

Supporting Information Part - II

Conformationally-constrained Indeno[2,1-c]quinolines - A New Class of Anti-mycobacterial agents**

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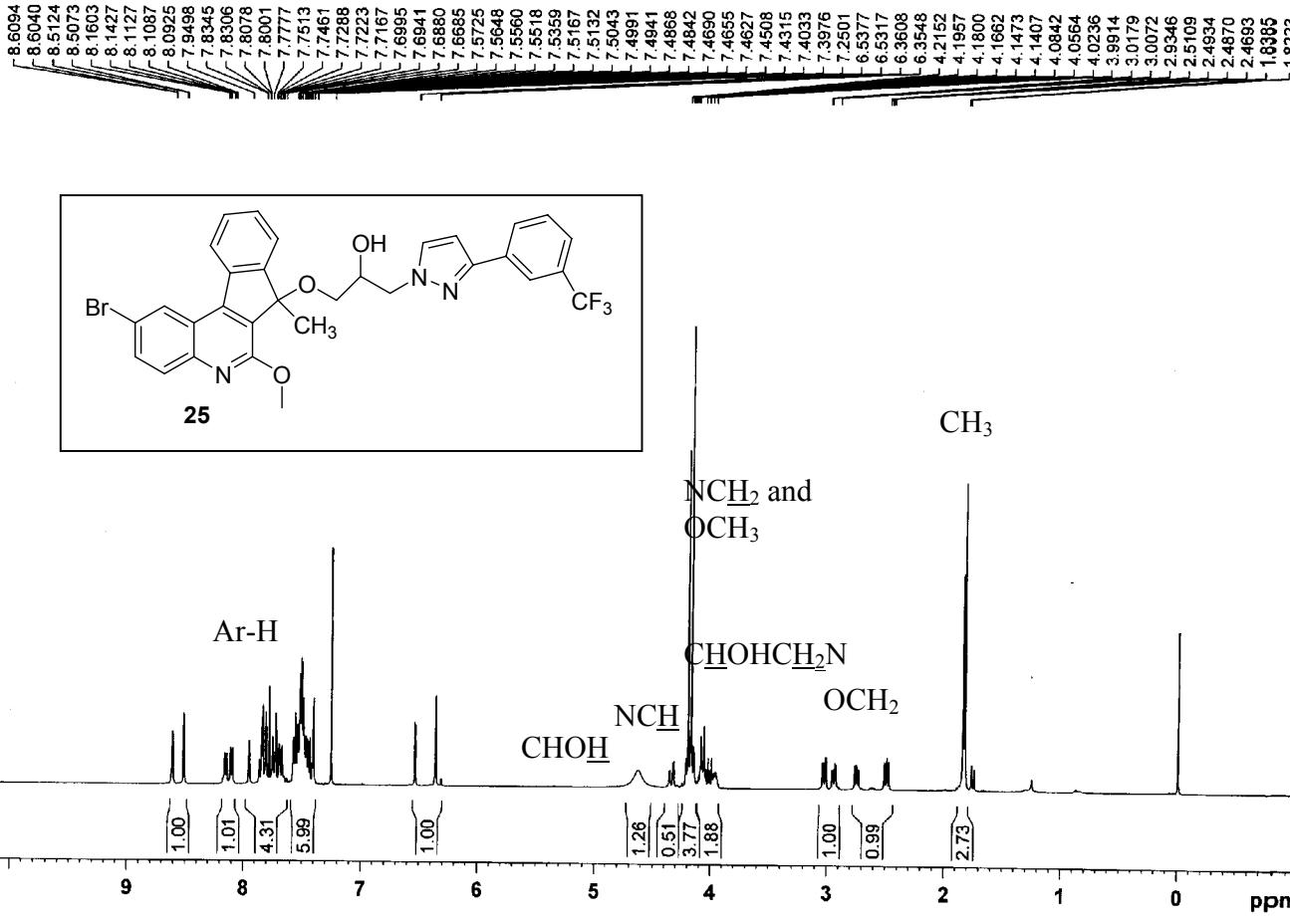
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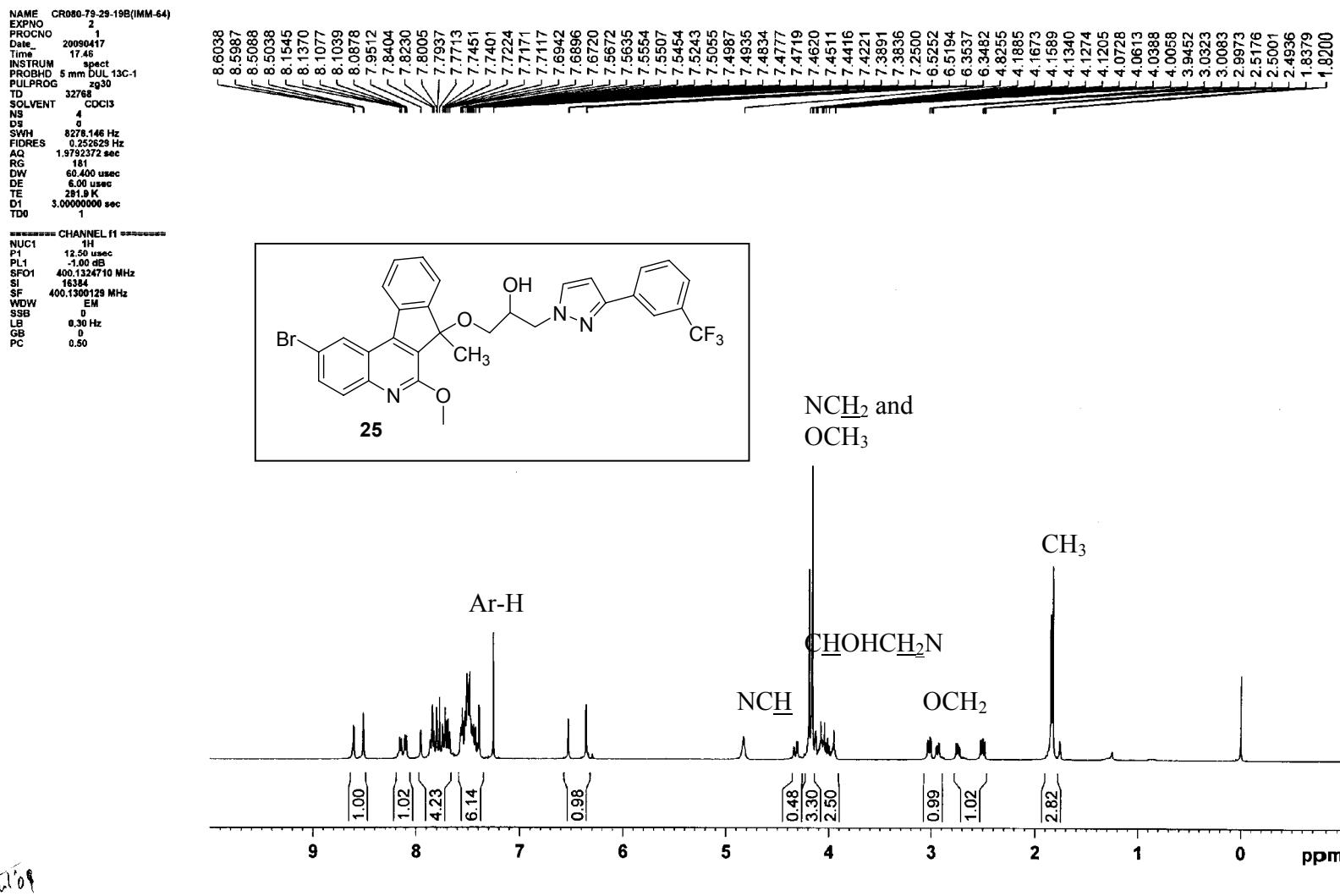
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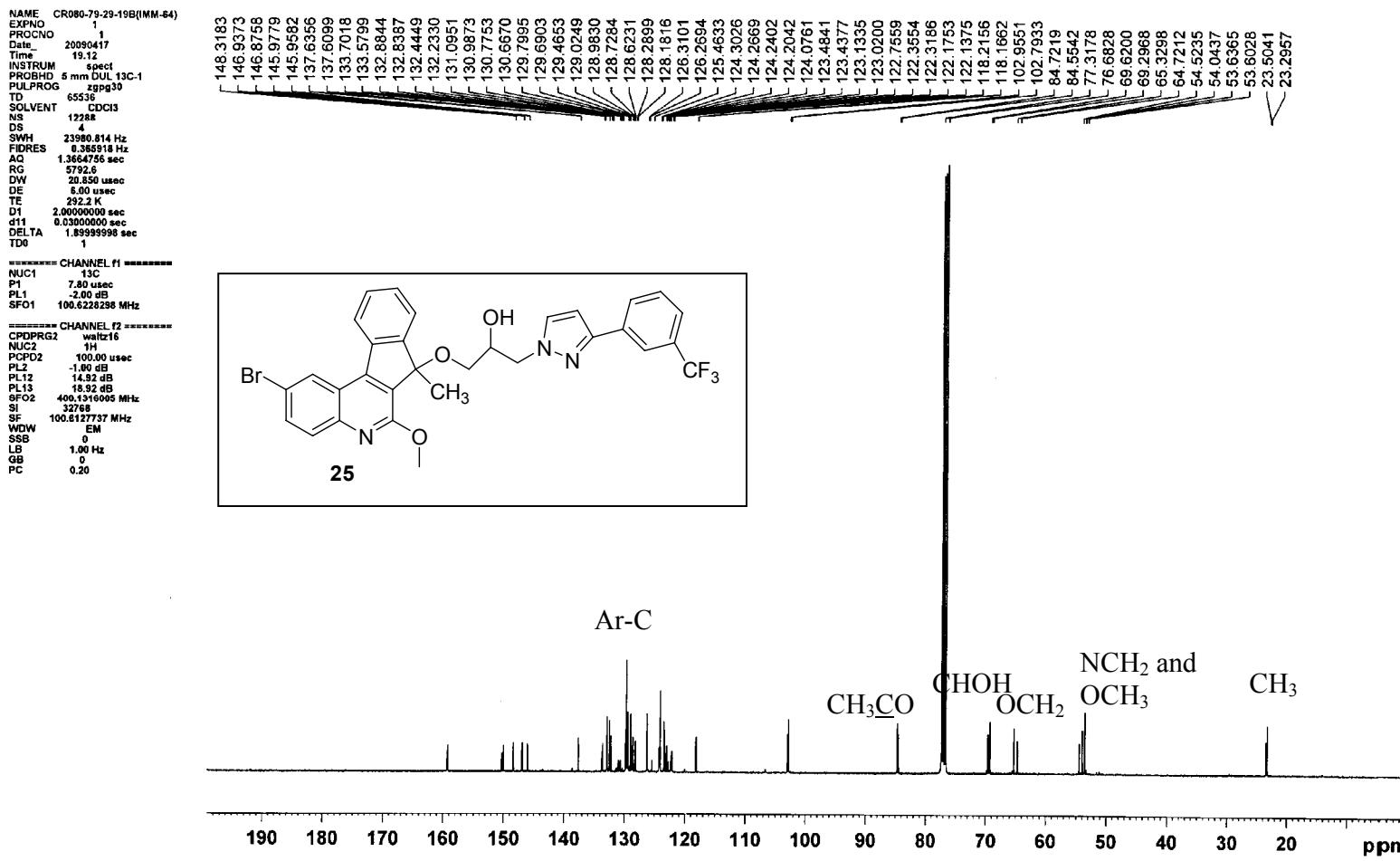
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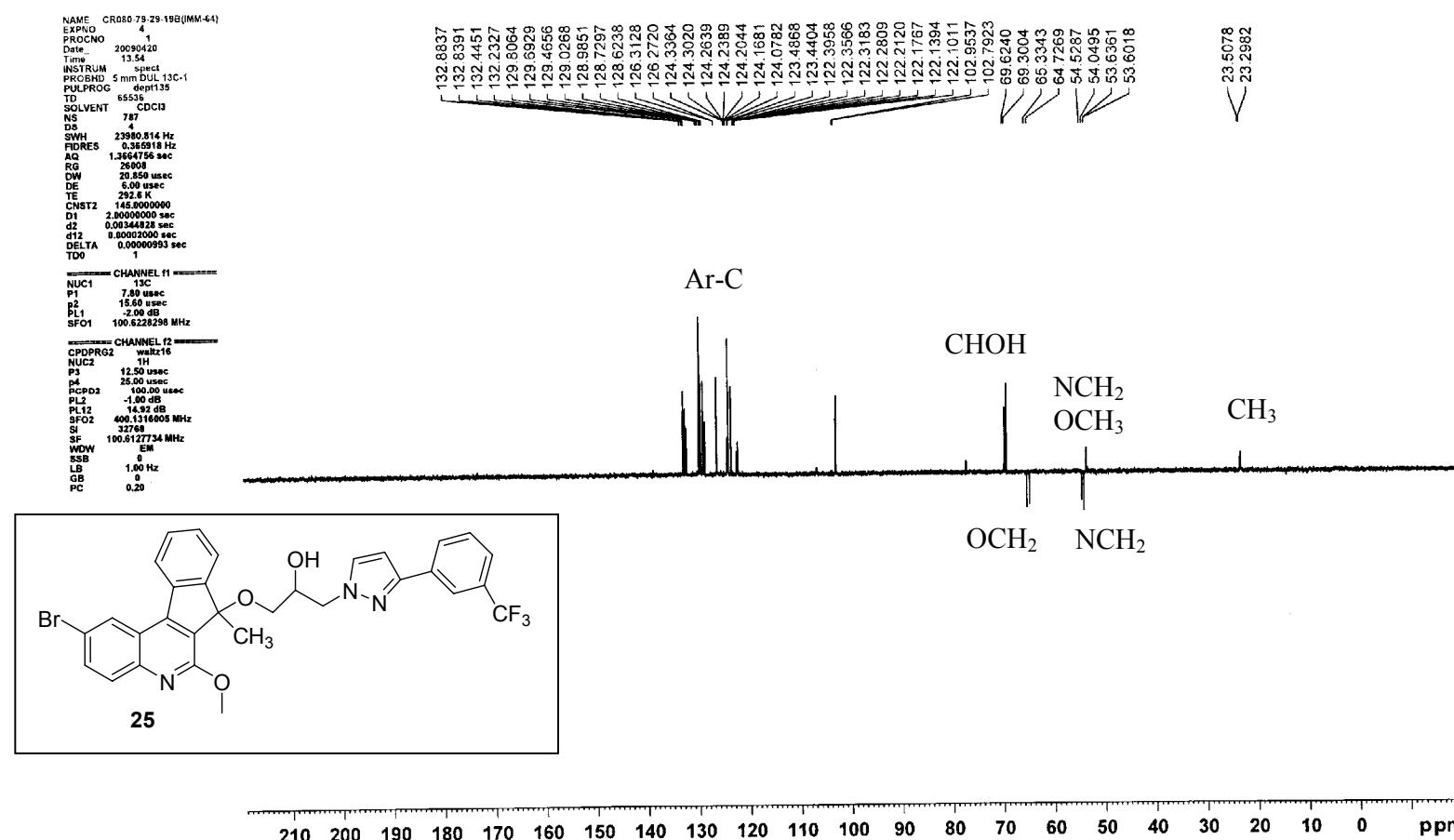
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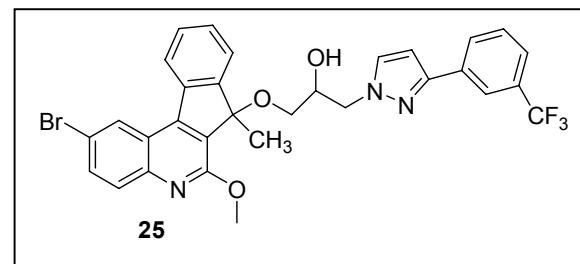
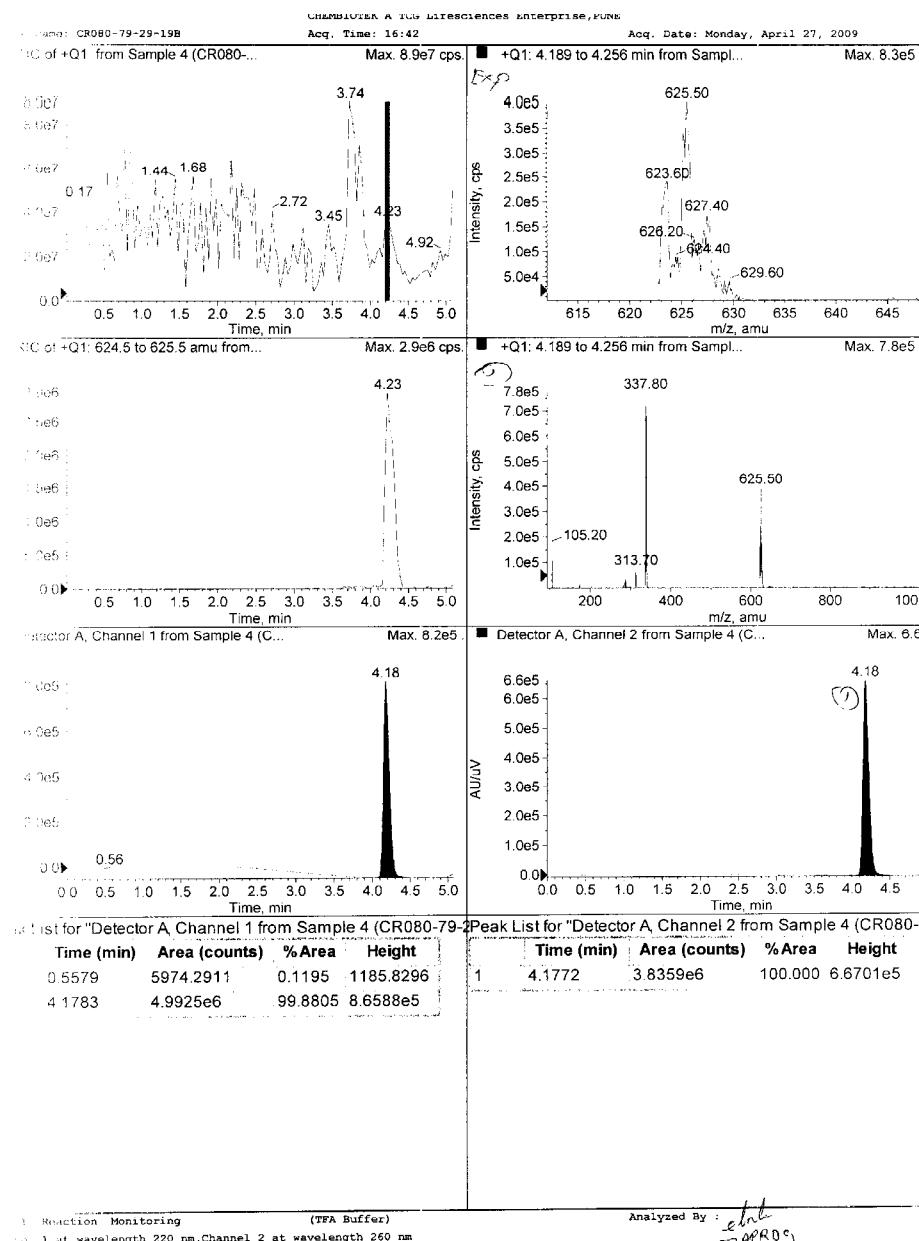


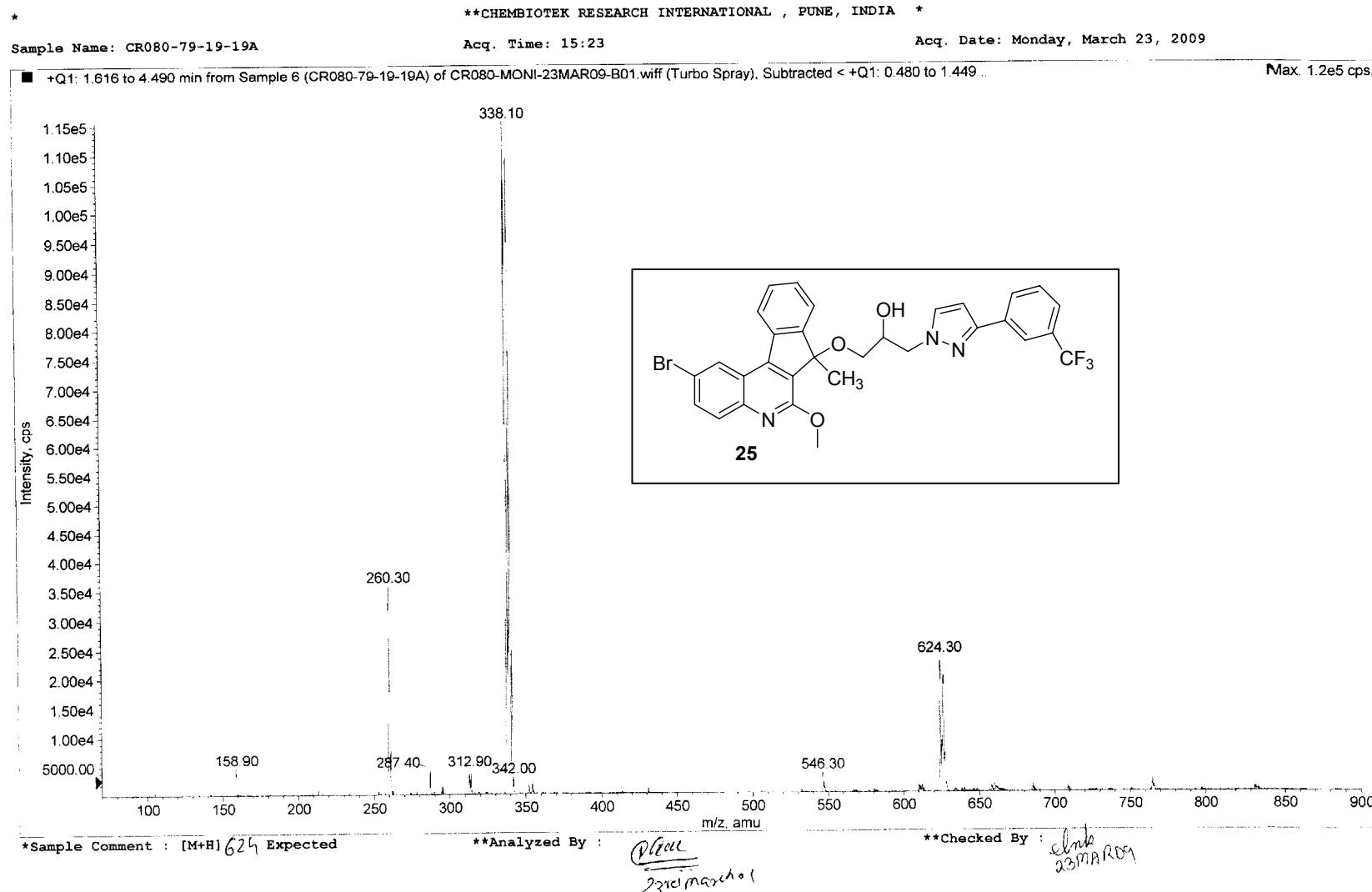






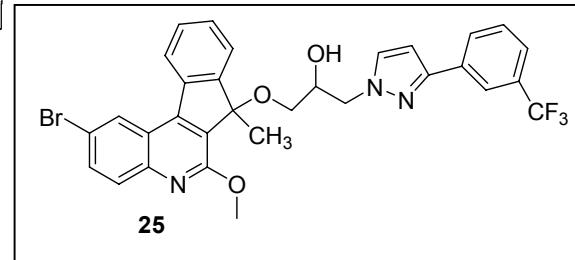
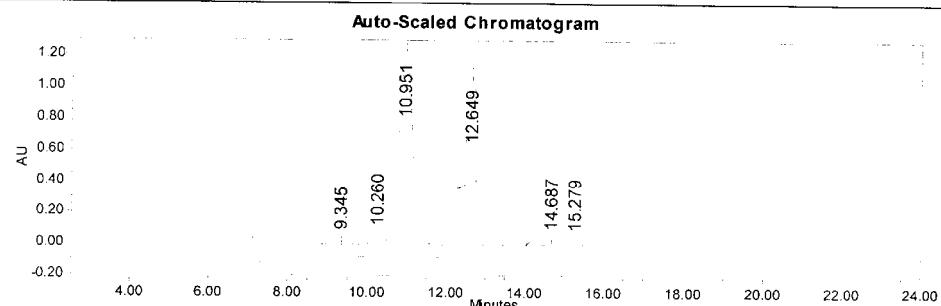
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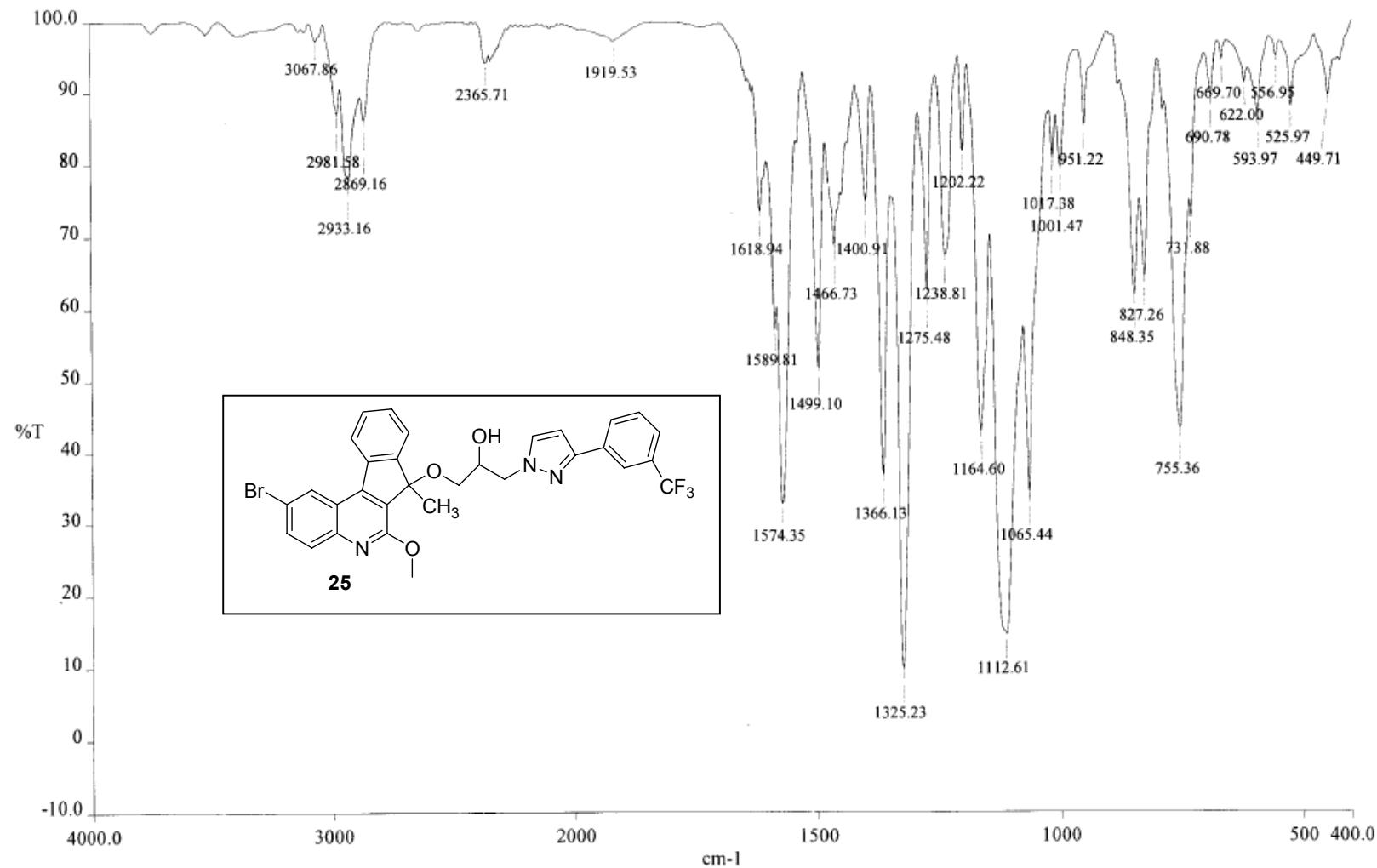
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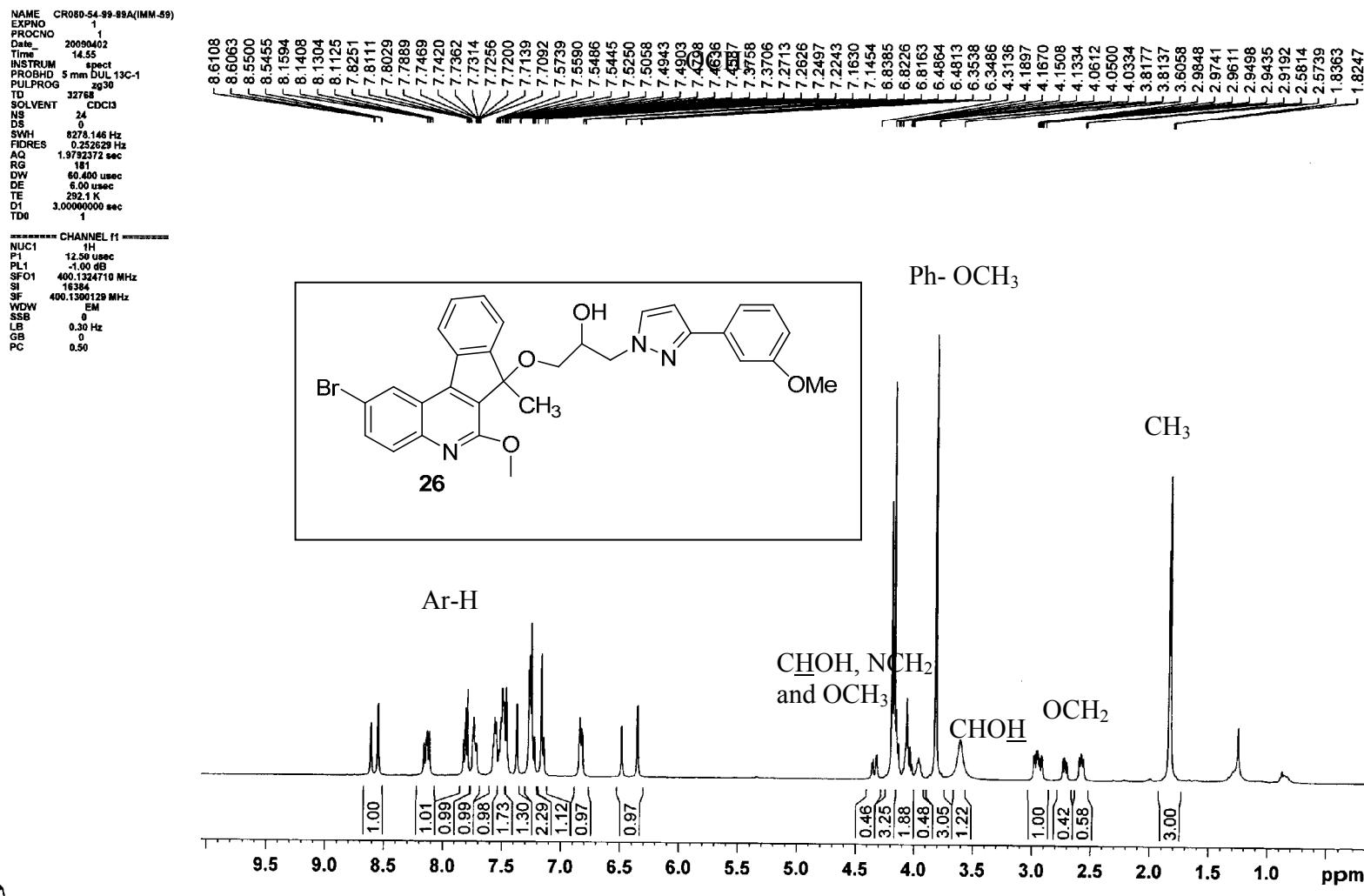
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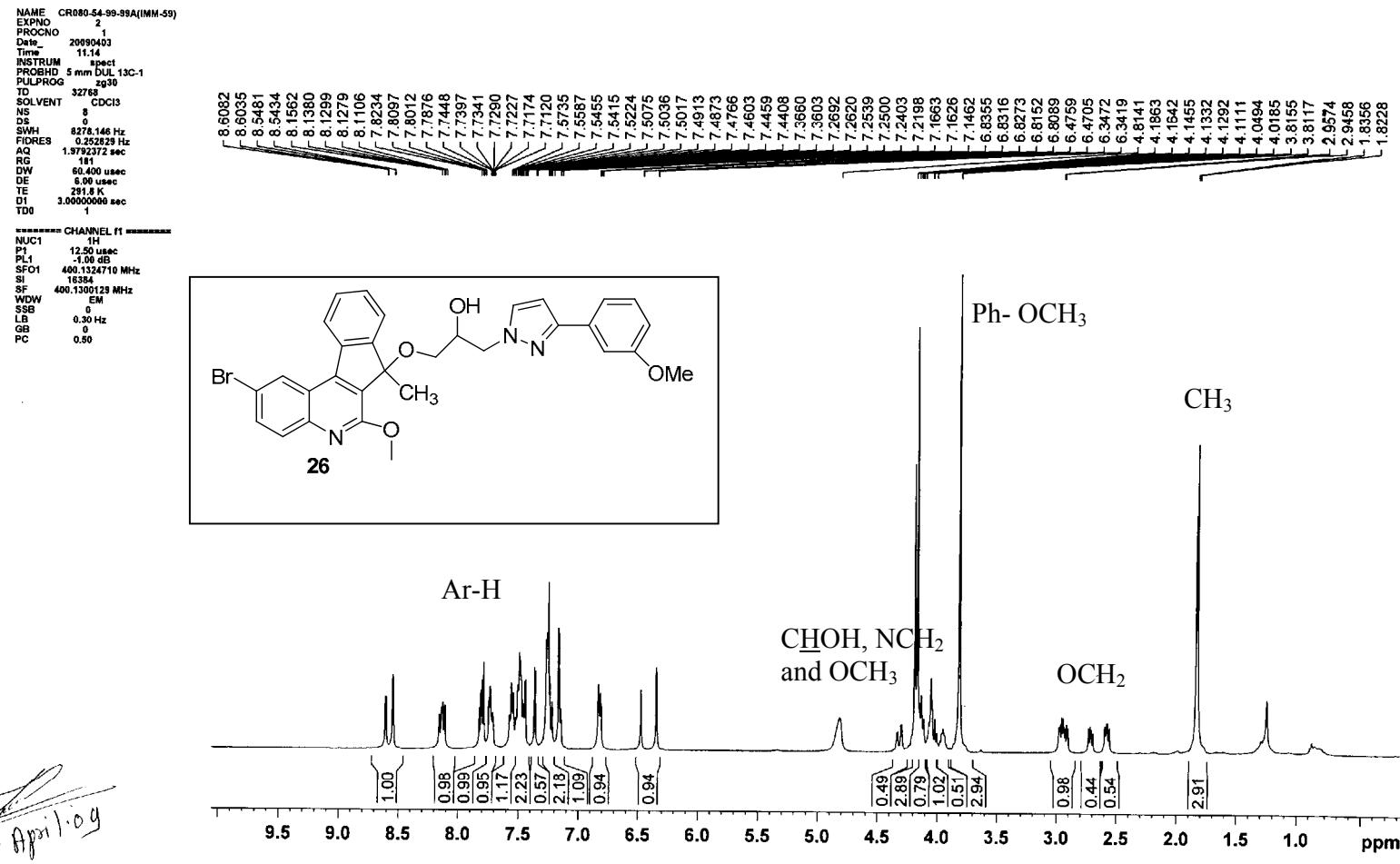
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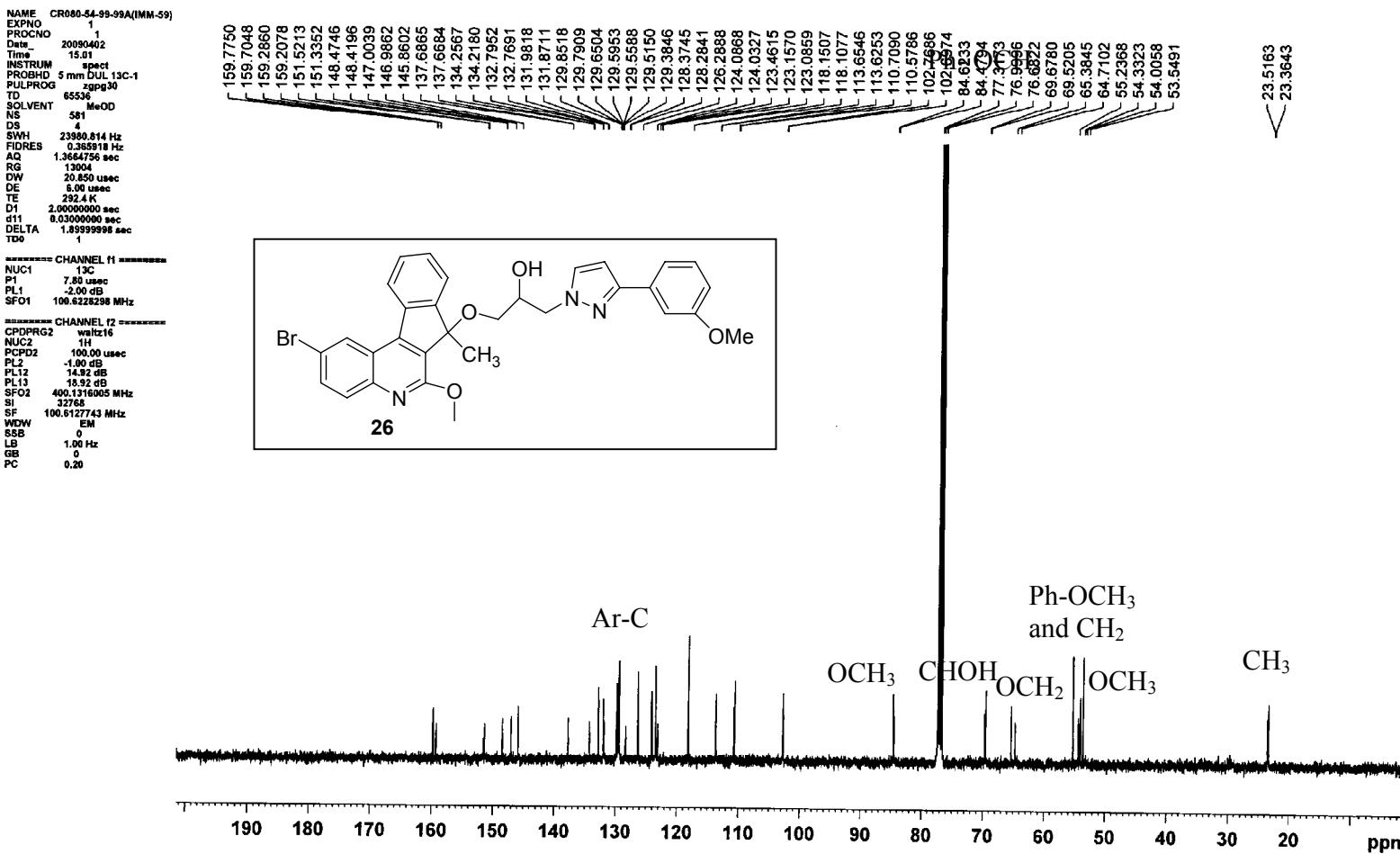
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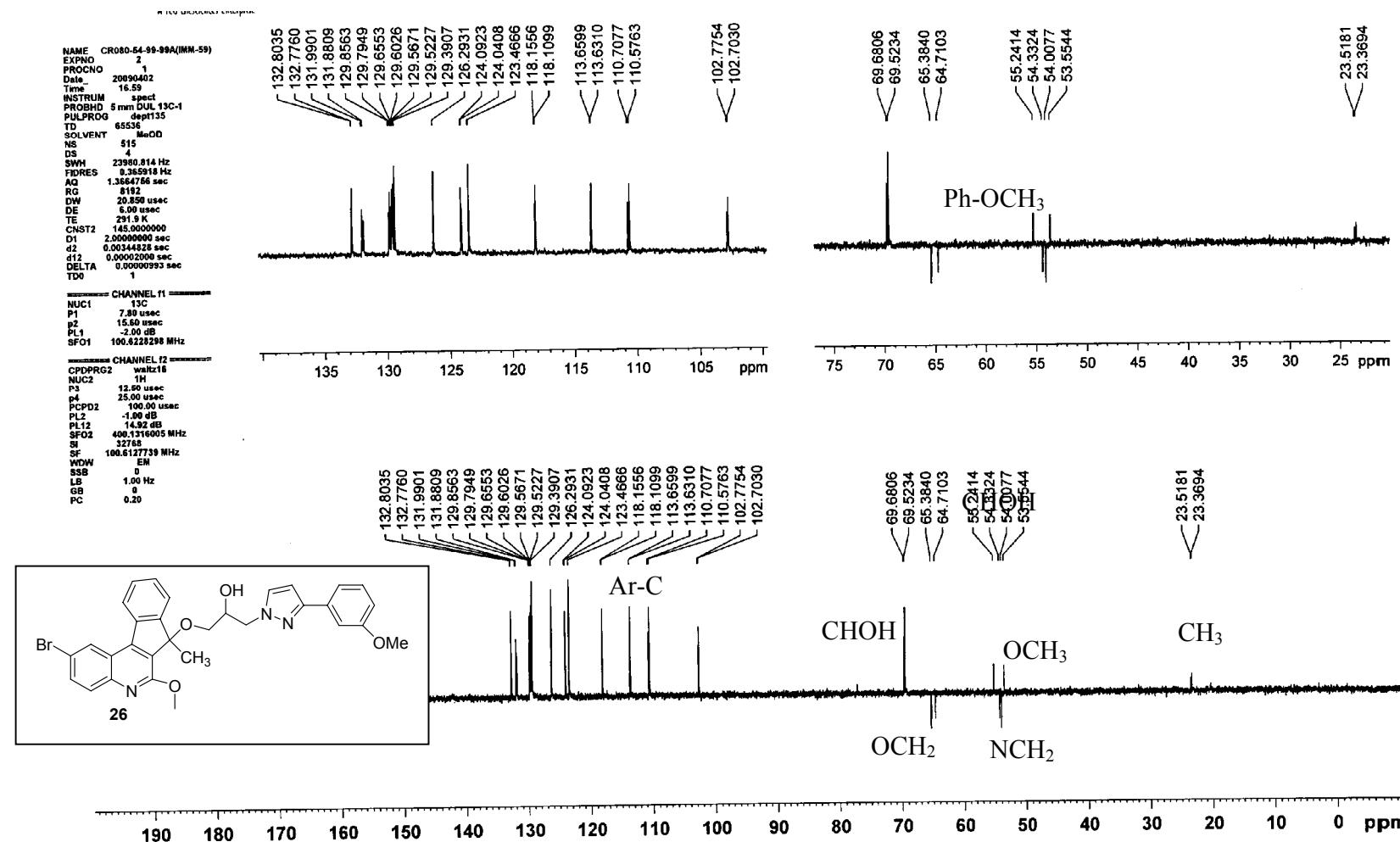
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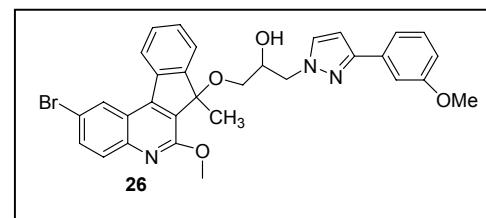
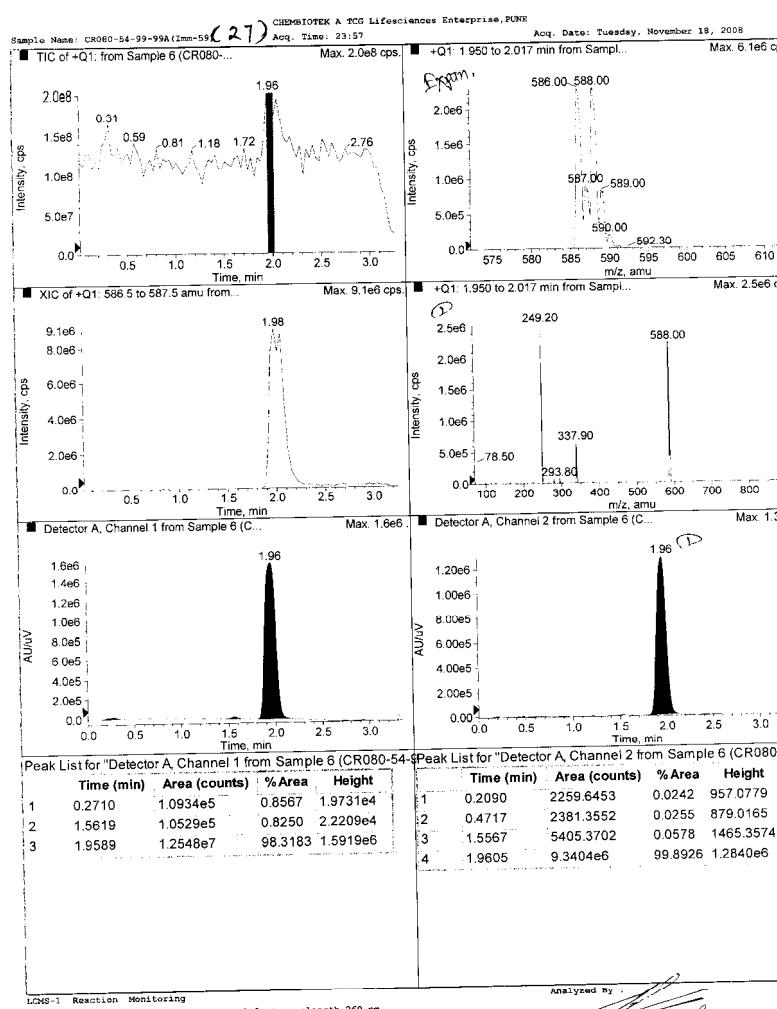


