

Innovation of 6-sulfonamide-2*H*-chromene as antidiabetic agents targeting α -amylase, α -glycosidase, and PPAR- γ inhibitors with *in-silico* molecular docking simulation

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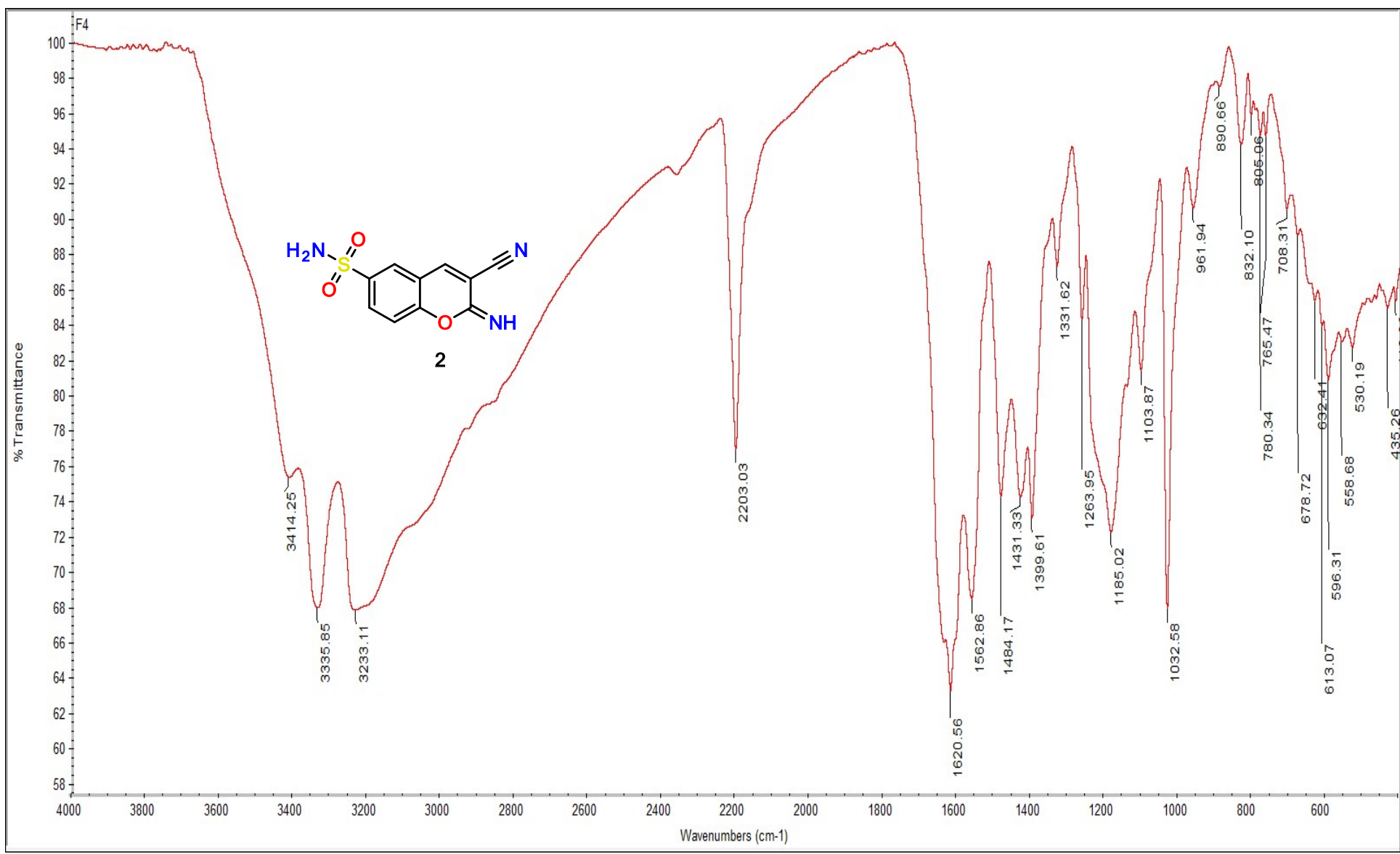
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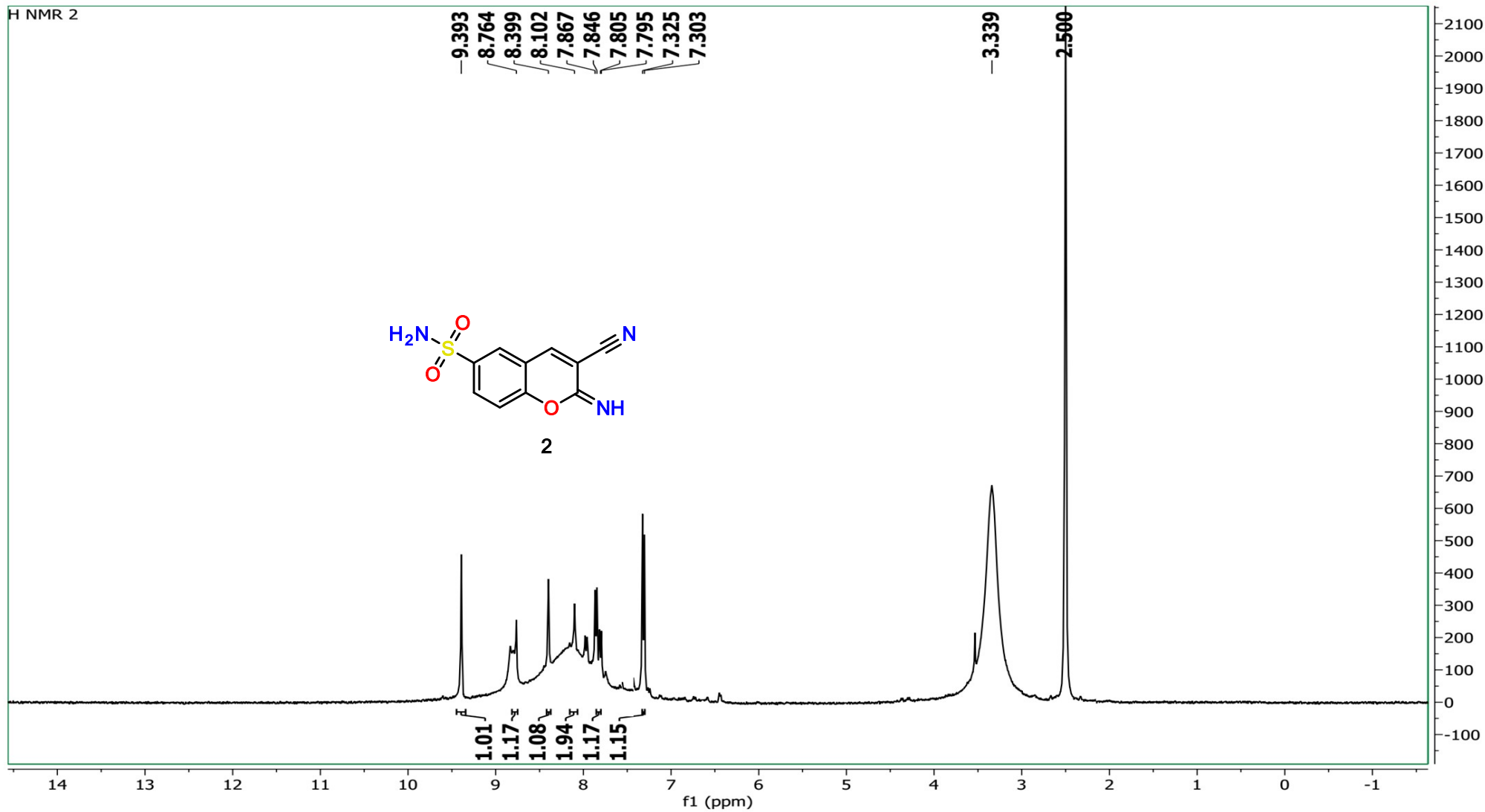
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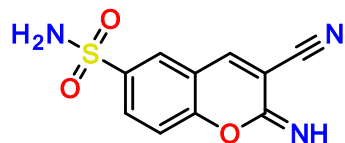
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H NMR 2

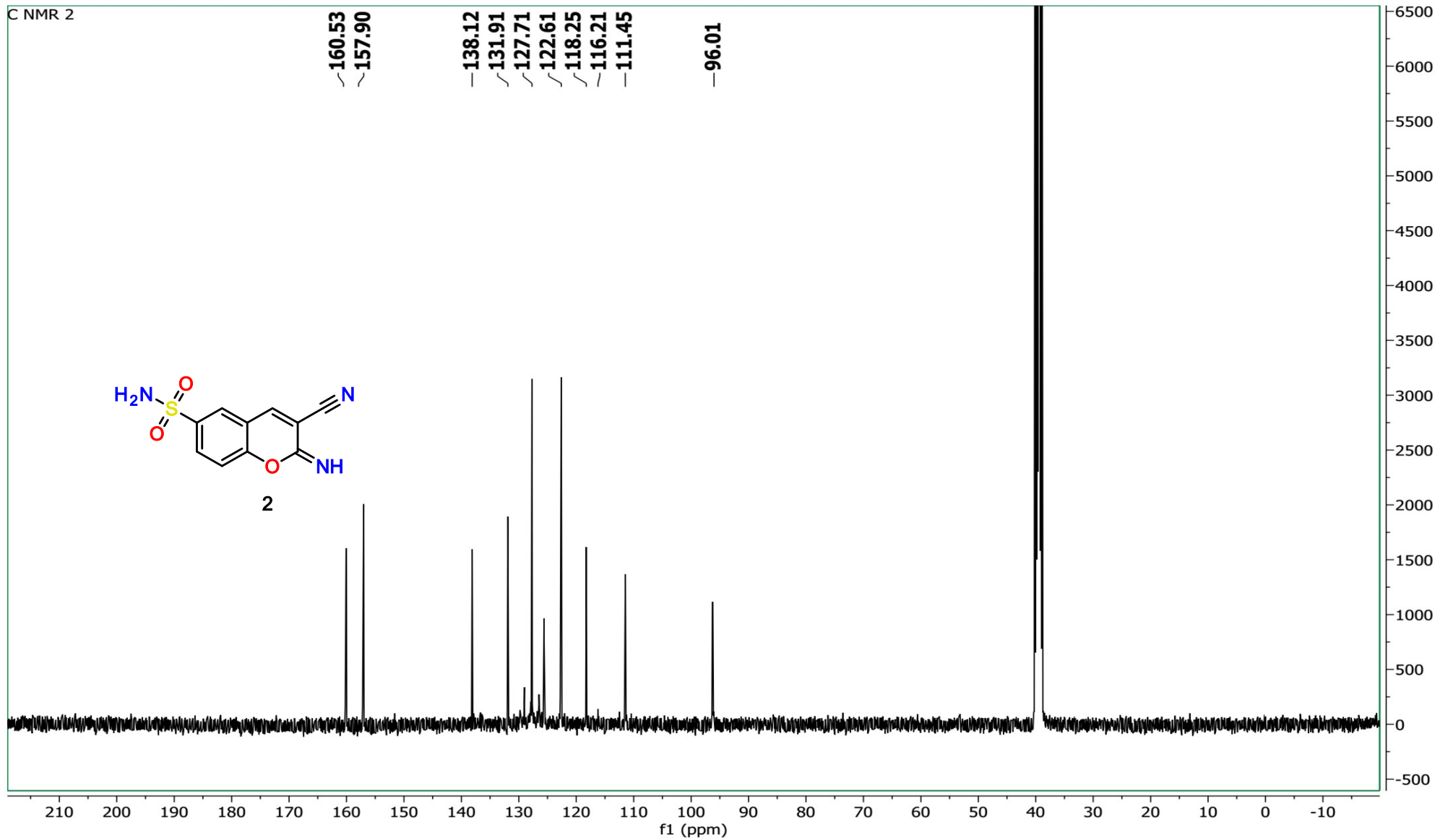


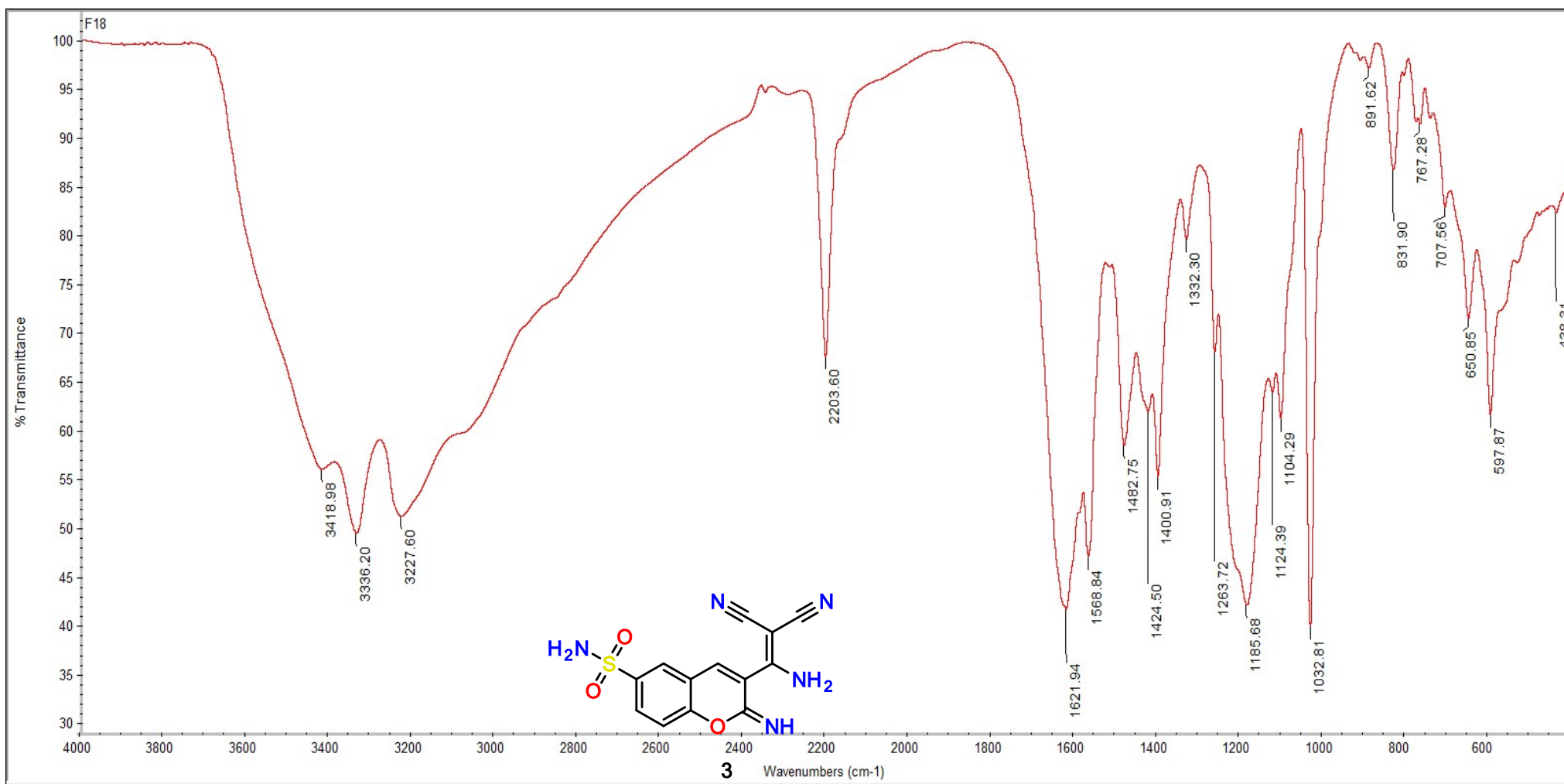
C NMR 2



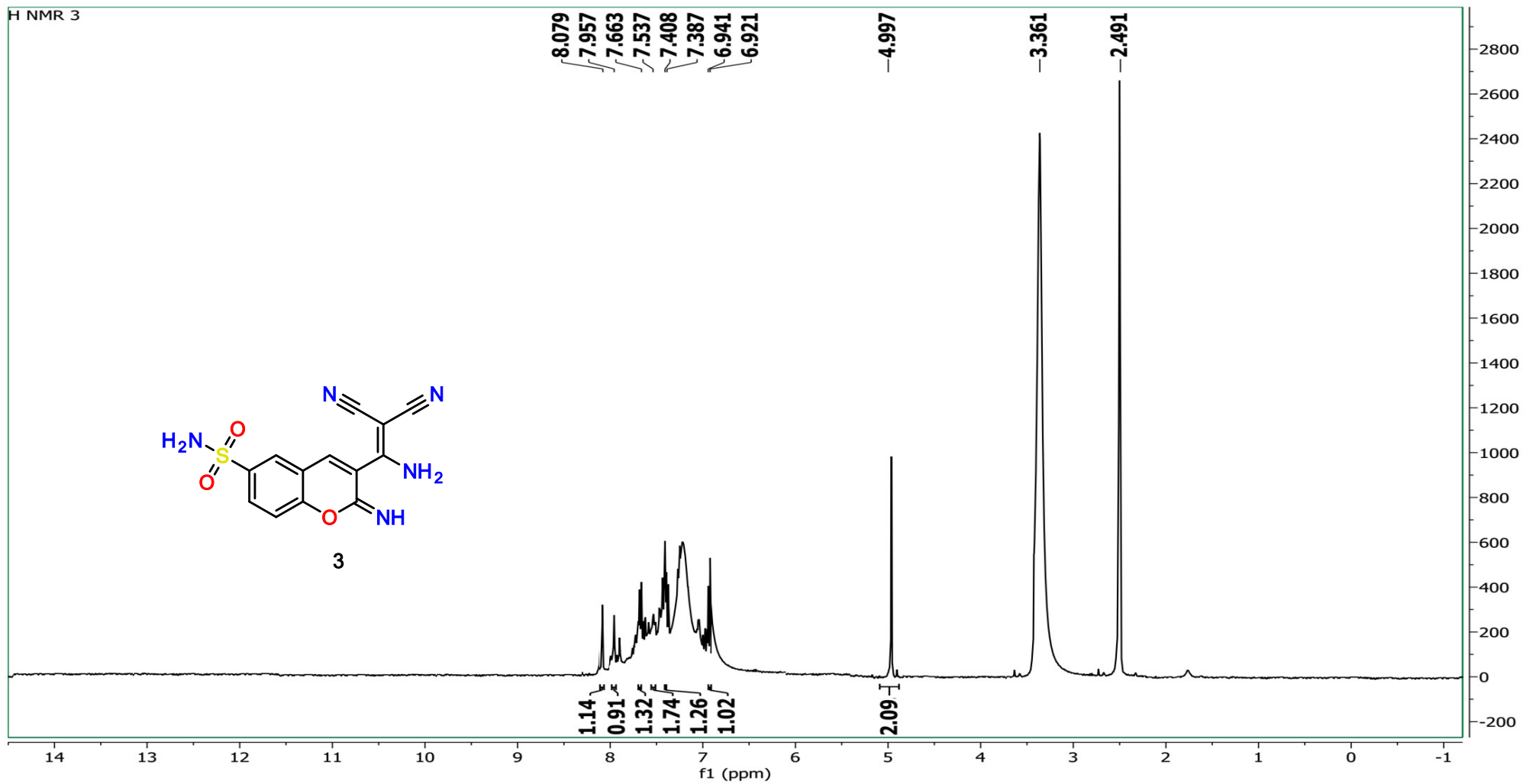
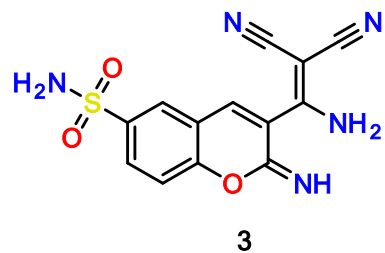
2

