The antimicrobial potentials and pharmacokinetic profiles of novel quinoline-based scaffolds: synthesis and *in silico* mechanistic studies as dual DNA gyrase and DHFR inhibitors

Supplementary Materials

Contents

Summary of docking results

Compound	ΔG, kcal/mol	H-bonding interactions		Hydrophobic interaction	
		Residue	Distance (Å)	Residue	Distance (Å)
1. DNA Gyrase					
15	-10.98	ILE 94	3.51	PRO 79	3.97
				LYS 103	3.98
				ASN 46	3.71
16	-10.96	GLY 101	3.27	PRO 79	3.83
		GLU 50	3.56	LYS 103	3.97
20	-11.21	THR 165	3.10	LYS 103	3.88
		LYS 103	2.84		
		VAL 120	3.40		
21	-10.33	ASP 73	2.94	ILE 78	4.53
				ILE 78	3.99
				PRO 79	3.61
				LYS 103	4.04
22	-10.71	ASP 73	2.90	LYS 103	3.93
RLI	-12.23	3.06	Arg76	-	
		3.15	Arg136		
		3.63 bidirectional	Gly101		
		2.81	Gly101		
2. DHFR					
15	-10.29	SER69	2.99	VAL70	4.15
16	-11.11	SER69	2.80	LEU32	4.02

Compound	ΔG, kcal/mol	H-bonding interactions		Hydrophobic interaction	
		Residue	Distance (Å)	Residue	Distance (Å)
				VAL70	4.57
20	-8.83	-	-	LEU32	4.43
				VAL70	3.90
21	-8.75	TYR162	3.08	GLY157	4.45
22	-8.45	TYR162	2.98	GLY157	3.16
H9G	-11.16	SER69	2.99	VAL70	4.15

Docking Against 4DUH (DNA Gyrase)

Docking details for the Co-crystallized ligand RLI in the active site of DNA Gyrase

Score -12.2316351

Ligand Interactions Report

4DUH: ISOMERASE/ISOMERASE INHIBITOR / 4DUH: ISOMERASE/ISOMERASE INHIBITOR

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
S11 11 O	GLY 101 (A)	H-donor	3.63	-1.0
N13 18 O	GLY 101 (A)	H-donor	2.81	-4.2
O12 14 NH1	ARG 136 (A)	H-acceptor	3.15	-1.7
O12 14 NH2	ARG 136 (A)	H-acceptor	3.06	-5.2
O12 14 NH2	ARG 76 (A)	ionic	3.64	-1.4
O12 14 NH1	ARG 136 (A)	ionic	3.15	-3.5
O12 14 NH2	ARG 136 (A)	ionic	3.06	-4.1

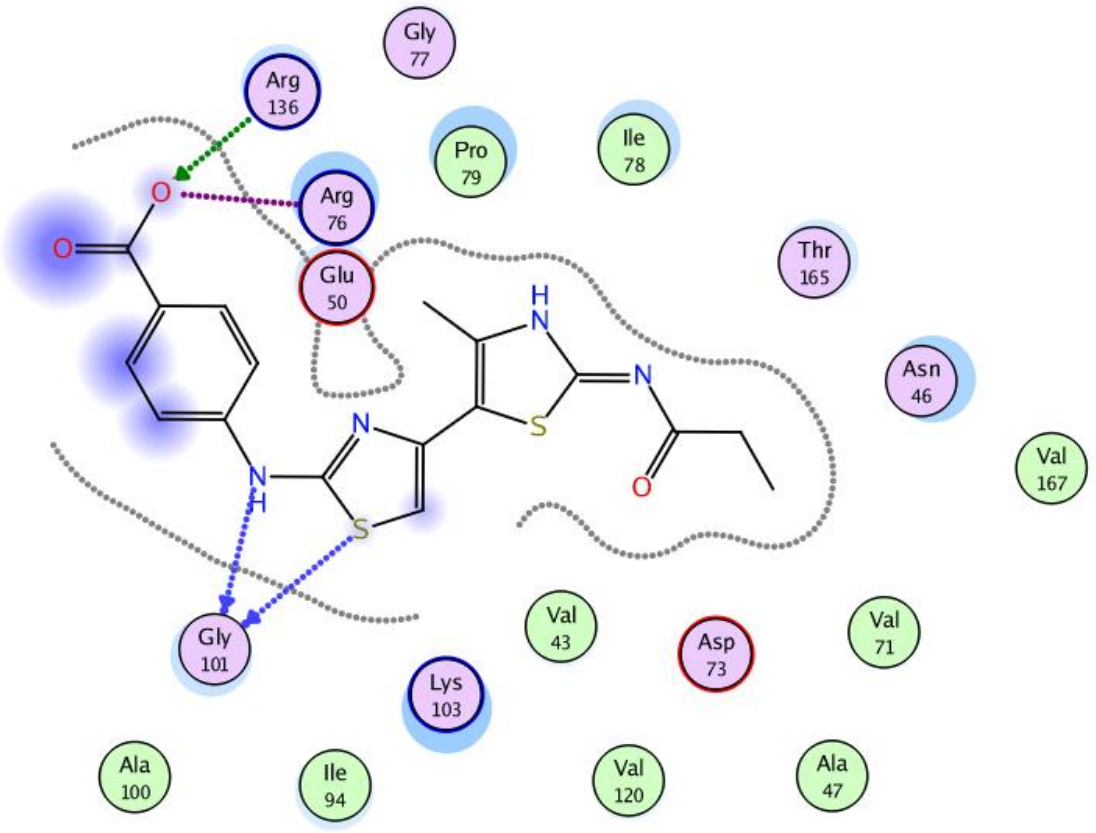


Figure 1: 2D interactions of the co-crystallized ligand, RLI in the active site of DNA Gyrase

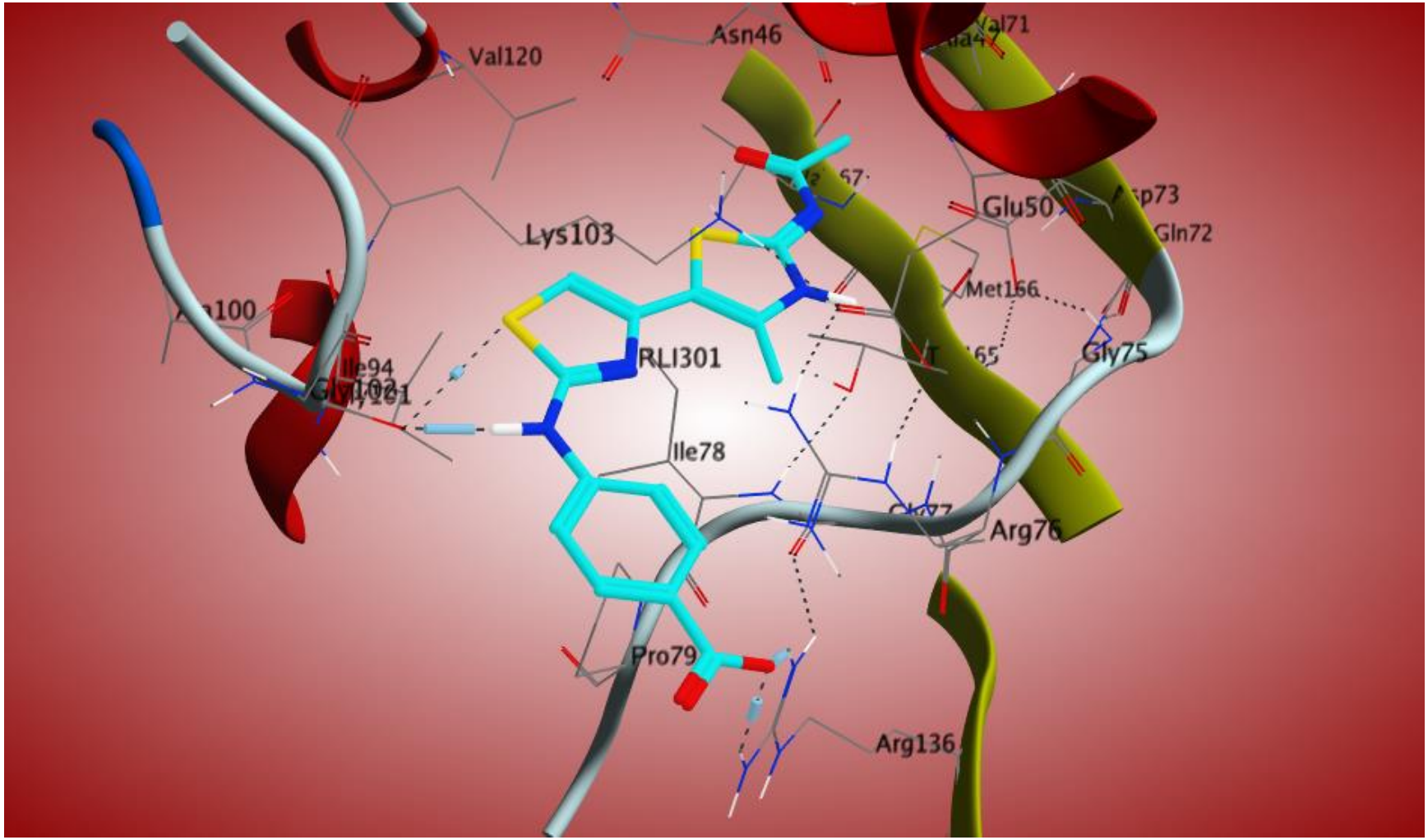


Figure 2: 3D interactions of the co-crystallized ligand, RLI in the active site of DNA Gyrase

Docking details for compound 15 in the active site of DNA Gyrase

Score -10.98

Ligand Interactions Report 1

4DUH: ISOMERASE/ISOMERASE INHIBITOR / 4DUH

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
6-ring	CD PRO 79 (A)	pi-H	3.97	-0.7
6-ring	CE LYS 103 (A)	pi-H	3.98	-0.7

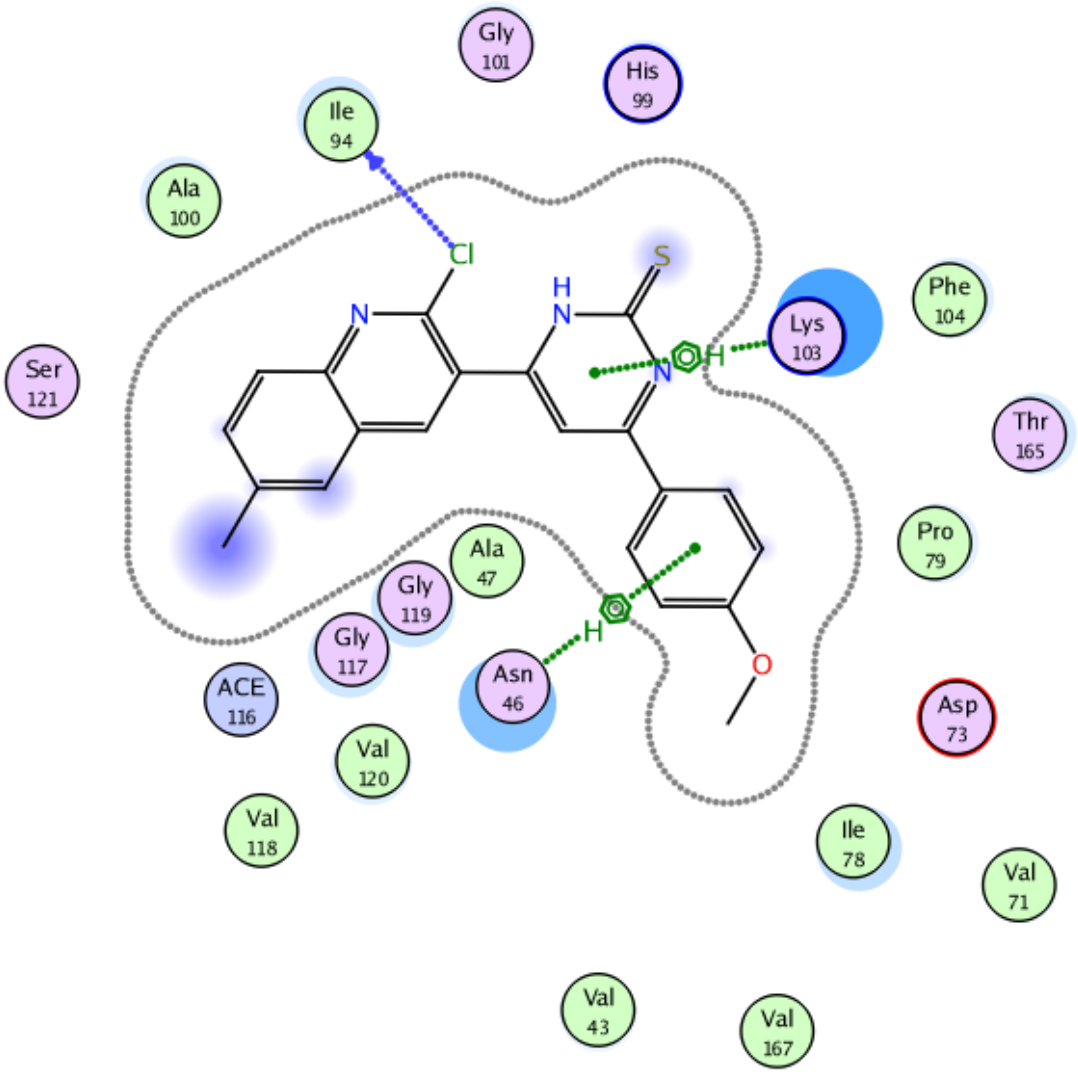


Figure 3: 2D interactions of the quinoline derivative 15 in the active site of DNA Gyrase

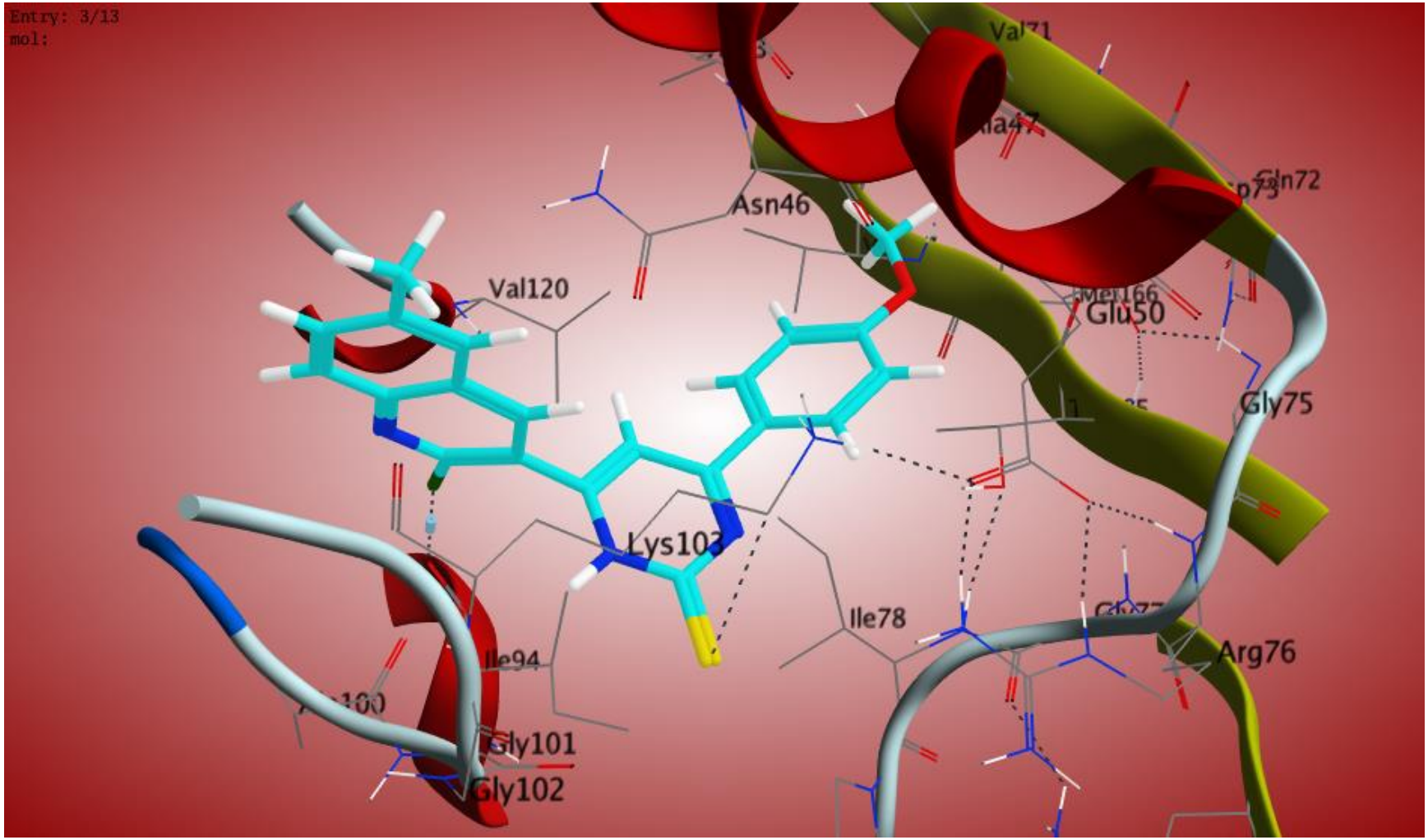


Figure 4: 2D interactions of the quinoline derivative 15 in the active site of DNA Gyrase

Docking details for compound 16 in the active site of DNA Gyrase

Ligand Interactions Report 2

4DUH: ISOMERASE/ISOMERASE INHIBITOR / 4DUH

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
C 10	O GLY 101 (A)	H-donor	3.27	-0.7

quinoline ring serves as a backbone HB acceptor

CL	12	OE2	GLU 50	(A)	H-donor	3.56	-0.3

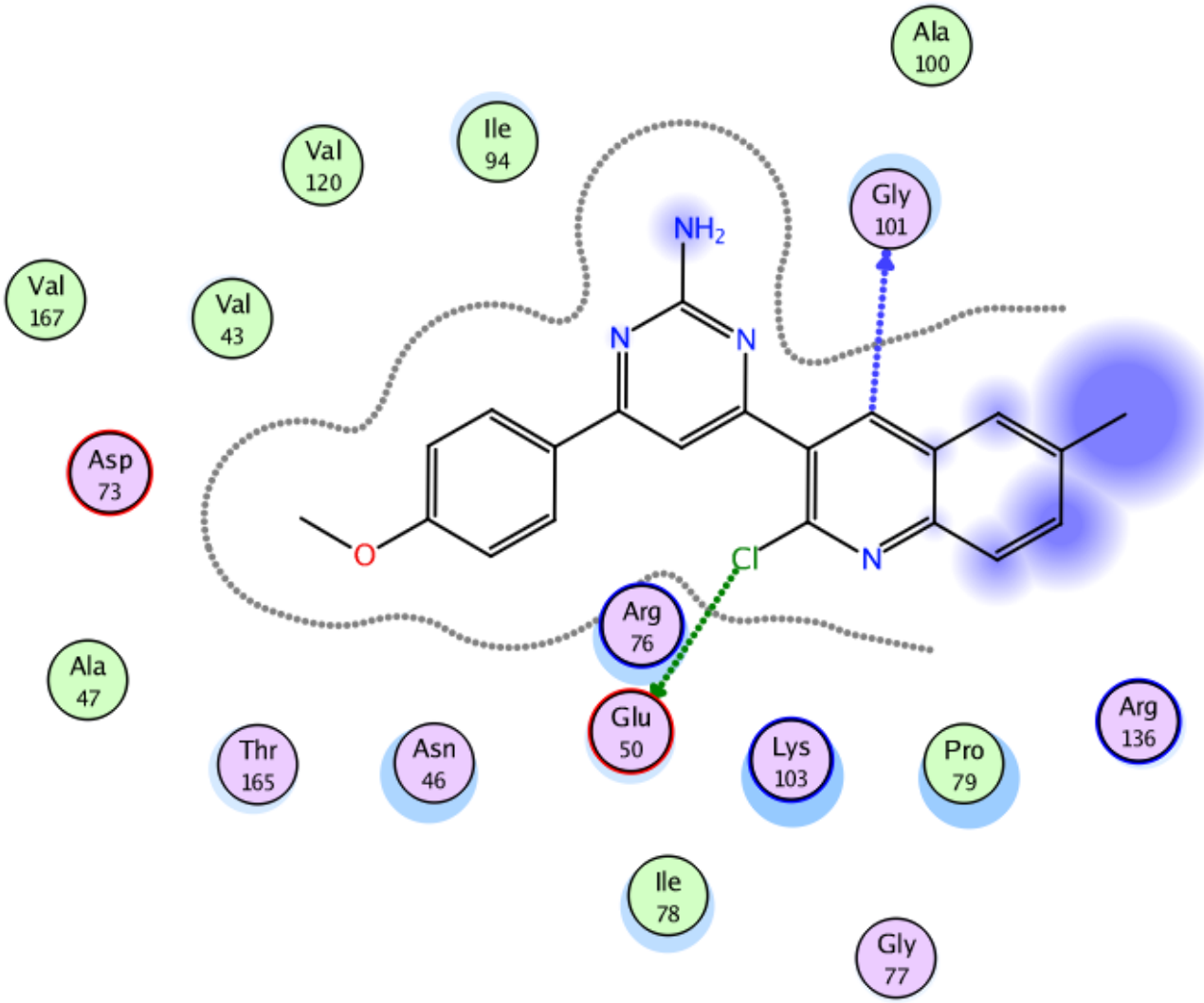


Figure 5: 2D interactions of the quinoline derivative 16 in the active site of DNA Gyrase

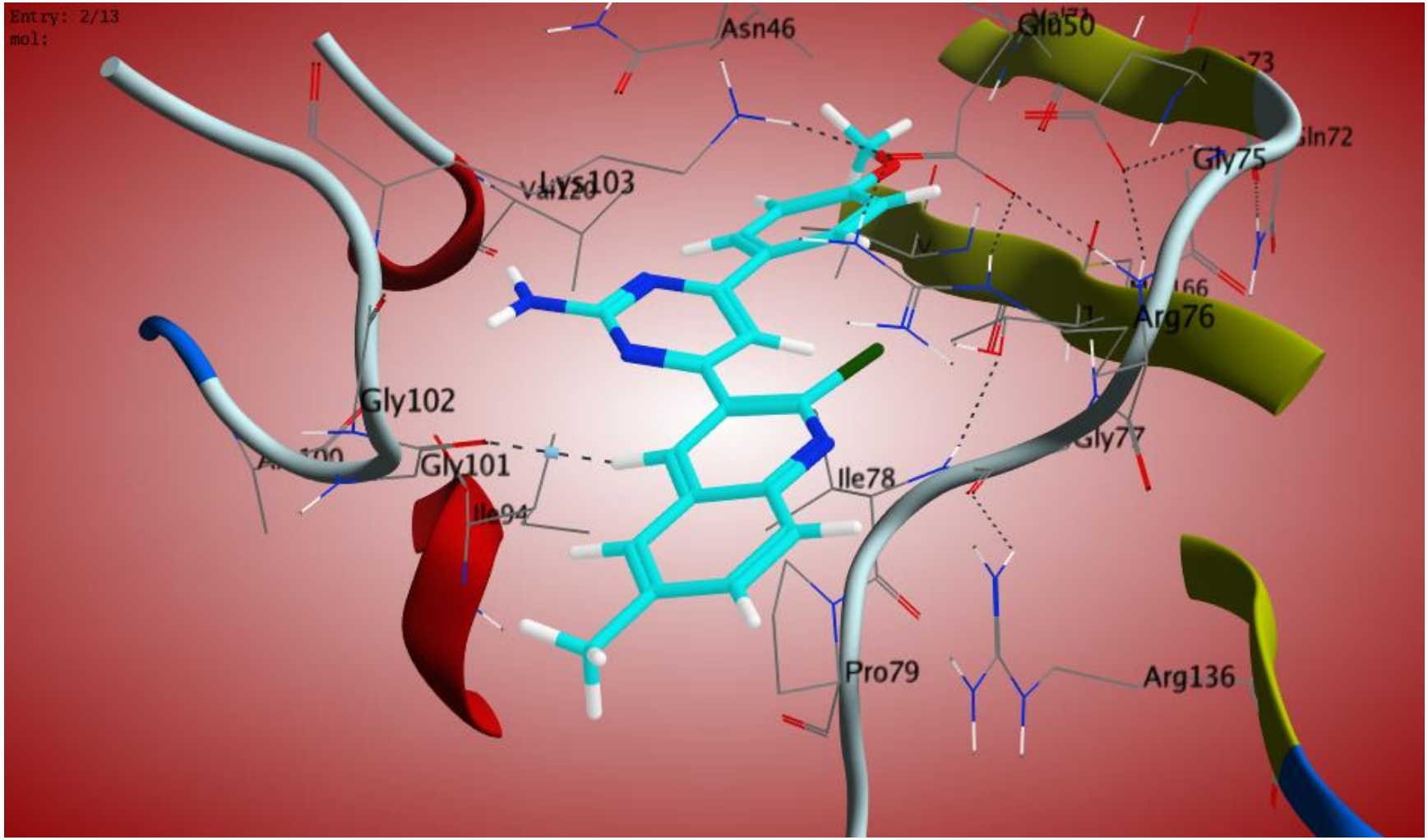


Figure 6: 3D interactions of the quinoline derivative 16

Docking details for compound 20 in the active site of DNA Gyrase

Score -11.2167978

Ligand Interactions Report 1

4DUH: ISOMERASE/ISOMERASE INHIBITOR / 4DUH

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
O 20	CB THR 165 (A)	H-acceptor	3.10	-0.8
6-ring	CE LYS 103 (A)	pi-H	3.88	-0.8

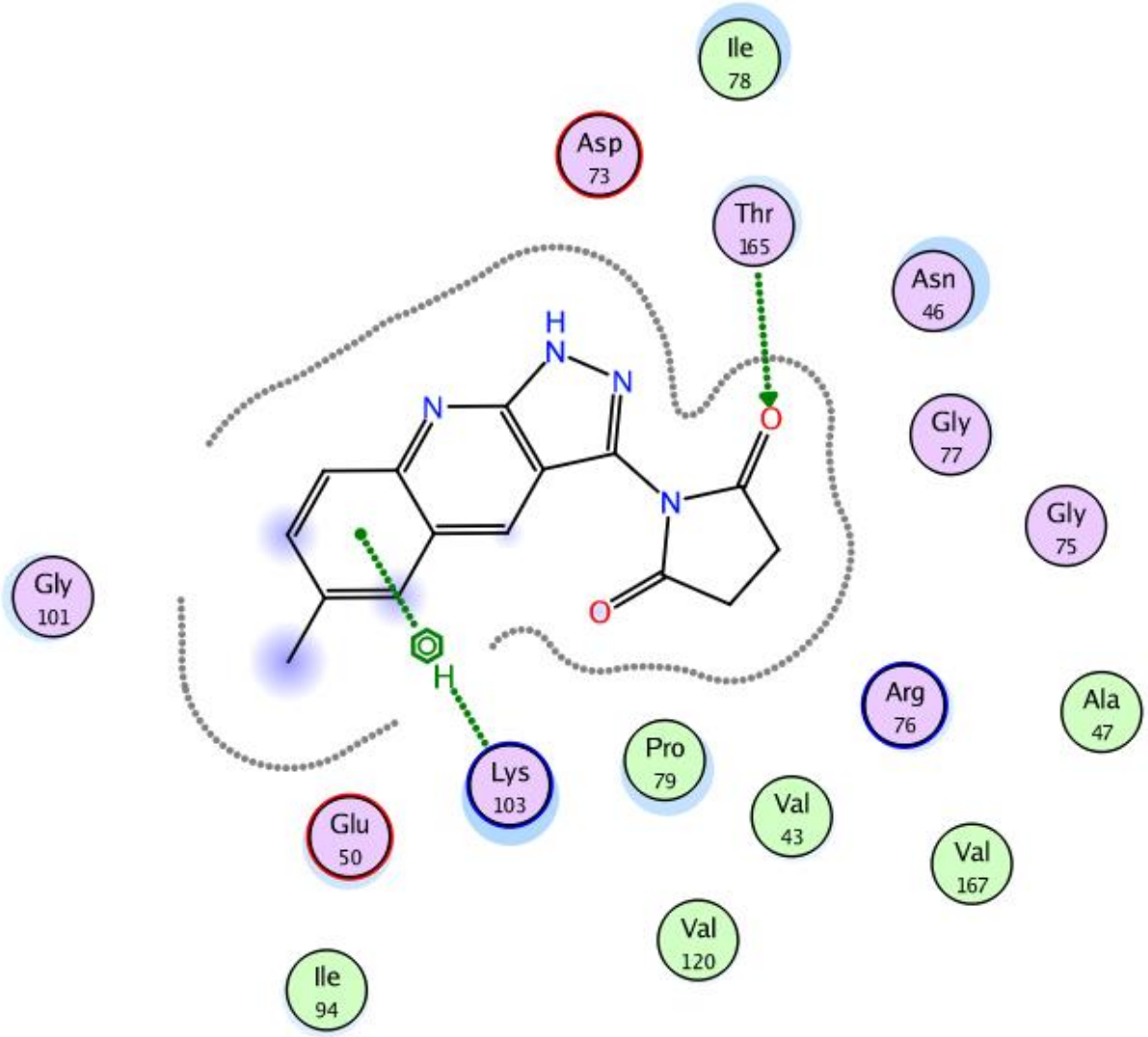


Figure 7: 2D interactions of the quinoline derivative 20 in the active site of DNA Gyrase

