861
			-7.3	20.235	18.843
			-7.2	22.241	21.138
			-7.1	21.702	20.314
			-7.1	22.496	18.821
			-7.1	24.277	20.133
			-6.8	6.579	5.905
D17.		300.1	-8.3	0	0
			-8	2.309	1.881
			-7.4	22.416	18.825
			-7.2	21.904	20.505
			-7.2	20.799	18.921
			-7.1	22.719	21.65
			-7	24.465	22.414
			-6.8	25.3	19.649

			-6.8	22.332	19.648
D18.		276.5	-8.7	0	0
			-8.3	10.719	1.268
			-7.6	20.11	18.239
			-7.4	22.199	18.458
			-6.9	24.976	19.417
			-6.9	24.276	22.259
			-6.9	20.396	19.101
			-6.9	22.375	20.75
			-6.8	20.54	18.712
D19.		275.96	-8.6	0	0
			-8.2	10.683	0.992
			-8.1	2.227	1.636
			-8	19.124	13.728
			-7.2	21.15	19.111
			-7.2	19.663	14.623
			-7.2	10.807	1.696

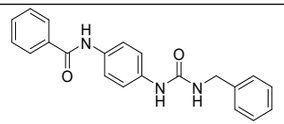
			-7.1	21.301	19.403
			-7	7.15	5.169
D20.		227.72	-8.6	0	0
			-8.4	3.013	2.467
			-8.3	1.699	1.362
			-7.8	10.744	1.543
			-7.4	21.898	20.411
			-7.3	10.279	1.891
			-7.3	21.079	19.93
			-7.3	19.509	18.169
			-7.1	19.801	18.133

Table D2. The interaction details of the native ligand molecule with the binding site residues.

Active Amino Acid Residue	Atom from Ligand	Bond Length (Å)	Bond Category	Bond Type
Native Ligand				
A:ILE133	Alkyl	4.78	Hydrophobic	Alkyl
A:CYS437	Alkyl	3.59	Hydrophobic	Alkyl
A:VAL370	Alkyl	3.91	Hydrophobic	Alkyl
A:ALA306	Alkyl	4.12	Hydrophobic	Alkyl
A:ILE133	Alkyl	4.00	Hydrophobic	Alkyl
A:ALA306	Alkyl	5.25	Hydrophobic	Alkyl
A:TRP224	Pi-Orbitals	5.23	Hydrophobic	Pi-Alkyl

Table D3. The interaction details of the designed molecules with the binding site residues.

Active Amino Acid Residue	Atom from Ligand	Bond Length (A^0)	Bond Category	Bond Type
D1				
A:LEU152	C-H	3.59141	Hydrophobic	Pi-Sigma
A:MET374	Sulfur	5.18676	Other	Pi-Sulfur
A:MET446	Sulfur	5.7763	Other	Pi-Sulfur
A:ILE133	Pi-Orbitals	4.73032	Hydrophobic	Pi-Alkyl
A:CYS437	Pi-Orbitals	5.02222	Hydrophobic	Pi-Alkyl
A:ALA306	Pi-Orbitals	4.43544	Hydrophobic	Pi-Alkyl
A:ALA307	Pi-Orbitals	4.86199	Hydrophobic	Pi-Alkyl
D2				
A:LEU152	C-H	3.60212	Hydrophobic	Pi-Sigma
A:MET446	Sulfur	5.69567	Other	Pi-Sulfur