160.53
157.90
138.12
131.91
127.71
122.61
118.25
116.21
111.45
96.01





H NMR 3



C NMR (3)

178.95

160.08

156.69

140.05

138.12

136.68

131.91

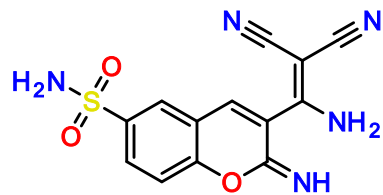
127.71

122.61

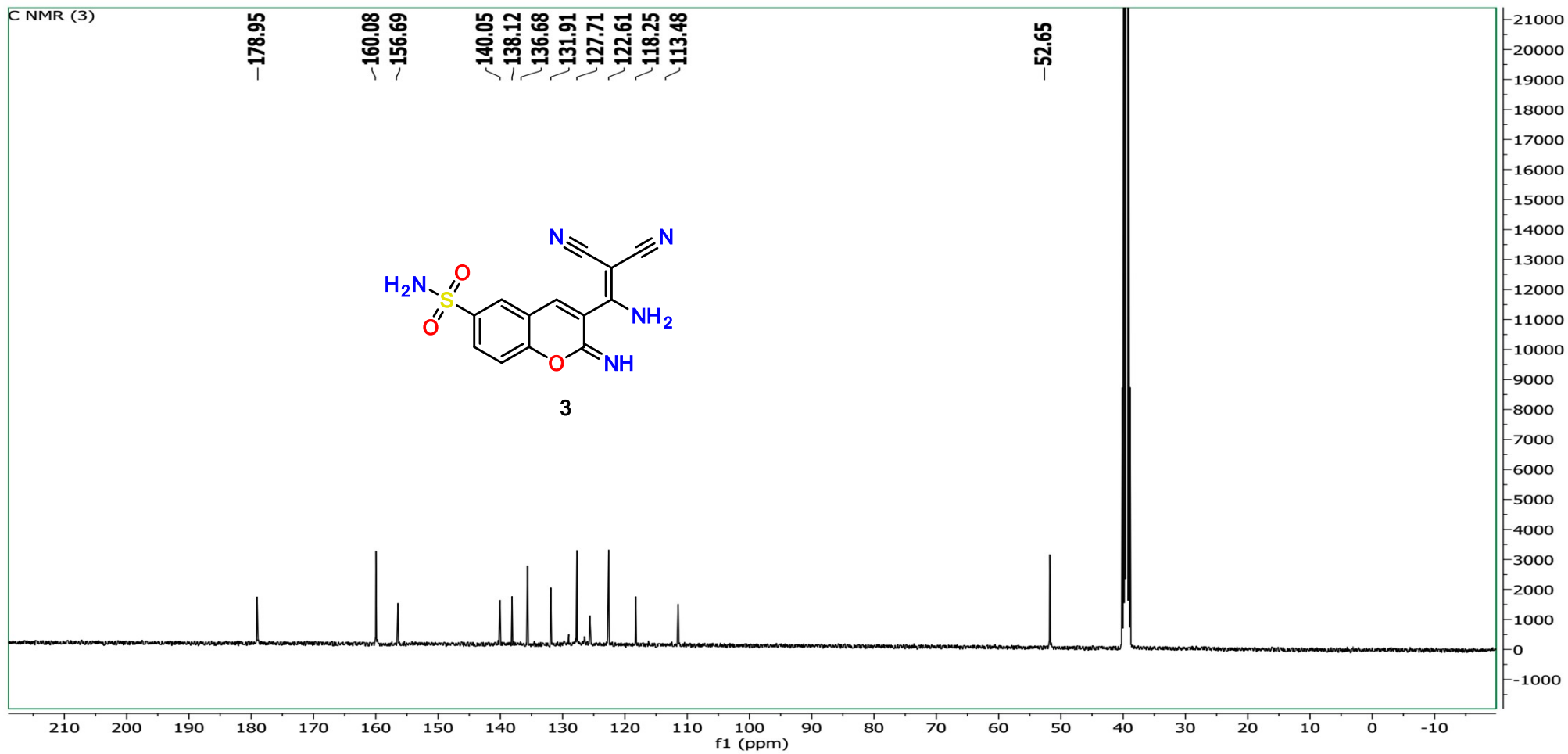
118.25

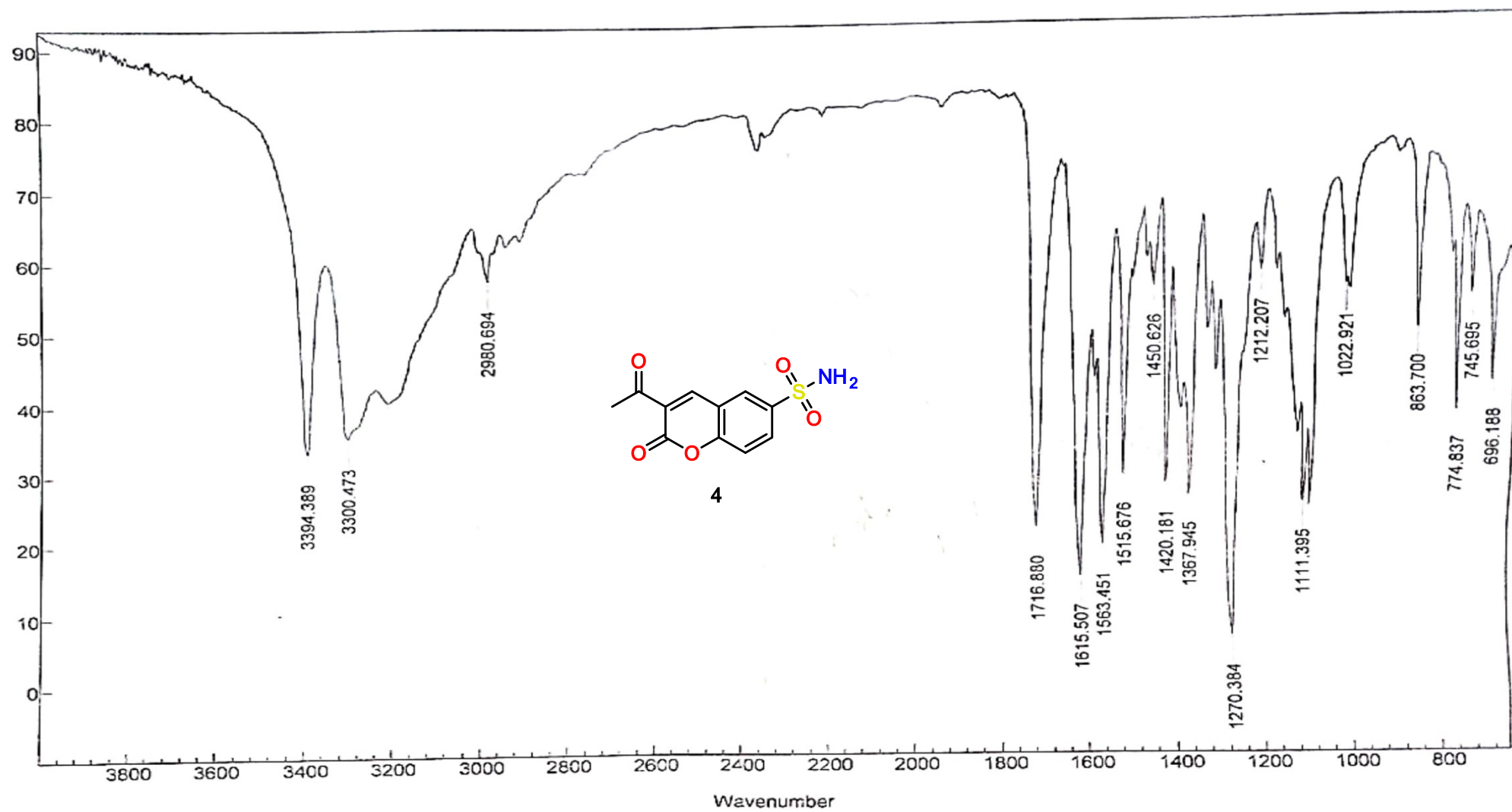
113.48

52.65

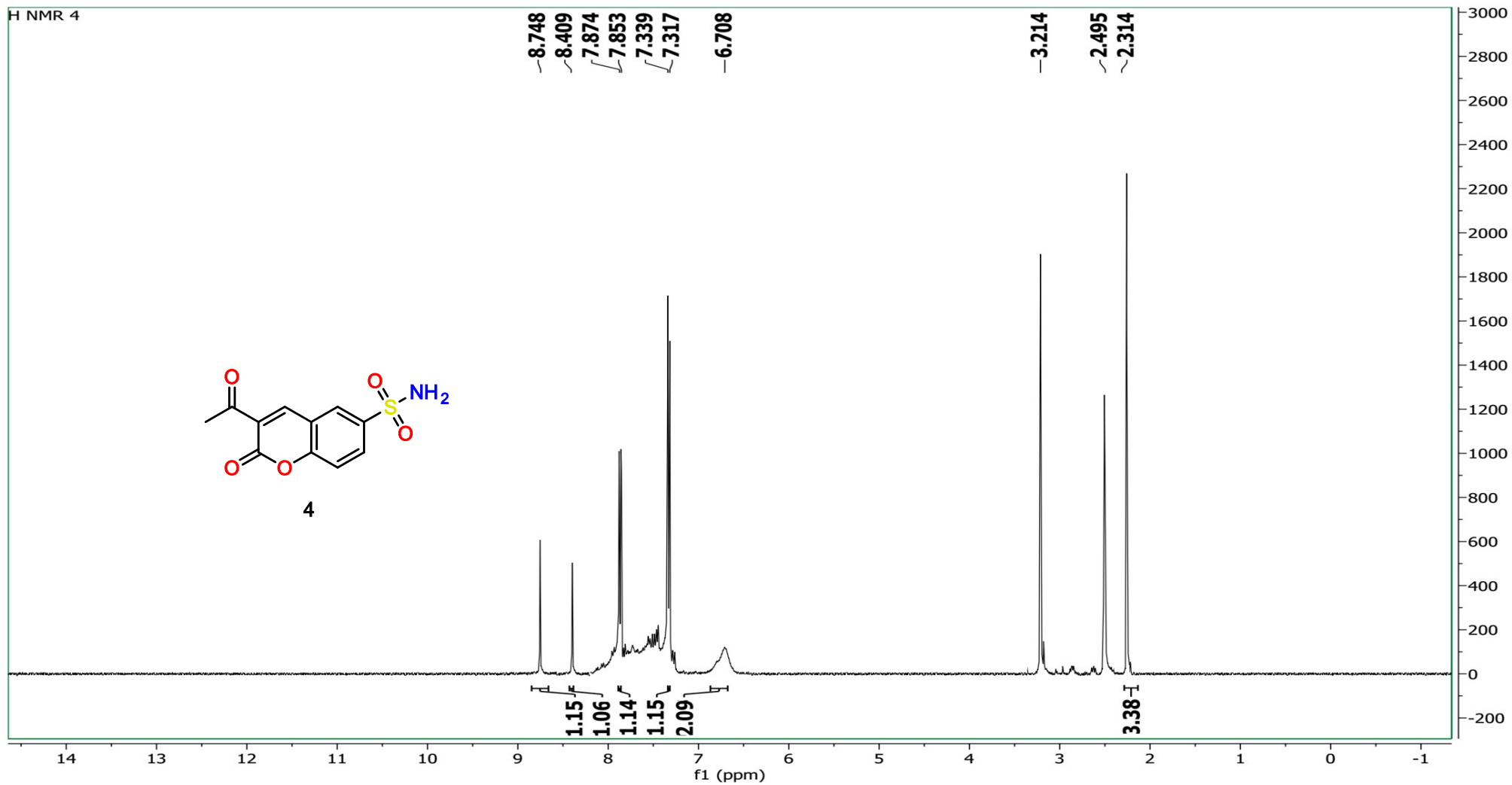
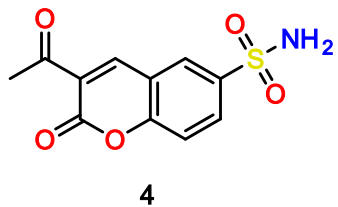


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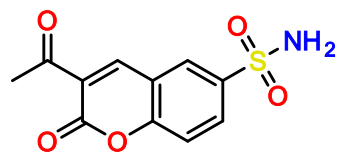




H NMR 4



C NMR 4



4

183.43

161.15

157.46

144.90

138.55

131.65

127.30

122.06

119.91

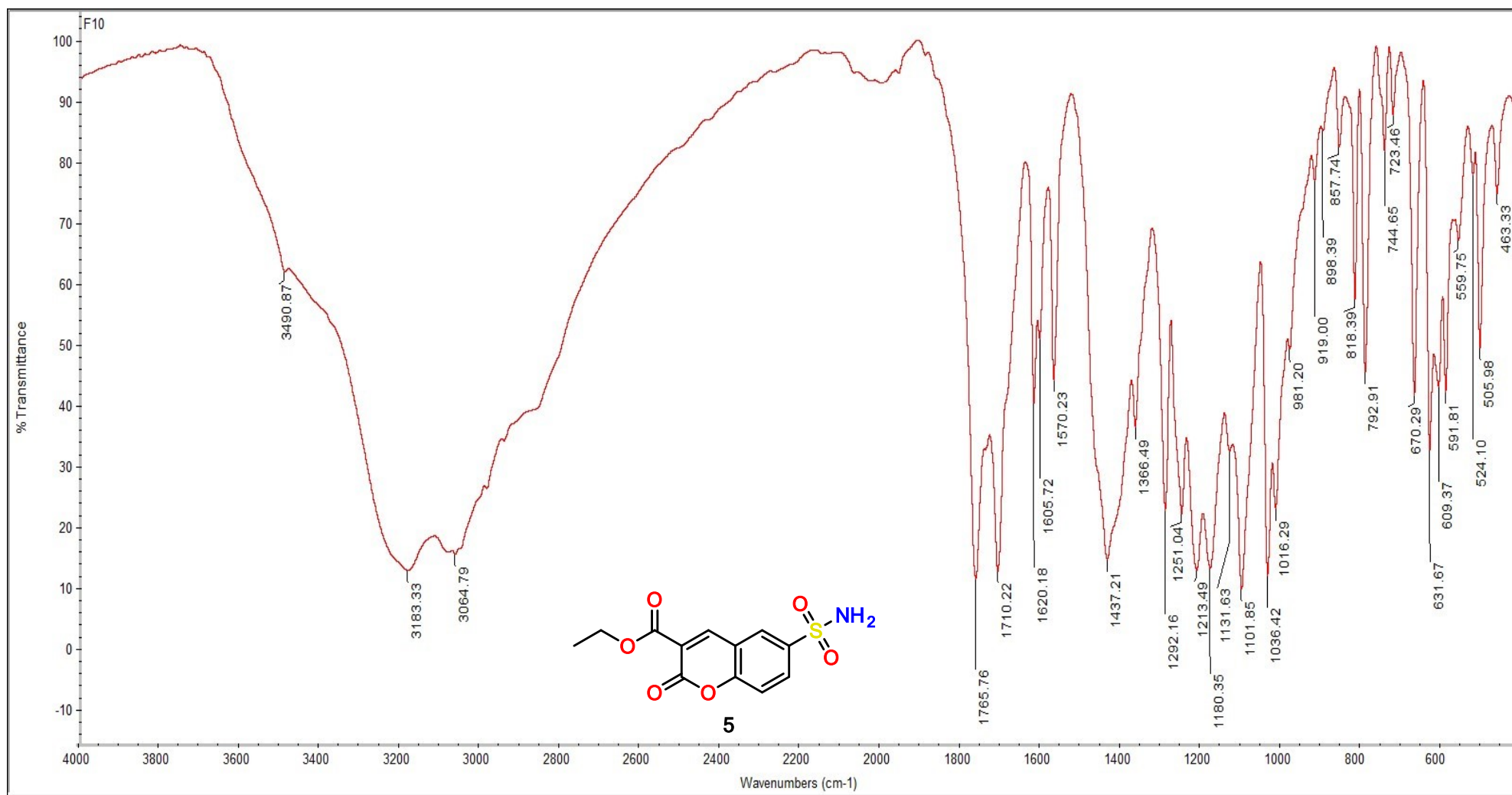
119.54

25.90

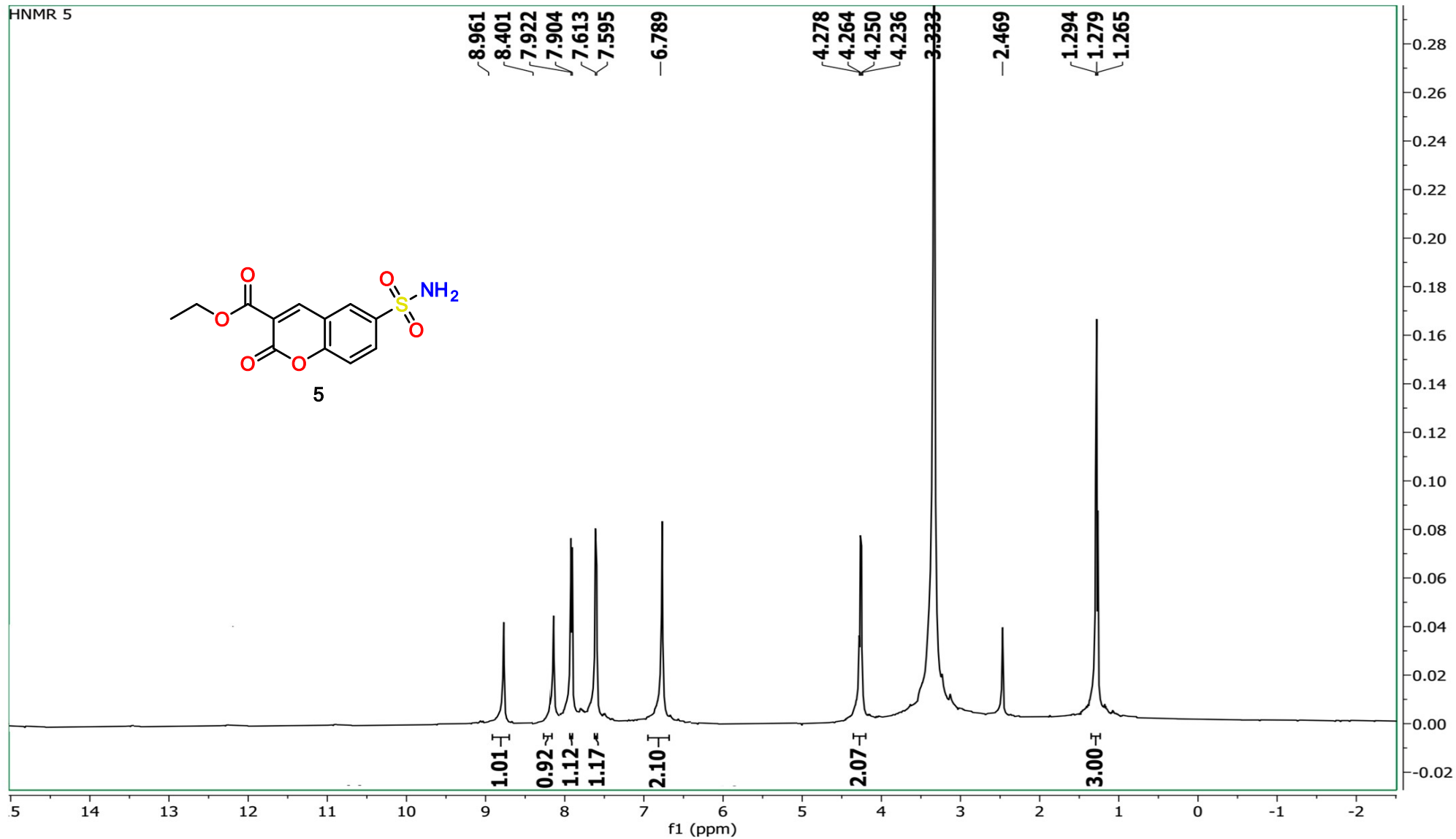
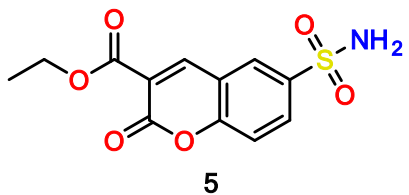
210 200 190 180 170 160 150 140 130 120 110 100 90 80 70 60 50 40 30 20 10 0 -10

f1 (ppm)