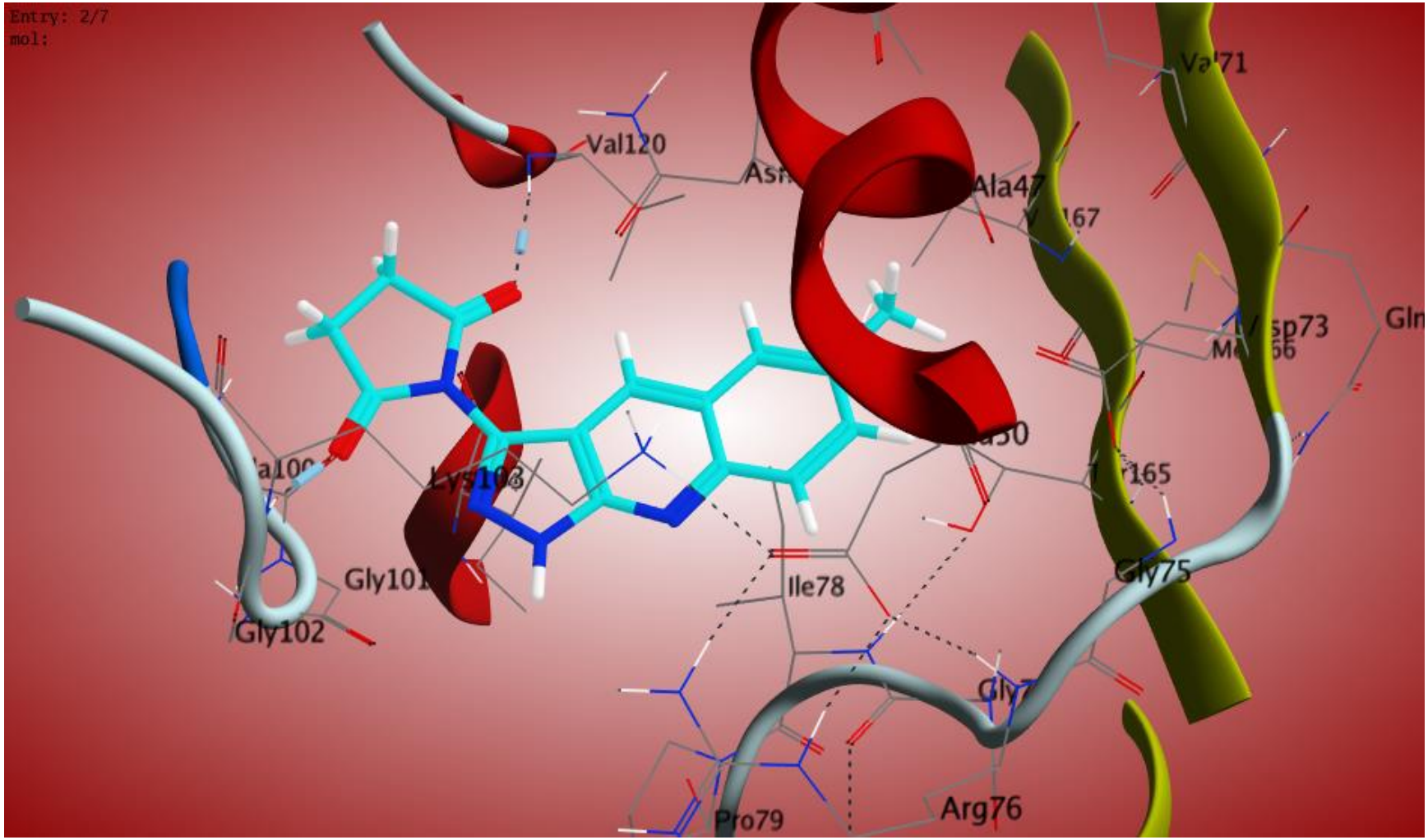


Figure 8: 3D interactions of the quinoline derivative 20

Docking details for compound 21 in the active site of DNA Gyrase

Score -10.3347683

Ligand Interactions Report 1

4DUH: ISOMERASE/ISOMERASE INHIBITOR / 4DUH

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
6-ring	CA ILE 78 (A)	pi-H	4.53	-0.6
6-ring	CA ILE 78 (A)	pi-H	3.99	-0.6
6-ring	CD PRO 79 (A)	pi-H	3.61	-0.7
6-ring	CE LYS 103 (A)	pi-H	4.04	-0.7

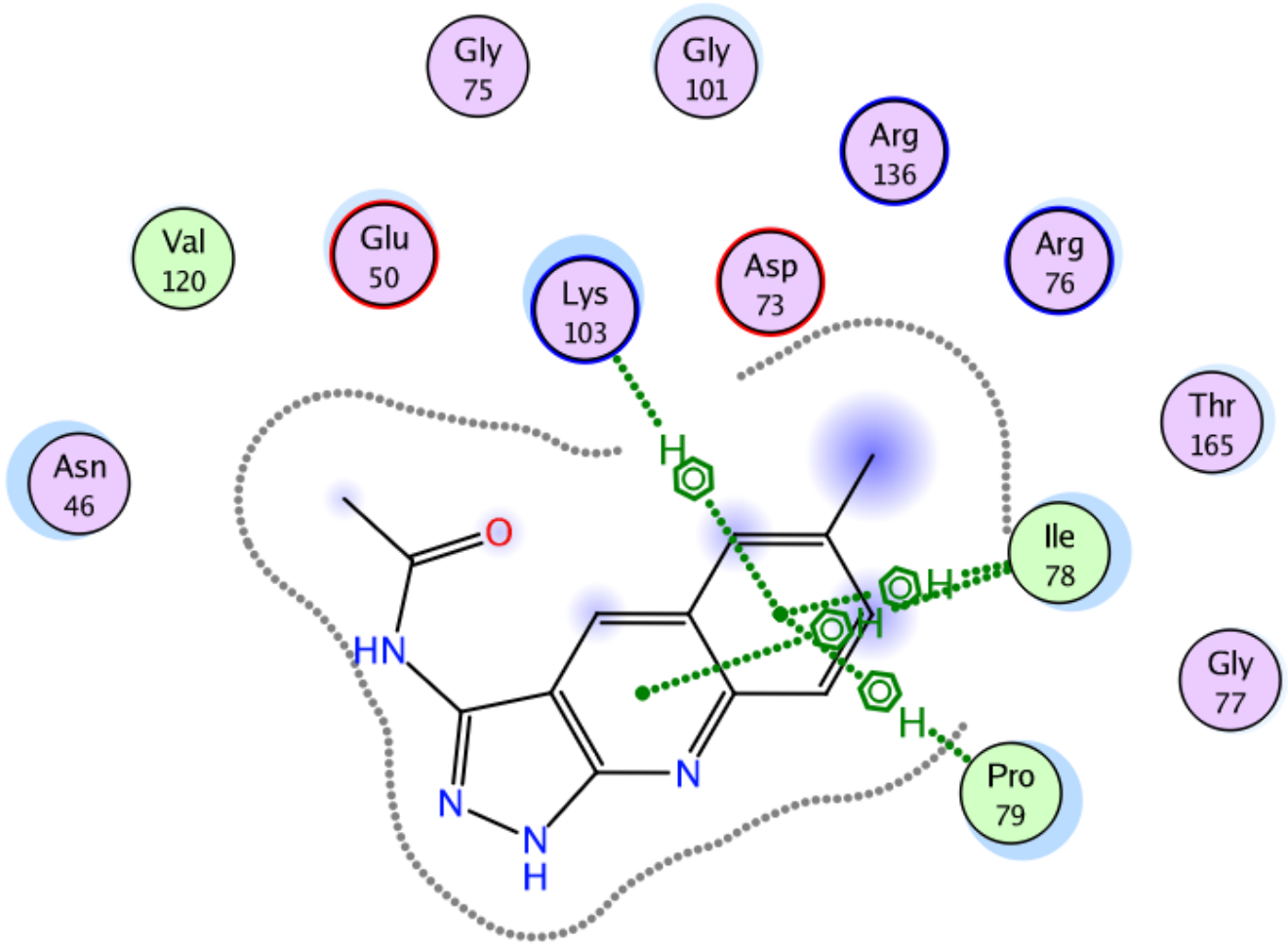


Figure 9: 2D interactions of the quinoline derivative 21 in the active site of DNA Gyrase

Ligand Interactions Report

4DUH: ISOMERASE/ISOMERASE INHIBITOR / 4DUH

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
N 15	OD1 ASP 73 (A)	H-donor	2.94	-7.2

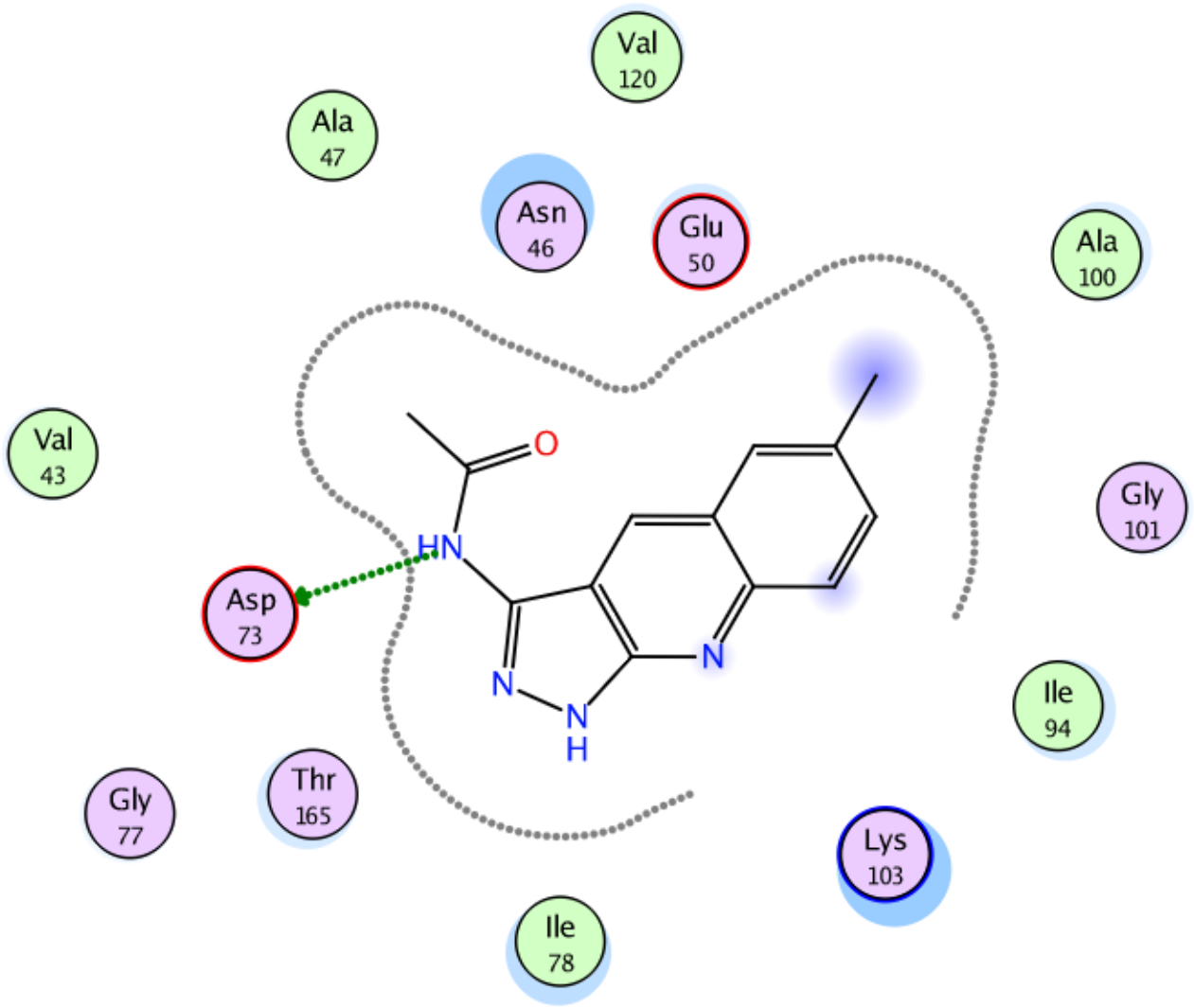


Figure 10: 2D interactions of the quinoline derivative 21, pose 2

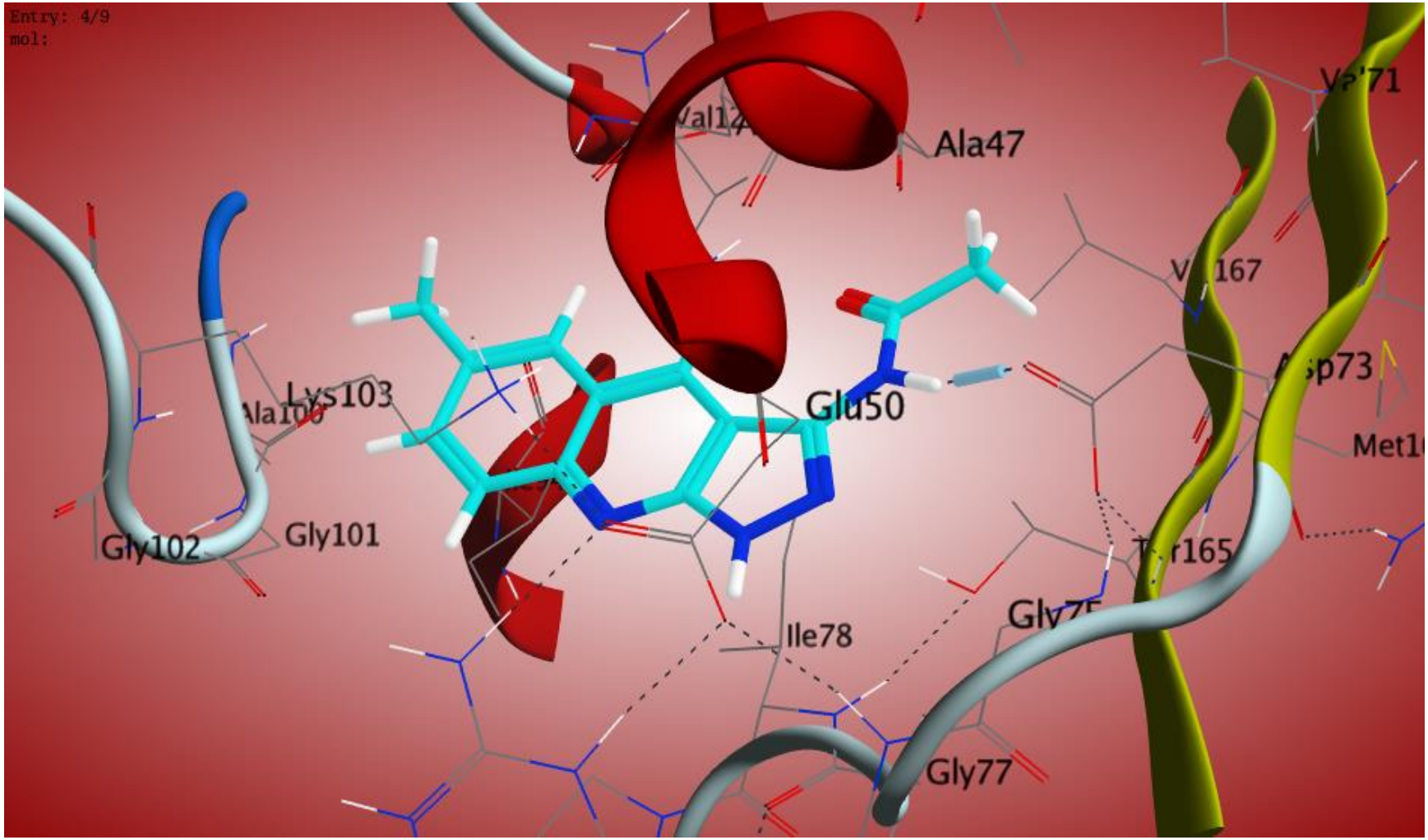


Figure 11: 3D interactions of the quinoline derivative 21

Docking details for compound 22 in the active site of DNA Gyrase

Score -10.7126884

Ligand Interactions Report 1

4DUH: ISOMERASE/ISOMERASE INHIBITOR / 4DUH

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
N 15	OD1 ASP 73 (A)	H-donor	3.01	-4.4
6-ring	CE LYS 103 (A)	pi-H	3.93	-0.7

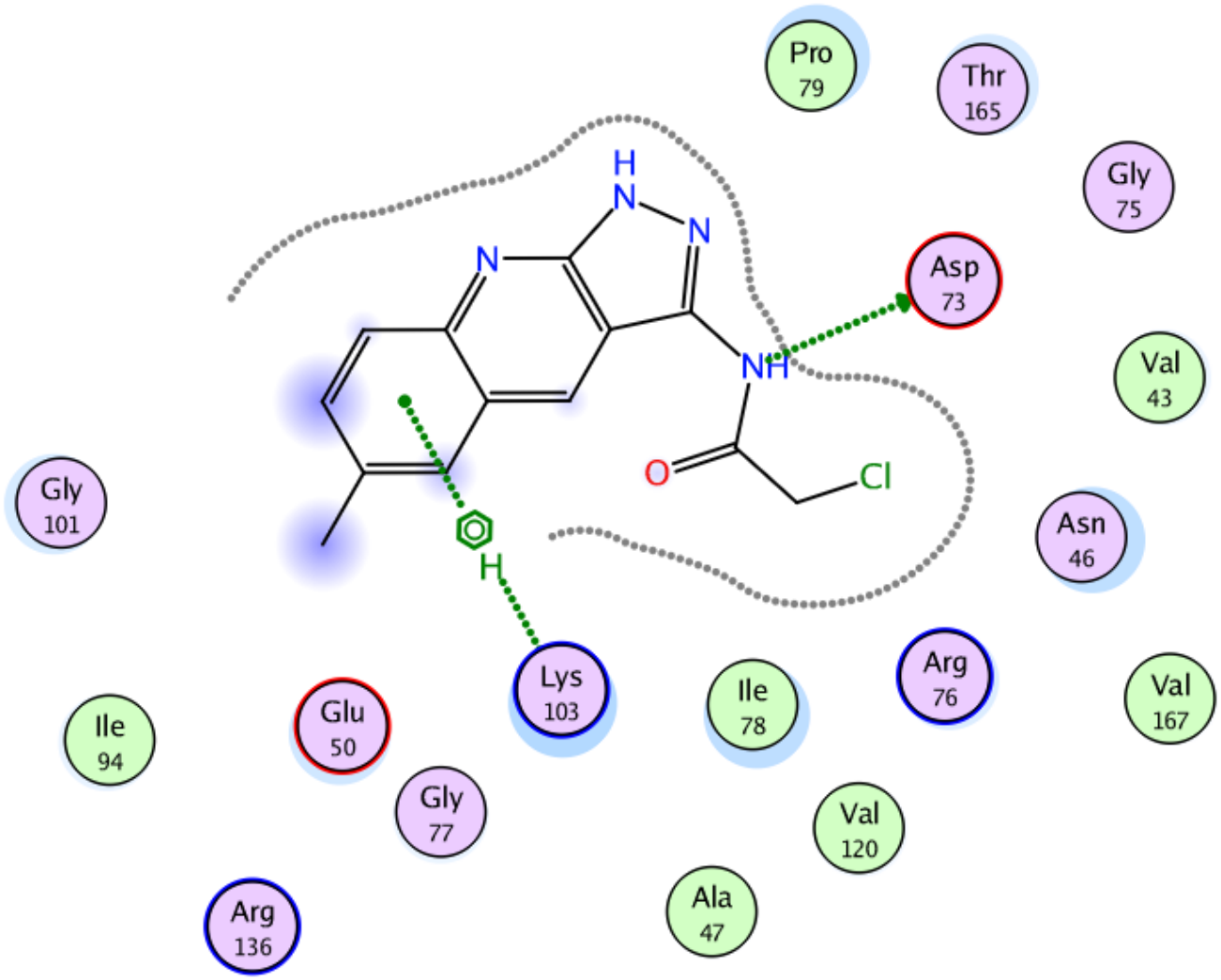


Figure 12: 2D interactions of the quinoline derivative 22, pose 1, in the active site of DNA Gyrase

Ligand Interactions Report 2

4DUH: ISOMERASE/ISOMERASE INHIBITOR / 4DUH

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
N 15	OD1 ASP 73 (A)	H-donor	2.90	-7.9

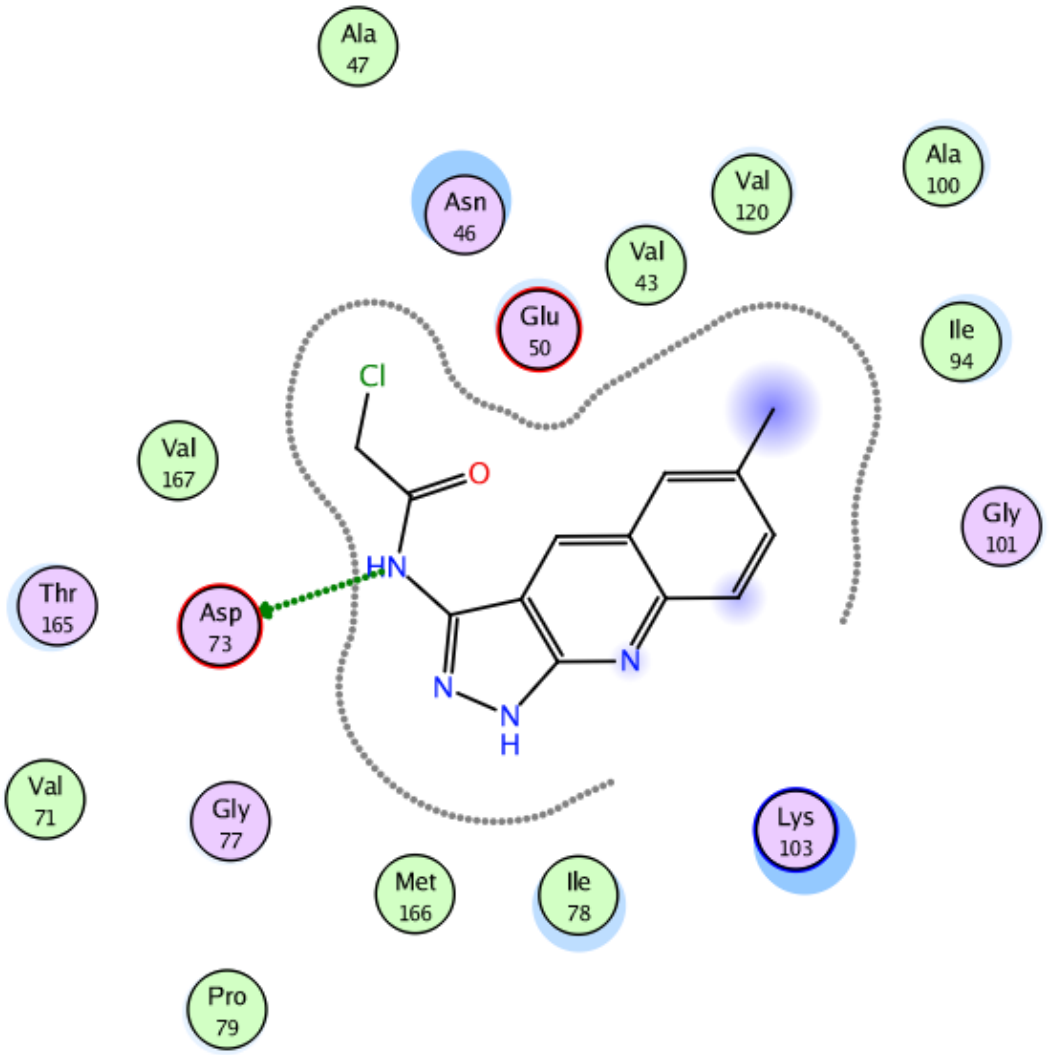


Figure 13: 2D interactions of the quinoline derivative 22, pose 2, in the active site of DNA Gyrase

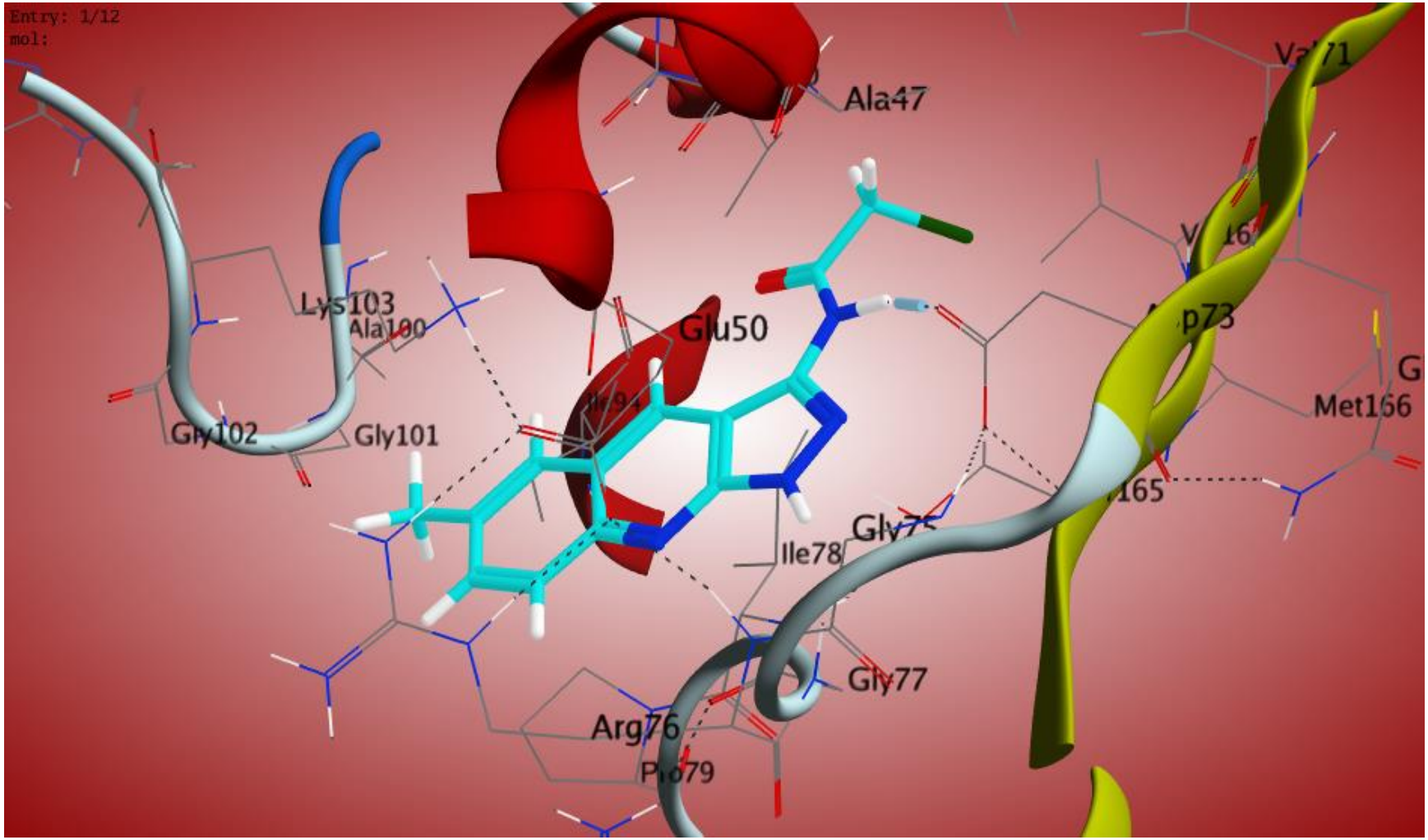


Figure 14: 3D interactions of the quinoline derivative 22 in the active site of DNA Gyrase

