

Supporting information

**Macrocyclic peptidomimetics with antimicrobial activity: synthesis,
bioassay, and molecular modeling studies**

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^f*Department of Pharmaceutical Chemistry, faculty of pharmacy, Damanhour University, Damanhour, Egypt*

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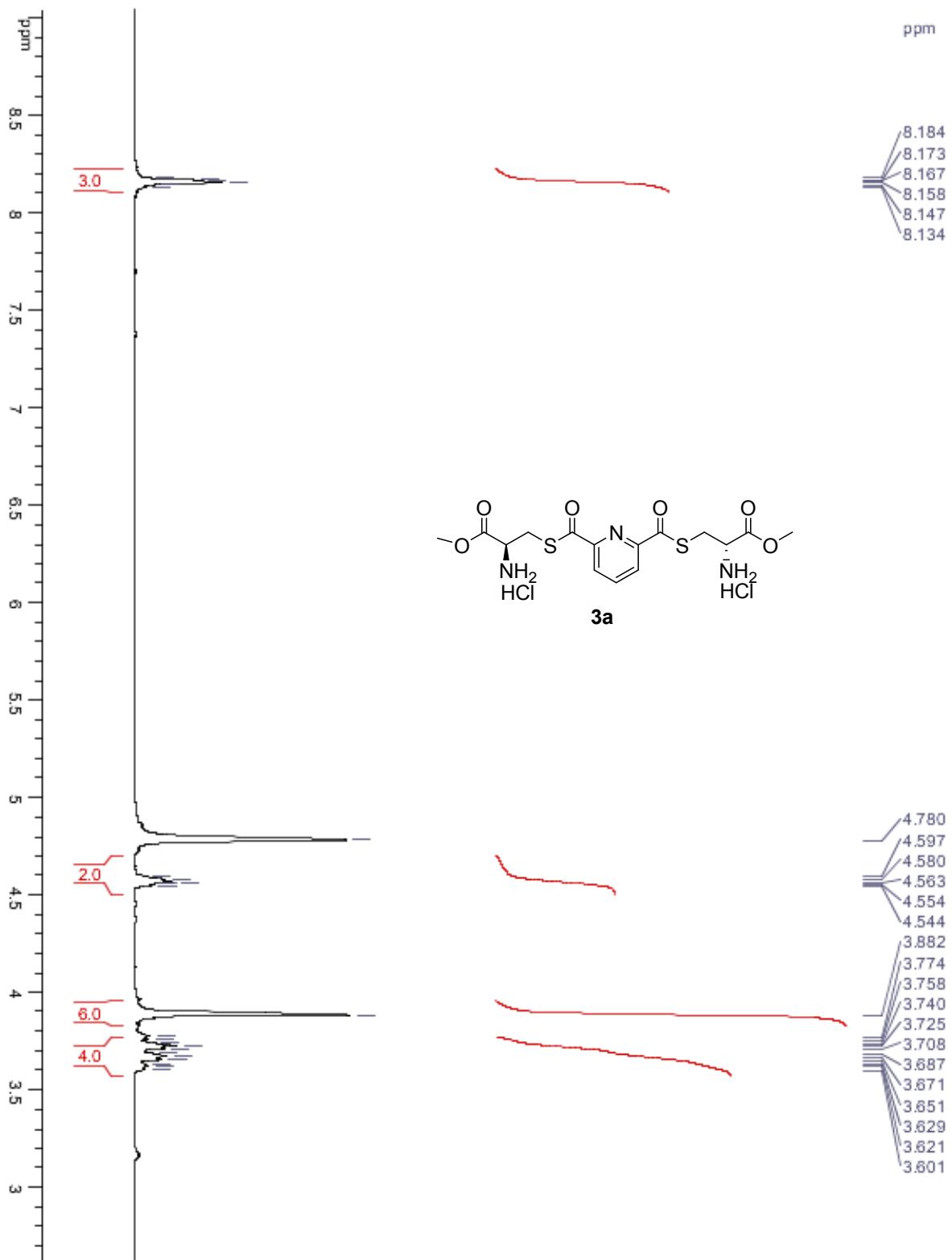
^h*Department of Chemistry, University of Tartu, 50411 Tartu, Estonia*

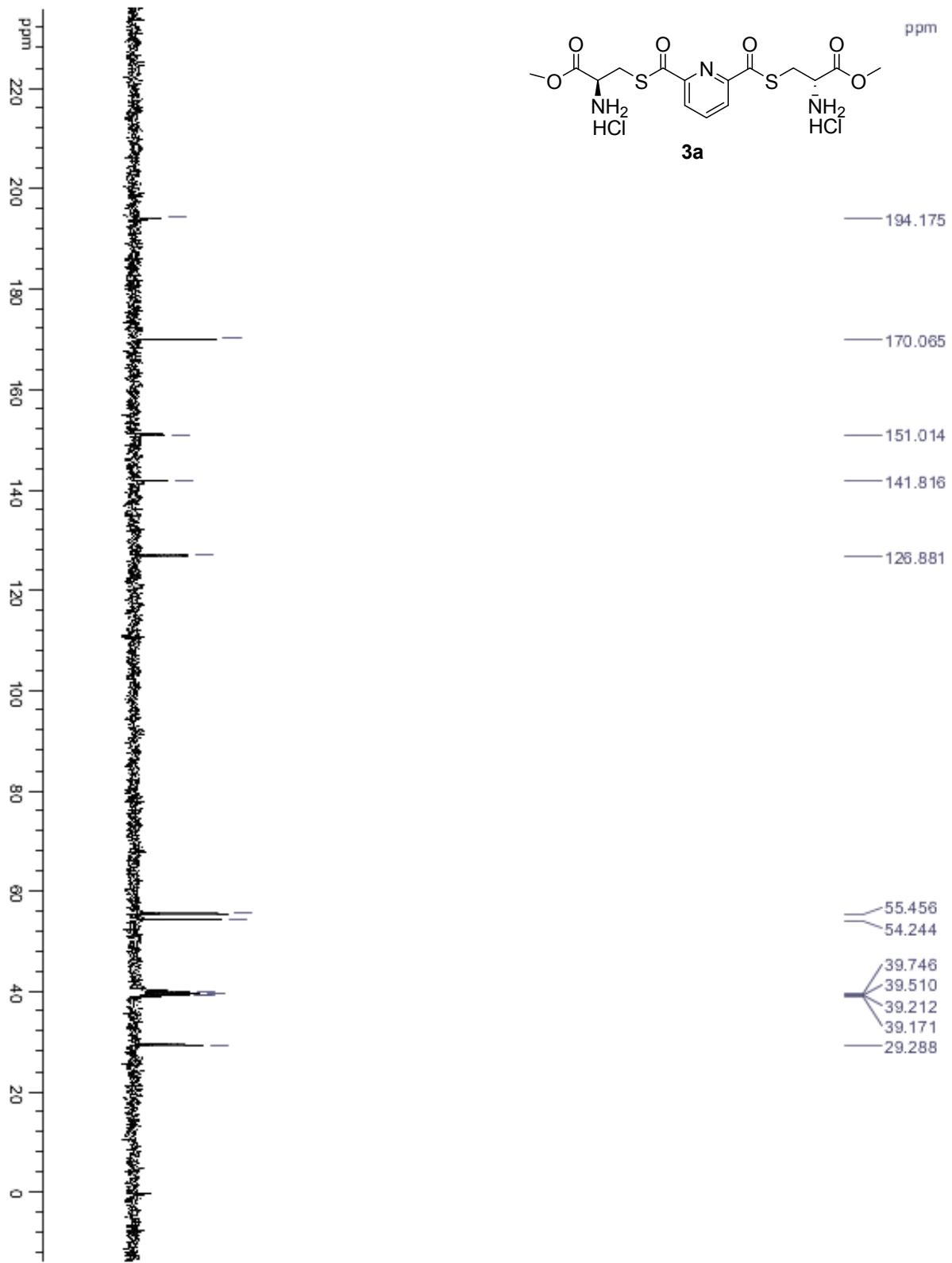
ⁱ*Department of Microbiology, Faculty of Veterinary Medicine, Cairo University, Cairo, Egypt*

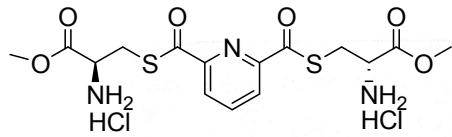
[†]*Deceased on February 10, 2014*

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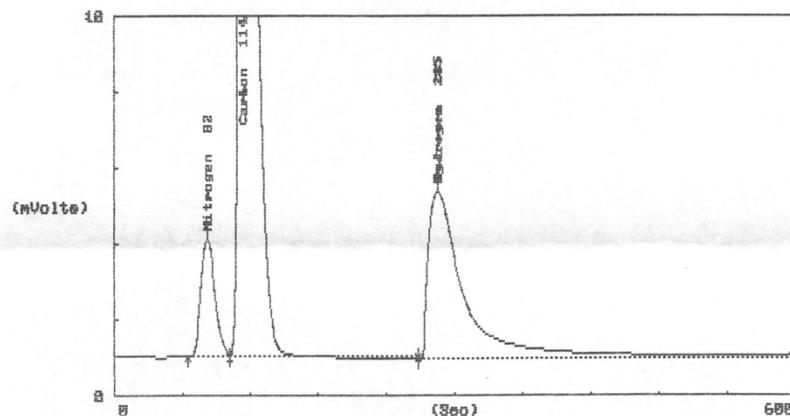






EAGER 200 Stripchart

Sample Ident. : 20 Maaa6esterHCl Filename : 266420
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EAGER 200 Peak Integration Report

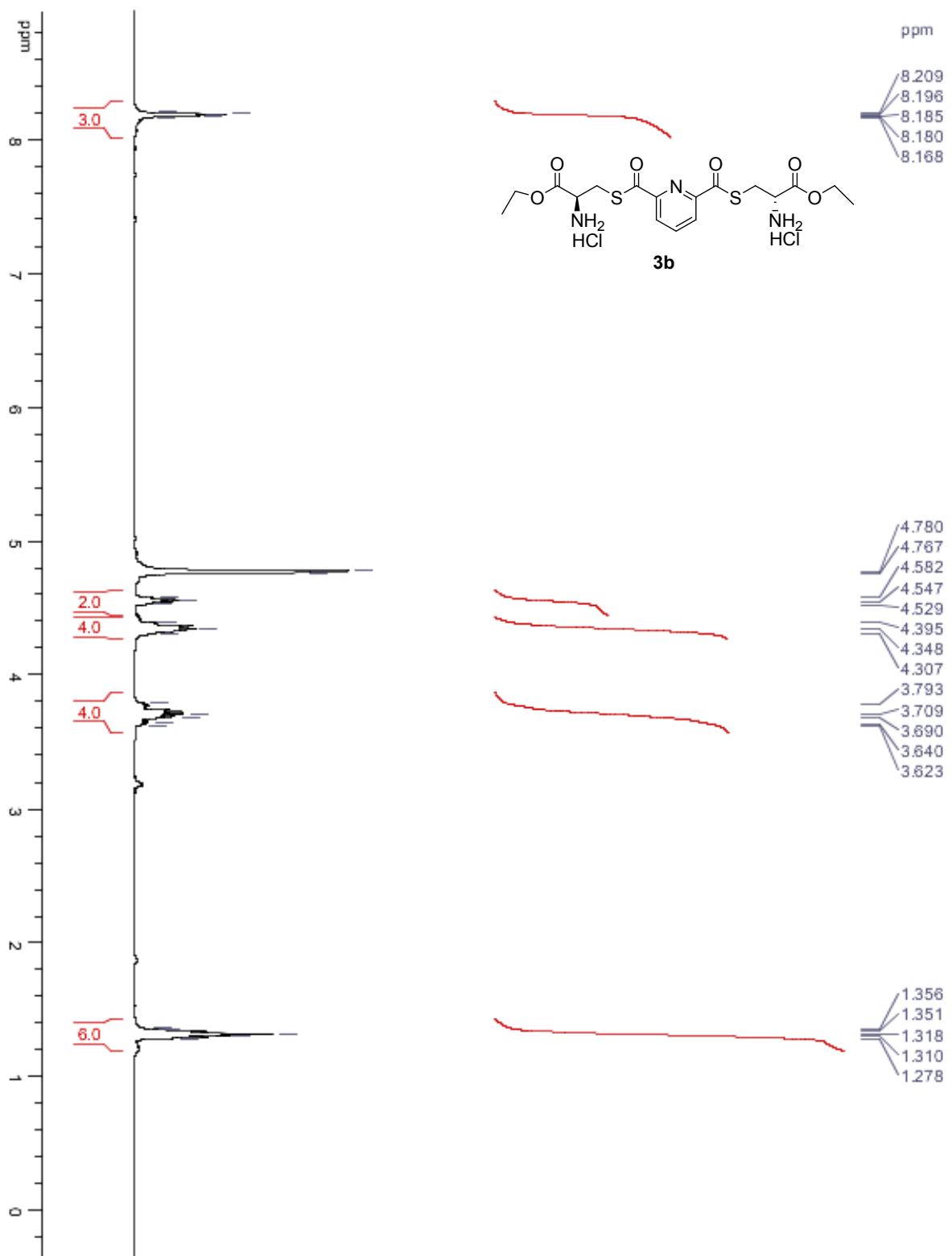
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 Company Name : U of Florida Operator Ident. : KOU
 Analysed : 01-11-12 08:53:19 Printed : 01-11-2012 09:03:21
 Sample Ident. : 20 Maaa6esterHCl Filename : 266420
 Sample Weight : 2.168 Calc.method: using 'K. Factors'

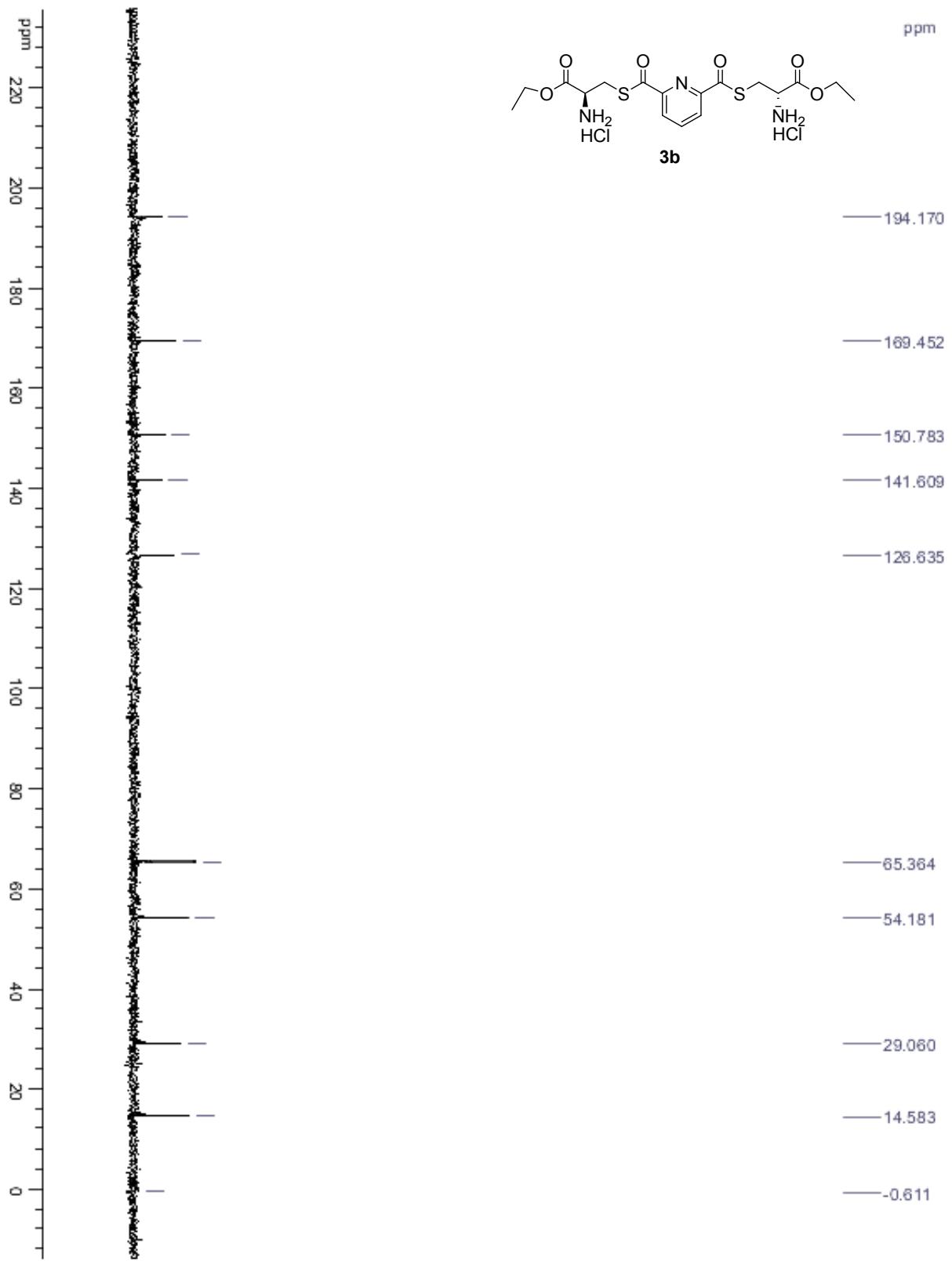
No.	Type	Start (#)	End (#)	Ret Time (Sec)	Height (fV)	Area (fV*Sec)	Area % (%)	Name
1	FU	65	102	82	3092.2	42236	6.08	Nitrogen
2	FU	102	268	114	33619.0	492721	70.94	Carbon
3	RS	268	598	285	4358.5	159626	22.98	Hydrogen
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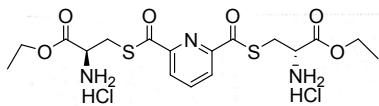
EAGER 200 Unk Report

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 Sample Ident. : 20 Maaa6esterHCl Filename : 266420
 Sample Weight : 2.168 Calc.method: using 'K. Factors'

Pk.	Ret Time (Sec)	Area (fV*Sec)	Element % (%)	Area Ratio	Name
1	82	42236	8.828	.116658E+02	Nitrogen
2	114	492721	37.745	.100000E+01	Carbon
3	285	159626	4.569	.308673E+01	Hydrogen

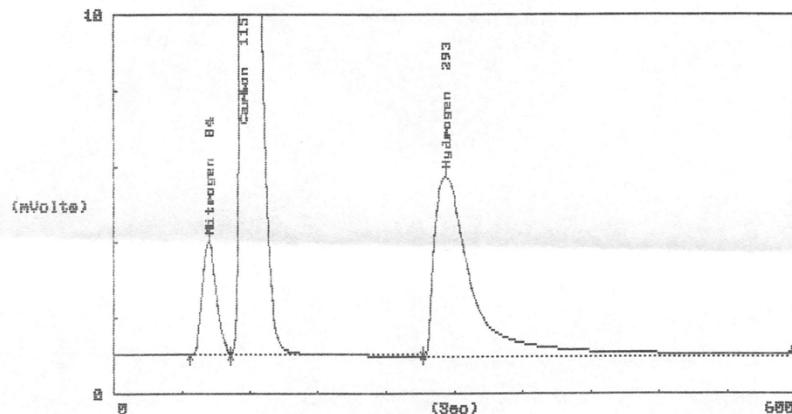






EAGER 200 Stripchart

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EAGER 200 Peak Integration Report