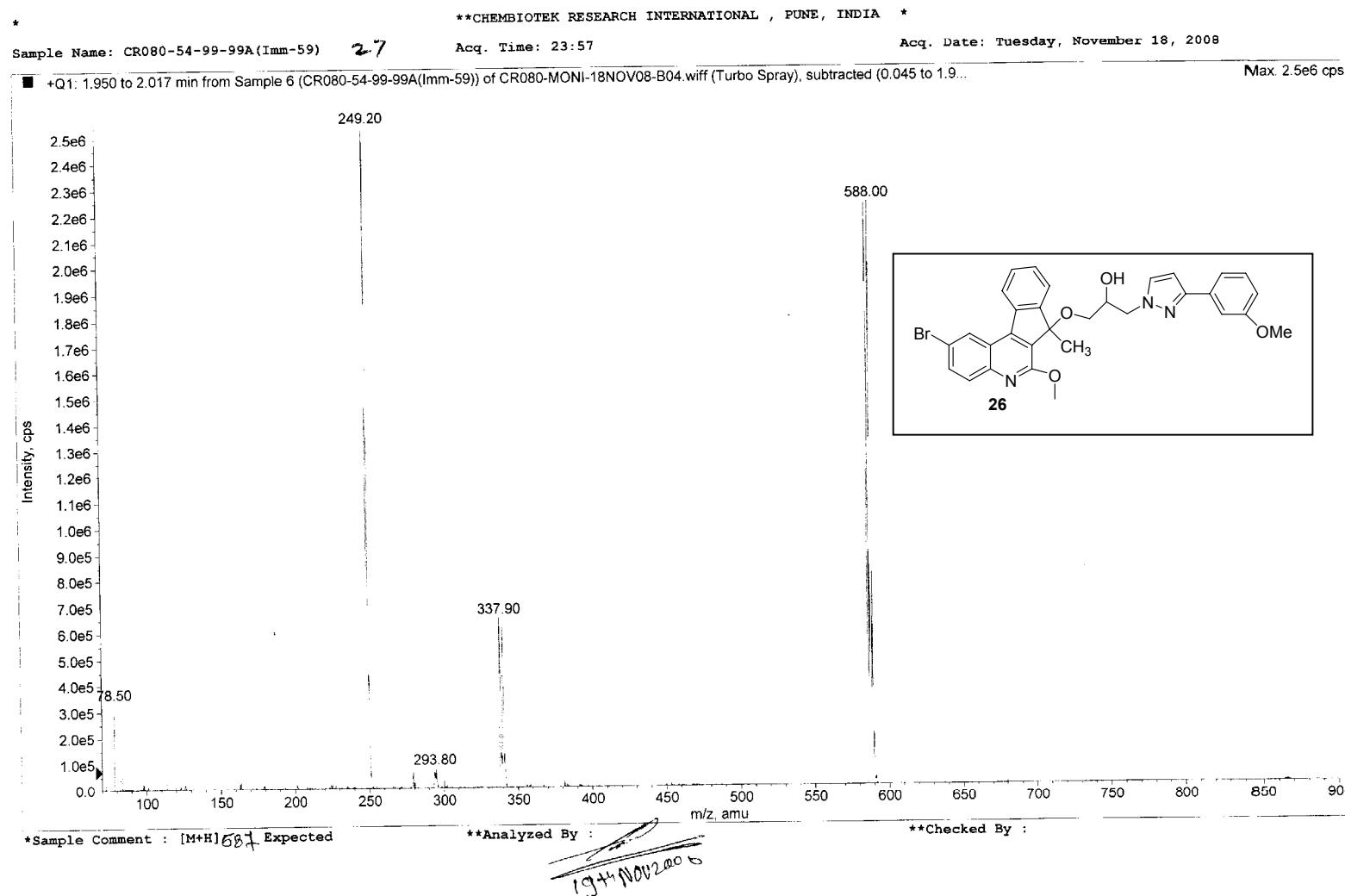


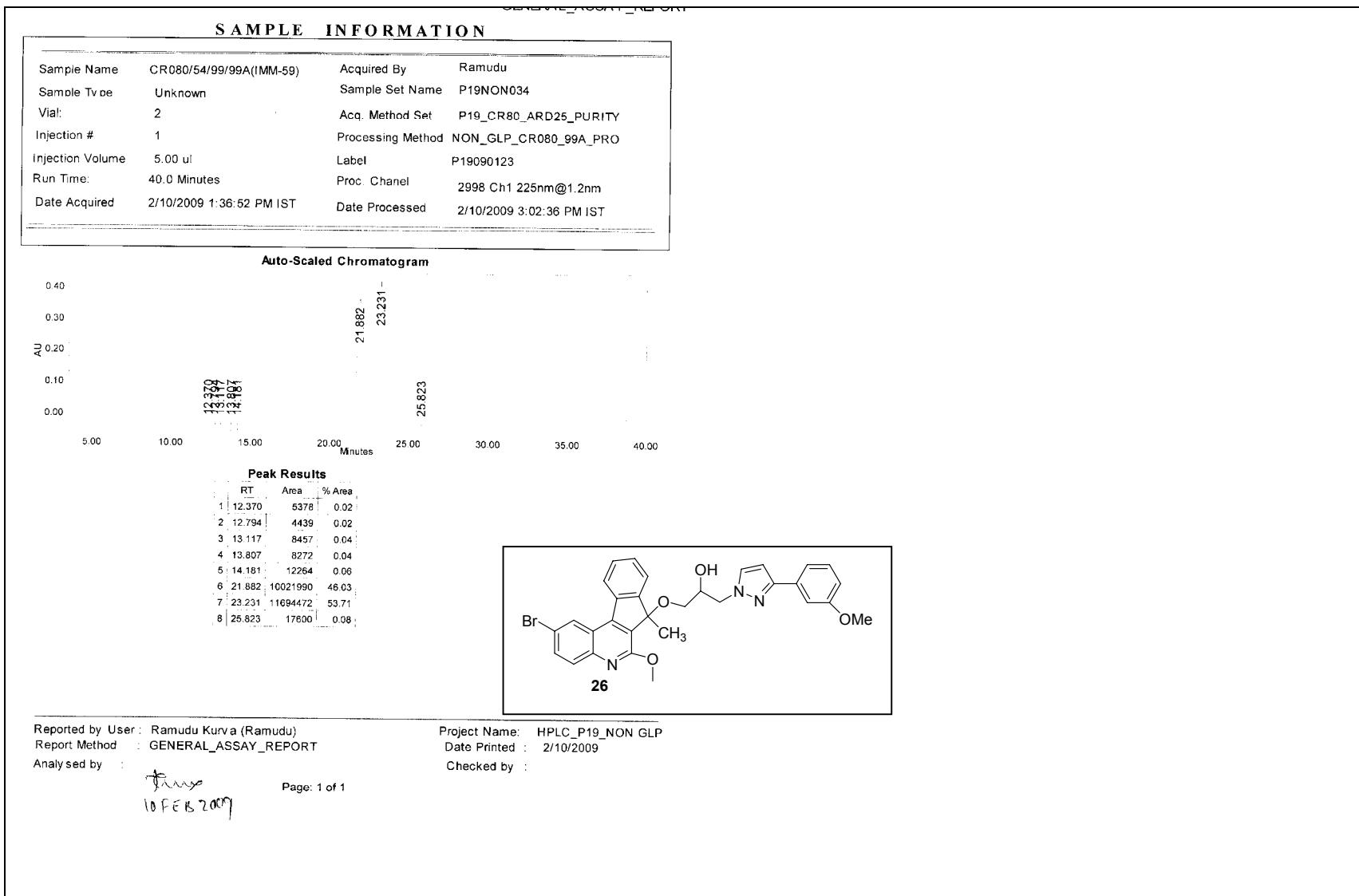


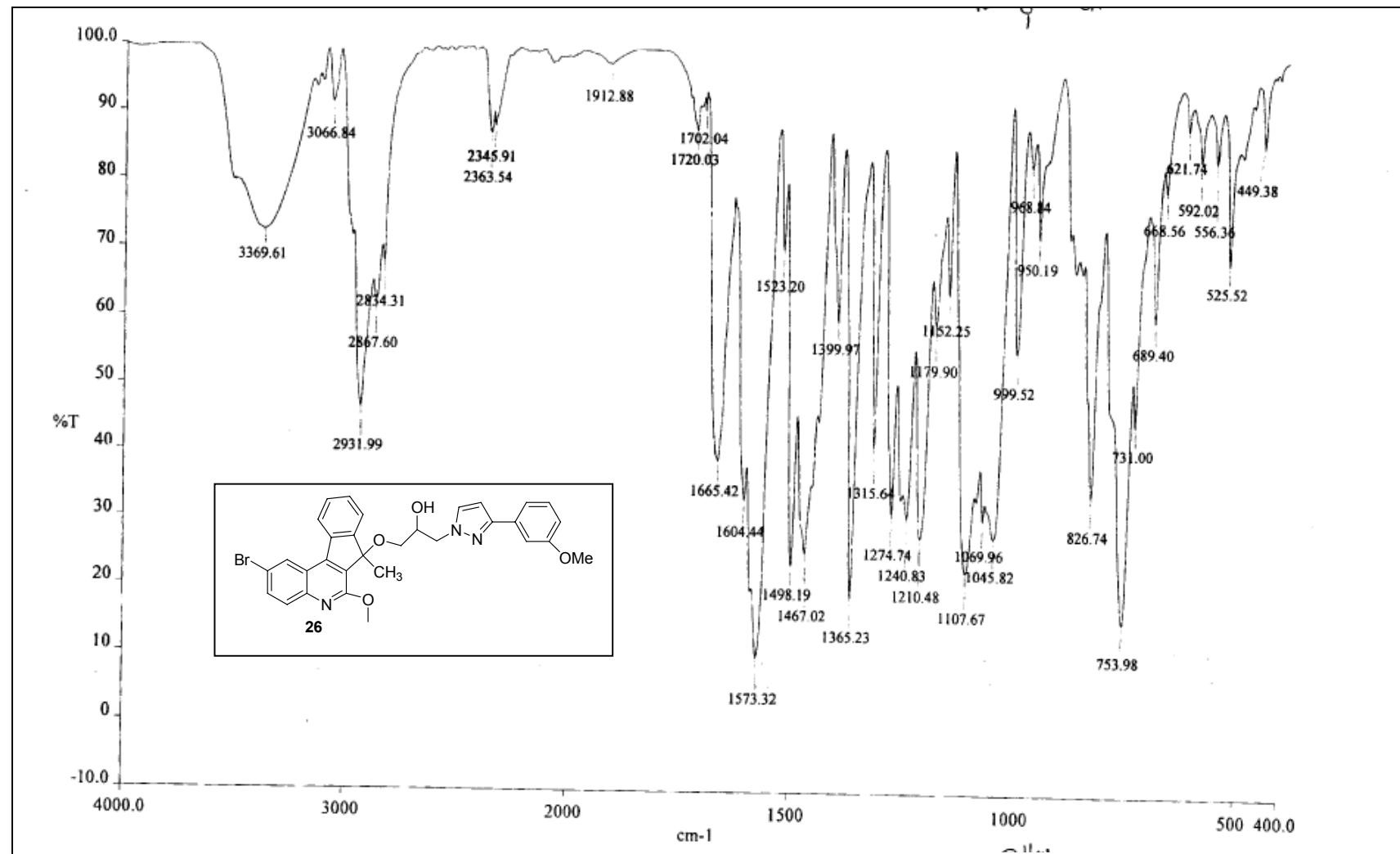


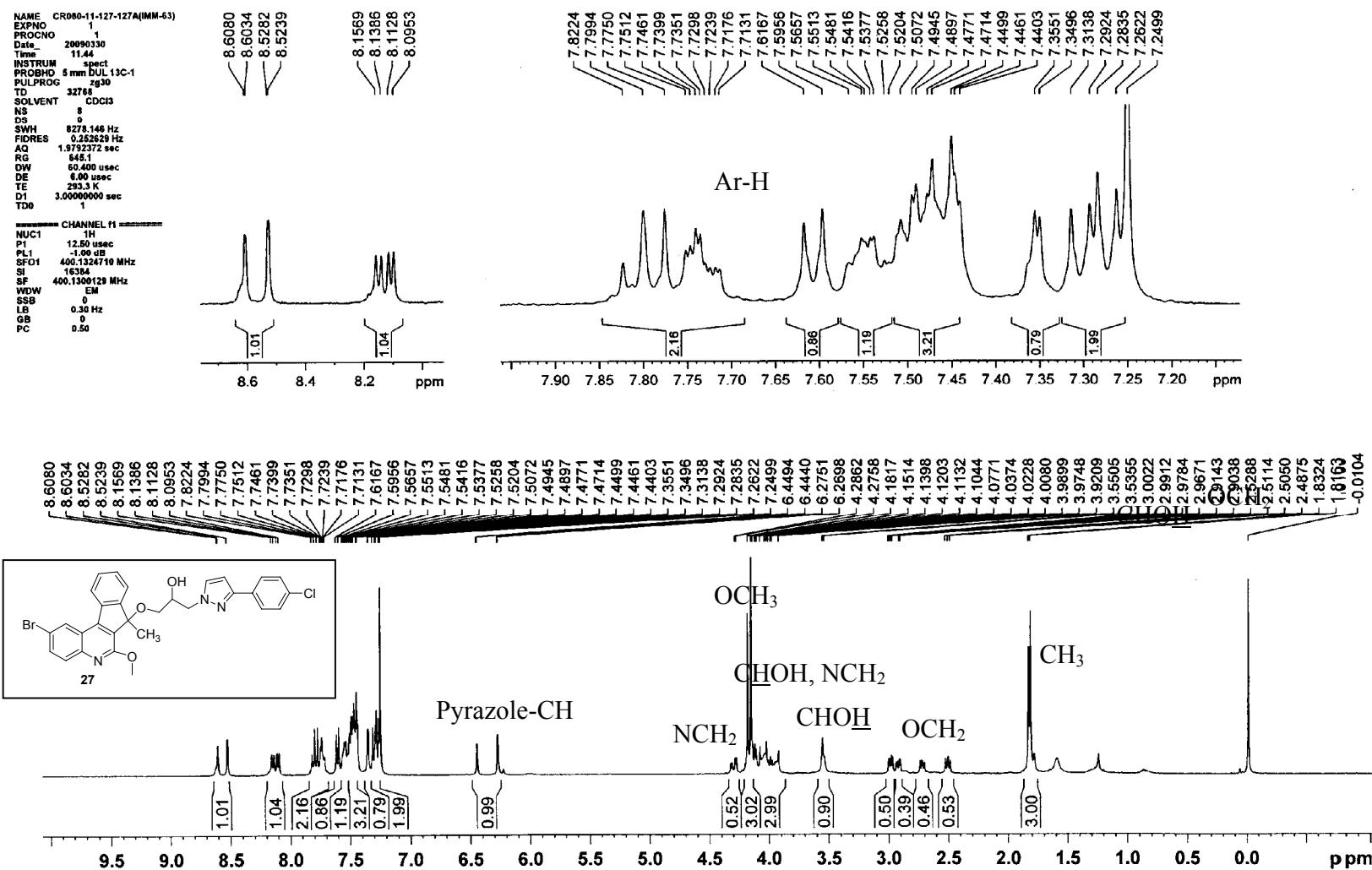


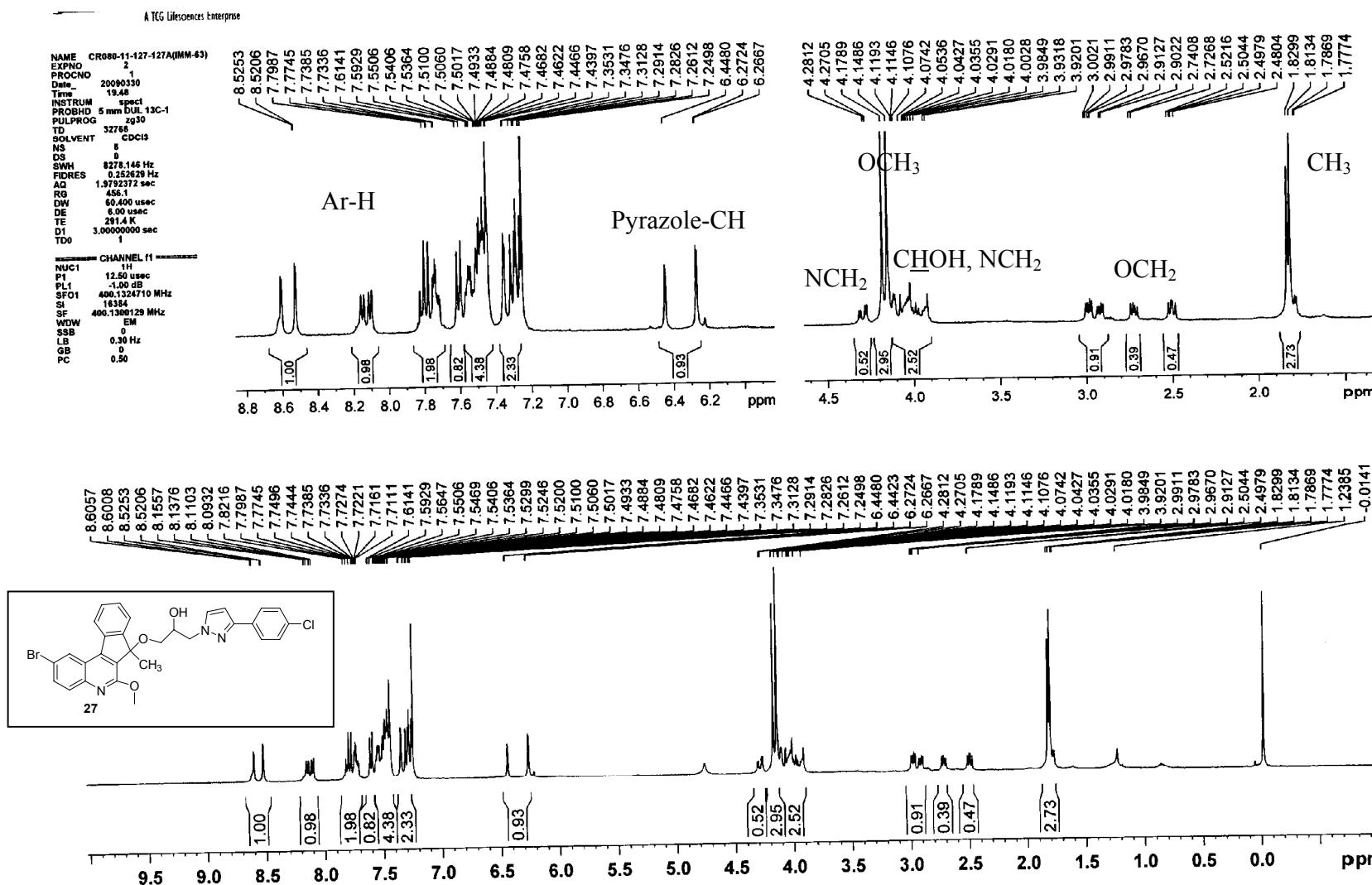


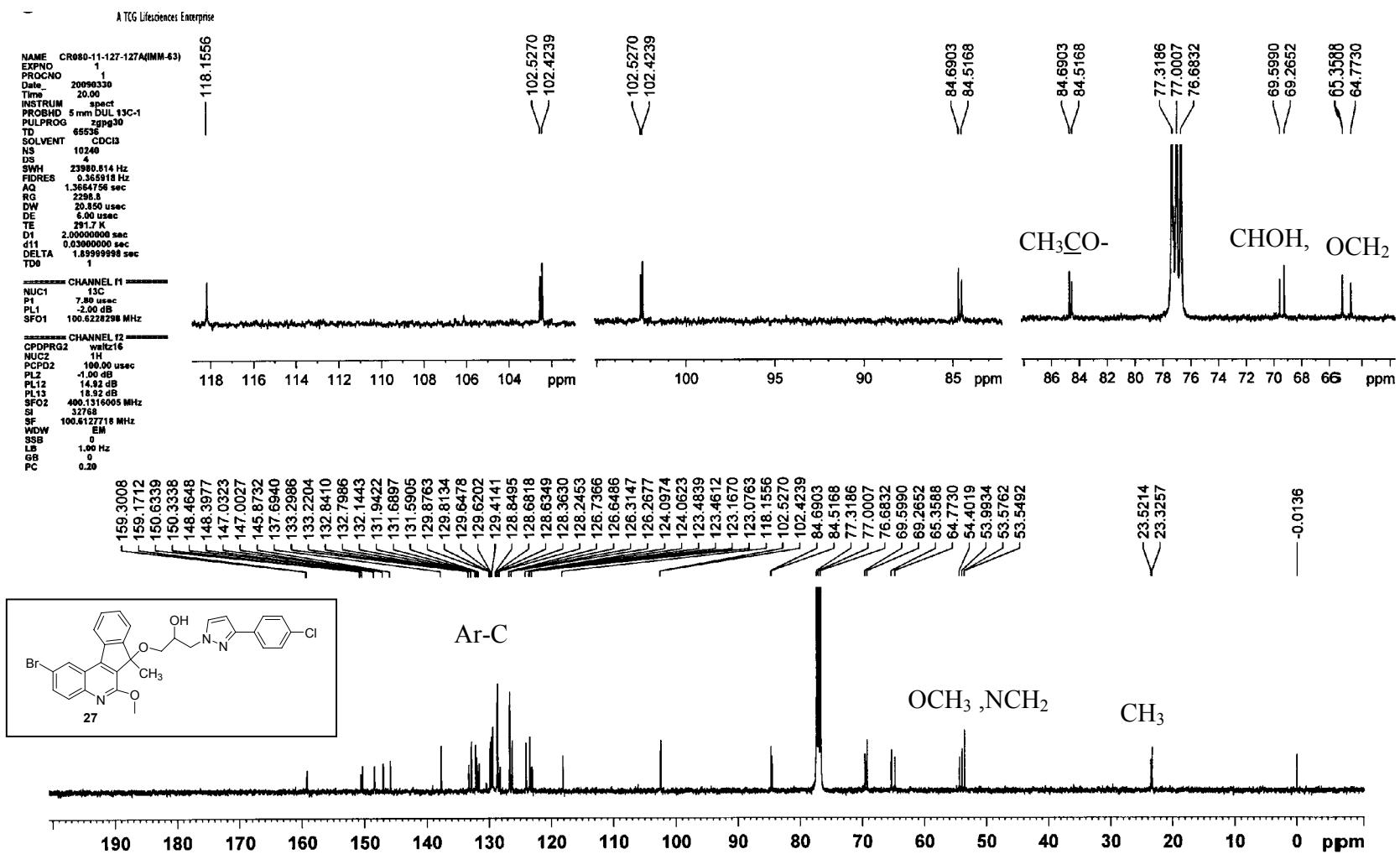


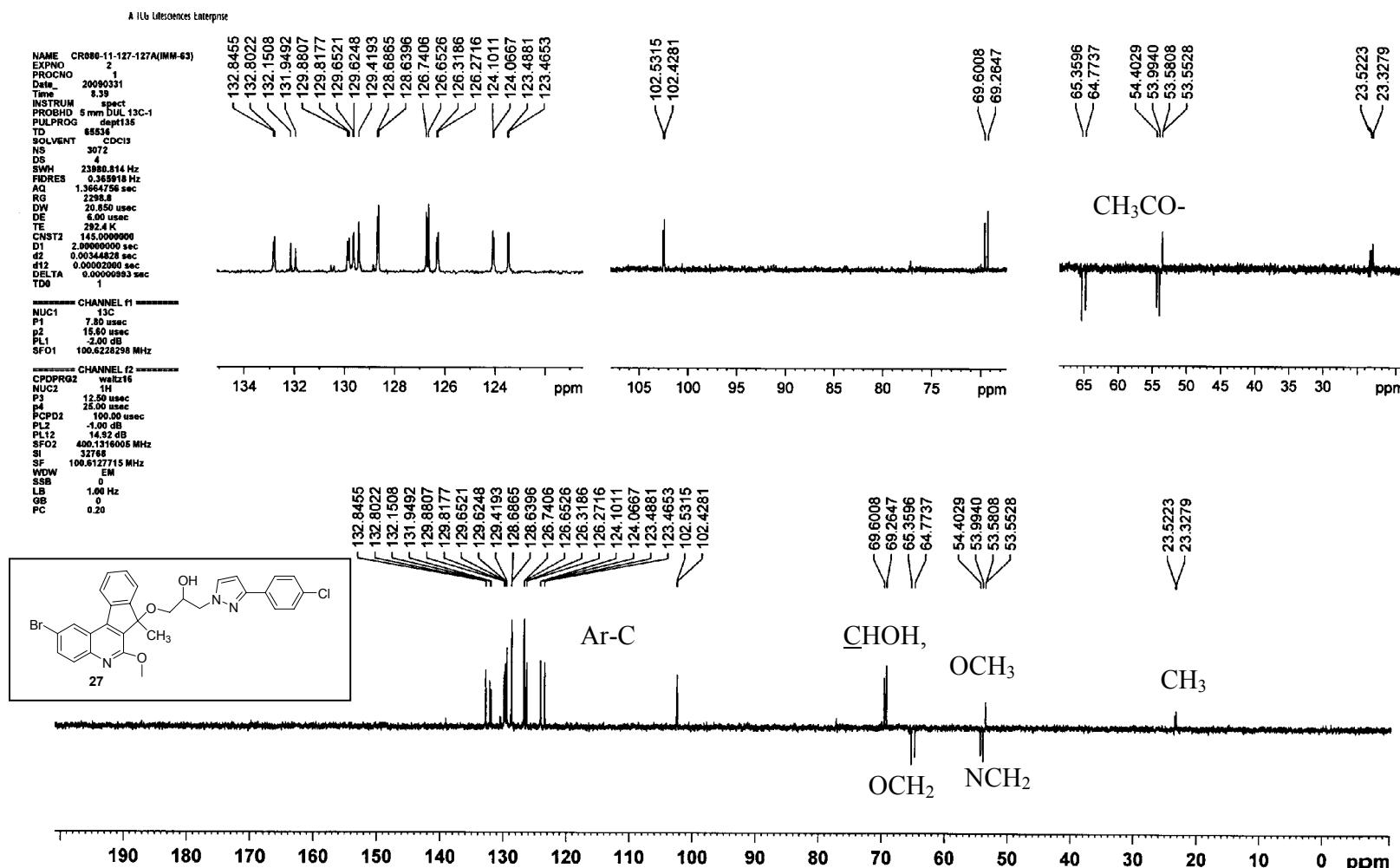


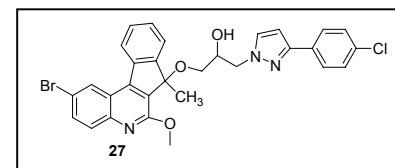
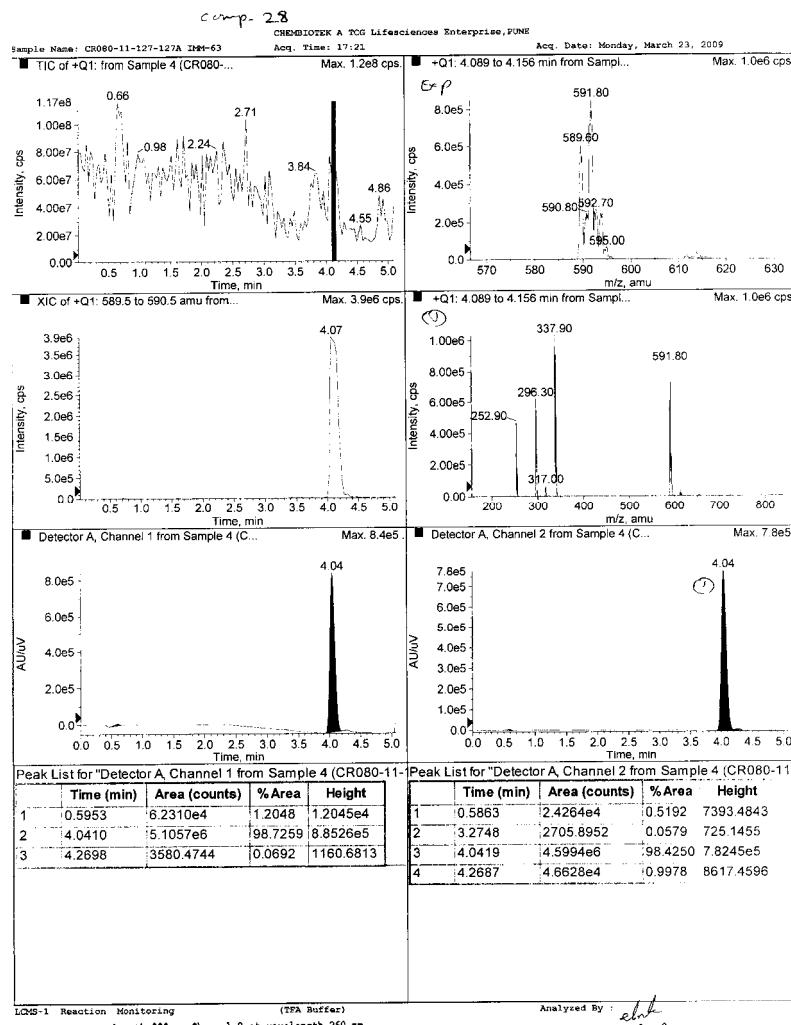