Docking Against 6DTH (DHFR)

Docking details for H9G in the active site of DHFR

Score -11.1688385

Ligand Interactions Report

6DTC: ANTIFUNGAL PROTEIN/INHIBITOR / 6DTC: ANTIFUNGAL PROTEIN/INHIBITOR

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
N12 16	O ILE 10 (A)	H-donor	2.97	-1.6
N13 19	OD1 ASP 40 (A)	H-donor	2.46	4.5
N22 31	NH1 ARG 80 (A)	H-acceptor	2.68	-8.6
N21 30	NH1 ARG 80 (A)	ionic	3.64	-1.4
N22 31	NH1 ARG 80 (A)	ionic	2.68	-7.0
N22 31	NH2 ARG 80 (A)	ionic	3.17	-3.5
N23 32	NH1 ARG 80 (A)	ionic	3.73	-1.1
N23 32	NH2 ARG 80 (A)	ionic	3.60	-1.5
5-ring	CD2 LEU 77 (A)	pi-H	3.73	-0.6

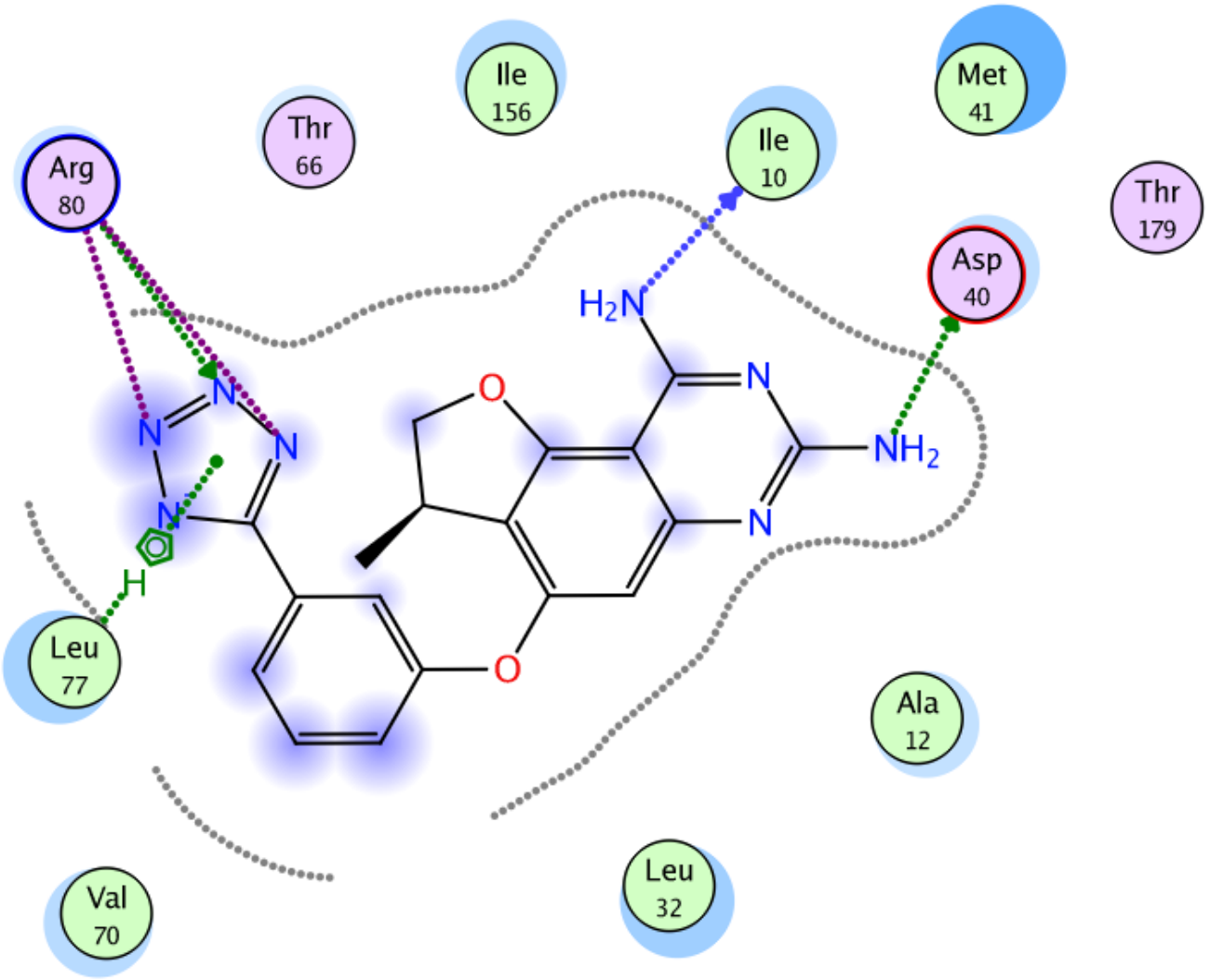


Figure 15: 2D interactions of quinoline derivative 15 in the active site of DHFR

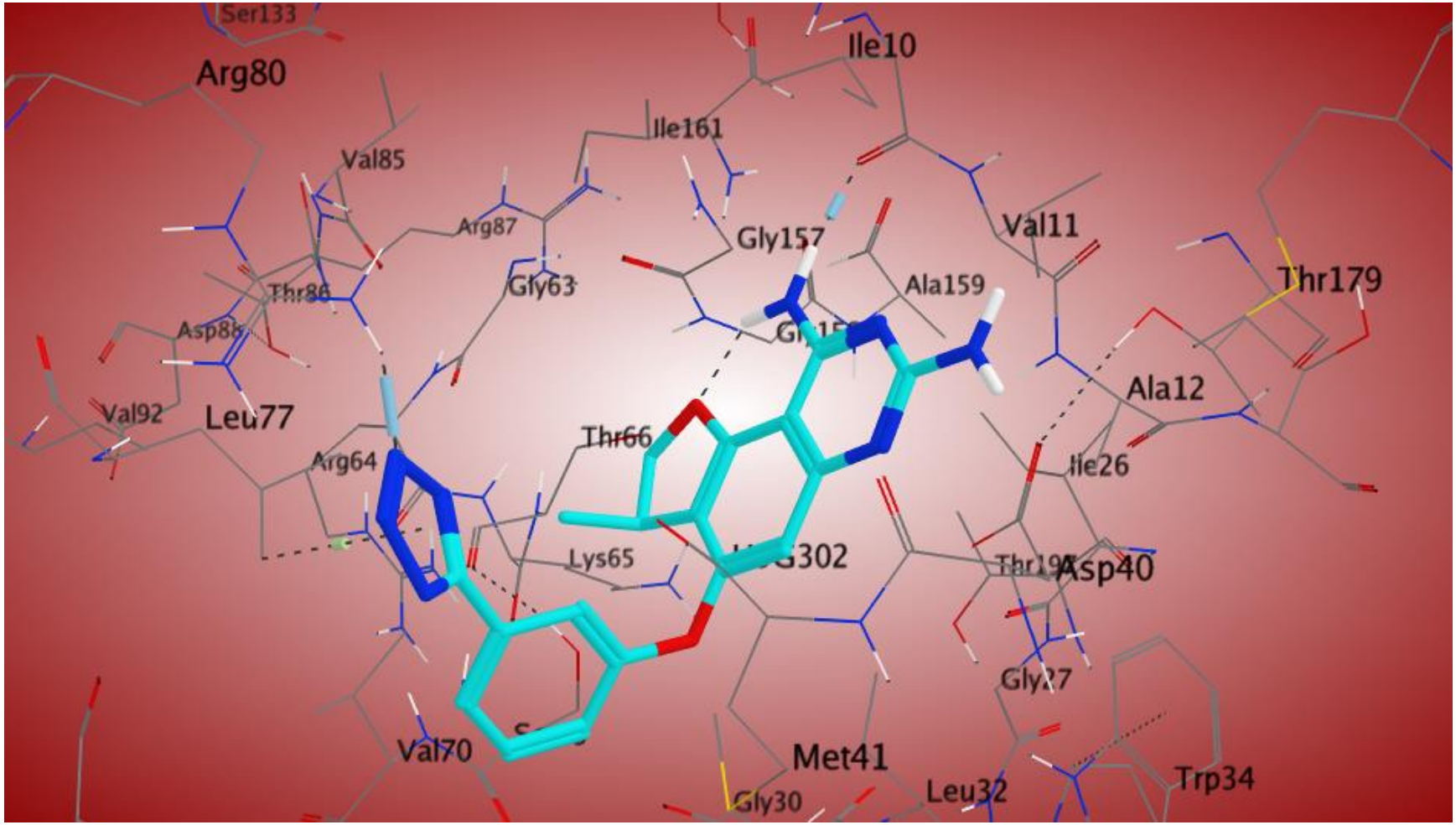


Figure 16: 3D interactions of quinoline derivative 15 in the active site of DHFR

Docking details for H9G redocked in the active site of DHFR

Score -11.16

Ligand Interactions Report

6DTC: ANTIFUNGAL PROTEIN/INHIBITOR / 6DTC

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
N 24	OD1 ASP 40 (A)	H-donor	2.99	-4.5
N 27	O ILE 10 (A)	H-donor	3.02	-2.2
N 27	O ILE 156 (A)	H-donor	2.89	-2.3
6-ring	6-ring PHE 44 (A)	pi-pi	4.00	-0.0

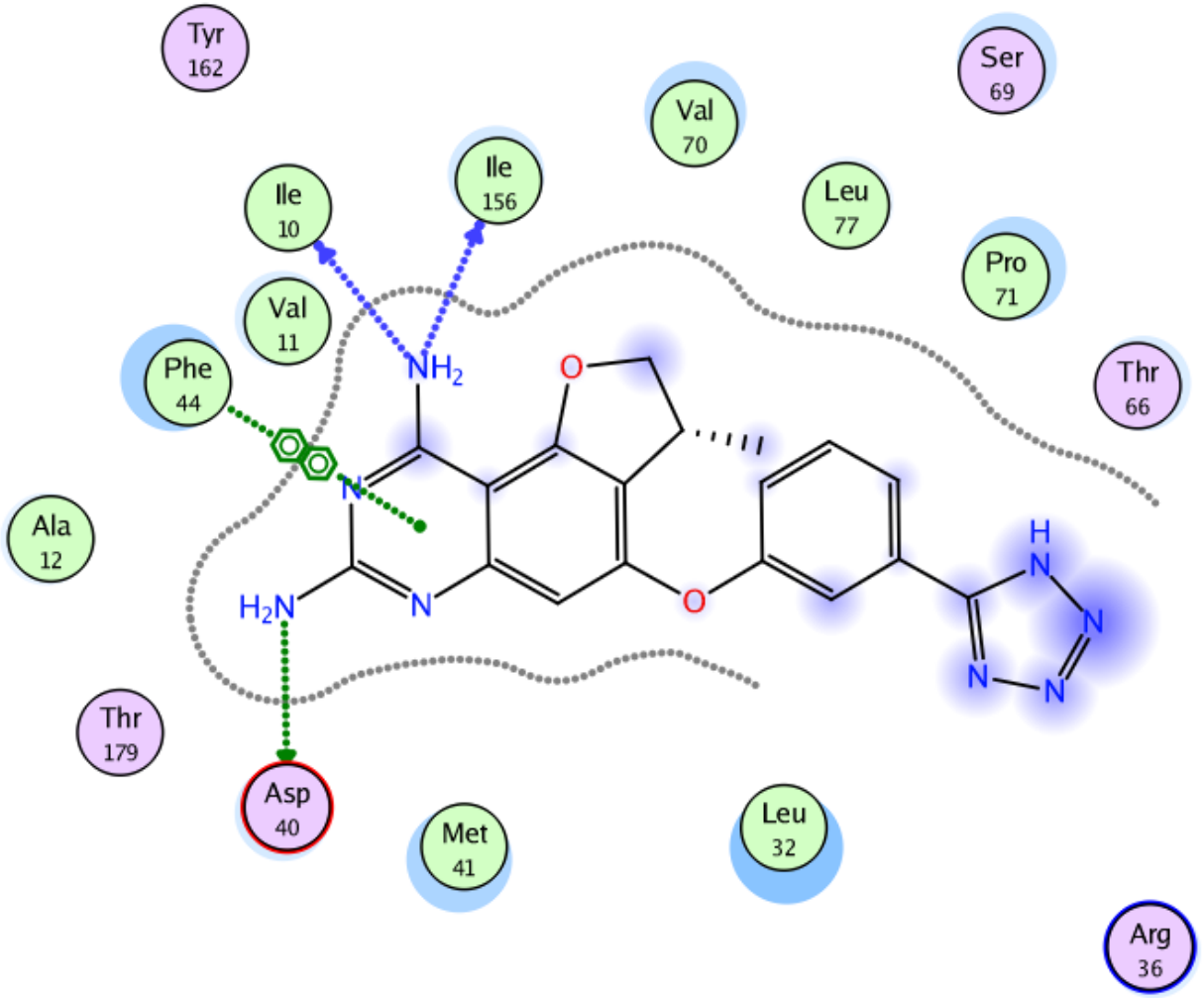


Figure 17: 2D interactions of H9G in the active site of DHFR

Docking details for compound 15 in the active site of DHFR

Score -10.2931118

Ligand Interactions Report

6DTC: ANTIFUNGAL PROTEIN/INHIBITOR / 6DTC

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
N 24	OG SER 69 (A)	H-donor	2.99	-1.3
6-ring	CG2 VAL 70 (A)	pi-H	4.15	-0.7

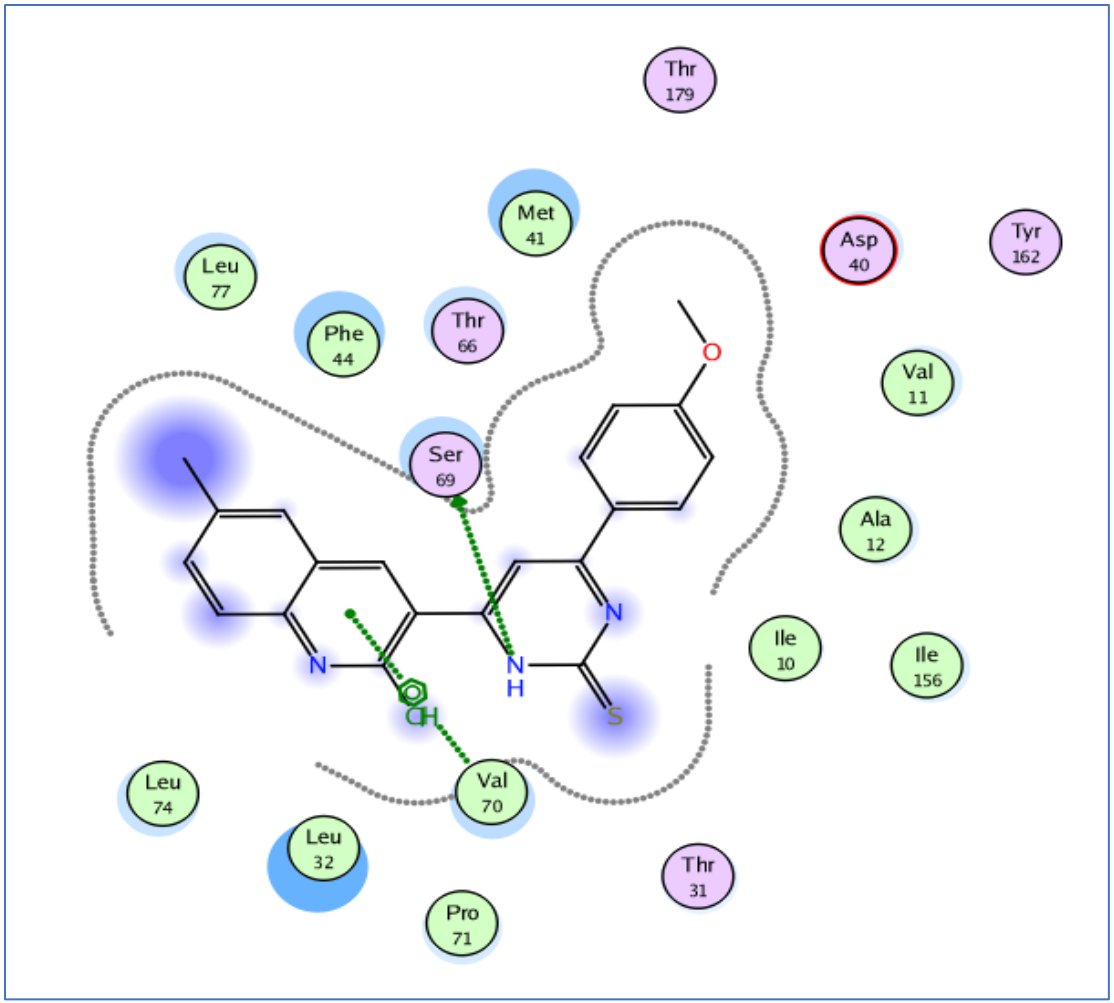


Figure 18: 2D interactions of quinoline derivative 15 in the active site of DHFR

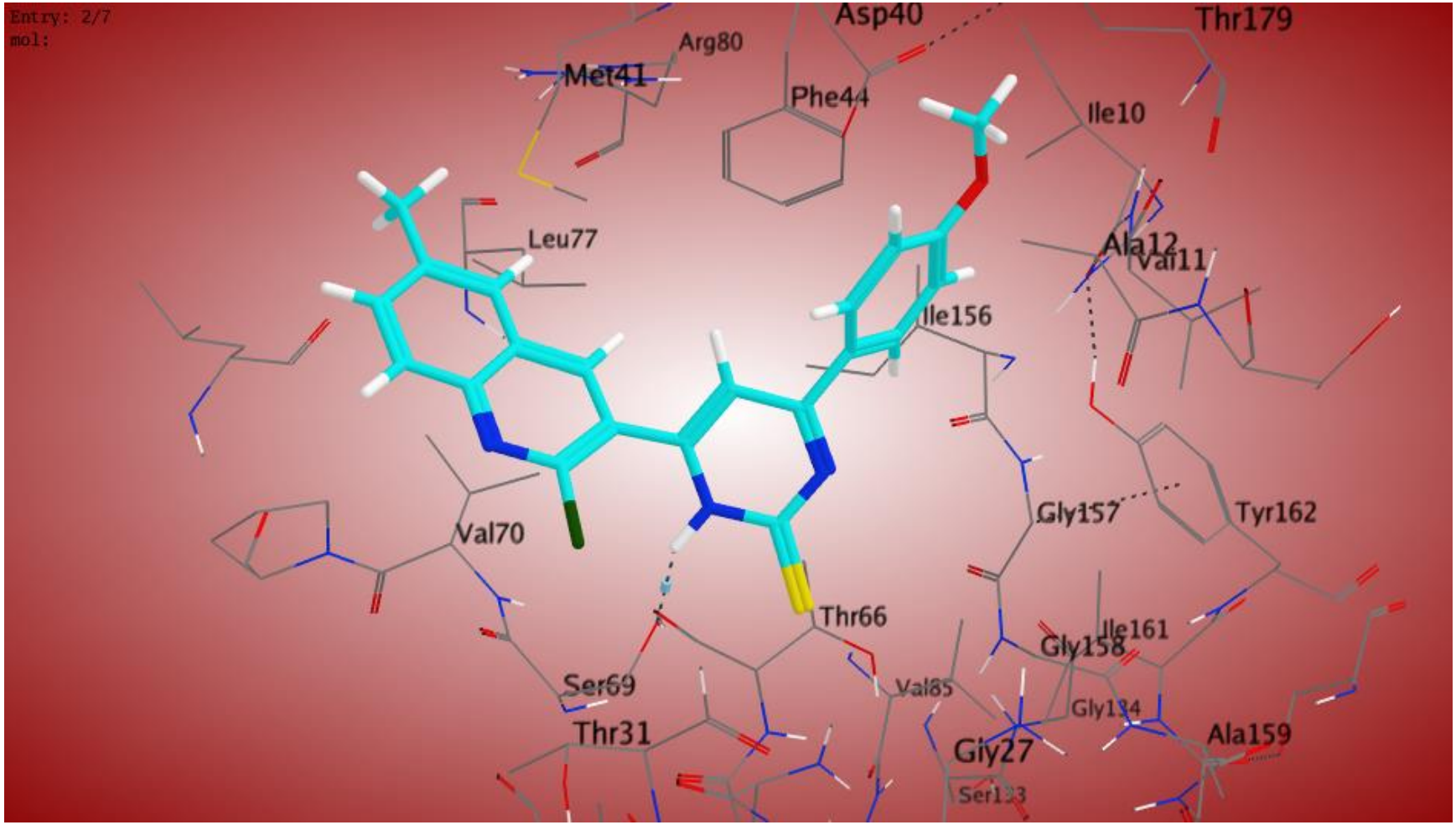


Figure 19: 3D interactions of quinoline derivative 15 in the active site of DHFR

Docking details for compound 16 in the active site of DHFR

Score -11.1149416

Ligand Interactions Report

6DTC: ANTIFUNGAL PROTEIN/INHIBITOR / 6DTC

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
N 26	OG SER 69 (A)	H-donor	2.80	-1.5
6-ring	CD2 LEU 32 (A)	pi-H	4.02	-0.6
6-ring	CG2 VAL 70 (A)	pi-H	4.57	-0.7

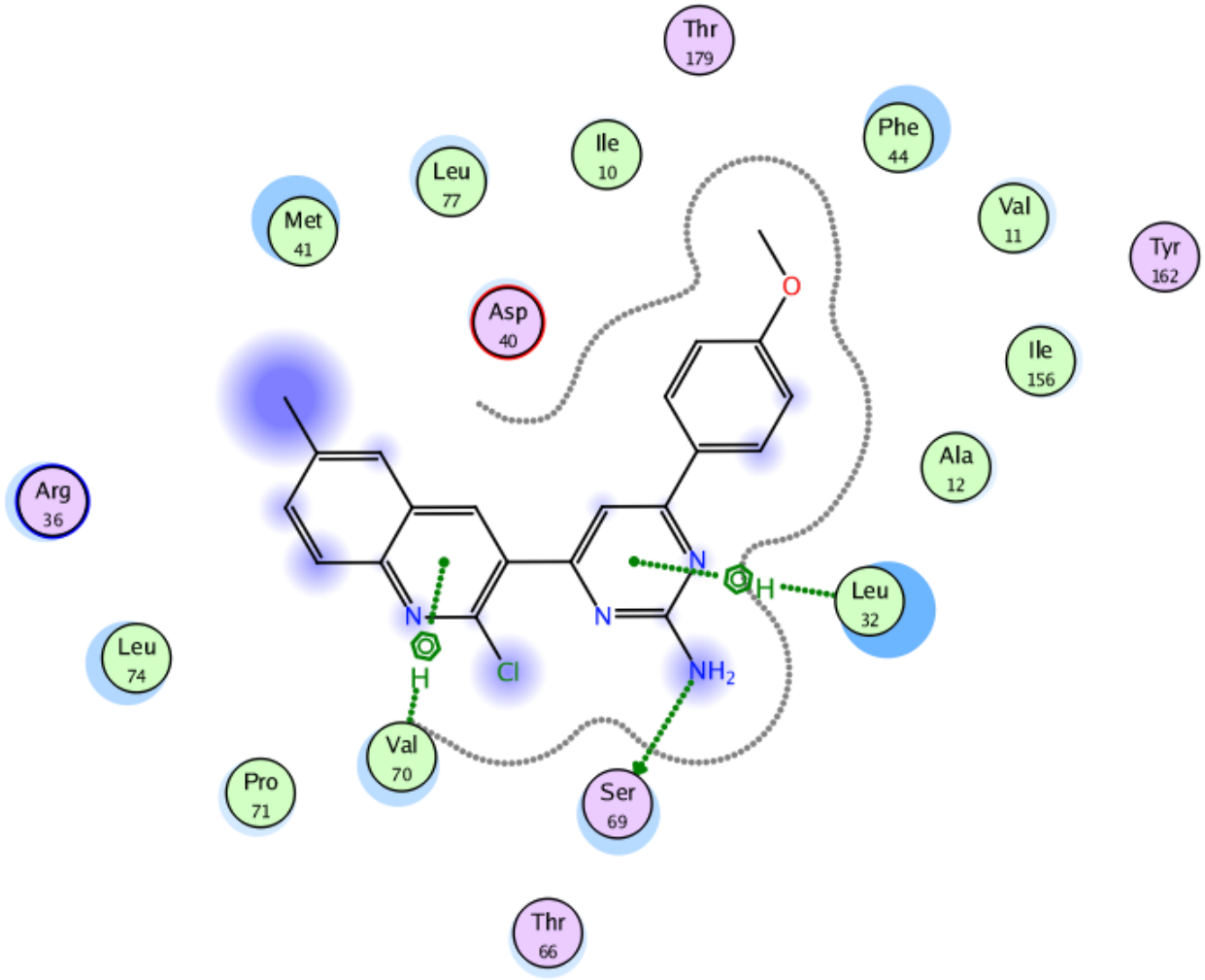


Figure 20: 2D interactions of quinoline derivative 16 in the active site of DHFR

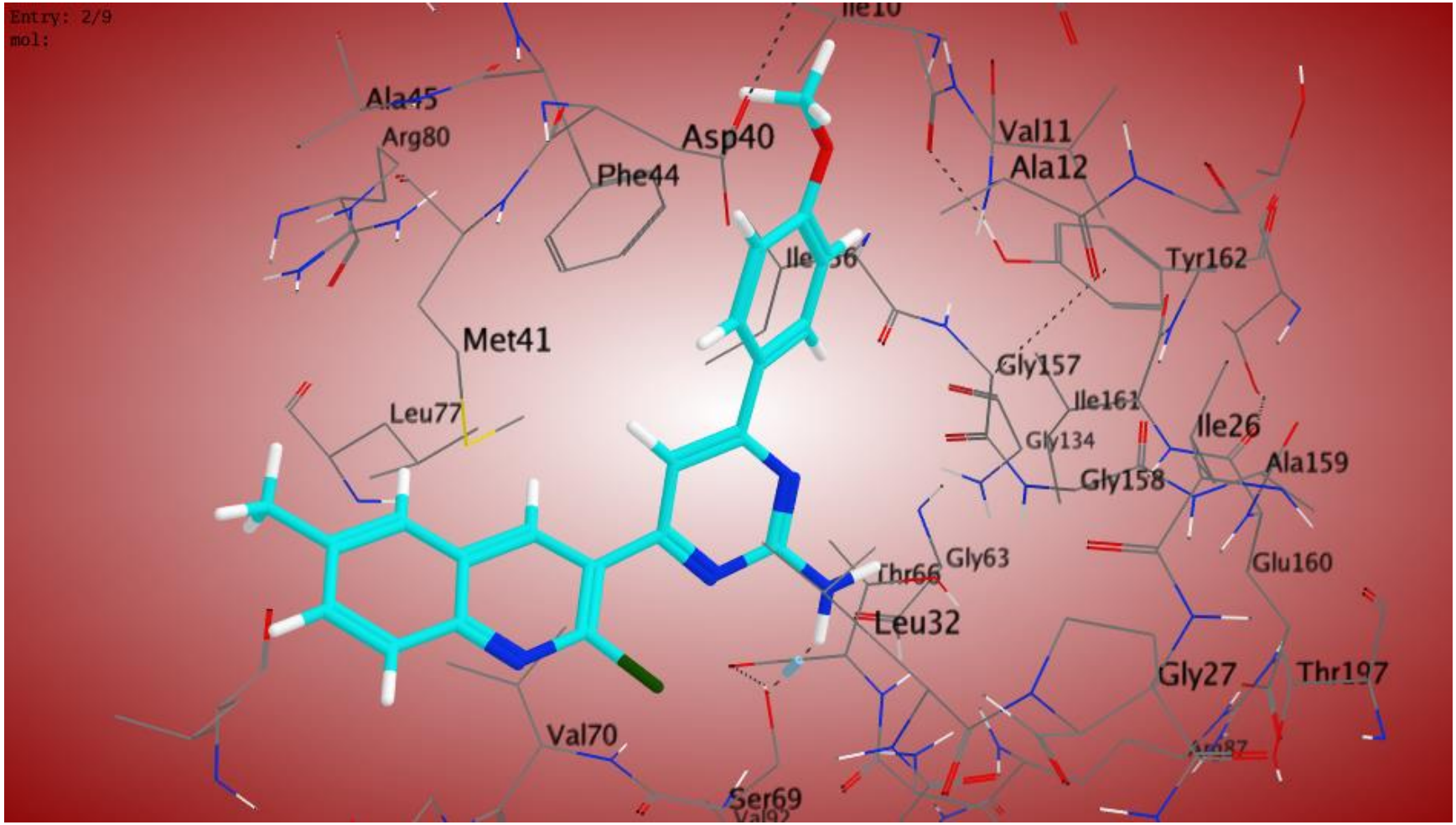


Figure 21: 3D interactions of quinoline derivative 16 in the active site of DHFR

Docking details for compound 20 in the active site of DHFR

Score -8.83793068

Ligand Interactions Report

6DTC: ANTIFUNGAL PROTEIN/INHIBITOR / 6DTC

Ligand	Receptor				Interaction	Distance	E (kcal/mol)
6-ring	CD2	LEU	32	(A)	pi-H	4.43	-0.6
5-ring	CG2	VAL	70	(A)	pi-H	3.90	-1.4