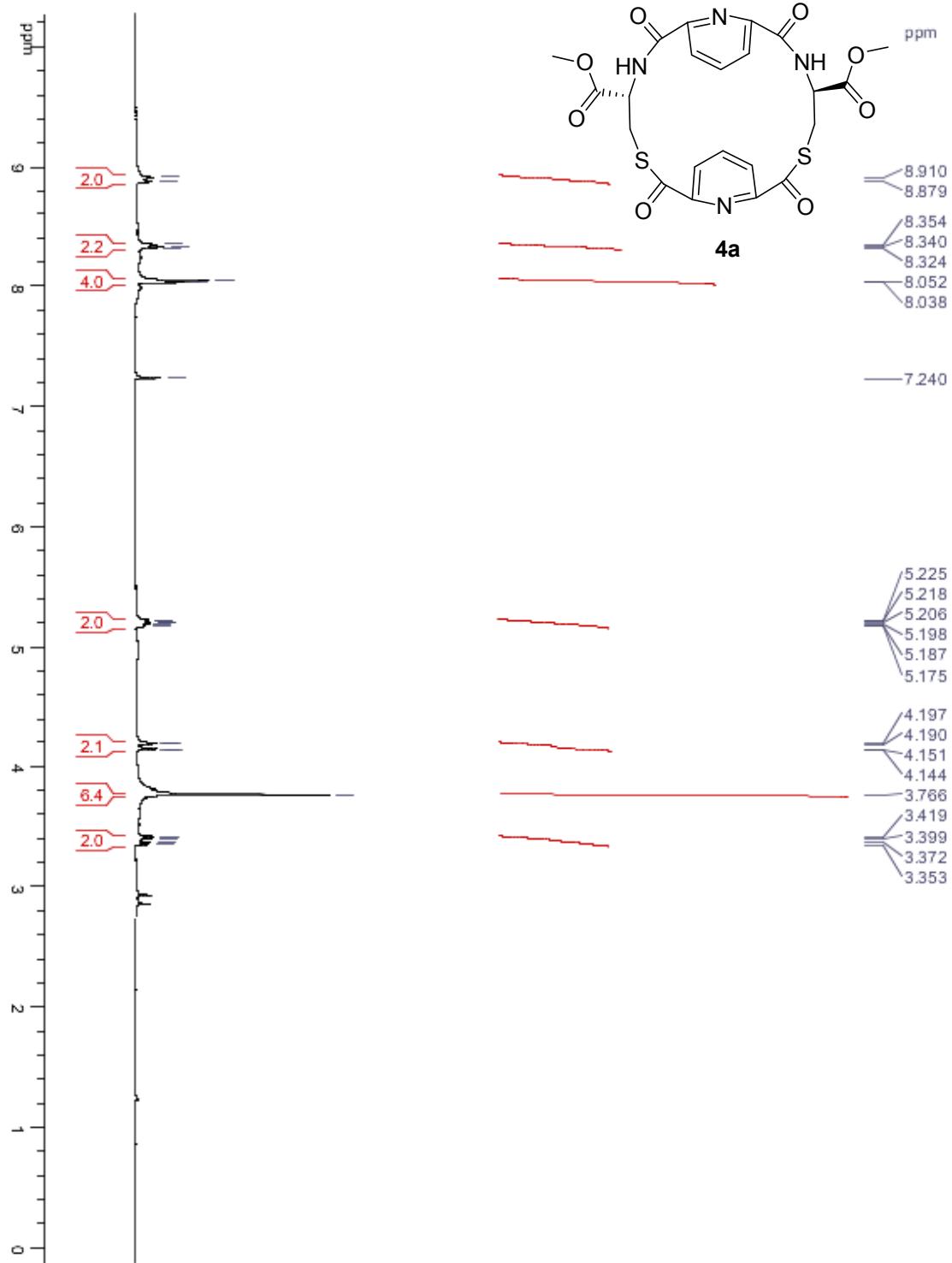
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Company Name :	U of Florida	Operator Ident. : KOU
Analysed :	02-14-12 08:47:21	Printed : 02-14-2012 08:57:24
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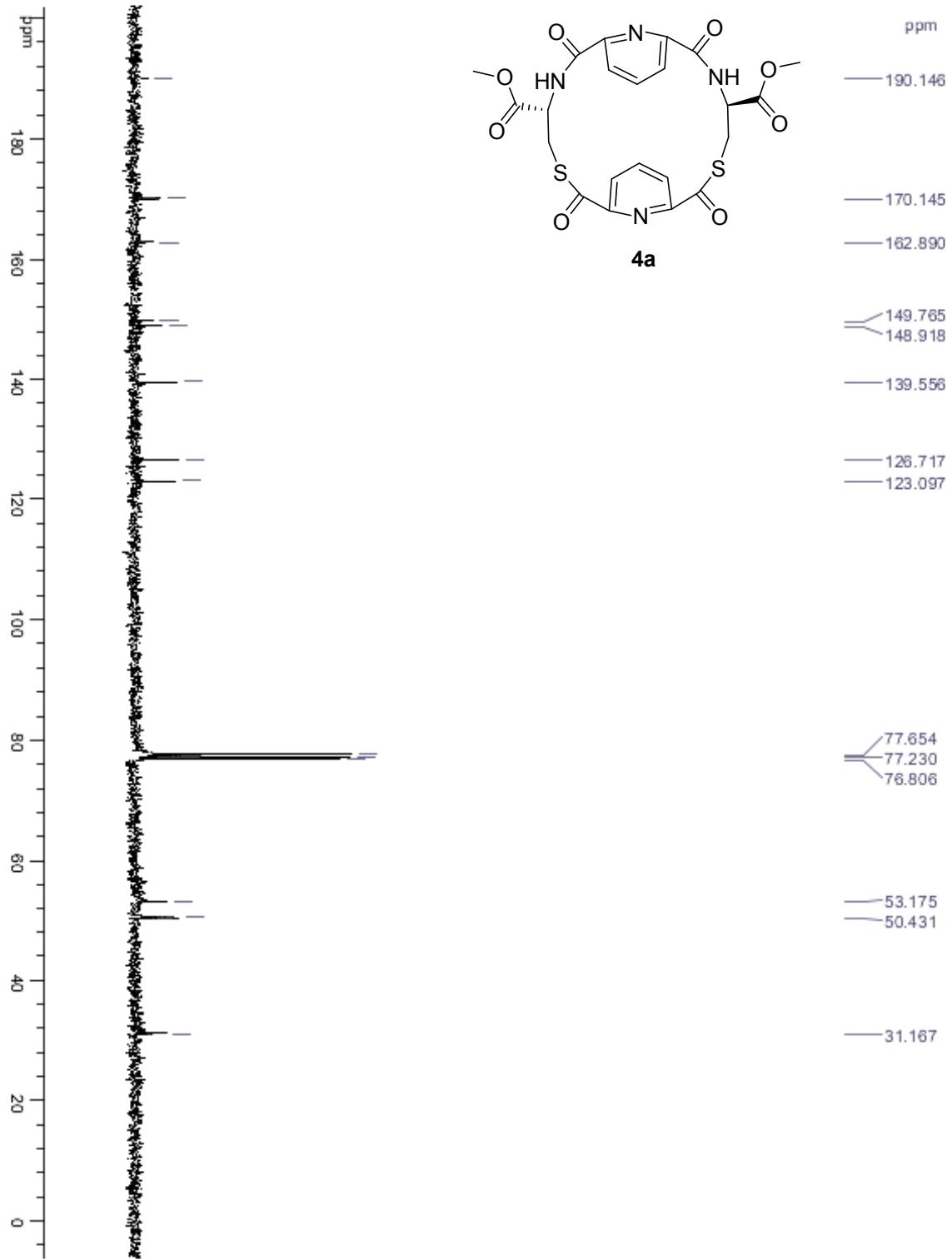
No.	Type	Start (#)	End (#)	Ret Time (Sec)	Height (fV)	Area (fV*Sec)	Area % (%)	Name
1	FU	67	103	84	2962.1	40633	5.34	Nitrogen
2	FU	103	272	115	36689.9	538909	70.78	Carbon
3	RS	272	597	293	4711.7	181833	23.88	Hydrogen
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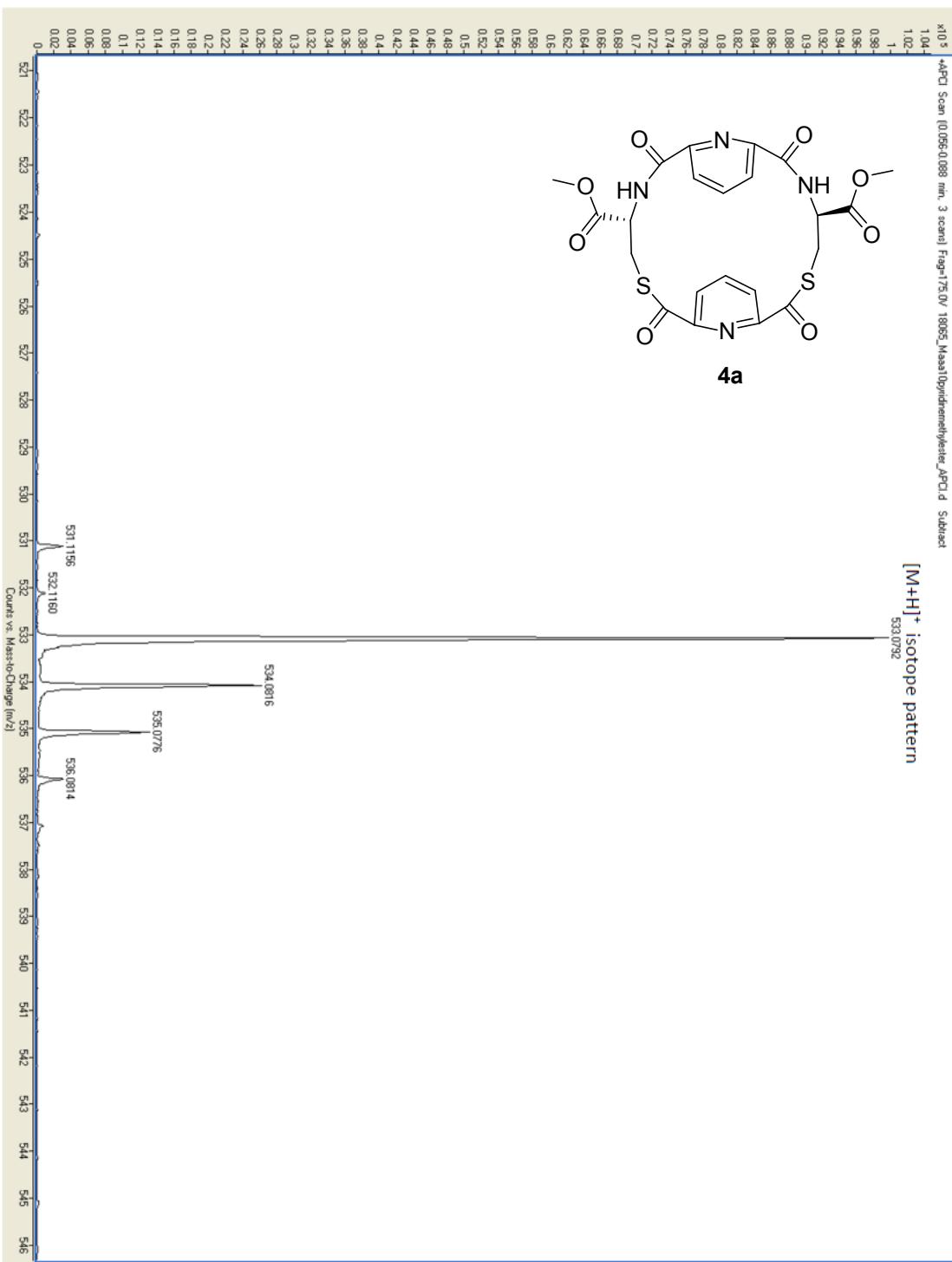
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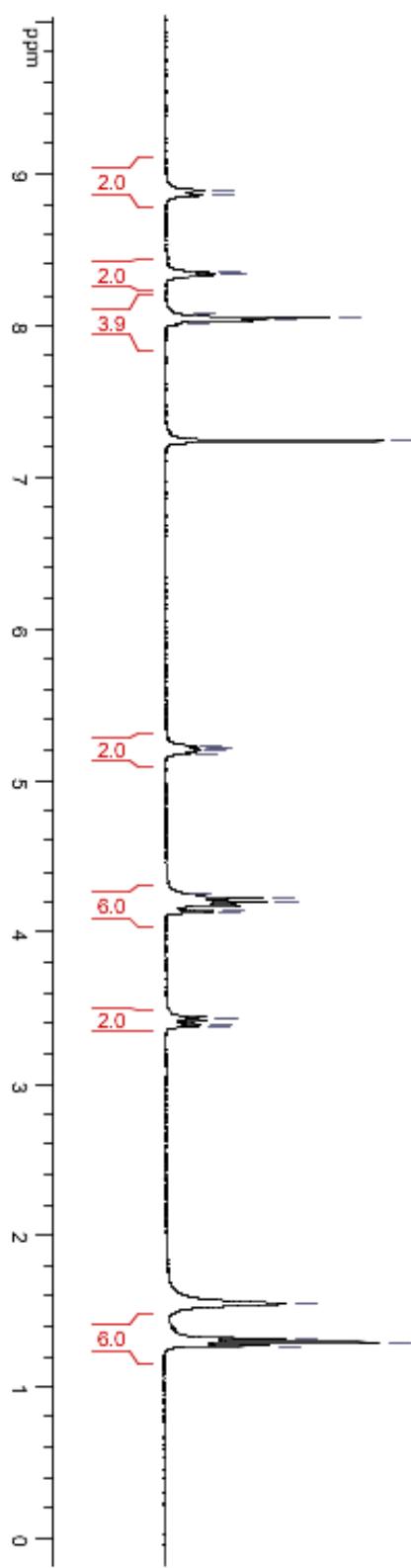
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Company Name :	U of Florida	Operator Ident. : KOU
Analysed :	02-14-12 08:47:21	Printed : 02-14-2012 08:57:24
Sample Ident. :	20 maaa6ethyl	Filename : 267120
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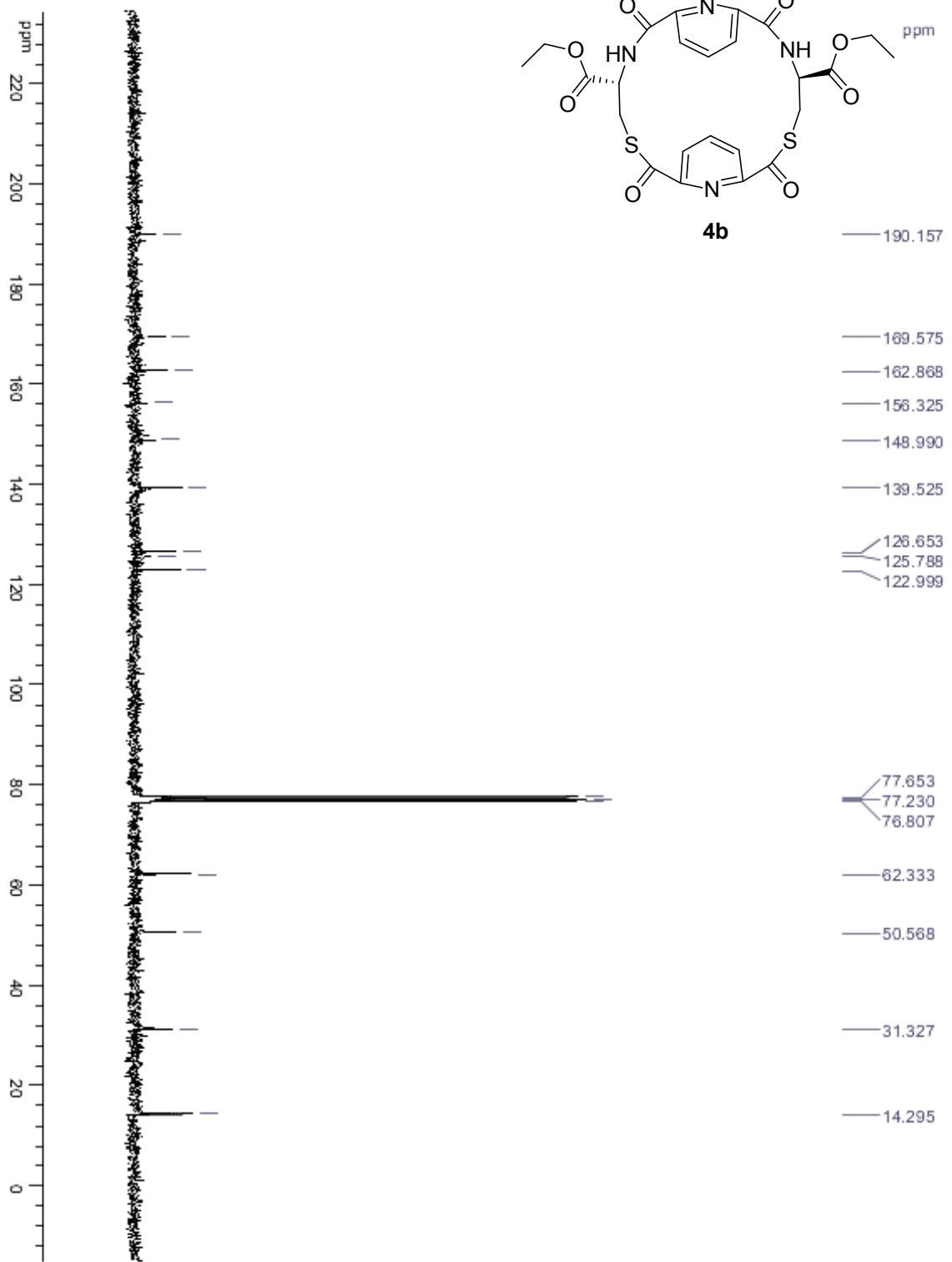
Pk. (#)	Ret Time (Sec)	Area (fV*Sec)	Element % (%)	Area Ratio	Name
1	84	40633	8.454	.132628E+02	Nitrogen
2	115	538909	40.999	.100000E+01	Carbon
3	293	181833	5.372	.296375E+01	Hydrogen