A:MET374	Alkyl	4.95459	Hydrophobic	Alkyl
A:ILE133	Pi-Orbitals	5.07191	Hydrophobic	Pi-Alkyl
A:ALA306	Pi-Orbitals	4.81635	Hydrophobic	Pi-Alkyl
A:CYS437	Pi-Orbitals	5.02515	Hydrophobic	Pi-Alkyl
A:ALA306	Pi-Orbitals	4.47315	Hydrophobic	Pi-Alkyl
A:ALA307	Pi-Orbitals	4.8061	Hydrophobic	Pi-Alkyl
A:PHE134	Pi-Orbitals	5.08734	Hydrophobic	Pi-Alkyl
D3				
A:THR310	H	2.998	Hydrogen Bond	Conventional Hydrogen Bond
A:ALA306	H	2.52969	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	H	2.00243	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	C-H	3.71566	Hydrophobic	Pi-Sigma
A:MET374	Sulfur	5.1018	Other	Pi-Sulfur
A:VAL370	Pi-Orbitals	5.23308	Hydrophobic	Pi-Alkyl
D4				
A:ALA306	H	2.58921	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	H	1.99588	Hydrogen Bond	Conventional Hydrogen Bond

A:THR310	C-H	3.76289	Hydrophobic	Pi-Sigma
A:MET446	C-H	3.82147	Hydrophobic	Pi-Sigma
A:MET374	Sulfur	5.15429	Other	Pi-Sulfur
A:VAL370	Pi-Orbitals	5.34159	Hydrophobic	Pi-Alkyl
A:LEU152	Pi-Orbitals	5.1788	Hydrophobic	Pi-Alkyl
A:ALA306	Pi-Orbitals	4.76943	Hydrophobic	Pi-Alkyl
A:ALA307	Pi-Orbitals	4.29899	Hydrophobic	Pi-Alkyl
A:ILE442	Pi-Orbitals	5.36139	Hydrophobic	Pi-Alkyl
D5				
A:THR310	H	2.90166	Hydrogen Bond	Conventional Hydrogen Bond
A:ALA306	H	2.73553	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	H	1.95289	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	C-H	3.83414	Hydrophobic	Pi-Sigma
A:MET446	C-H	3.96889	Hydrophobic	Pi-Sigma
A:MET374	Sulfur	5.05165	Other	Pi-Sulfur
A:VAL370	Pi-Orbitals	5.24051	Hydrophobic	Pi-Alkyl
A:LEU152	Pi-Orbitals	5.3237	Hydrophobic	Pi-Alkyl

A:ALA306	Pi-Orbitals	4.51771	Hydrophobic	Pi-Alkyl
A:ALA307	Pi-Orbitals	4.24055	Hydrophobic	Pi-Alkyl
D6				
A:GLY117	O	2.46014	Hydrogen Bond	Conventional Hydrogen Bond
A:LYS376	O	2.27727	Hydrogen Bond	Conventional Hydrogen Bond
A:LYS376	Positive	4.13478	Electrostatic	Pi-Cation
A:GLU92	Negative	3.5594	Electrostatic	Pi-Anion
A:GLY117; SER118	Amide	3.63876	Hydrophobic	Amide-Pi Stacked
A:LYS376	Pi-Orbitals	5.48565	Hydrophobic	Pi-Alkyl
A:PRO138	Pi-Orbitals	4.01776	Hydrophobic	Pi-Alkyl
D7				
A:THR310	H	2.96757	Hydrogen Bond	Conventional Hydrogen Bond
A:ALA306	H	2.62519	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	H	1.87699	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	C-H	3.89798	Hydrophobic	Pi-Sigma
A:MET446	C-H	3.92962	Hydrophobic	Pi-Sigma
A:MET374	Sulfur	5.11903	Other	Pi-Sulfur

A:VAL370	Pi-Orbitals	5.38799	Hydrophobic	Pi-Alkyl
A:LEU152	Pi-Orbitals	5.23351	Hydrophobic	Pi-Alkyl
A:ALA306	Pi-Orbitals	4.61904	Hydrophobic	Pi-Alkyl
A:ALA307	Pi-Orbitals	4.30702	Hydrophobic	Pi-Alkyl
D8				
A:ALA306	H	3.07047	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	H	2.12731	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	C-H	3.72459	Hydrophobic	Pi-Sigma
A:MET374	Sulfur	5.14288	Other	Pi-Sulfur
A:MET446	Sulfur	5.48999	Other	Pi-Sulfur
A:VAL370	Pi-Orbitals	5.16372	Hydrophobic	Pi-Alkyl
A:LEU152	Pi-Orbitals	5.28988	Hydrophobic	Pi-Alkyl
A:ALA306	Pi-Orbitals	4.17509	Hydrophobic	Pi-Alkyl
A:ALA307	Pi-Orbitals	4.22316	Hydrophobic	Pi-Alkyl
D9				
A:CYS124	H	2.62578	Hydrogen Bond	Conventional Hydrogen Bond
A:CYS124	H	1.96848	Hydrogen Bond	Conventional Hydrogen Bond