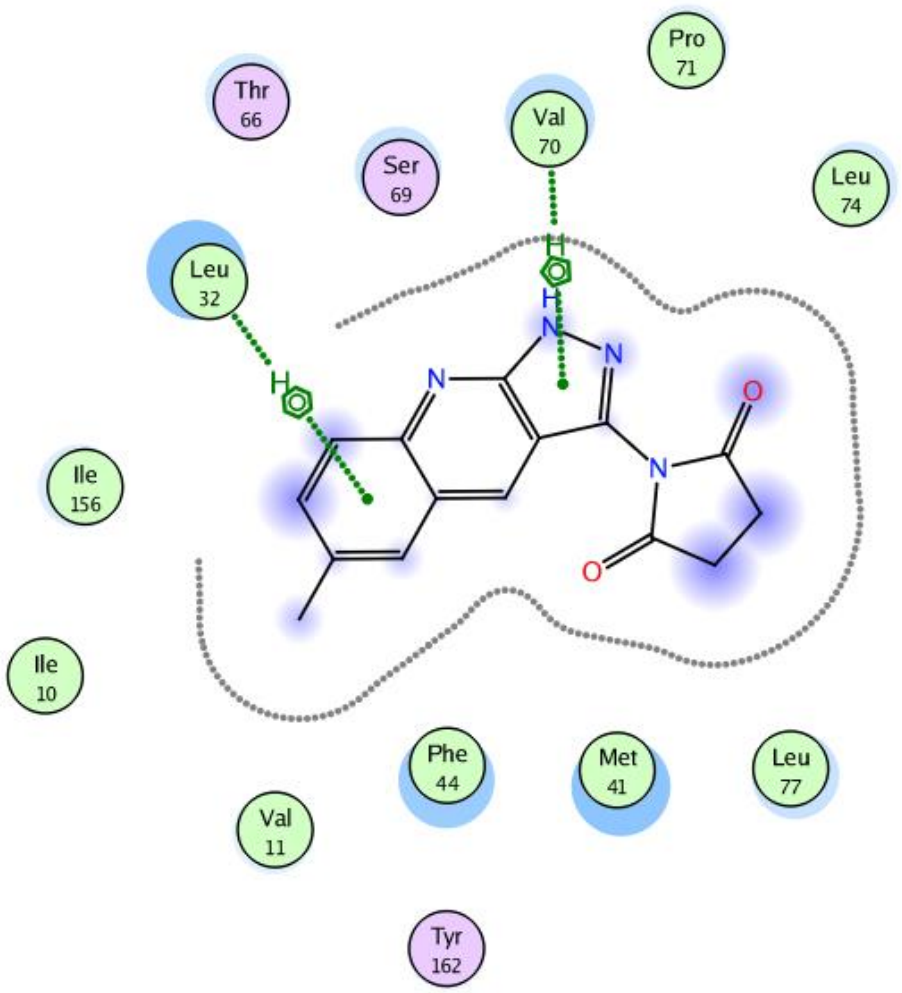


Figure 22: 2D interactions of quinoline derivative 20 in the active site of DHFR

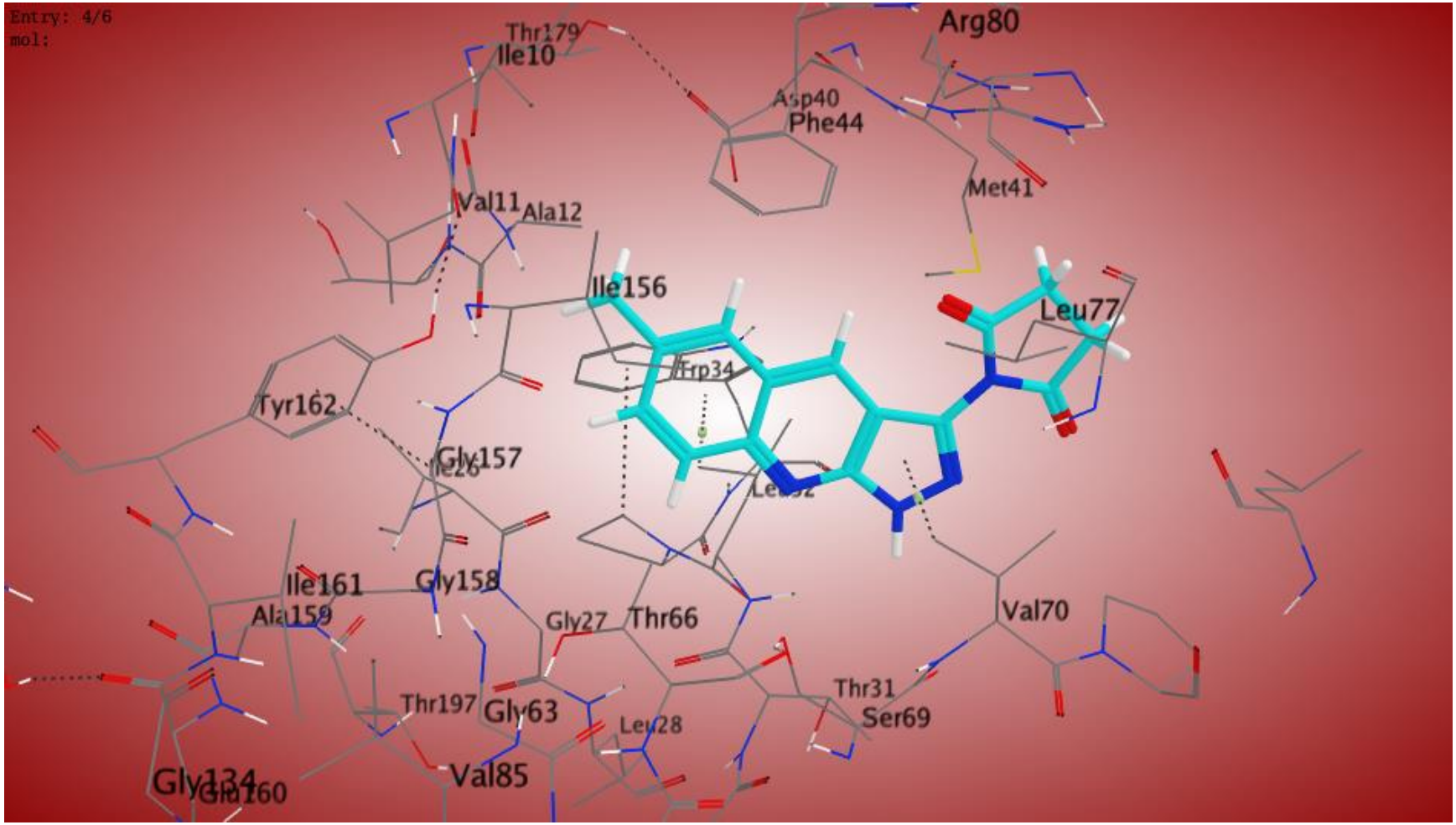


Figure 23: 3D interactions of quinoline derivative 20 in the active site of DHFR

Docking details for compound 21 in the active site of DHFR

Score -8.75586033

Ligand Interactions Report

6DTC: ANTIFUNGAL PROTEIN/INHIBITOR / 6DTC

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
N 12	OH TYR 162 (A)	H-donor	3.08	-0.6
5-ring	CA GLY 157 (A)	pi-H	4.45	-1.0

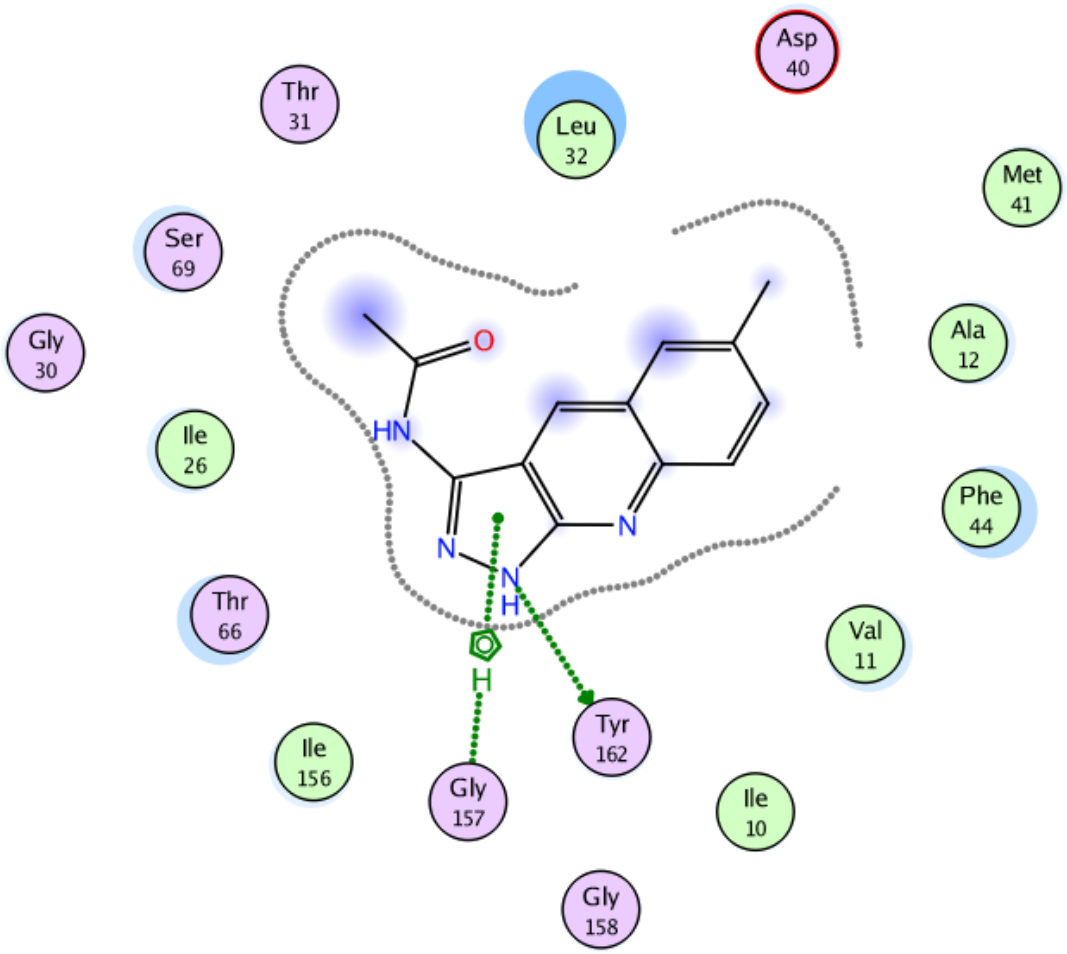


Figure 24: 2D interactions of quinoline derivative 21 in the active site of DHFR

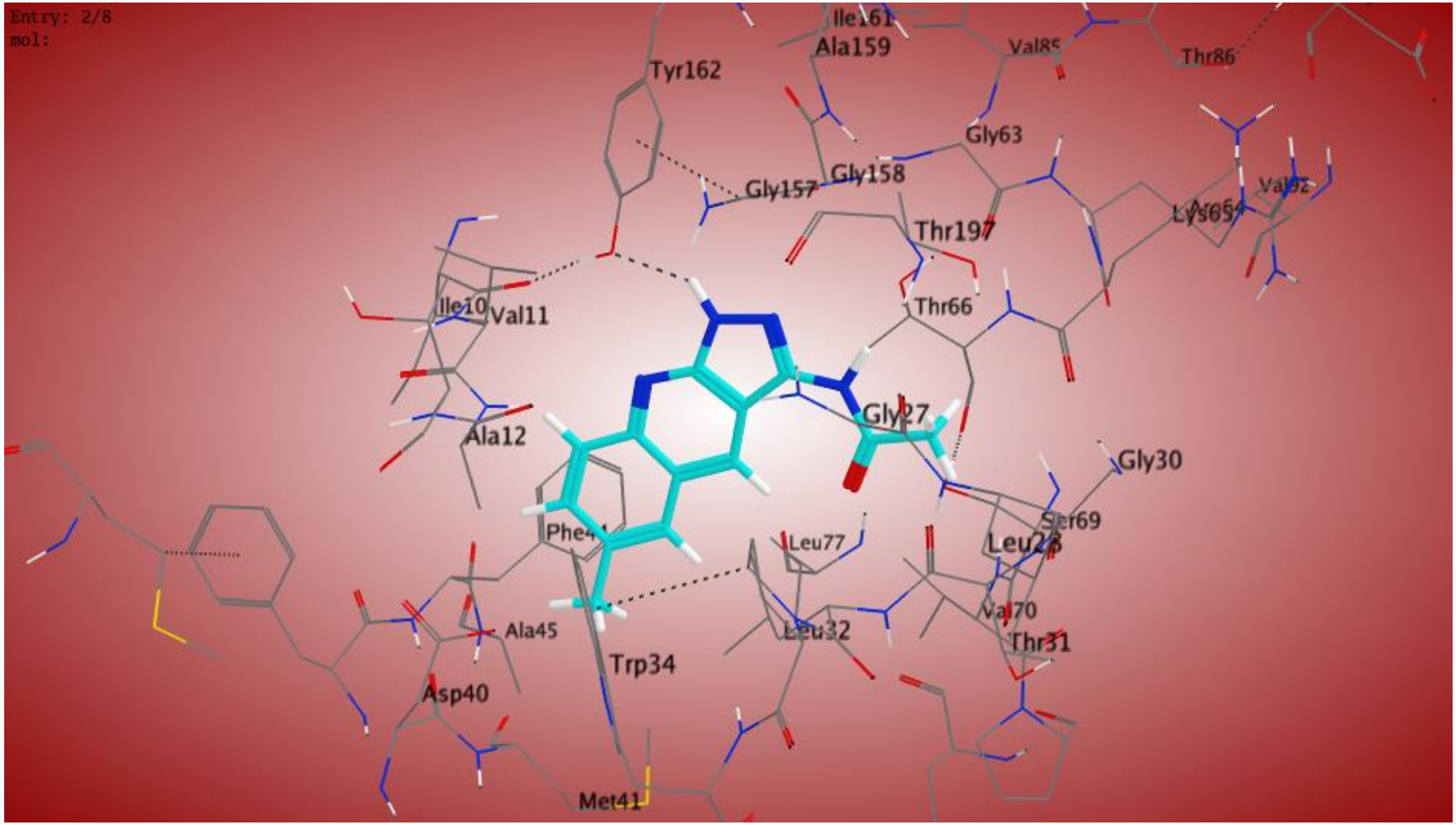


Figure 25: 3D interactions of quinoline derivative 21 in the active site of DHFR

Docking details for compound 21 in the active site of DHFR

Score -8.45339394

Ligand Interactions Report

6DTC: ANTIFUNGAL PROTEIN/INHIBITOR / 6DTC

Ligand	Receptor	Interaction	Distance	E (kcal/mol)
N 12	OG SER 69 (A)	H-donor	2.98	-1.1

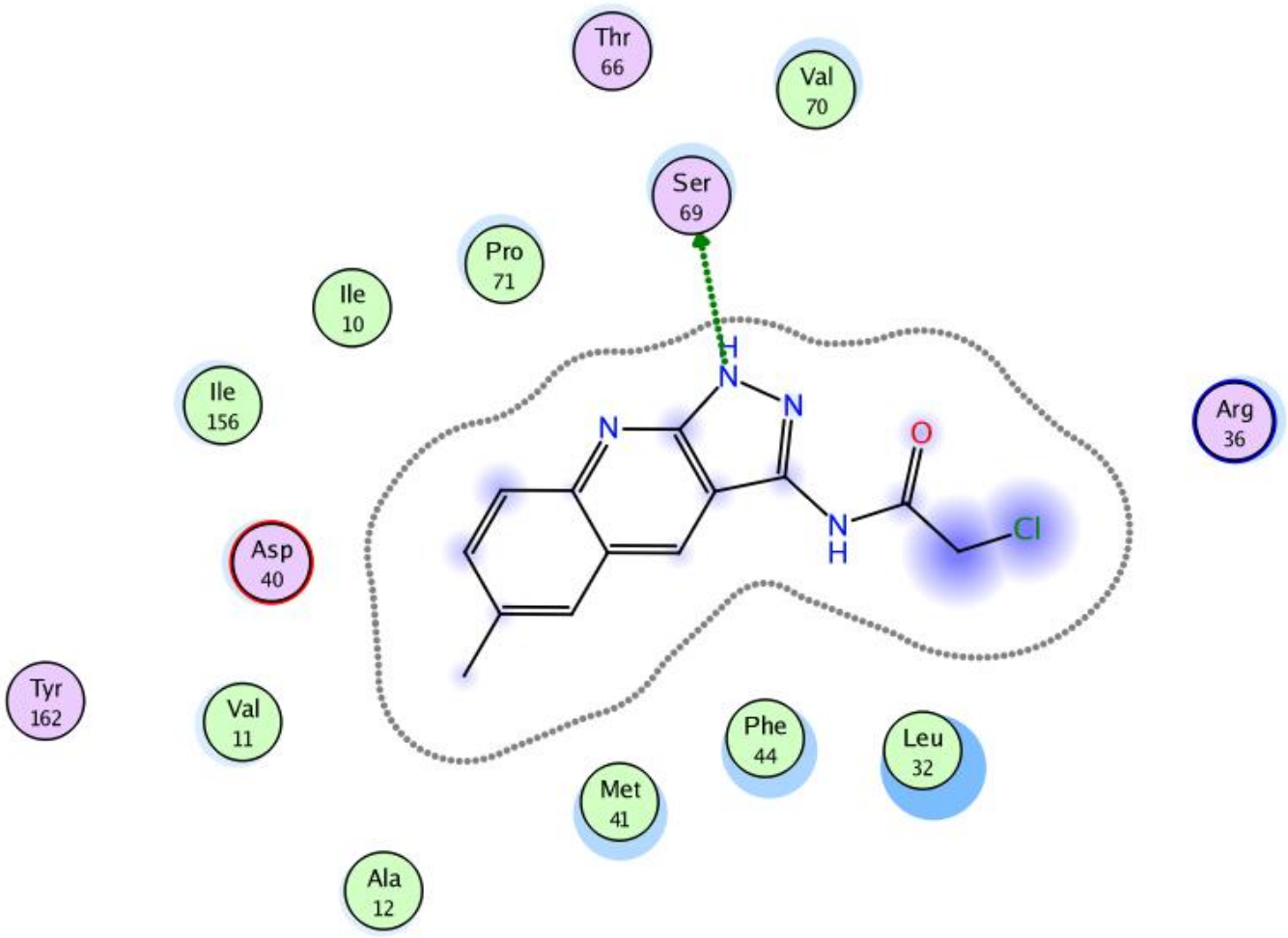


Figure 26: 2D interactions of quinoline derivative 22 in the active site of DHFR

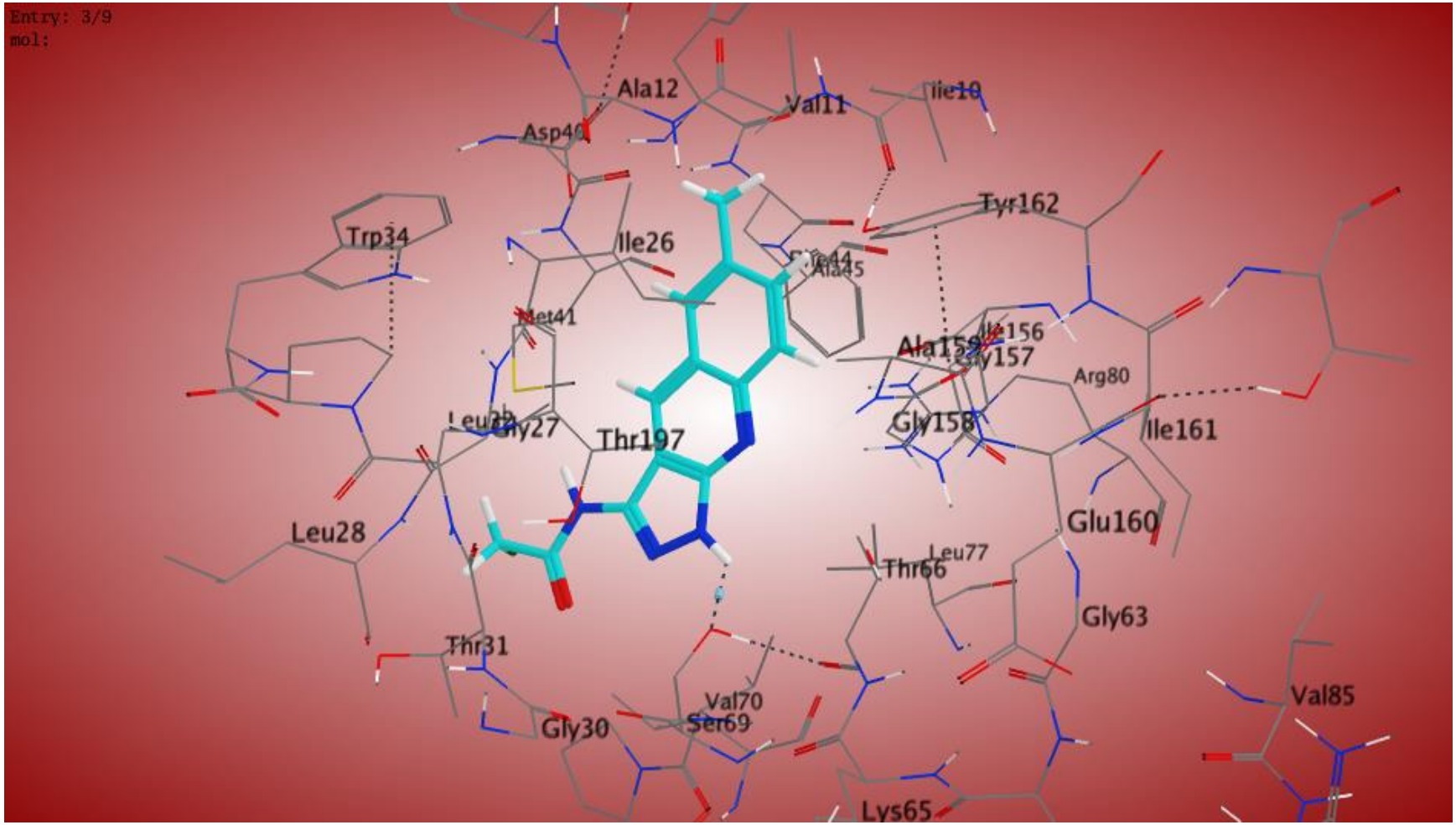
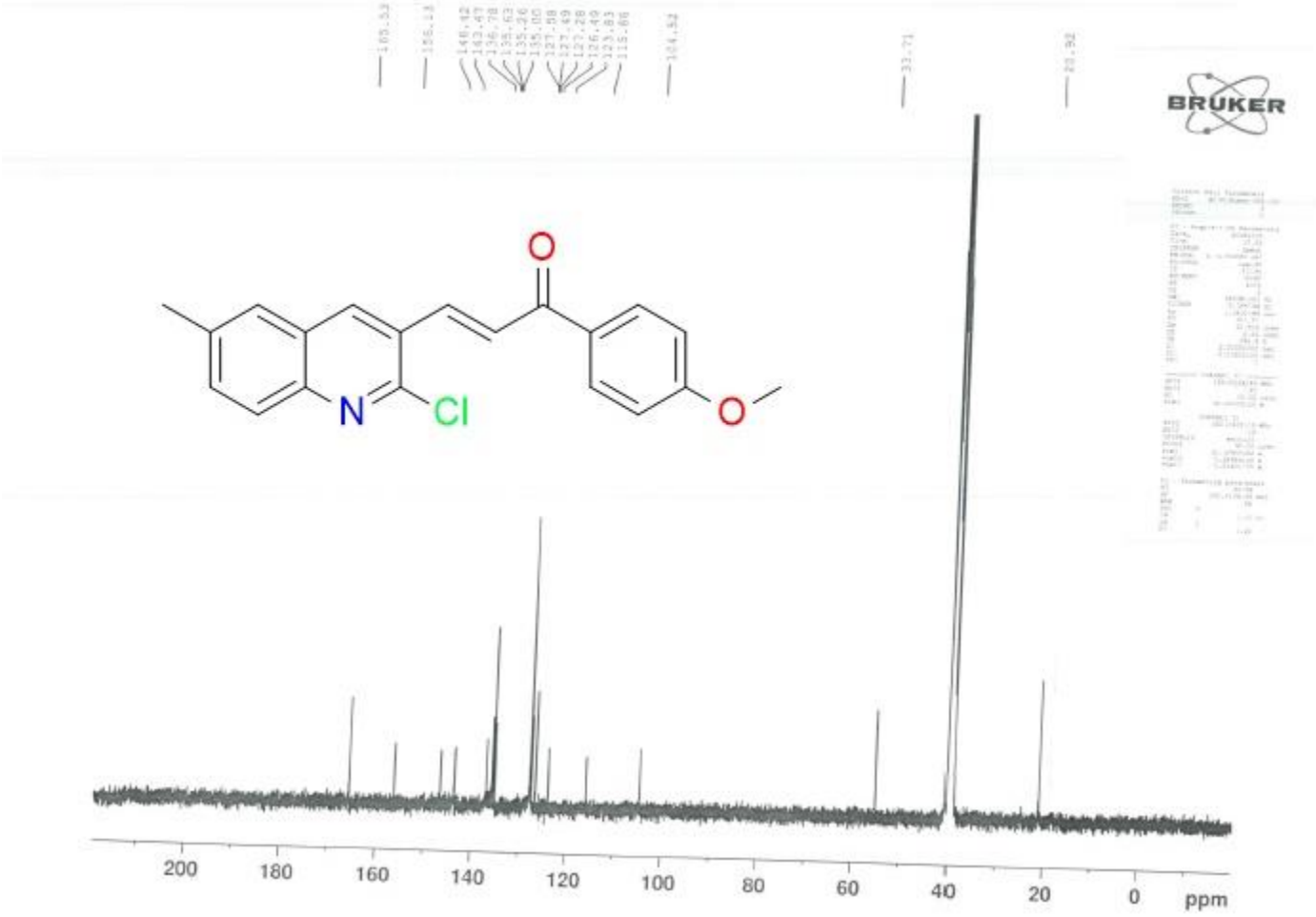