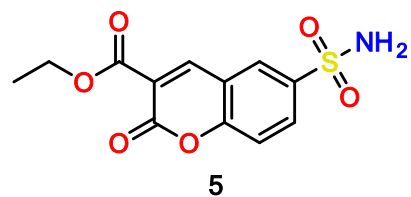
17000
16000
15000
14000
13000
12000
11000
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
-1000



HNMR 5



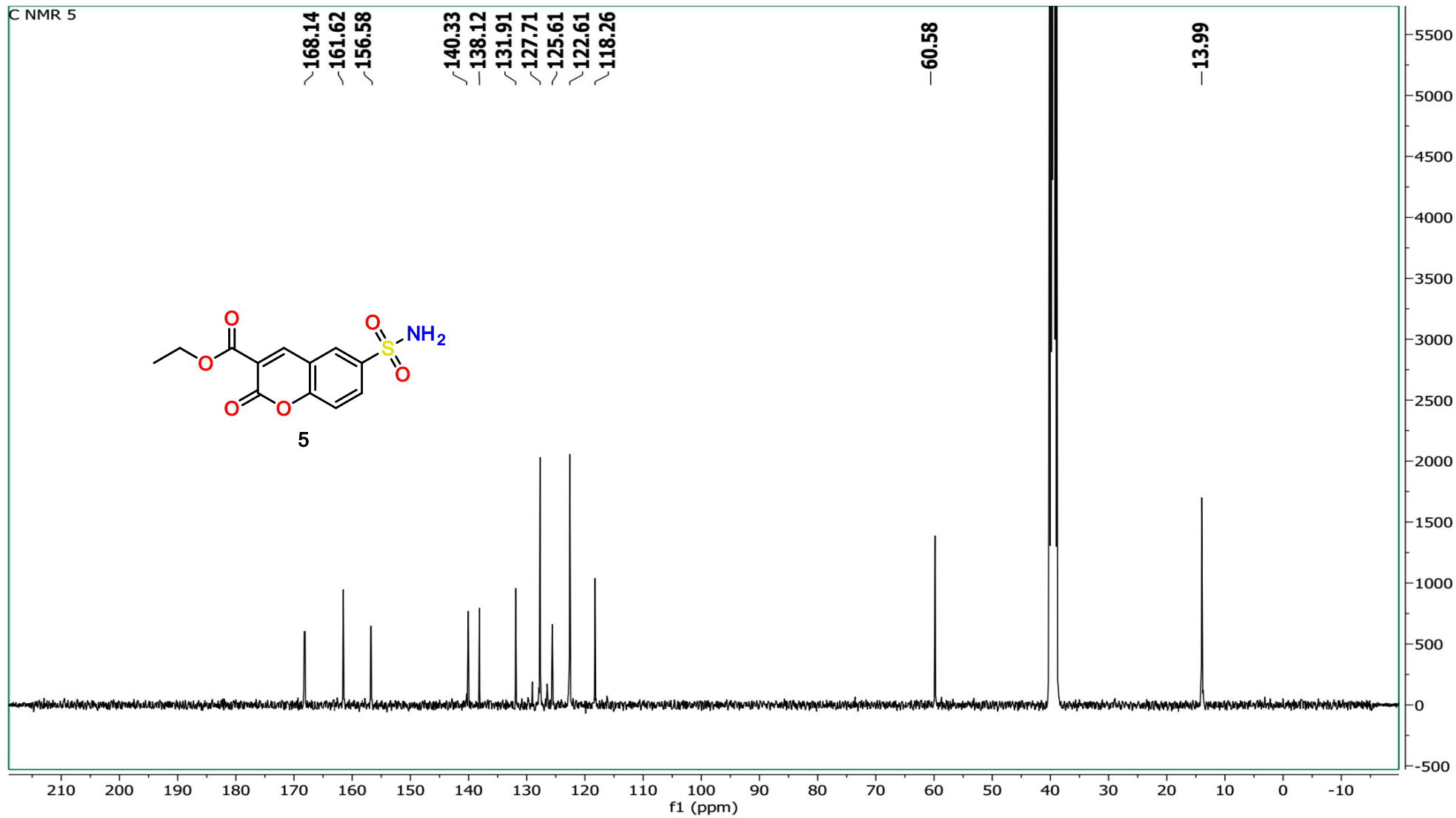
C NMR 5

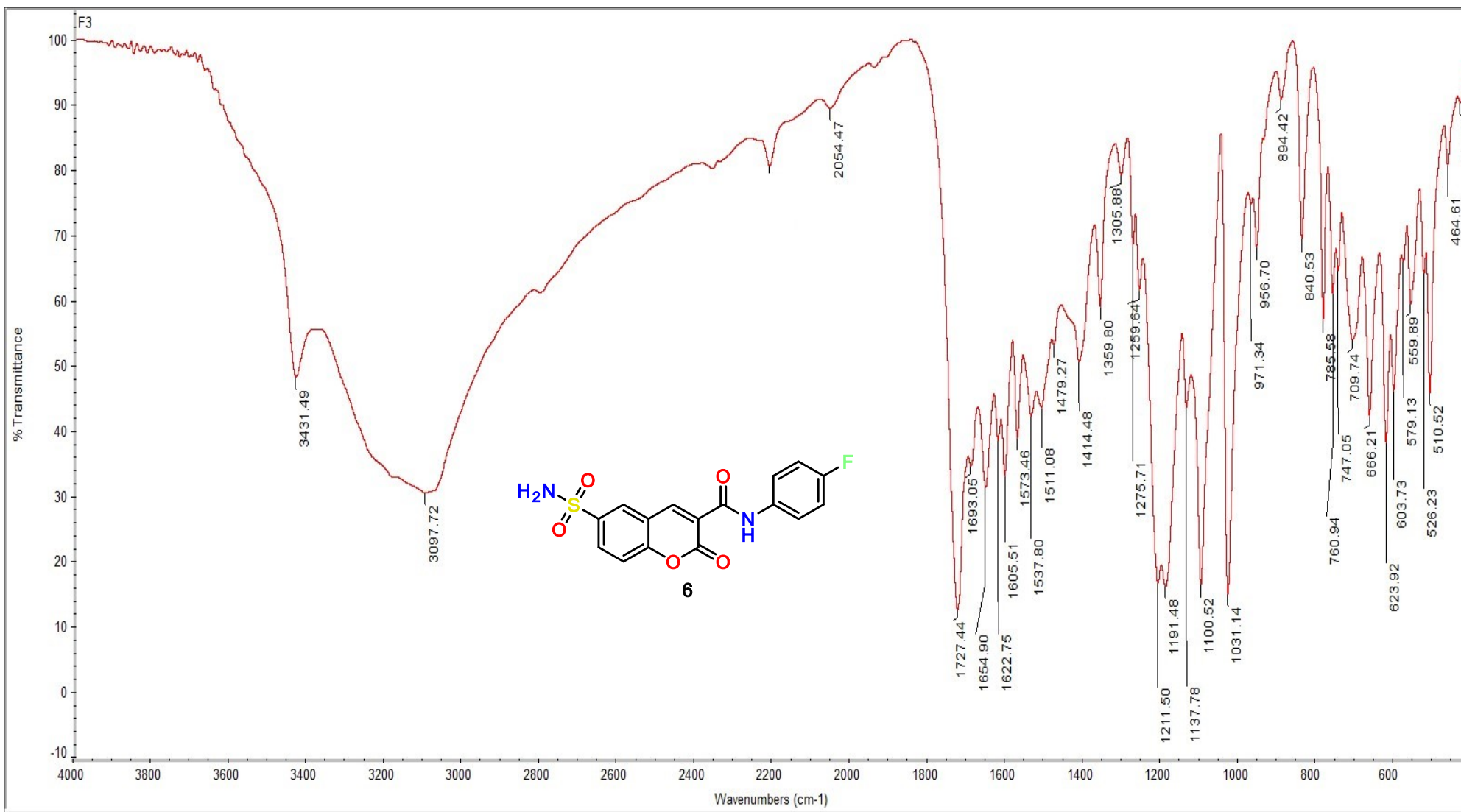


168.14
161.62
156.58
140.33
138.12
131.91
127.71
125.61
122.61
118.26

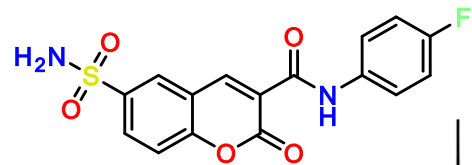
60.58

13.99





H NMR 6



10.466
8.433
8.341
7.843
7.766
7.745
7.724
7.702
7.696
7.673
7.211
7.190
6.901

3.333

2.500

6

0.85

0.90

0.99

0.90

2.29

1.18

2.24

1.98

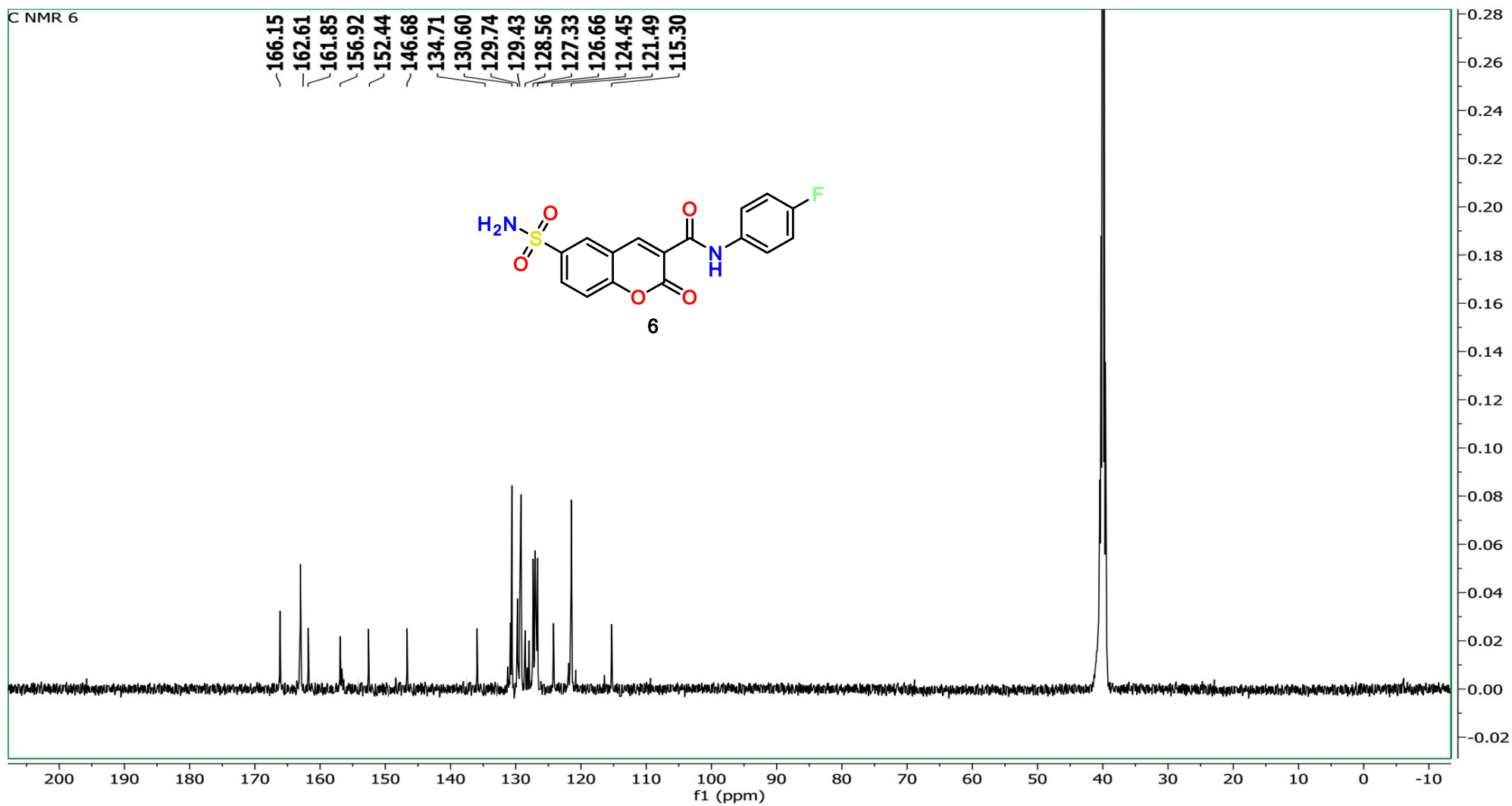
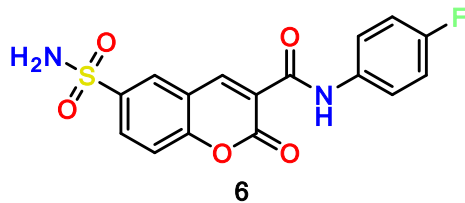
14 13 12 11 10 9 8 7 6 5 4 3 2 1 0 -1

f1 (ppm)

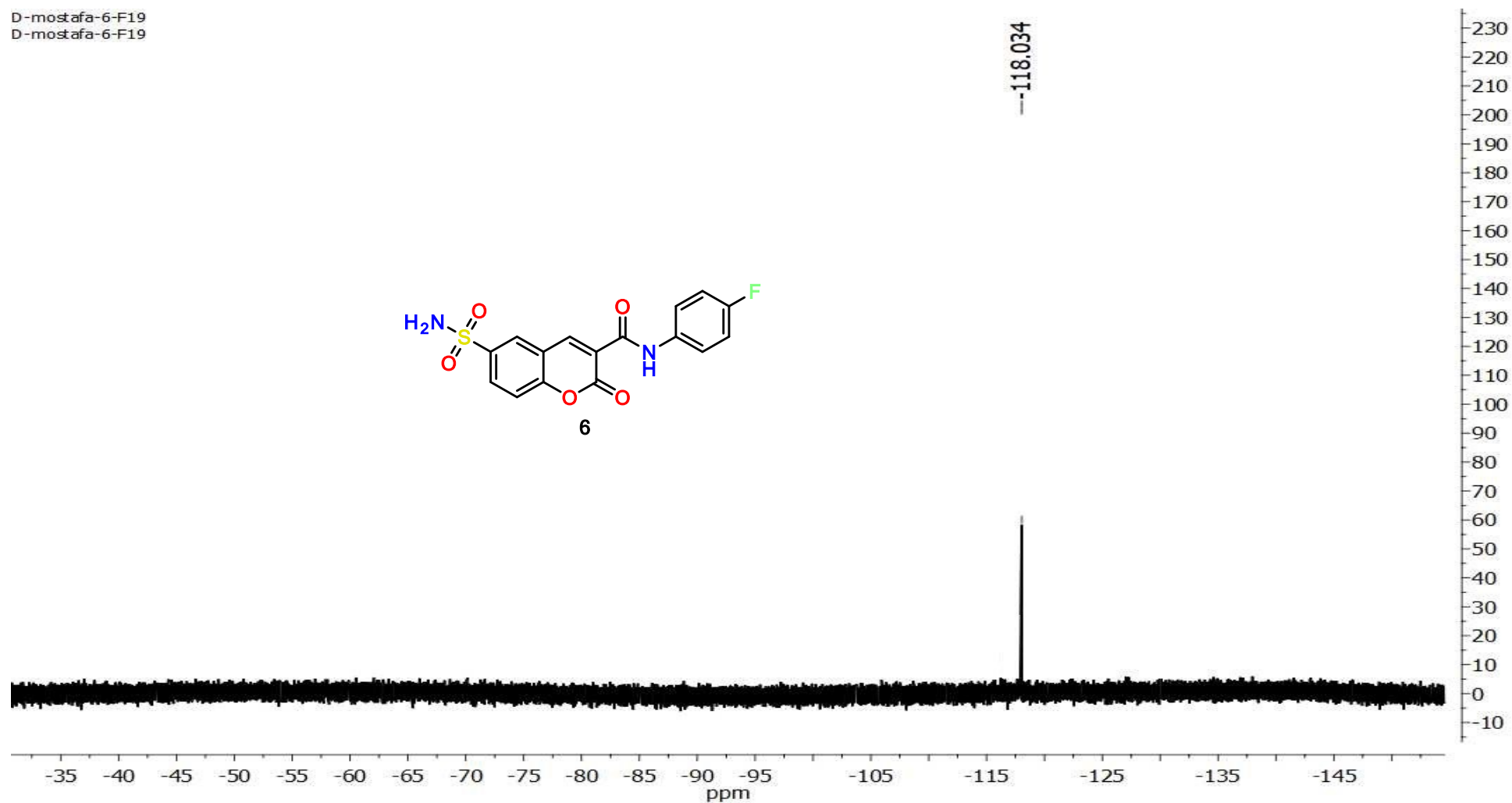
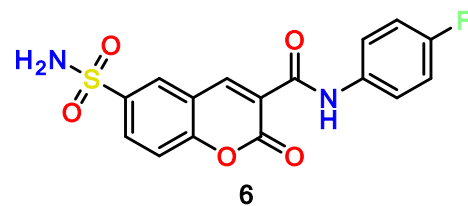
13000
12000
11000
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
-1000