A:TYR241	HH	2.54449	Hydrogen Bond	Conventional Hydrogen Bond
A:CYS124	Sulfur	5.56438	Other	Pi-Sulfur
A:TYR241	Pi-Orbitals	5.34825	Hydrophobic	Pi-Pi Stacked
A:PHE235; LYS236	Amide	3.85212	Hydrophobic	Amide-Pi Stacked
A:VAL248	Pi-Orbitals	5.46931	Hydrophobic	Pi-Alkyl
A:LYS249	Pi-Orbitals	4.6032	Hydrophobic	Pi-Alkyl
A:LYS236	Pi-Orbitals	4.92931	Hydrophobic	Pi-Alkyl
D10				
A:GLY117	H	2.0319	Hydrogen Bond	Conventional Hydrogen Bond
A:GLY117	H	2.67471	Hydrogen Bond	Conventional Hydrogen Bond
A:GLU129	NH	2.5366	Hydrogen Bond	Conventional Hydrogen Bond
A:ASN136	H	2.55066	Hydrogen Bond	Conventional Hydrogen Bond
A:GLU92	Negative	4.05003	Electrostatic	Pi-Anion
A:LYS119	NH	3.08756	Hydrogen Bond	Pi-Donor Hydrogen Bond
D11				
A:THR310	H	2.73917	Hydrogen Bond	Conventional Hydrogen Bond
A:PRO429	H	2.16876	Hydrogen Bond	Conventional Hydrogen Bond

A:PRO429	H	2.33609	Hydrogen Bond	Conventional Hydrogen Bond
A:VAL370	O	2.77996	Hydrogen Bond	Conventional Hydrogen Bond
A:ALA306	C-H	3.89756	Hydrophobic	Pi-Sigma
A:MET303	Sulfur	5.44002	Other	Pi-Sulfur
A:VAL370	Pi-Orbitals	5.31721	Hydrophobic	Pi-Alkyl
A:CYS437	Pi-Orbitals	4.78236	Hydrophobic	Pi-Alkyl
A:ALA443	Pi-Orbitals	5.36601	Hydrophobic	Pi-Alkyl
A:LEU152	Pi-Orbitals	5.46632	Hydrophobic	Pi-Alkyl
A:ALA307	Pi-Orbitals	4.55727	Hydrophobic	Pi-Alkyl
D12				
A:ALA306	H	2.48419	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	H	1.97834	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	C-H	3.85939	Hydrophobic	Pi-Sigma
A:MET374	Sulfur	5.6163	Other	Pi-Sulfur
A:ALA306	Pi-Orbitals	5.0647	Hydrophobic	Pi-Alkyl
D13				
A:GLU129	H	3.03697	Hydrogen Bond	Conventional Hydrogen Bond