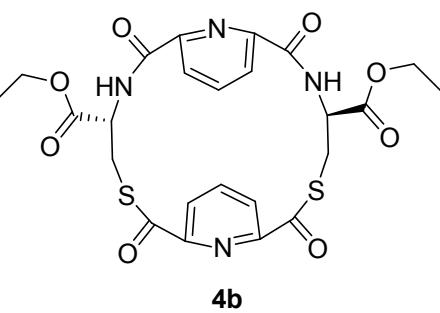


Theoretical $[M+H]^+$ = 561.1108

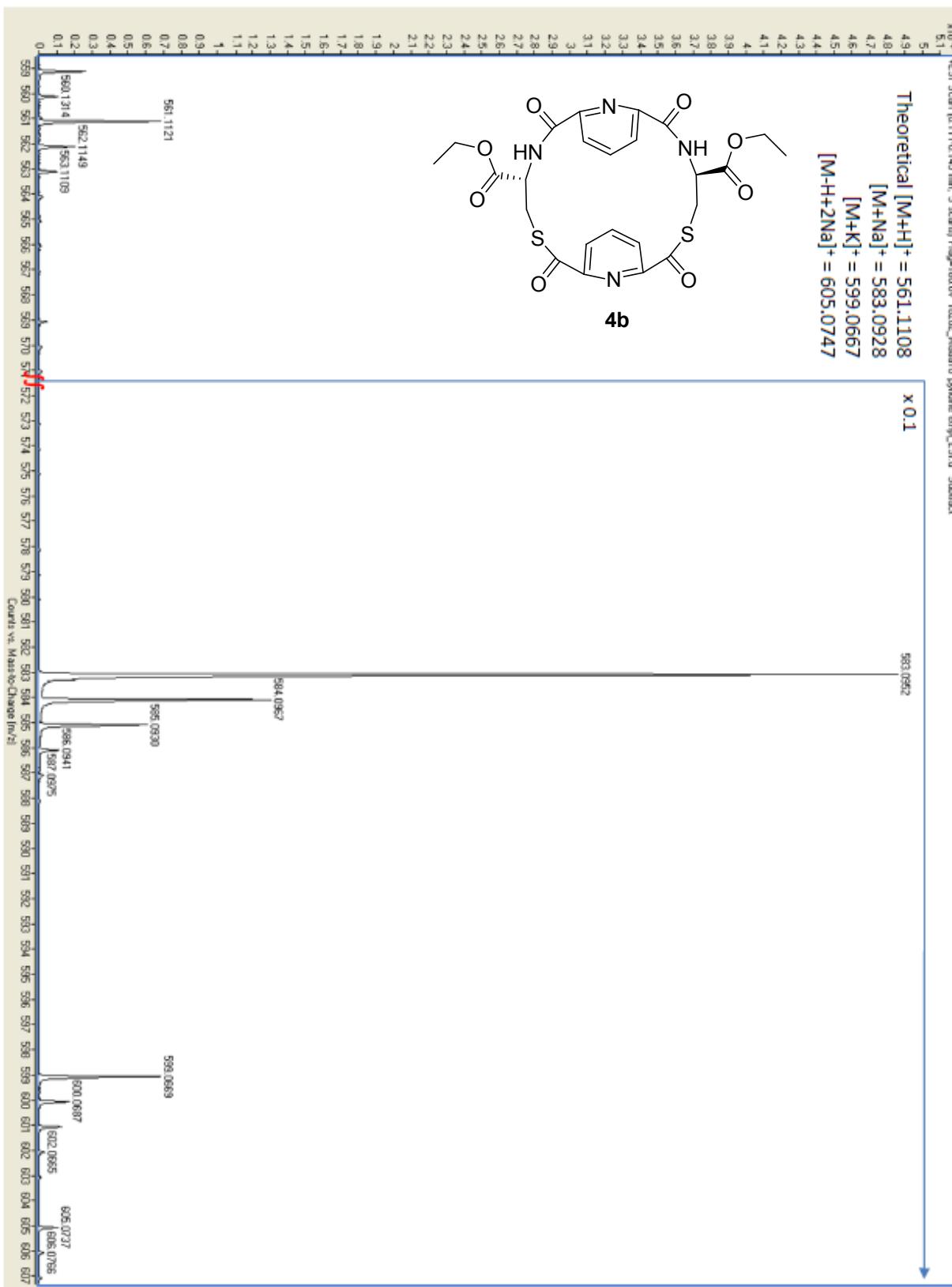
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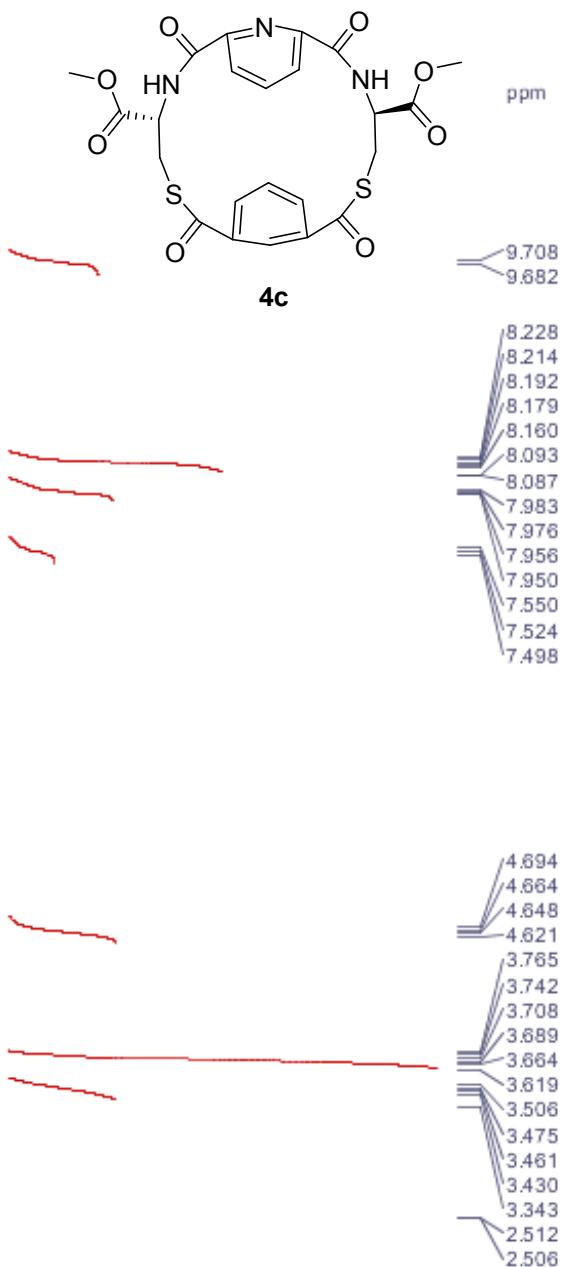
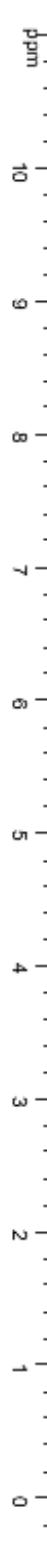
$[M+K]^+$ = 599.0667

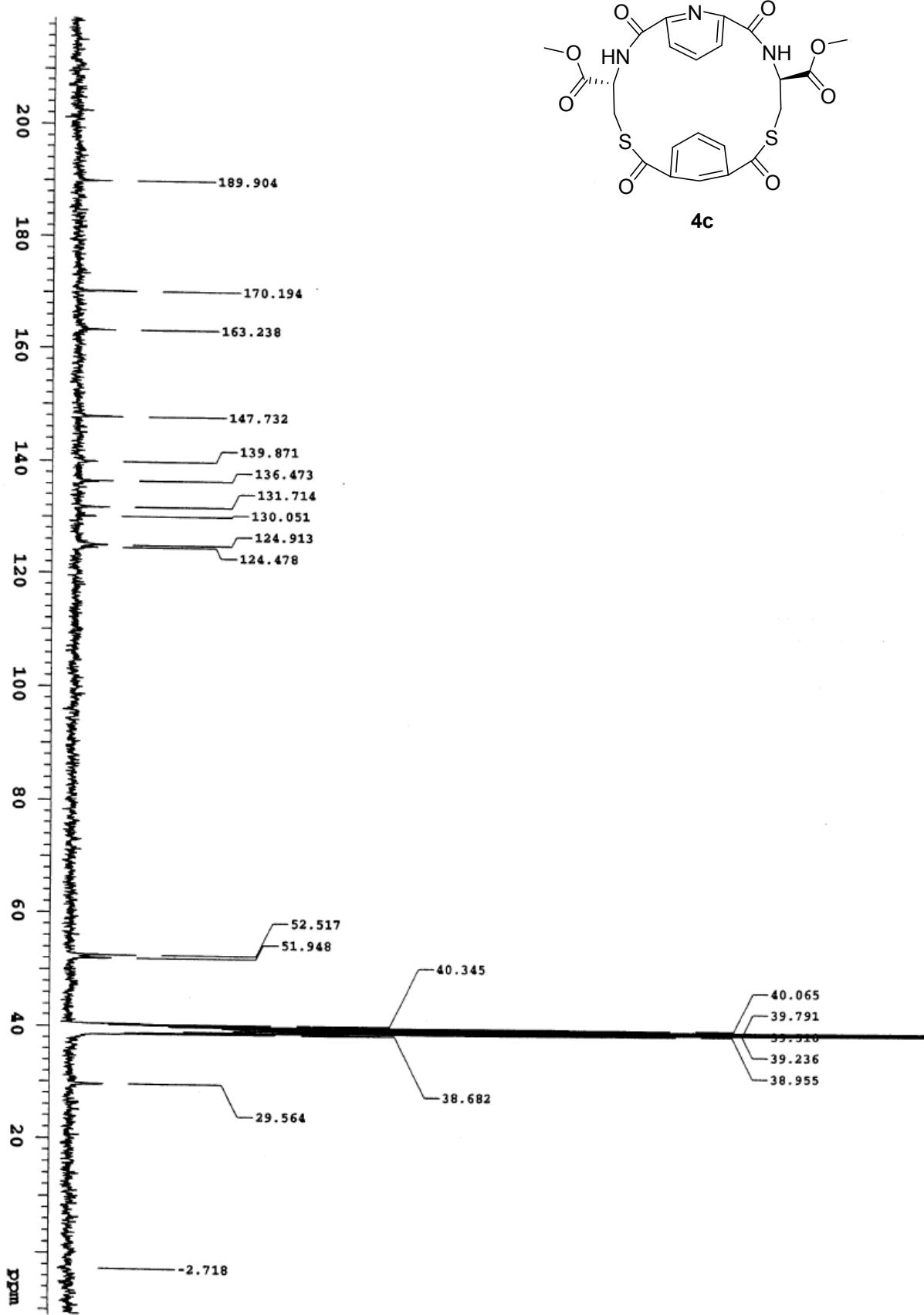
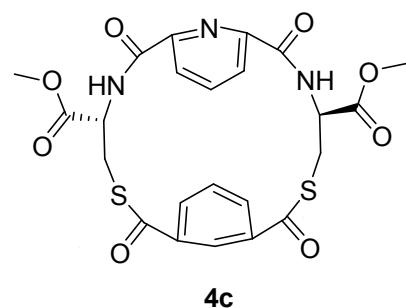
$[M-H+2Na]^+$ = 605.0747



4b

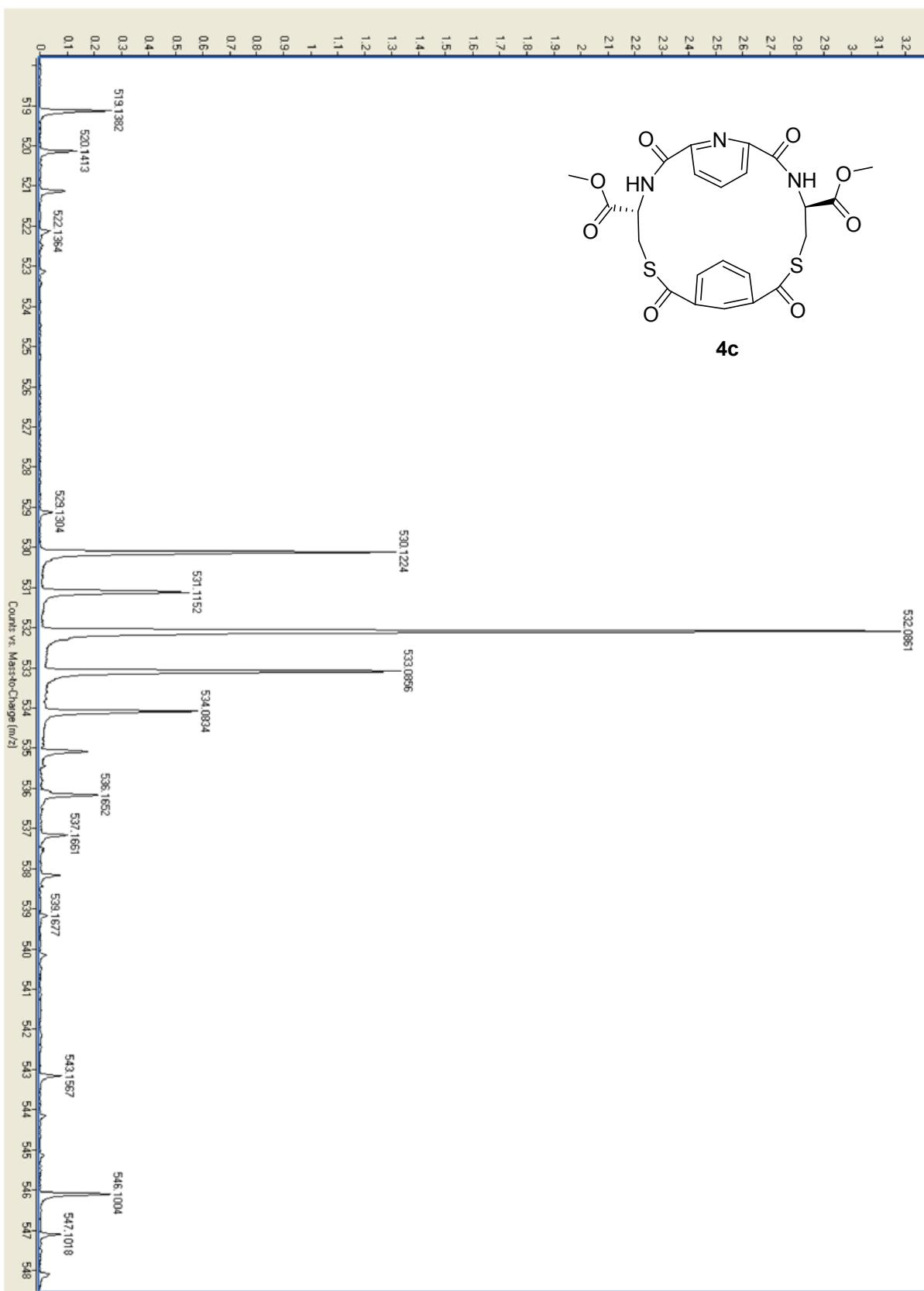
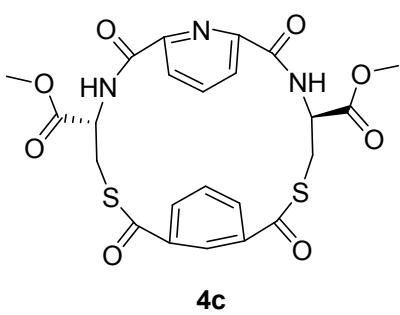


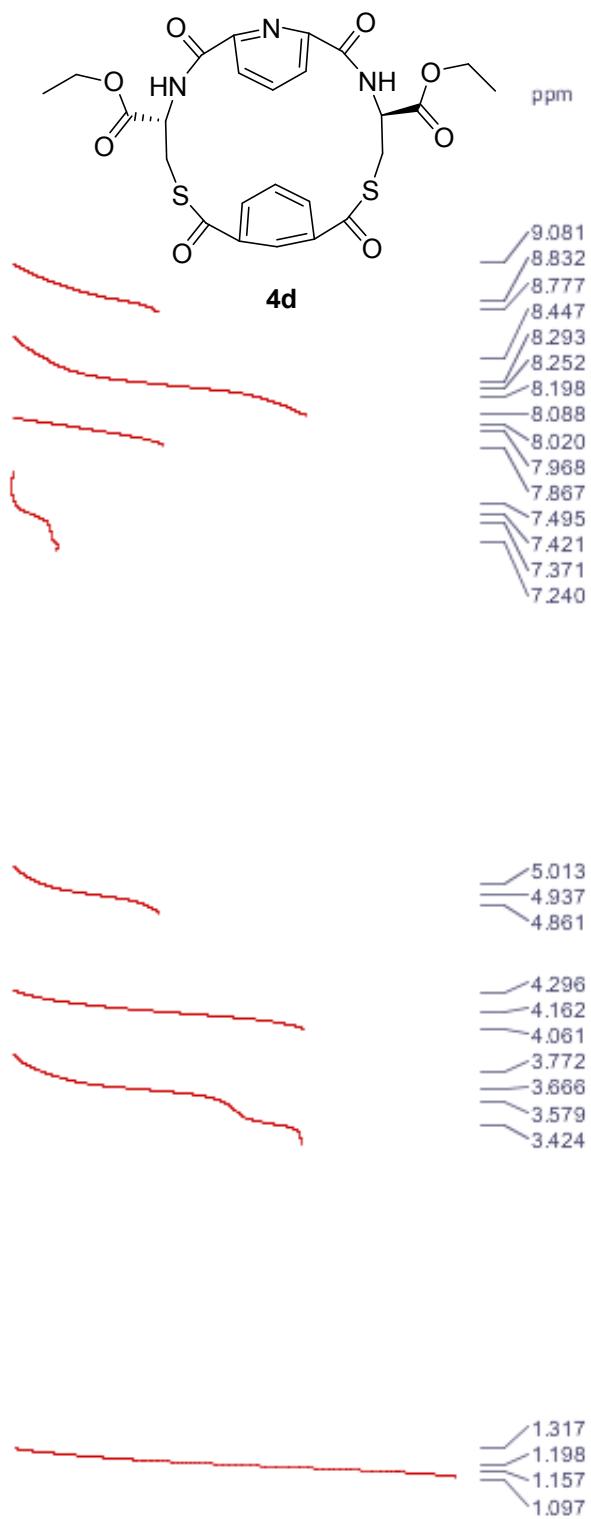
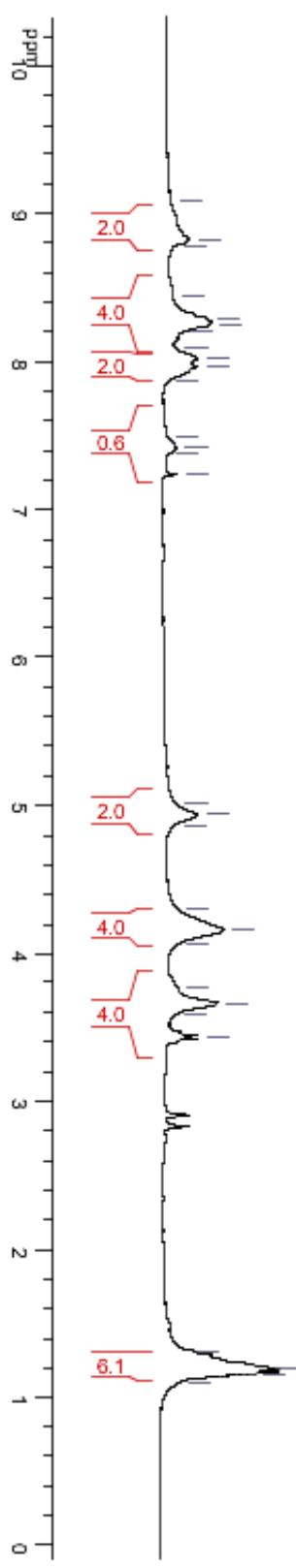


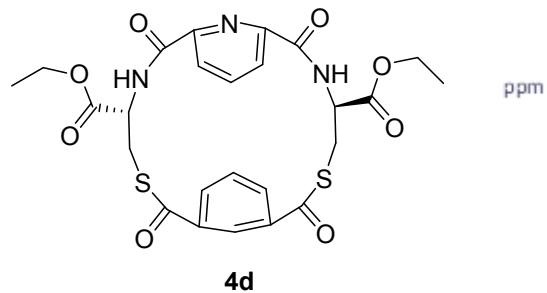
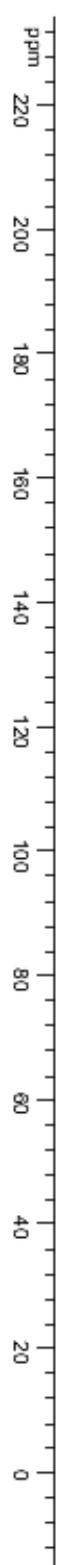


x10⁴
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Theoretical [M+H]⁺ = 532.0843

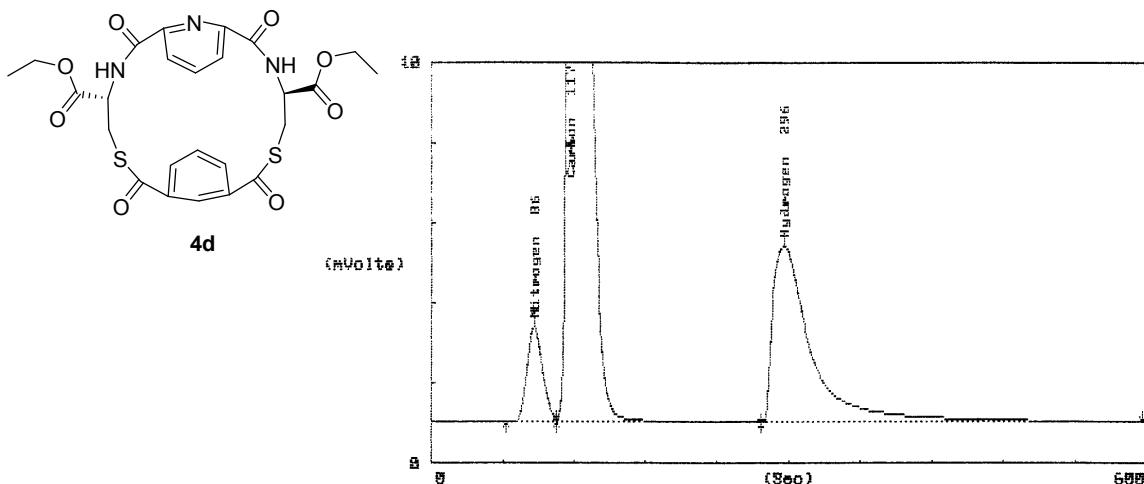






EAGER 200 Stripchart

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EAGER 200 Peak Integration Report