C NMR 6

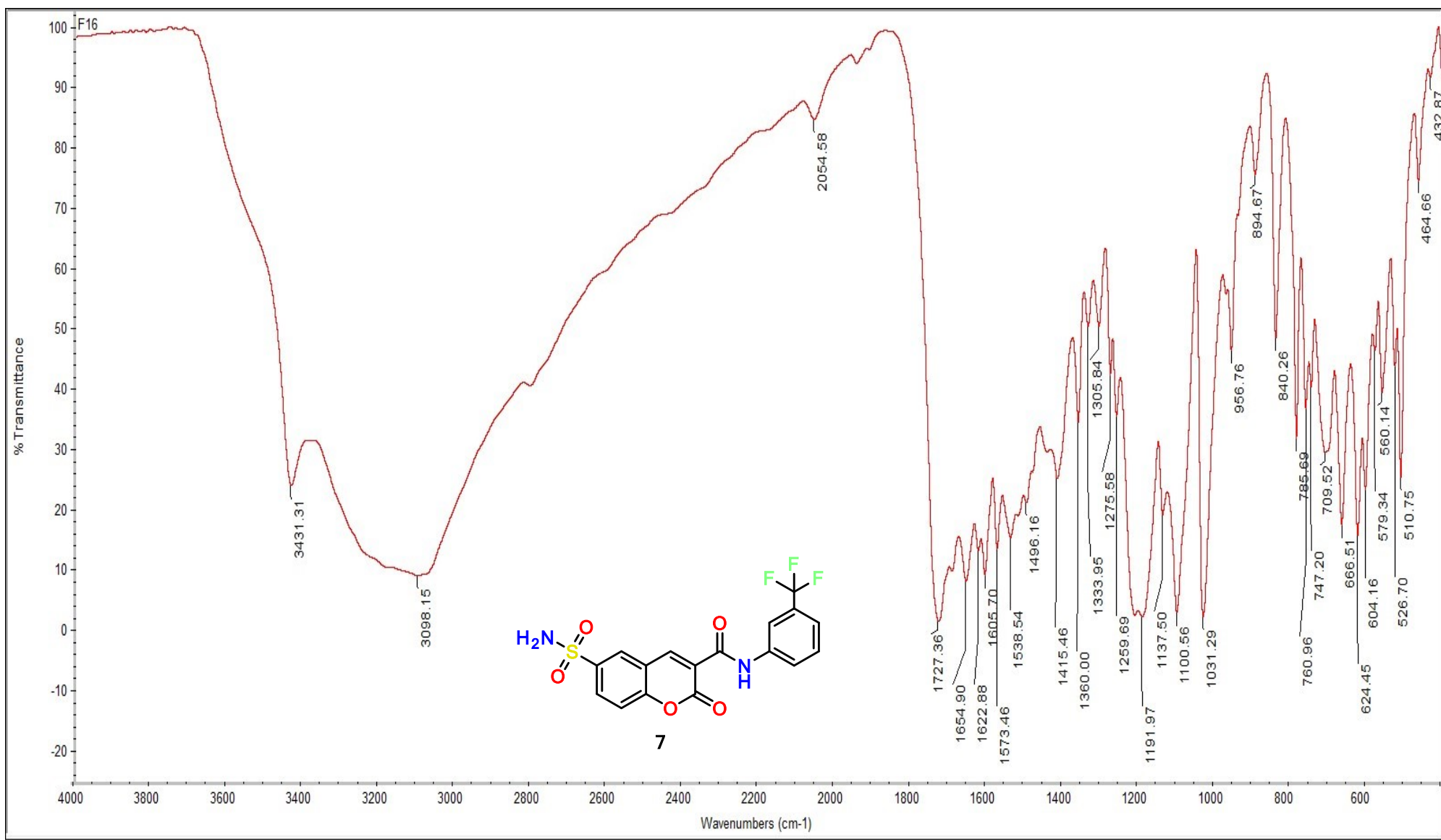
166.15
162.61
161.85
156.92
152.44
146.68
134.71
130.60
129.74
129.43
128.56
127.33
126.66
124.45
121.49
115.30



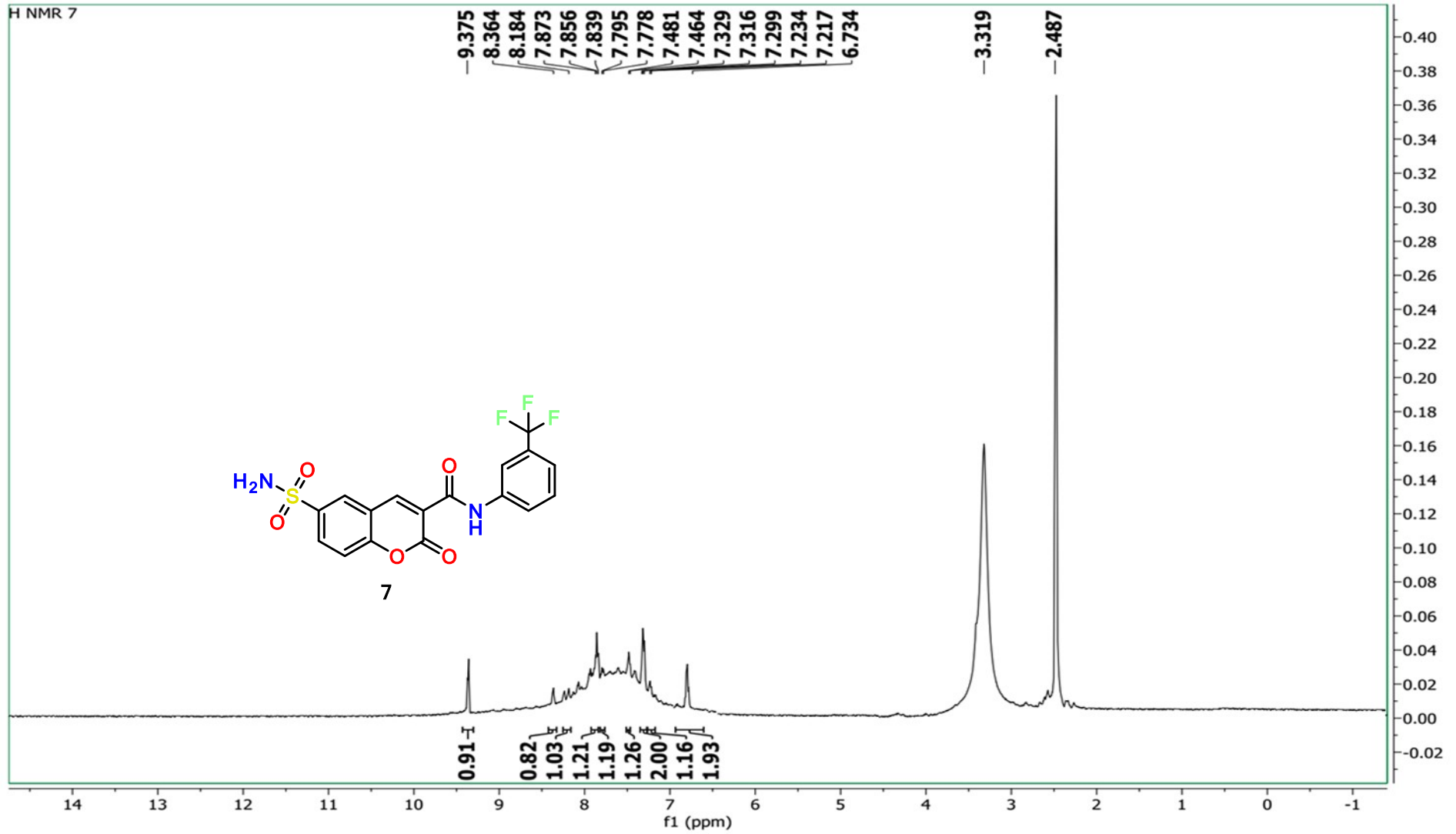
D-mostafa-6-F19
D-mostafa-6-F19



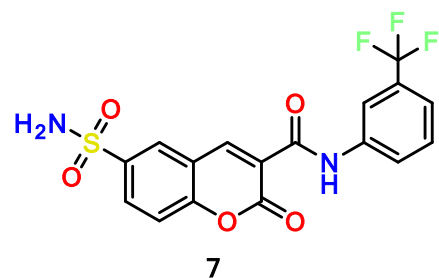
¹⁹F NMR of compound 6 in (376 MHz, DMSO-d₆)



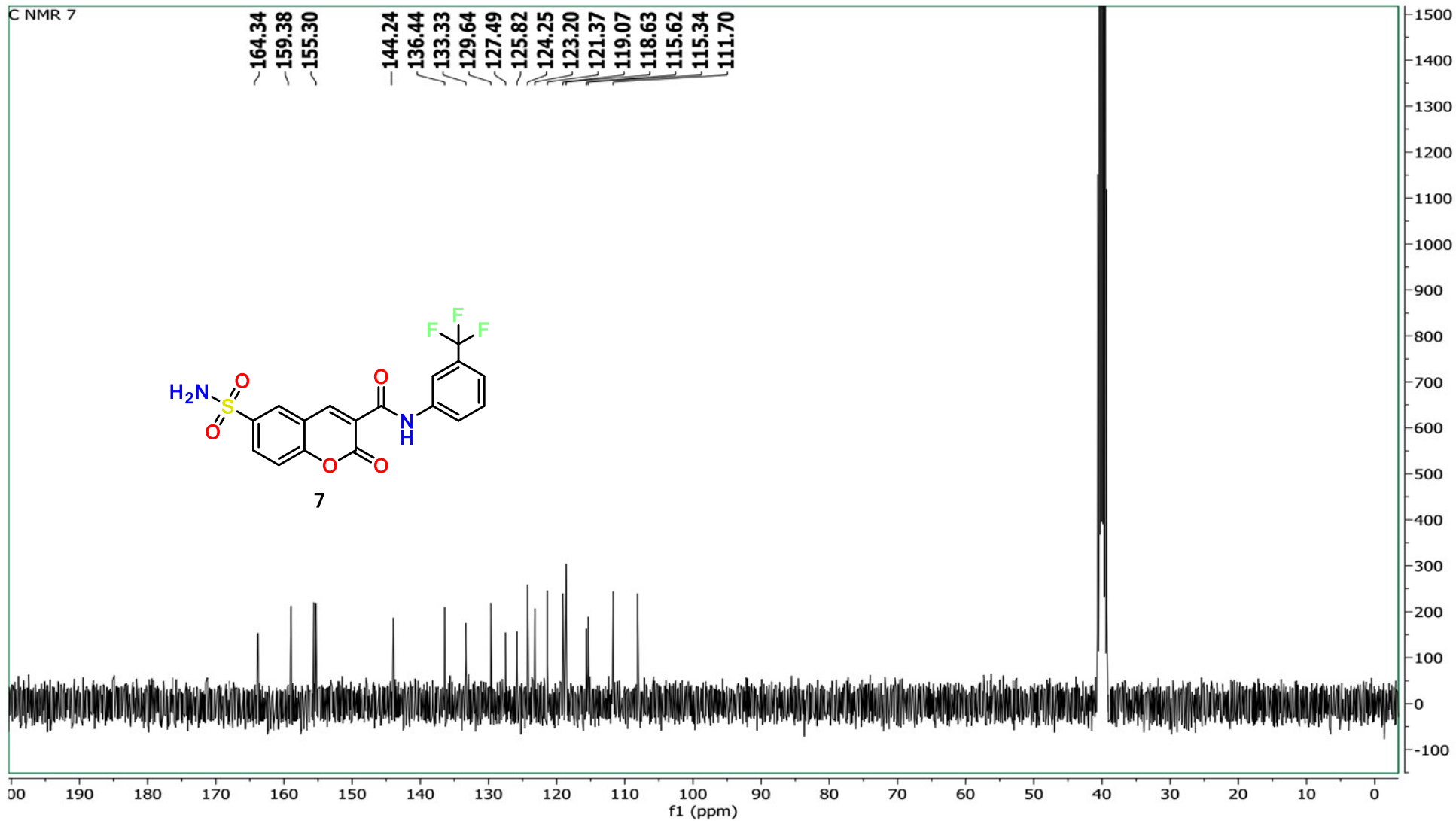
H NMR 7



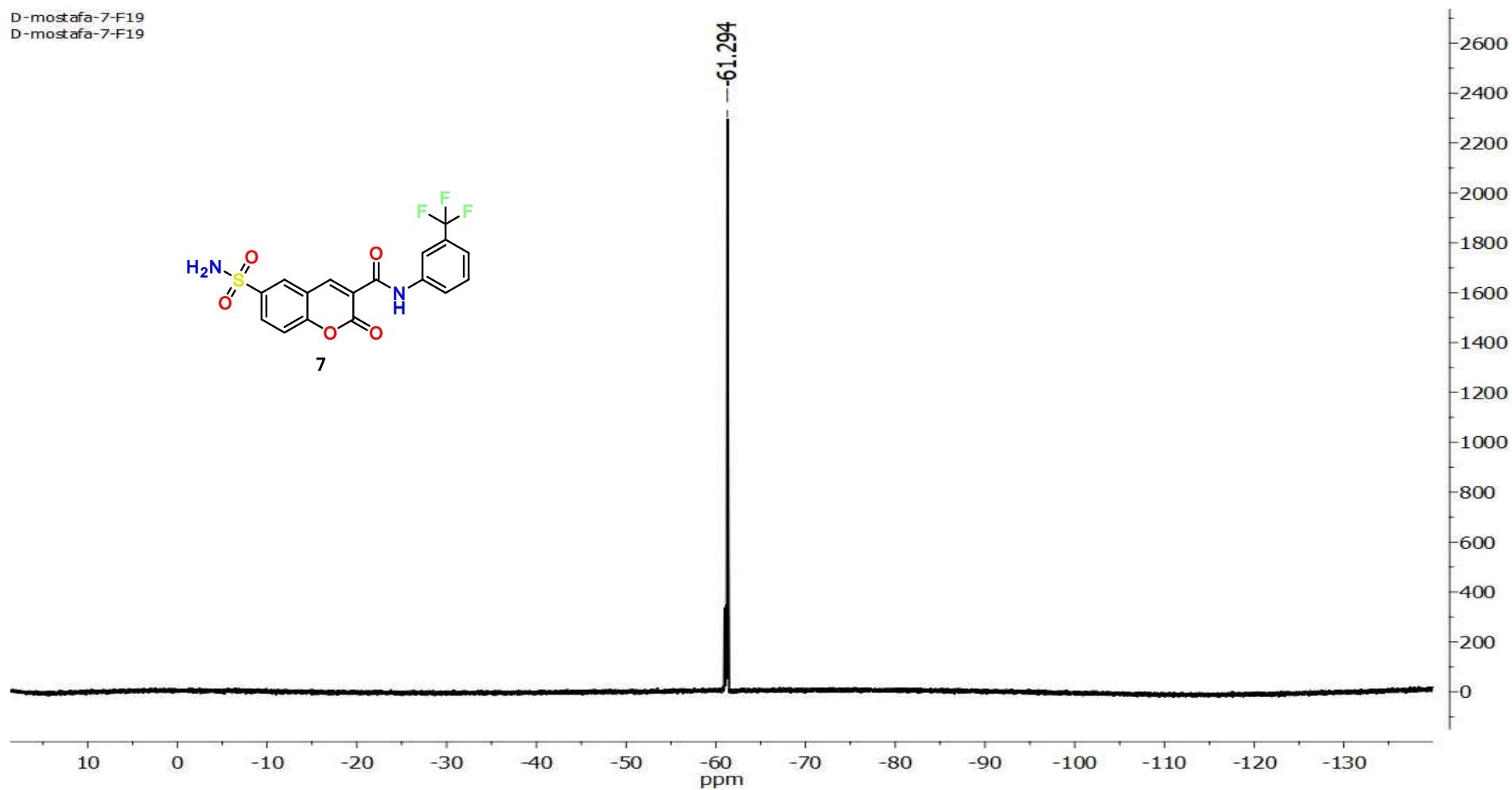
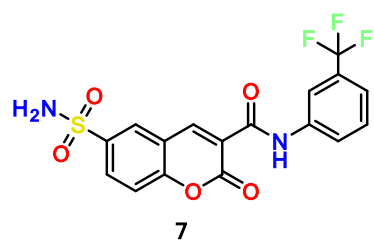
C NMR 7



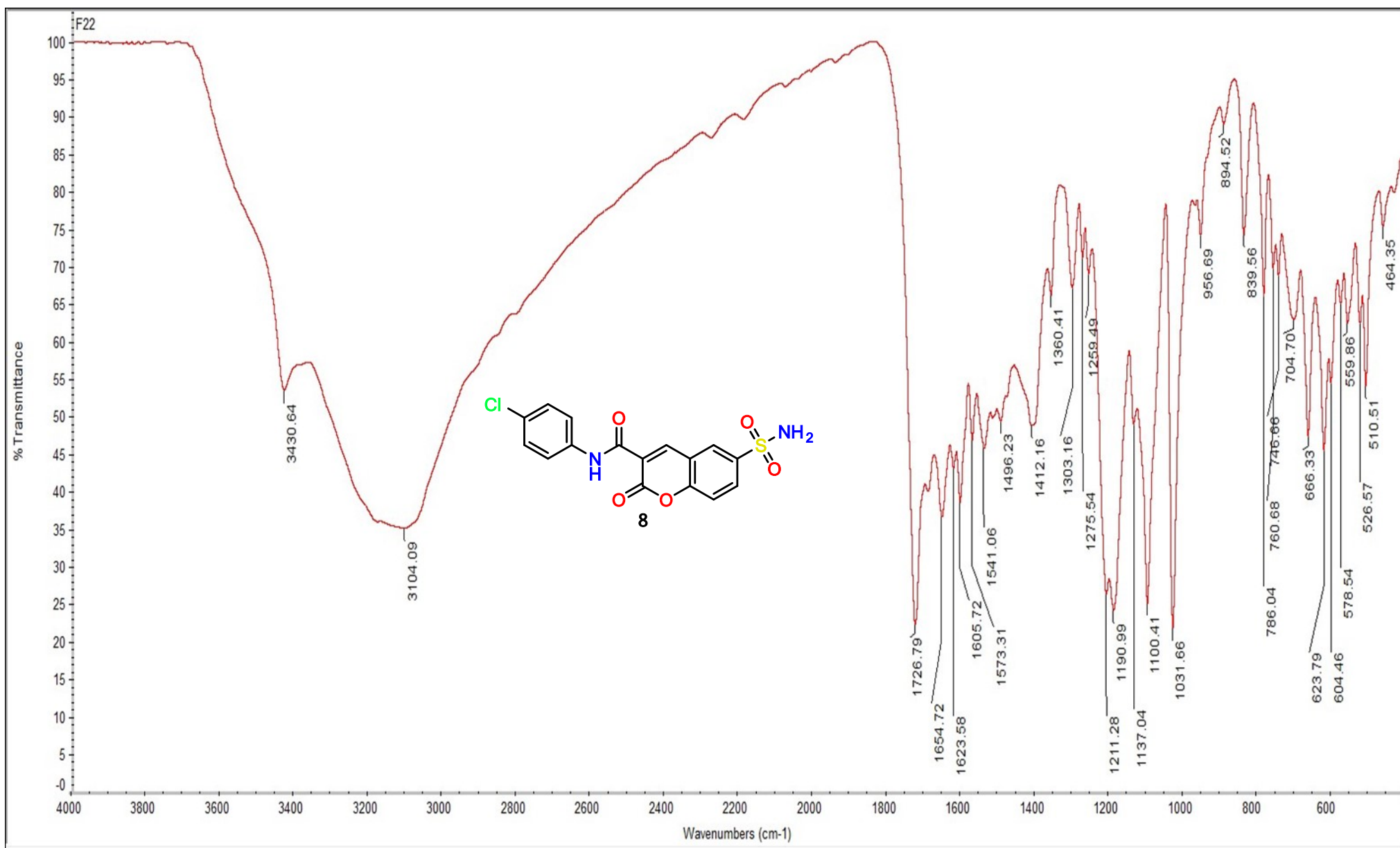
164.34
159.38
155.30
144.24
136.44
133.33
129.64
127.49
125.82
124.25
123.20
121.37
119.07
118.63
115.62
115.34
111.70