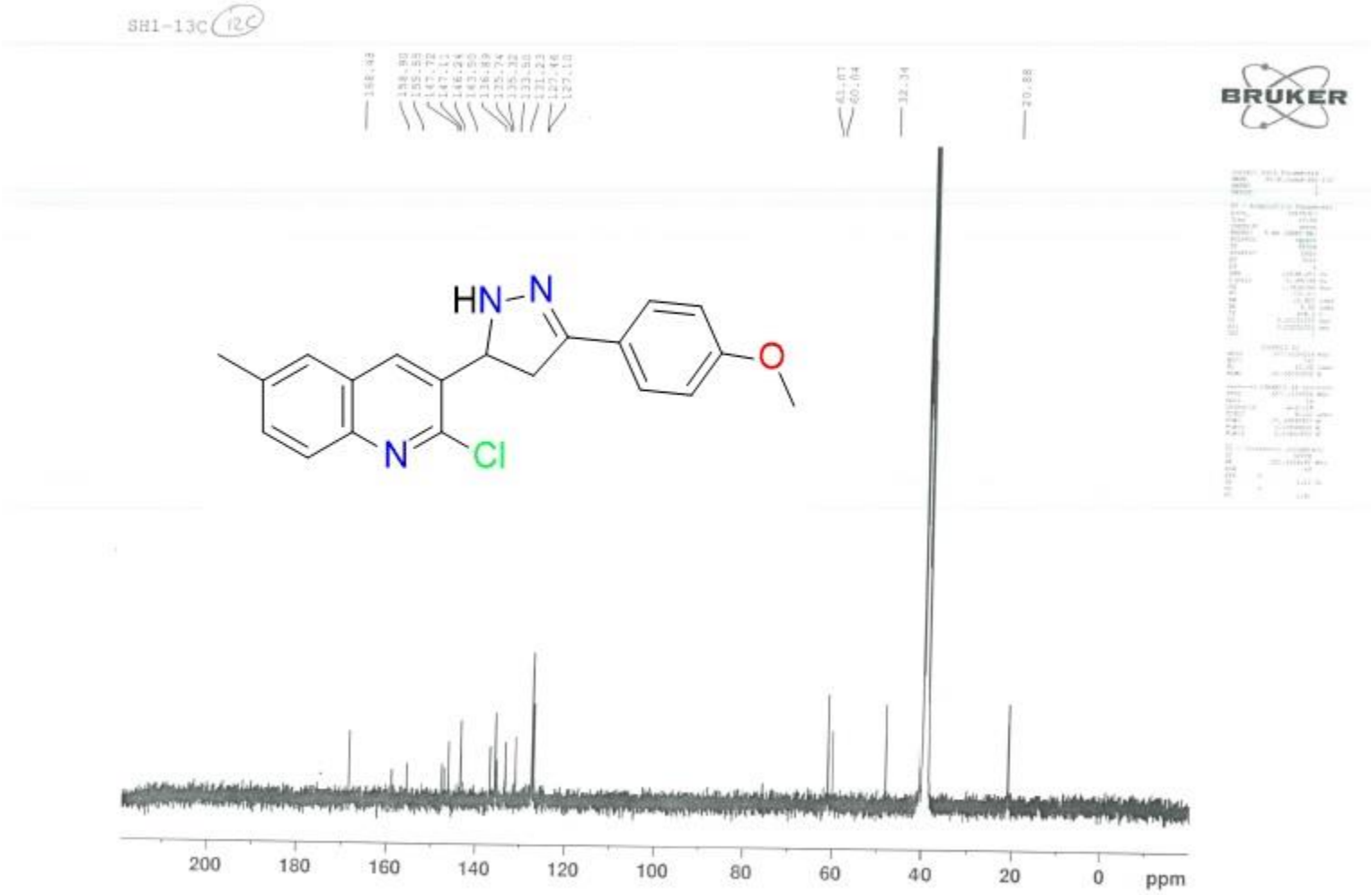
Figure 27: 3D interactions of quinoline derivative 22 in the active site of DHFR