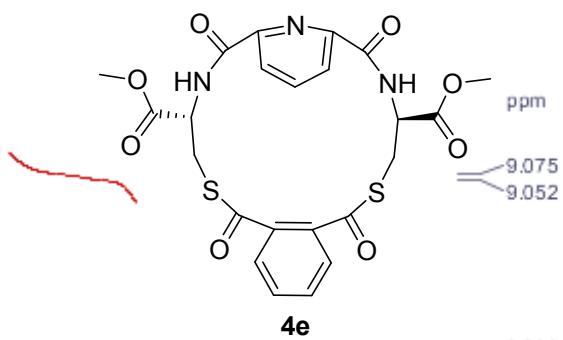
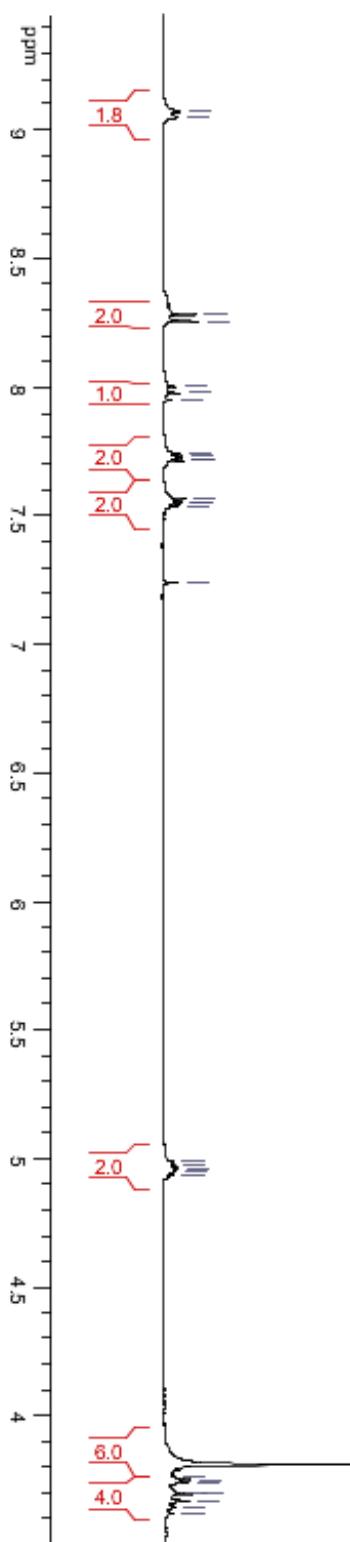
Instrument name : Instrument #1 Bline drift (fV): 6.8
 Company Name : U of Florida Operator Ident. : KOU
 Analysed : 04-25-12 08:12:19 Printed : 04-25-2012 08:22:22
 Sample Ident. : 23 1985-01 Filename : 269423
 Sample Weight : 2.111 Calc.method: using 'K. Factors'

No.	Type	Start (#)	End (#)	Ret Time (Sec)	Height (fV)	Area (fV*Sec)	Area % (%)	Name
1	FU	63	105	86	2391.2	34425	3.82	Nitrogen
2	FU	105	277	117	44233.0	696815	77.23	Carbon
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-----								902252 100.00

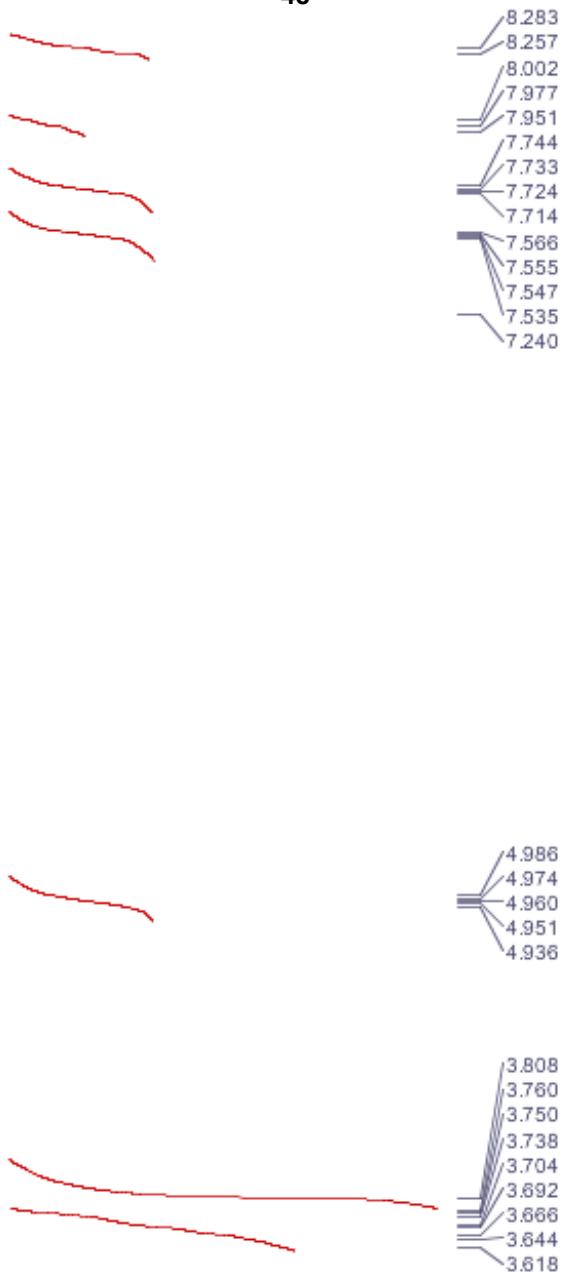
EAGER 200 Unk Report

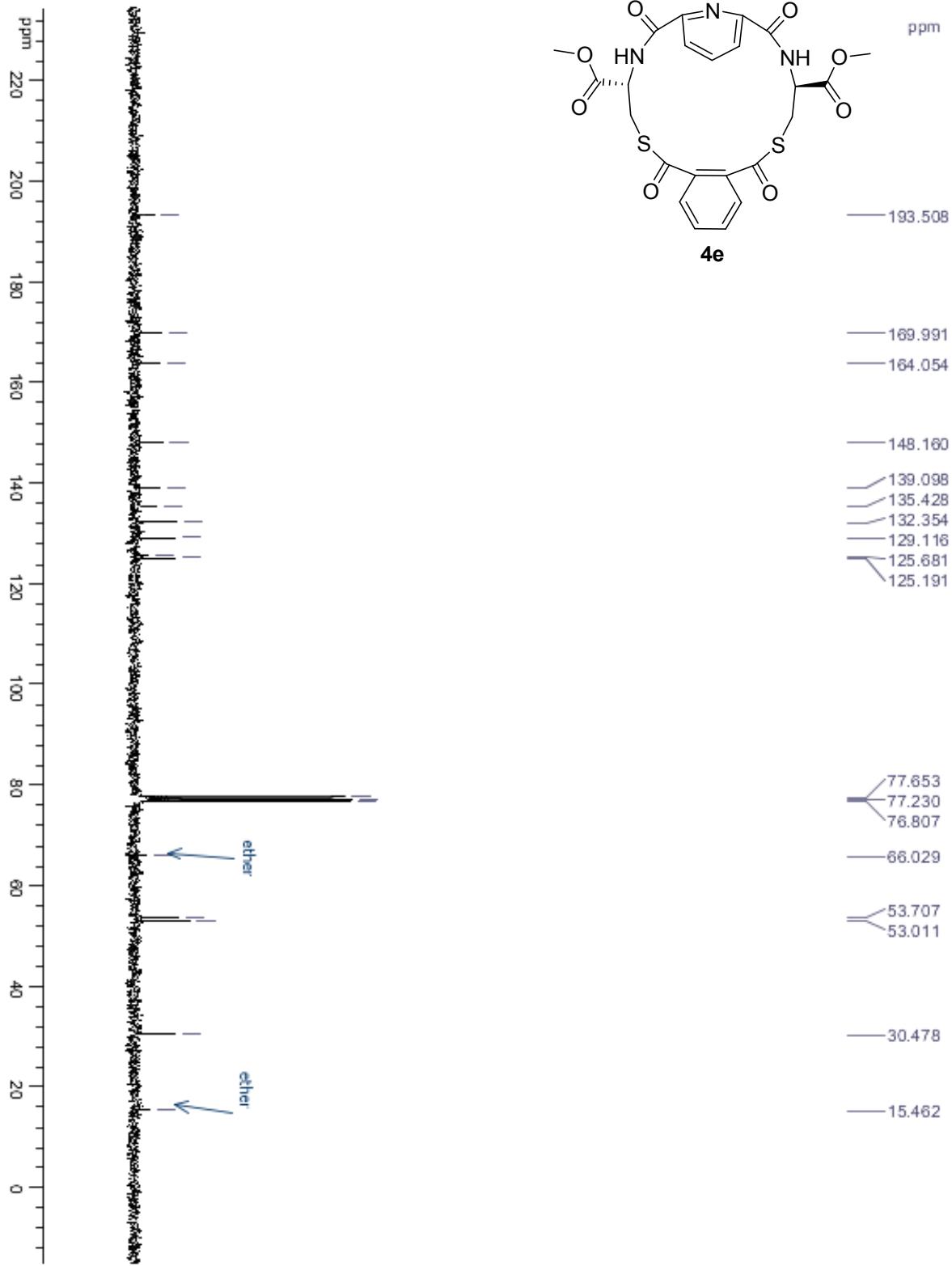
Instrument name : Instrument #1 Bline drift (fV): 6.8
 Company Name : U of Florida Operator Ident. : KOU
 Analysed : 04-25-12 08:12:19 Printed : 04-25-2012 08:22:22
 Sample Ident. : 23 1985-01 Filename : 269423
 Sample Weight : 2.111 Calc.method: using 'K. Factors'

Pk. (#)	Ret Time (Sec)	Area (fV*Sec)	Element % (%)	Area Ratio	Name
1	86	34425	7.248	.202415E+02	Nitrogen
2	117	696815	53.546	.100000E+01	Carbon
3	296	171012	4.749	.407465E+01	Hydrogen



4e





EI/ESI Scan [0.1980.19] min, 3 scans] Range [80.0V, 1820.0V, Mass[10 pHmE, methanol/ESI/d Subnan]

Theoretical $[M+H]^+$ = 532.0843

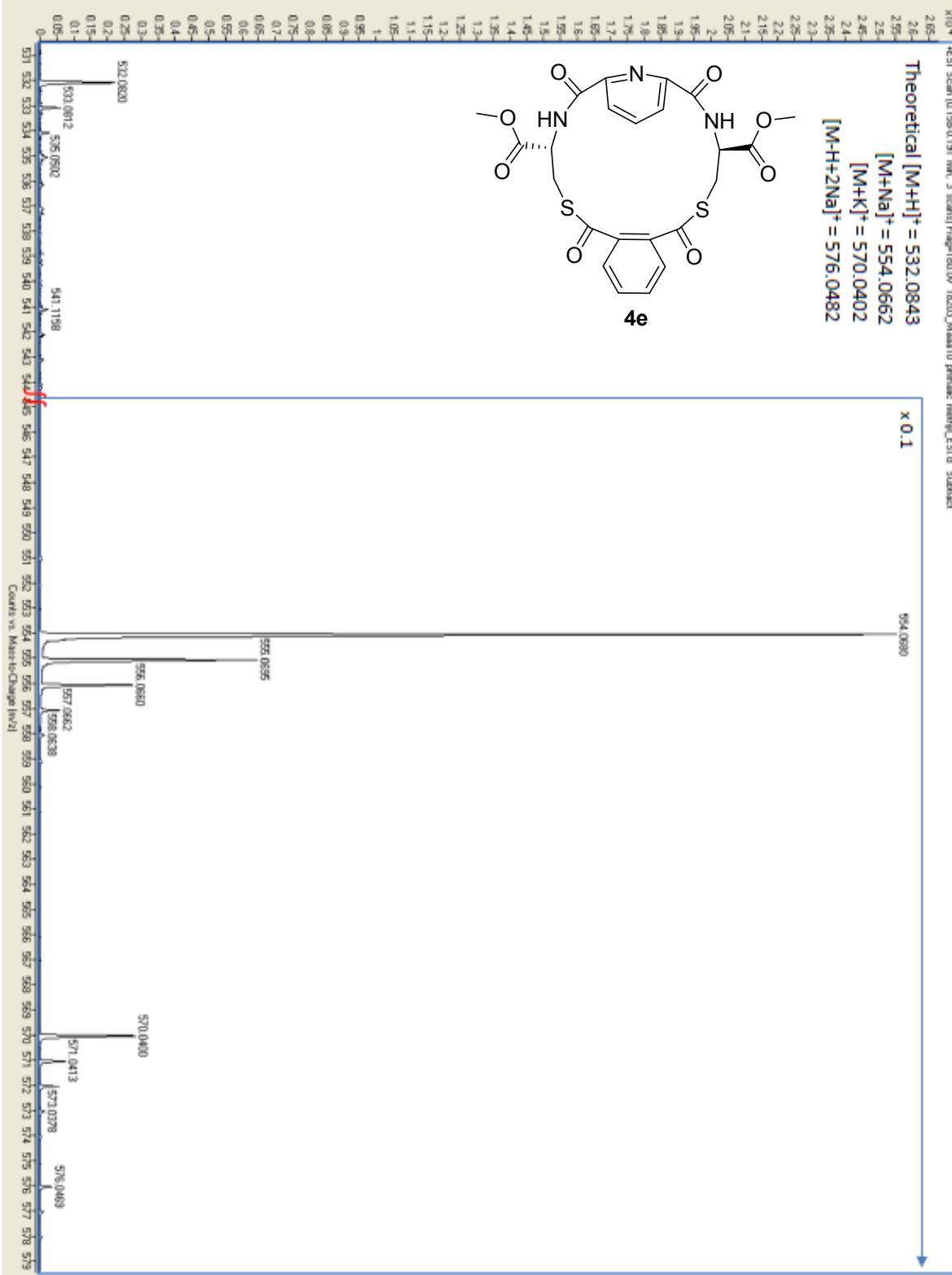
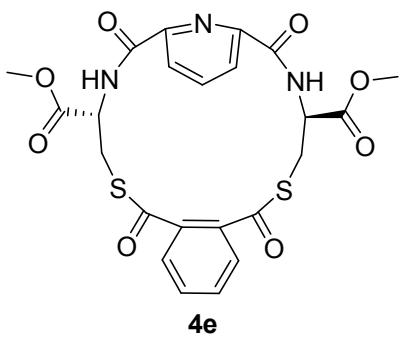
$[M+Na]^+$ = 534.0662

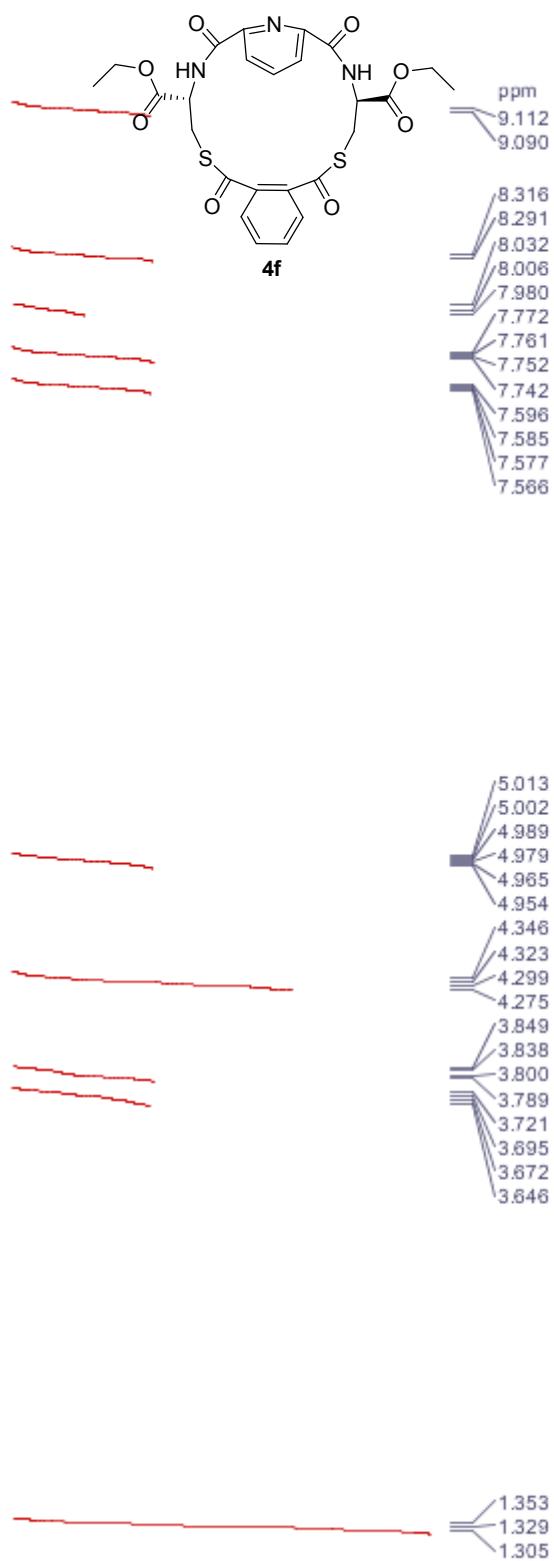
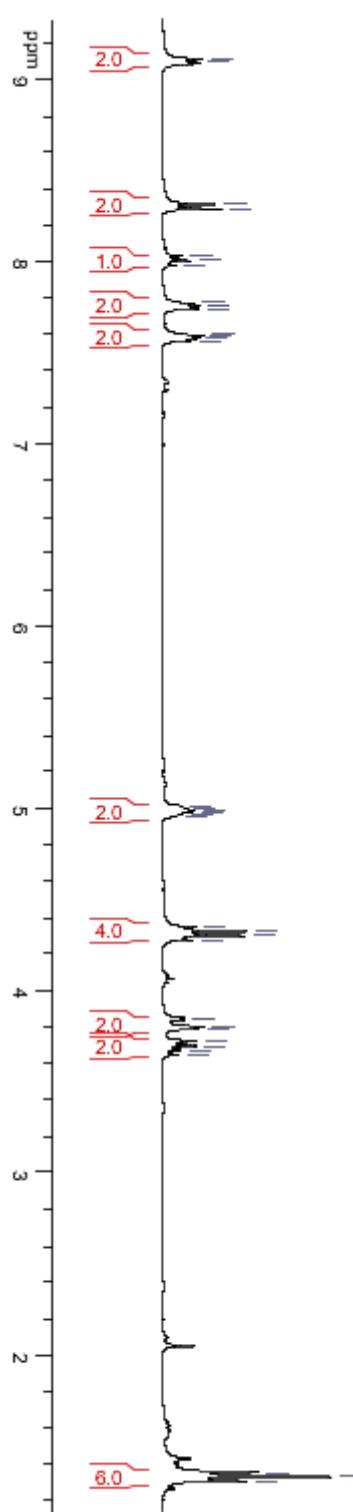
$[M+K]^+$ = 570.0402