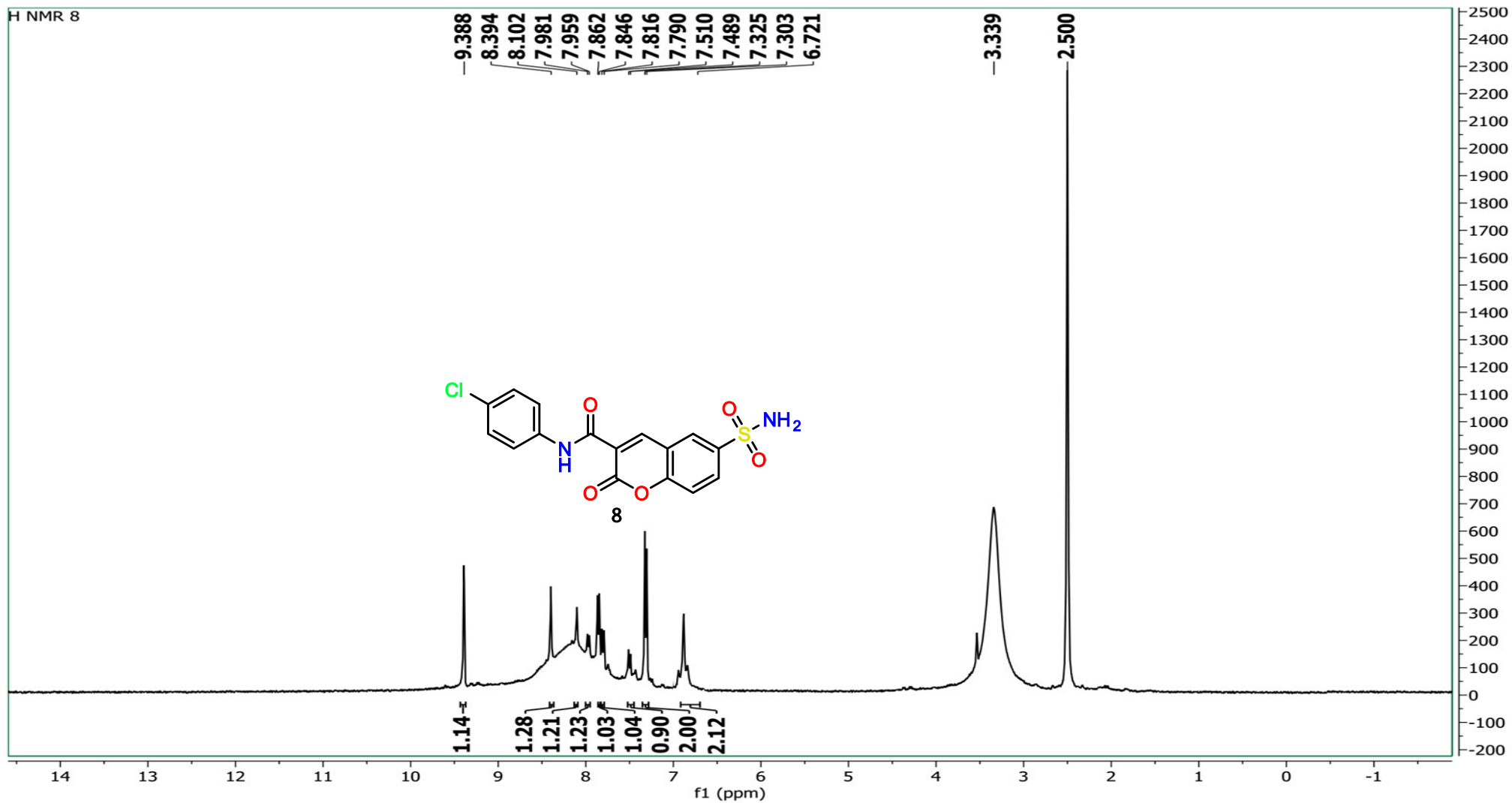


D-mostafa-7-F19
D-mostafa-7-F19



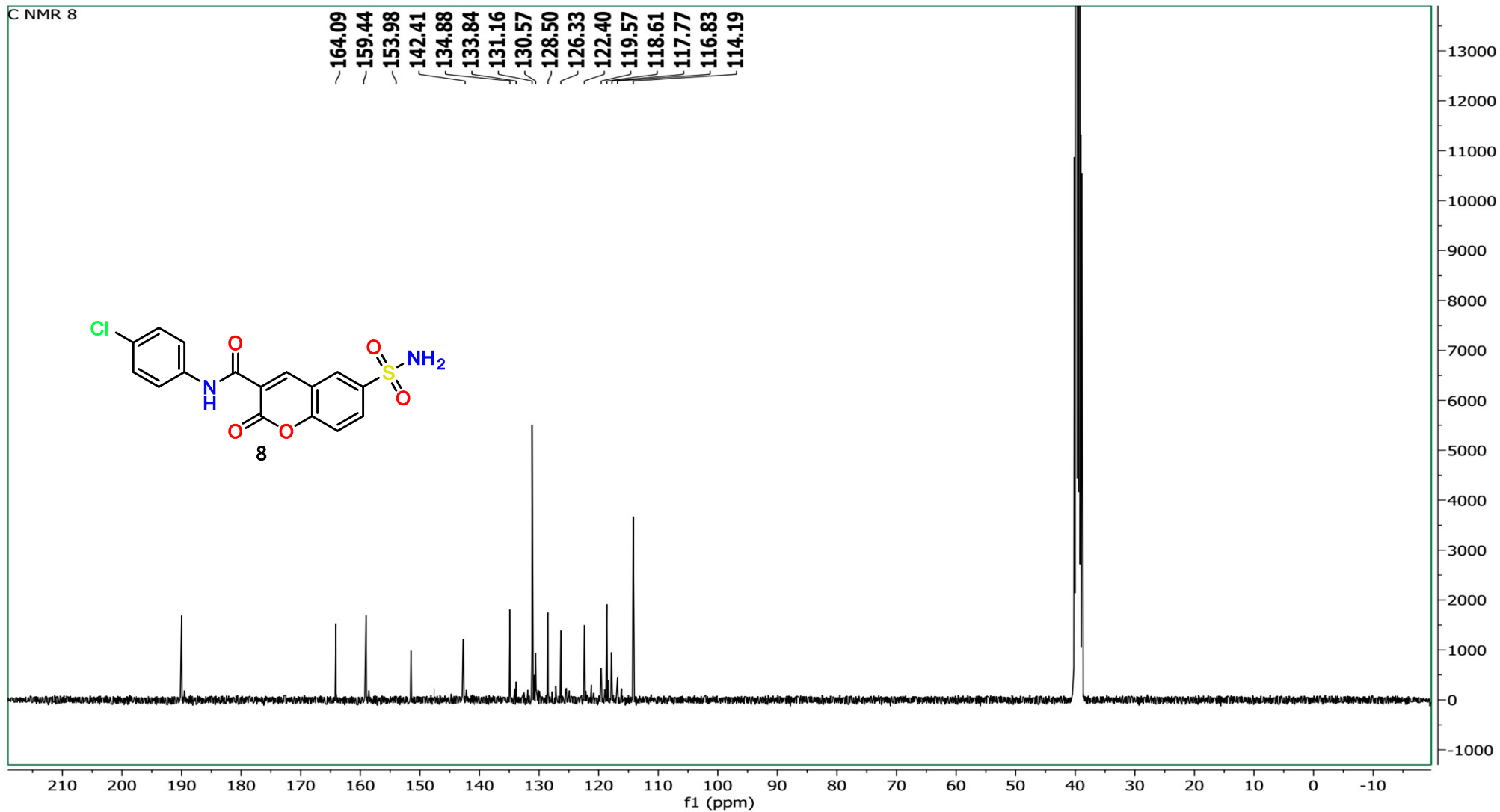
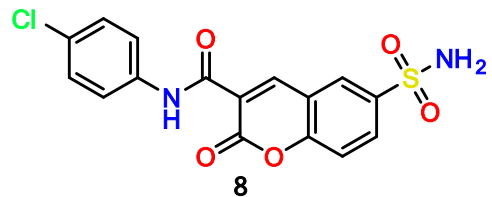
¹⁹F NMR of compound 7 in (376 MHz, DMSO-d₆)

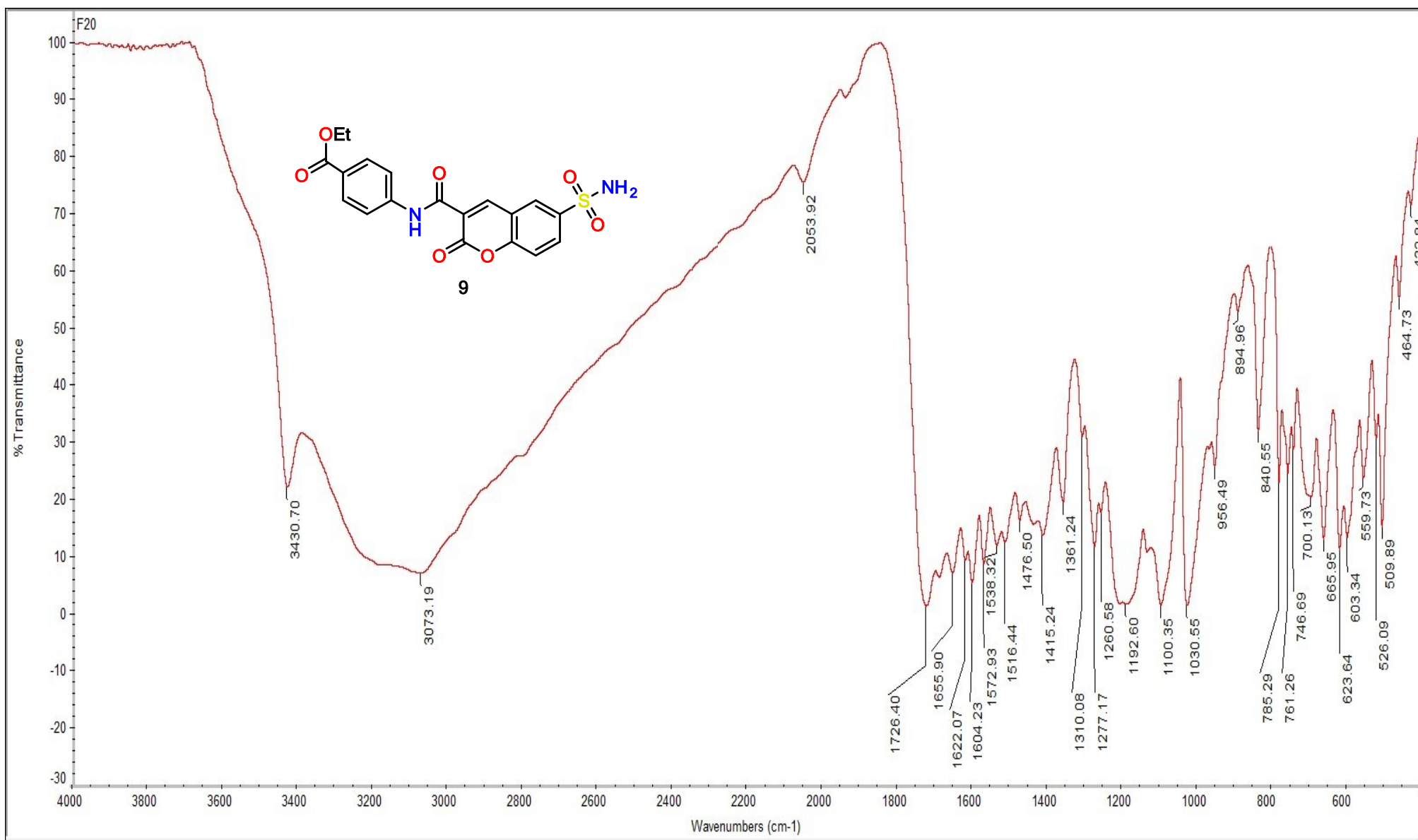




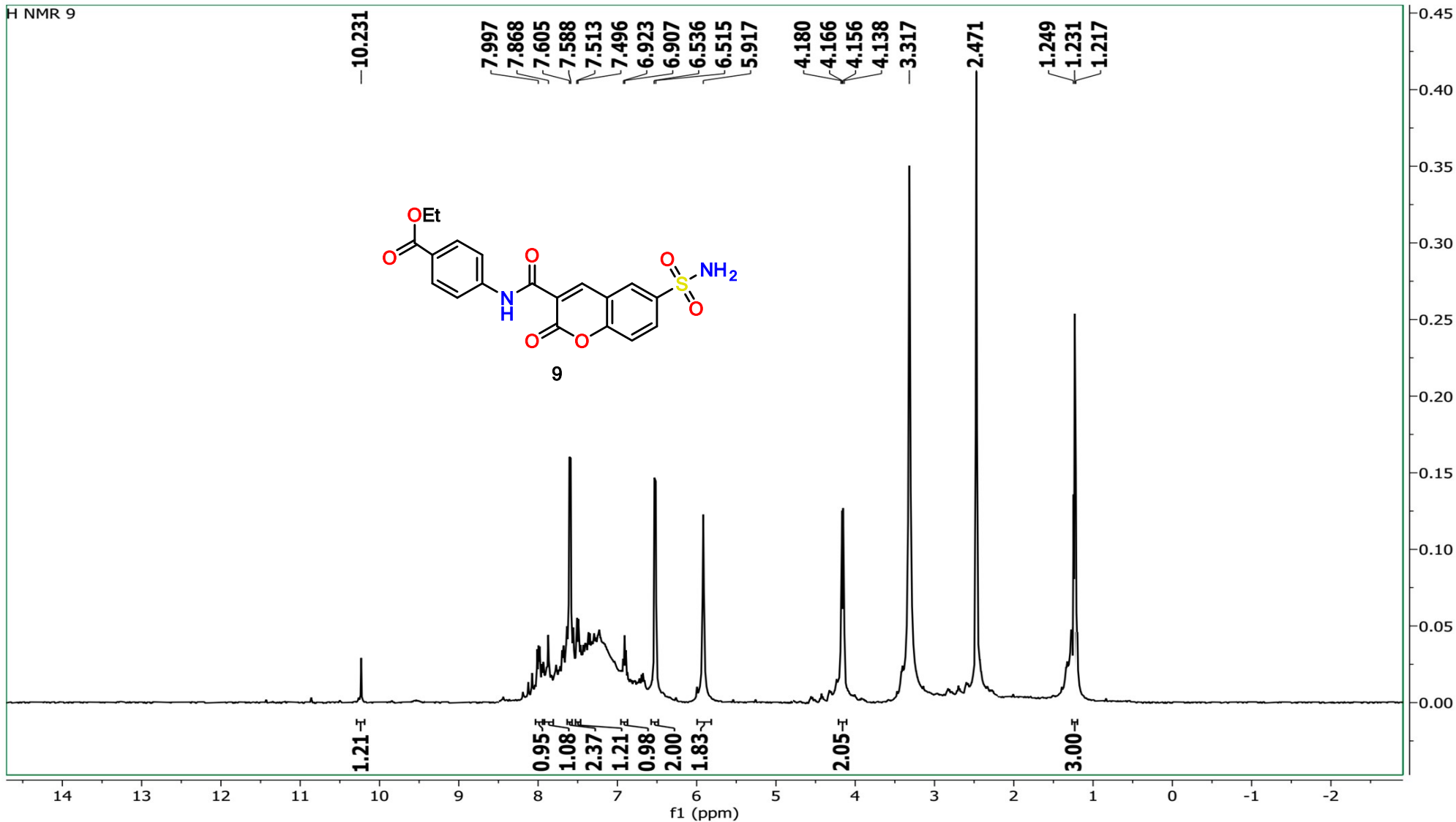
C NMR 8

164.09
159.44
153.98
142.41
134.88
133.84
131.16
130.57
128.50
126.33
122.40
119.57
118.61
117.77
116.83
114.19

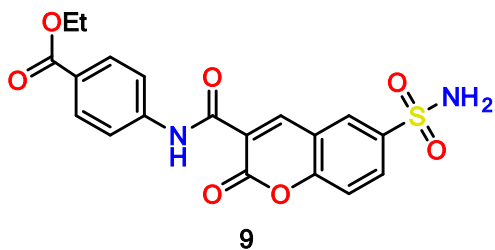




H NMR 9



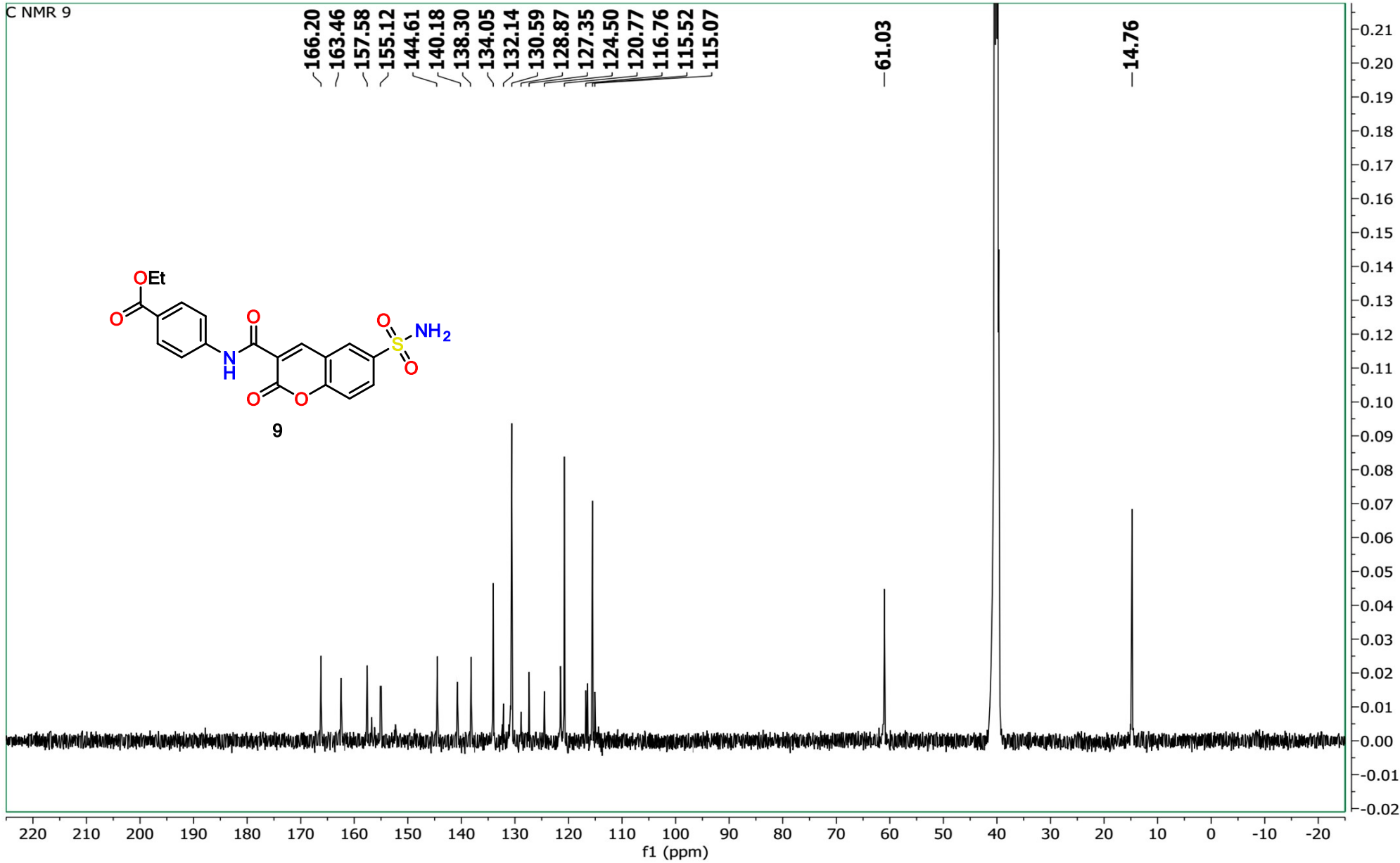
C NMR 9



- 166.20
- 163.46
- 157.58
- 155.12
- 144.61
- 140.18
- 138.30
- 134.05
- 132.14
- 130.59
- 128.87
- 127.35
- 124.50
- 120.77
- 116.76
- 115.52
- 115.07

61.03

14.76



Biological evaluation

Researcher	: Dr.Yosri ammar	email:	mob.
Date	: 30-11-2023		
Assay	: α-Amylase assay		
Samples	: 08 samples .		