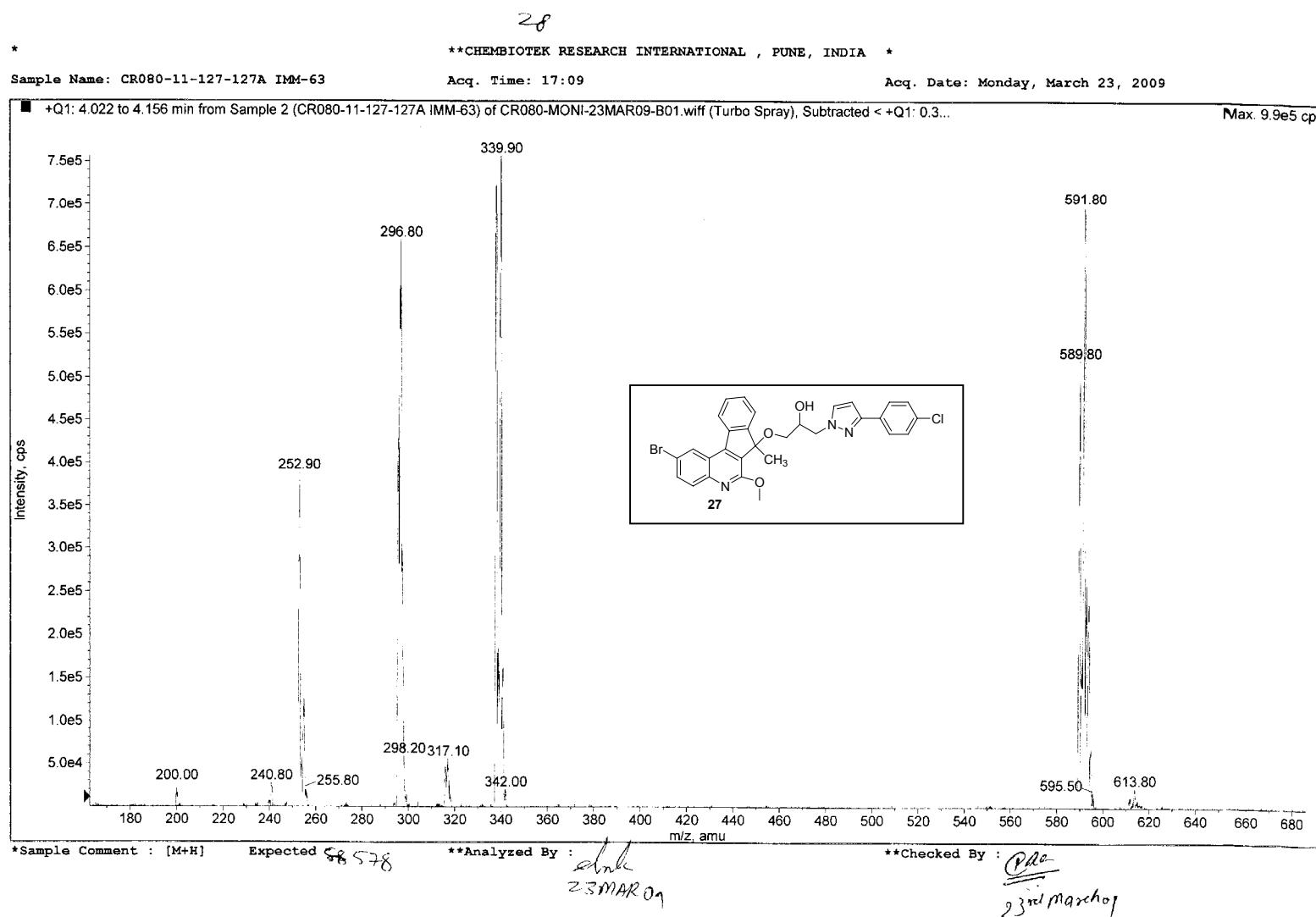




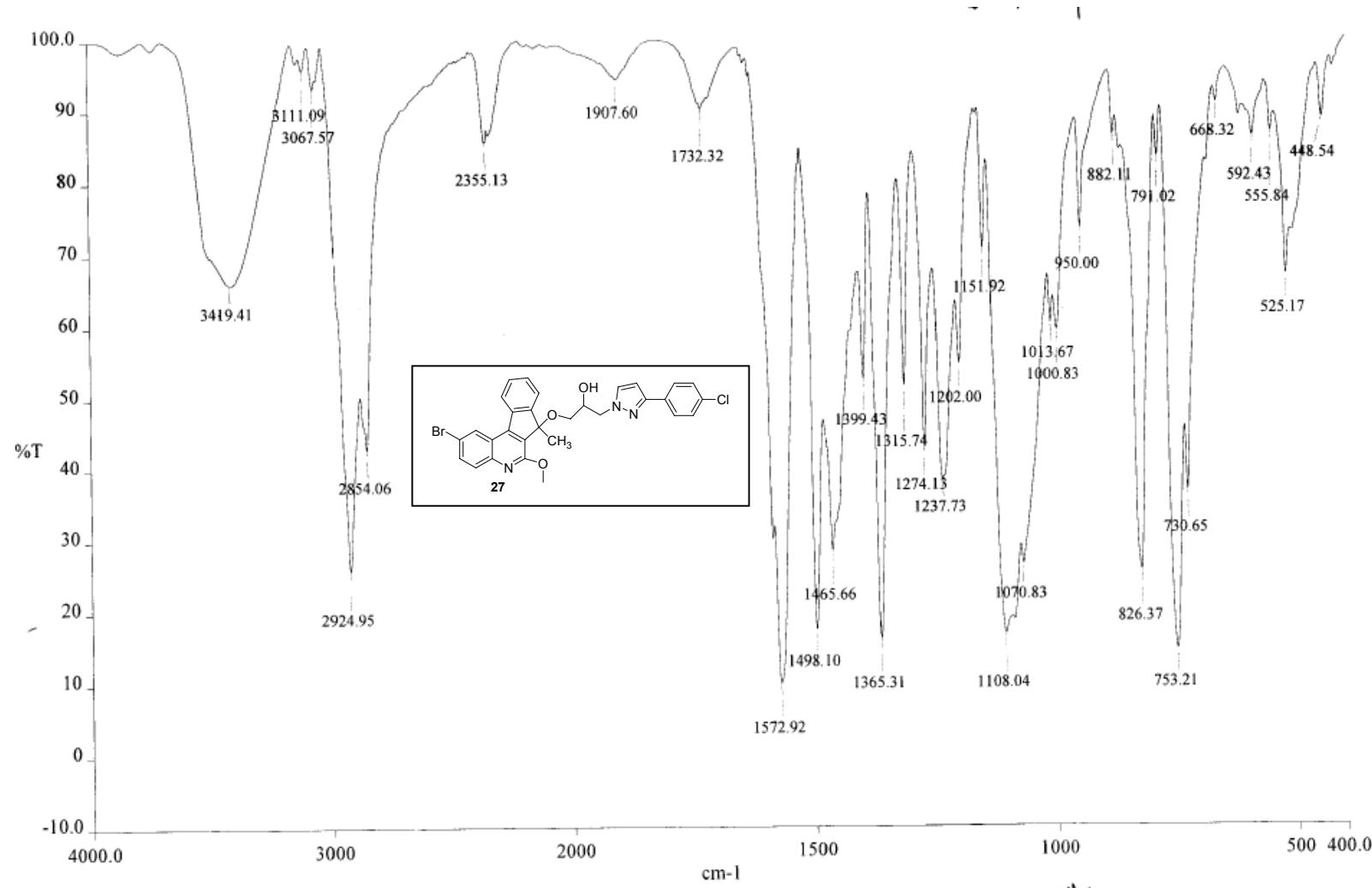


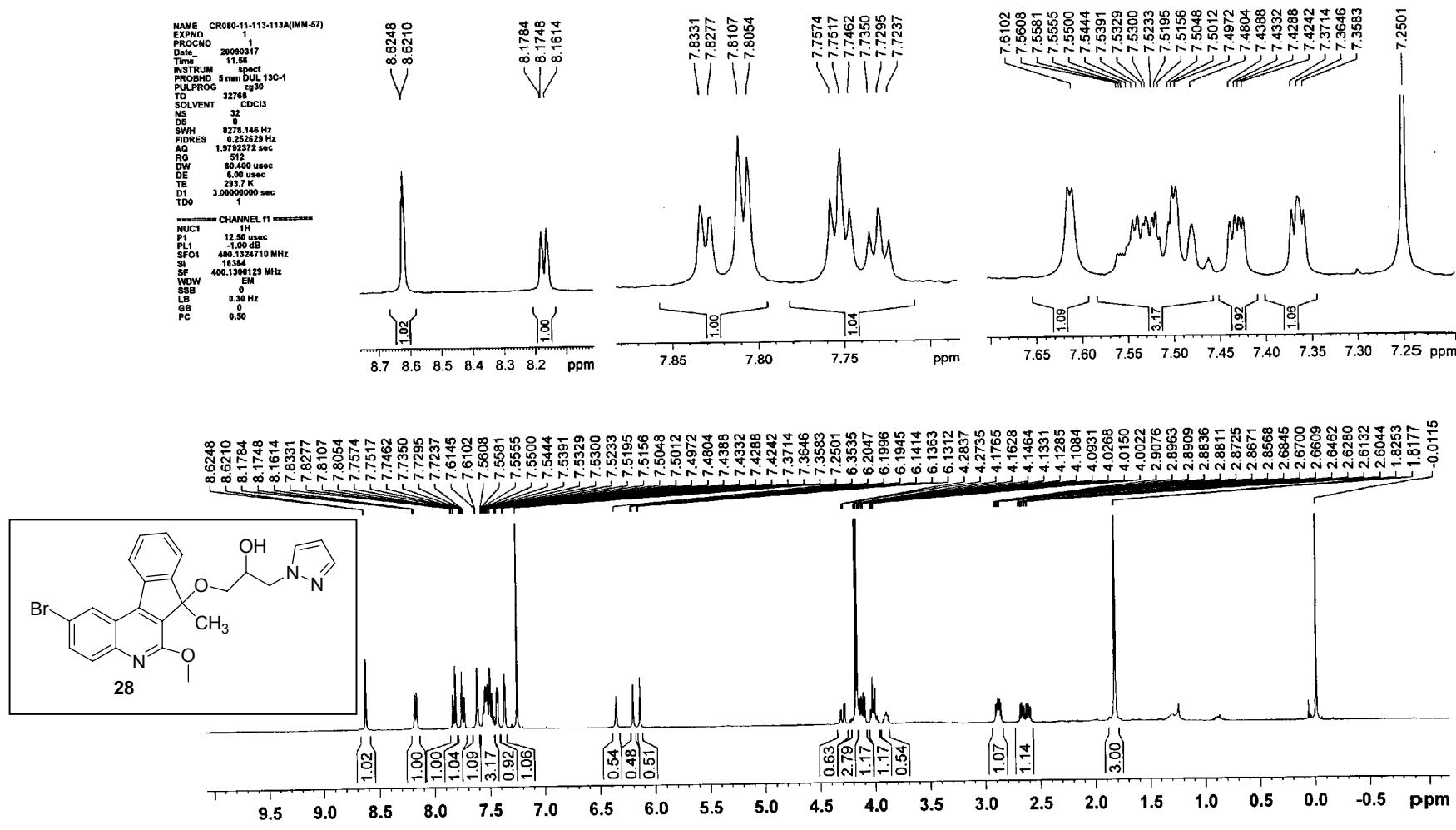


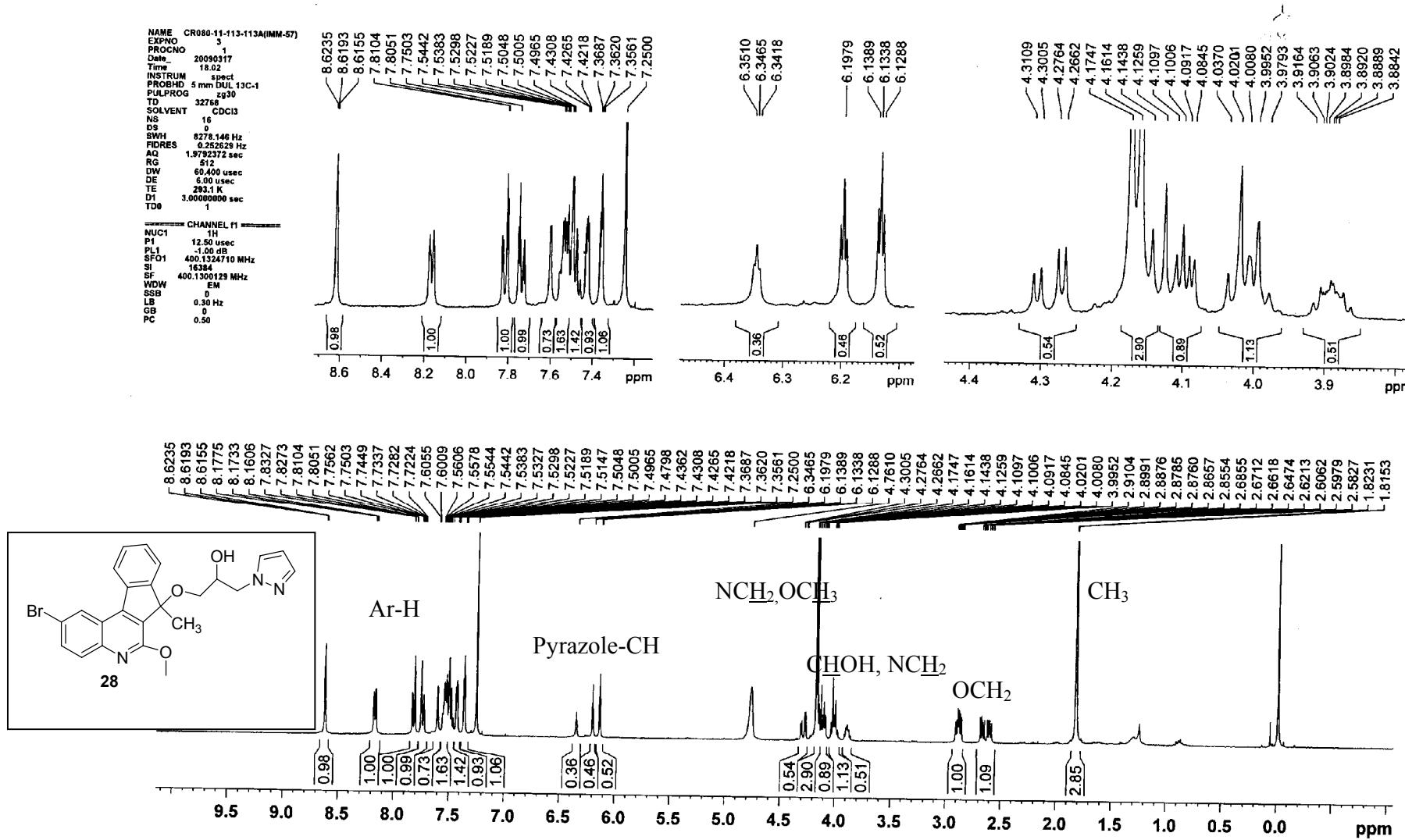


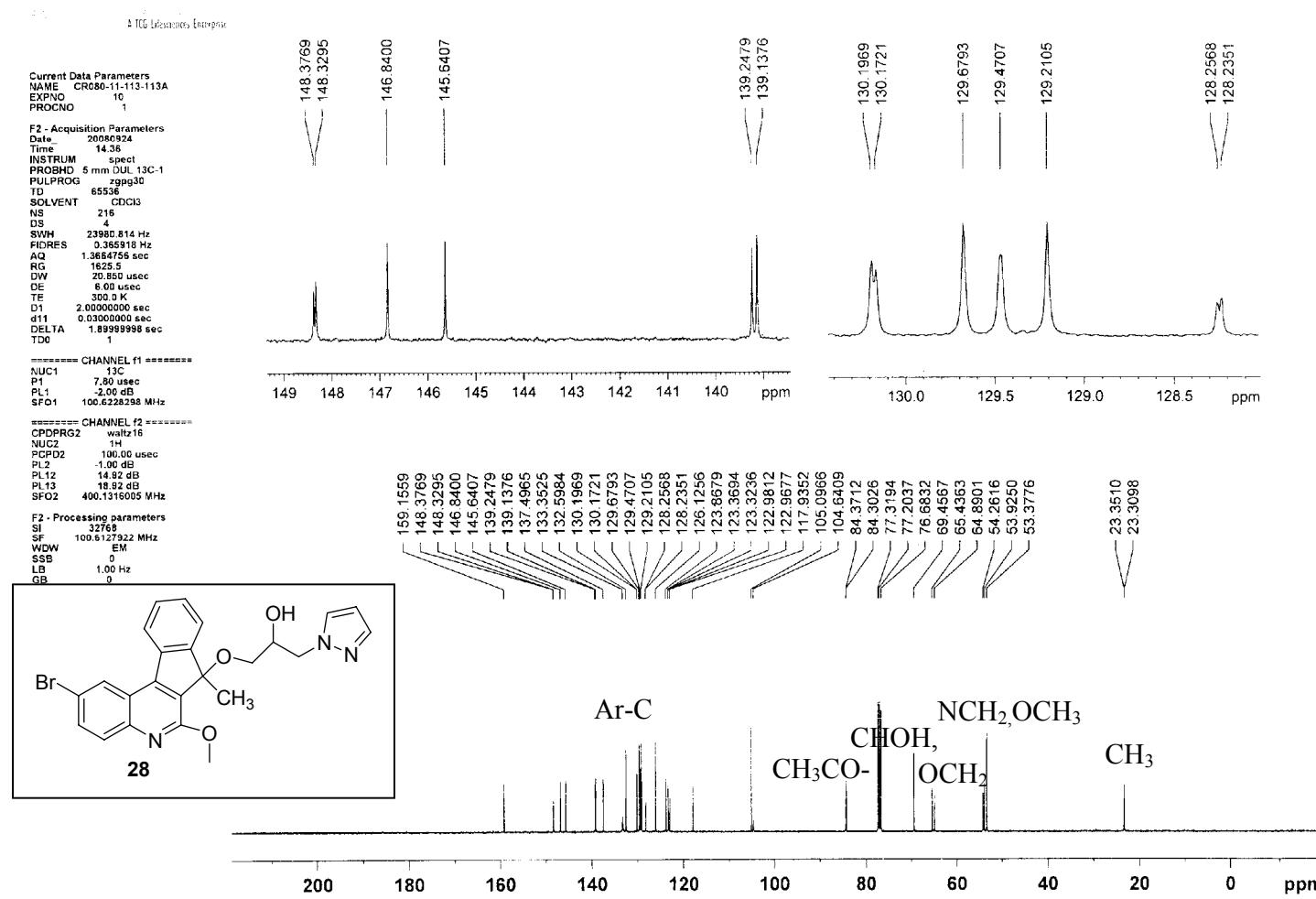


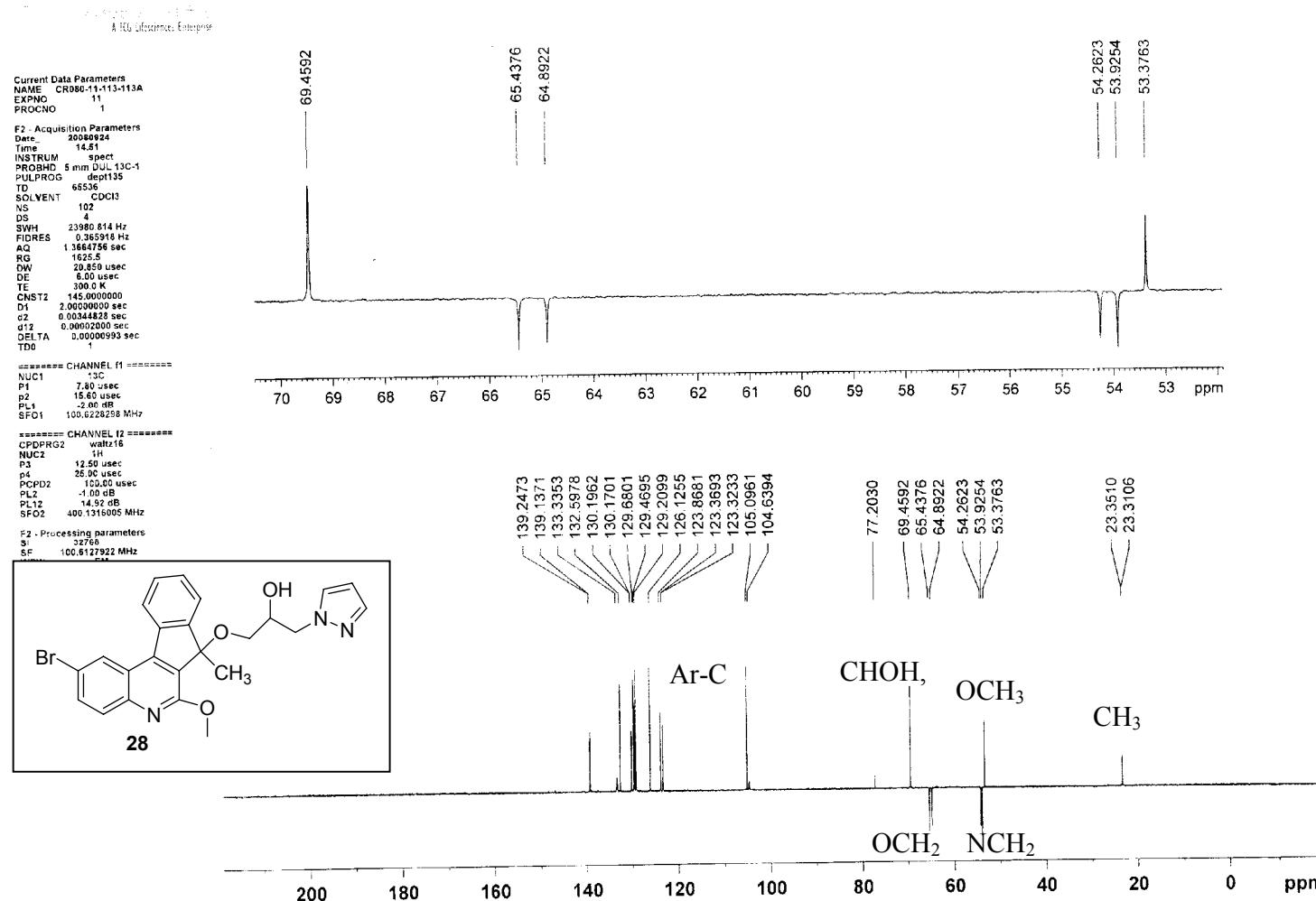
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Auto-Scaled Chromatogram		Auto-Scaled Chromatogram																																											
Peak Results <table border="1" style="margin-left: auto; margin-right: auto;"> <thead> <tr> <th>RT</th> <th>Area</th> <th>% Area</th> </tr> </thead> <tbody> <tr><td>1 8.781</td><td>161018</td><td>0.37</td></tr> <tr><td>2 16.677</td><td>54771</td><td>0.13</td></tr> <tr><td>3 17.168</td><td>41092</td><td>0.09</td></tr> <tr><td>4 22.623</td><td>1605958</td><td>3.67</td></tr> <tr><td>5 24.023</td><td>21860013</td><td>50.00</td></tr> <tr><td>6 25.512</td><td>20001364</td><td>45.74</td></tr> </tbody> </table>		RT	Area	% Area	1 8.781	161018	0.37	2 16.677	54771	0.13	3 17.168	41092	0.09	4 22.623	1605958	3.67	5 24.023	21860013	50.00	6 25.512	20001364	45.74	Peak Results <table border="1" style="margin-left: auto; margin-right: auto;"> <thead> <tr> <th>RT</th> <th>Area</th> <th>% Area</th> </tr> </thead> <tbody> <tr><td>1 8.781</td><td>161018</td><td>0.37</td></tr> <tr><td>2 16.677</td><td>54771</td><td>0.13</td></tr> <tr><td>3 17.168</td><td>41092</td><td>0.09</td></tr> <tr><td>4 22.623</td><td>1605958</td><td>3.67</td></tr> <tr><td>5 24.023</td><td>21860013</td><td>50.00</td></tr> <tr><td>6 25.512</td><td>20001364</td><td>45.74</td></tr> </tbody> </table>		RT	Area	% Area	1 8.781	161018	0.37	2 16.677	54771	0.13	3 17.168	41092	0.09	4 22.623	1605958	3.67	5 24.023	21860013	50.00	6 25.512	20001364	45.74
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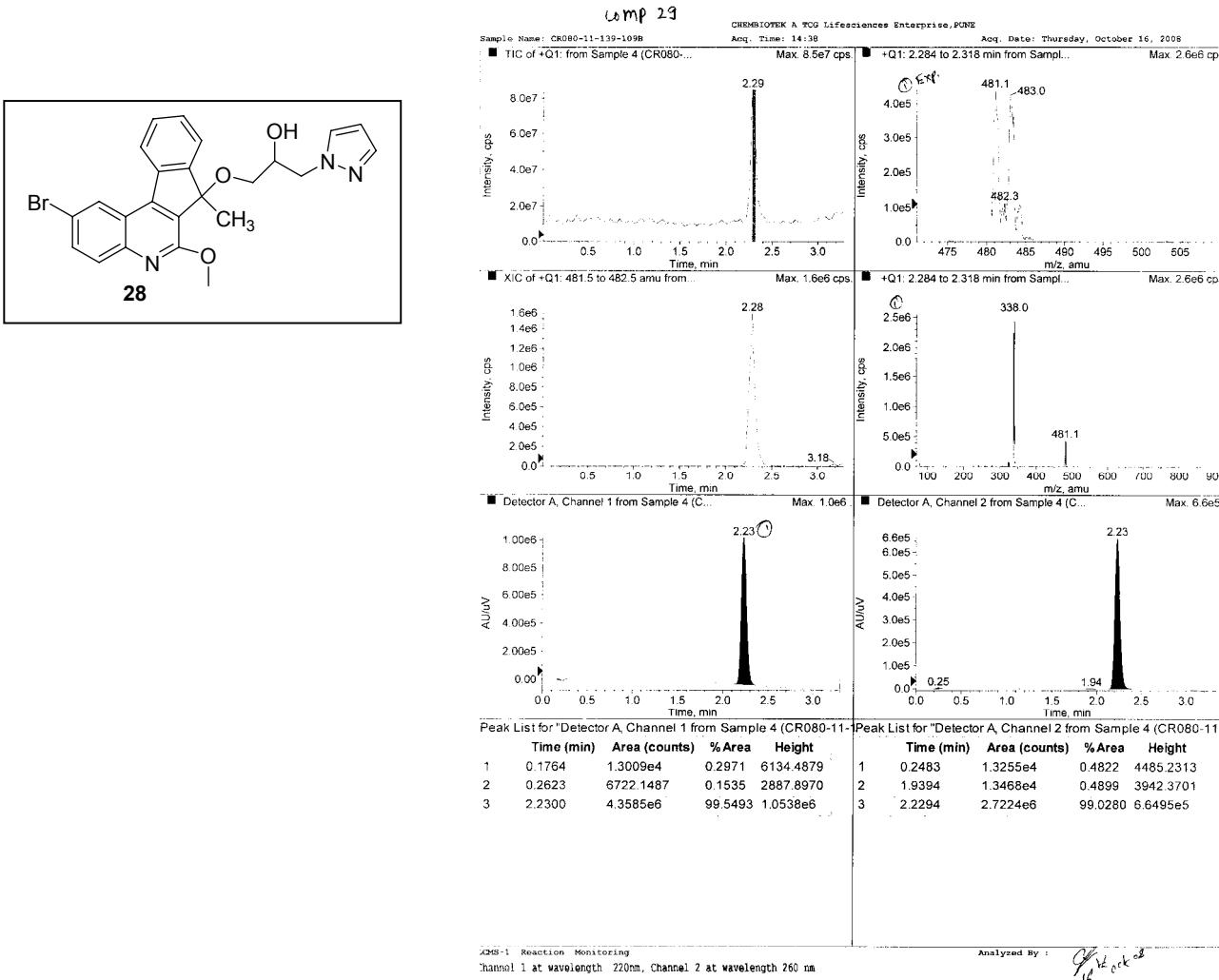