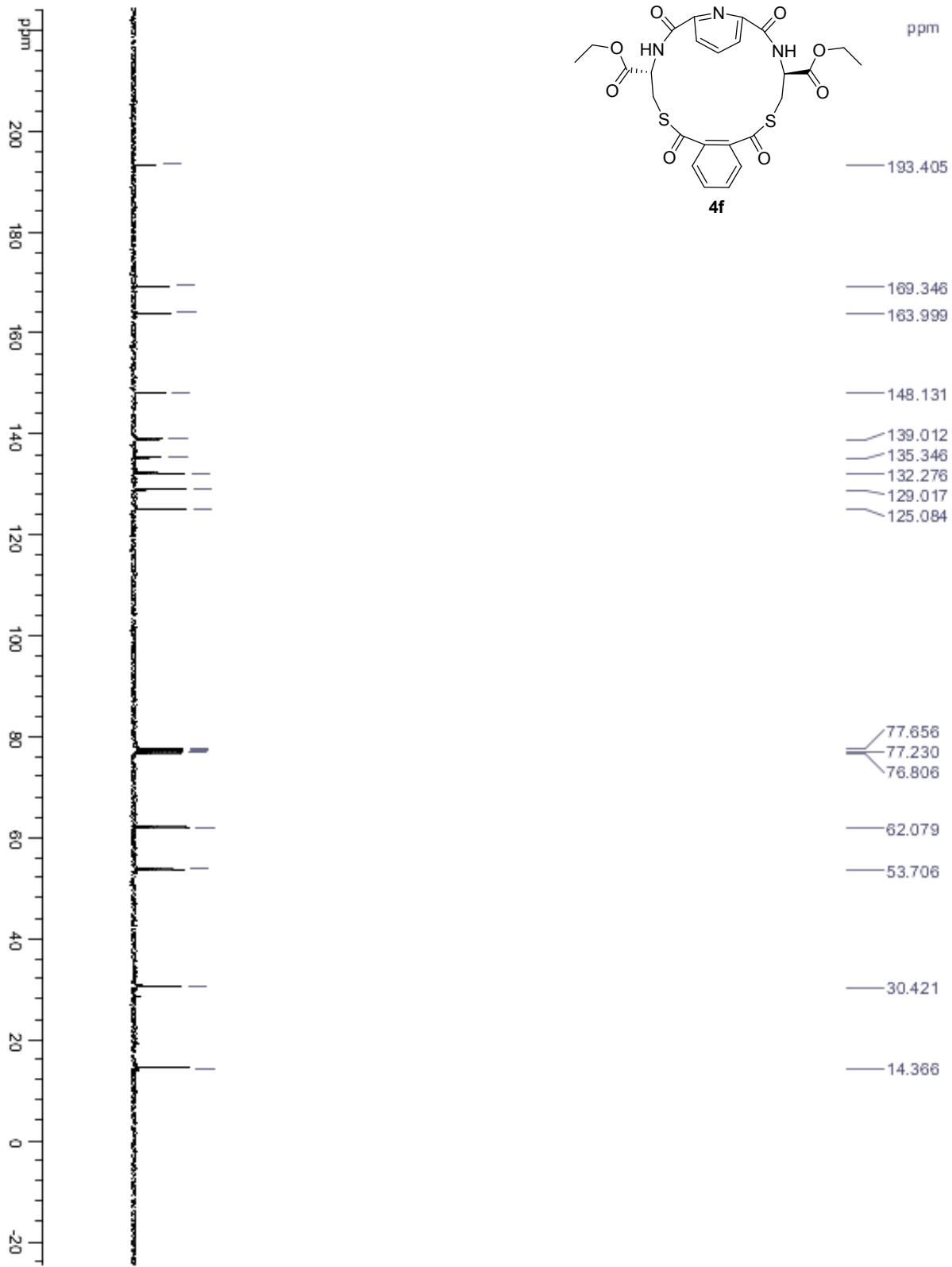
$[M-H+2Na]^+$ = 576.0482

x 0.1

534.0662







x 0.5

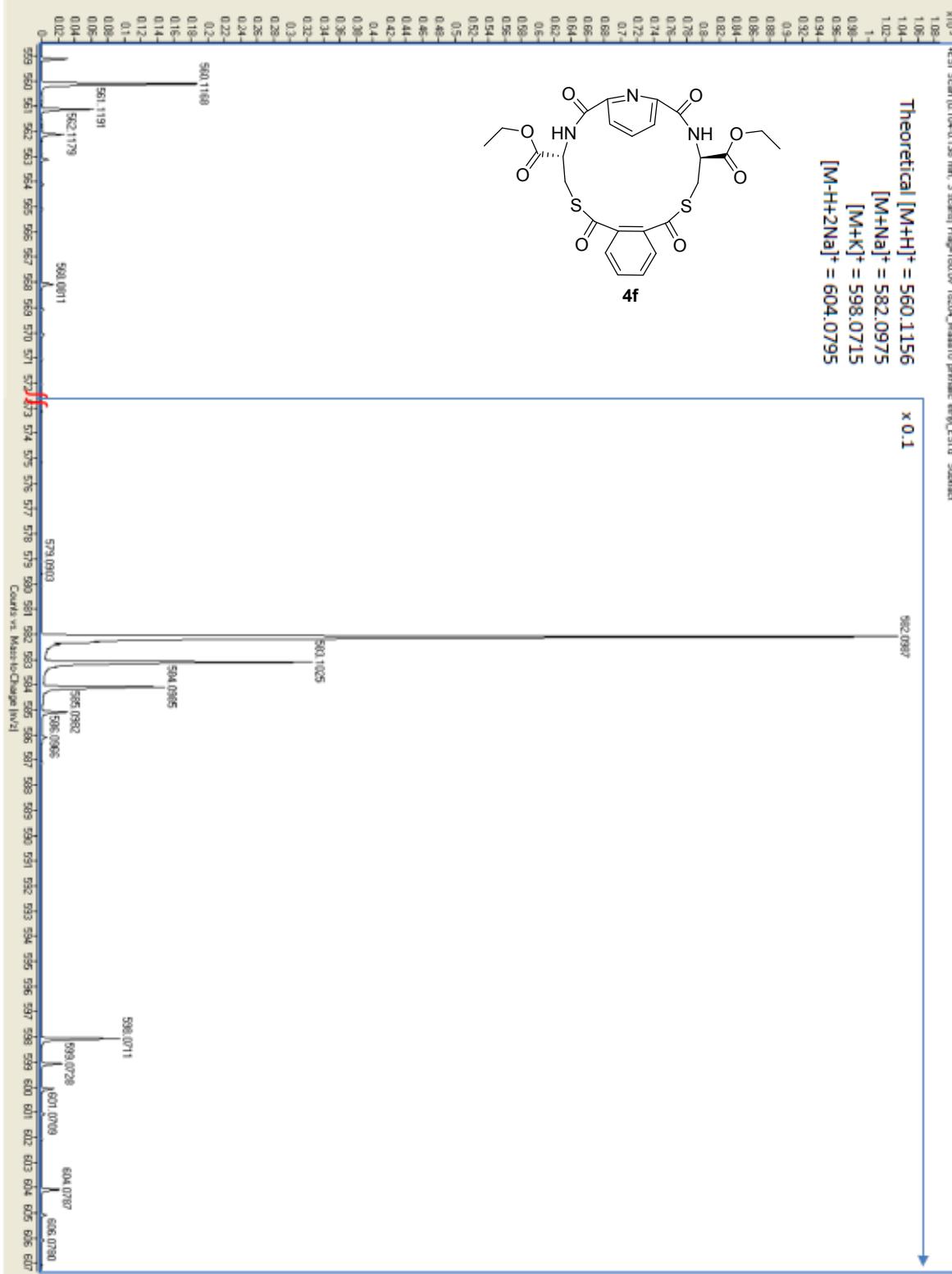
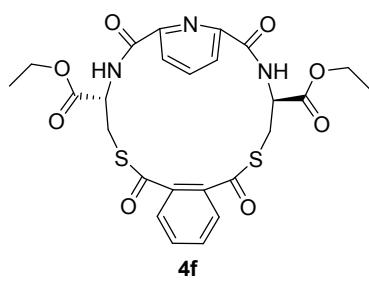
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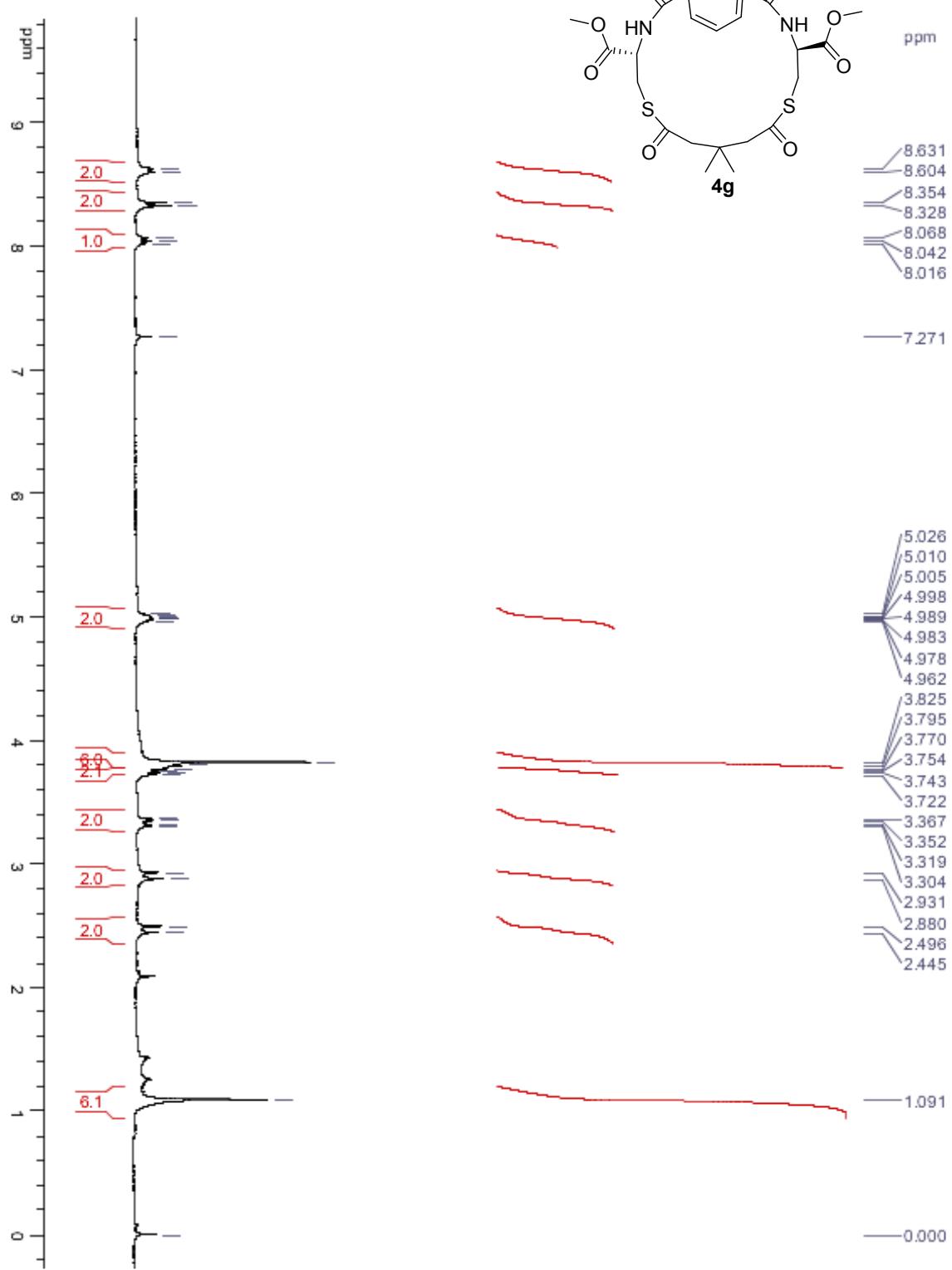
Theoretical $[M+H]^+$ = 560.1156

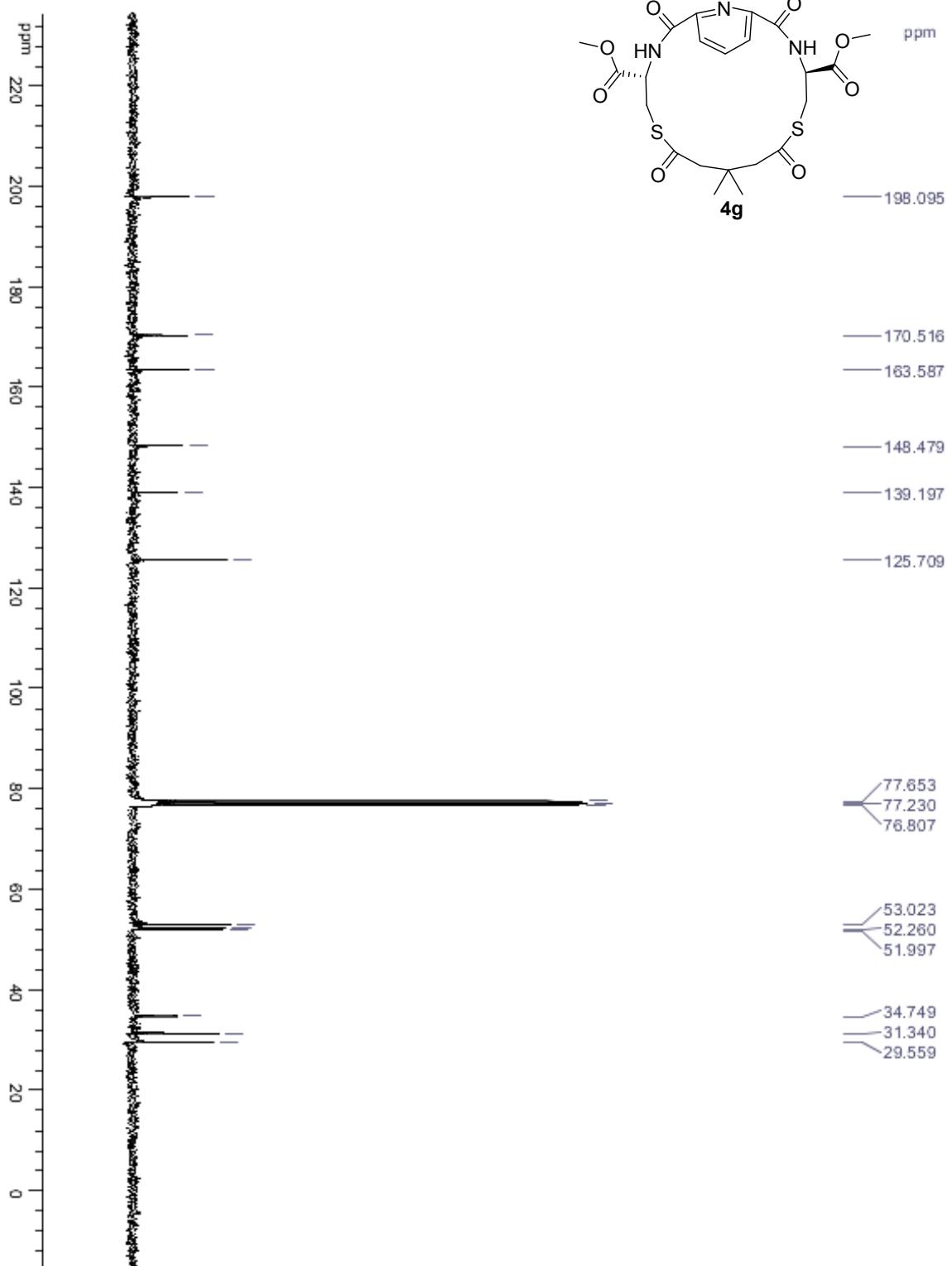
$[M+Na]^+$ = 582.0975

$[M+K]^+$ = 598.0715

$[M-H+2Na]^+$ = 604.0795







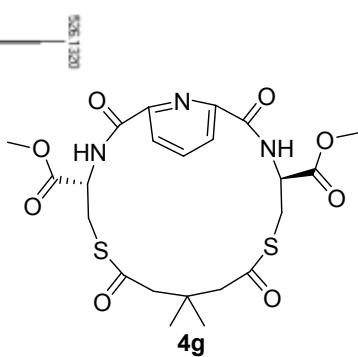
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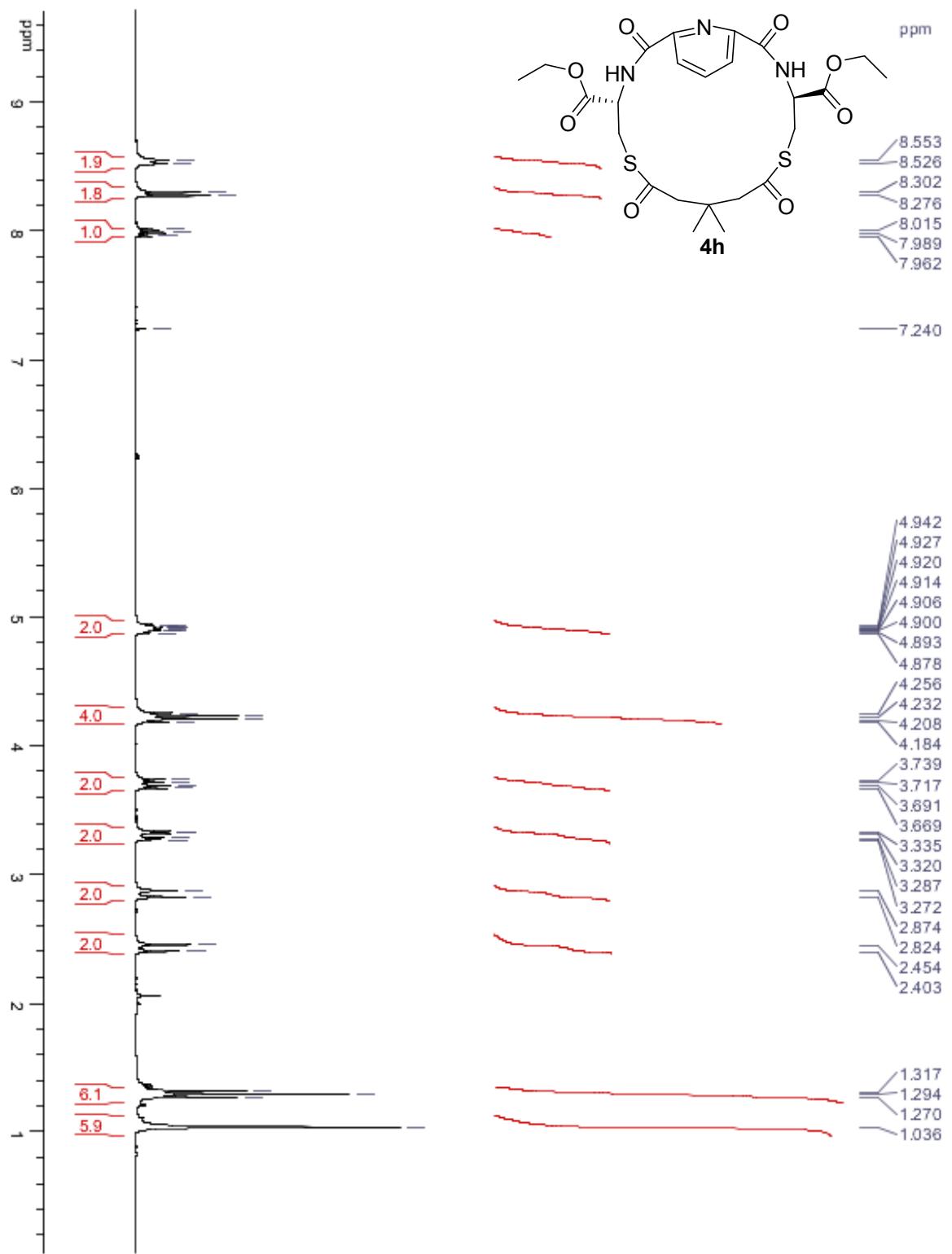
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0.05-
0.04-
0.03-
0.02-
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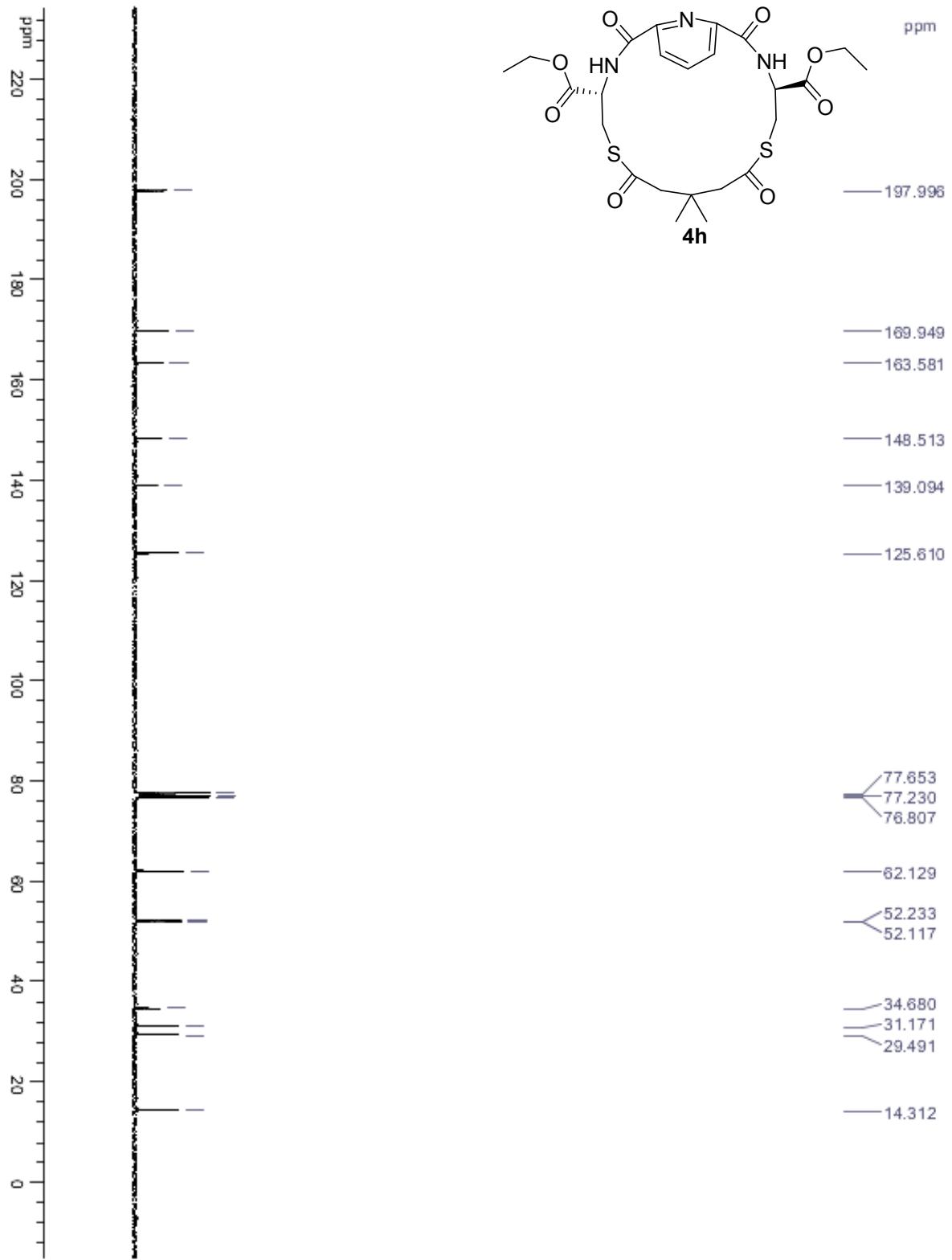
Theoretical $[M+H]^+$ = 526.1312