Lab Report II

ser	compound			α- Amylase	DF=100
	Original code	Manuscript No.	conc mg/ml		SD ±
1	F3	6	361.35	2.11	0.03
2	F4	2	249.24	1.75	0.01
3	F10	5	297.28	32.53	0.33
4	F16	7	411.36	4.39	0.06
5	F18	3	316.29	14.62	0.16
6	F20	9	415.42	1.08	0.02
7	F22	8	401.48	4.23	0.06
8	F6	4	267.26	8.551	0.312
***	Acarbose		361.35	0.43	0.01

Detailed results.

α- Amylase

Code	IC50	conc	log	%inh	T2	T1	ΔT	RFU2	RFU1	ΔRFU	slope	K.Activity
f3	100	2	95.4	30	0	30	4.62	0	4.62	3.333	5.544	
	10	1	88.6	30	0	30	11.41	0	11.41	3.333	13.692	
	1	0	81.2	30	0	30	18.77	0	18.77	3.333	22.524	
	0.1	-1	70.1	30	0	30	29.91	0	29.91	3.333	35.892	
	0.01	-2	43.7	30	0	30	56.29	0	56.29	3.333	67.548	
EC			0	30	0	30	100	0	100	3.333	120	
code	IC50	conc	log	%inh	T2	T1	ΔT	RFU2	RFU1	ΔRFU	slope	K.Activity
f4	100	2	96.1	30	0	30	3.88	0	3.88	3.333	4.656	
	10	1	91.2	30	0	30	8.79	0	8.79	3.333	10.548	
	1	0	77.8	30	0	30	22.15	0	22.15	3.333	26.58	
	0.1	-1	68.9	30	0	30	31.14	0	31.14	3.333	37.368	
	0.01	-2	50.3	30	0	30	49.67	0	49.67	3.333	59.604	
EC			0	30	0	30	100	0	100	3.333	120	
code	IC50	conc	log	%inh	T2	T1	ΔT	RFU2	RFU1	ΔRFU	slope	K.Activity
f10	100	2	93.4	30	0	30	6.59	0	6.59	3.333	7.908	

	10	1	85.6	30	0	30	14.38	0	14.38	3.333	17.256
	1	0	72	30	0	30	28.02	0	28.02	3.333	33.624
	0.1	-1	48.8	30	0	30	51.18	0	51.18	3.333	61.416
	0.01	-2	31.6	30	0	30	68.43	0	68.43	3.333	82.116
EC			0	30	0	30	100	0	100	3.333	120

code	IC50	conc	log	%inh	T2	T1	ΔT	RFU2	RFU1	ΔRFU	slope	K.Activity
f16	100	2	96.2	30	0	30	3.76	0	3.76	3.333	4.512	
	10	1	89.6	30	0	30	10.42	0	10.42	3.333	12.504	
	1	0	80.8	30	0	30	19.15	0	19.15	3.333	22.98	
	0.1	-1	54.9	30	0	30	45.13	0	45.13	3.333	54.156	
	0.01	-2	46.1	30	0	30	53.89	0	53.89	3.333	64.668	
EC			0	30	0	30	100	0	100	3.333	120	

code	IC50	conc	log	%inh	T2	T1	ΔT	RFU2	RFU1	ΔRFU	slope	K.Activity
f18	100	2	96	30	0	30	3.99	0	3.99	3.333	4.788	
	10	1	88	30	0	30	12.03	0	12.03	3.333	14.436	
	1	0	73.5	30	0	30	26.51	0	26.51	3.333	31.812	
	0.1	-1	60.2	30	0	30	39.77	0	39.77	3.333	47.724	
	0.01	-2	33.8	30	0	30	66.18	0	66.18	3.333	79.416	
EC			0	30	0	30	100	0	100	3.333	120	

code	IC50	conc	log	%inh	T2	T1	ΔT	RFU2	RFU1	ΔRFU	slope	K.Activity
f20		100	2	96.6	30	0	30	3.39	0	3.39	3.333	4.068
		10	1	90	30	0	30	9.95	0	9.95	3.333	11.94
		1	0	82.6	30	0	30	17.41	0	17.41	3.333	20.892
		0.1	-1	73.5	30	0	30	26.54	0	26.54	3.333	31.848
		0.01	-2	45.8	30	0	30	54.15	0	54.15	3.333	64.98
EC				0	30	0	30	100	0	100	3.333	120
code	IC50	conc	log	%inh	T2	T1	ΔT	RFU2	RFU1	ΔRFU	slope	K.Activity
f22		100	2	95.4	30	0	30	4.61	0	4.61	3.333	5.532
		10	1	88.6	30	0	30	11.39	0	11.39	3.333	13.668
		1	0	75.8	30	0	30	24.16	0	24.16	3.333	28.992
		0.1	-1	60.5	30	0	30	39.51	0	39.51	3.333	47.412
		0.01	-2	44.5	30	0	30	55.47	0	55.47	3.333	66.564
EC				0	30	0	30	100	0	100	3.333	120
F6	IC50	conc	log	%inh	T2	T1	ΔT	RFU2	RFU1	ΔRFU	slope	K.Activity
		100	2	94.2	30	0	30	5.75	0	5.75	3.333	6.9
		10	1	84.7	30	0	30	15.29	0	15.29	3.333	18.348
		1	0	70.5	30	0	30	29.46	0	29.46	3.333	35.352
		0.1	-1	52.6	30	0	30	47.41	0	47.41	3.333	56.892
		0.01	-2	31.8	30	0	30	68.22	0	68.22	3.333	81.864

				0	30	0	30	100	0	100	3.333	120
code	IC50	conc	log	%inh	T2	T1	ΔT	RFU2	RFU1	ΔRFU	slope	K.Activity
Acarbose		100	2	96.5	30	0	30	3.45	0	3.45	3.333	4.14
		10	1	90.2	30	0	30	9.81	0	9.81	3.333	11.772
		1	0	84.3	30	0	30	15.73	0	15.73	3.333	18.876
		0.1	-1	75.4	30	0	30	24.63	0	24.63	3.333	29.556
		0.01	-2	47.5	30	0	30	52.46	0	52.46	3.333	62.952
EC				0	30	0	30	100	0	100	3.333	120

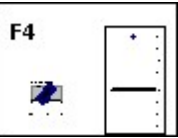


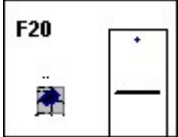
Lab Report I

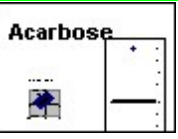
ser	compound			α -glucosidase IC50	DF=100
	code		M.W	mg/ml	SD \pm
1	F4	2	---	0.548	0.02
2	F20	9	---	2.435	0.09
***	Acarbose		---	0.604	0.02

Detailed results.

α- Glucosidase

code	IC50	conc	log	%inh	T2	T1	ΔT	RFU2	RFU1	ΔRFU	slope	K.Activity
F4		10	1	90.7	30	0	30	9.33	0	9.33	3.333	11.196
		5	0.7	76.4	30	0	30	23.62	0	23.62	3.333	28.344
		1	0	53.4	30	0	30	46.55	0	46.55	3.333	55.86
		0.1	-1	20.6	30	0	30	79.35	0	79.35	3.333	95.22
		0.01	-2	8.98	30	0	30	91.02	0	91.02	3.333	109.22
	EC				0	30	0	30	100	0	100	3.333

code	IC50	conc	log	%inh	T2	T1	ΔT	RFU2	RFU1	ΔRFU	slope	K.Activity
F20		10	1	83.8	30	0	30	16.23	0	16.23	3.333	19.476
		5	0.7	54.2	30	0	30	45.77	0	45.77	3.333	54.924
		1	0	20.6	30	0	30	79.38	0	79.38	3.333	95.256
		0.1	-1	8.85	30	0	30	91.15	0	91.15	3.333	109.38
		0.01	-2	3.45	30	0	30	96.55	0	96.55	3.333	115.86
	EC				0	30	0	30	100	0	100	3.333

code	IC50	conc	log	%inh	T2	T1	ΔT	RFU2	RFU1	ΔRFU	slope	K.Activity
Acarbose		10	1	90.1	30	0	30	9.86	0	9.86	3.333	11.832
		5	0.7	82.6	30	0	30	17.44	0	17.44	3.333	20.928
		1	0	51.4	30	0	30	48.63	0	48.63	3.333	58.356
		0.1	-1	13.8	30	0	30	86.22	0	86.22	3.333	103.46
		0.01	-2	5.95	30	0	30	94.05	0	94.05	3.333	112.86
	EC				0	30	0	30	100	0	100	3.333

Lab Report

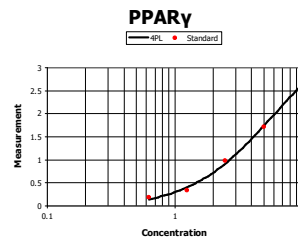
ser	sample			PPAR γ	FLD
	Original code number	Manuscript number	Type	ug/ml	
1	F4	2		3.152±0.03	1.365
2	F20	--9-		3.706±0.32	1.605
3	pioglitazone	---		4.884±0.29	2.115
4	control	---		2.309±0.02	1

Detailed Results:

Standard conc.

ST	Conc .
St.1	10
St.2	5
St.3	2.5
St.4	1.25
St.5	0.625

Plate map



Calibrator	Wells	Conc.	Raw (Corrected)	Backfit	Recovery %
Standard1	A1	10	2.64	10.06	100.6
Standard2	B1	5	1.71	4.89	97.8
Standard3	C1	2.5	0.984	2.662	106.5
Standard4	D1	1.25	0.33	1.079	86.29
Standard5	E1	0.625	0.177	0.7074	113.2

Sample	Wells	Raw	Background Corrected	Conc.	Conc. (Average)	%CV	SD	SEM
F4	E2	1.17	1.17	3.128	3.152	1.07	0.0336	0.0238
	F2	1.18		3.176				
F20	G2	1.44	1.35	3.937	3.706	8.84	0.328	0.232
	H2	1.29		3.474				
pioglitazone	A3	1.77	1.71	5.094	4.884	6.08	0.297	0.21
	B3	1.66		4.674				
control	C3	0.862	0.846	2.328	2.309	1.15	0.0265	0.0187
	D3	0.847		2.291				
Blank	F1	0.015	0	0.2304	0.2087	9.36	0.0195	0.0113
	G1	0.004		0.1926				
	H1	0.007		0.2031				

Docking simulation figures

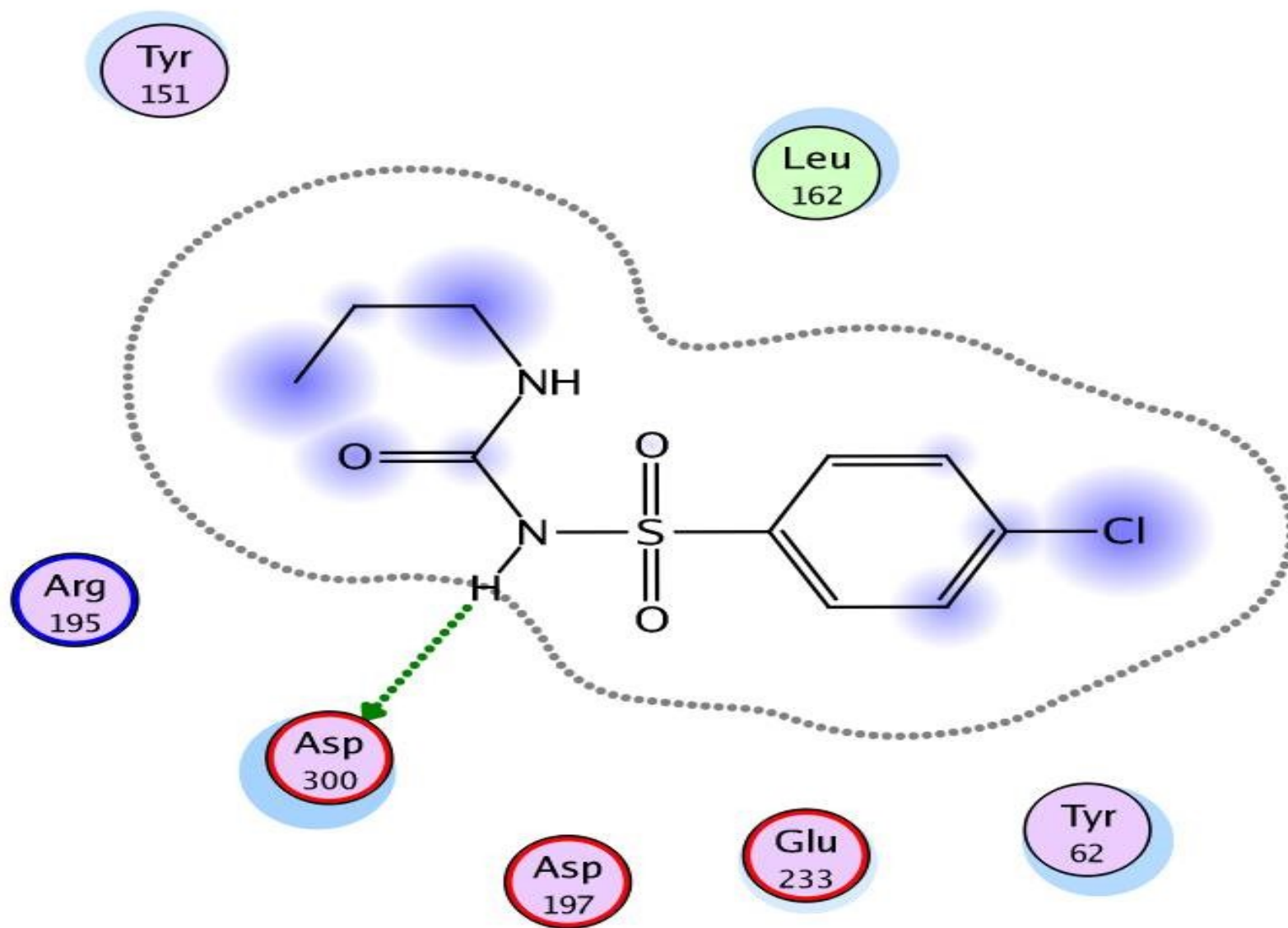


Figure S1: 2D interaction of **Chlorpropamide** inside the active site of α -amylase (PDB: 2QV4)

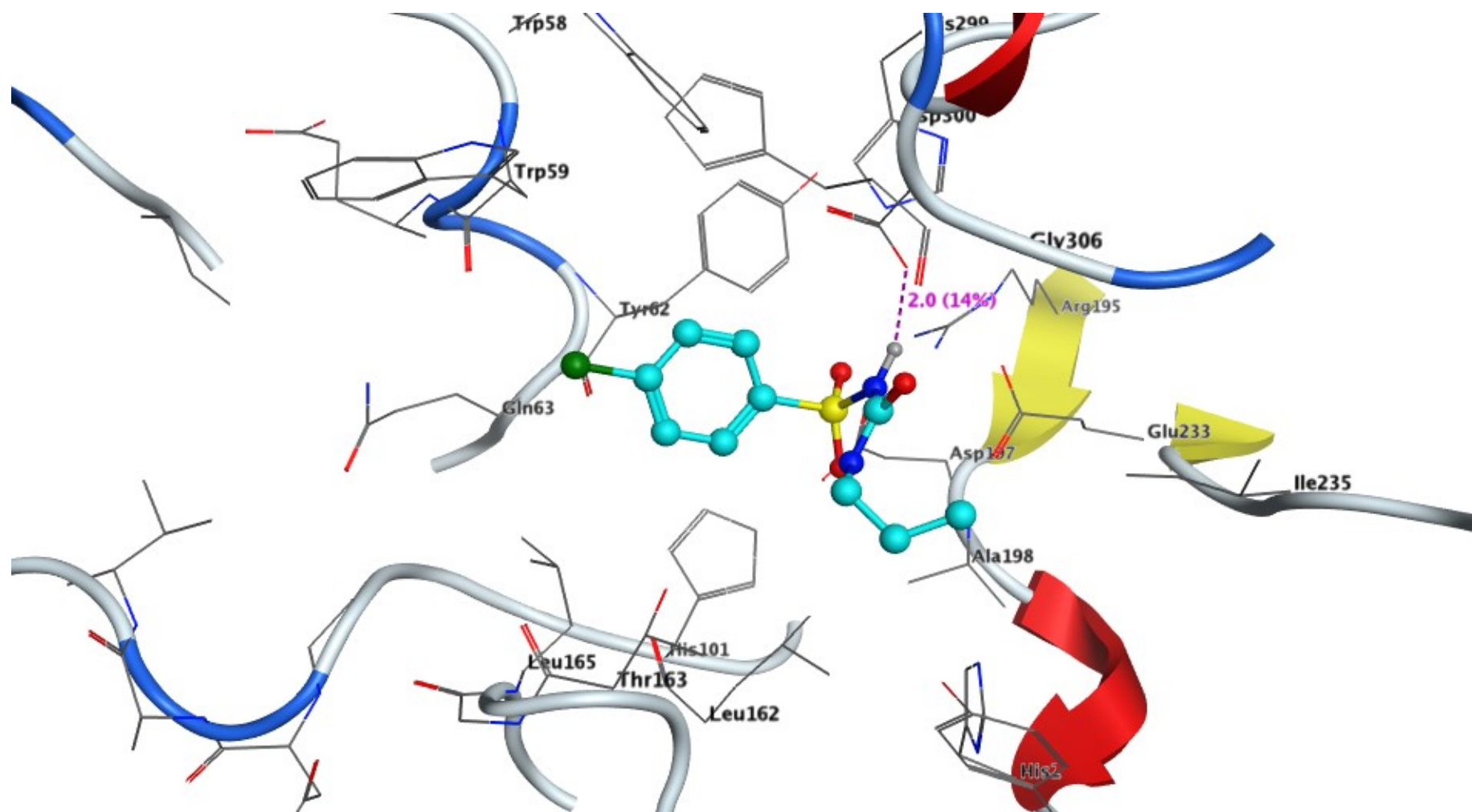


Figure S2: 3D interaction of **Chlorpropamide** inside the active site of α -amylase (PDB: 2QV4)