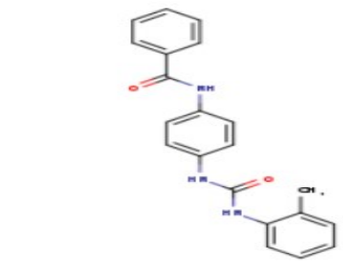
A:LYS376	O	2.24868	Hydrogen Bond	Conventional Hydrogen Bond
A:GLU92	Negative	3.36261	Electrostatic	Pi-Anion
A:LYS119	Pi-Orbitals	5.16566	Hydrophobic	Pi-Alkyl
D14				
A:ALA306	H	2.34066	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	C-H	3.75713	Hydrophobic	Pi-Sigma
A:MET374	Sulfur	5.15477	Other	Pi-Sulfur
A:ALA306	Pi-Orbitals	5.2536	Hydrophobic	Pi-Alkyl
D15				
A:TYR361	H	2.65387	Hydrogen Bond	Conventional Hydrogen Bond
A:MET444	Pi-Orbitals	5.0067	Hydrophobic	Pi-Alkyl
A:PRO429	Pi-Orbitals	5.00342	Hydrophobic	Pi-Alkyl
A:ILE347	Pi-Orbitals	5.37876	Hydrophobic	Pi-Alkyl
A:ILE350	Pi-Orbitals	5.04232	Hydrophobic	Pi-Alkyl
D16				
A:MET303	H	2.09588	Hydrogen Bond	Conventional Hydrogen Bond
A:SER199	O	2.15246	Hydrogen Bond	Conventional Hydrogen Bond

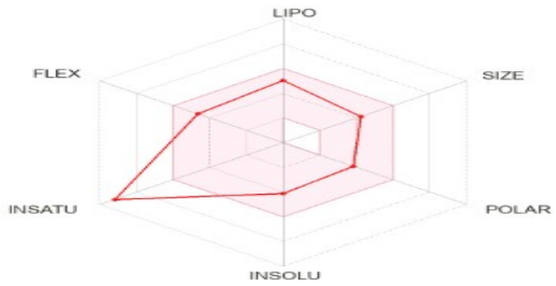
A:LEU152	C-H	3.75542	Hydrophobic	Pi-Sigma
A:MET374	Sulfur	5.14397	Other	Pi-Sulfur
A:MET446	Sulfur	5.58993	Other	Pi-Sulfur
A:ILE133	Pi-Orbitals	4.80249	Hydrophobic	Pi-Alkyl
A:CYS437	Pi-Orbitals	5.08104	Hydrophobic	Pi-Alkyl
A:ALA306	Pi-Orbitals	4.38019	Hydrophobic	Pi-Alkyl
A:ALA307	Pi-Orbitals	4.55999	Hydrophobic	Pi-Alkyl
D17				
A:LEU152	C-H	3.69749	Hydrophobic	Pi-Sigma
A:MET374	Sulfur	5.12605	Other	Pi-Sulfur
A:MET446	Sulfur	5.61916	Other	Pi-Sulfur
A:ILE133	Pi-Orbitals	4.78448	Hydrophobic	Pi-Alkyl
A:CYS437	Pi-Orbitals	5.0598	Hydrophobic	Pi-Alkyl
A:ALA306	Pi-Orbitals	4.42012	Hydrophobic	Pi-Alkyl
A:ALA307	Pi-Orbitals	4.64893	Hydrophobic	Pi-Alkyl
D18				
A:LEU152	C-H	3.69301	Hydrophobic	Pi-Sigma

A:MET374	Sulfur	5.16266	Other	Pi-Sulfur
A:CYS437	Sulfur	4.72024	Other	Pi-Sulfur
A:ALA307	Alkyl	3.744	Hydrophobic	Alkyl
A:MET446	Alkyl	4.75034	Hydrophobic	Alkyl
A:ILE133	Pi-Orbitals	5.02984	Hydrophobic	Pi-Alkyl
A:ALA306	Pi-Orbitals	4.20068	Hydrophobic	Pi-Alkyl
A:ALA307	Pi-Orbitals	5.08251	Hydrophobic	Pi-Alkyl
A:PHE203	Pi-Orbitals	4.77675	Hydrophobic	Pi-Alkyl
D19				
A:THR310	H	3.02233	Hydrogen Bond	Conventional Hydrogen Bond
A:ALA306	H	2.77767	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	H	1.94013	Hydrogen Bond	Conventional Hydrogen Bond
A:THR310	C-H	3.65298	Hydrophobic	Pi-Sigma
A:MET374	Sulfur	5.15383	Other	Pi-Sulfur
A:ALA443	Alkyl	3.38822	Hydrophobic	Alkyl
A:MET446	Alkyl	5.45268	Hydrophobic	Alkyl
A:VAL370	Pi-Orbitals	5.18741	Hydrophobic	Pi-Alkyl