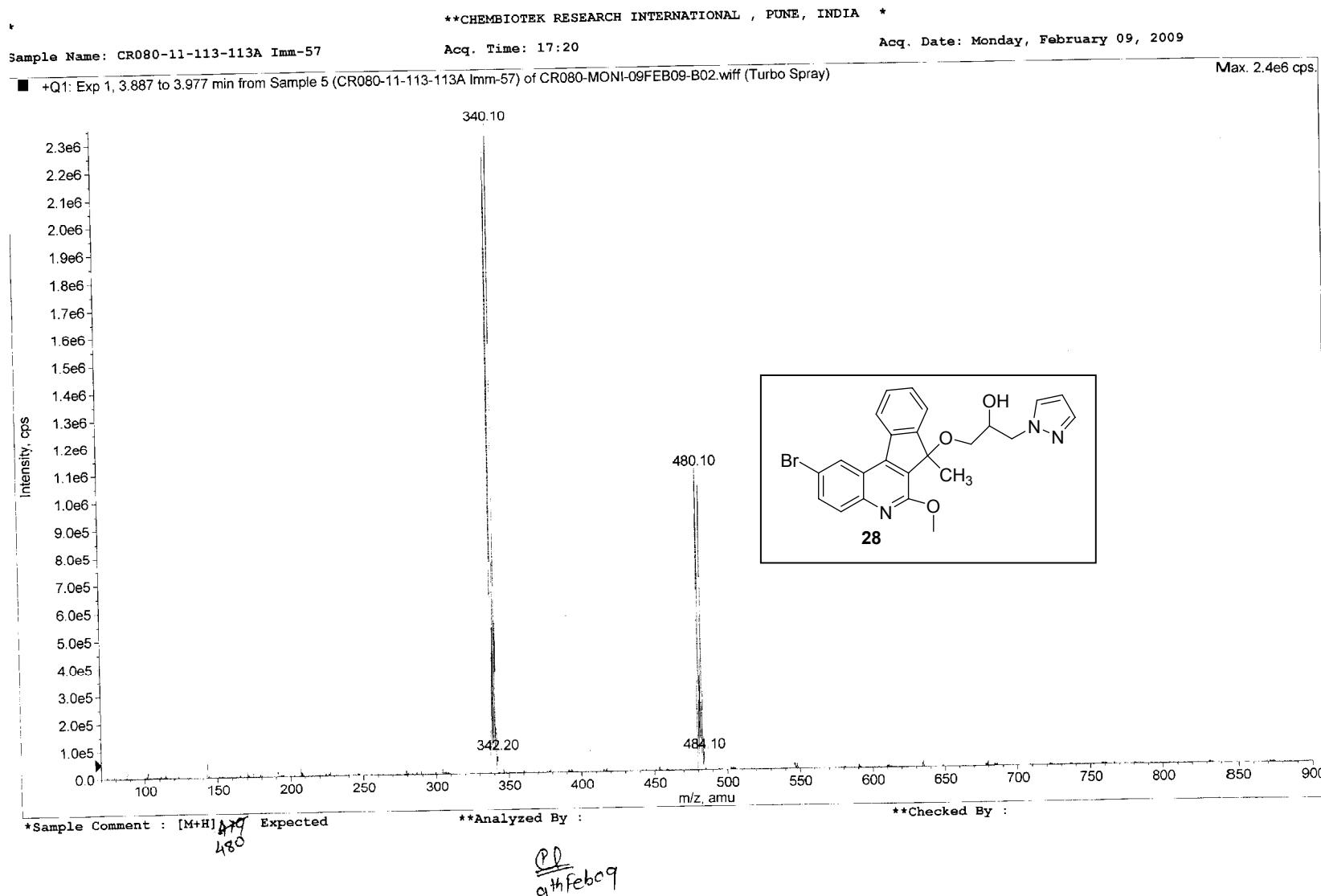


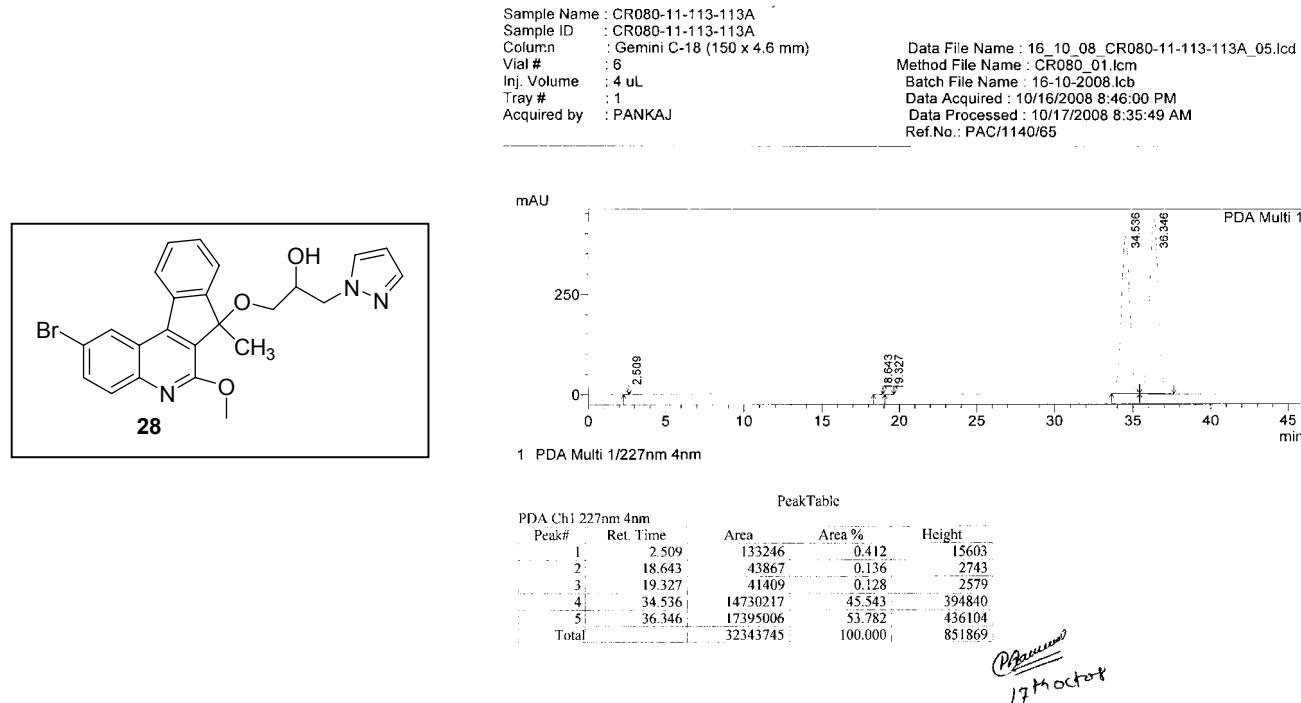


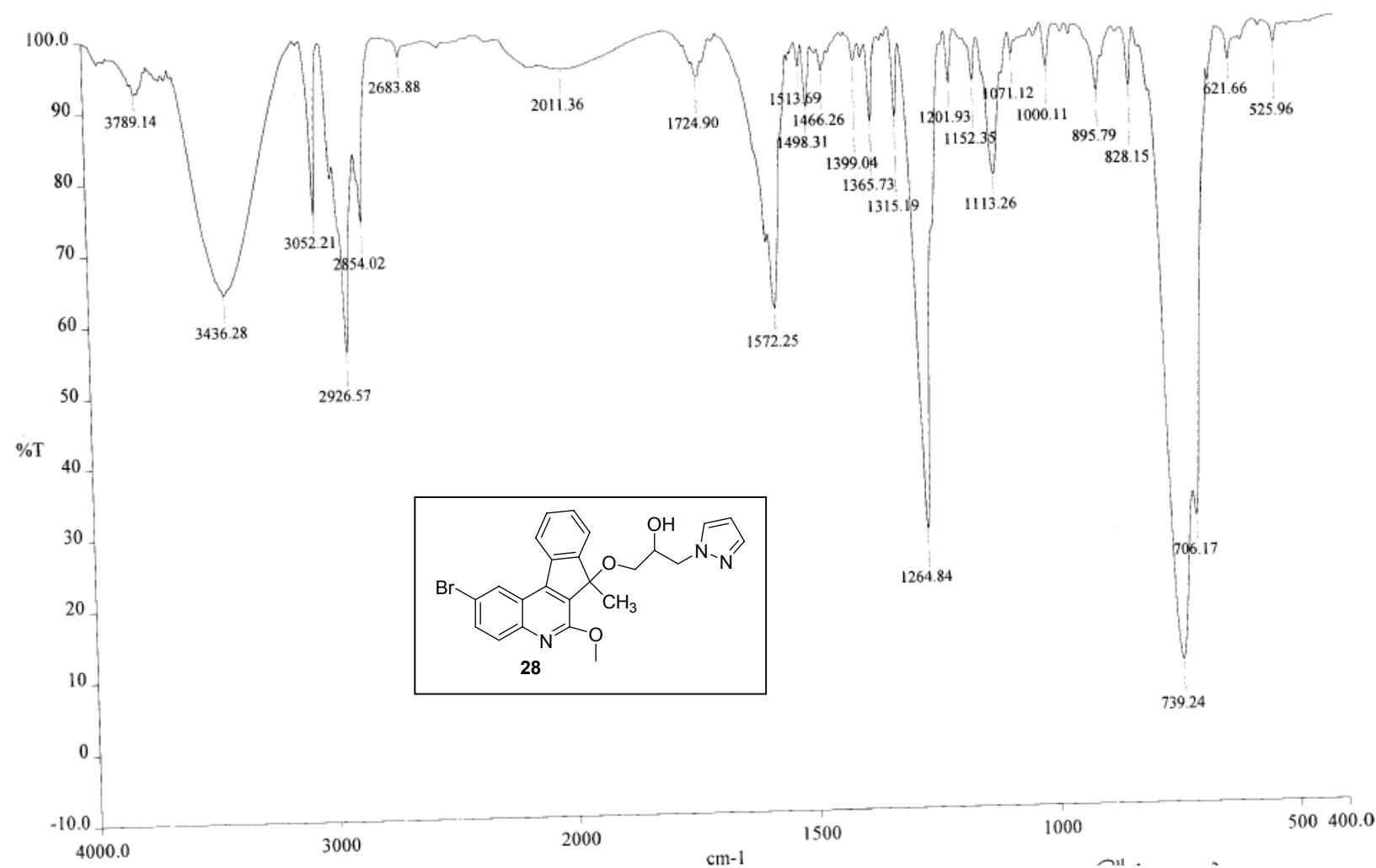


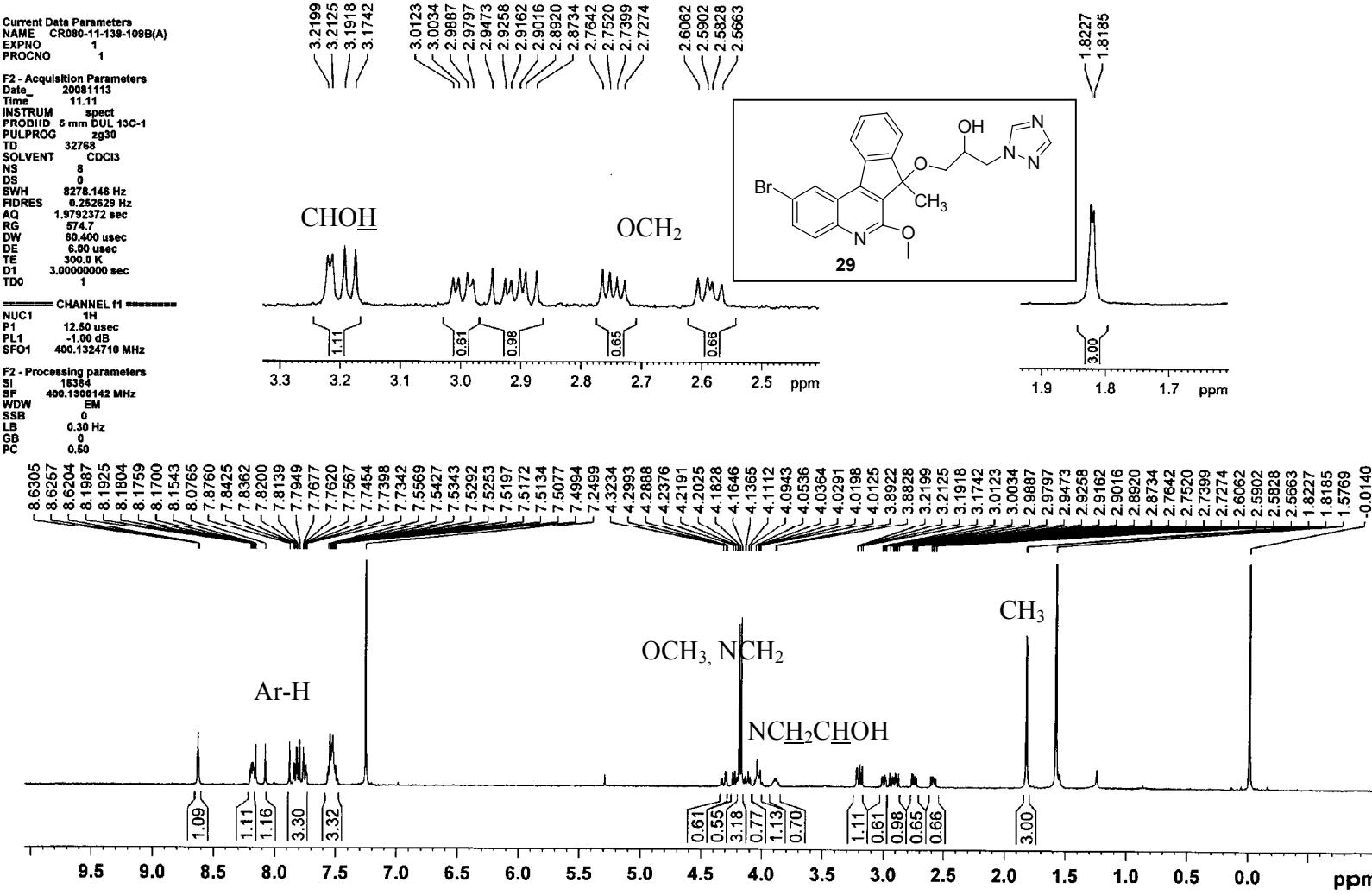










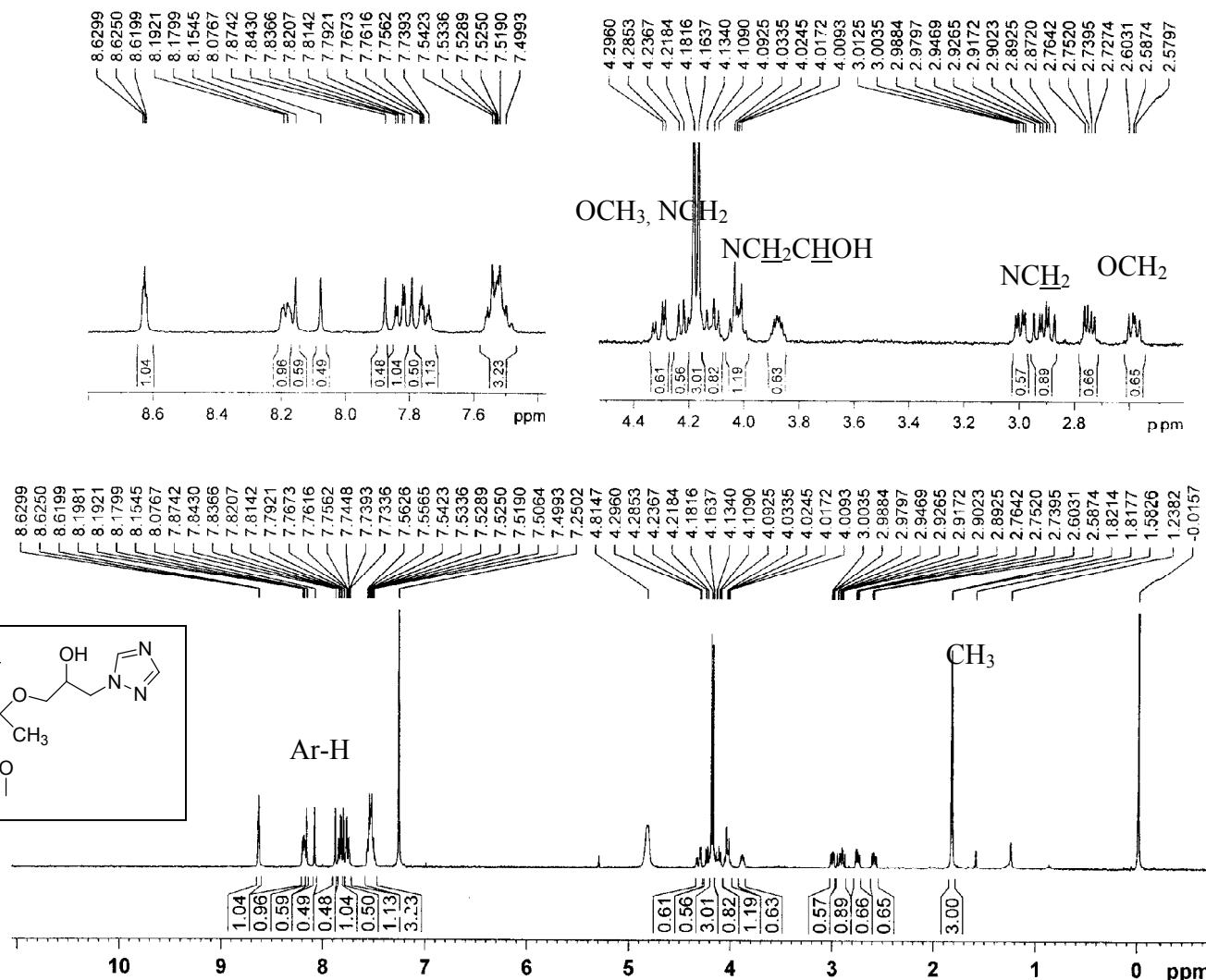
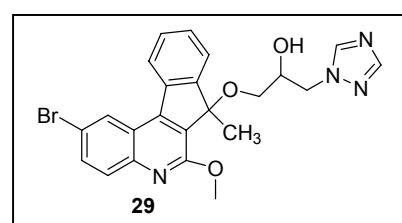


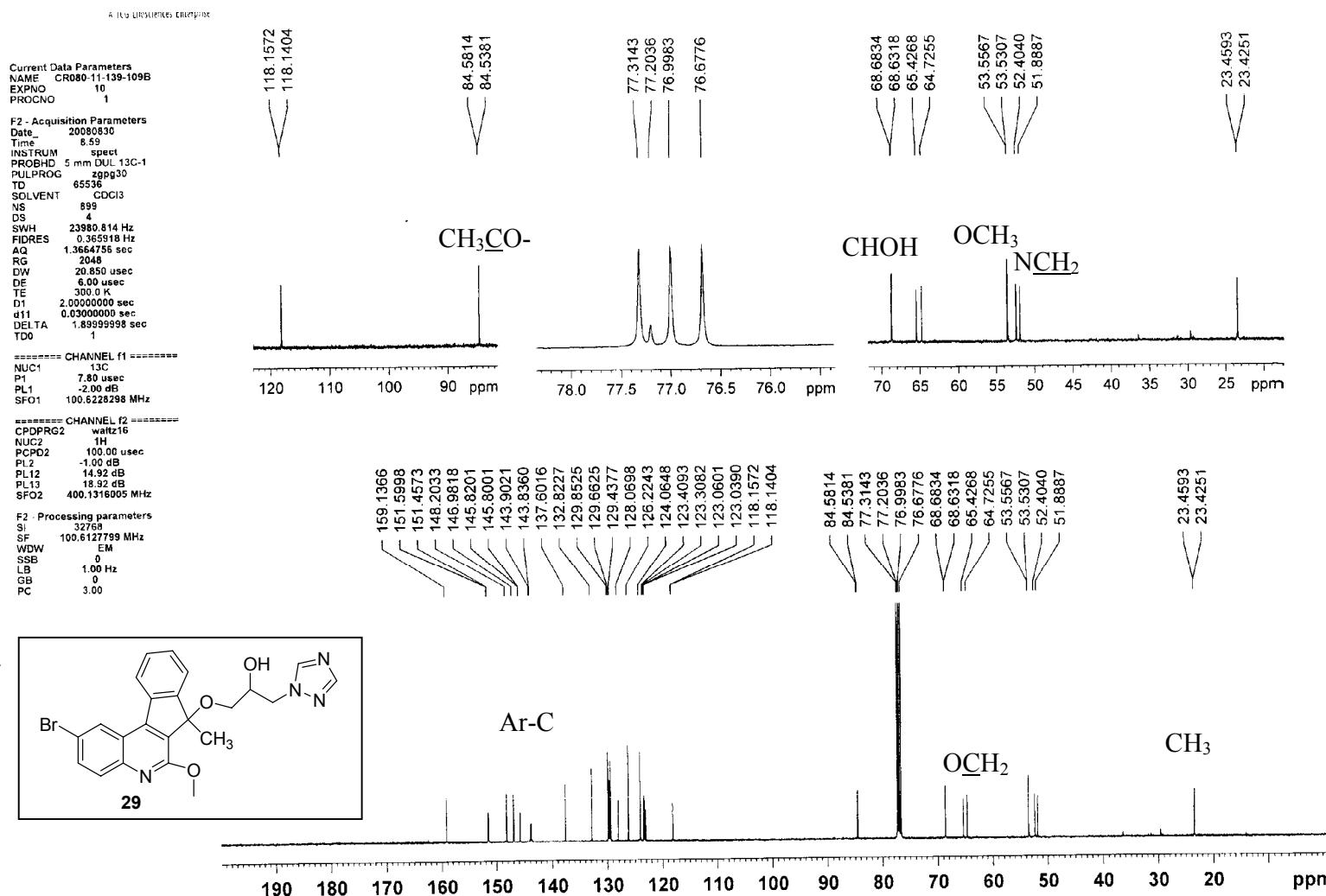
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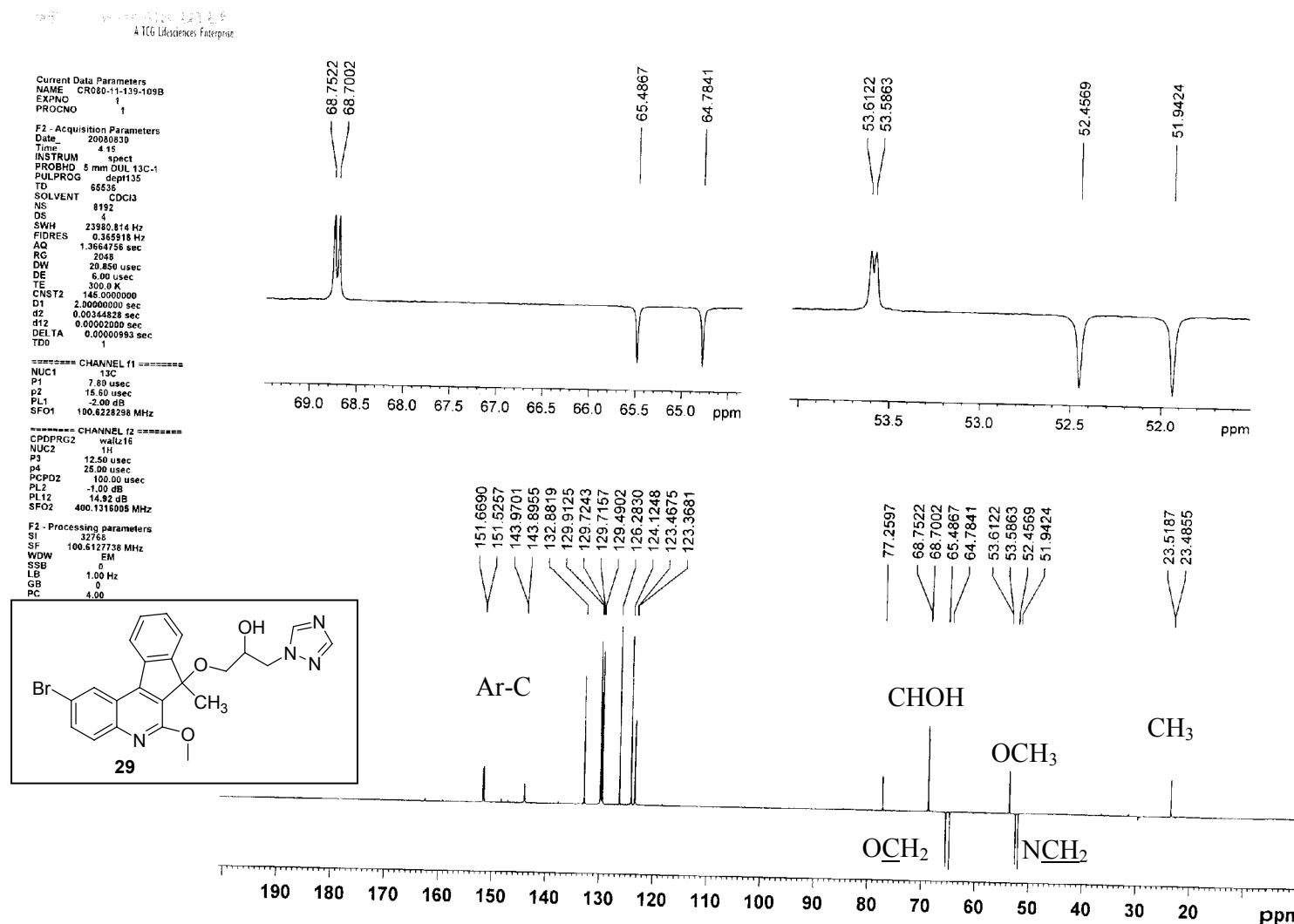
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 SWH 8278.146 Hz
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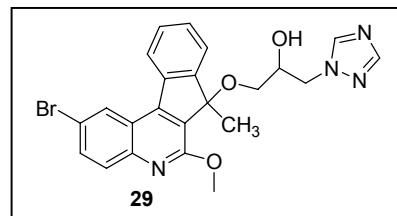
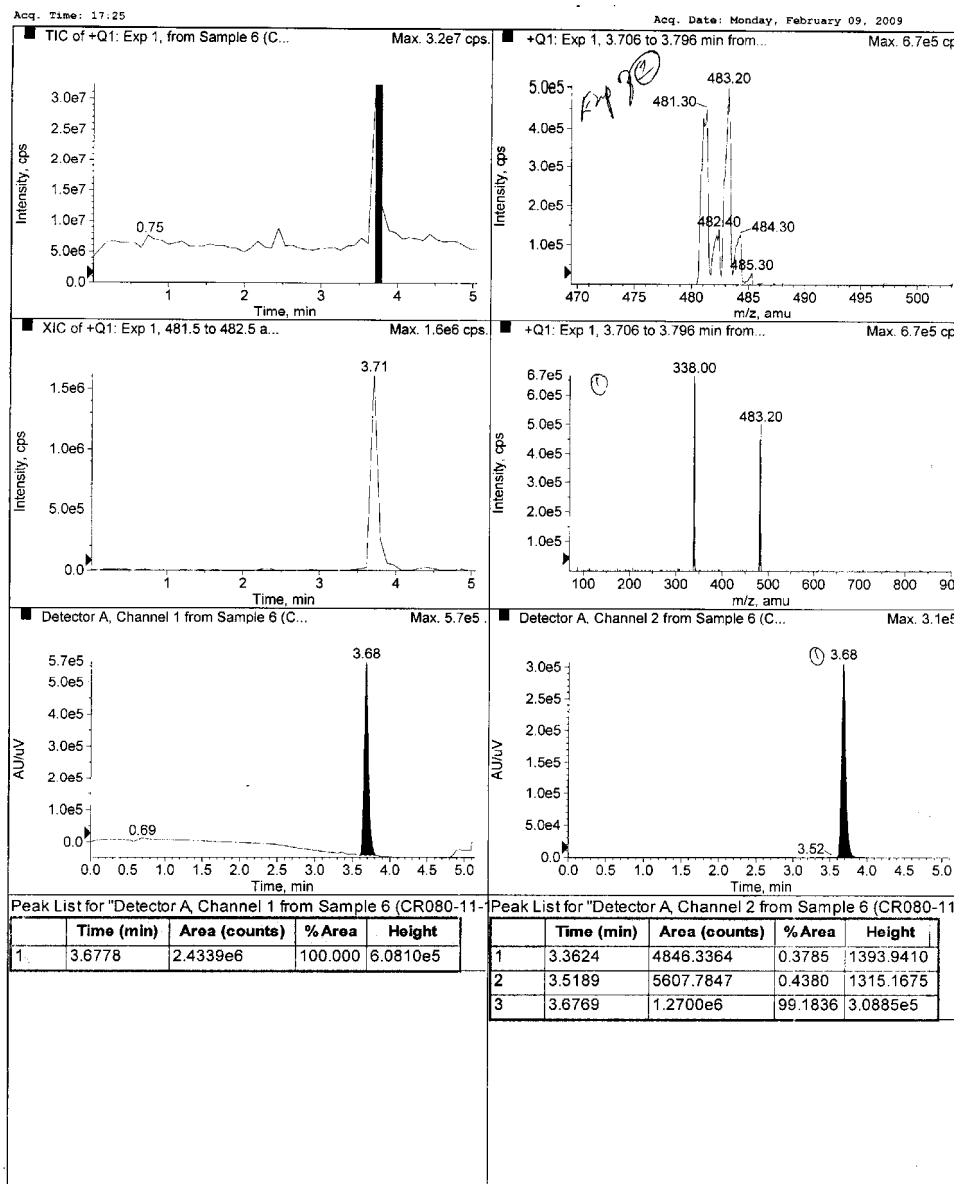
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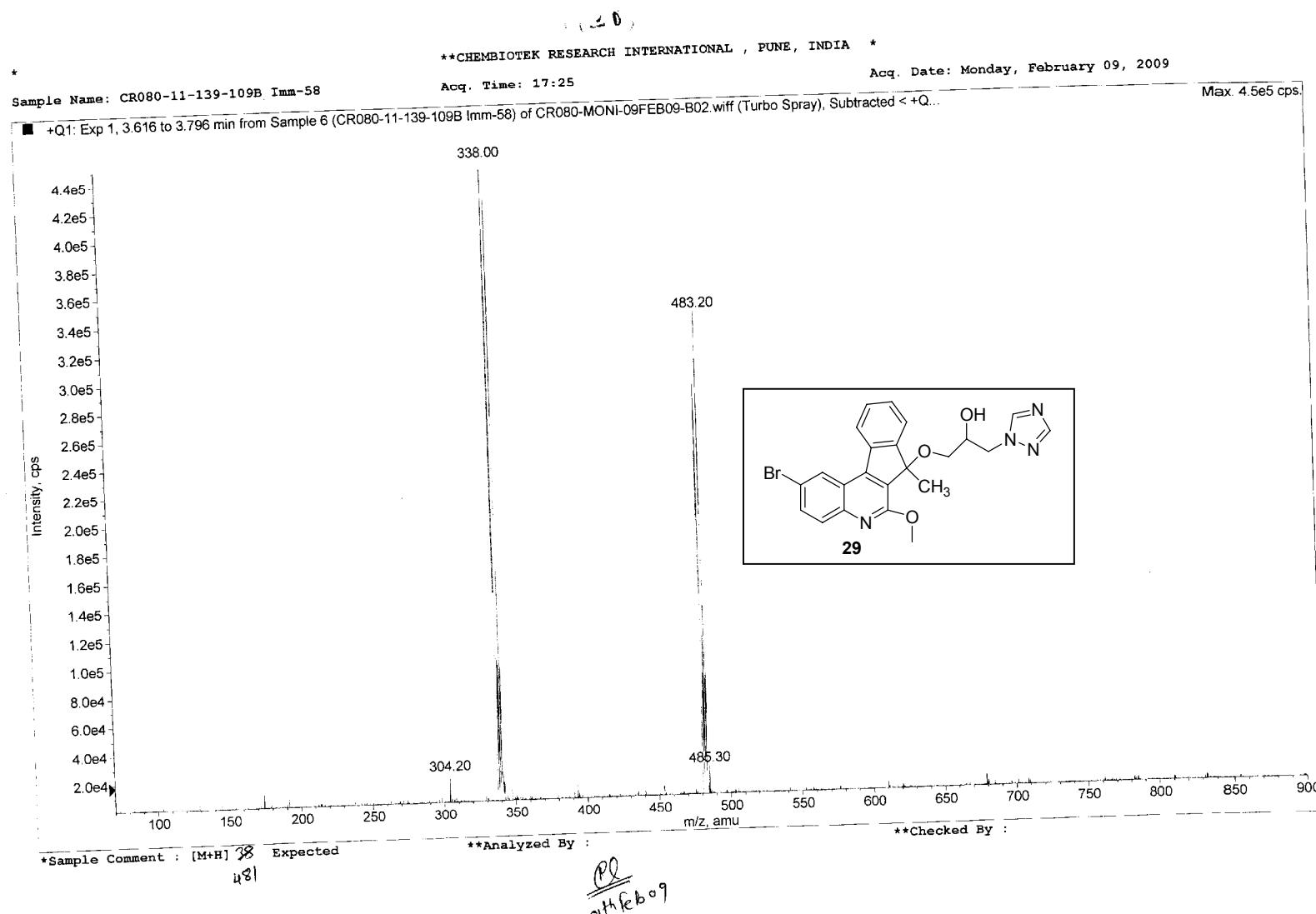






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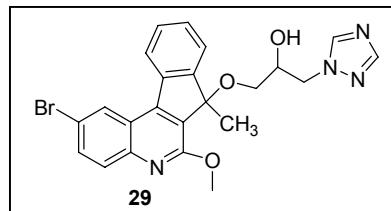
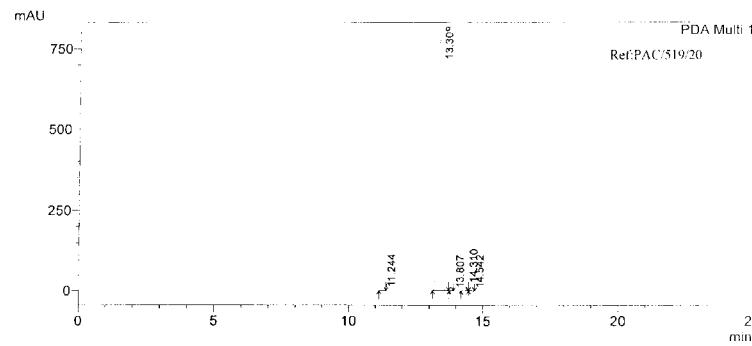
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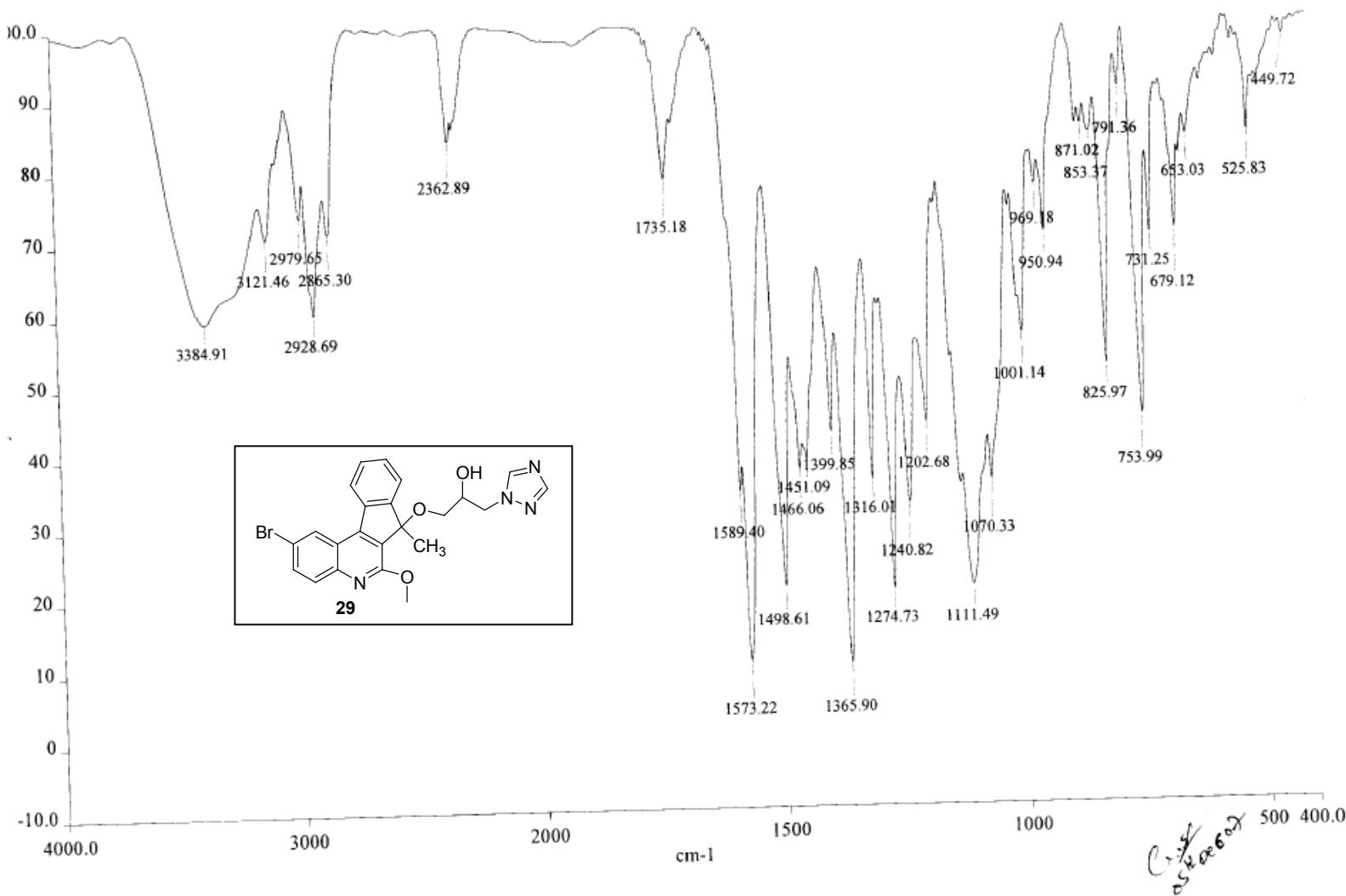
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Acquired by : Pankaj

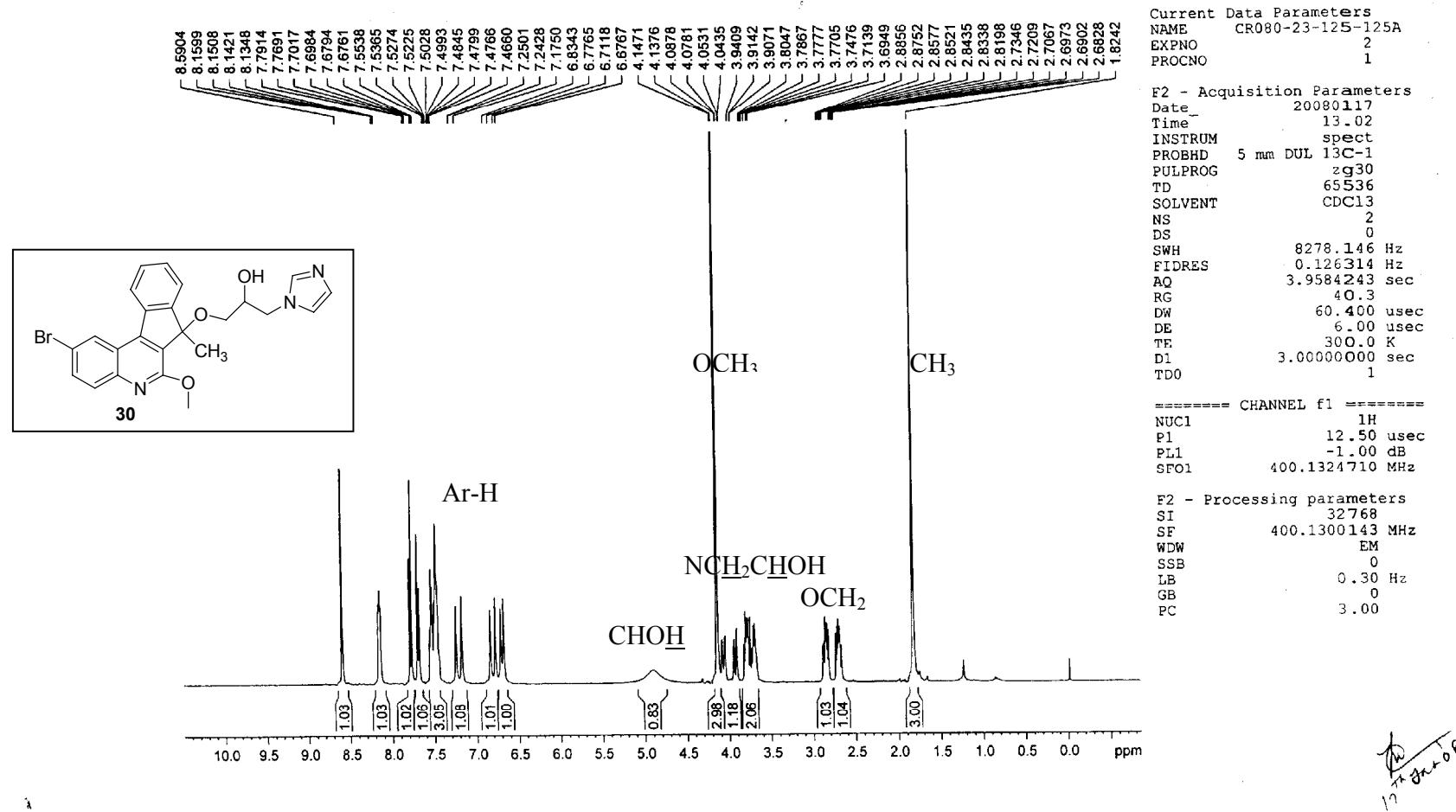
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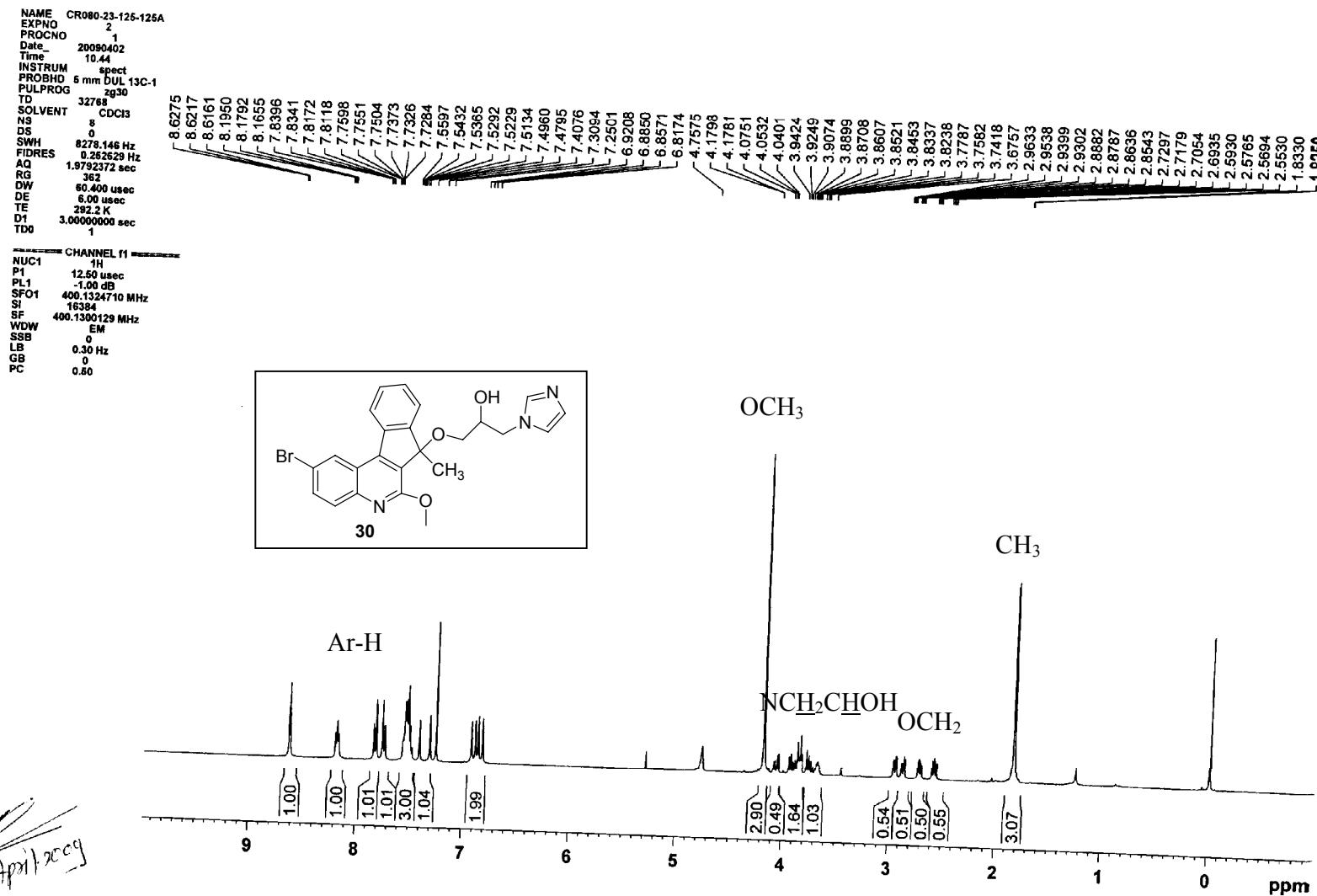
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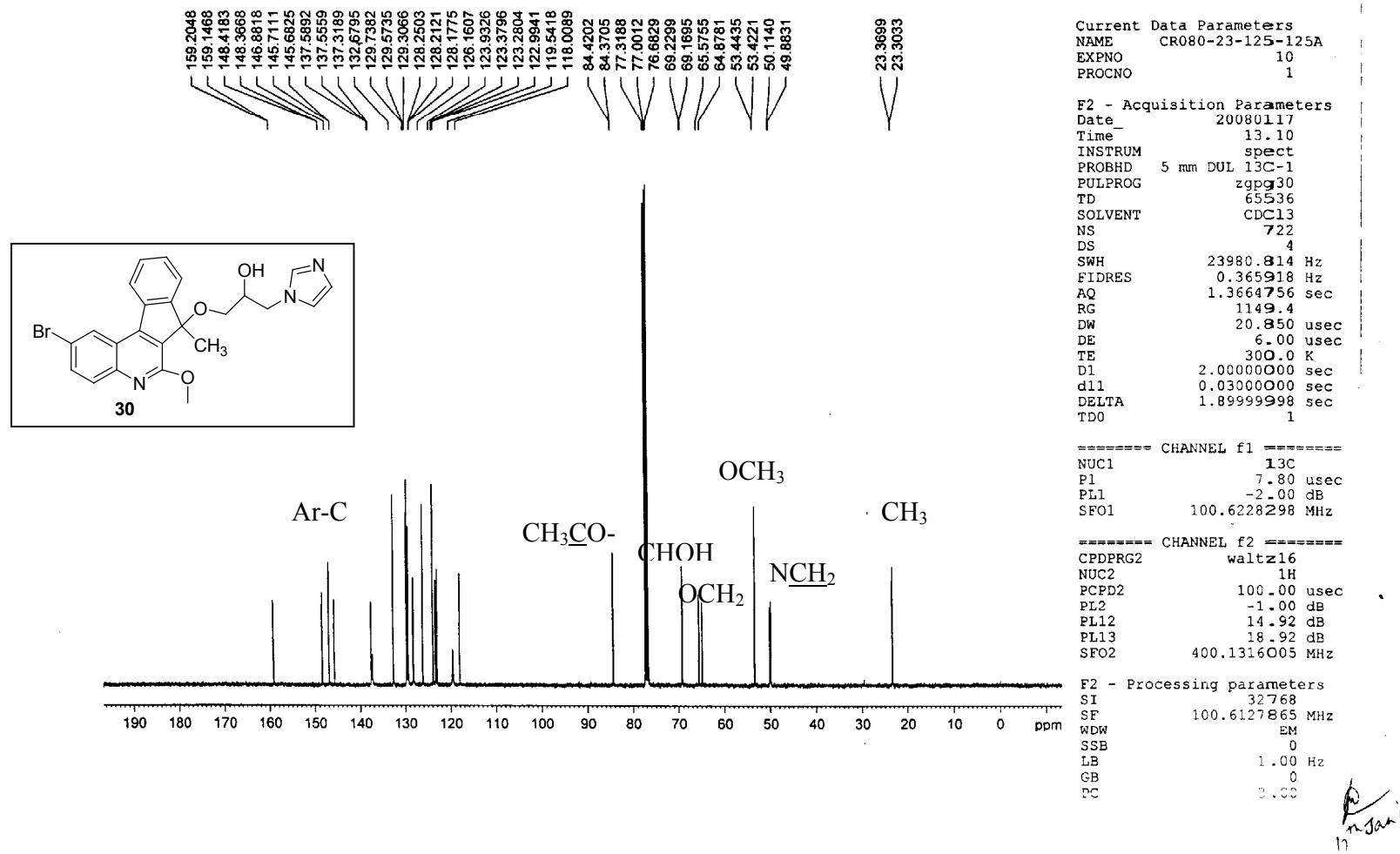