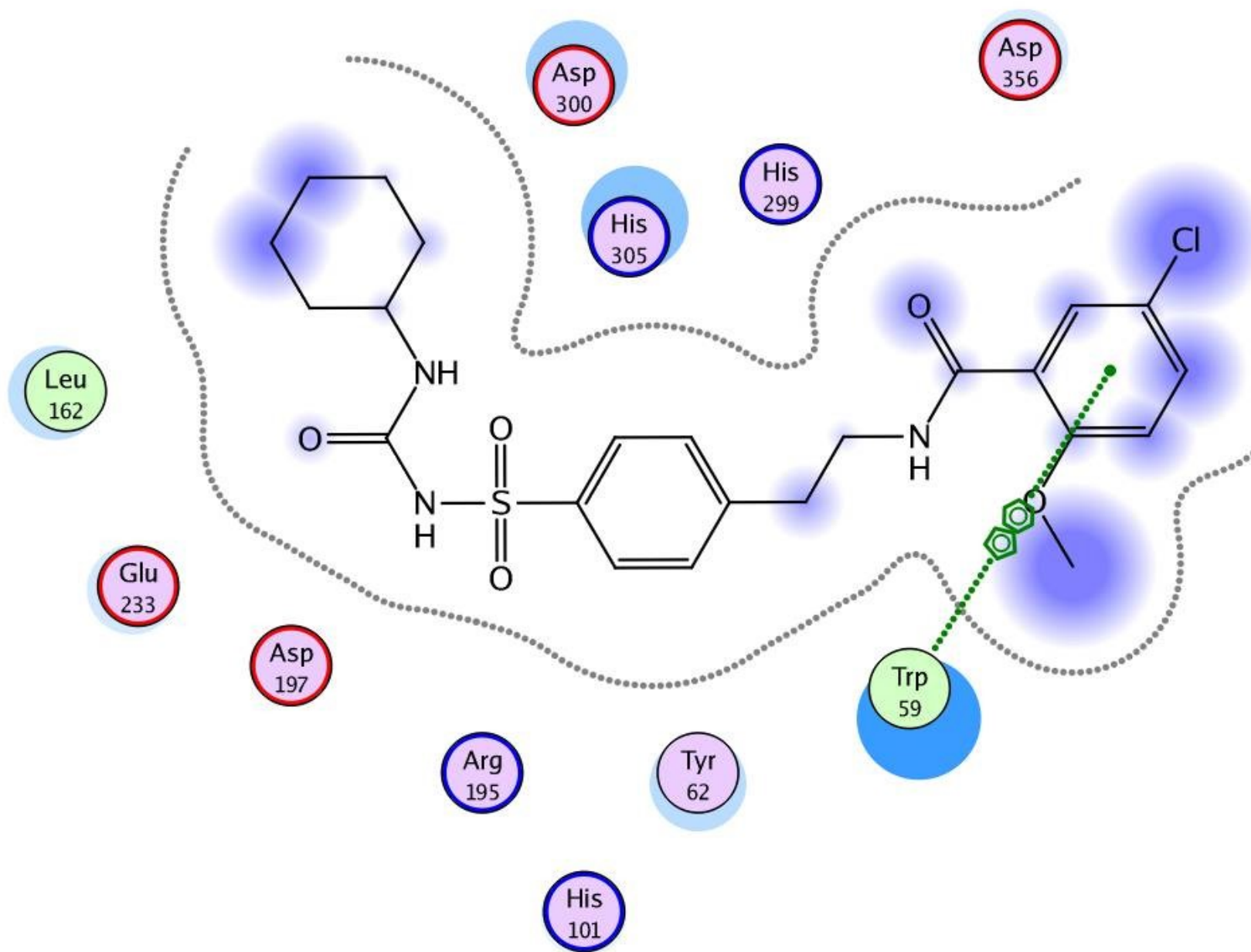


Figure S3: 2D interaction of **Glibenclamide** inside the active site of α -amylase (PDB: 2QV4)

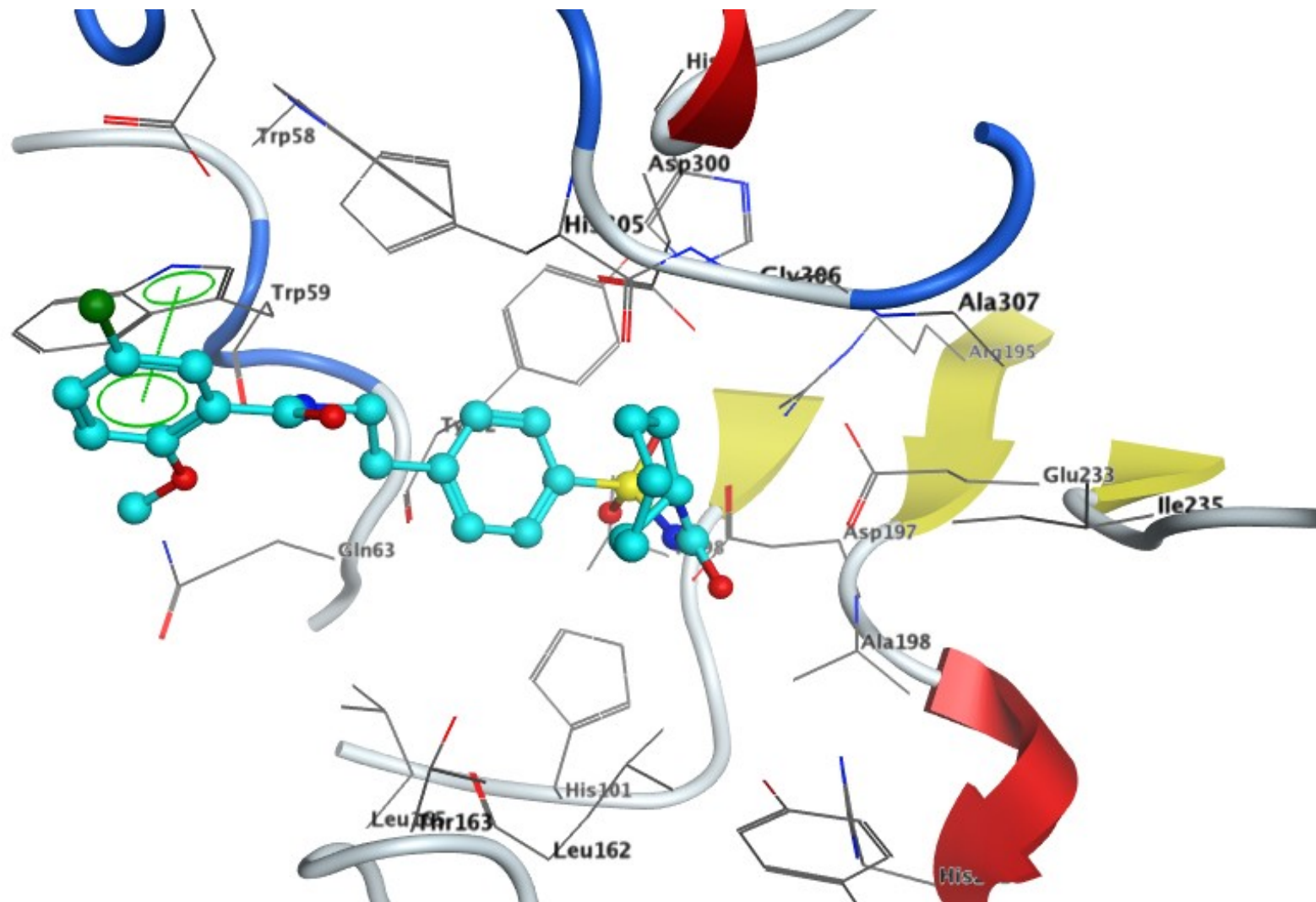


Figure S4: 3D interaction of **Glibenclamide** inside the active site of α -amylase (PDB: 2QV4)

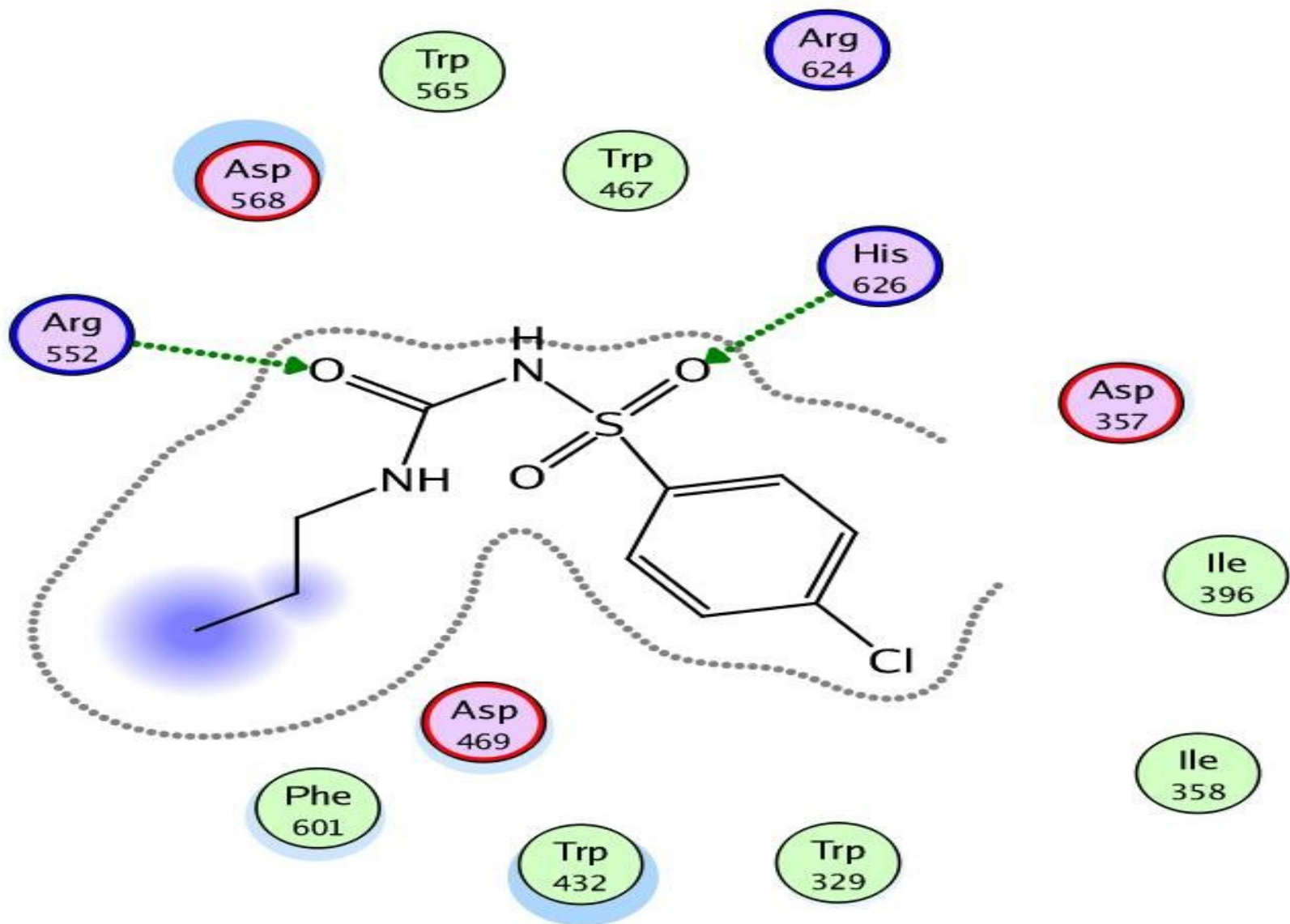


Figure S5: 2D interaction of **Chlorpropamide** inside the active site of α -glucosidase (PDB: 3w37)

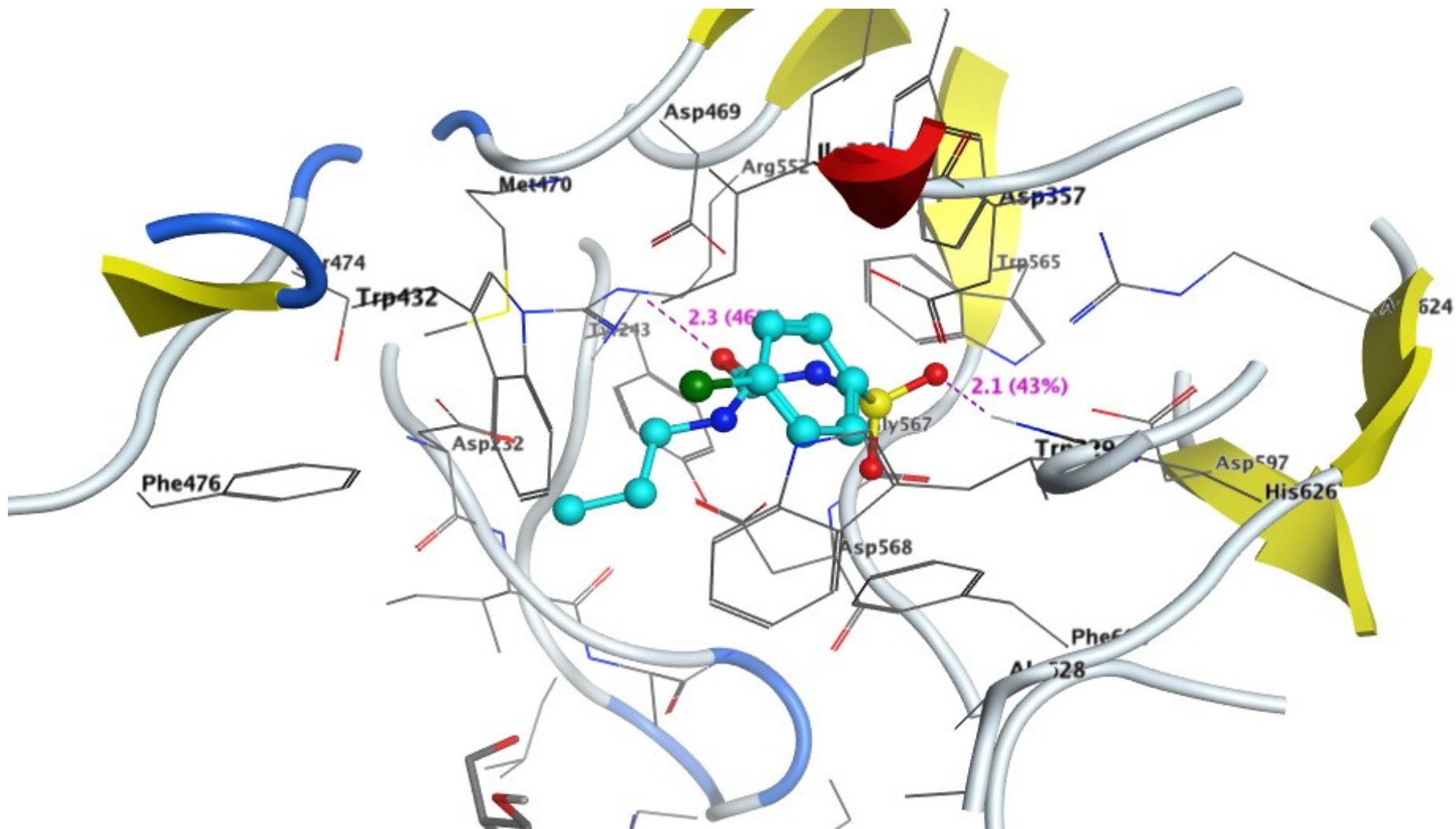


Figure S6: 3D interaction of **Chlorpropamide** inside the active site of α -glucosidase (PDB: 3w37)

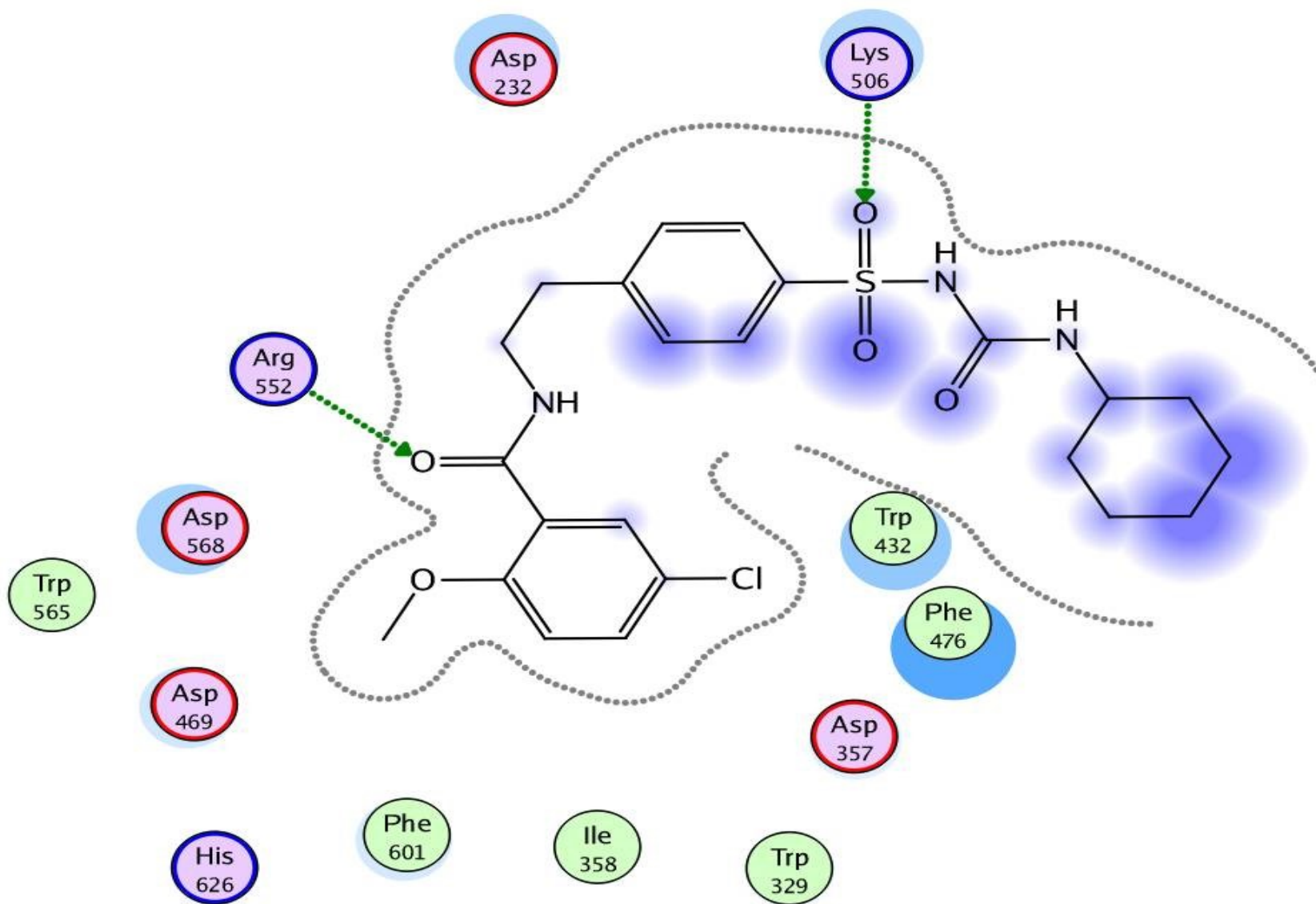


Figure S7: 2D interaction of **Glibenclamide** inside the active site of α -glucosidase (PDB: 3w37)