$[M+Na]^+$ = 548.1132
 $[M+K]^+$ = 564.0871

548.1148

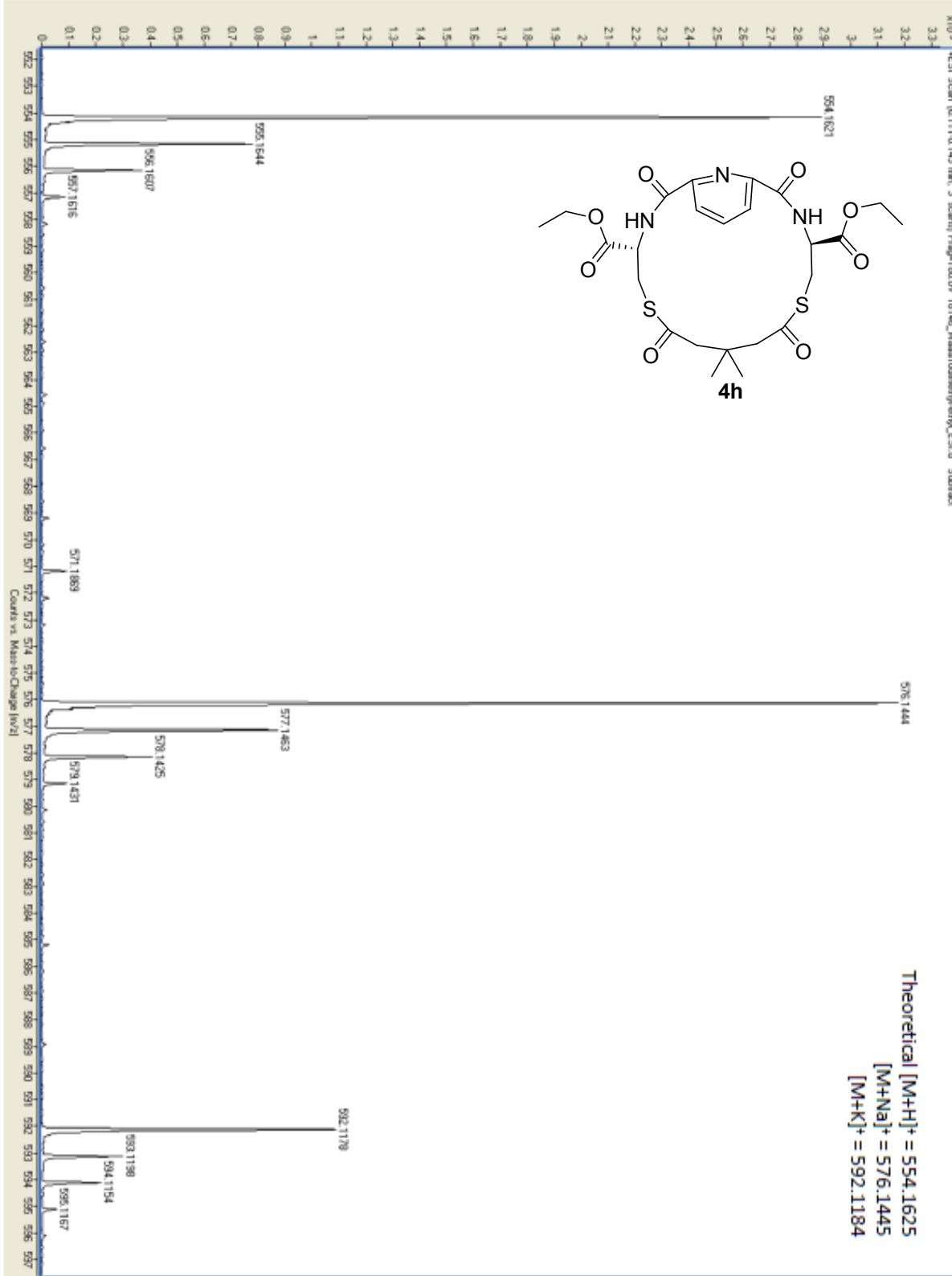
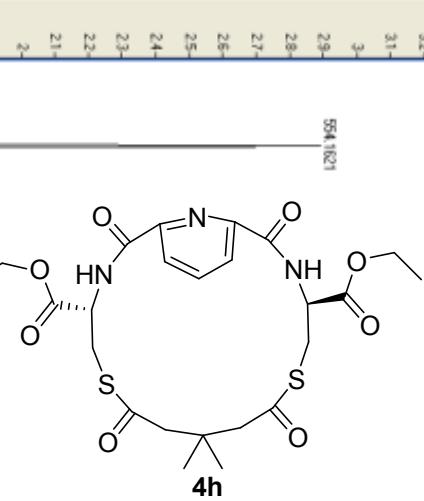


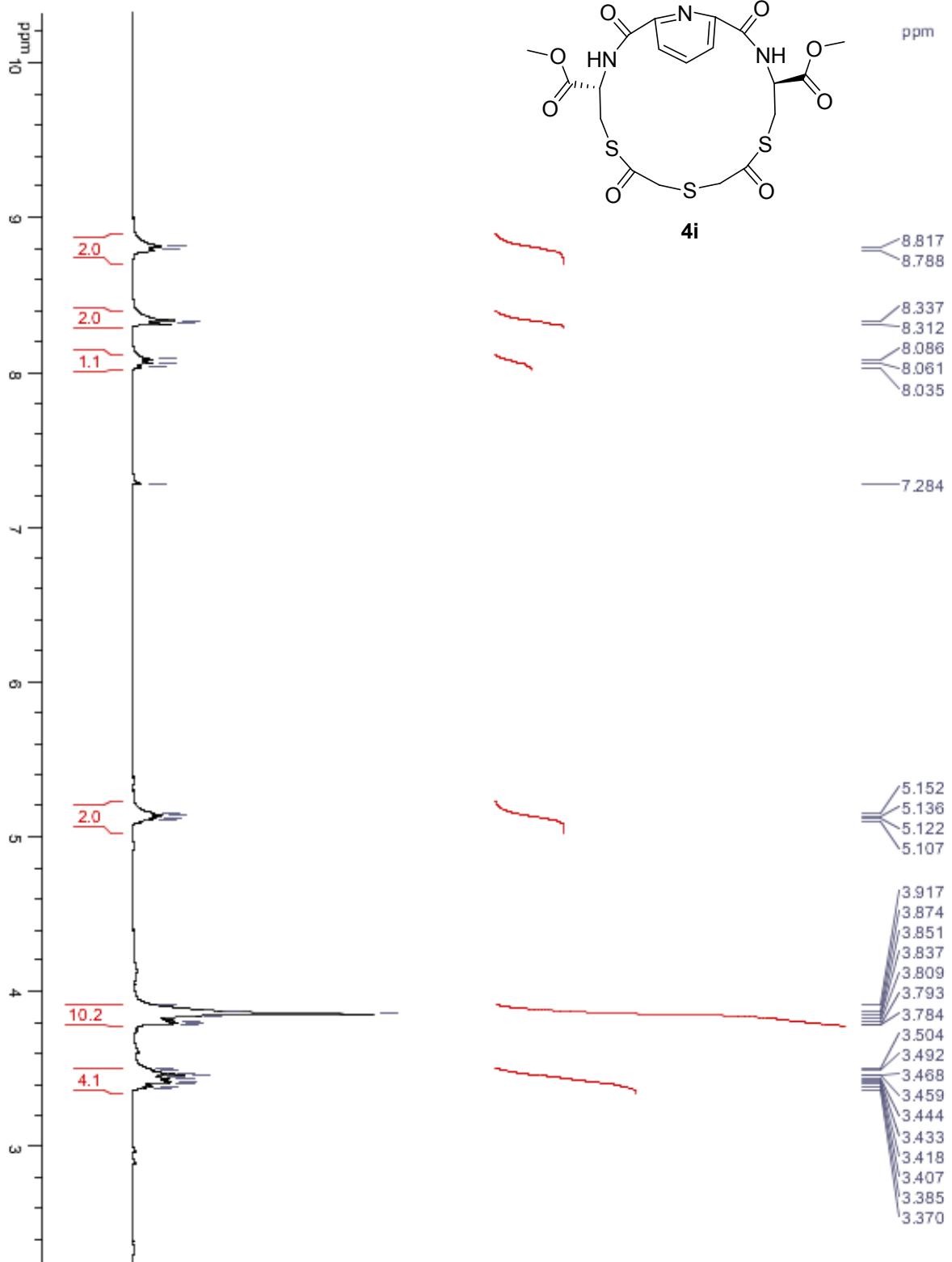


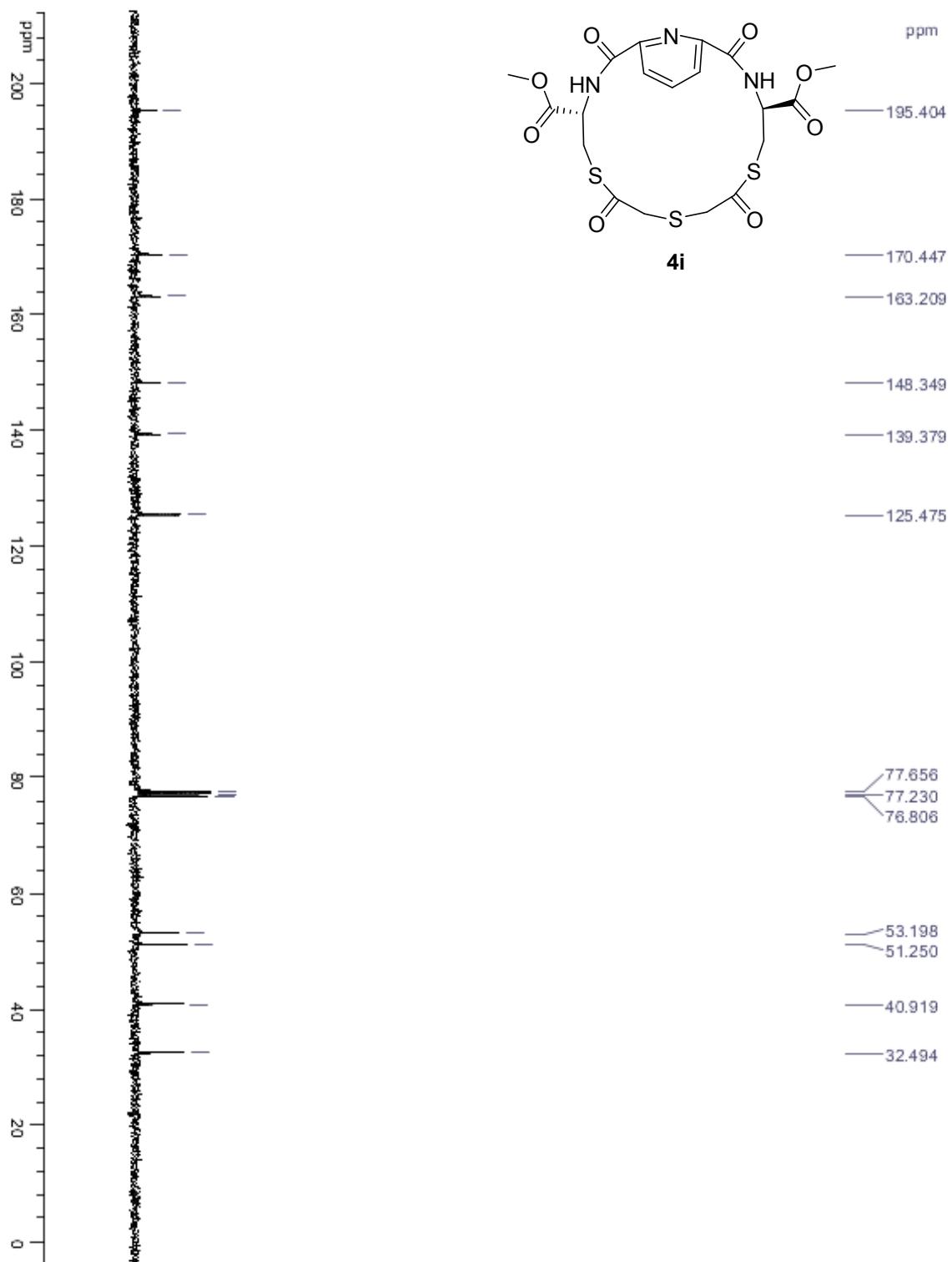


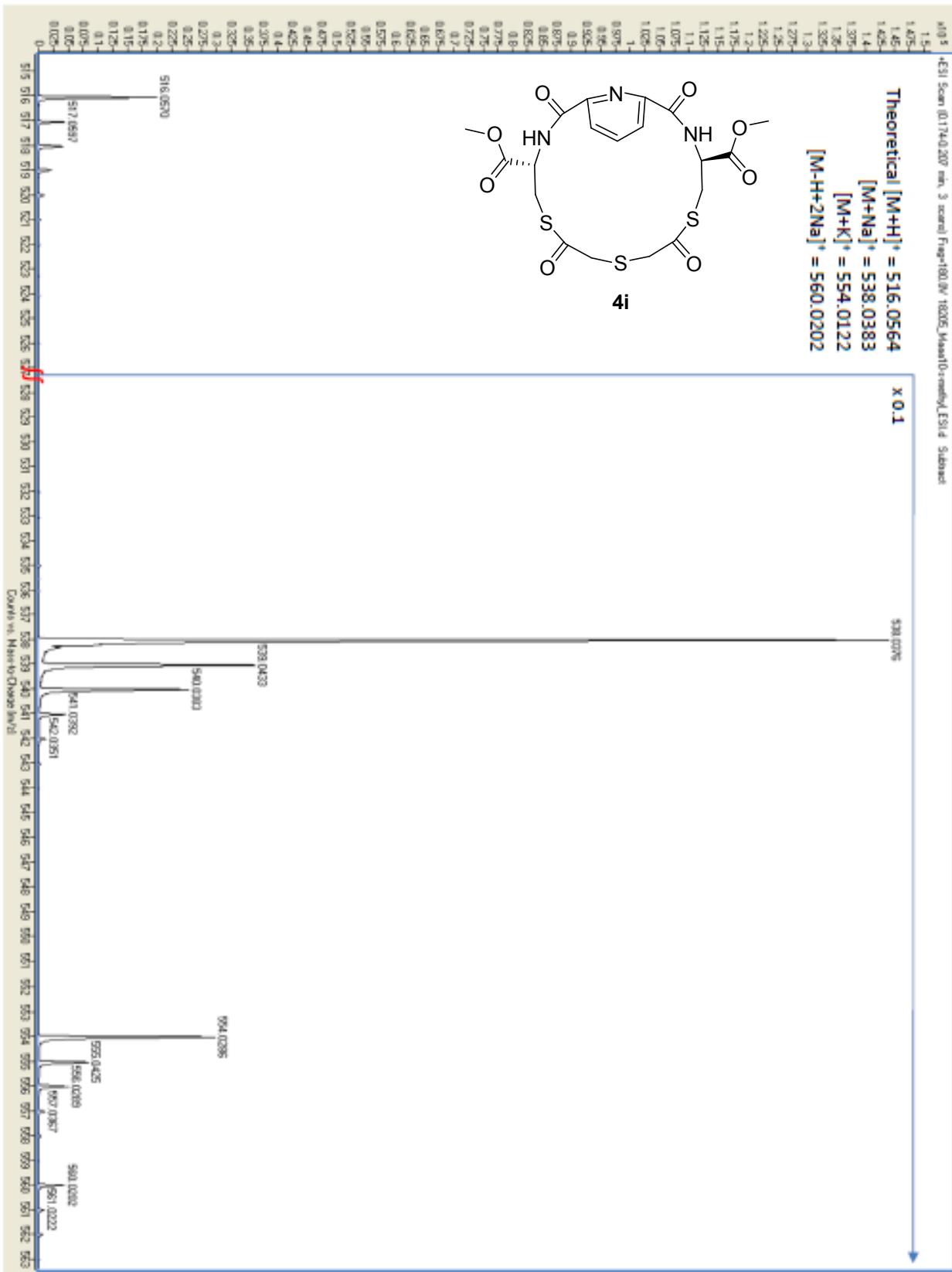
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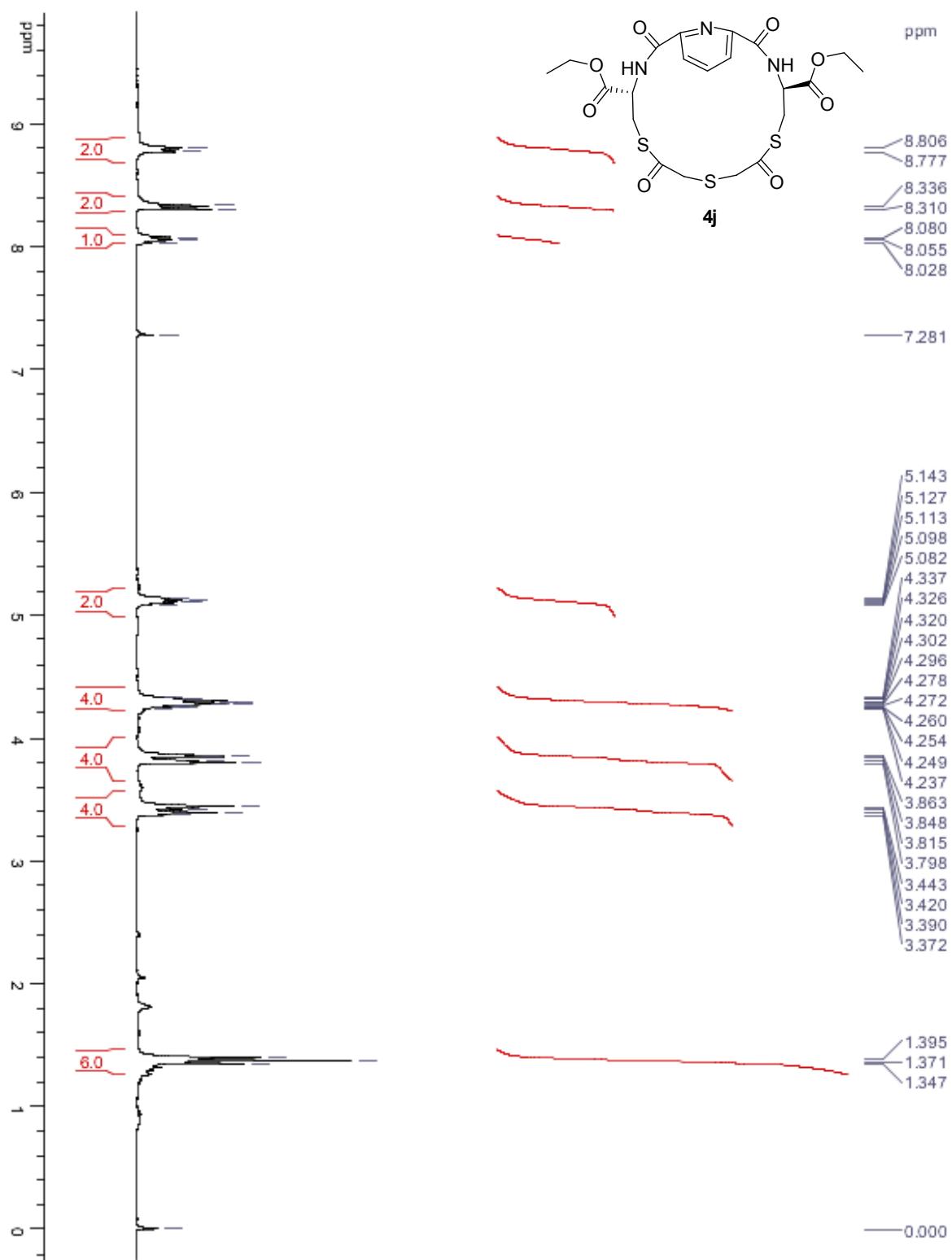
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 $[M+Na]^+$ = 576.1445
 $[M+K]^+$ = 592.1184