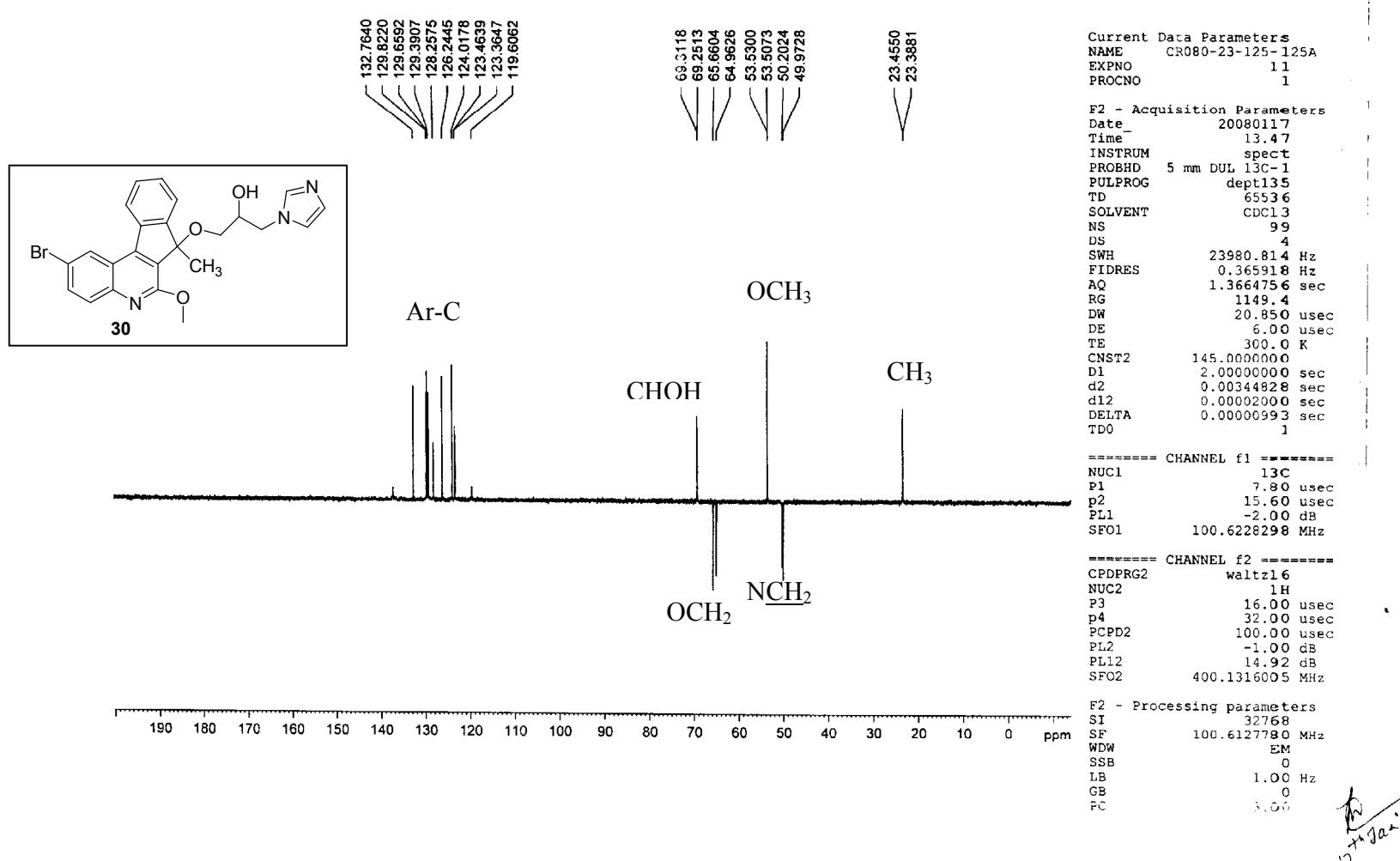
(Pankaj)
22nd June 07

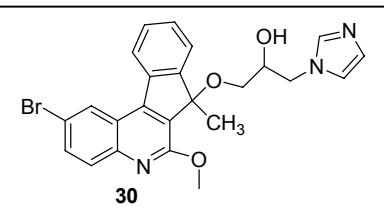












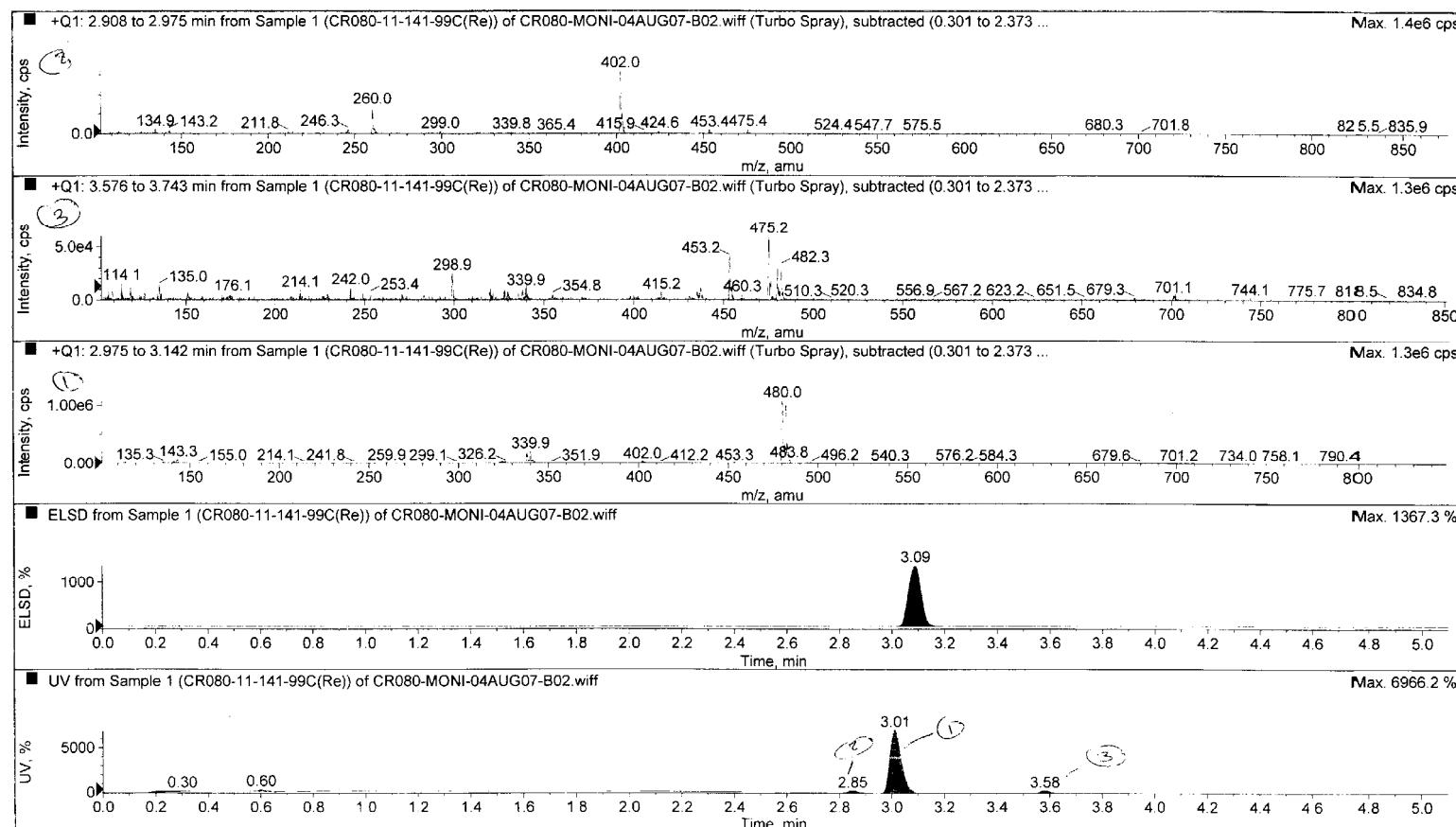
(Comp - 31)

**CHEMBIOTEK RESEARCH INTERNATIONAL , PUNE, INDIA *

Sample Name: CR080-11-141-99C(Re) (IMM-60)

Acq. Time: 18:54

Acq. Date: Saturday, August 04, 2007



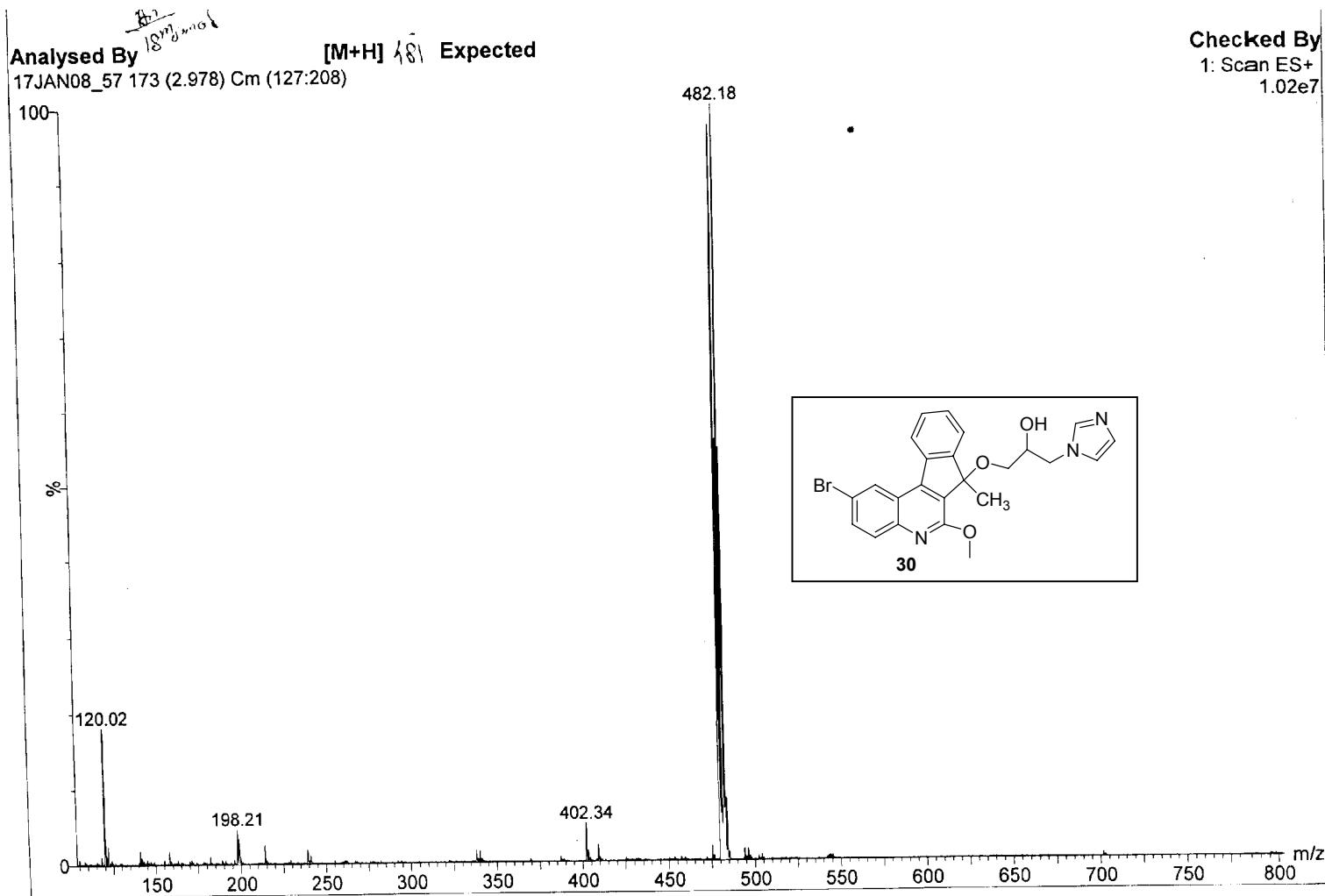
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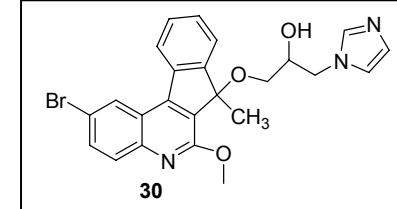
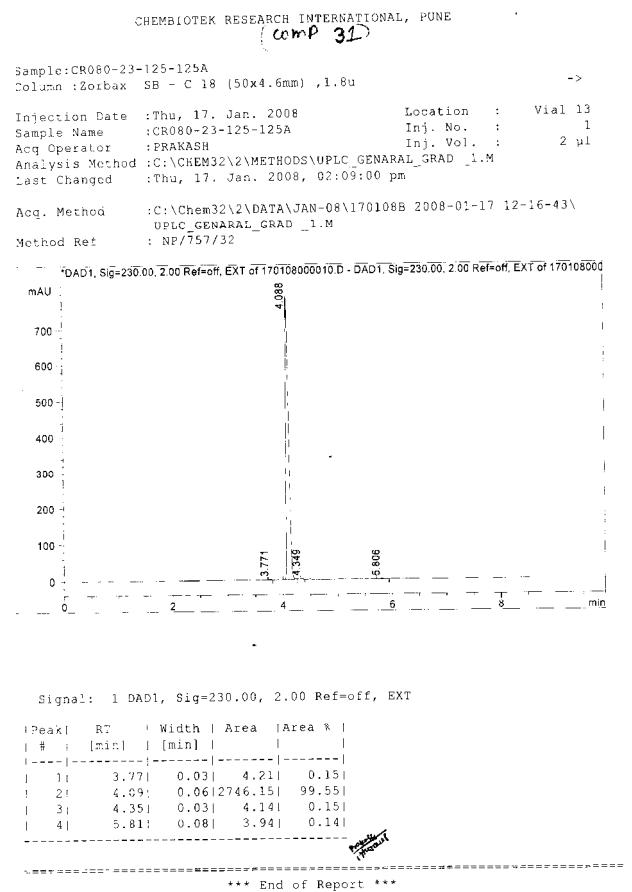
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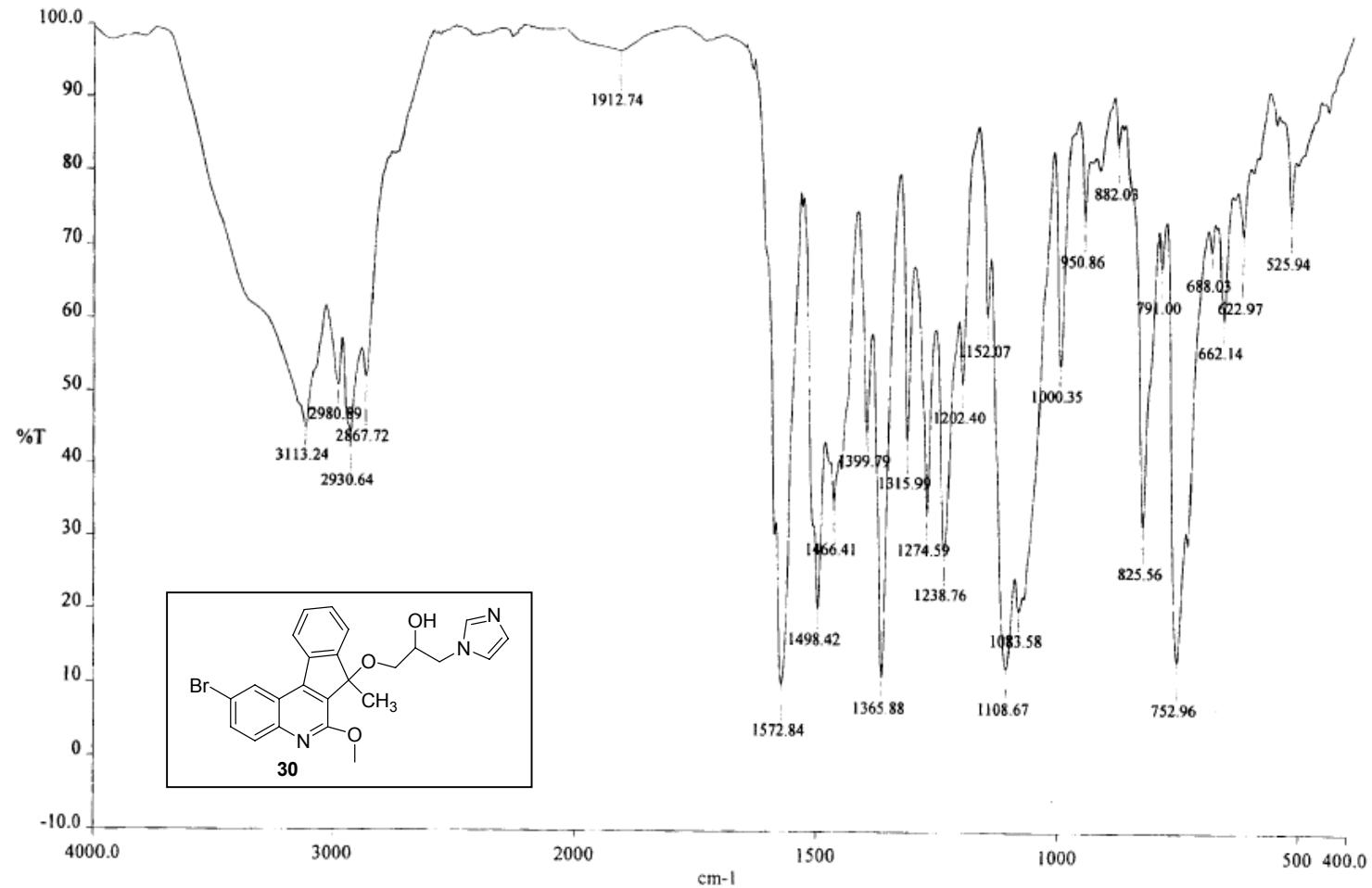
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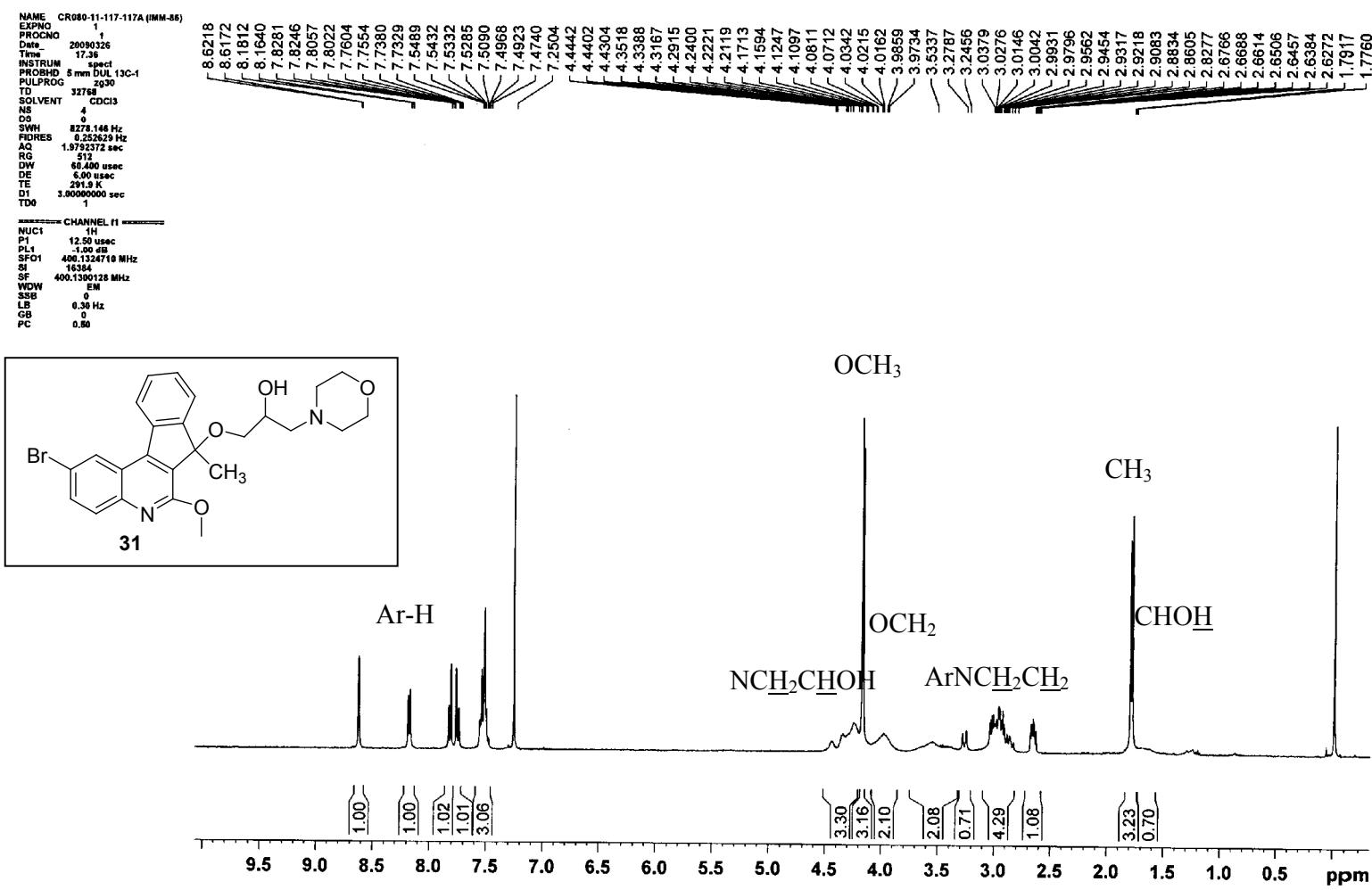
An
14th August 2007

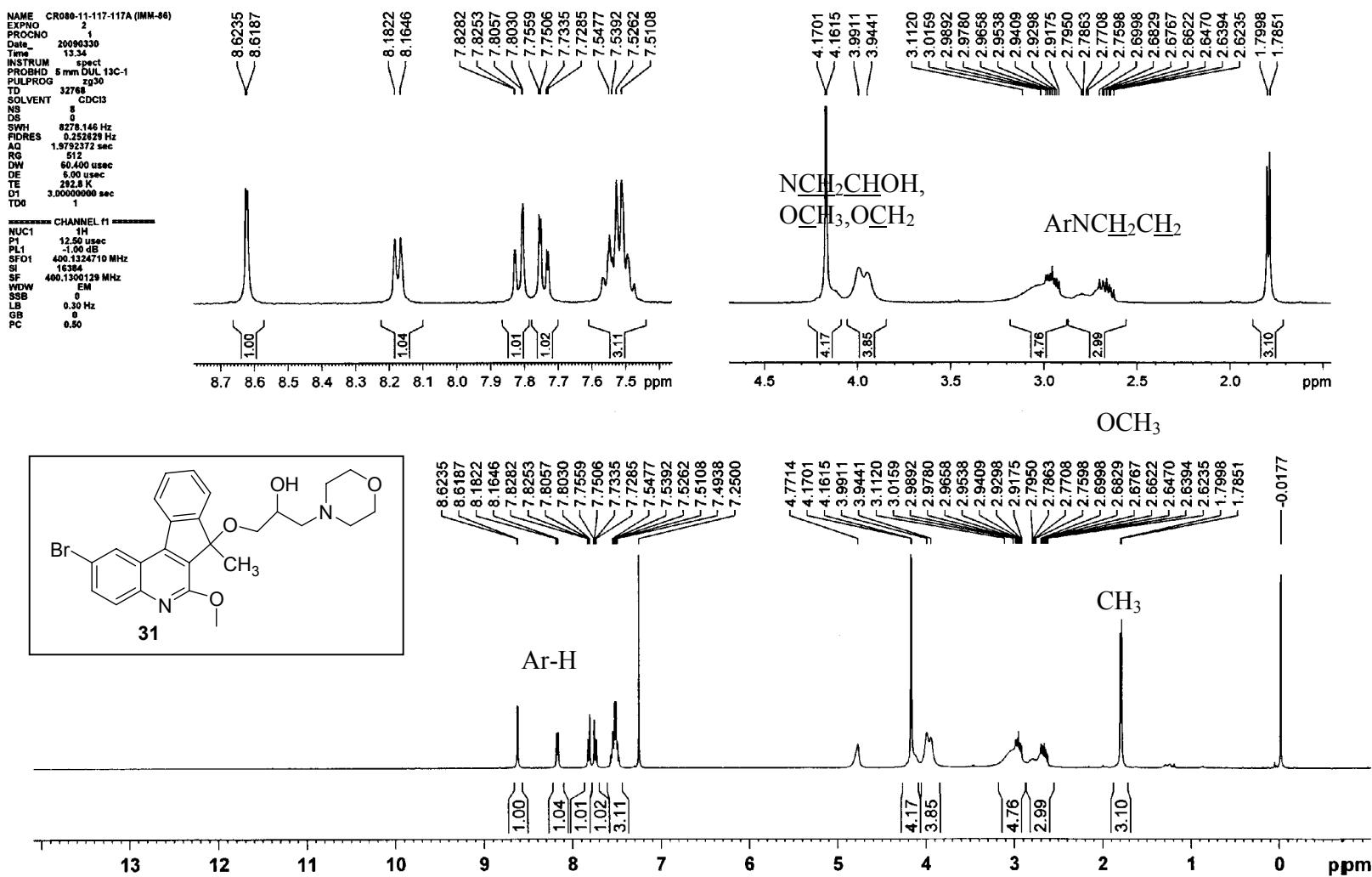
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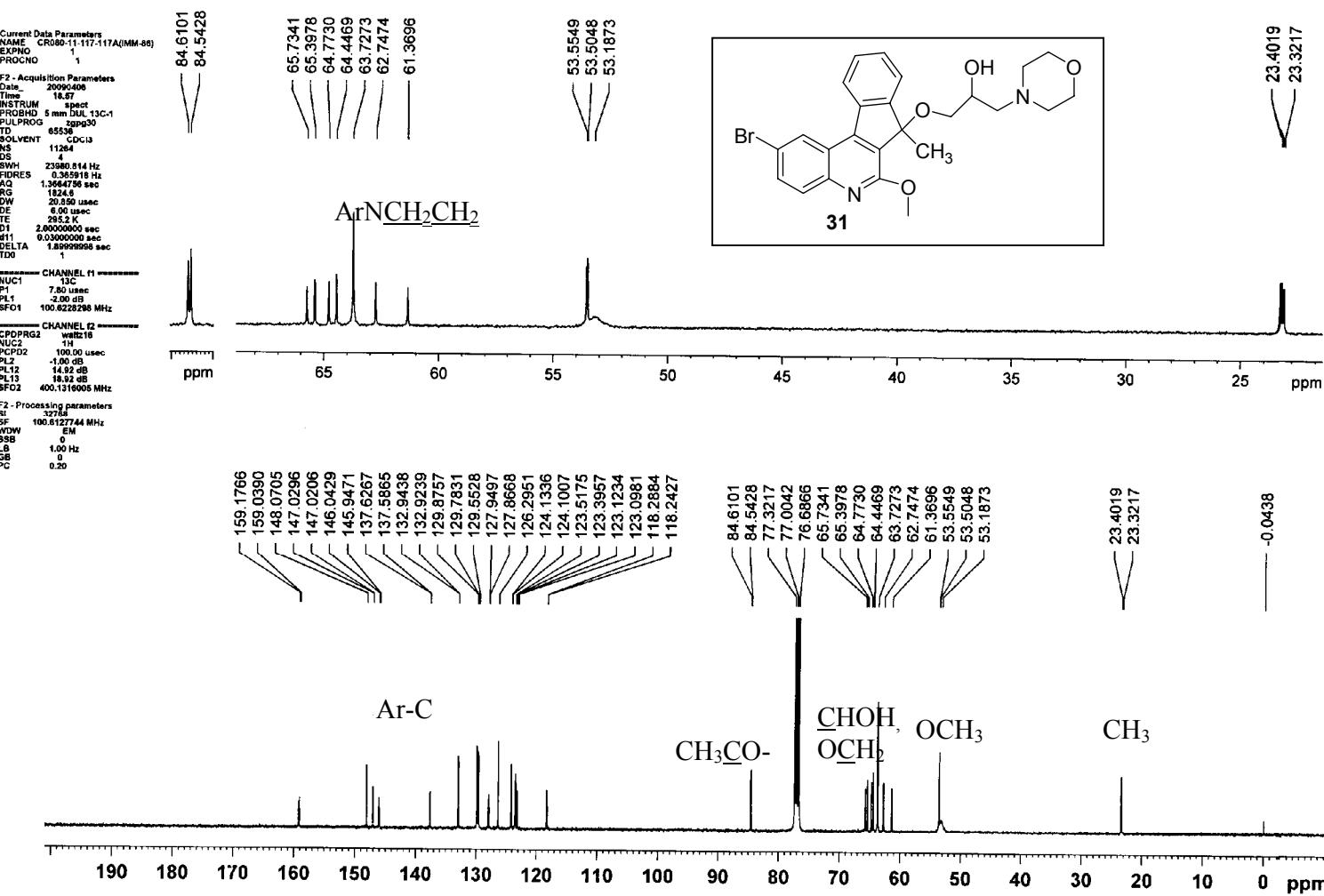


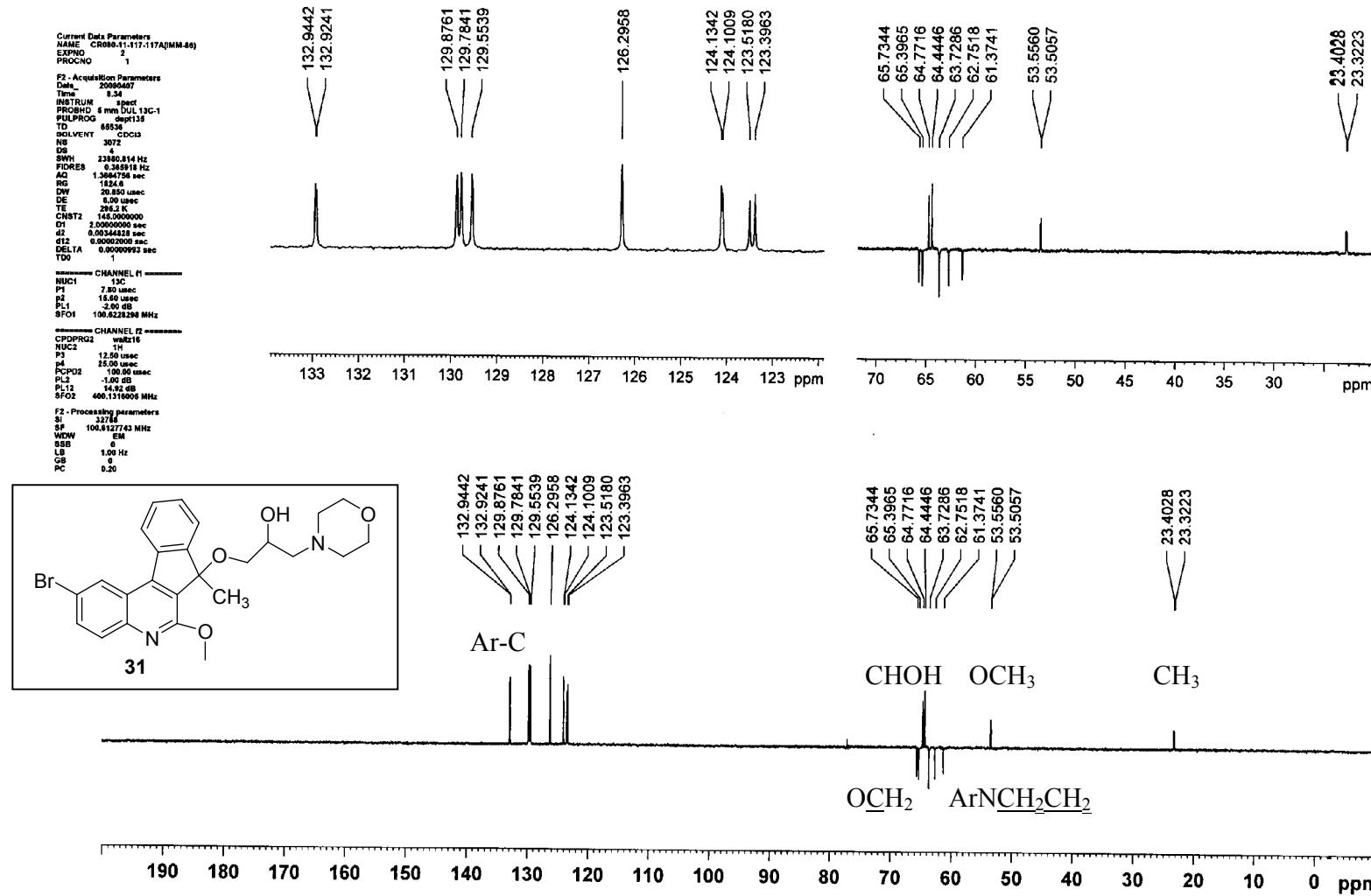


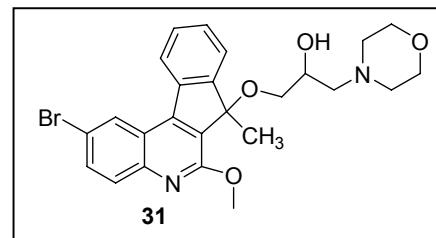
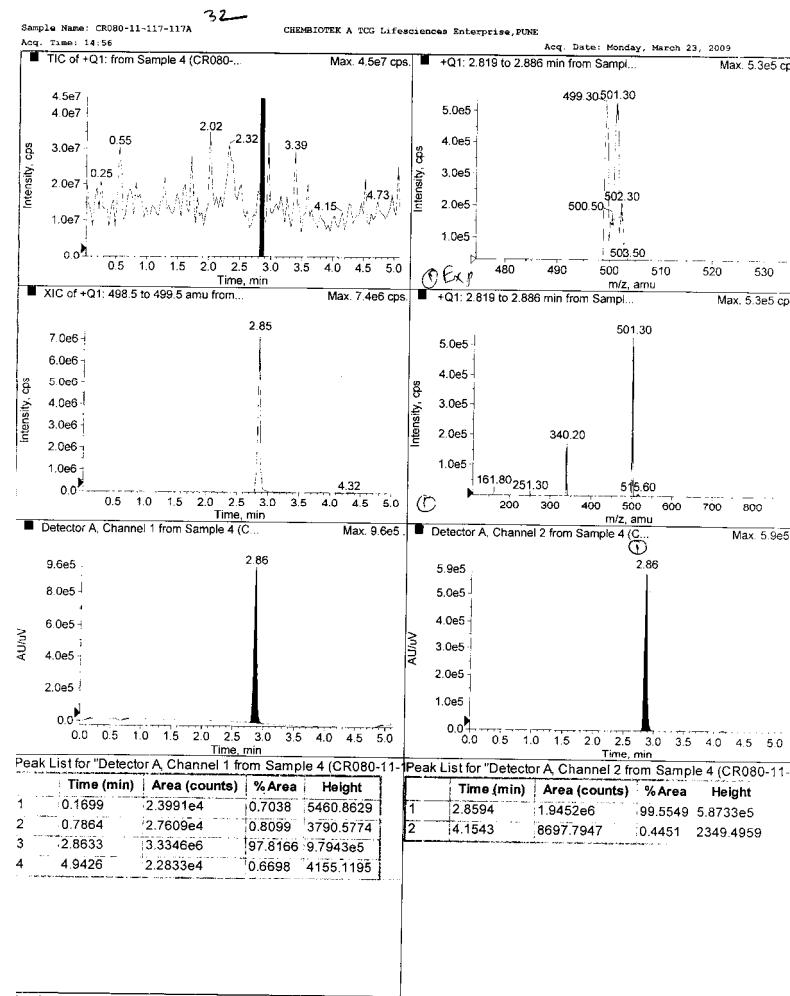