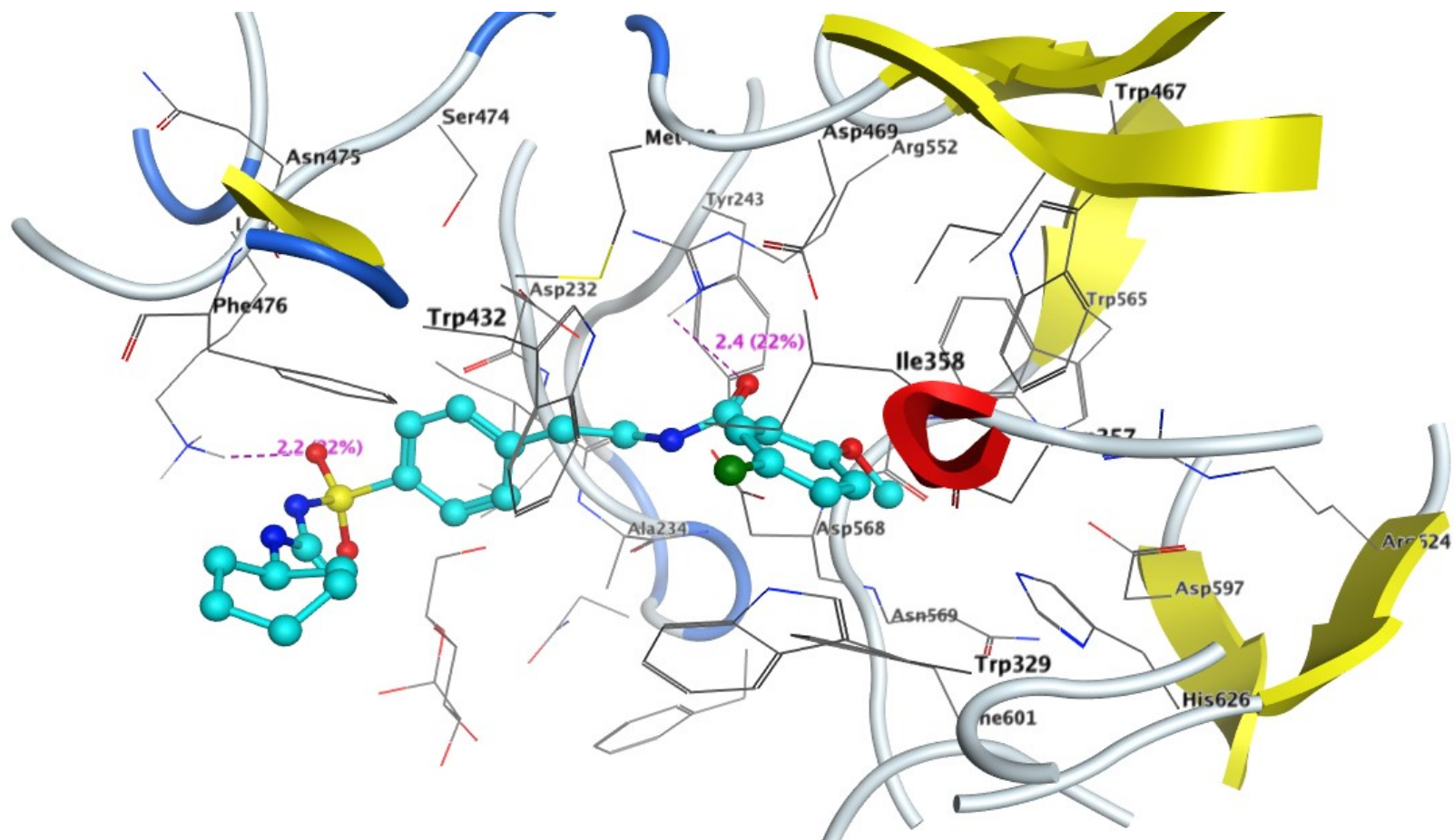


Figure S8: 3D interaction of **Glibenclamide** inside the active site of α -glucosidase (PDB: 3w37)

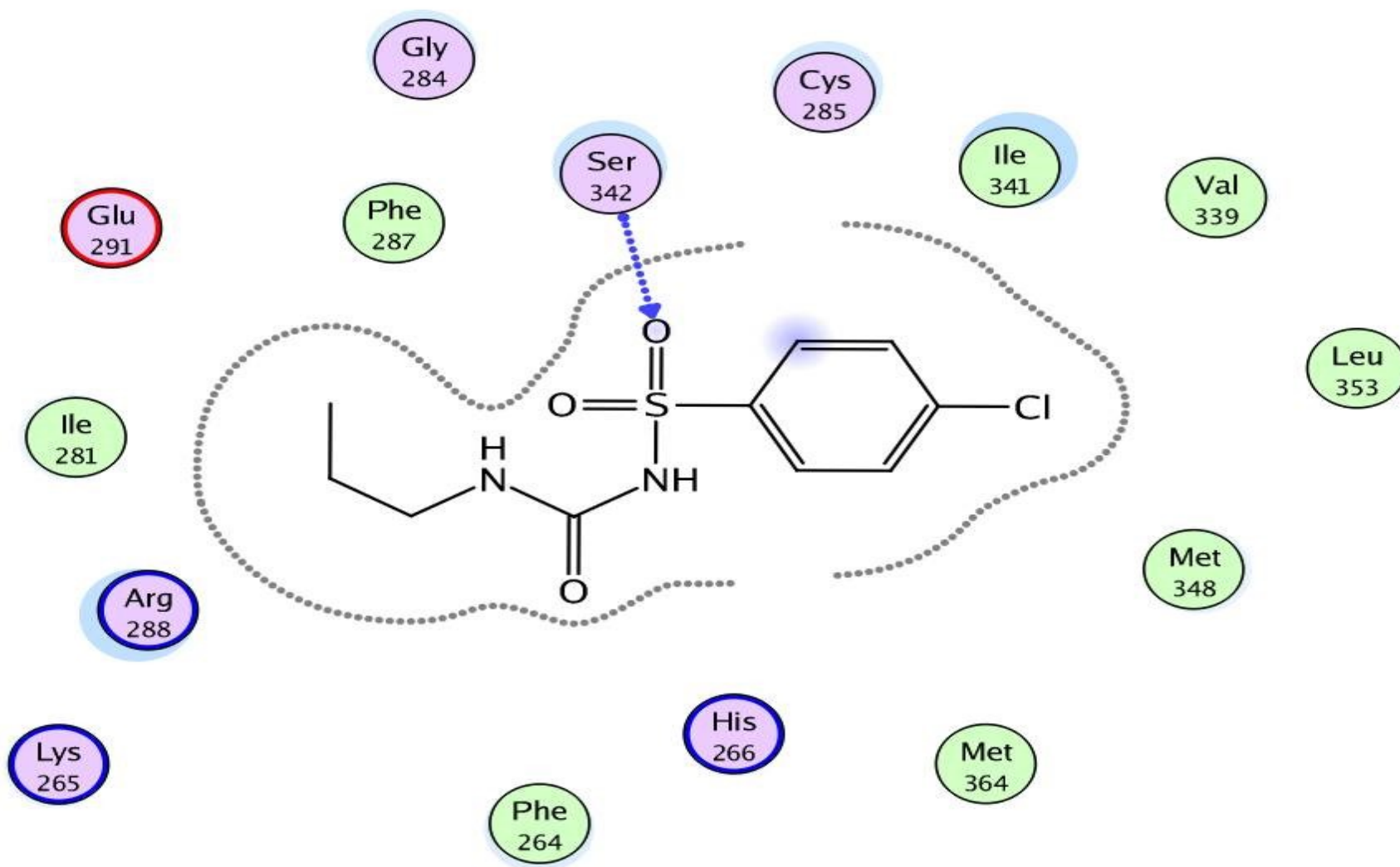


Figure S9: 2D interaction of **Chlorpropamide** inside the active site of PPAR- γ (PDB: 3SZ1)

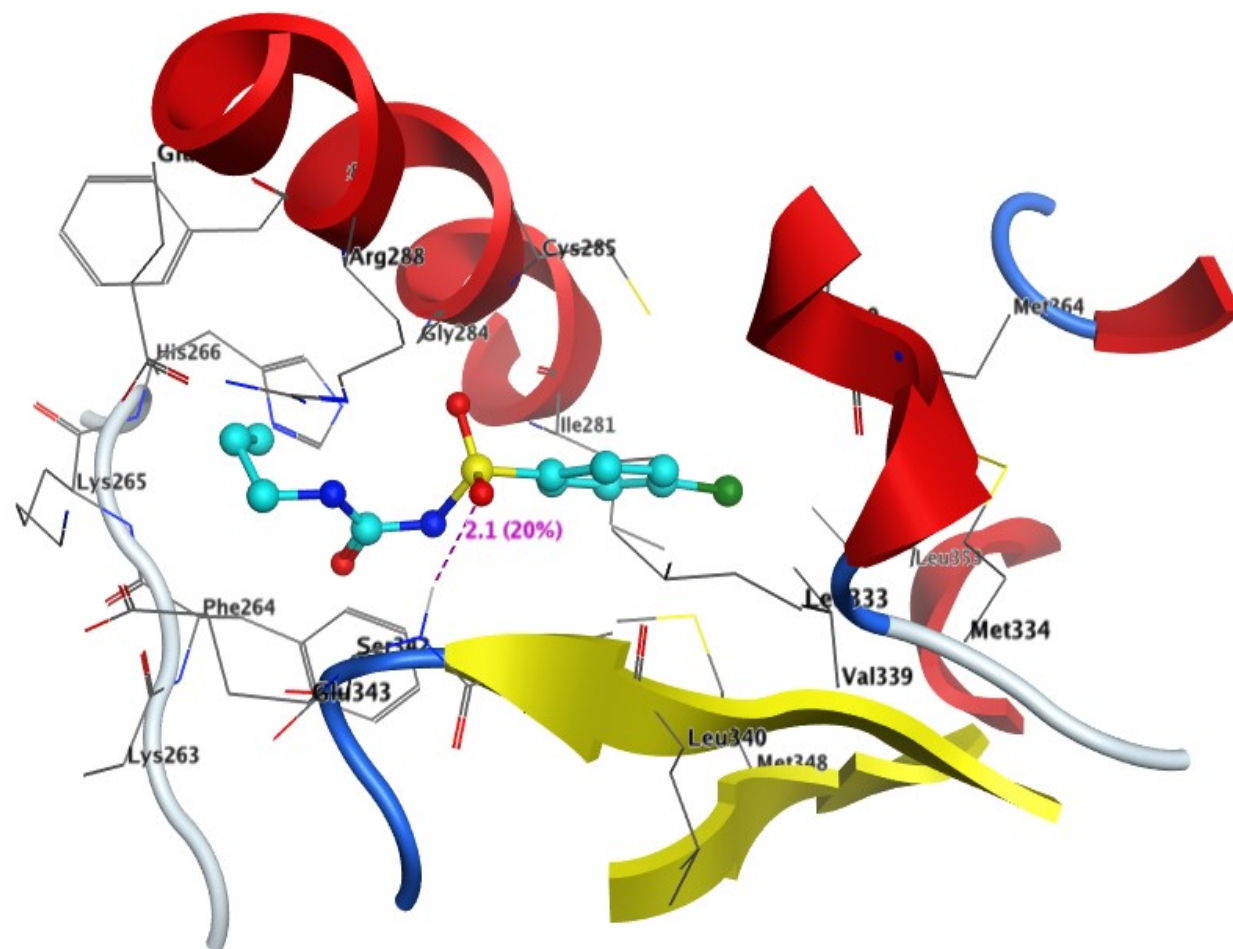


Figure S10: 3D interaction of **Chlorpropamide** inside the active site of PPAR-γ (PDB: 3SZ1)

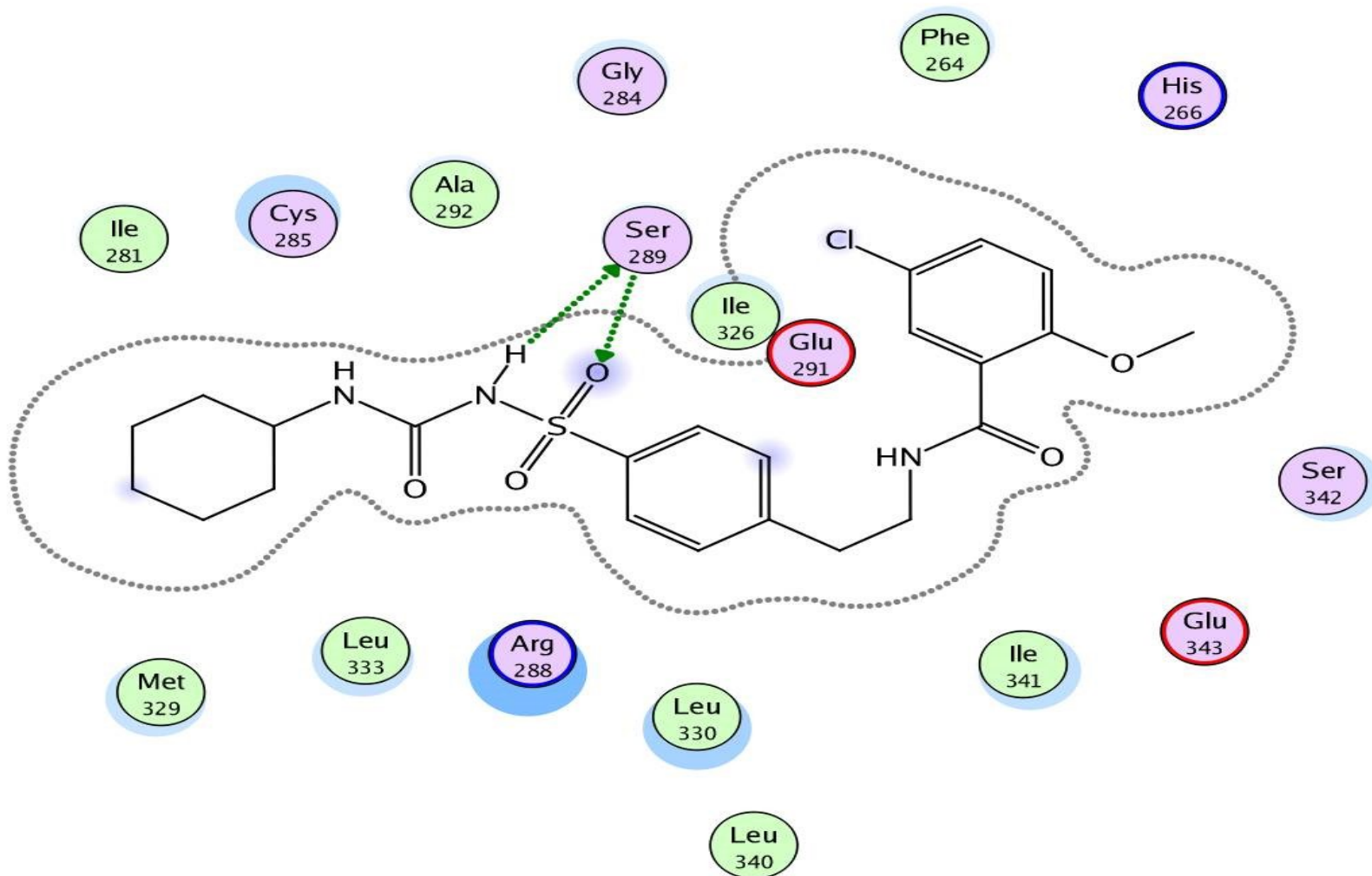


Figure S11: 2D interaction of **Glibenclamide** inside the active site of PPAR-γ (PDB: 3SZ1)

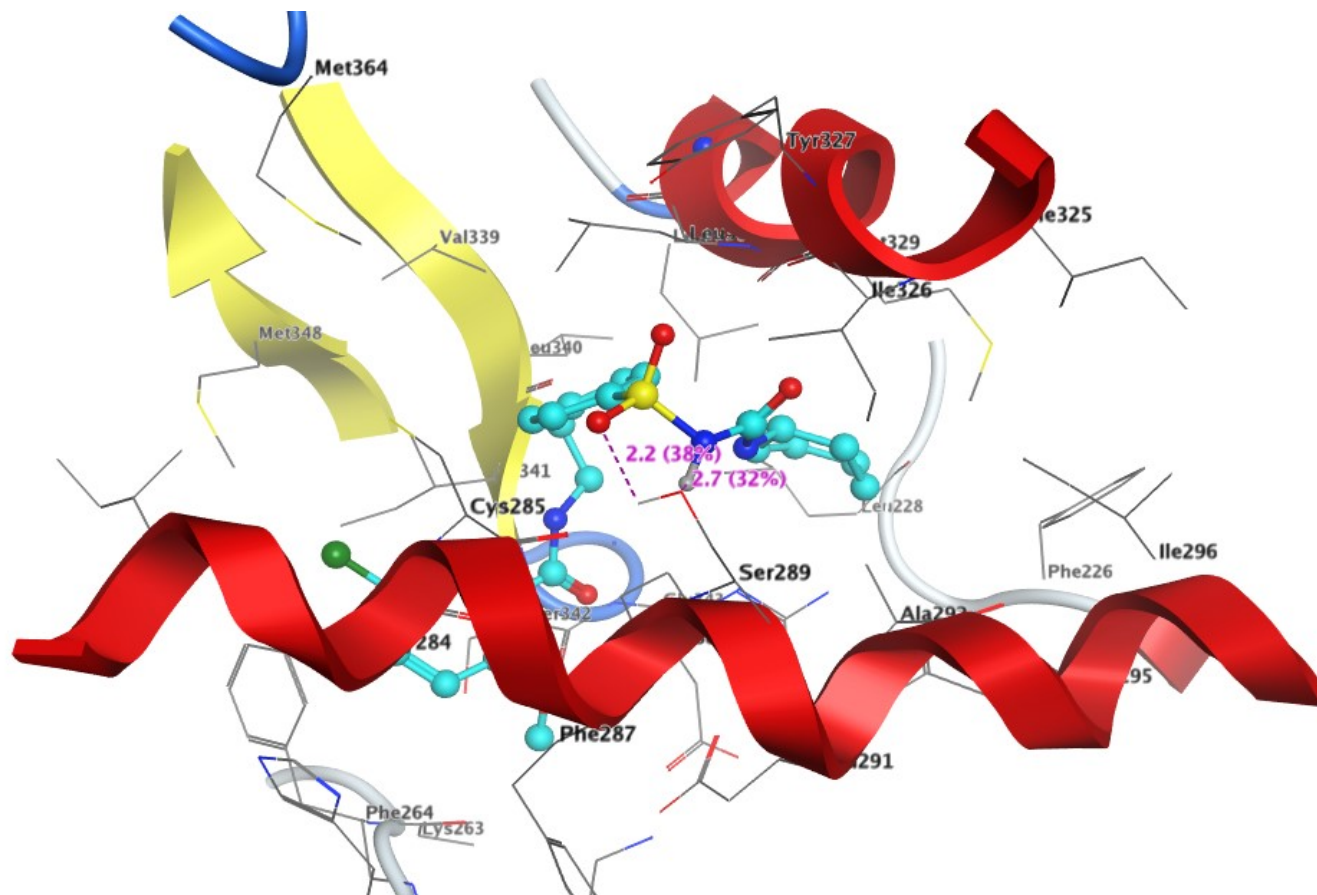


Figure S12: 3D interaction of **Glibenclamide** inside the active site of PPAR-γ (PDB: 3SZ1)