Representative spectral data of new compounds

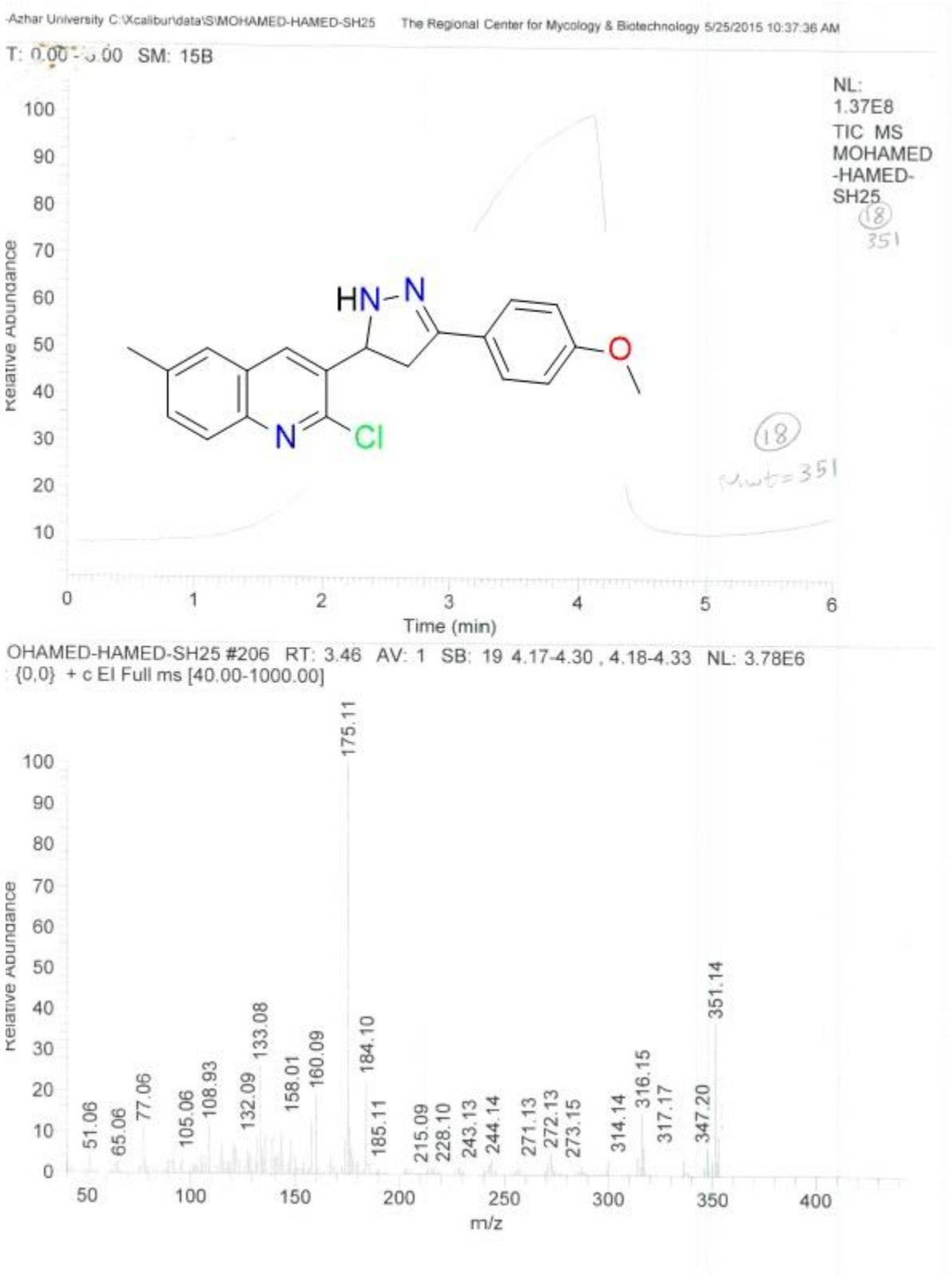
^{13}C NMR spectrum of compound 12



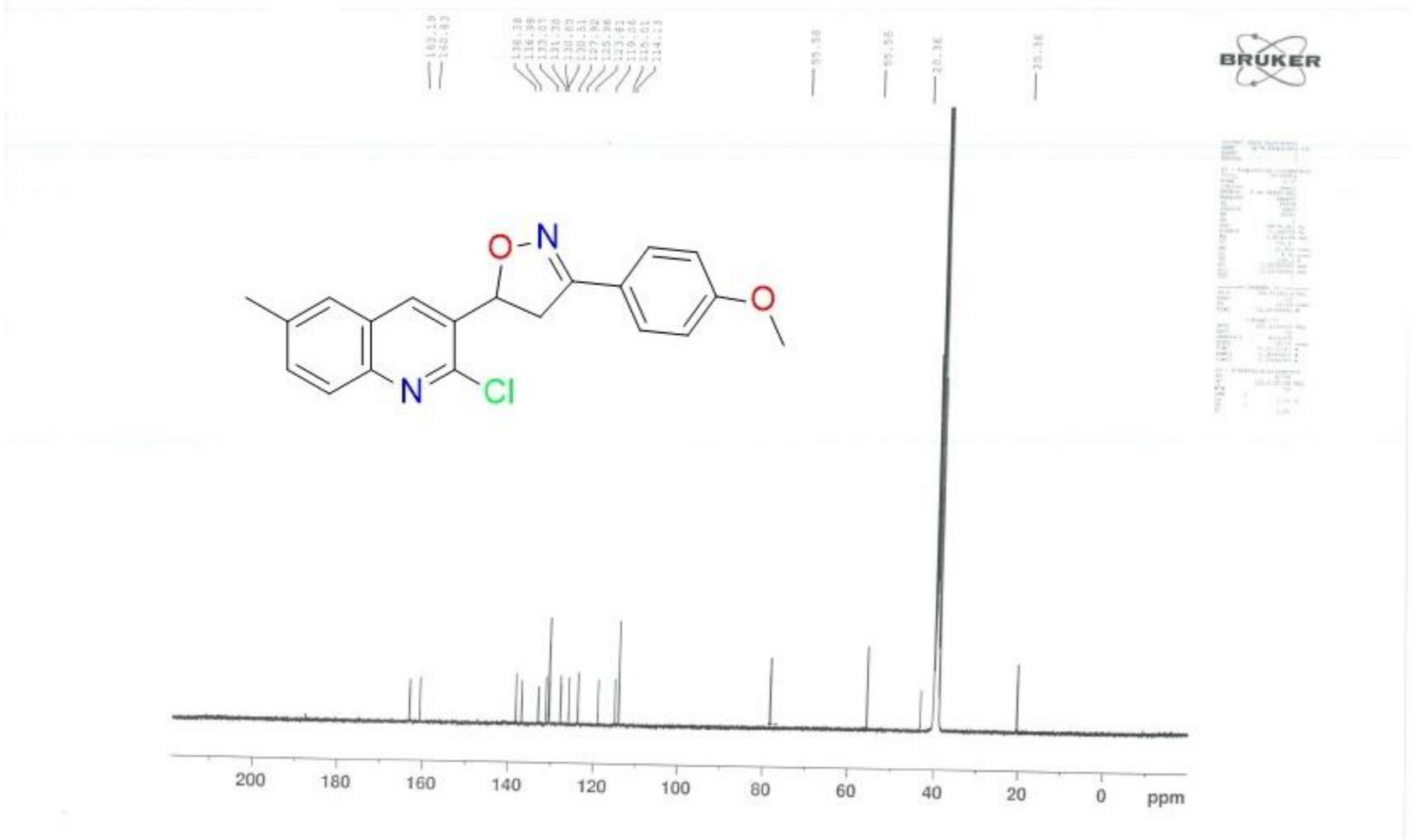
^{13}C NMR spectrum of compound 13



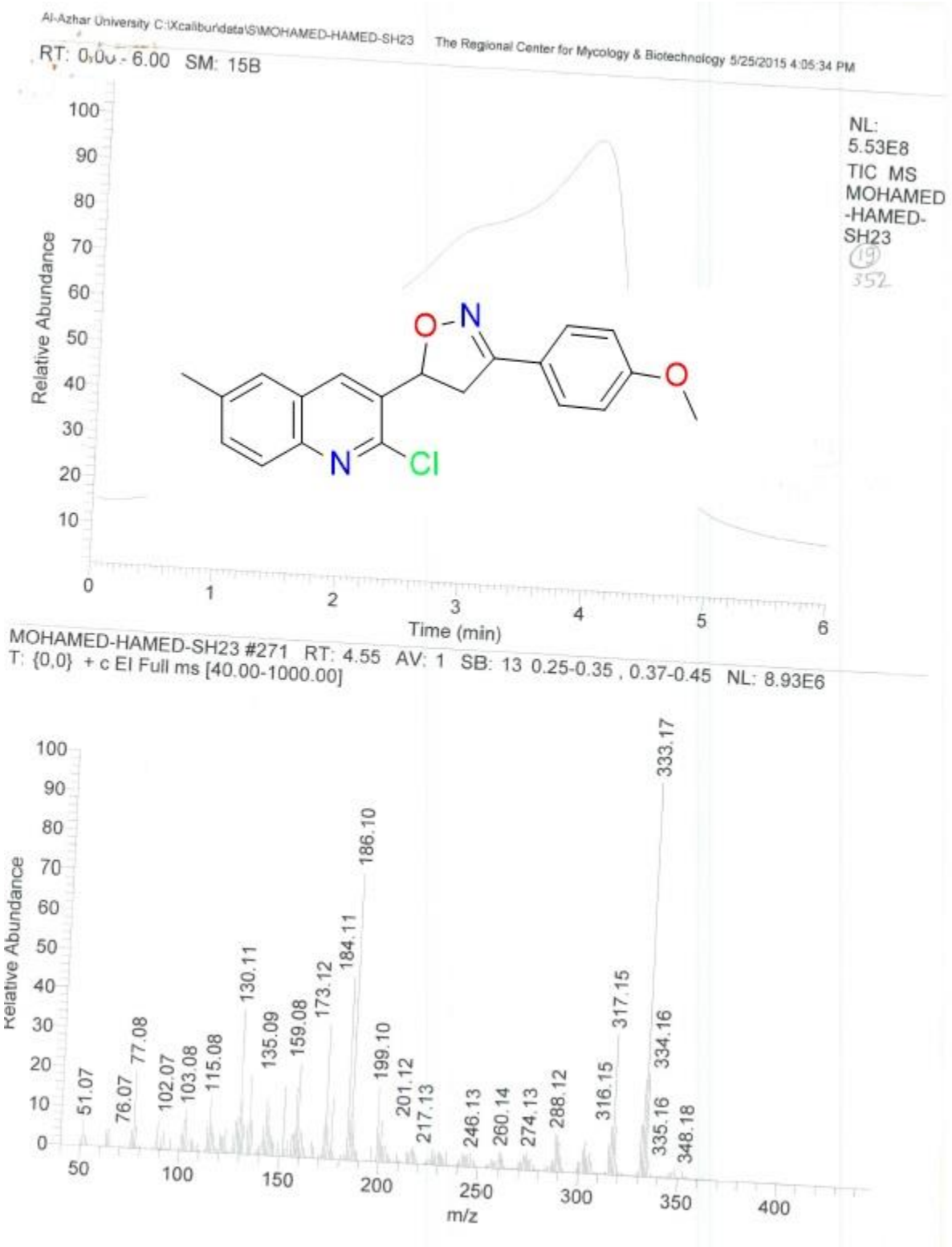
Mass Spectrum of compound 13



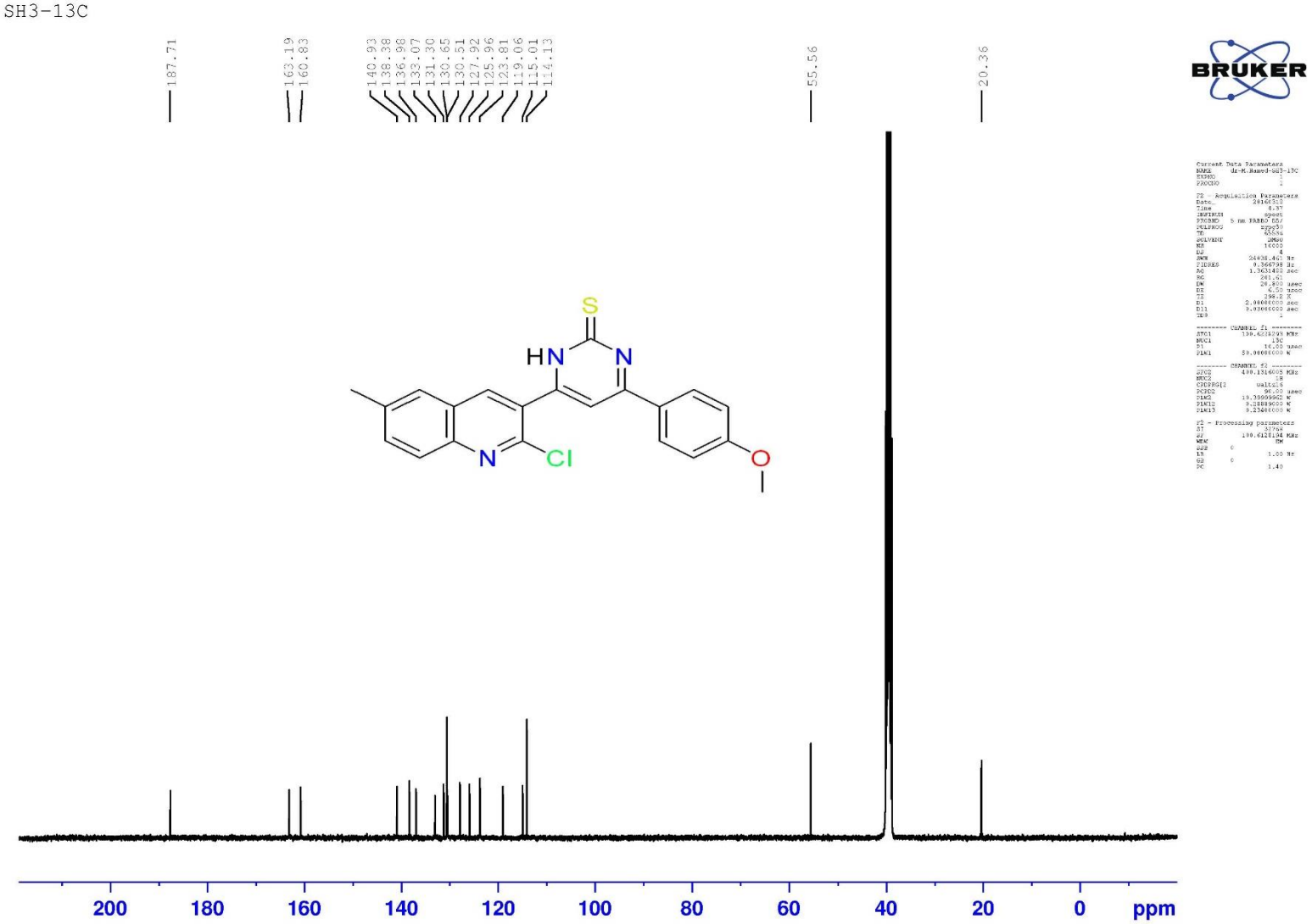
13C NMR spectrum of compound 14



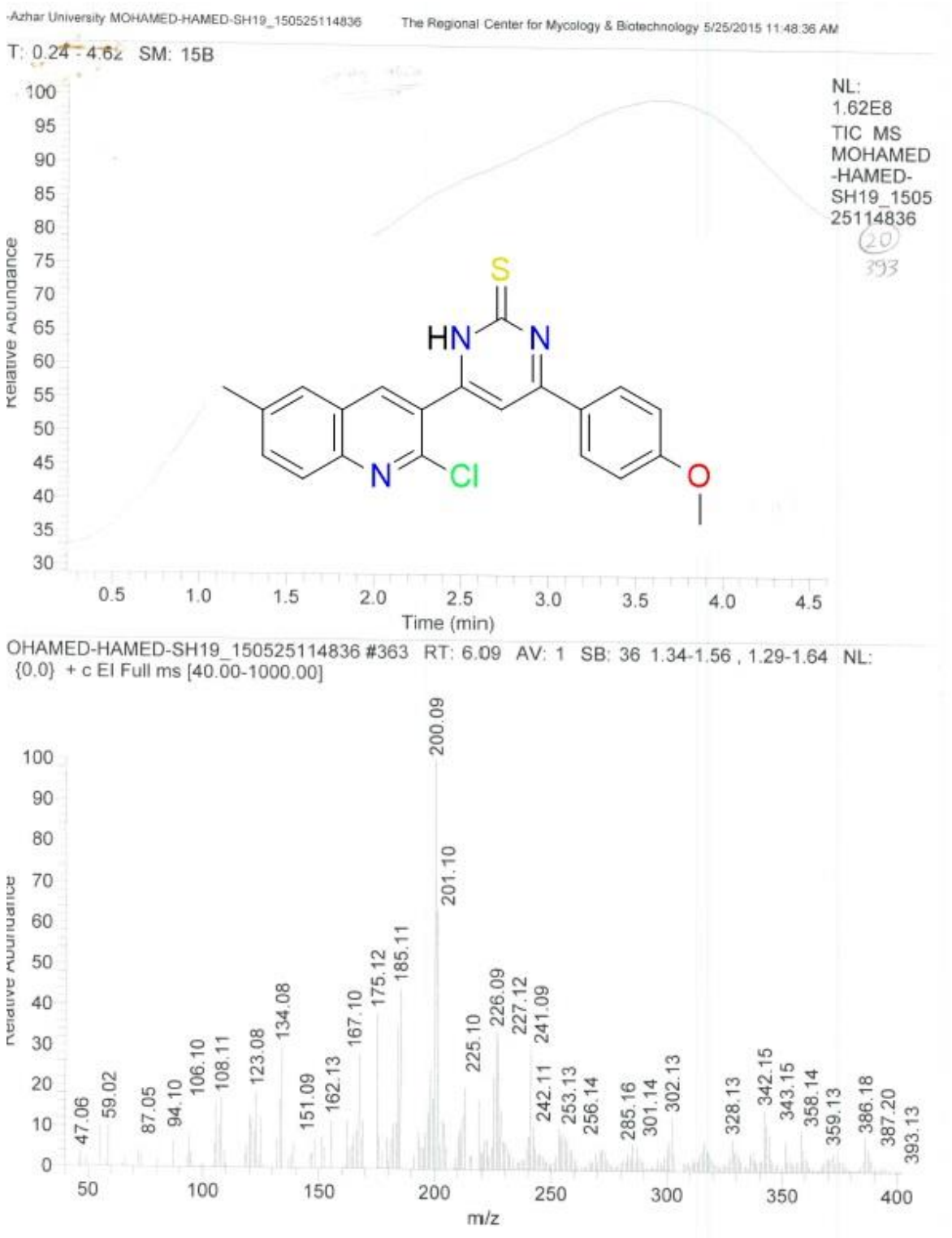
Mass spectrum of compound 14



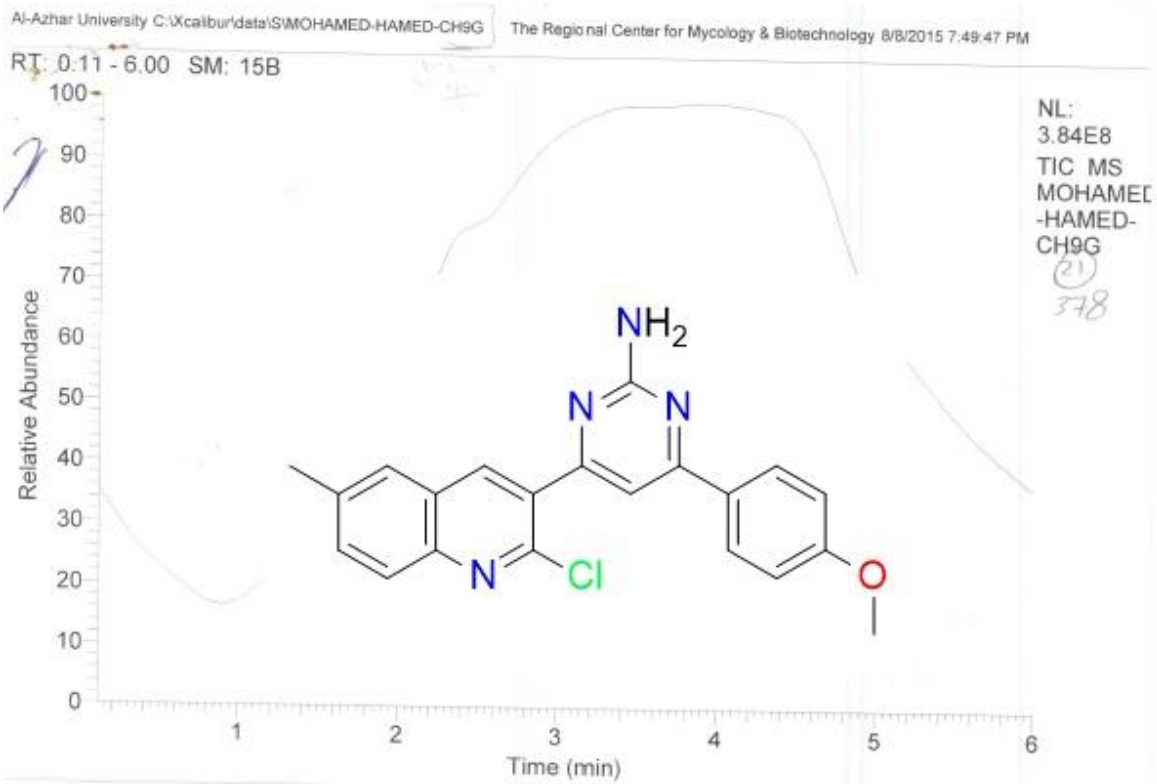
^{13}C NMR spectrum of compound 15

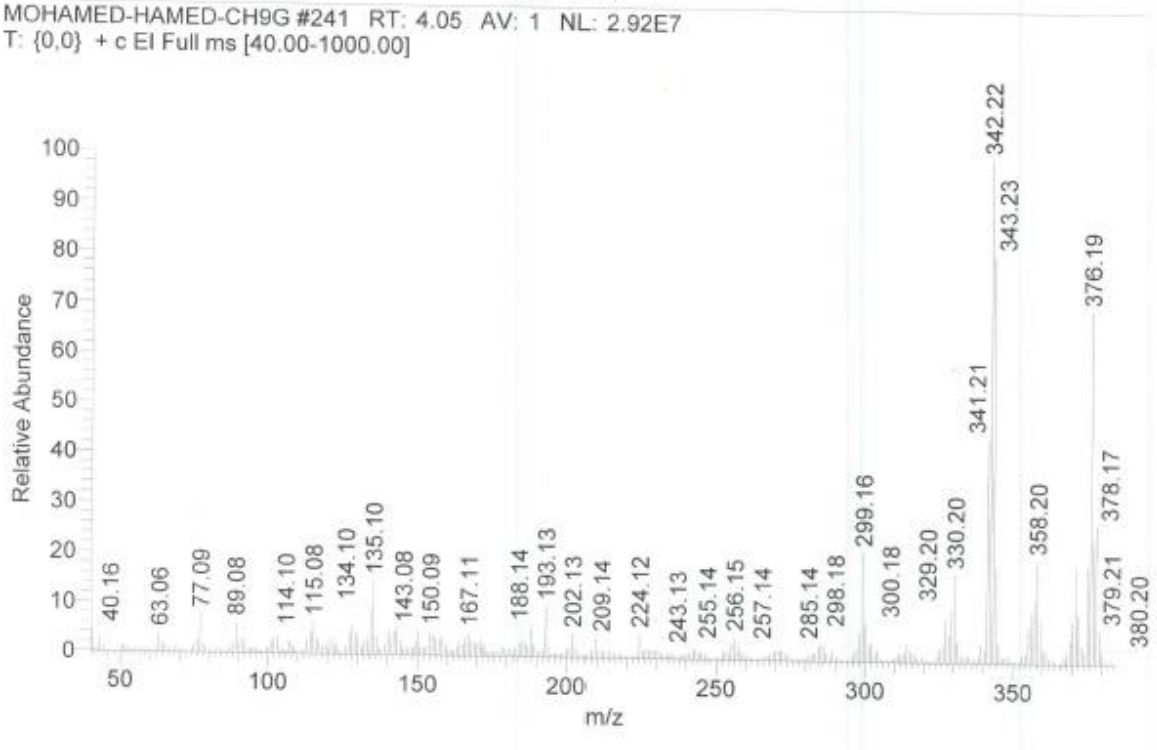


Mass spectrum of compound 15

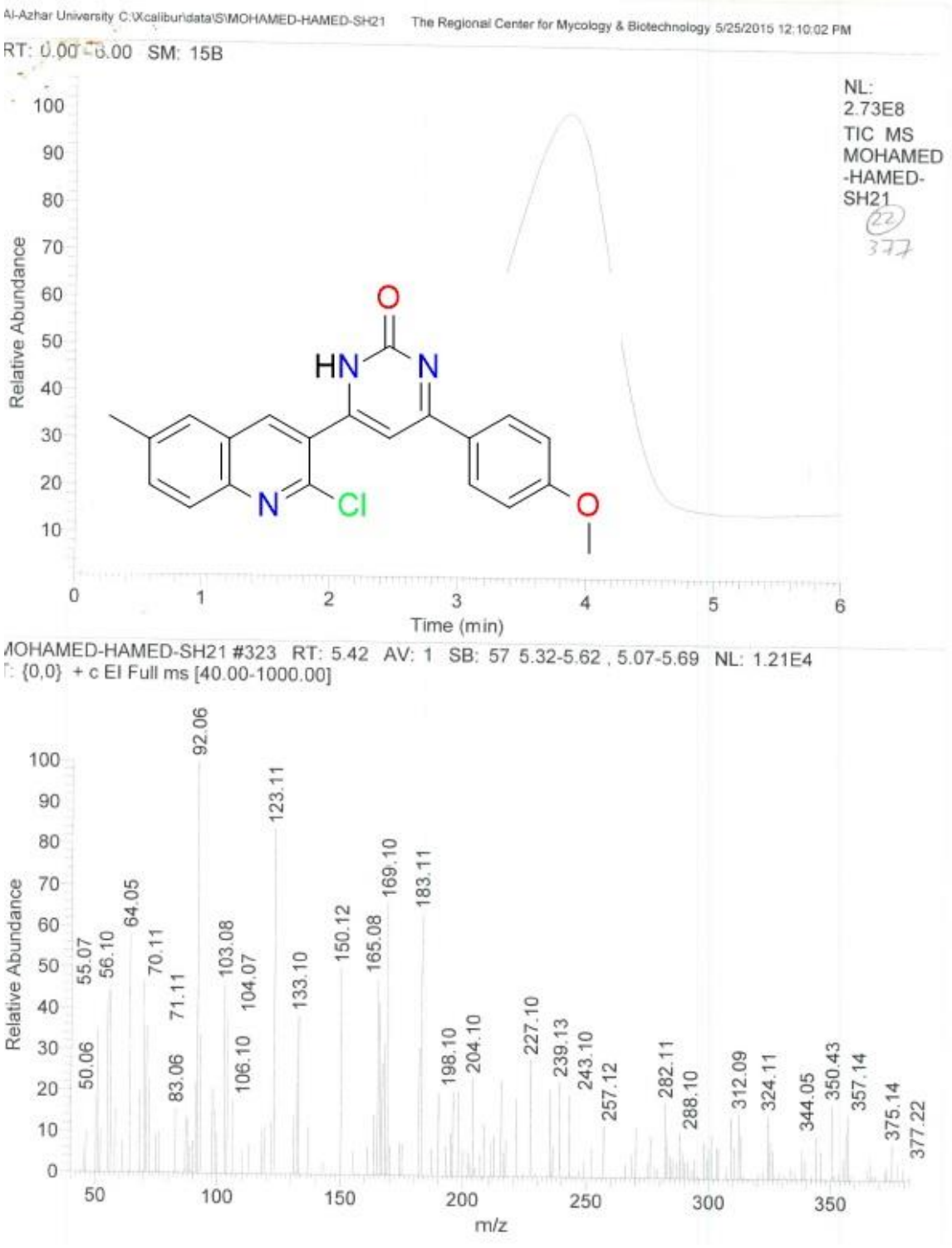


Mass spectrum of compound 16

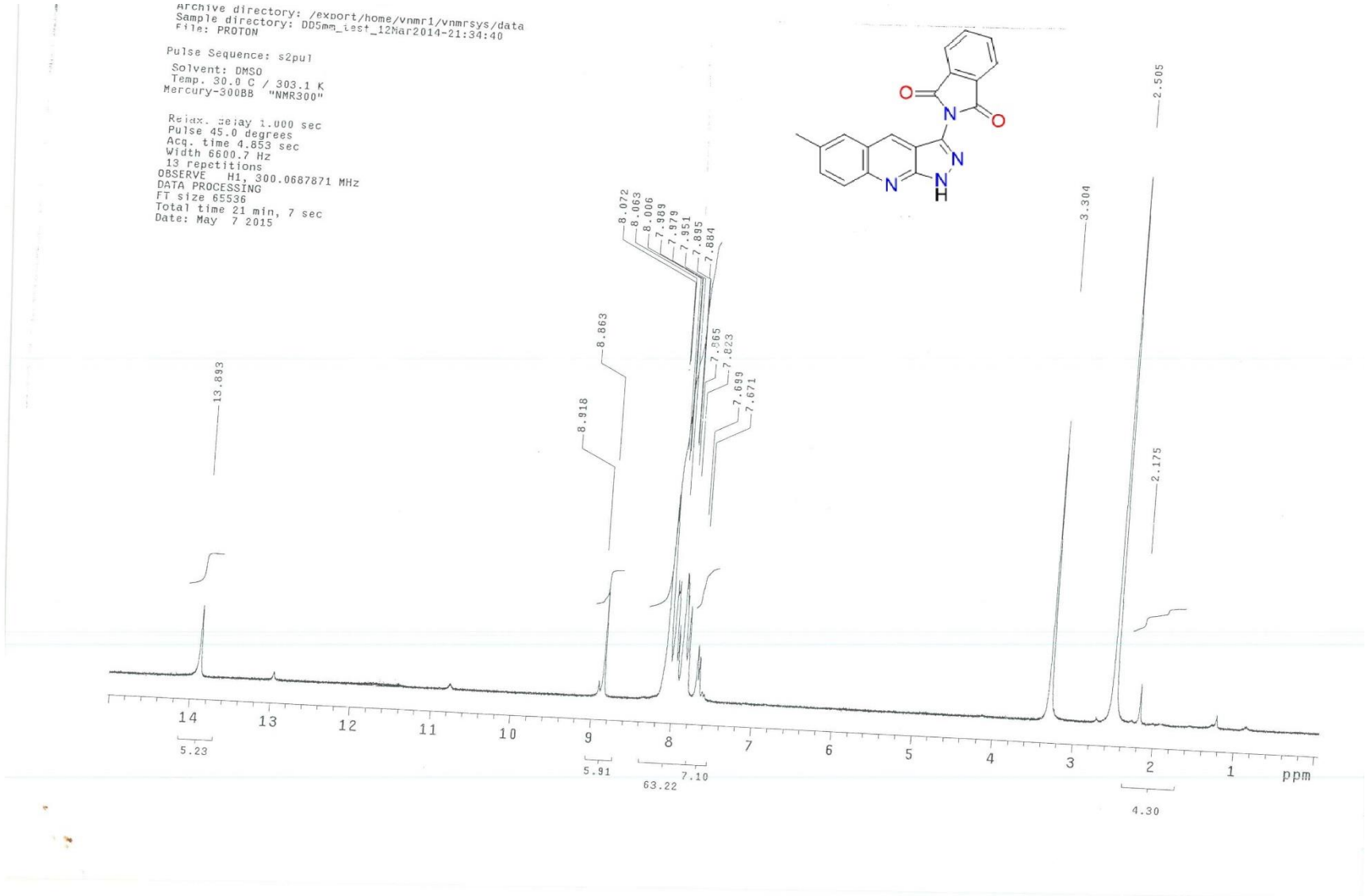