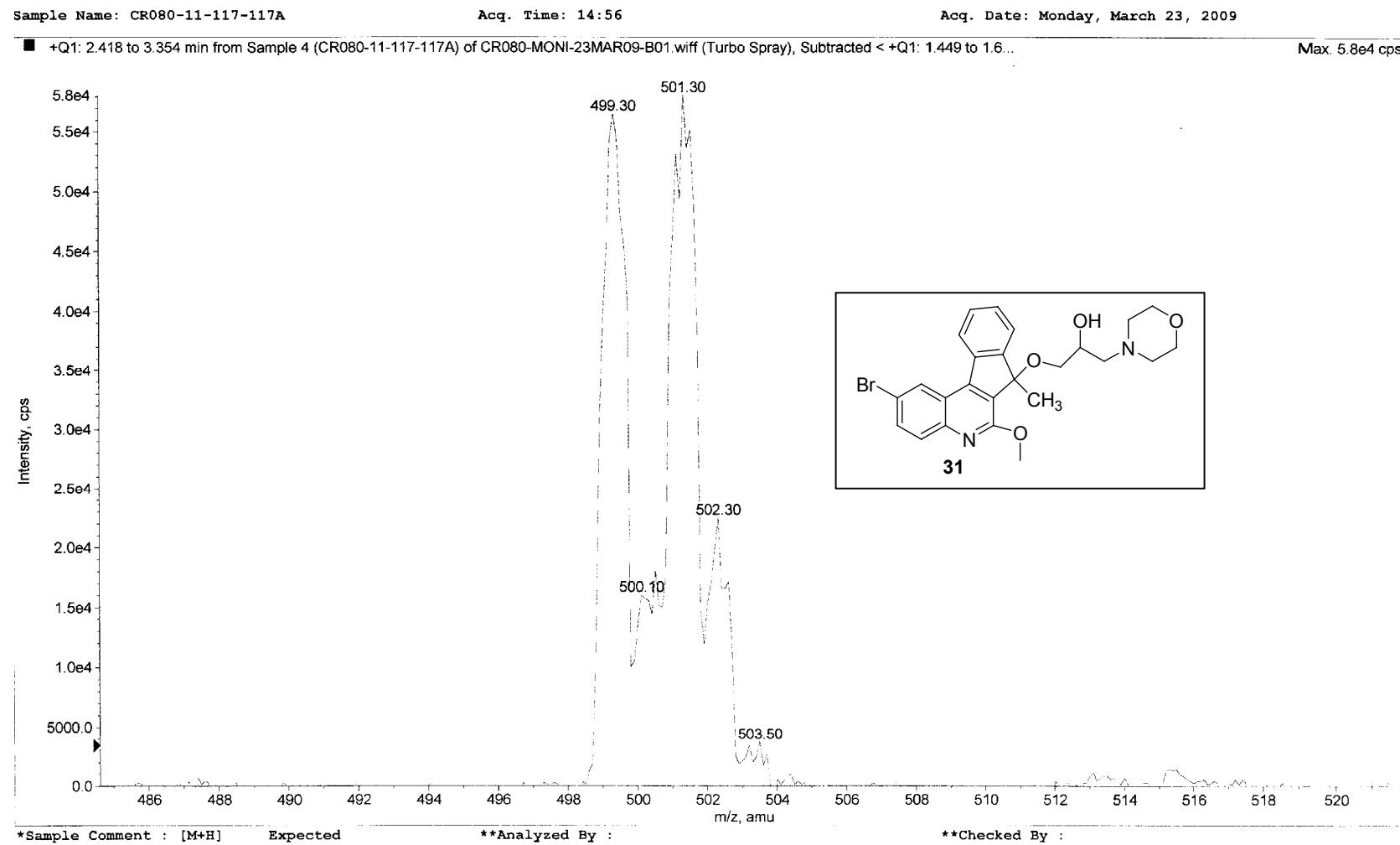






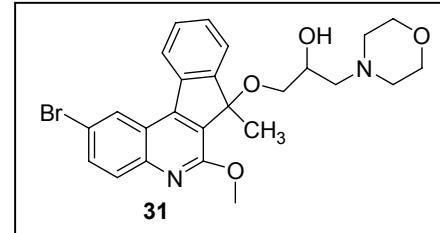
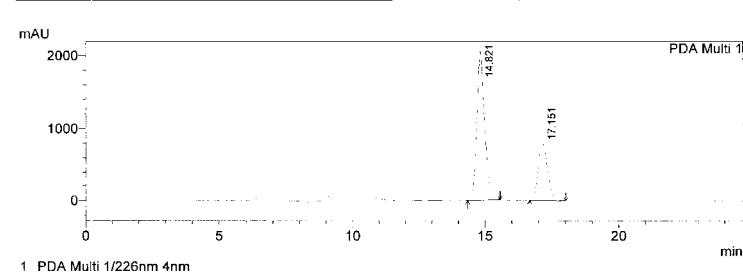






Sample Name : CR080-11-117-117A
Sample ID : CR080-11-117-117A
Column : CHIRALPAK AD-H (250 x 4.6 mm)
Vial # : 11
Inj. Volume : 10 uL
Tray # : 1
Acquired by : PANKAJ

Data File Name : 04_10_08_CR080-11-117-117A_05.lcd
Method File Name : CR156_01.lcm
Batch File Name :
Data Acquired : 10/4/2008 12:35:19 PM
Data Processed : 10/4/2008 1:00:02 PM

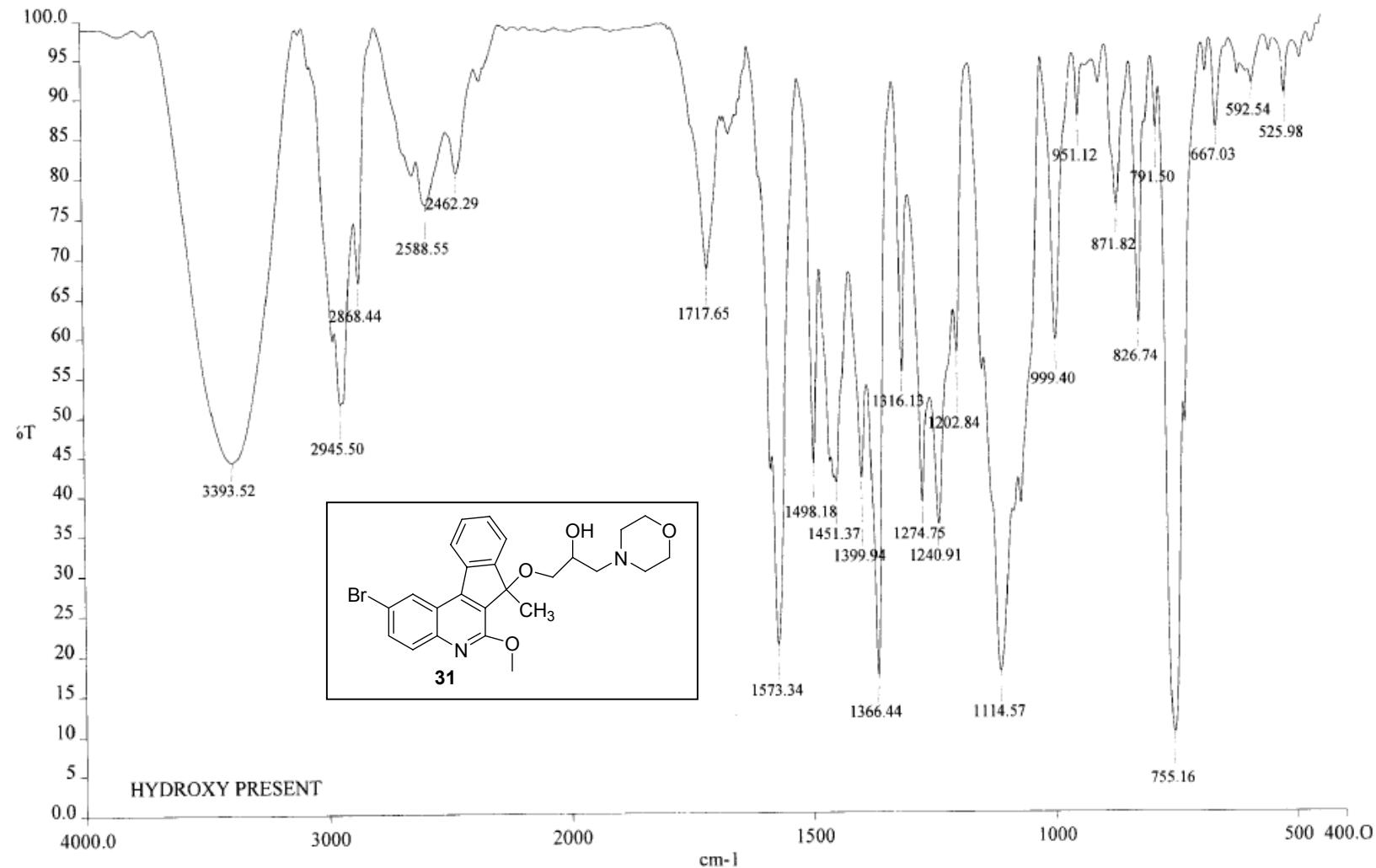


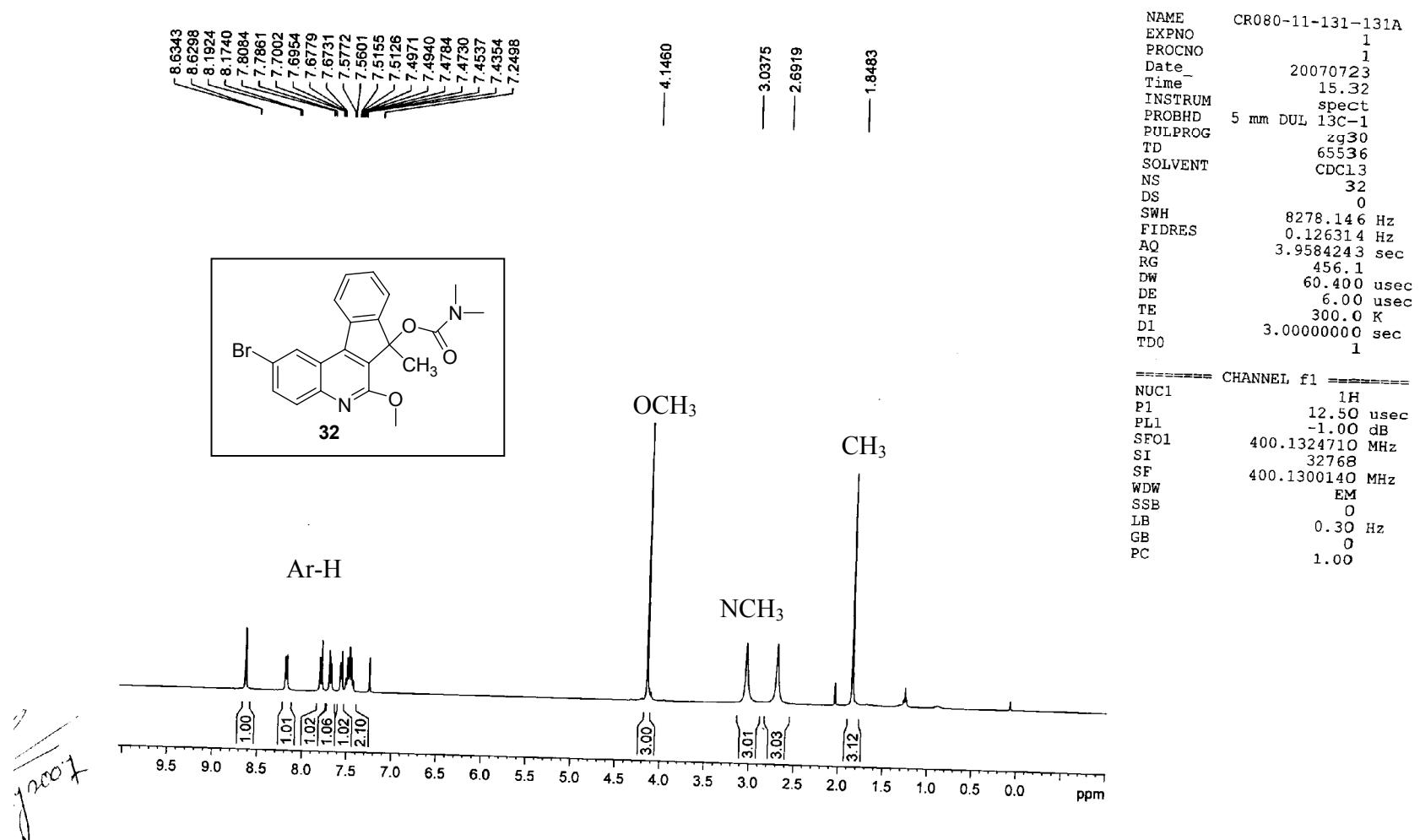
PeakTable				
Peak#	Ret. Time	Area	Area %	Height
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2	17.151	19509390	31.842	798966
Total		61269357	100.000	2868964

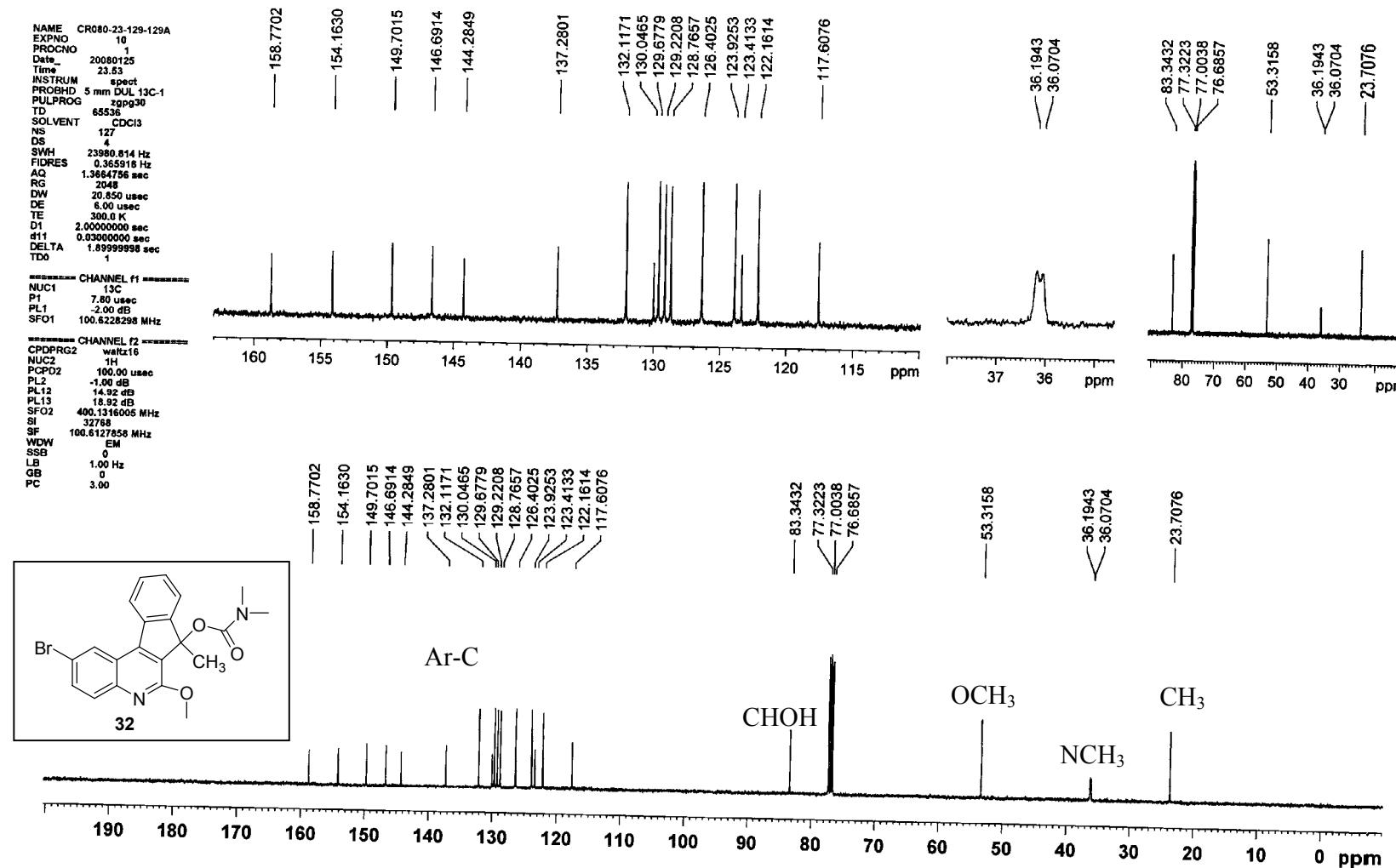
Phenomenex
10³ octadec

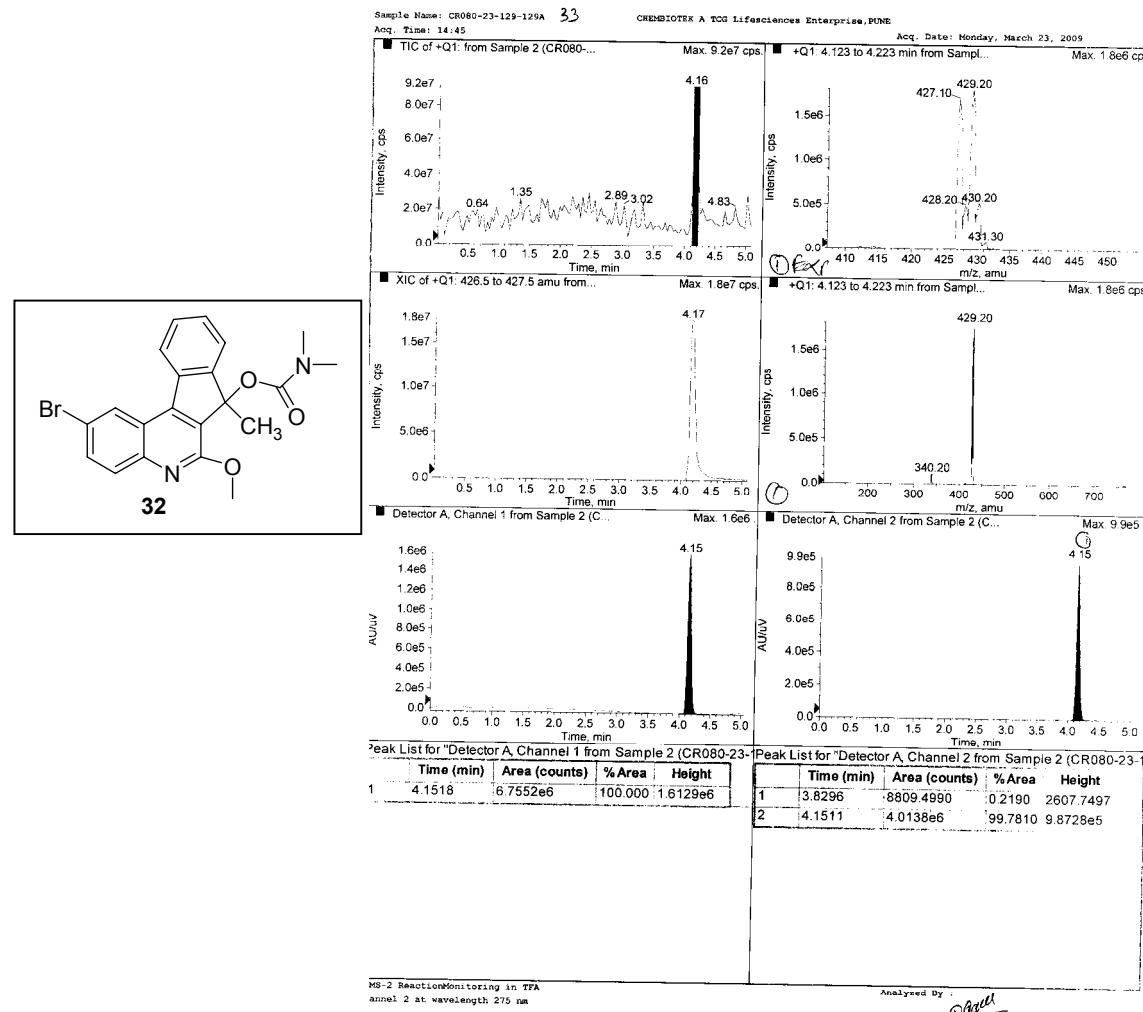
Normal phase.

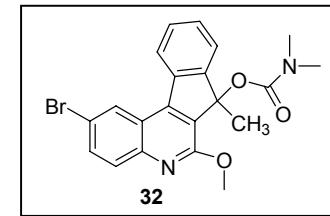
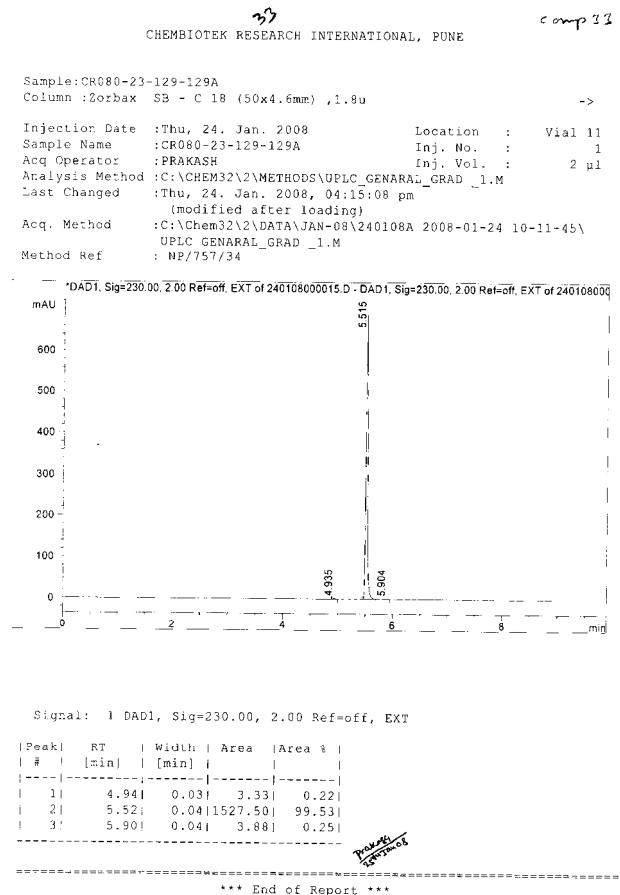
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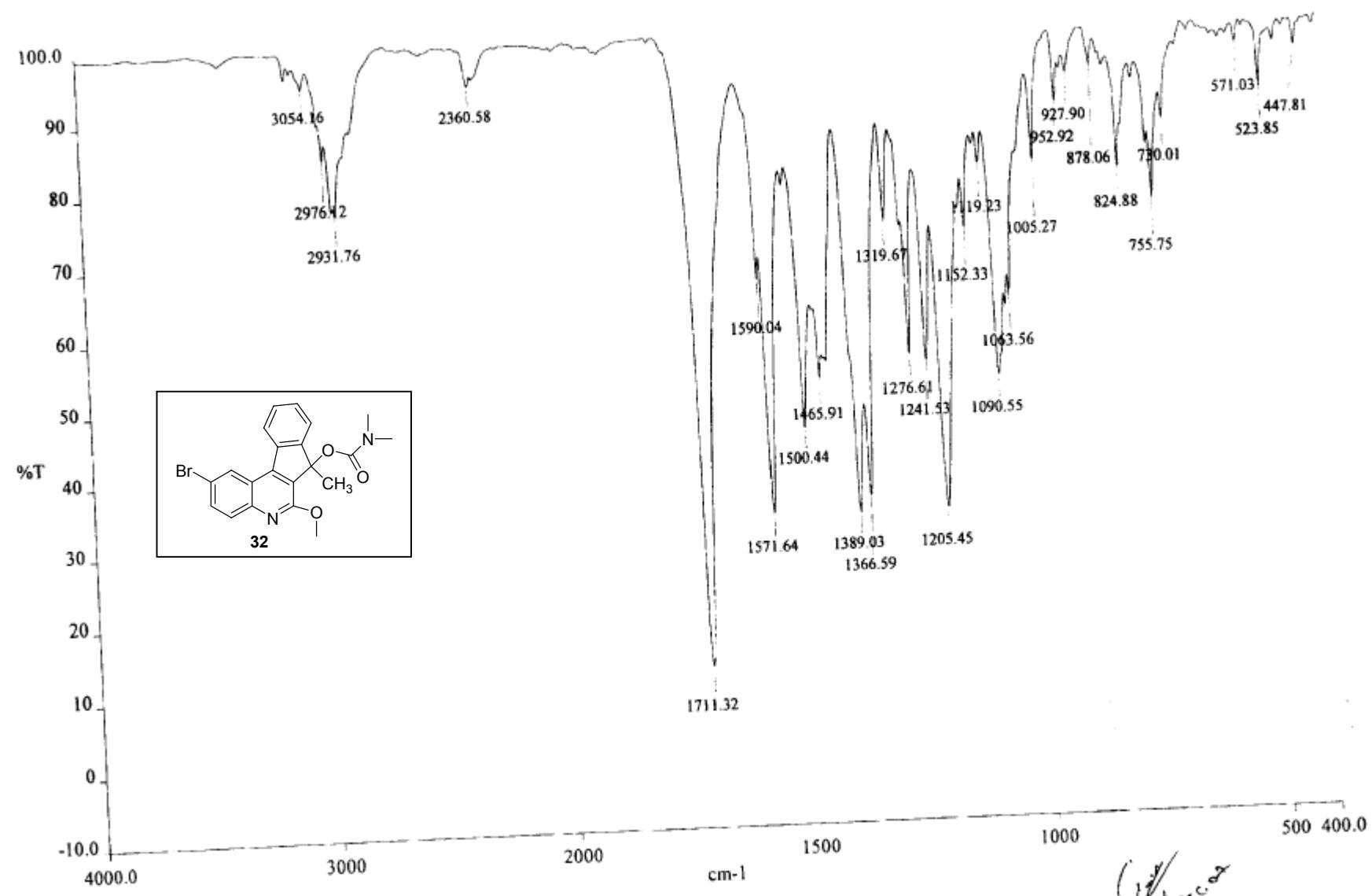