A:LEU152	Pi-Orbitals	5.14384	Hydrophobic	Pi-Alkyl
A:ALA306	Pi-Orbitals	4.52294	Hydrophobic	Pi-Alkyl
A:ALA307	Pi-Orbitals	4.29137	Hydrophobic	Pi-Alkyl
D20				
A:LEU152	C-H	3.87865	Hydrophobic	Pi-Sigma
A:MET446	Sulfur	5.88582	Other	Pi-Sulfur
A:PHE134	Pi-Orbitals	5.05611	Hydrophobic	Pi-Pi Stacked
A:ILE133	Pi-Orbitals	4.78005	Hydrophobic	Pi-Alkyl
A:CYS437	Pi-Orbitals	5.01985	Hydrophobic	Pi-Alkyl
A:ALA306	Pi-Orbitals	4.11183	Hydrophobic	Pi-Alkyl
A:ALA307	Pi-Orbitals	4.65537	Hydrophobic	Pi-Alkyl
A:MET374	Pi-Orbitals	5.12173	Hydrophobic	Pi-Alkyl

ADMET predictions of D19 molecule:





SMILES O=C(Nc1ccccc1C)Nc1ccc(cc1)NC(=O)c1ccccc1

Physicochemical Properties	
Formula	C21H19N3O2
Molecular weight	345.39 g/mol
Num. heavy atoms	26
Num. arom. heavy atoms	18
Fraction Csp3	0.05
Num. rotatable bonds	7
Num. H-bond acceptors	2
Num. H-bond donors	3
Molar Refractivity	104.34
TPSA	70.23 Å²
Lipophilicity	
Log $P_{o/w}$ (iLOGP)	2.73
Log $P_{o/w}$ (XLOGP3)	3.30
Log $P_{o/w}$ (WLOGP)	4.32
Log $P_{o/w}$ (MLOGP)	3.84
Log $P_{o/w}$ (SILICOS-IT)	3.05
Consensus Log $P_{o/w}$	3.45

Water Solubility	
Log *S* (ESOL)	-4.11
Solubility	2.68e-02 mg/ml ; 7.75e-05 mol/l
Class	Moderately soluble
Log *S* (Ali)	-4.45
Solubility	1.22e-02 mg/ml ; 3.54e-05 mol/l
Class	Moderately soluble
Log *S* (SILICOS-IT)	-7.83
Solubility	5.05e-06 mg/ml ; 1.46e-08 mol/l
Class	Poorly soluble
Pharmacokinetics	
GI absorption	High
BBB permeant	Yes
P-gp substrate	No
CYP1A2 inhibitor	Yes
CYP2C19 inhibitor	Yes
CYP2C9 inhibitor	Yes
CYP2D6 inhibitor	Yes
CYP3A4 inhibitor	Yes
Log K_p (skin permeation)	-6.06 cm/s
Druglikeness	
Lipinski	Yes; 0 violation
Ghose	Yes
Veber	Yes
Egan	Yes
Muegge	Yes
Bioavailability Score	0.55
Medicinal Chemistry	
PAINS	0 alert
Brenk	0 alert
Leadlikeness	Yes
Synthetic accessibility	2.15

Toxicity prediction:

ID	Value
algae_at	0.0212129
Ames_test	mutagen
Carcino_Mouse	positive
Carcino_Rat	positive
daphnia_at	0.0310858
hERG_inhibition	high_risk
medaka_at	0.00205667
minnow_at	0.00386286
TA100_10RLI	positive
TA100_NA	negative
TA1535_10RLI	negative
TA1535_NA	negative