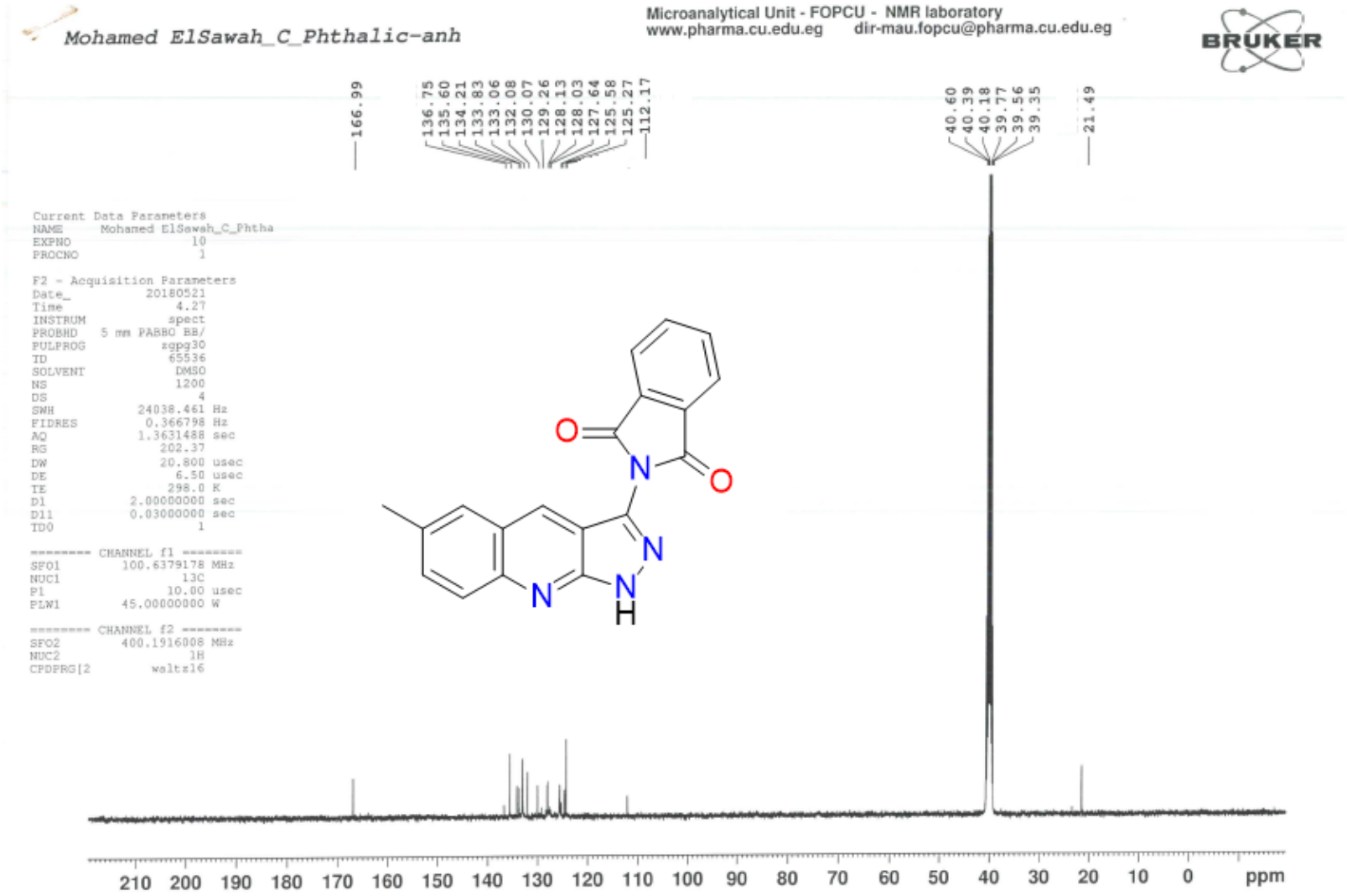
Mass spectrum of compound 17



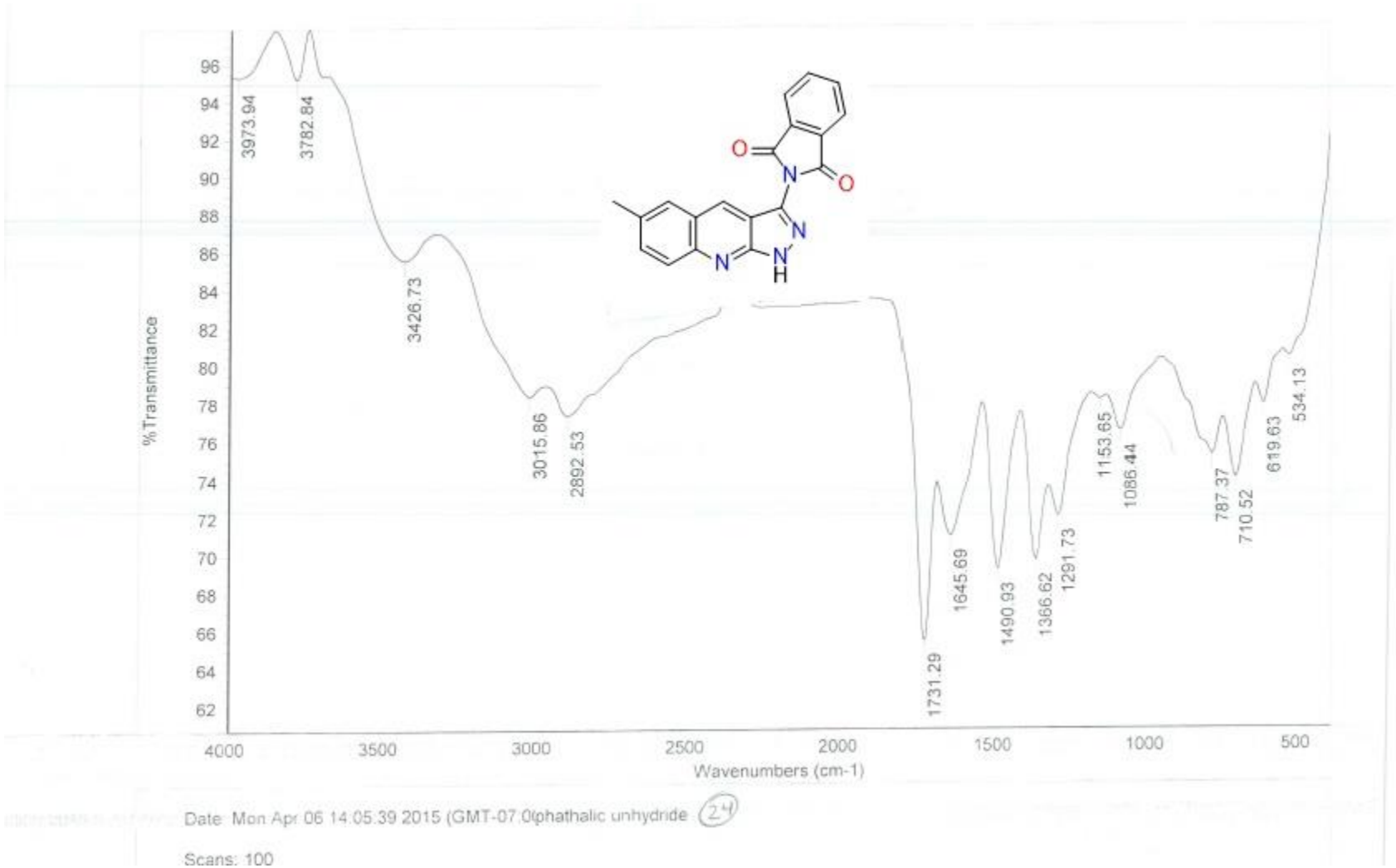
^{1}H NMR spectrum of compound 18



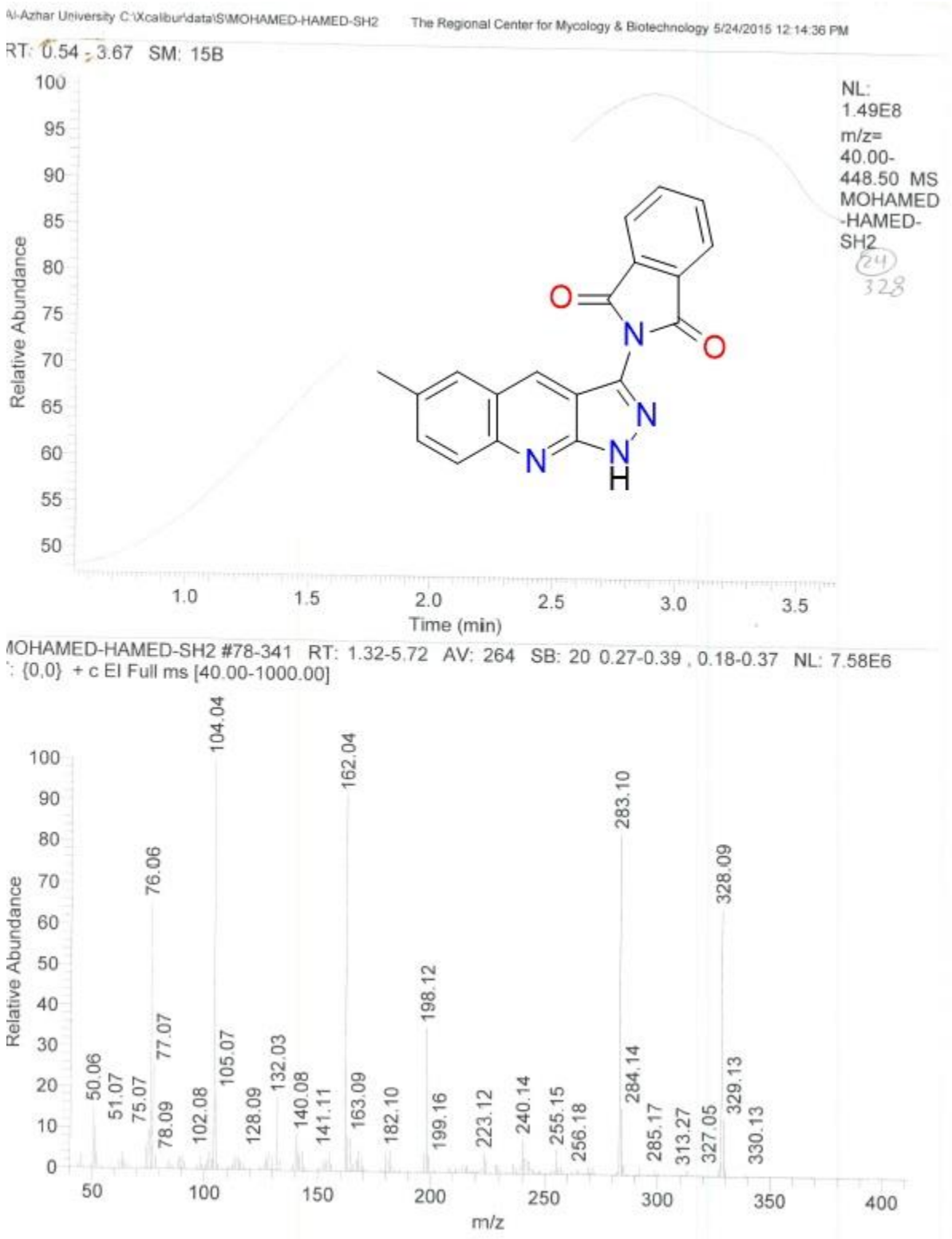
^{13}C NMR spectrum of compound 18



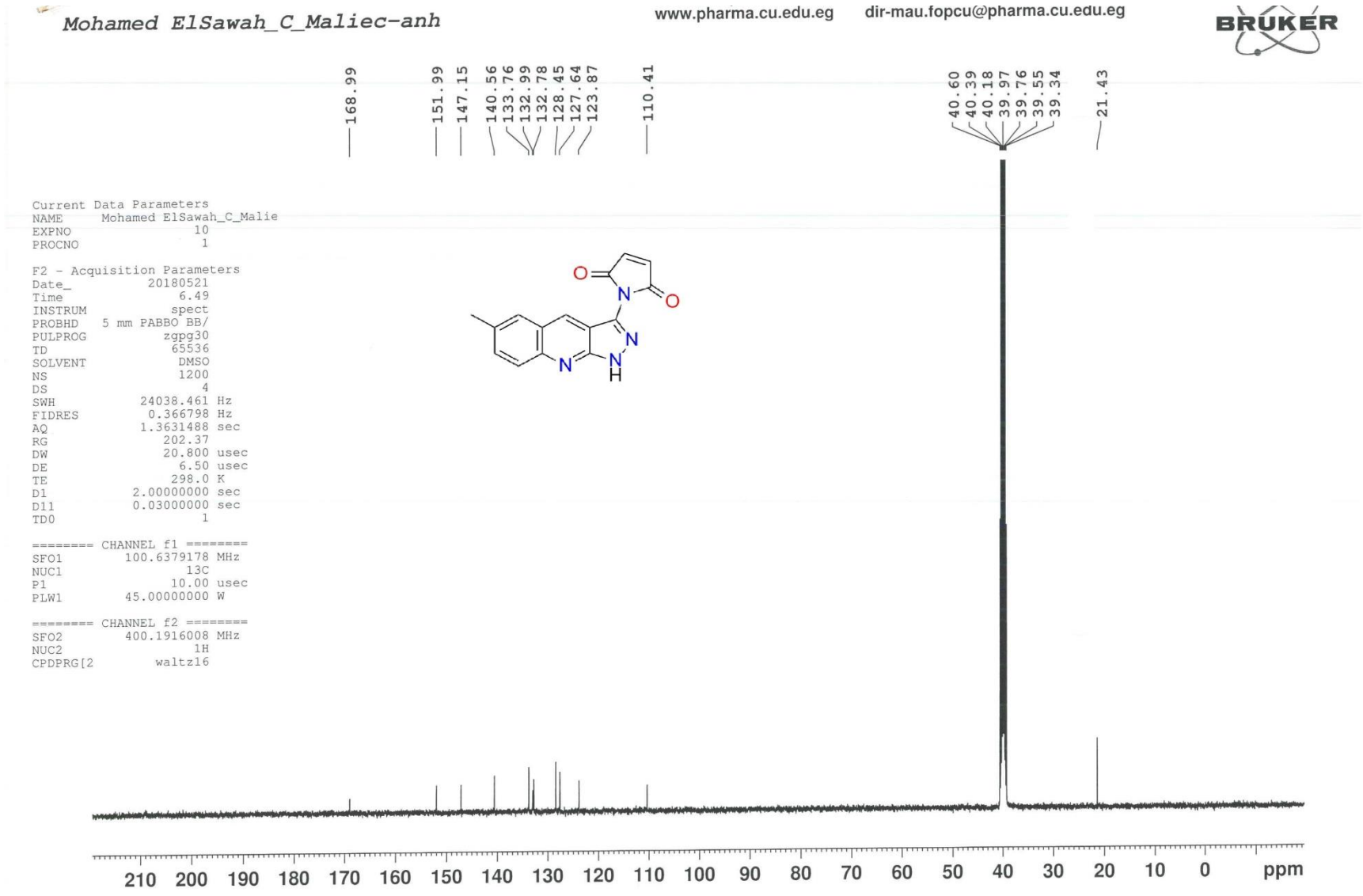
IR spectrum of compound 18



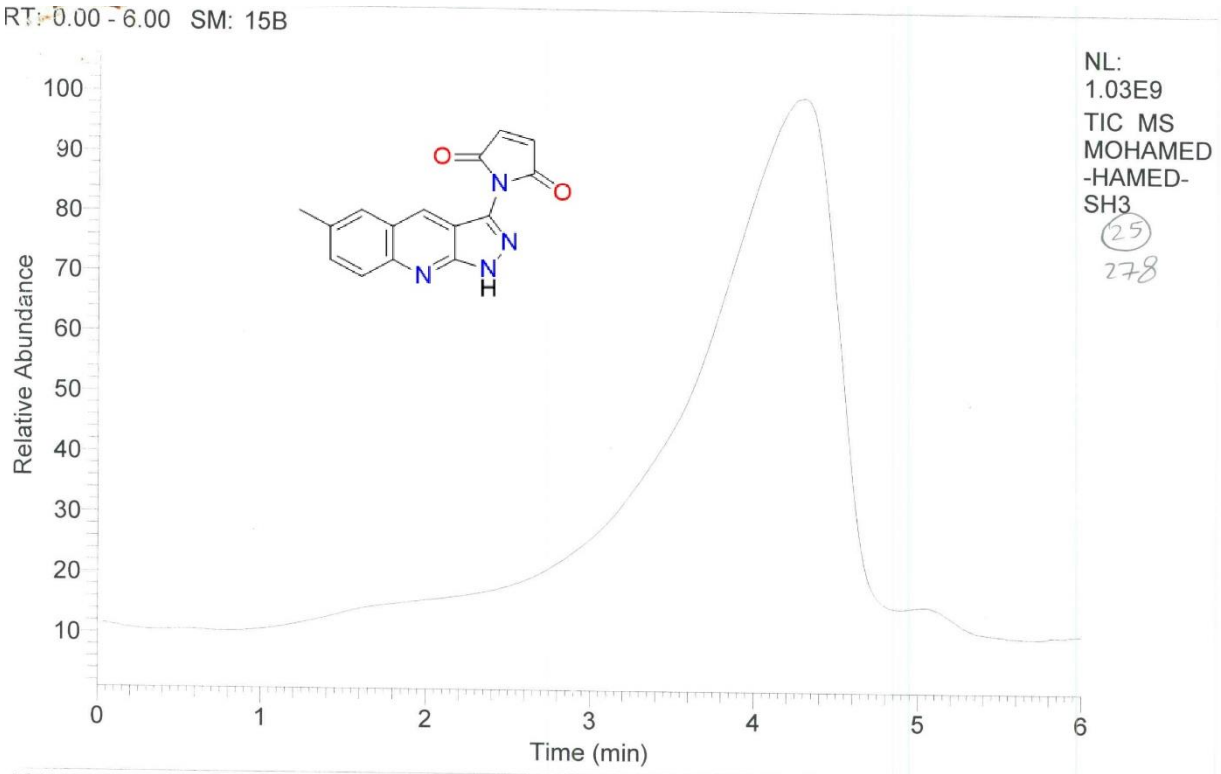
Mass spectrum of compound 18



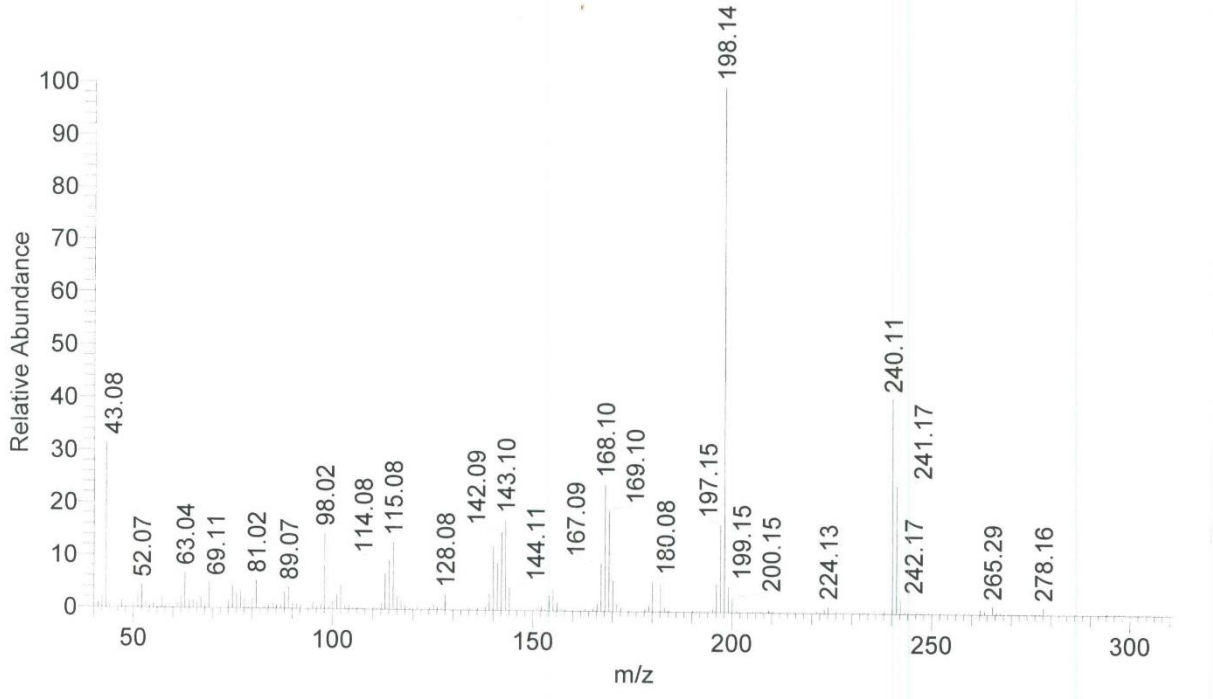
^{13}C NMR spectrum of compound 19



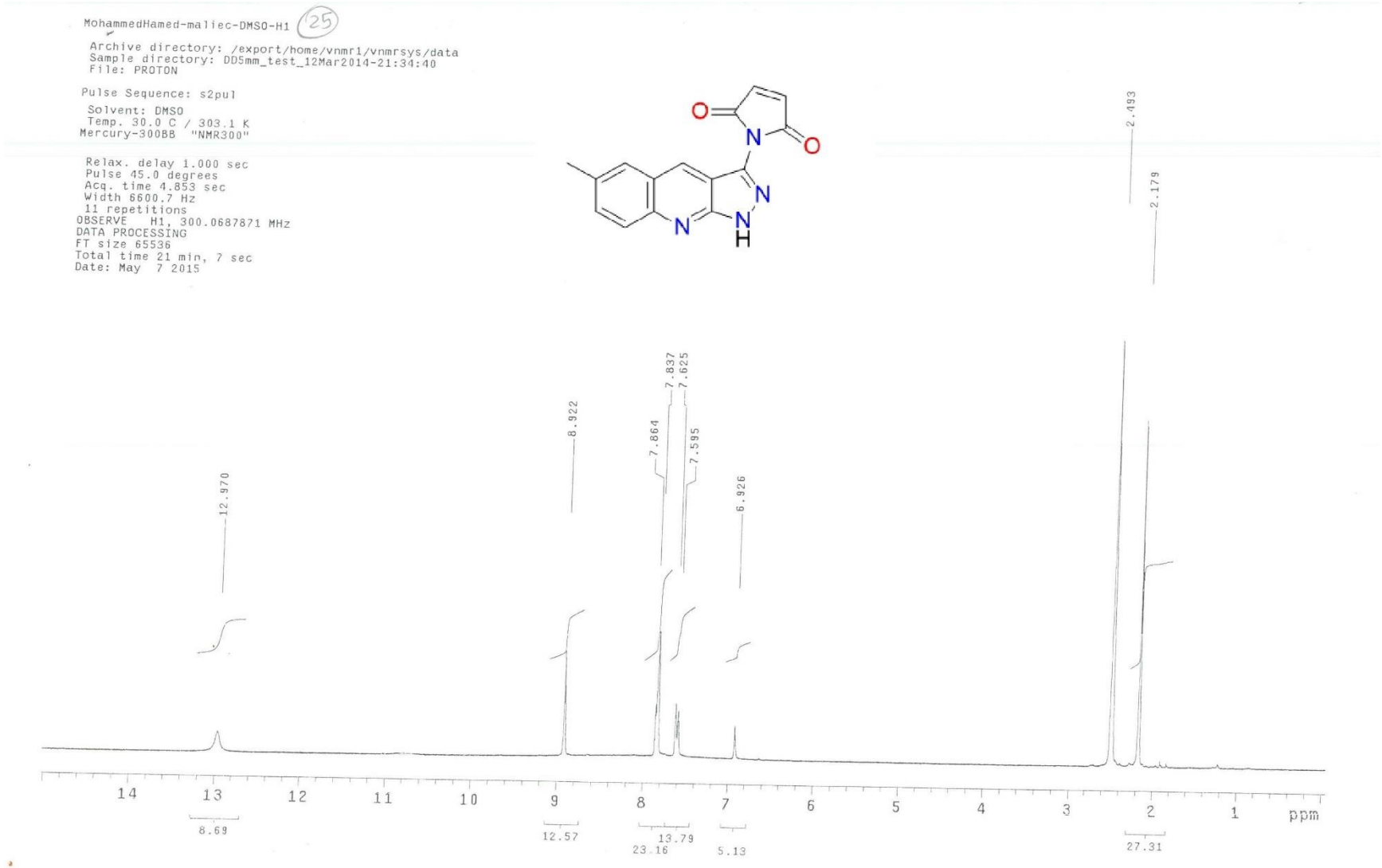
Mass spectrum of compound 19



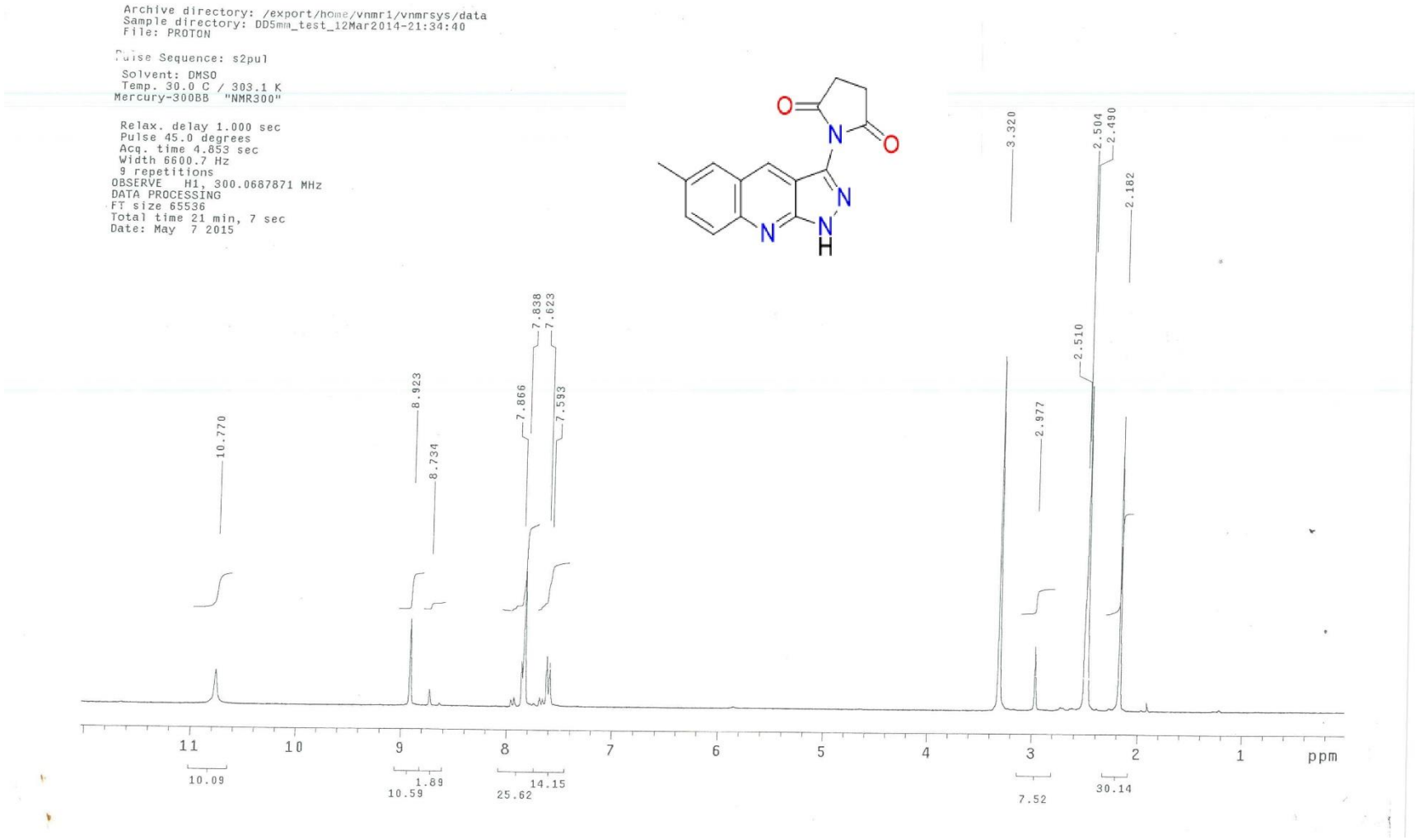
MOHAMED-HAMED-SH3 #219 RT: 3.68 AV: 1 SB: 22 3.58-3.73 , 3.55-3.73 NL: 3.43E6
T: {0,0} + c EI Full ms [40.00-1000.00]