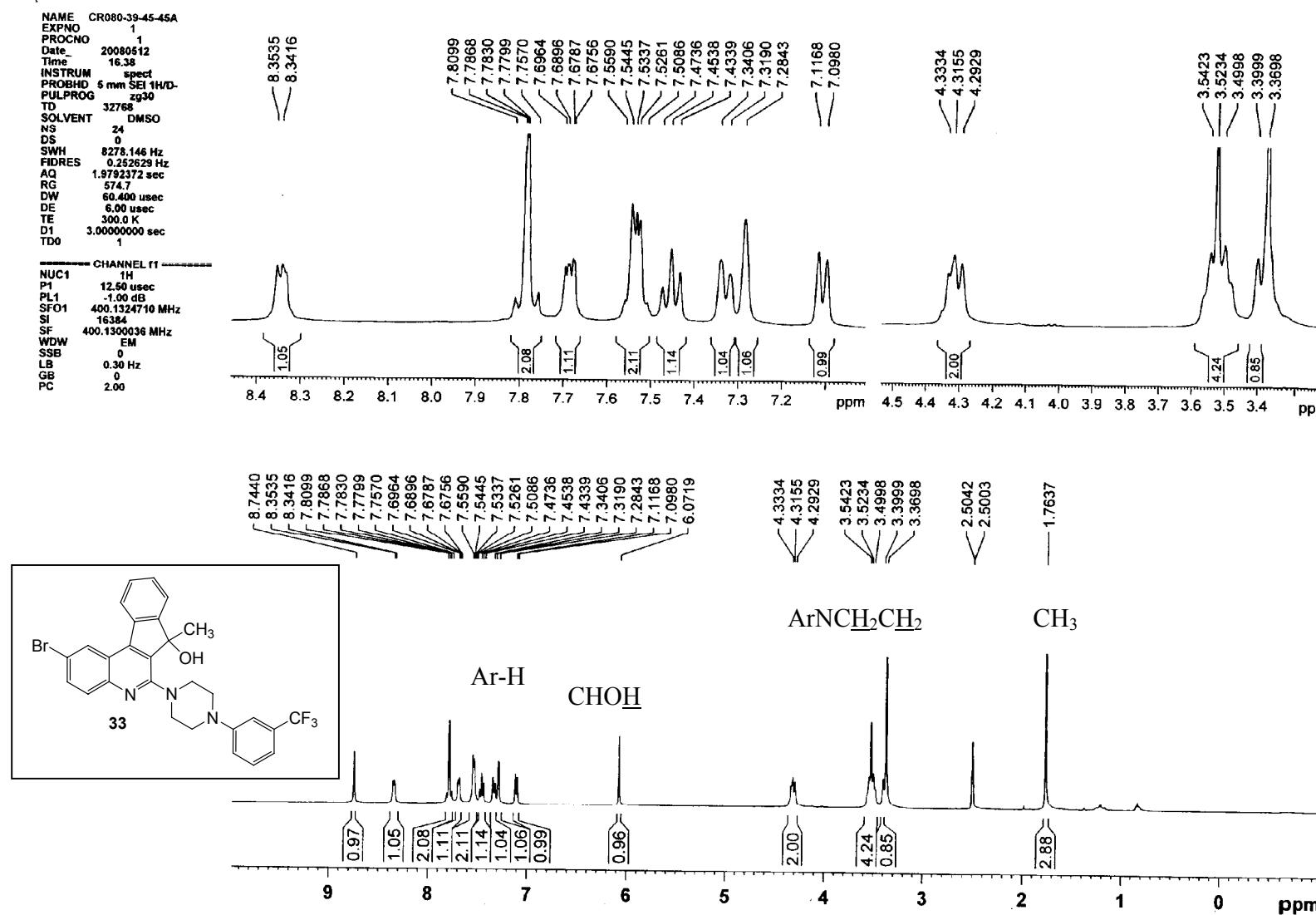






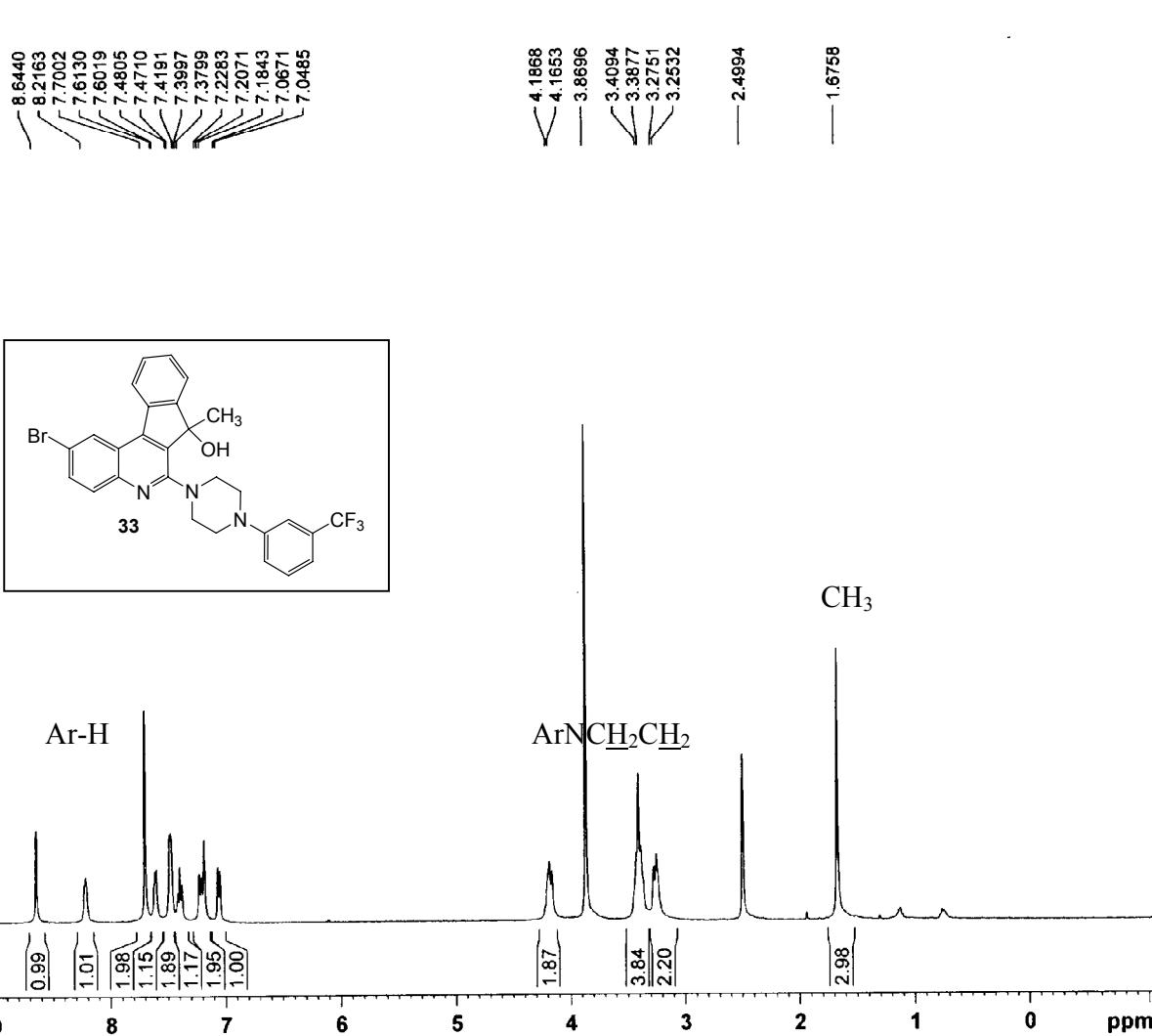


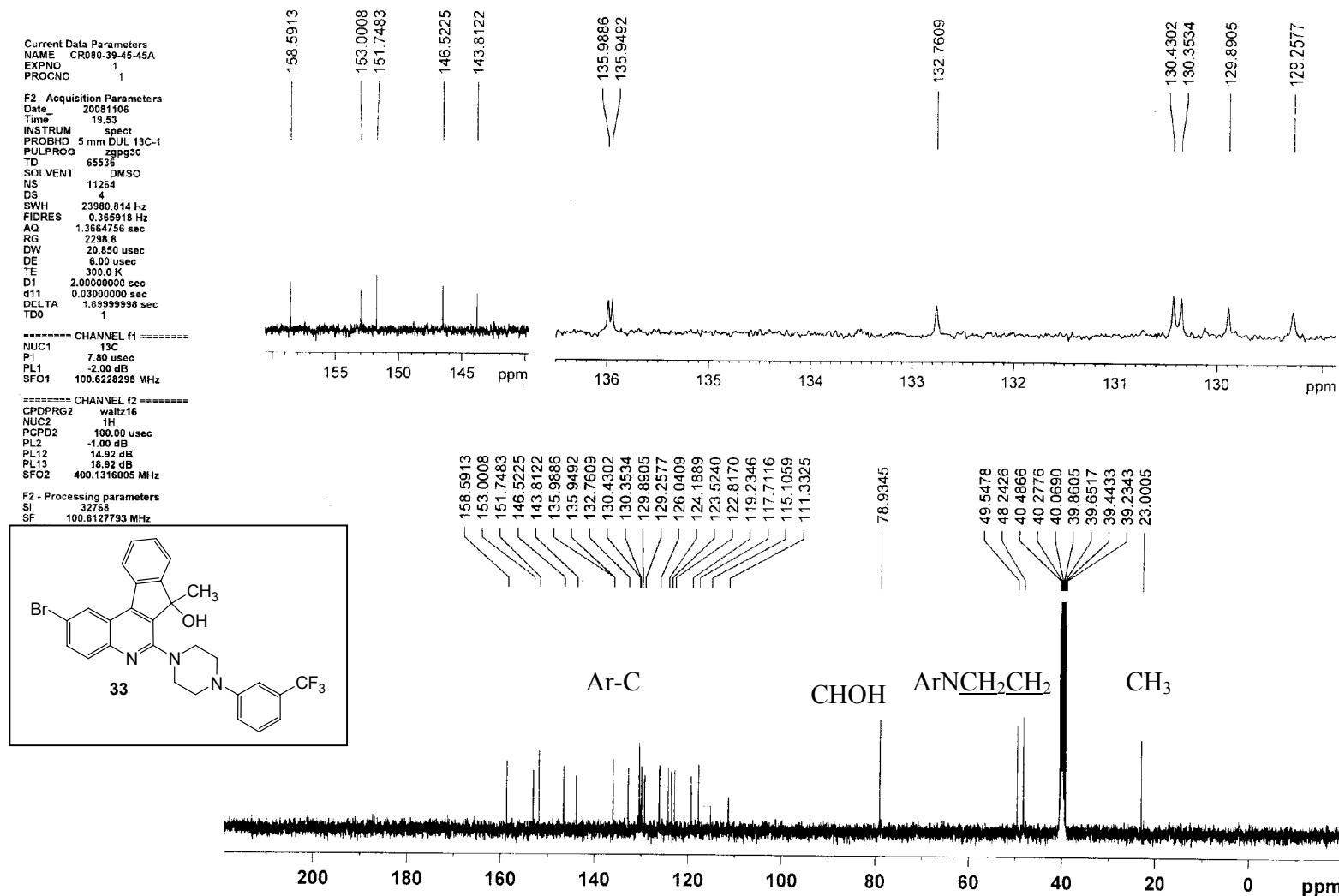


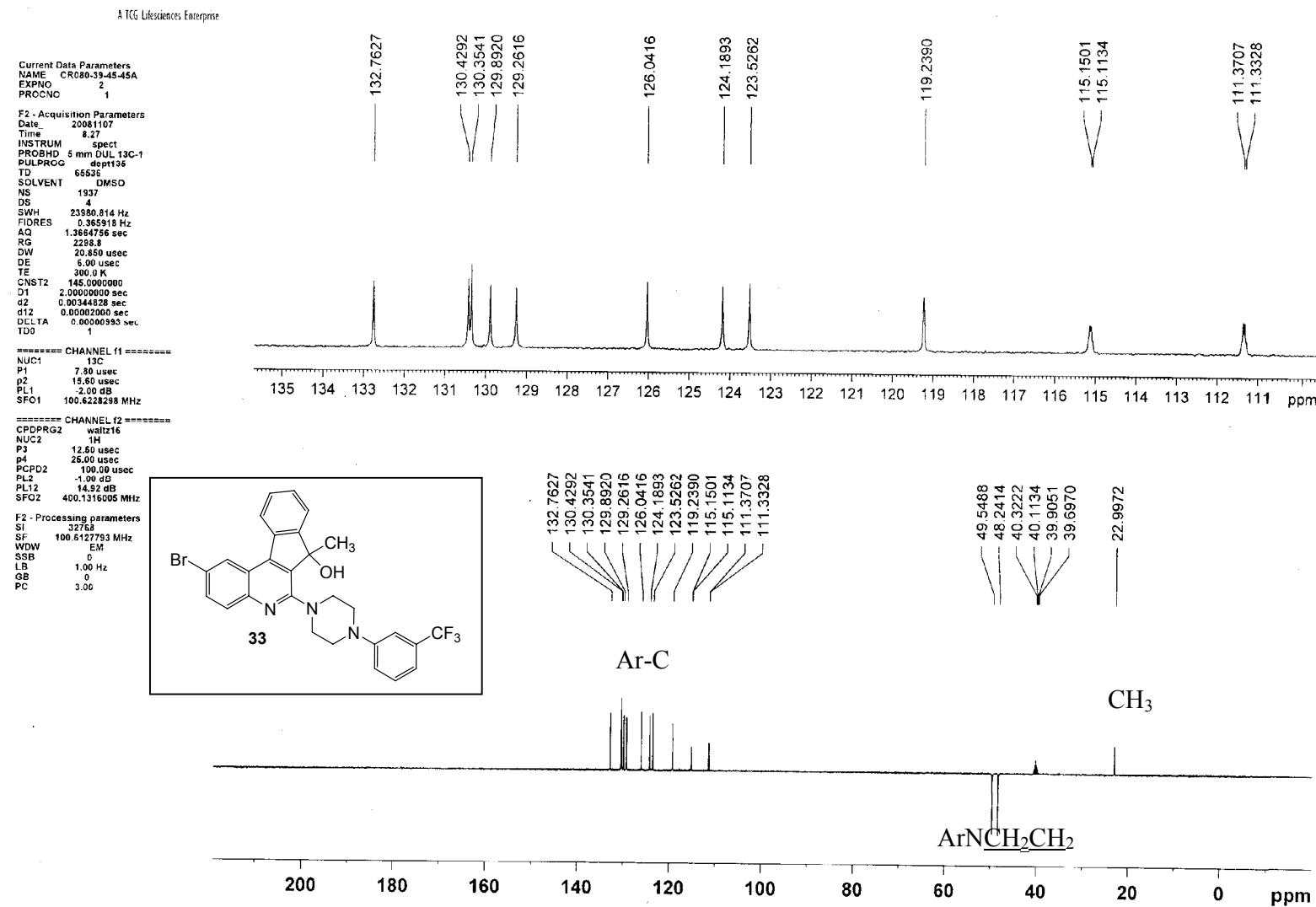


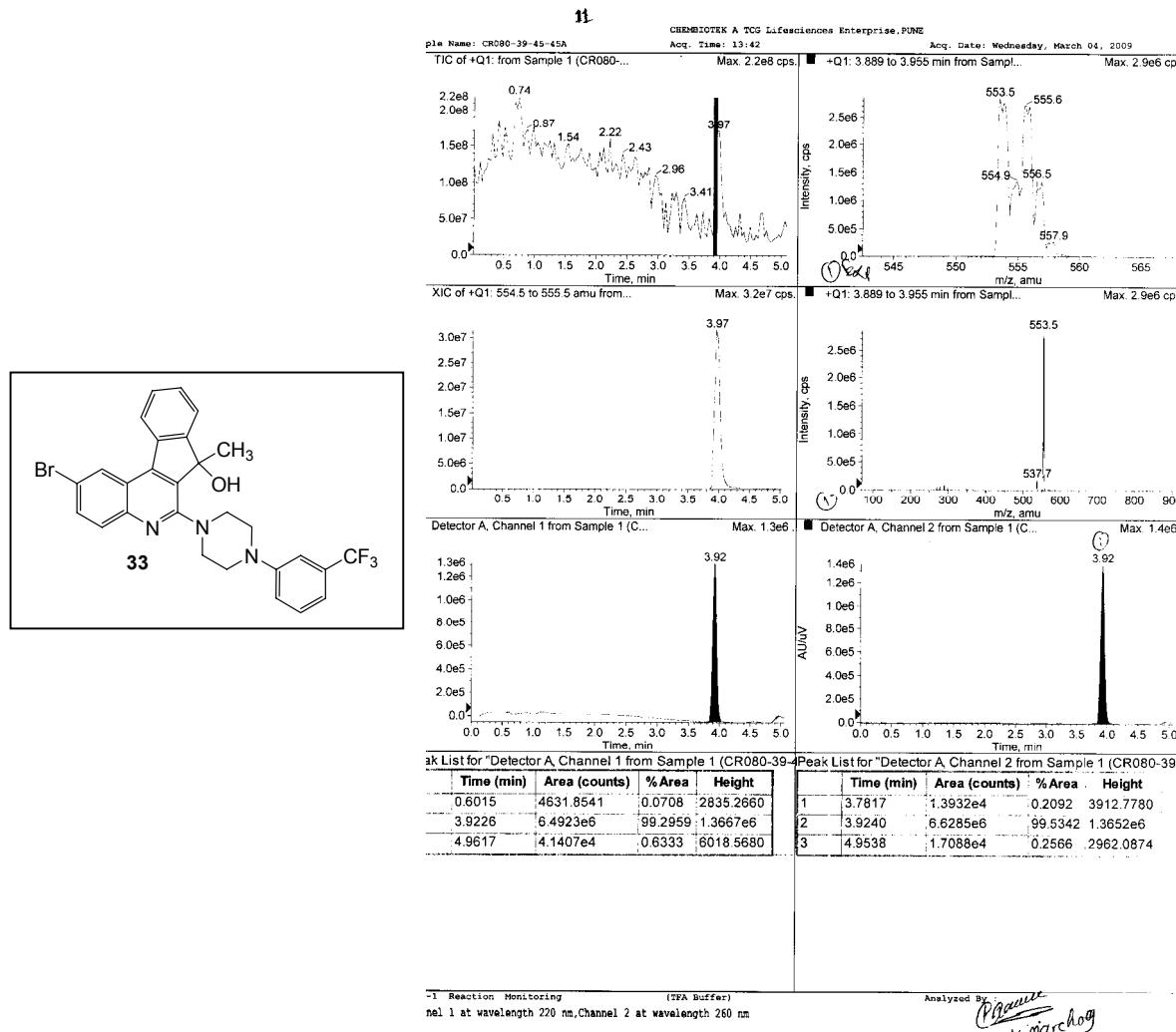
NAME CR080-39-46-45A
EXPNO 2
PROCNO 1
Date 20080513
Time 13.03
INSTRUM spect
PROBHD 5 mm SEI 1H/D-
PLP/PROG z930
TD 32768
SOLVENT DMSO
NS 4
DS 0
SWH 8278.146 Hz
FIDRES 0.252629 Hz
AQ 1.8782372 sec
RG 574.7
DW 60.400 usec
DE 6.00 usec
TE 300.0 K
D1 3.0000000 sec
TD0 1

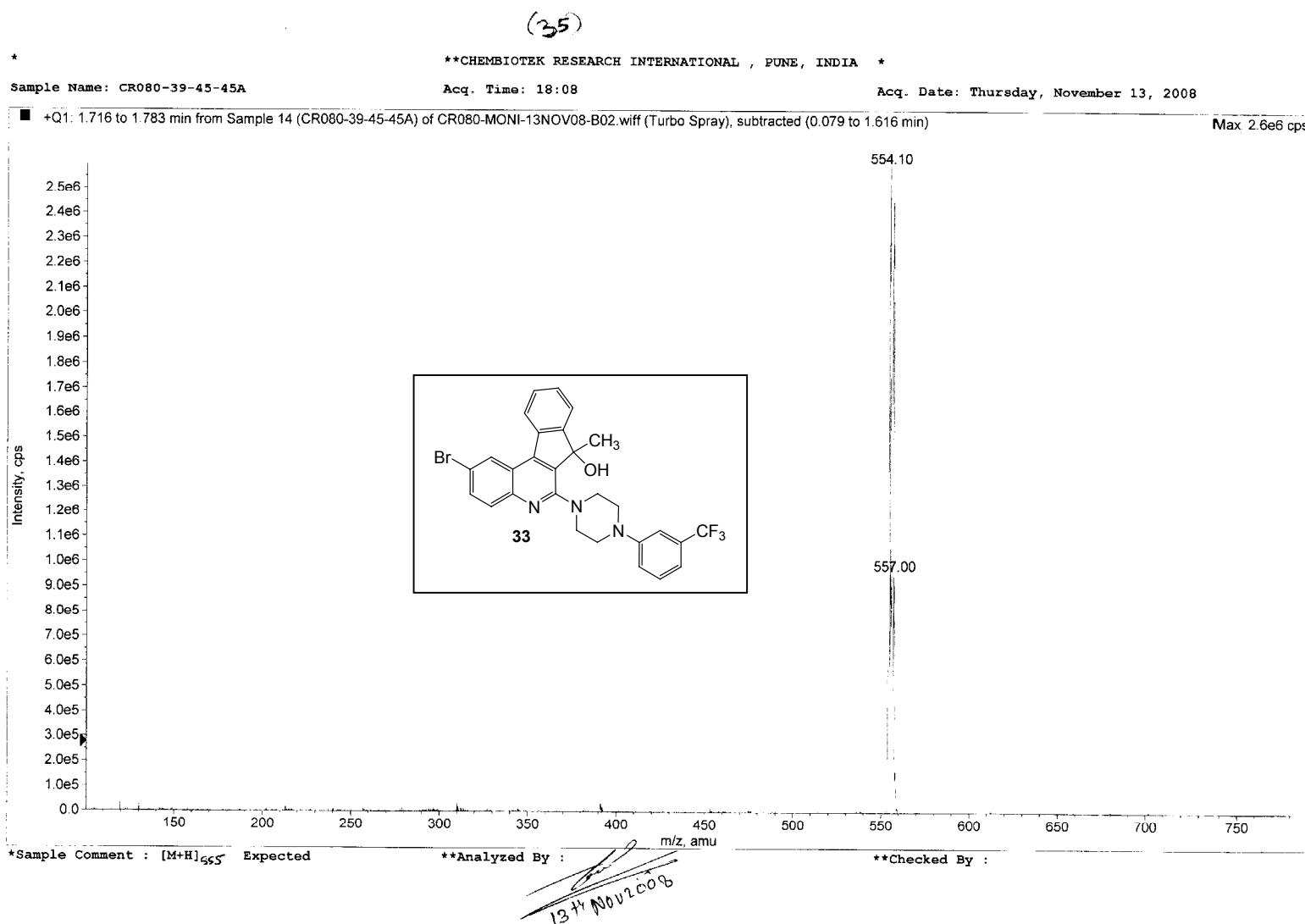
===== CHANNEL f1 =====
NUC1 1H
P1 12.60 usec
PL1 -1.00 dB
SFO1 400.1324710 MHz
SI 16384
SF 400.1300059 MHz
WDW EM
SSB 0
LB 0.30 Hz
GB 0
PC 2.00

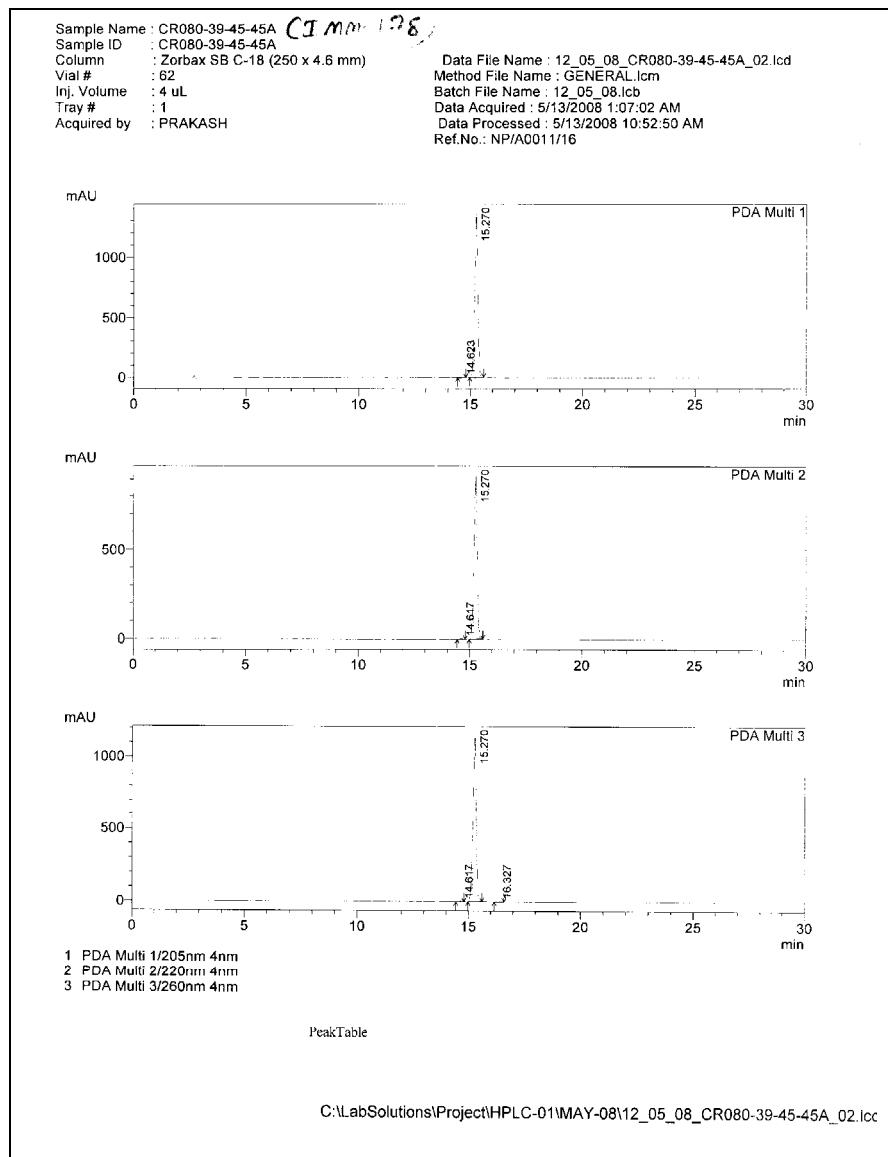












HPLC-01 PDA Ch1 205nm 4nm				
Peak#	Ret. Time	Area	Area %	Height
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2	15.270	13134395	99.830	1361208
Total		13156782	100.000	1364090

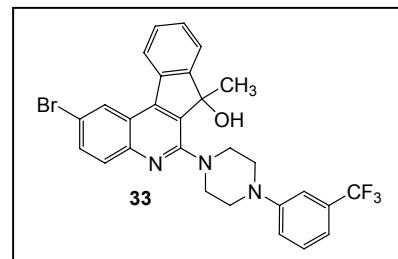
PeakTable

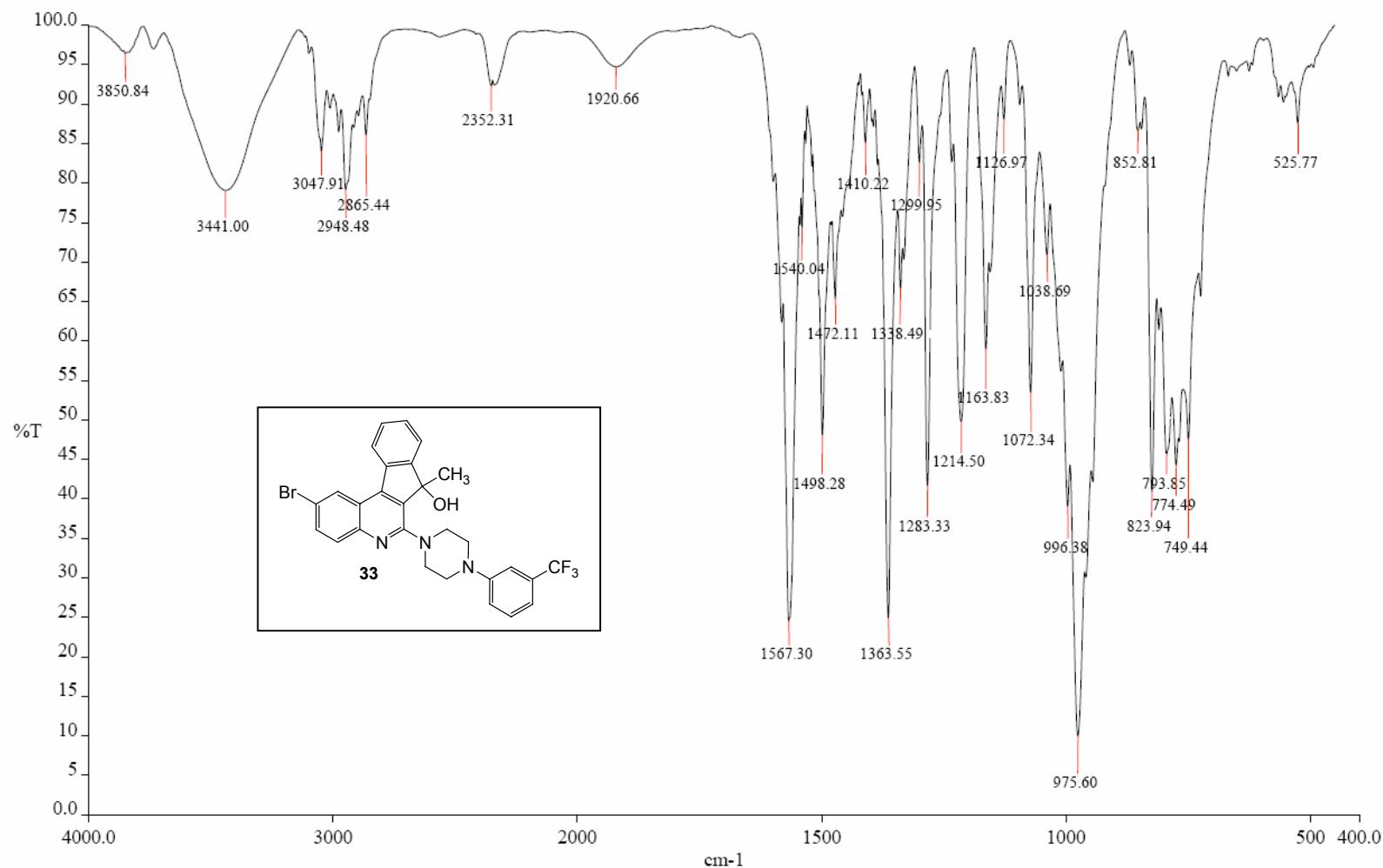
HPLC-01 PDA Ch2 220nm 4nm				
Peak#	Ret. Time	Area	Area %	Height
1	14.617	17830	0.194	2289
2	15.270	9151775	99.806	922278
Total		9169605	100.000	924567

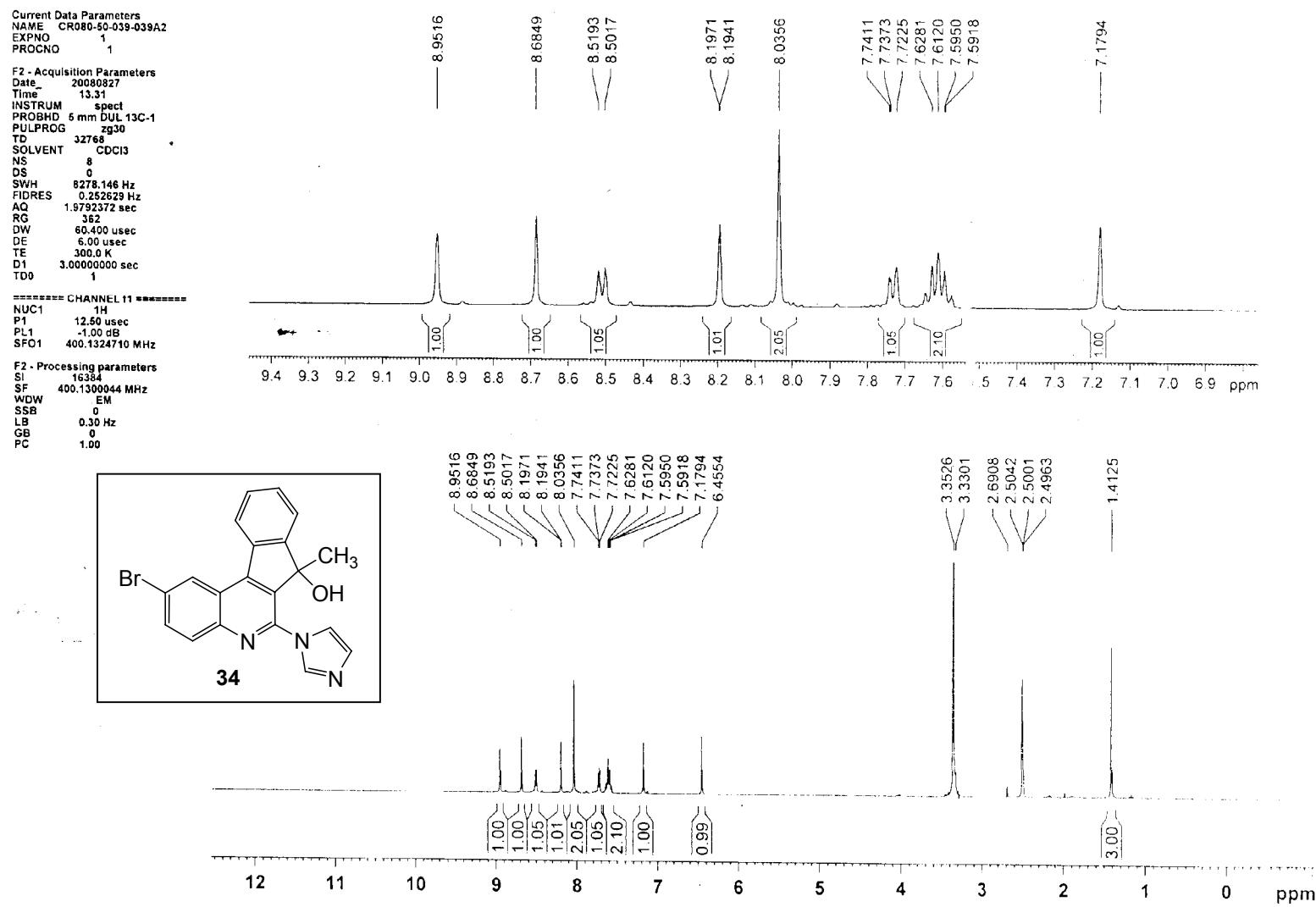
PeakTable

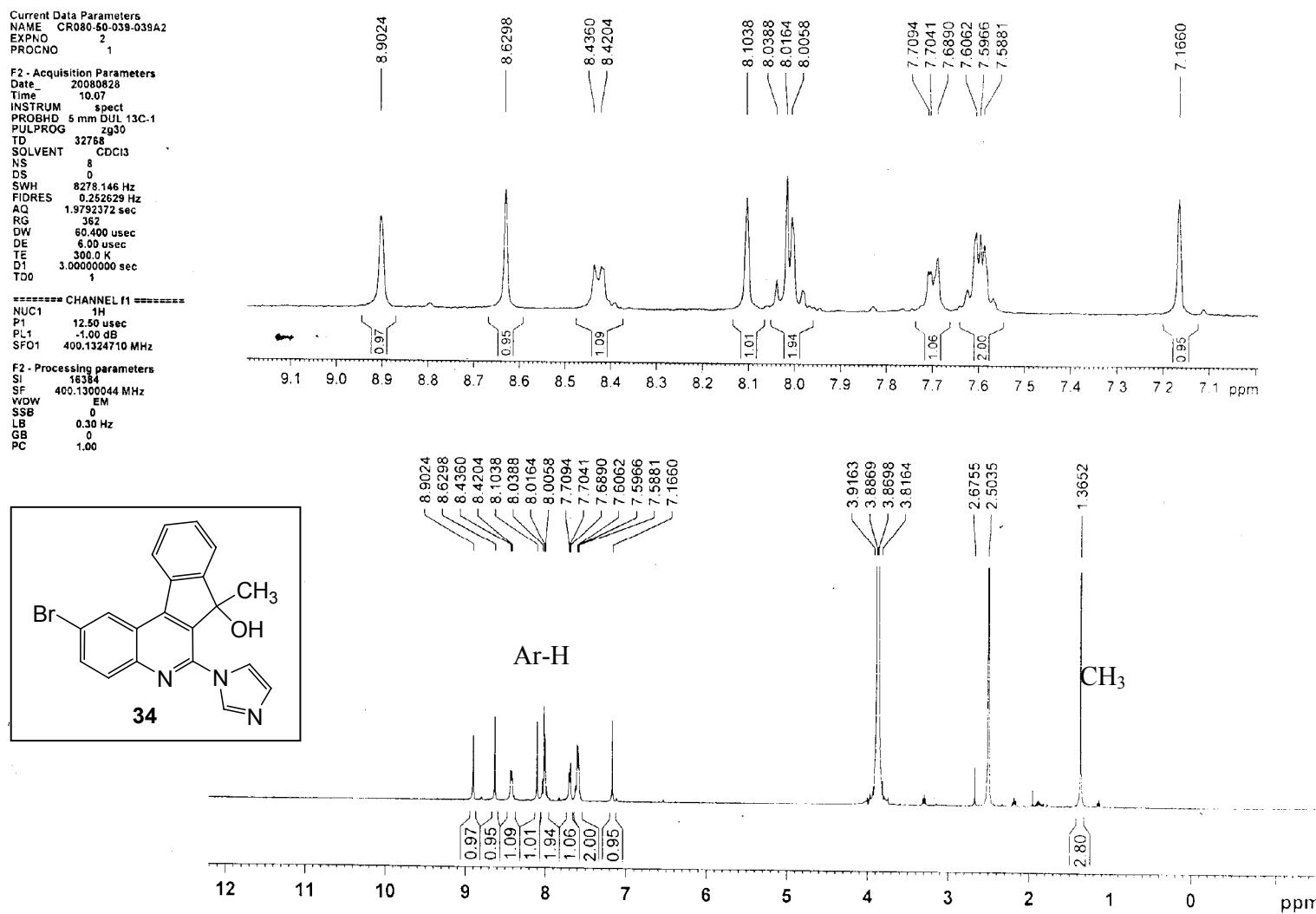
HPLC-01 PDA Ch3 260nm 4nm				
Peak#	Ret. Time	Area	Area %	Height
1	14.617	21224	0.186	2721
2	15.270	11373125	99.707	1146475
3	16.327	12188	0.107	1056
Total		11406537	100.000	1150252

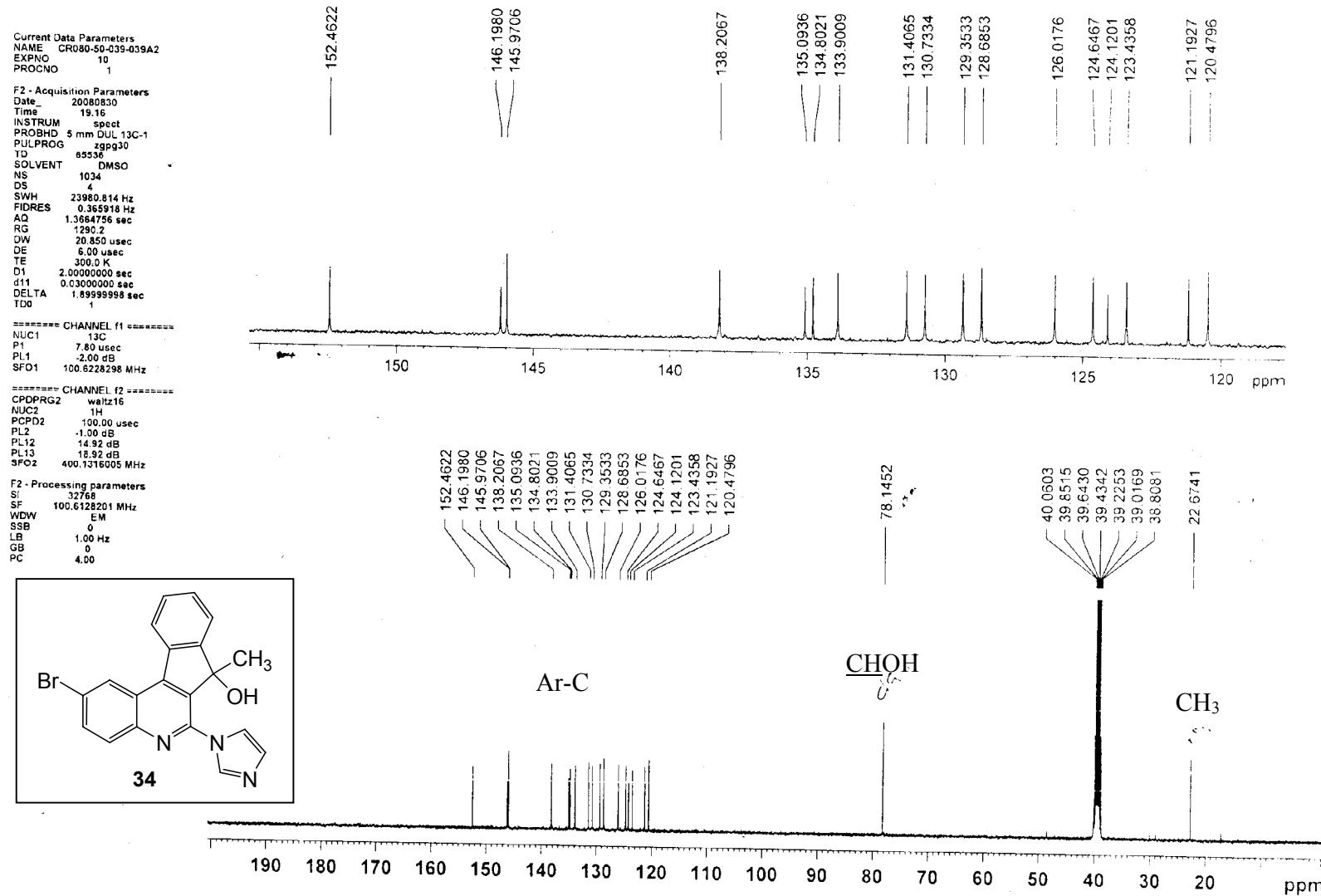
*Peak 1
 14.617 min*

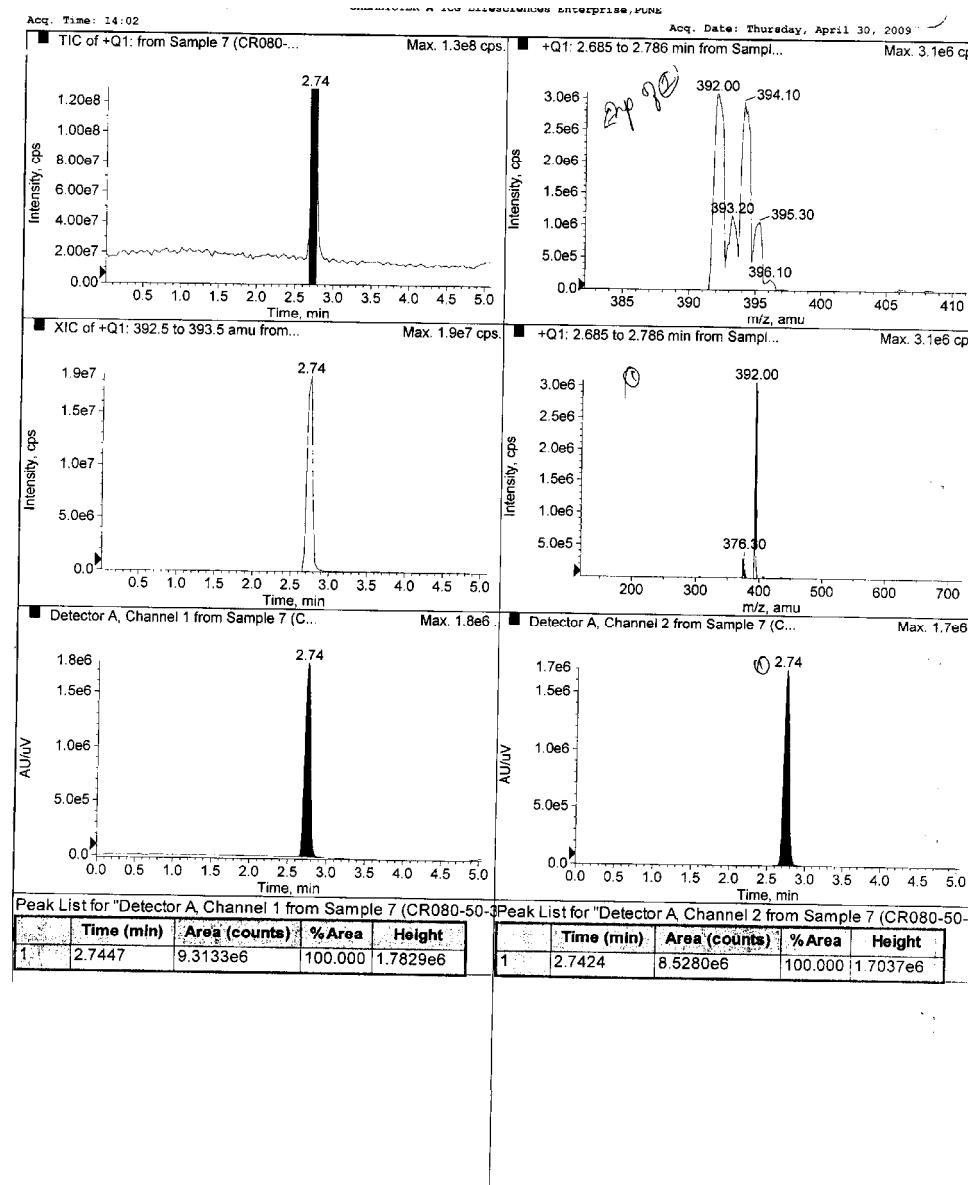
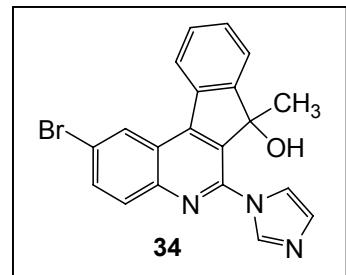