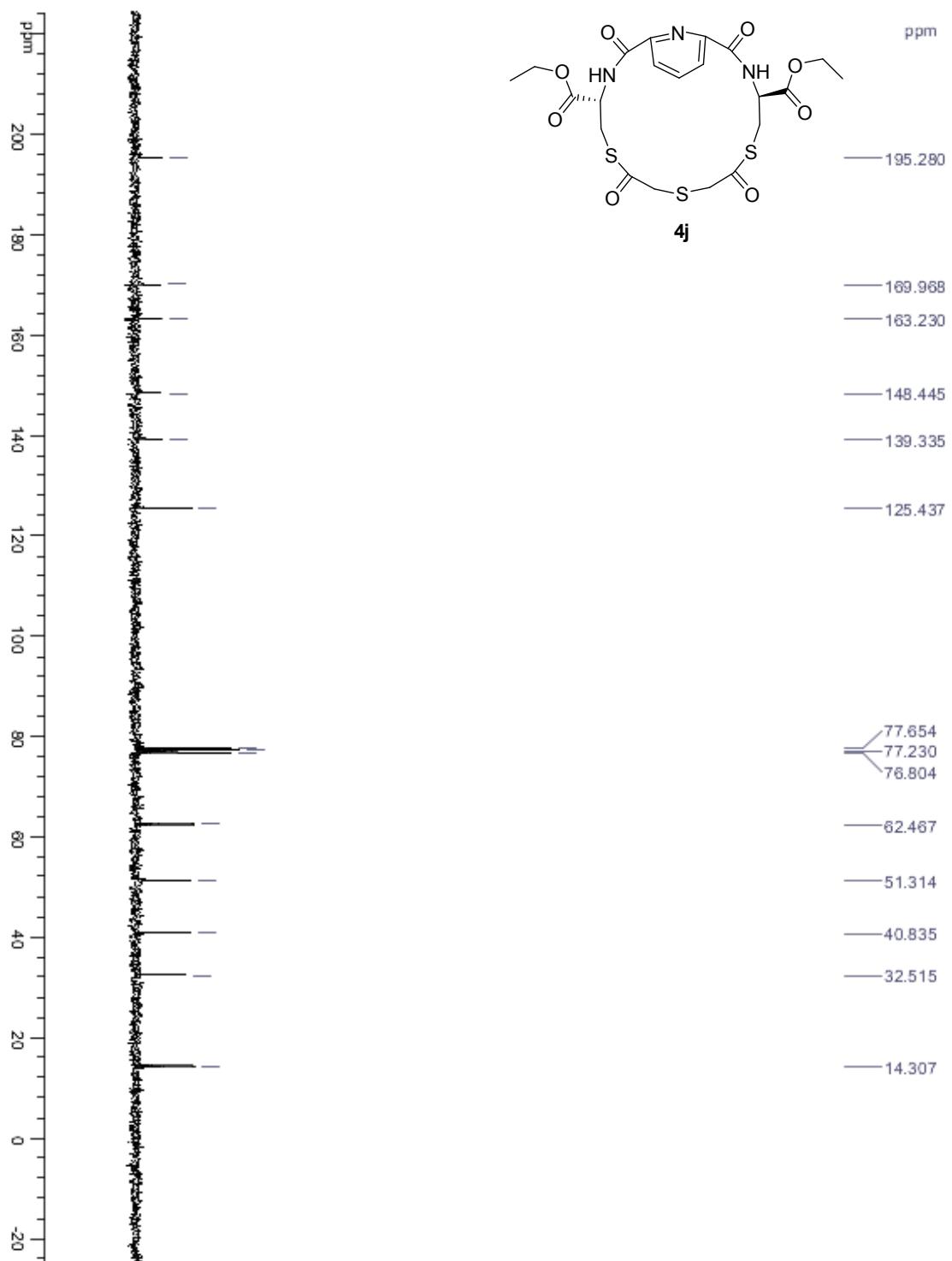






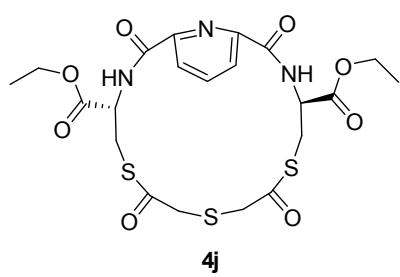




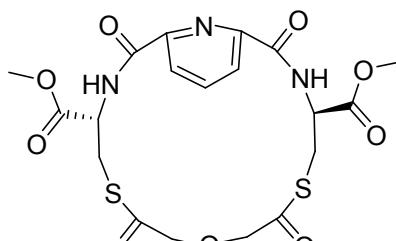
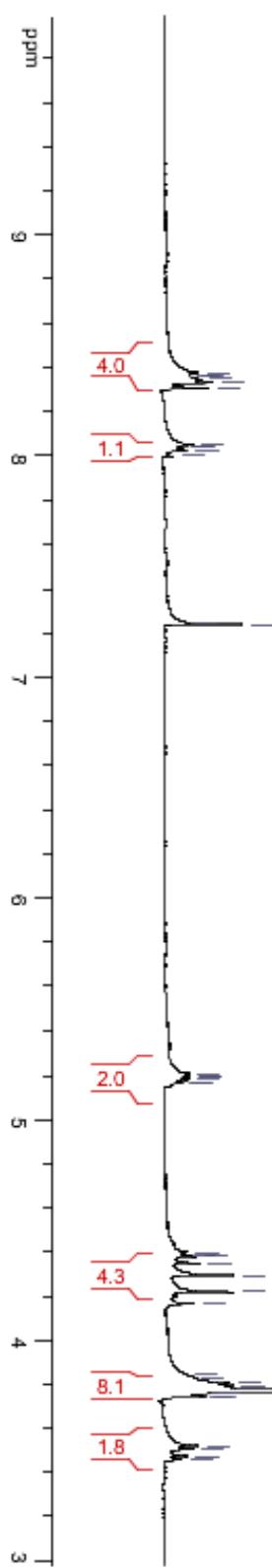


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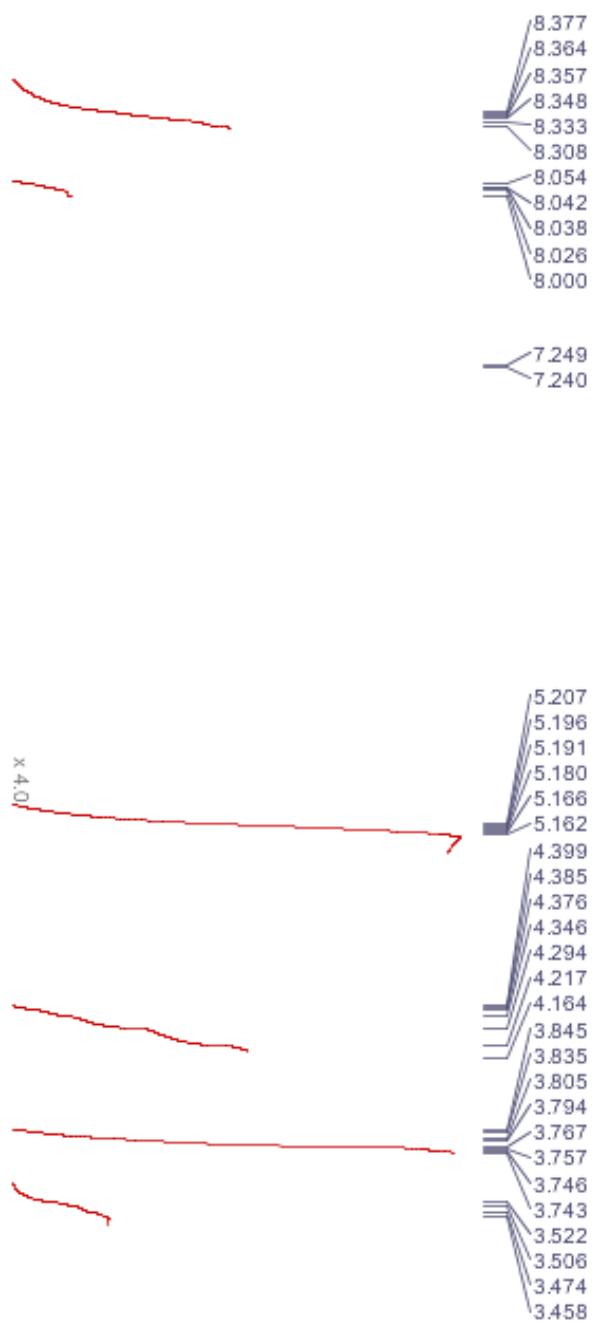
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1.06-
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0.9-
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0.7-
0.68-
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0.64-
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0.58-
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0.3-
0.28-
0.26-
0.24-
0.22-
0.2-
0.18-
0.16-
0.14-
0.12-
0.1-
0.08-
0.06-
0.04-
0.02-
0.00-
566.0719
568.0687
569.0701
570.0695
572.0604
573.0696
574.0685
575.0674
576.0663
577.0653
578.0642
579.0631
580.0620
581.0609
582.0598
583.0587
584.0576
585.0565
586.0553
587.0542
588.0531
589.0520
590.0509
591.0498
592.0487
593.0476
594.0465
595.0453
596.0442
597.0431
598.0420
599.0409
600.0398
601.0387
602.0376
603.0365
604.0354
605.0343
606.0332
607.0321
608.0310
609.0300
610.0289
611.0278
612.0267
613.0256
614.0245
615.0234
616.0223
617.0212
618.0201
619.0190
620.0179
621.0168
622.0157
623.0146
624.0135
625.0124
626.0113
627.0102
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632.0047
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635.0014
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637.0000

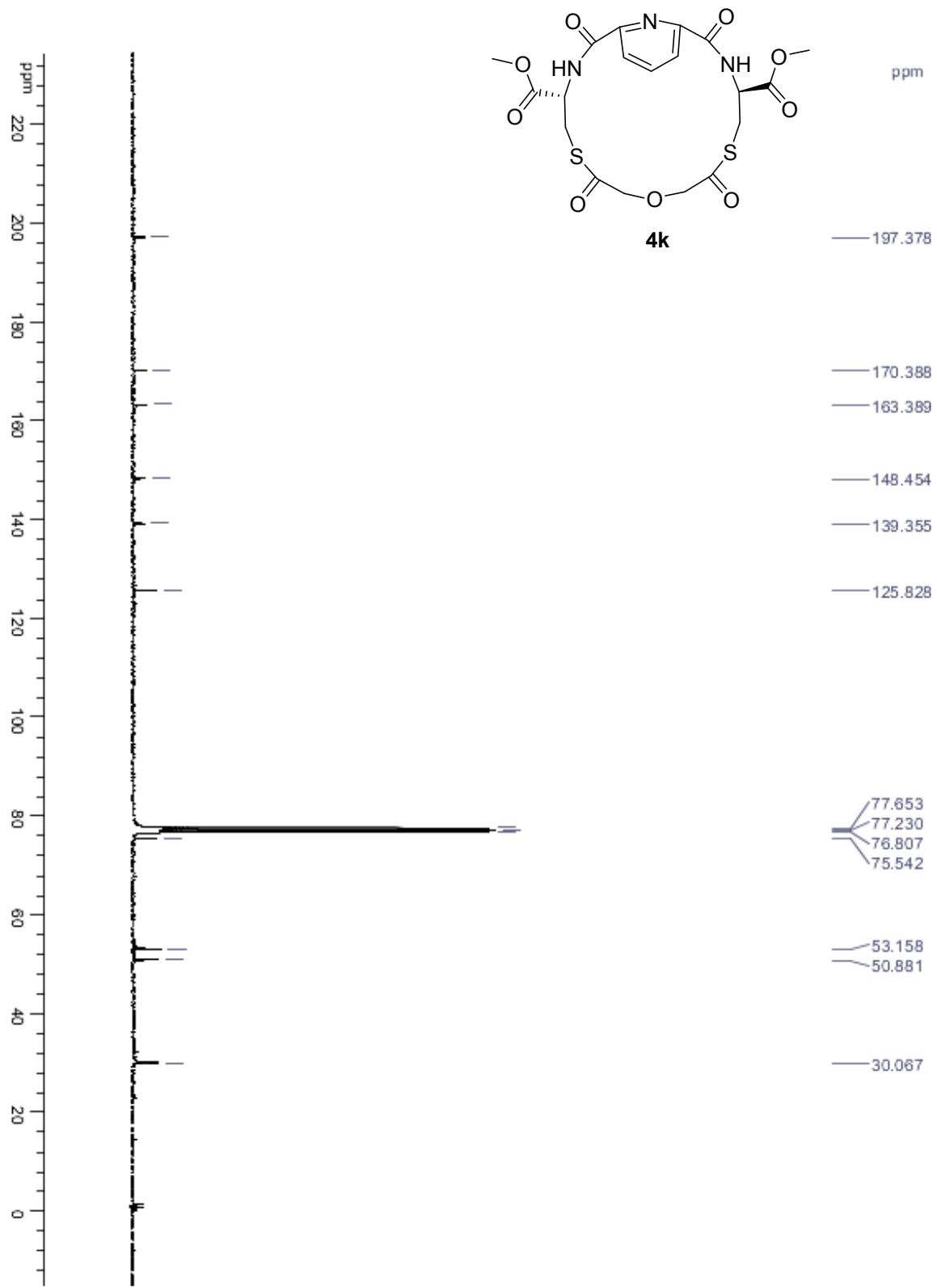


Theoretical [M+Na]⁺ = 566.0696
[M+K]⁺ = 582.0435
[M-H+2Na]⁺ = 588.0515



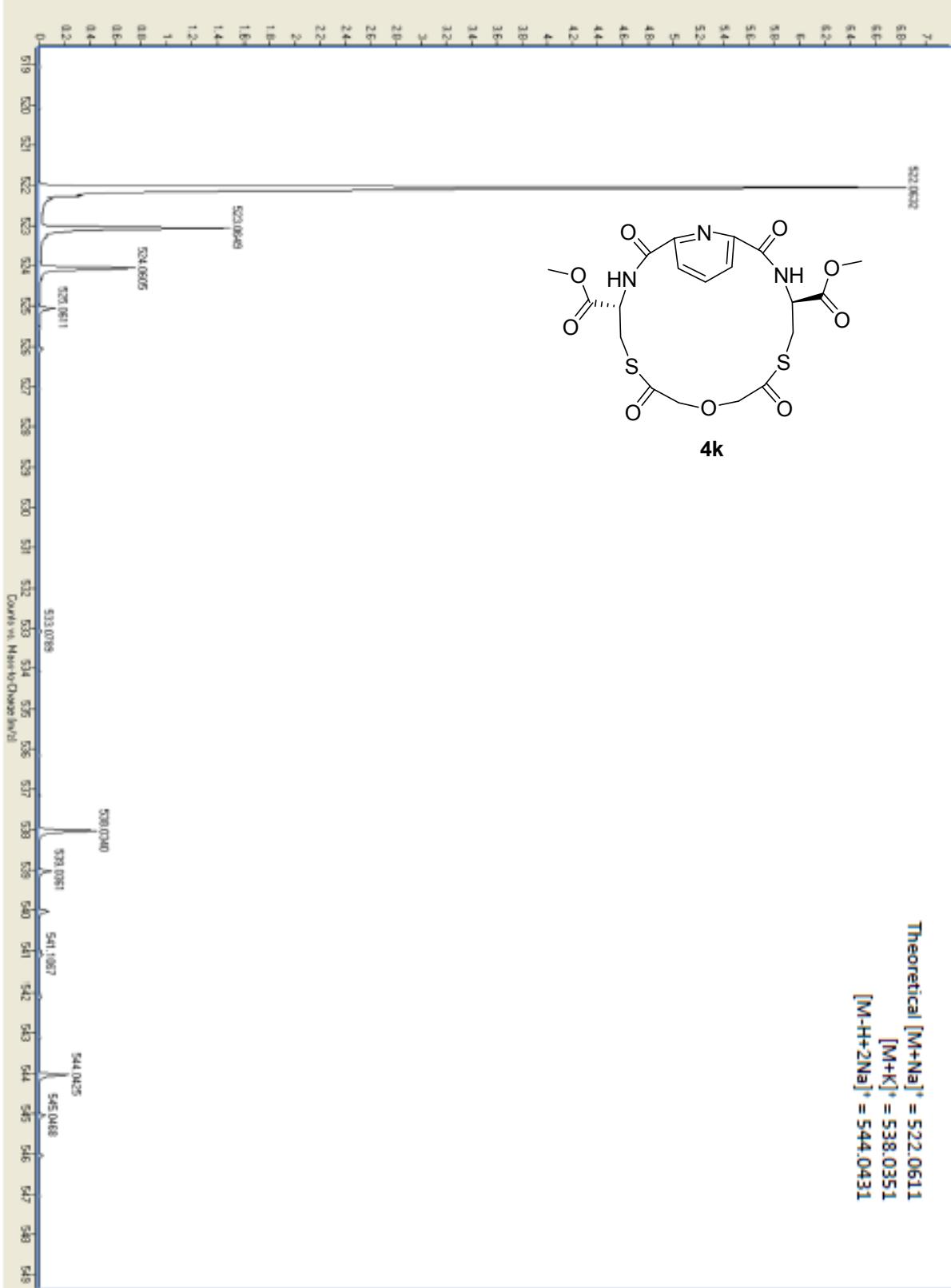
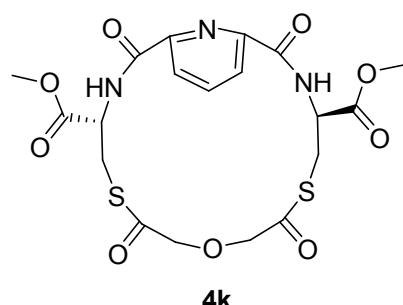
4k