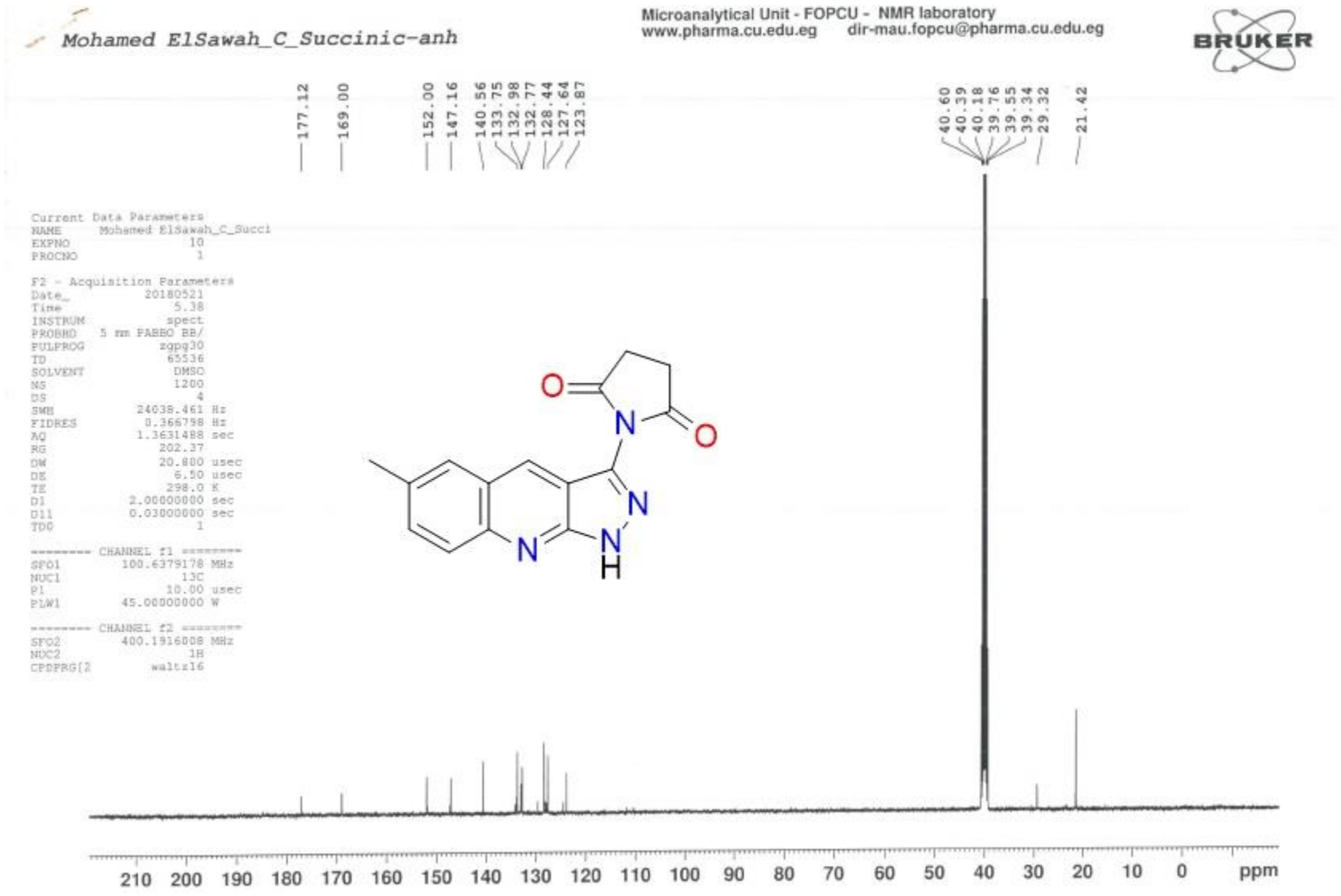
^{1}H NMR spectrum of compound 19



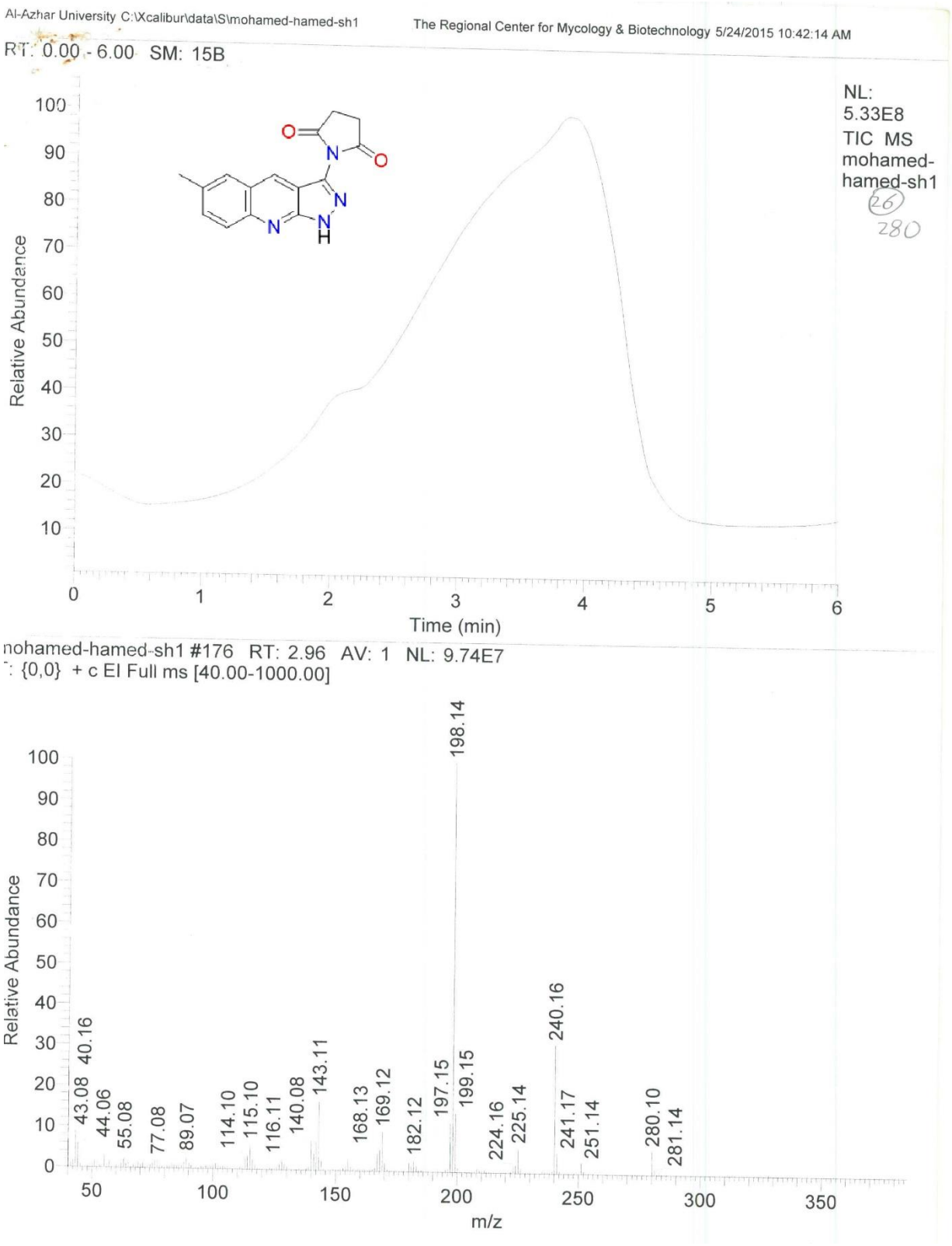
^{1}H NMR spectrum of compound 20



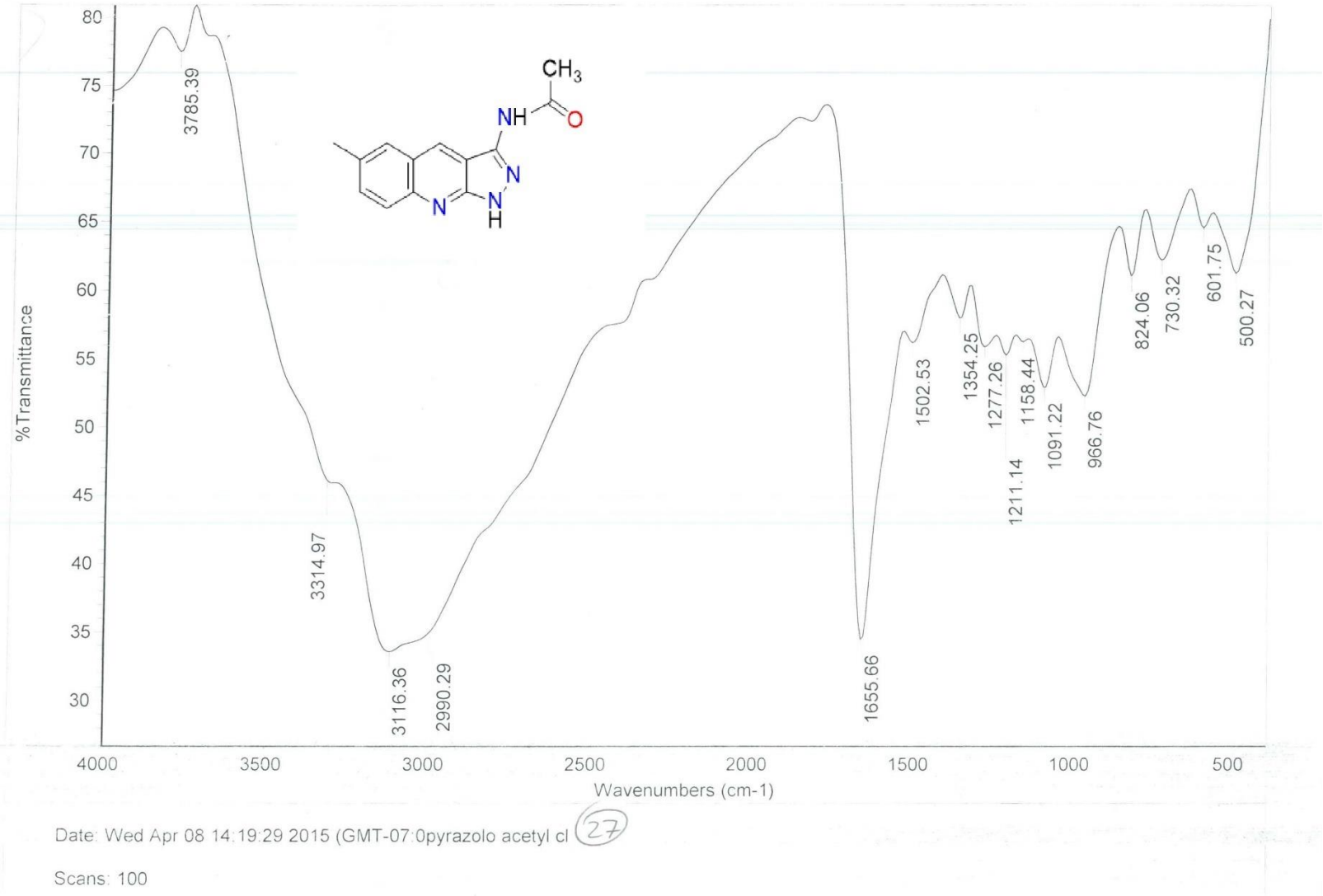
^{13}C NMR spectrum of compound 20



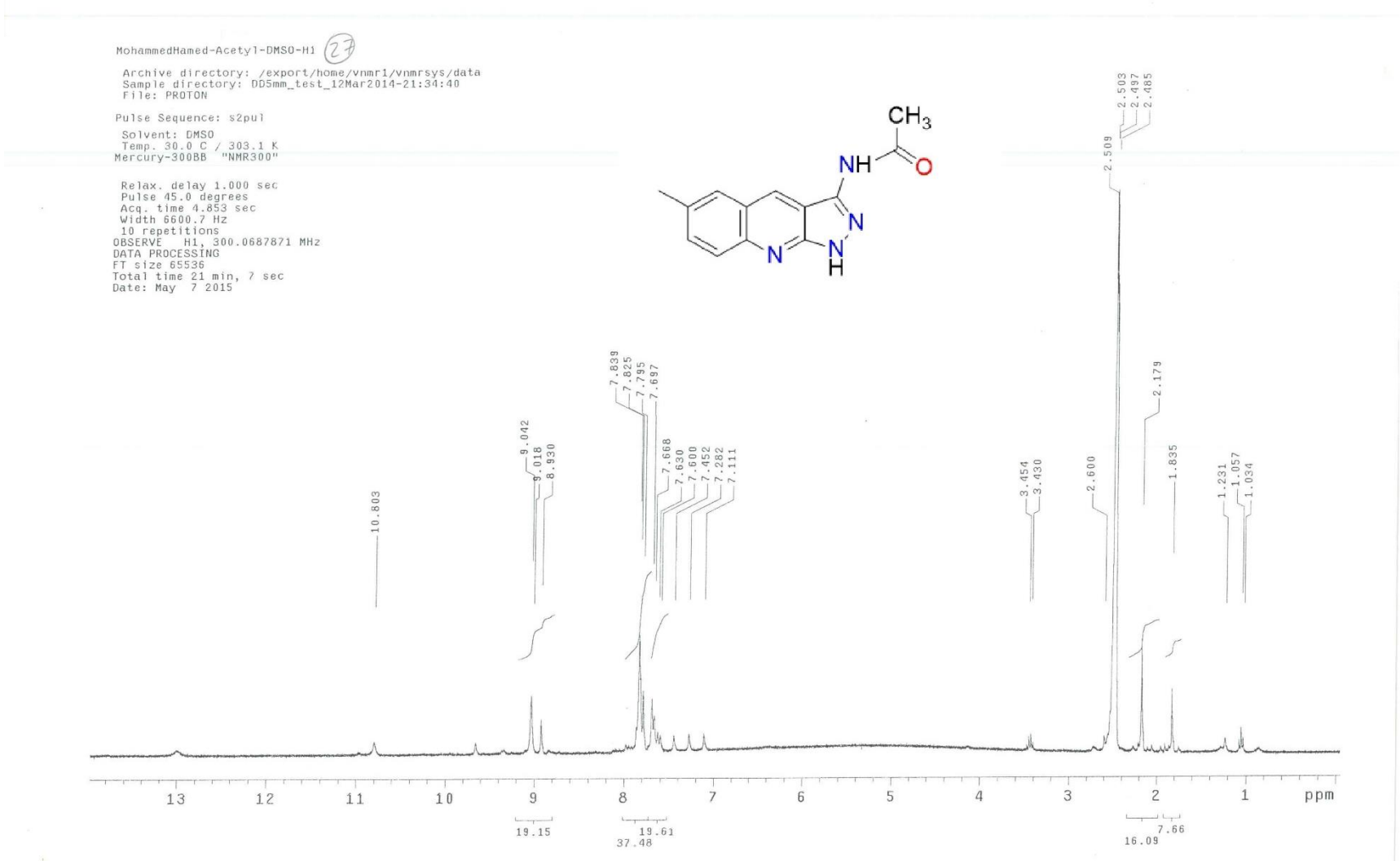
Mass spectrum of compound 20



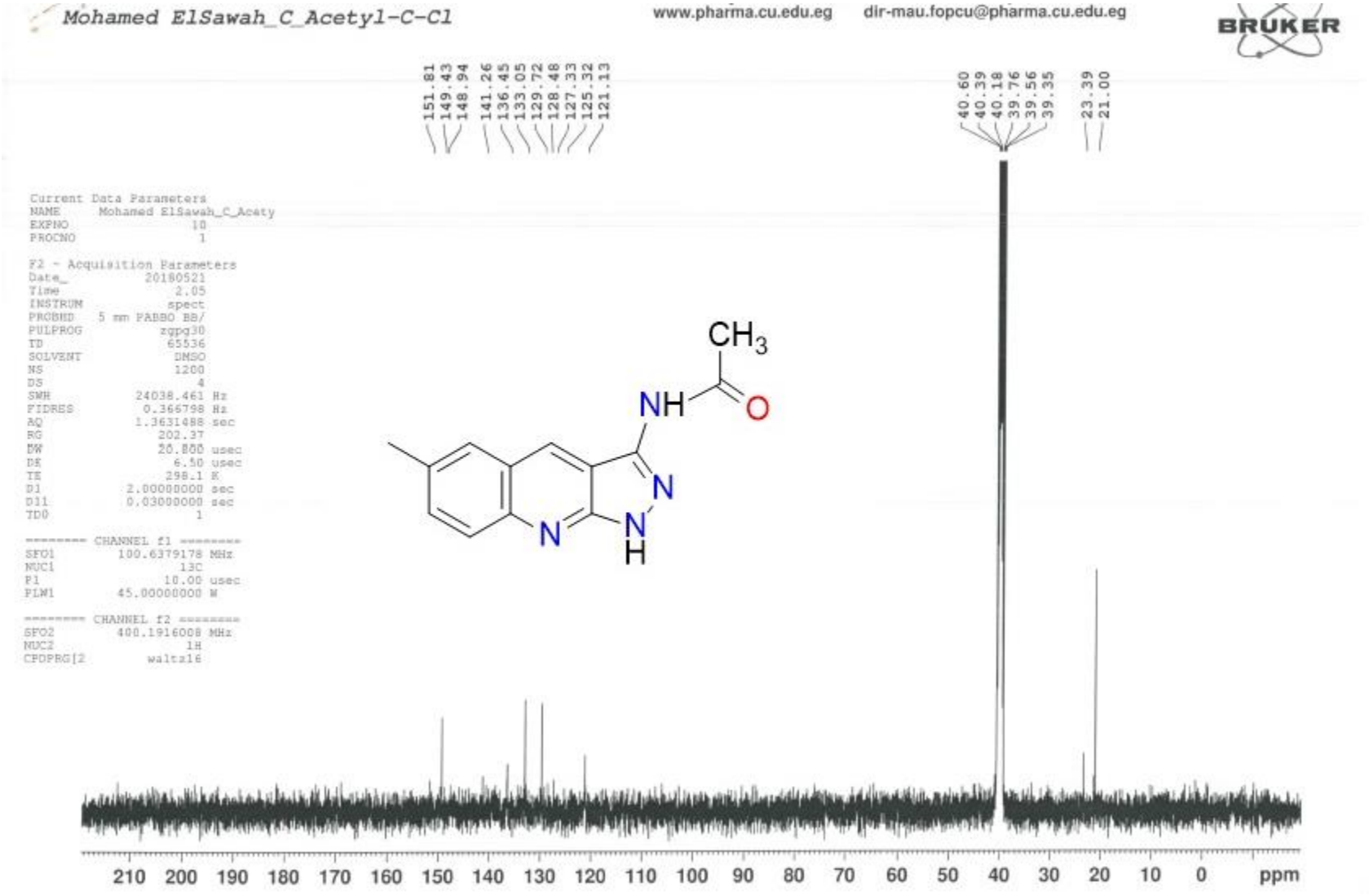
IR spectrum of compound 21



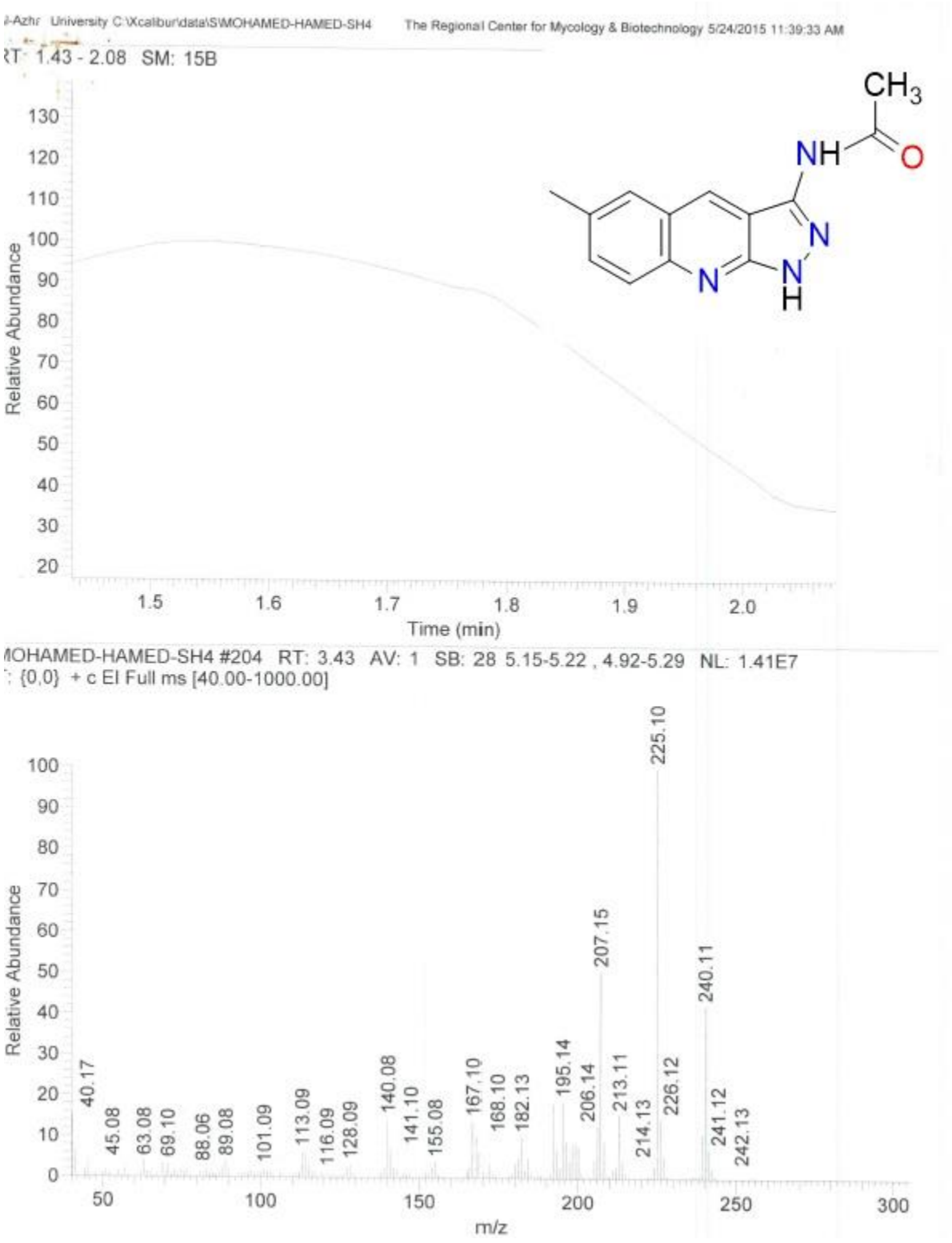
^{1}H NMR spectrum of compound 21



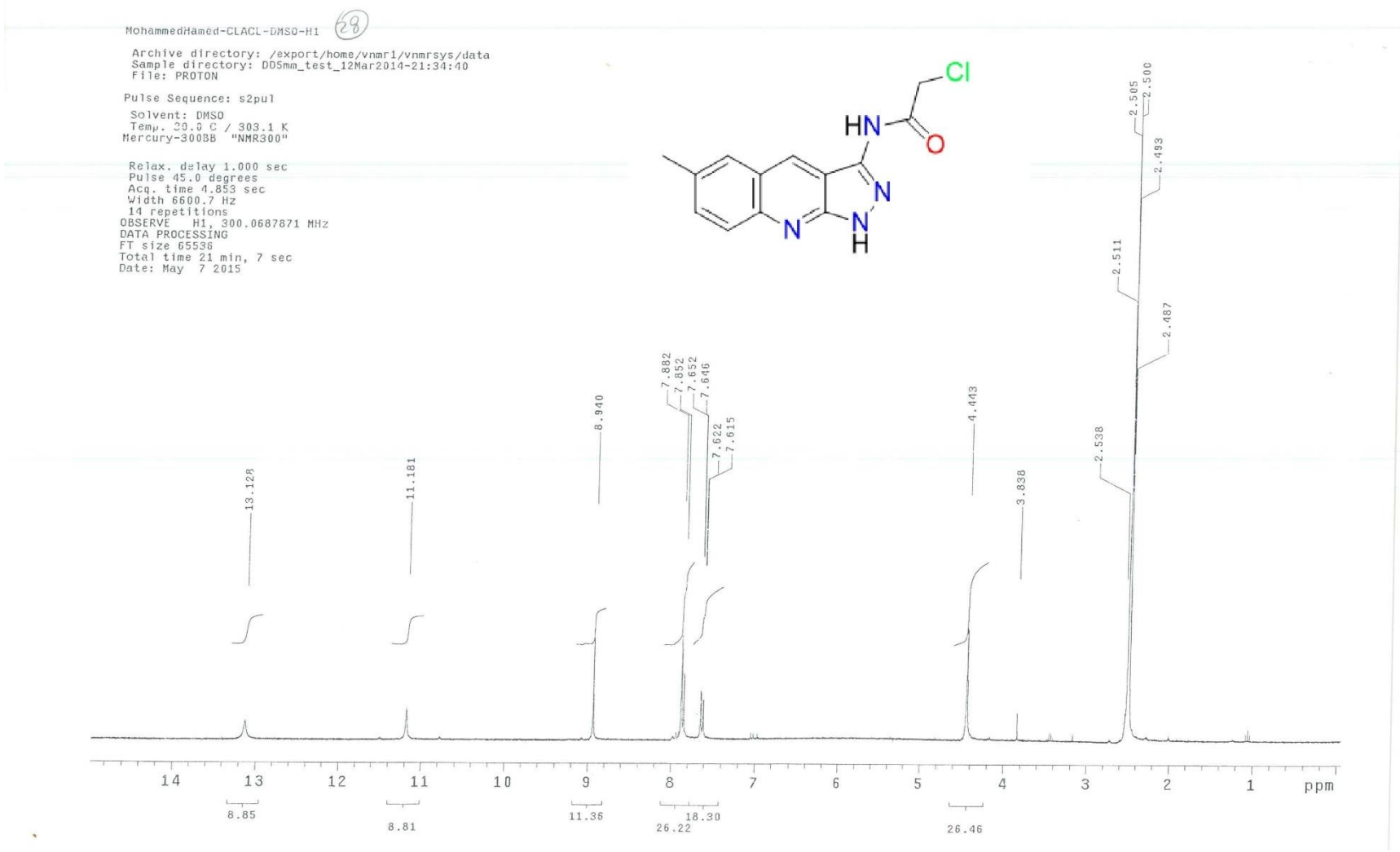
^{13}C NMR spectrum of compound 21



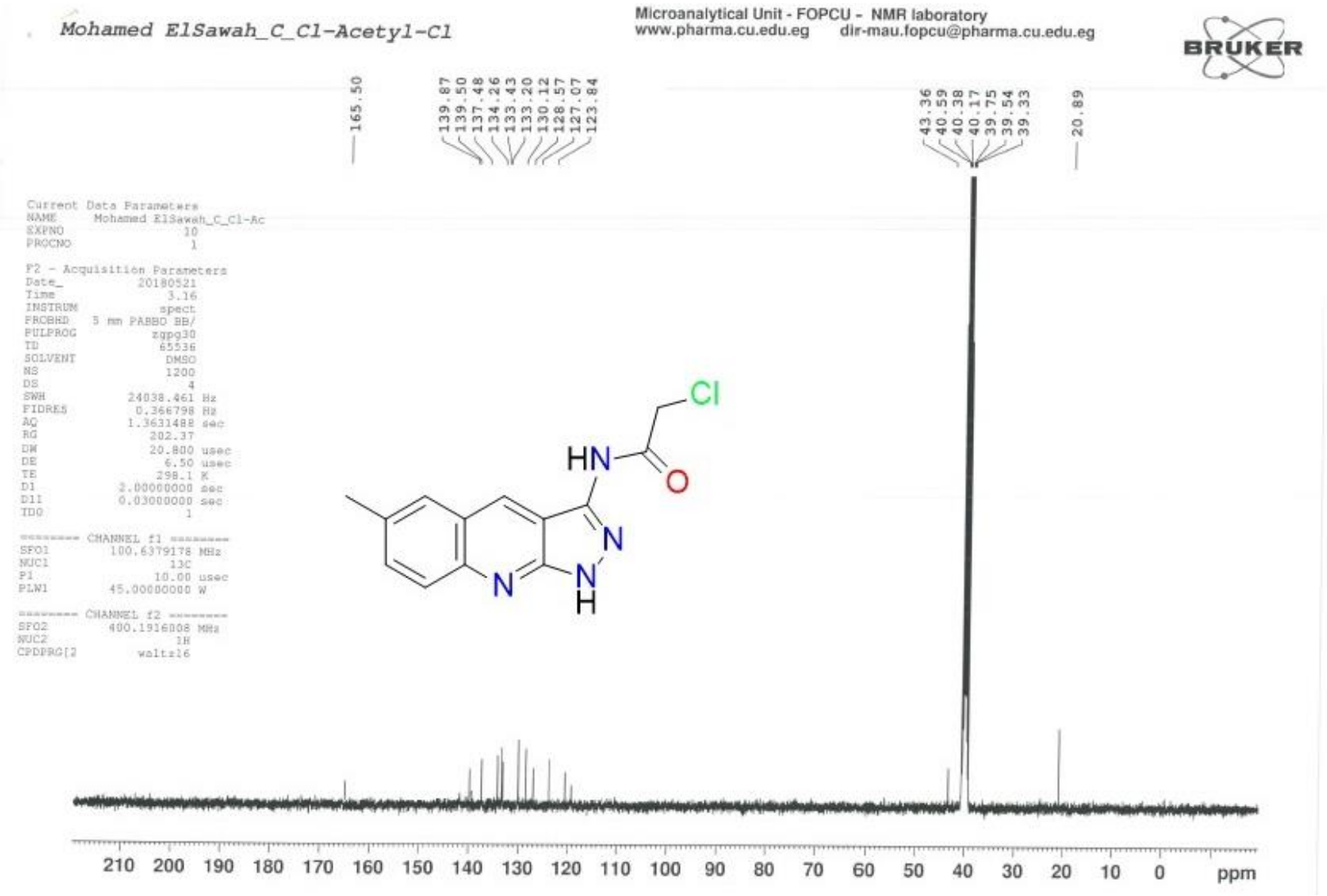
Mass spectrum of compound 21



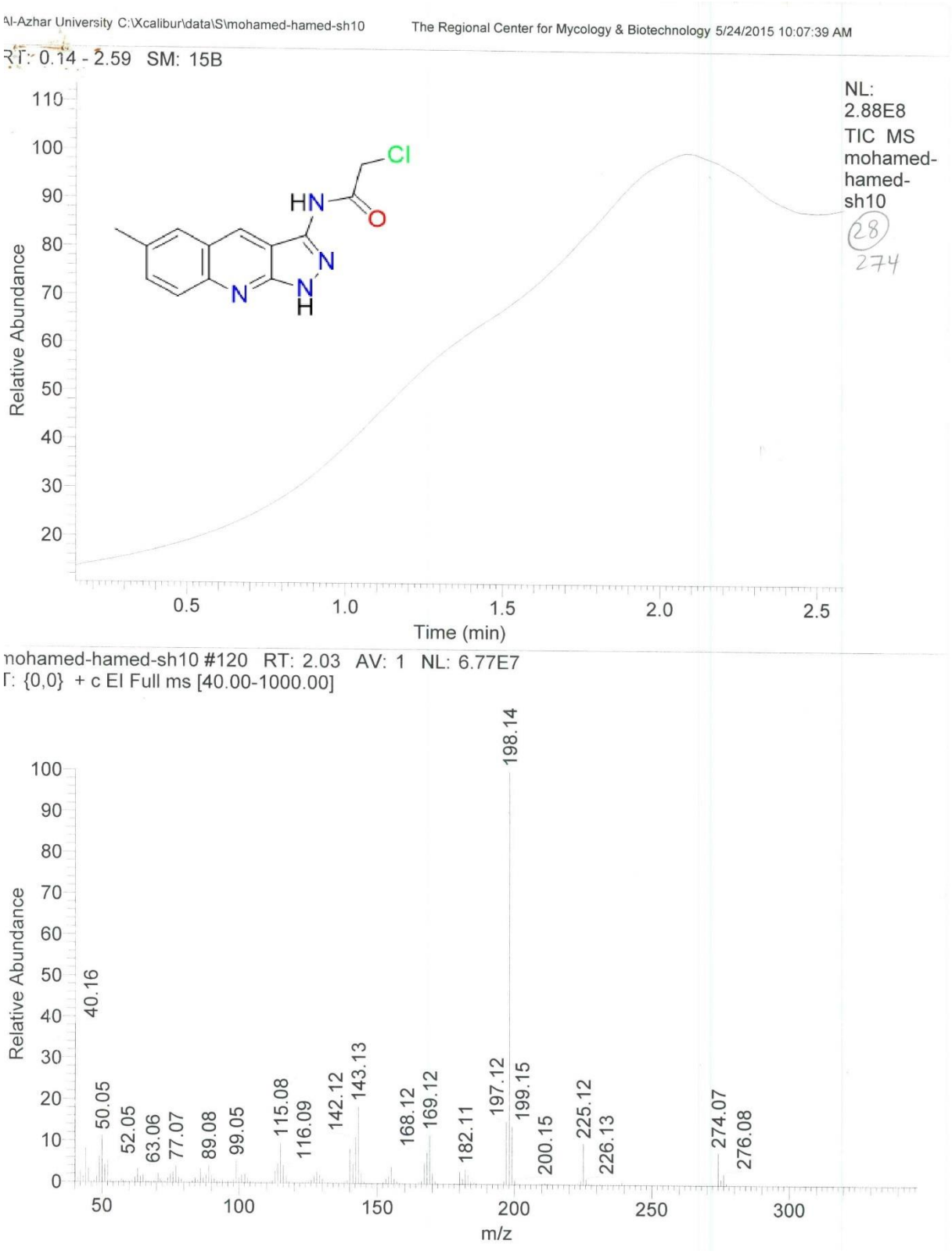
^{1}H NMR spectrum of compound 22



^{13}C NMR spectrum of compound 22



Mass spectrum of compound 22



Elemental analyses data of the new compounds

Al-Azhar University
The Regional Center for Mycology and Biotechnology

Requester Data:

Name: Dr. Mohamed Hamed
Authority: Faculty of Pharmacy,
Al-Azhar University

Sample Data:

Ten samples had been submitted for elemental analysis.

Analysis Report:

Sample Code	C%	H%	N%
SH 1 12a	61.98	4.48	10.53
SH 2 12c	64.12	5.43	9.61
SH 3 14a	70.23	5.09	11.94
SH 4 14b	75.18	5.39	9.34
SH 5 15a	62.21	3.81	11.67
SH 6 15b	69.37	4.98	12.31
SH 7 15c	56.89	3.28	10.69
SH 8 15e	66.34	4.78	11.81
SH 9 15f	60.59	3.70	15.03
SH 10 15g	40.18	2.16	7.52

INVESITIGATOR **DIRECTOR**

Al-Azhar University Campus - Nasr City, Cairo, Egypt.
Tel: 0202 22620373 Fax: 0202 22620373
E.mail: rcmb@azhar.edu.eg
Website: http://www.azhar.edu.eg.htm * http://www.azhar.edu.eg/pages/fungi_center.htm
Facebook: RCMB AZHAR P.O. box mail : 11751 Nasr City Cairo, Egypt.

Al-Azhar University
The Regional Center for Mycology and Biotechnology

Requester Data:

Name: Dr. Mohamed Hamed
Authority: Faculty of Pharmacy,
Al-Azhar University

Sample Data:

Ten samples had been submitted for elemental analysis.

Analysis Report:

Sample Code	C%	H%	N%
SH 11 16	69.94	5.38	11.89
SH 12 18	68.41	5.22	12.13
SH 13 20	64.20	4.13	10.88
SH 14 21	67.28	4.62	15.01
SH 15 13	57.51	4.48	20.74
SH 16 24	69.84	3.75	17.19
SH 17 25	64.89	3.67	20.41
SH 18 26	64.37	4.30	20.36
SH 19 27	65.13	5.18	23.60
SH 20 28	57.08	4.11	20.59

INVESTIGATOR **DIRECTOR**

Al-Azhar University Campus - Nasr City, Cairo, Egypt.
Tel: 0202 22620373 Fax: 0202 22620373
E.mail: rcmb@azhar.edu.eg
Website: http://www.azhar.edu.eg.htm * http://www.azhar.edu.eg/pages/fungi_center.htm
Facebook: RCMB AZHAR P.O. box mail : 11751 Nasr City Cairo, Egypt.

Results of the In vitro antimicrobial evaluation study

THE REGIONAL CENTER FOR MYCOLOGY AND BIOTECHNOLOGY

ANTIMICROBIAL ACTIVITY UNIT

REFERRED FROM: Dr.: MOHAMED HAMED

Mean zone of inhibition in mm ± Standard deviation beyond well diameter (6 mm) produced on a range of environmental and clinically pathogenic microorganisms using (1mg/ml) concentration of tested samples. Results are depicted in the following table:

Sample / Tested microorganisms	SH26	SH27	SH29	SH32	SH31	St.
FUNGI						*Amphotericin B*
Aspergillus fumigatus (RCMB 02568)	NA	24.2 ± 0.58	20.3± 1.2	21.3 ± 1.5	23.2± 0.58	23.7± 0.63
Syncephalastrum racemosum (RCMB 05922)	NA	22.3 ± 1.2	19.3± 0.63	20.4 ± 0.72	21.4 ± 1.5	19.7± 0.72
Geotricum candidum (RCMB 05097)	NA	27.3± 0.58	22.4± 2.1	23.2± 0.58	24.6± 0.44	28.7± 0.58
Candida albicans (RCMB 05036)	NA	NA	NA	NA	NA	25.4± 0.63
Gram Positive Bacteria:						*Ampicillin*
Streptococcus pneumoniae (RCMB 010010)	16.3± 1.2	26.8± 1.63	21.3 ± 0.63	20.6 ± 2.1	24.3 ± 2.1	23.8± 0.2
Bacillis subtilis (RCMB 010067)	18.2± 2.1	28.1± 0.58	23.6 ± 2.1	22.4 ± 1.5	26.2 ± 0.58	32.4± 0.58
Gram negativeBacteria:						*Gentamicin*
Pseudomonas aeruginosa (RCMB 010043)	NA	NA	NA	NA	NA	17.3± 0.63
Escherichia coli (RCMB 010059)	15.4± 0.72	22.3 ±1.5	20.3± 1.6	18.3± 0.58	18.6± 0.72	21.3± 0.58

- The test was done using the diffusion agar technique, Well diameter: 6.0 mm …… …… (100 µl was tested), RCMB: Regional Center for Mycology and Biotechnology Antimicrobial unit test organisms *NA: No activity, data are expressed in the form of mean ± SD.

Some of your antimicrobial results are promising, so determination of the Minimum Inhibitory Concentration (MIC) for the tested sample(s) is recommended.

Investigators

Dr. MARWA MOSTAFA

DIRECTOR

Prof. Dr. H.H. Elsheikh

Postal address:p.o.box:8104- Nasr City 11371 Cairo- Egypt Tel: 01114313001 E – mail: marwa2rcmb@ Yahoo.com

THE REGIONAL CENTER FOR MYCOLOGY AND BIOTECHNOLOGY

ANTIMICROBIAL ACTIVITY UNIT

REFERRED FROM: Dr.: MOHAMED HAMED

Mean zone of inhibition in mm ± Standard deviation beyond well diameter (6 mm) produced on a range of environmental and clinically pathogenic microorganisms using (1mg/ml) concentration of tested samples. Results are depicted in the following table:

Sample / Tested microorganisms	SH1 (26)	SH2 (24)	SH3 (25)	SH4 (14a)	SH5 (14b)	St.
FUNGI						*Amphotericin B*
Aspergillus fumigatus (RCMB 02568)	14.6 ± 1.5	16.3± 1.2	16.9± 0.63	20.3± 2.1	13.2± 0.58	23.7± 0.63
Syncephalastrum racemosum (RCMB 05922)	13.4± 0.44	14.2 ± 0.58	15.2 ± 1.2	19.2± 0.72	11.3± 1.2	19.7± 0.72
Geotricum candidum (RCMB 05097)	15.4± 1.2	15.9 ± 2.1	16.3 ± 0.42	22.3± 1.5	14.1± 0.63	28.7± 0.58
Candida albicans (RCMB 05036)	NA	NA	NA	NA	NA	25.4± 0.63
Gram Positive Bacteria:						*Ampicillin*
Streptococcus pneumoniae (RCMB 010010)	16.3± 1.5	16.8 ± 0.58	17.1± 1.5	21.3 ± 0.63	14.3± 2.1	23.8± 0.2
Bacillis subtilis (RCMB 010067)	18.1± 0.58	19.1± 0.63	19.6± 0.63	22.4±0.58	16.1± 0.58	32.4± 0.58
Gram negativeBacteria:						*Gentamicin*
Pseudomonas aeruginosa (RCMB 010043)	NA	NA	NA	NA	NA	17.3± 0.63
Escherichia coli (RCMB 010059)	14.8 ± 2.1	15.6 ± 0.63	16.3± 0.72	20.6 ±1.2	12.4 ± 1.5	21.3± 0.58

♦ The test was done using the diffusion agar technique, Well diameter: 6.0 mm …… …… (100 µl was tested), RCMB: Regional Center for Mycology and Biotechnology Antimicrobial unit test organisms *NA: No activity, data are expressed in the form of mean ± SD.

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Postal address:p.o.box:8104- Nasr City 11371 Cairo- Egypt Tel: 01114313001 E – mail: marwa2rcmb@ Yahoo.com

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Sample / Tested microorganisms	SH6 (12c)	SH7 (16)	SH8 (12b)	SH9 (15e)	SH10 (28)	St.
FUNGI						*Amphotericin B*
Aspergillus fumigatus (RCMB 02568)	17.3± 2.1	NA	NA	NA	22.3 ± 1.2	23.7± 0.63
Syncephalastrum racemosum (RCMB 05922)	16.4 ± 0.58	NA	NA	NA	20.7 ± 0.58	19.7± 0.72
Geotricum candidum (RCMB 05097)	19.1 ± 1.5	NA	NA	NA	25.2 ± 0.63	28.7± 0.58
Candida albicans (RCMB 05036)	NA	NA	NA	NA	NA	25.4± 0.63
Gram Positive Bacteria:						*Ampicillin*
Streptococcus pneumoniae (RCMB 010010)	18.3± 0.63	13.6± 1.2	15.7 ± 2.1	17.1± 0.44	22.8± 2.1	23.8± 0.2
Bacillis subtilis (RCMB 010067)	20.4± 0.63	15.2± 1.5	16.1 ± 0.58	17.9± 0.63	26.8± 0.58	32.4± 0.58
Gram negativeBacteria:						*Gentamicin*
Pseudomonas aeruginosa (RCMB 010043)	NA	NA	NA	NA	NA	17.3± 0.63
Escherichia coli (RCMB 010059)	17.5± 2.1	12.4± 0.58	15.2± 0.63	16.7 ±2.1	23.4 ±0.63	21.3± 0.58

♦ The test was done using the diffusion agar technique, Well diameter: 6.0 mm …… …… (100 µl was tested), RCMB: Regional Center for Mycology and Biotechnology Antimicrobial unit test organisms *NA: No activity, data are expressed in the form of mean ± SD.

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REFERRED FROM: Dr.: MOHAMED HAMED

Mean zone of inhibition in mm ± Standard deviation beyond well diameter (6 mm) produced on a range of environmental and clinically pathogenic microorganisms using (1mg/ml) concentration of tested samples. Results are depicted in the following table:

Sample / Tested microorganisms	SH16 (15f)	SH17 (12a)	SH18 (13)	SH19 (20)	SH20	St.
FUNGI						*Amphotericin B*
Aspergillus fumigatus (RCMB 02568)	18.3± 1.2	19.3 ± 0.63	19.5± 1.2	19.8± 1.2	21.3± 1.2	23.7± 0.63
Syncephalastrum racemosum (RCMB 05922)	19.3 ± 0.58	19.9 ± 2.1	20.1± 0.63	20.5 ± 0.25	20.4 ± 0.58	19.7± 0.72
Geotricum candidum (RCMB 05097)	20.4 ± 2.1	20.6 ± 0.58	21.3± 2.1	21.4 ± 2.1	21.9± 0.58	28.7± 0.58
Candida albicans (RCMB 05036)	NA	NA	NA	NA	NA	25.4± 0.63
Gram Positive Bacteria:						*Ampicillin*
Streptococcus pneumoniae (RCMB 010010)	19.3± 0.58	20.3 ± 0.58	20.7 ± 0.72	21.3 ± 0.44	22.4 ± 0.63	23.8± 0.2
Bacillis subtilis (RCMB 010067)	21.2± 0.72	21.4 ± 1.2	21.8± 0.63	22.1± 0.63	23.8± 0.63	32.4± 0.58
Gram negativeBacteria:						*Gentamicin*
Pseudomonas aeruginosa (RCMB 010043)	NA	NA	NA	NA	NA	17.3± 0.63
Escherichia coli (RCMB 010059)	18.3 ± 0.63	20.3 ± 0.58	20.9 ± 0.58	21.2 ± 0.58	18.9± 0.72	21.3± 0.58

- The test was done using the diffusion agar technique, Well diameter: 6.0 mm …… …… (100 µl was tested), RCMB: Regional Center for Mycology and Biotechnology Antimicrobial unit test organisms *NA: No activity, data are expressed in the form of mean ± SD.

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Postal address:p.o.box:8104- Nasr City 11371 Cairo- Egypt Tel: 01114313001 E – mail: marwa2rcmb@ Yahoo.com

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ANTIMICROBIAL ACTIVITY UNIT

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Mean zone of inhibition in mm ± Standard deviation beyond well diameter (6 mm) produced on a range of environmental and clinically pathogenic microorganisms using (1mg/ml) concentration of tested samples. Results are depicted in the following table:

Sample / Tested microorganisms	SH11 (15a)	SH12 (15b)	SH13 (15c)	SH14 (15d)	SH15 (15g)	St.
FUNGI						*Amphotericin B*
Aspergillus fumigatus (RCMB 02568)	19.3 ± 2.1	17.3± 1.2	NA	20.1 ± 1.2	NA	23.7± 0.63
Syncephalastrum racemosum (RCMB 05922)	17.2 ± 0.25	16.2± 0.44	NA	18.3± 0.58	NA	19.7± 0.72
Geotricum candidum (RCMB 05097)	19.9 ± 1.5	18.3± 2.1	NA	20.1 ± 2.1	NA	28.7± 0.58
Candida albicans (RCMB 05036)	NA	NA	NA	NA	NA	25.4± 0.63
Gram Positive Bacteria:						*Ampicillin*
Streptococcus pneumoniae (RCMB 010010)	17.4 ± 0.58	18.1± 0.72	NA	19.3 ± 0.58	NA	23.8± 0.2
Bacillis subtilis (RCMB 010067)	19.1± 0.63	20.2± 0.58	NA	20.8±0.67	NA	32.4± 0.58
Gram negativeBacteria:						*Gentamicin*
Pseudomonas aeruginosa (RCMB 010043)	NA	NA	NA	NA	NA	17.3± 0.63
Escherichia coli (RCMB 010059)	15.2 ± 0.58	16.6 ± 0.72	NA	19.2 ±0.63	NA	21.3± 0.58

- The test was done using the diffusion agar technique, Well diameter: 6.0 mm .... (100 µl was tested), RCMB: Regional Center for Mycology and Biotechnology Antimicrobial unit test organisms *NA: No activity, data are expressed in the form of mean ± SD.

Some of your antimicrobial results are promising, so determination of the Minimum Inhibitory Concentration (MIC) for the tested sample(s) is recommended.

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