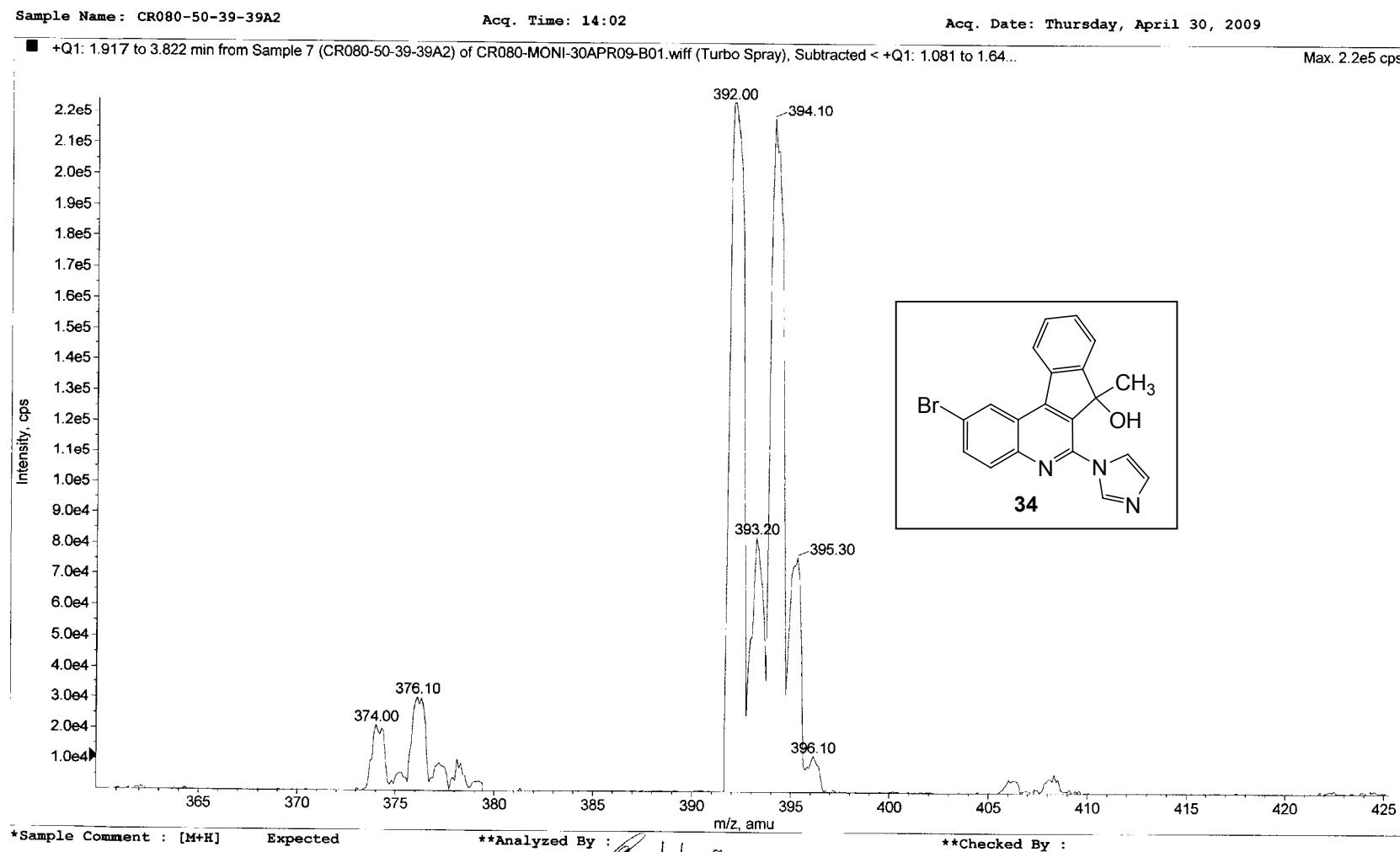


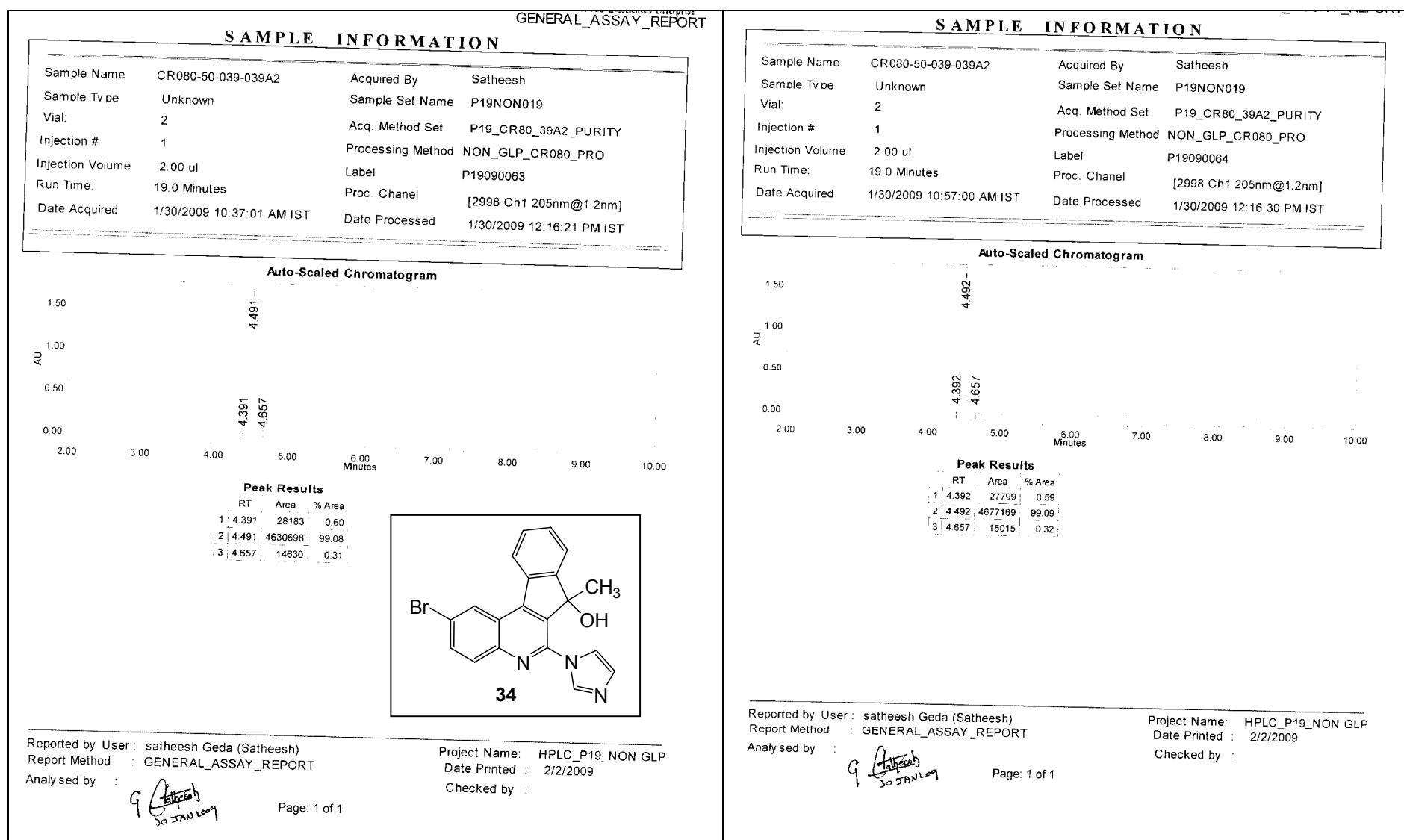


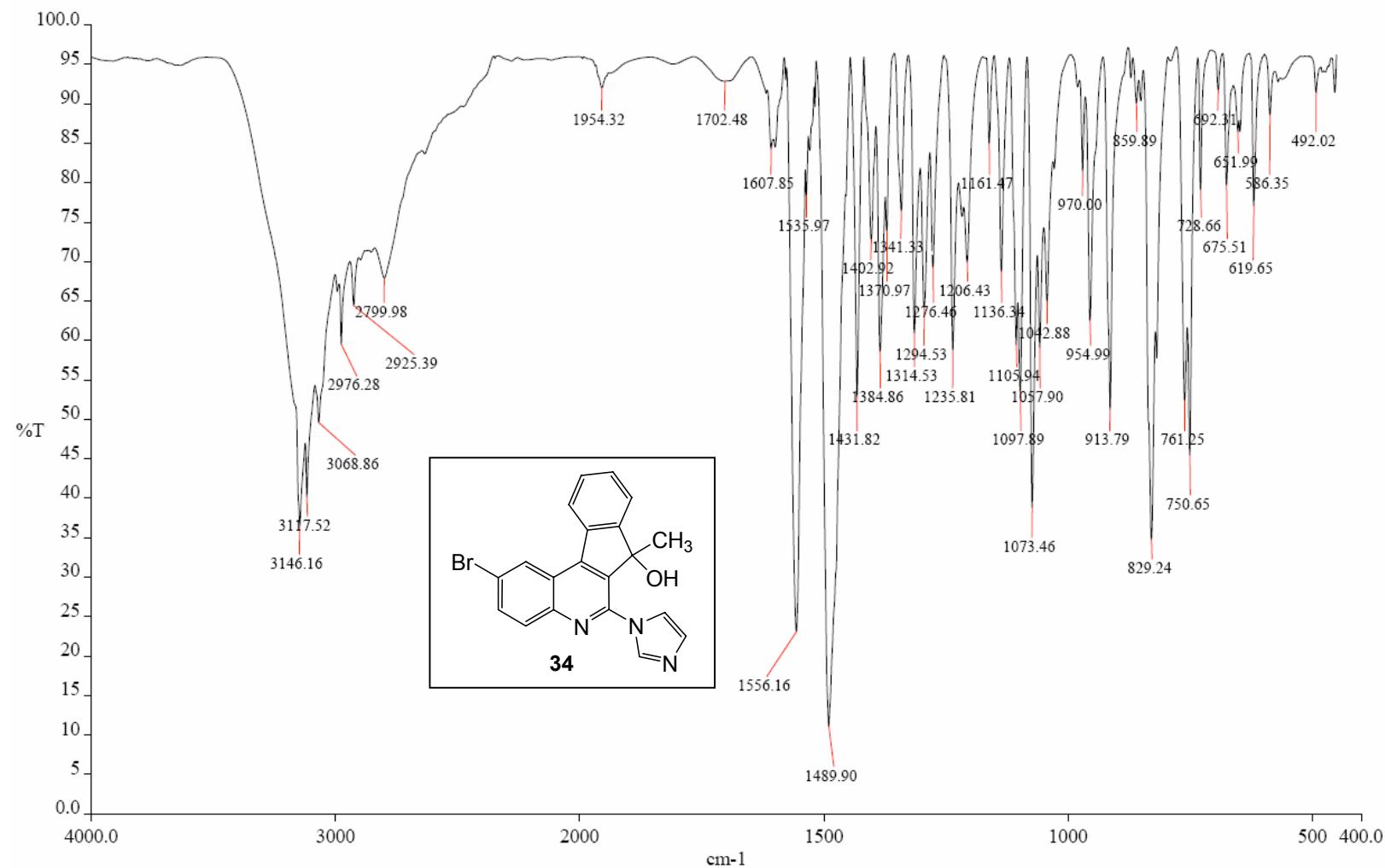


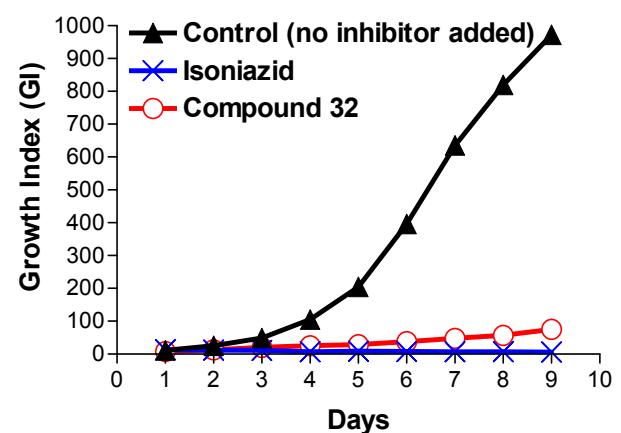
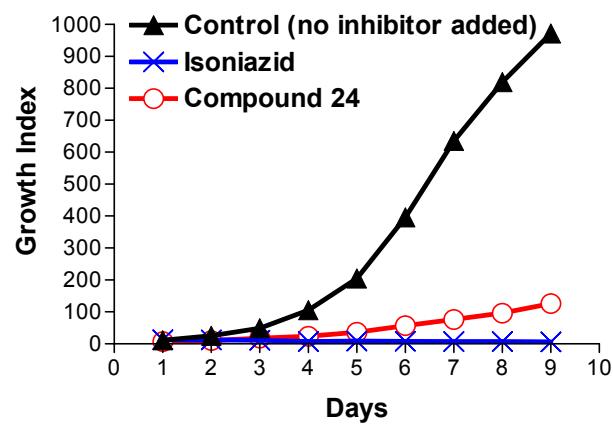
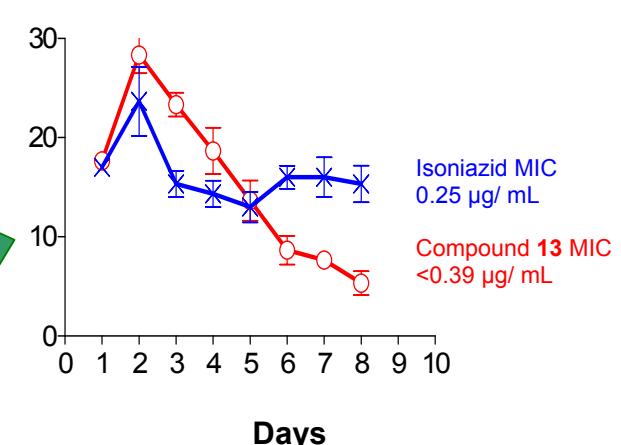
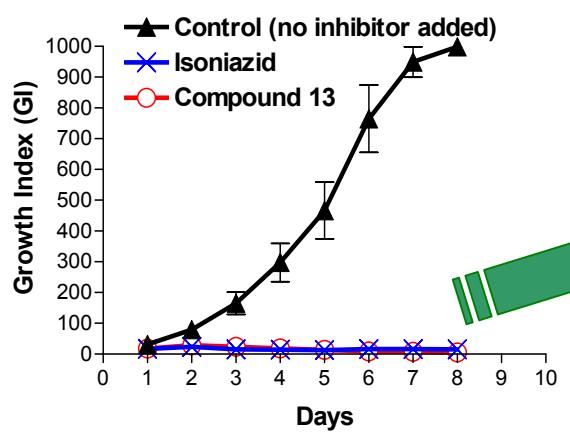
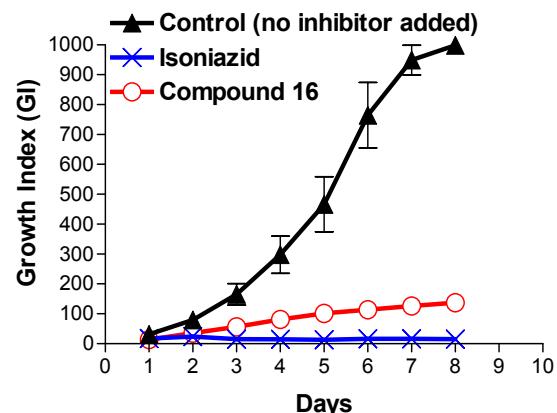
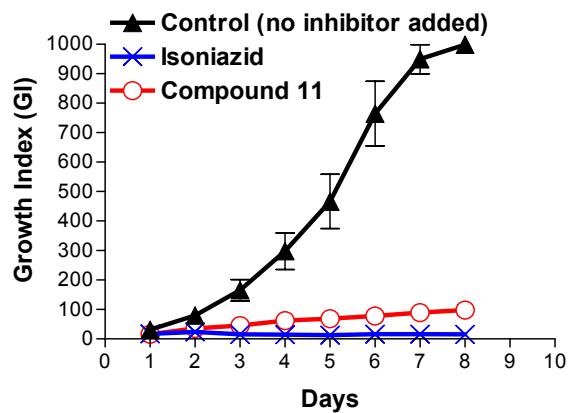












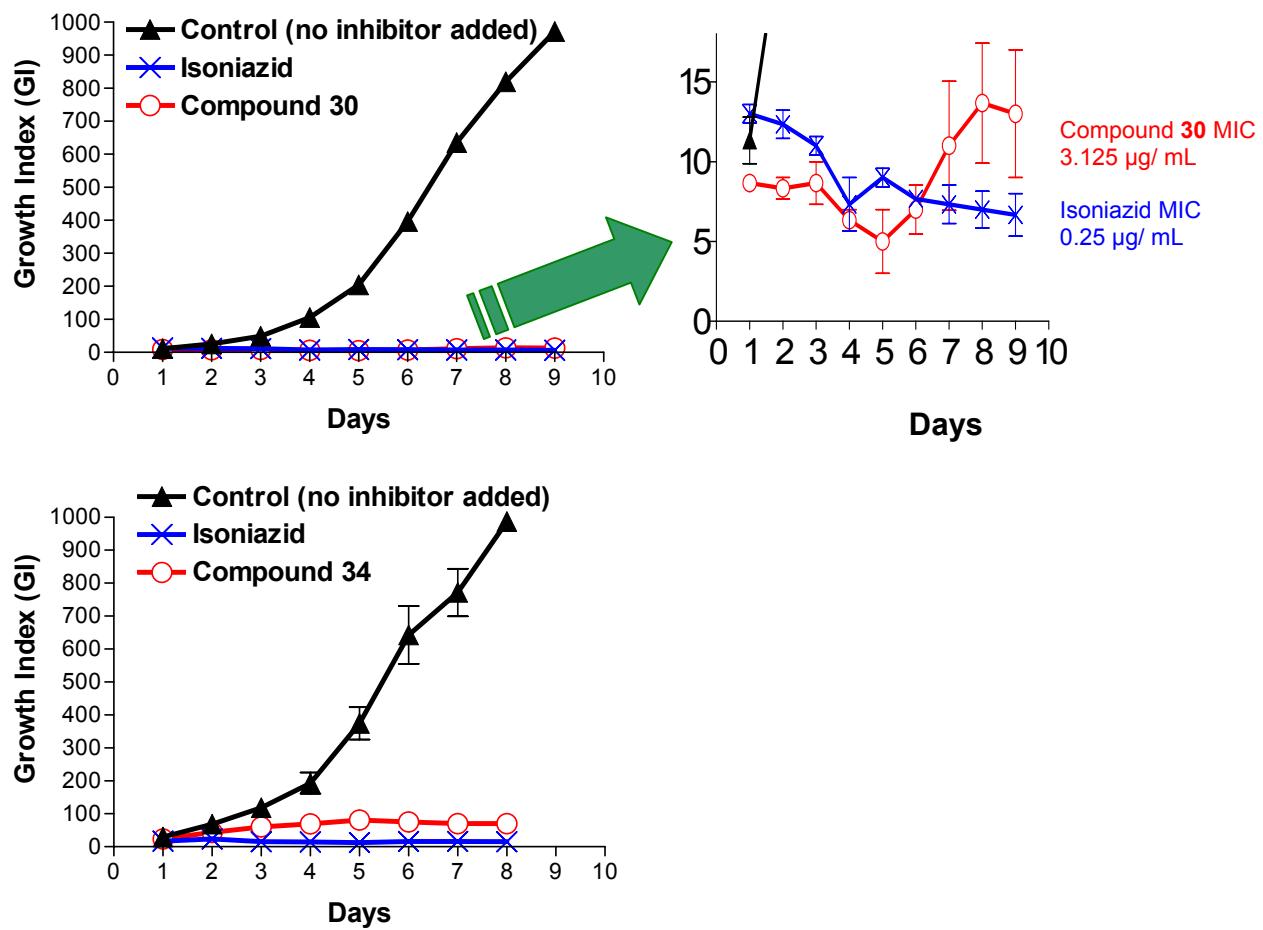


Figure S1: Plots showing Growth Index (GI) of TB H37Rv strain with standard deviation for 8 consecutive days for compounds **11**, **13**, **16**, **24**, **30**, **32** and **34** in comparison with isoniazid at a fixed concentration of 6.25 µg/mL upon single-administration of each of the substances on day-one. Standard deviation are shown in Table S1 in supplementary data.

Antimycobacterial activity:

All the compounds were screened for antimycobacterial activity against mycobacterium tuberculosis by BACTEC 460 radiometric methods. The broth based BACTEC 460 TB system was used for the growth of Mycobacteria. In this growth system, *Mycobacterium Tuberculosis* H37Rv was grown in the C¹⁴ labelled substrate in 7H12 medium, substrate is utilized by growing *mycobacteria* and ¹⁴CO₂ is produced, which is detected in the form of '**Growth Index**' (GI), which reflects the rate and amount of growth in the medium vial. If an antituberculosis drug will be added to the medium vial, it will suppress the growth of the bacteria which is detected by the decrease of the GI values as compared to the control vial. The positive controls taken in the experiment were the standard therapeutic drugs presently used for the treatment of the tuberculosis, Isoniazid and Rifampin.

The rate of increase in GI values or the change in GI over the previous day GI is called delta (Δ) GI, is compared with that of control values. If Δ GI of the drug-containing vial is equal to or greater than (\geq) than that in control vial the organisms are considered resistant to the drug. On the contrary if Δ GI of the drug-containing vial is less ($<$) than that in control vial the organisms are considered susceptible.

On the basis of the values calculated for Δ G, out of all screened compounds, seven compounds i.e. **11, 13, 16, 24, 30, 32** and **34** were found to act as active antimycobacterial agents. Below given table depicts Δ G of the compounds tested.

Table S1: Biological activity data table

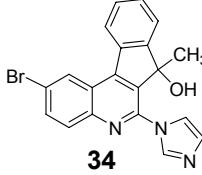
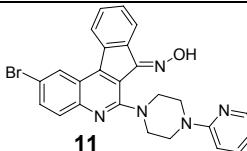
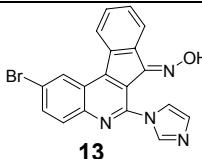
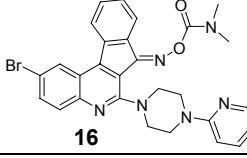
 34	Days	1	2	3	4	5	6	Δ GI	7	Δ GI	8	Δ GI	% Inhibition
	GI	24	44	59	69	83	81	-2	83	2	90	7	91
		24	44	61	67	74	63	-11	52	-11	46	6	95.4
	SD	22	44	62	73	88	83	-5	76	-7	74	-2	92.6
 11	GI	16	35	47	65	79	90	11	107	17	121	14	88.0
		17	39	48	70	75	84	9	97	13	112	15	89.0
	SD	15	32	42	51	53	60	7	64	04	60	4	94.0
													4.54
 13	GI	18	26	24	18	14	9	-5	8	-1	6	-2	99.4
		17	27	21	15	10	6	-4	8	-2	3	-5	99.7
	SD	18	32	25	23	17	11	-6	7	-4	7	0	99.3
													0.29
 16	GI	13	31	54	76	101	108	7	129	21	138	8	86.2
		16	44	71	97	123	142	19	156	14	161	5	84.0
	SD	12	31	43	70	80	92	12	95	03	111	17	89.0
													3.54
Isoniazid	GI	17	30	14	13	11	14	3	14	0	13	-1	99.7
		18	18	14	13	12	16	4	14	-2	14	0	99.6
	SD	16	23	18	17	16	18	2	20	2	19	-1	98.0
													1.35
Control	GI	31	76	157	278	461	834	373	999	165	999	0	
		40	110	231	414	629	910	281	999	89	999	0	
	SD	22	52	107	201	310	550	240	850	300	999	149	

Table S2: Biological activity data table

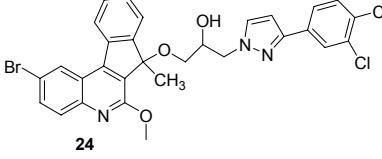
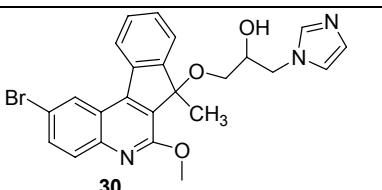
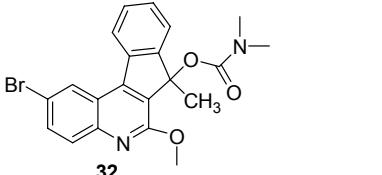
	Days	1	2	3	4	5	6	7	Δ GI	8	Δ GI	9	Δ GI	% Inhibition
		GI	7	10	17	24	35	53	77	14	98	21	121	23
		6	10	16	19	31	50	63	13	80	17	107	27	89.3
		8	12	21	28	42	68	88	20	112	24	150	38	85.0
	SD													3.11
	GI	9	9	10	7	7	9	11	2	14	3	17	3	98.3
		9	9	10	7	7	8	18	10	20	2	17	-3	98.3
	SD	8	7	6	5	1	4	4	0	7	3	5	2	99.5
	GI	11	16	25	30	30	39	46	7	55	9	69	14	93.0
		7	11	18	23	28	39	49	10	59	10	73	14	92.7
	SD	7	11	17	24	28	36	48	12	58	10	83	25	91.7
Isoniazid	GI	17	30	14	13	11	14	14	0	13	-1			99.7
		18	18	14	13	12	16	14	-2	14	0			99.6
		16	23	18	17	16	18	20	2	19	-1			98.0
	SD													1.35
Control	GI	14	30	57	122	216	431	643	212	788	145	999	211	
		11	24	43	99	192	384	622	238	801	179	918	117	
		9	21	46	95	206	374	641	267	869	228	999	130	
	SD													

Table S3: Docking, scoring and interaction energy data of compounds (data set I and II).

Comp. Number*	AD4			AD4.1			Interaction Energy			PMF ^j	Xscore ^k
	vdw ^a	elec ^b	IE ^c	vdw ^d	elec ^e	IE ^f	vdw ^g	elec ^h	Tot ⁱ		
Data Set I											
10	-7.87	-0.06	-7.92	-8.7710	-0.0534	-8.8244	-44.97	-6.70	-51.68	-243.79	6.60
11	-2.25	-0.13	-2.38	-5.6198	-0.1250	-5.7448	-56.09	-26.55	-82.65	-258.73	7.40
12	1.51	-0.15	1.36	-1.9850	-0.1456	-2.1306	-59.43	-15.18	-74.62	-228.93	7.08
13	-5.54	-0.05	-5.59	-7.2919	-0.0425	-7.3344	-50.09	-9.22	-59.32	-244.70	6.59
14	-5.50	-0.04	-5.53	-7.2565	-0.0334	-7.2899	-49.47	-9.47	-58.95	-238.64	6.68
15	-9.21	-0.07	-9.28	-10.4583	-0.0602	-10.5185	-54.72	-10.10	-64.82	-275.21	6.81
16	-1.32	0.03	-1.29	-5.3645	0.0056	-5.3589	-62.32	-24.30	-86.63	-307.29	7.49
17	0.20	-0.06	0.14	-4.3858	-0.0716	-4.4574	-67.11	-18.48	-85.59	-269.78	7.42
18	-12.55	-0.05	-12.60	-14.0854	-0.0453	-14.1307	-64.09	-13.71	-77.86	-244.50	8.48
19	7.18	-0.17	7.02	0.5409	-0.1677	0.3732	-78.22	-3.77	-81.99	-238.18	8.29
20	1.46	-0.03	1.43	-4.4473	-0.0394	-4.4867	-73.09	-18.54	-91.64	-247.44	8.74
Data Set II											
23	-9.82	-0.21	-10.03	-13.0369	-0.1881	-13.2250	-77.06	-25.71	-102.78	-316.12	8.22
24	-7.64	-0.02	-7.67	-11.1361	-0.0325	-11.1686	-68.35	-37.46	-105.81	-325.07	8.22
25	-8.55	0.05	-8.50	-11.1767	0.0467	-11.1300	-68.53	-17.83	-86.36	-287.88	8.68
26	-6.20	-0.07	-6.27	-9.4045	-0.0581	-9.4626	-69.95	-19.98	-89.93	-340.26	8.02
27	-9.44	-0.04	-9.48	-12.4930	-0.0371	-12.5301	-70.12	-8.04	-78.17	-298.04	8.17
28	-8.91	-0.02	-8.93	-10.7990	-0.0290	-10.8280	-56.00	-9.16	-65.17	-291.67	7.14
29	-8.88	-0.02	-8.90	-10.8636	-0.0194	-10.8830	-60.95	-6.10	-67.05	-290.93	6.98

30	-7.46	-0.14	-7.60	-9.7438	-0.1171	-9.8609	-57.26	-5.96	-63.22	150.14	6.63
31	-9.20	-0.37	-9.57	-10.9241	-0.3550	-11.2791	-59.45	-19.56	-79.01	-298.87	6.99
32	-7.37	-0.07	-7.44	-9.0900	-0.0619	-9.1519	-51.78	-6.90	-58.68	-298.59	6.71
33	2.93	-0.10	2.83	-1.5763	-0.1042	-1.6805	-59.85	-15.12	-74.98	-237.39	7.48
34	-5.14	-0.03	-5.17	-7.0758	-0.0248	-7.1006	-50.52	-10.24	-60.77	-248.23	6.70
37	-9.11	0.06	-9.05	-12.1413	0.0435	-12.0978	-69.99	-33.58	-103.5	155.01	8.24

vdw^a Autodock 4 (AD4) van der Waals, hydrogen bond and desolvation energy

elec^b Autodock 4 (AD4) electrostatic energy

IE^c Autodock 4 (AD4) intermolecular energy

vdw^d Autodock 4.1 (AD4.1) van der Waals, hydrogen bond and desolvation energy

elec^e Autodock 4.1 (AD4.1) electrostatic energy

IE^f Autodock 4.1 (AD4.1) intermolecular energy

vdw^g van der Waals energy from energy minimised protein-ligand complex

elec^h electrostatic energy from energy minimised protein-ligand complex

Totⁱ total interaction energy from energy minimised protein-ligand complex

PMF^j Potential of mean force score (in kcal/mol)

Xscore^k Average of HPscore, HMScore and HSScore

Theoretical Methods

Homology model comprising of 1 subunit A and 2 subunit C of ATP-synthase of *Mycobacterium tuberculosis*, was generated as described before.¹ The protonation state of three critical amino acid residues was kept as: Glu61^C (deprotonated) – Arg186^A (protonated) – Glu61^C (protonated).

Ligand molecules were sketched in Ghemical² irrespective of their stereochemistry and refined with 2500 steps of energy minimisation. Further, a random conformational analysis was performed on all the ligand molecules, with 2000 search steps and each step followed by 300 steps of energy minimisation. Finally, conformation with lowest energy was selected for docking. Ligand molecules were docked into the previously discussed binding site of ATP-synthase^{1,3} using AutoDock Tools⁴ and AutoDock.⁵ Grid size of 64Å×42Å×44Å was used. Docking parameters; population size, number of energy evaluations and number of Lamarckian Genetic Algorithm runs were kept at 250, 25000000 and 100, respectively. The initial position of ligand was defined same as the grid center position (*tran0* option in AutoDock).

AutoDock clustering (with 2Å root mean square) was used to select the ligand conformation/pose. In most of the cases, the best cluster of ligand conformations was the lowest energy cluster too, suggesting statistical significance of results. In this case, the conformation with lowest binding energy was selected. In case of scattered clustering or that best cluster didn't coincide with lowest energy cluster, the conformation with lowest binding energy was selected for further analysis. In most of the cases our results have high statistical significance because of good root mean square clustering. The *.pdbqt files of selected protein-ligand complexes were saved for further use.

Protein-ligand complexes of all the compounds were subjected to energy minimisation in AMBER.⁶ Amino acid residues of protein were treated with *ff03* forcefield,⁷ while General Amber Force Field (GAFF)⁸ was used for the ligand molecules. Partial charges of ligand molecules were calculated based on AM1-BCC⁹ methodology implemented in *antechamber*.¹⁰ The complete protein-ligand system was minimised for 2500 steps of conjugate gradients and 2500 steps of steepest descent minimisation in

AMBER using *sander*. Protein-ligand interaction energy (sum of van der Waals and electrostatic energy) was calculated for the minimised complex of each compound using NAMDEnergy, implemented in NAMD/Visual Molecular Dynamics (VMD).^{11,12}

Additional scoring tools such as PMF scoring available in Molden¹⁵ and Xscore¹⁶ were used. The protein-ligand complex was loaded in Molden and PMF score was calculated as shown by the plots of PMF score (y-axis) vs conformation (x-axis). During the analysis, the hydrogen bond distance and angle criteria were: Donor-H.....Acceptor distance < 3.5Å and Donor-H-Acceptor angle > 150°. All visualisation of molecules was done using Visual Molecular dynamics (VMD). Docking and forcefield based calculations were performed on 2.2GHz AMD Dual core computing machine running with Red Hat Enterprise Linux 5.

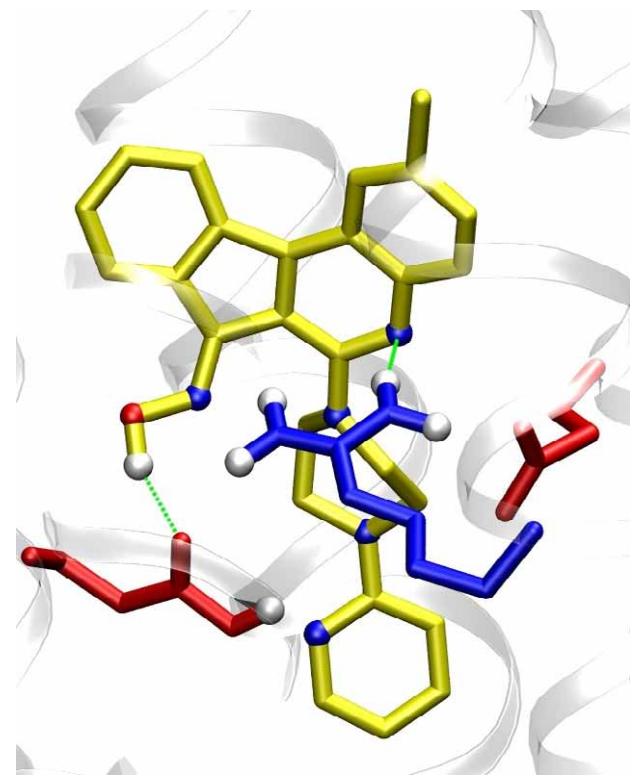


Figure S2: Protein-ligand interactions shown for compound **11**. Glu61^C, Arg186^A and ligand molecule are shown in red, blue and yellow licorice respectively. Nitrogen, Oxygen and Hydrogen are shown as blue, red and white spheres, respectively. Transmembrane helices are shown with light-grey ribbons. Interactions are shown with green dotted line.

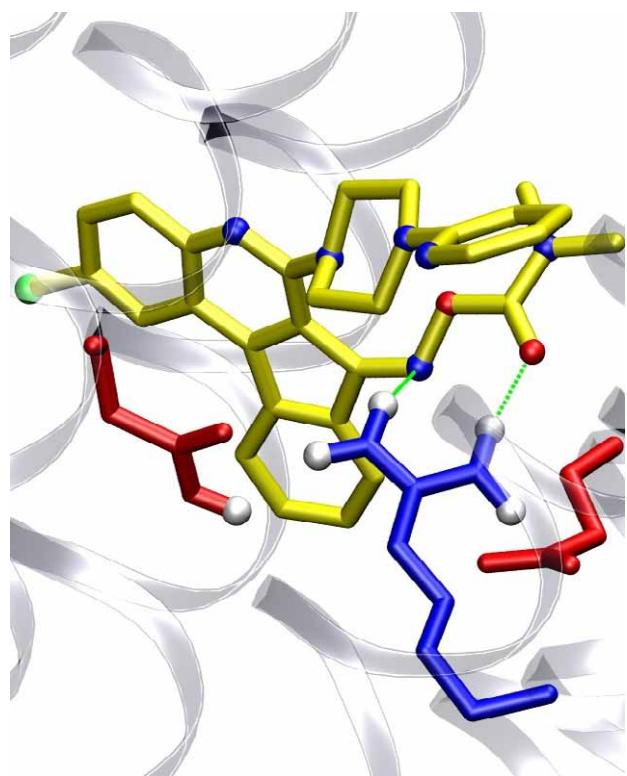


Figure S3: Protein-ligand interactions shown for compound **16**. Glu61^C, Arg186^A and ligand molecule are shown in red, blue and yellow licorice respectively. Nitrogen, Oxygen and Hydrogen are shown as blue, red and white spheres, respectively. Transmembrane helices are shown with light-grey ribbons. Interactions are shown with green dotted line.

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