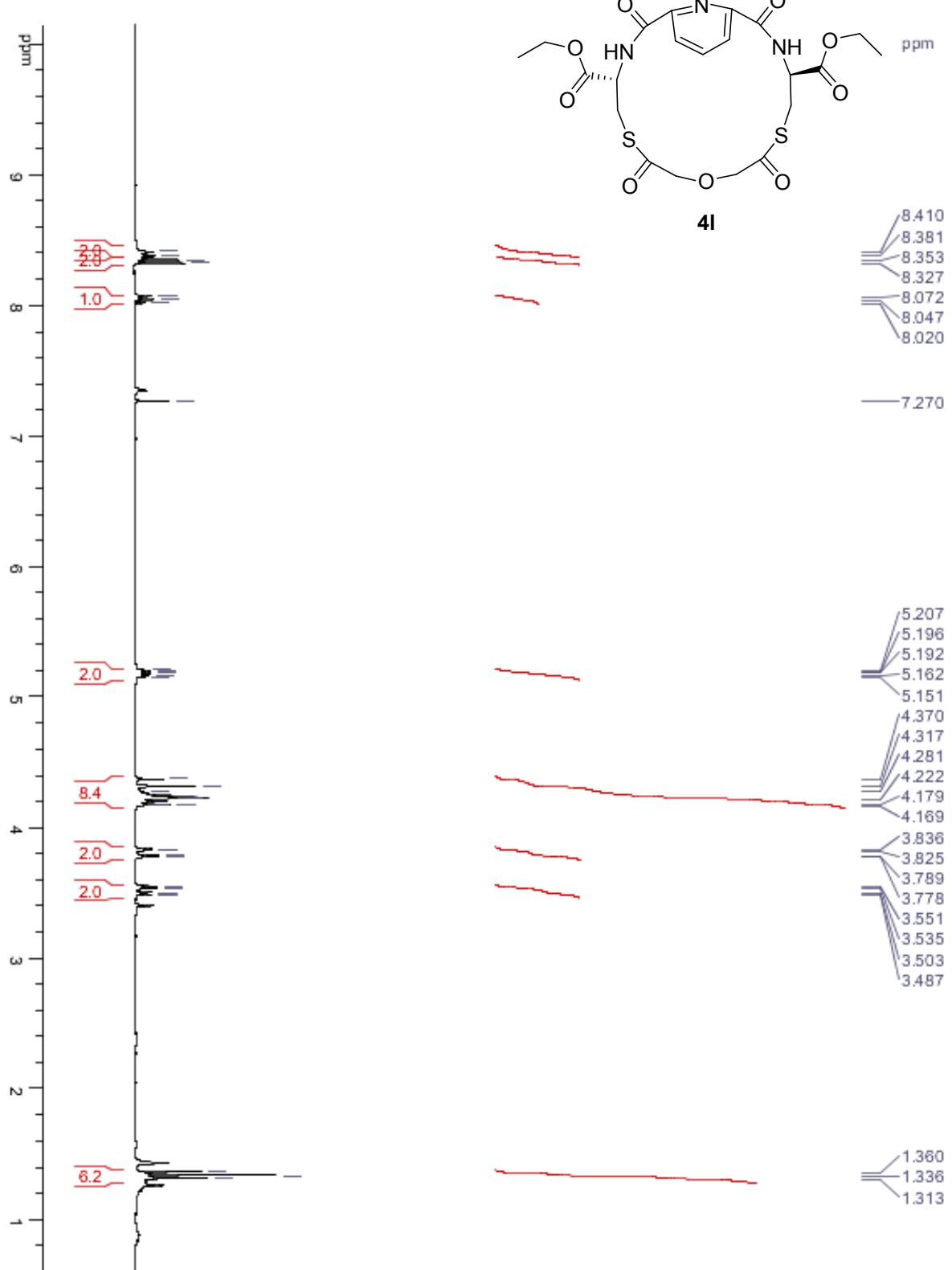


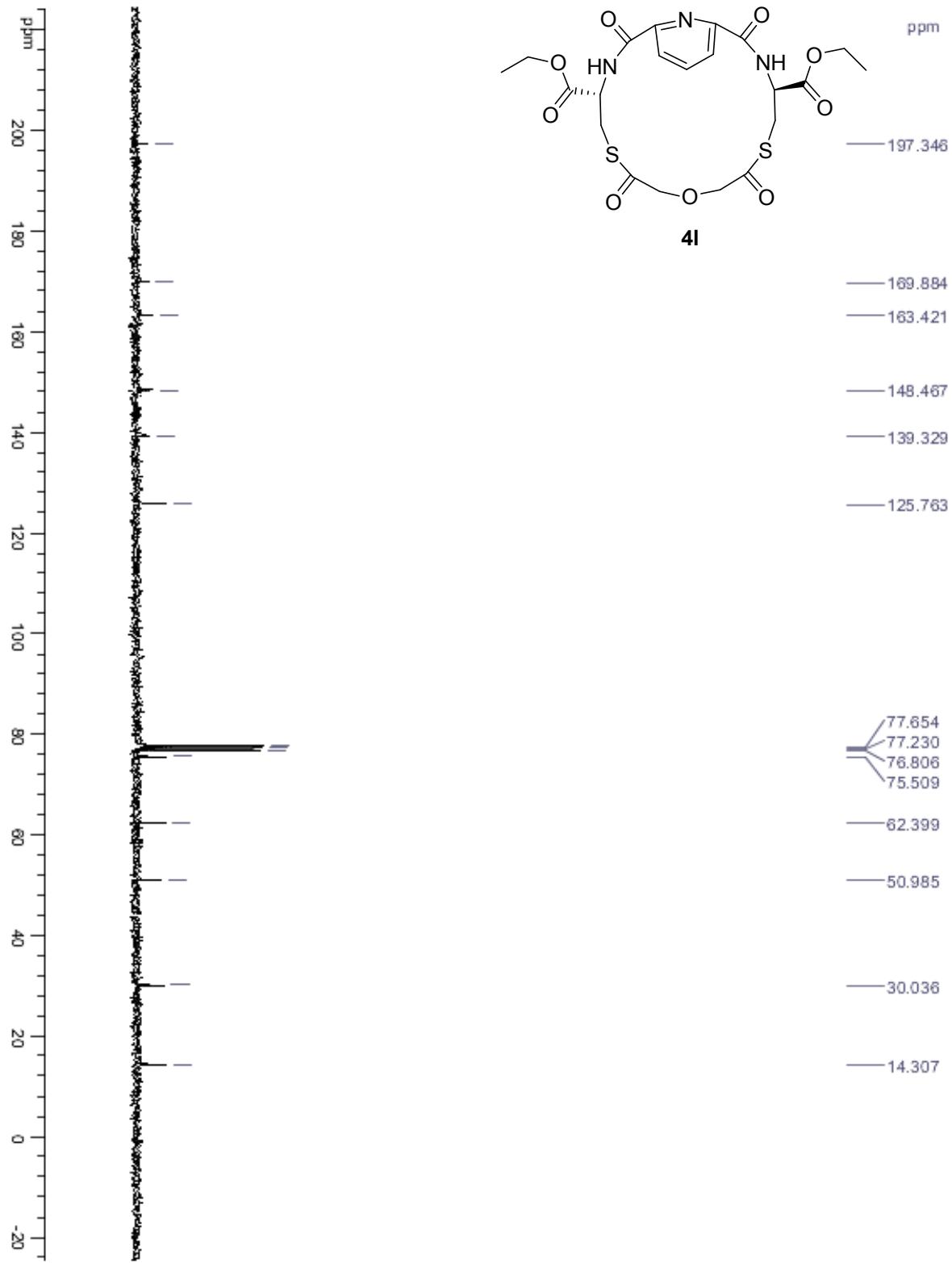


#135 +ESI Scan (0.103.0.136 min, 3 scans) Frag(102.94/ 1620.7, Meas=10.0, methyl, ESI:d, Subtract

Theoretical $[M+Na]^+$ = 522.0611
 $[M+K]^+$ = 538.0351
 $[M-H+2Na]^+$ = 544.0431







*ESI Scan [0.2140.242 min, 3 scans] File#180.m MassL0.msf ESI.ms1 Subset

Theoretical $[M+H]^+$ = 528.1105

$[M+Na]^+$ = 550.0924

$[M+K]^+$ = 566.0664

$[M-H+2Na]^+$ = 572.0744

X 0.1
#550940

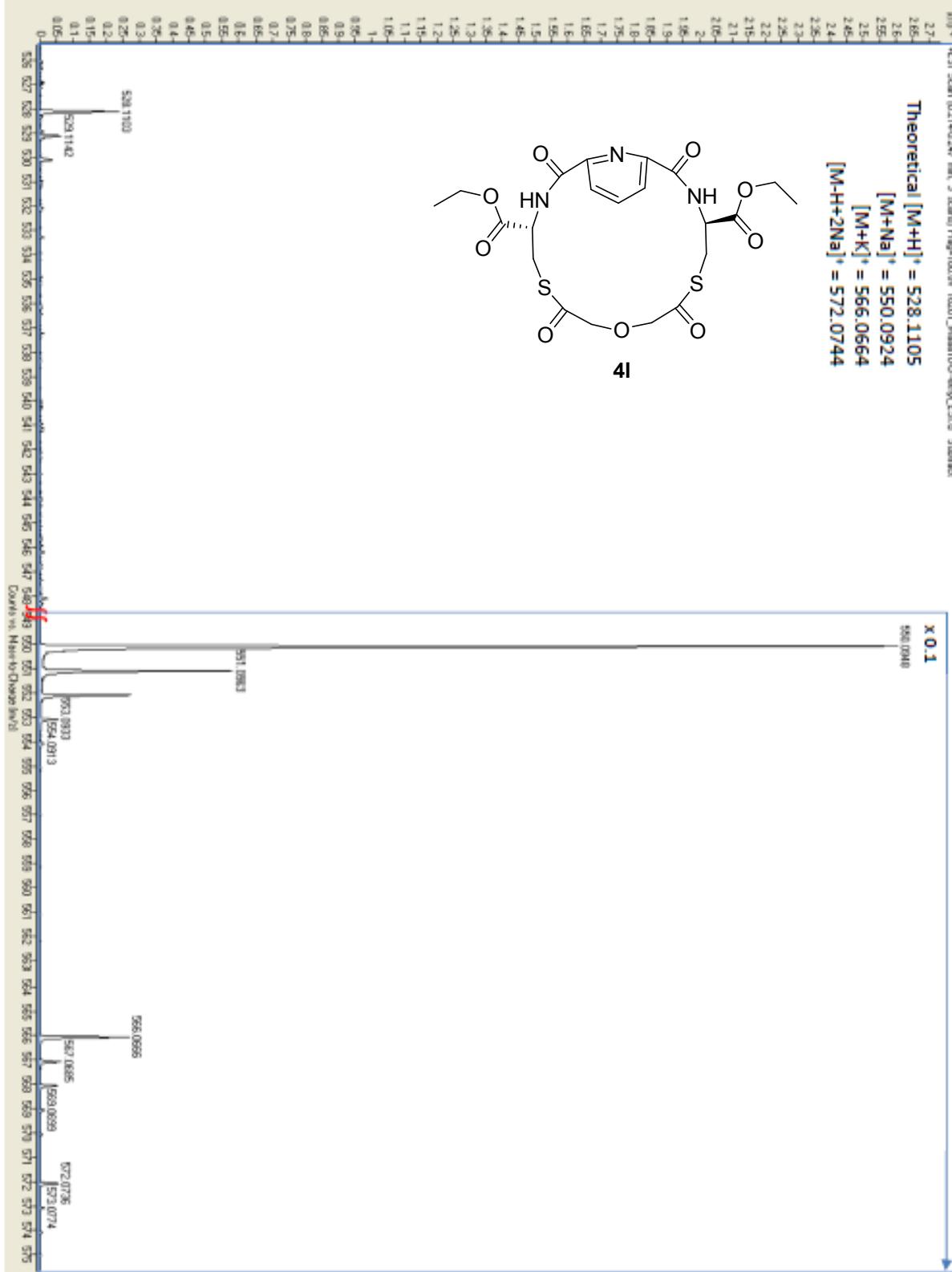
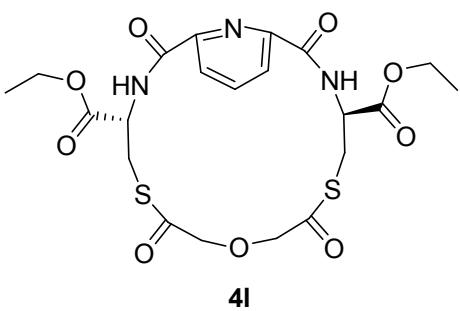


Table S1. Molecular descriptor values of the BMLR-QSAR model for the antifungal active macrocyclic peptidomimetics.

Entry	Compd.	Descriptors*		
		D ₁	D ₂	D ₃
1	4a	0.0043	-1153.12	19.5355
2	4b	0.0046	-1209.1	19.4839
3	4c	0.00623	-1264.3	19.5096
4	4d	0.00455	-1460.3	19.5223
5	4e	0.00944	-1268.36	19.5329
6	4f	0.0091	-1300.97	19.4882
7	4g	0.00238	-1221.38	19.468
8	4h	0.00213	-1061.68	19.4667
9	4i	0.00559	-1047.9	19.4659
10	4j	0.00159	-1017.77	19.4645
11	4k	0.00755	-934.668	19.5165
12	4l	0.00235	-1179.24	19.4717
13	5	0.01884	-1221.8	19.5034
14	6	0.02522	-1232.66	19.5044
15	7	0.01537	-900.929	19.472

*D₁ = FHDCA Fractional HDCA (HDCA/TMSA) (MOPAC PC), D₂ = WNSA-2 Weighted PNSA (PNSA2*TMSA/1000) (MOPAC PC), D₃ = Max. total interaction for bond C-C.

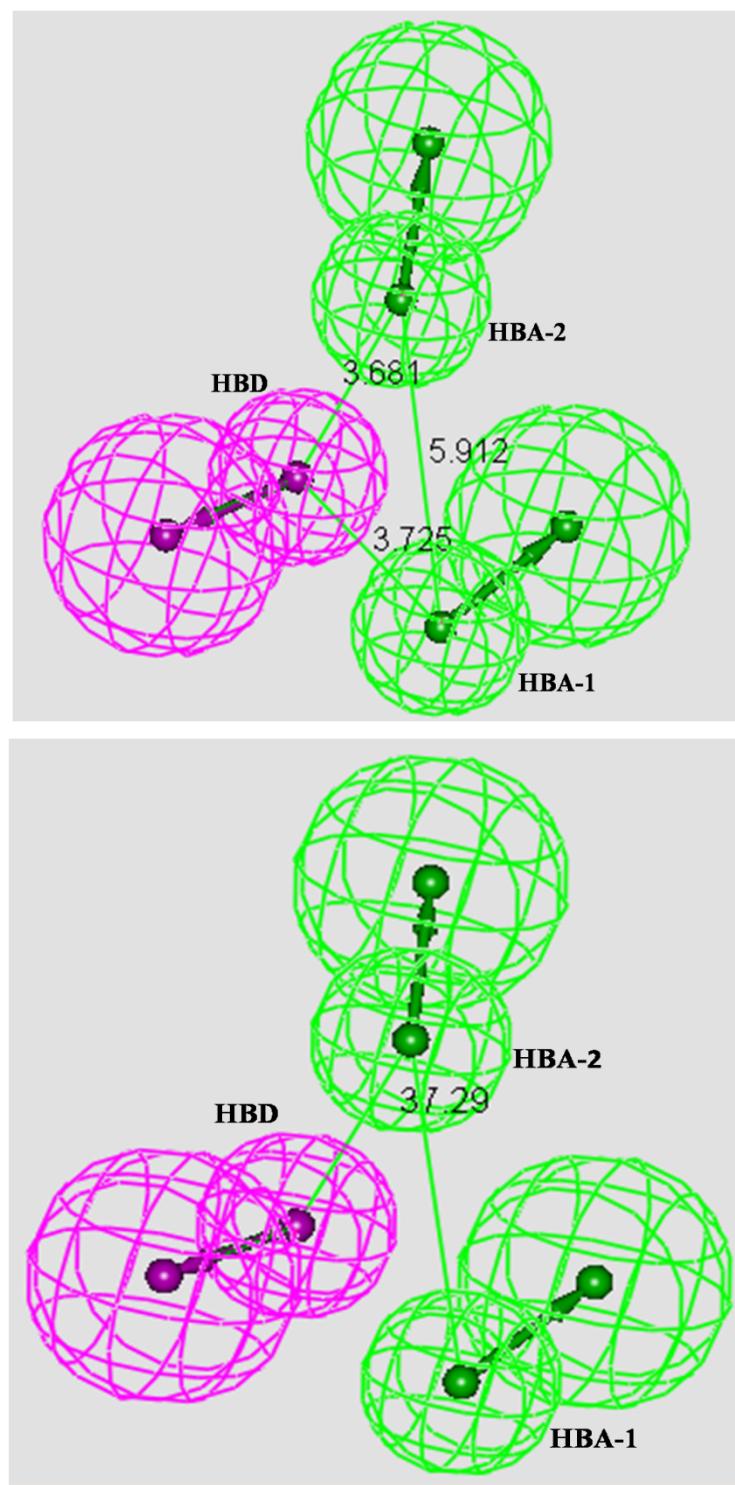
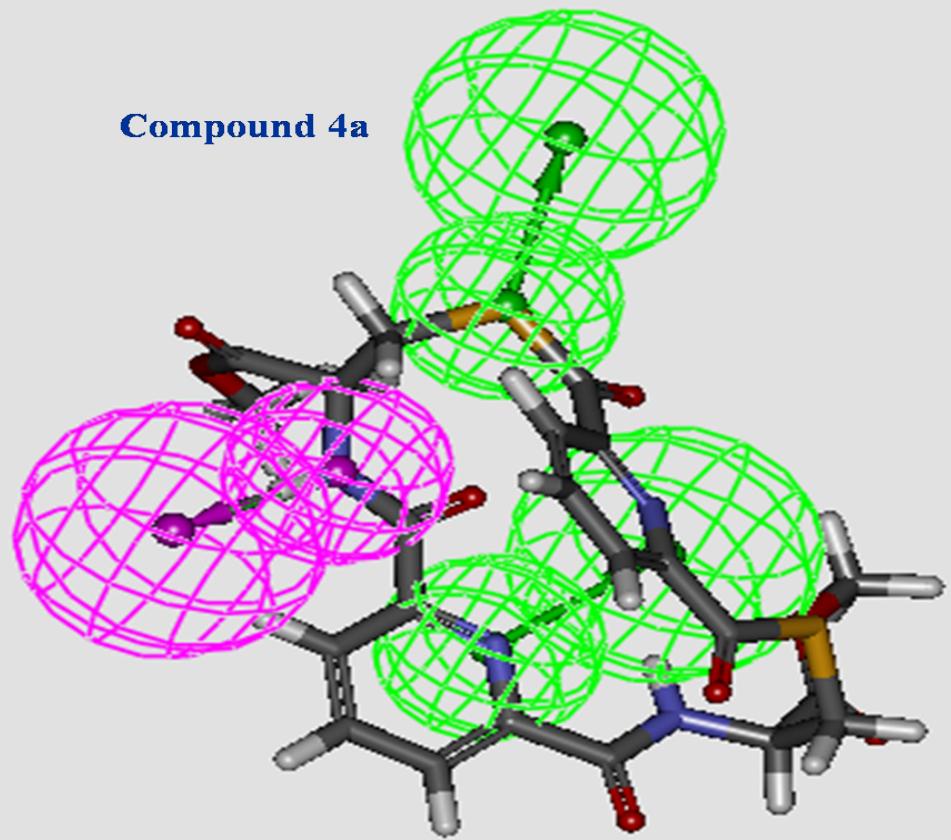
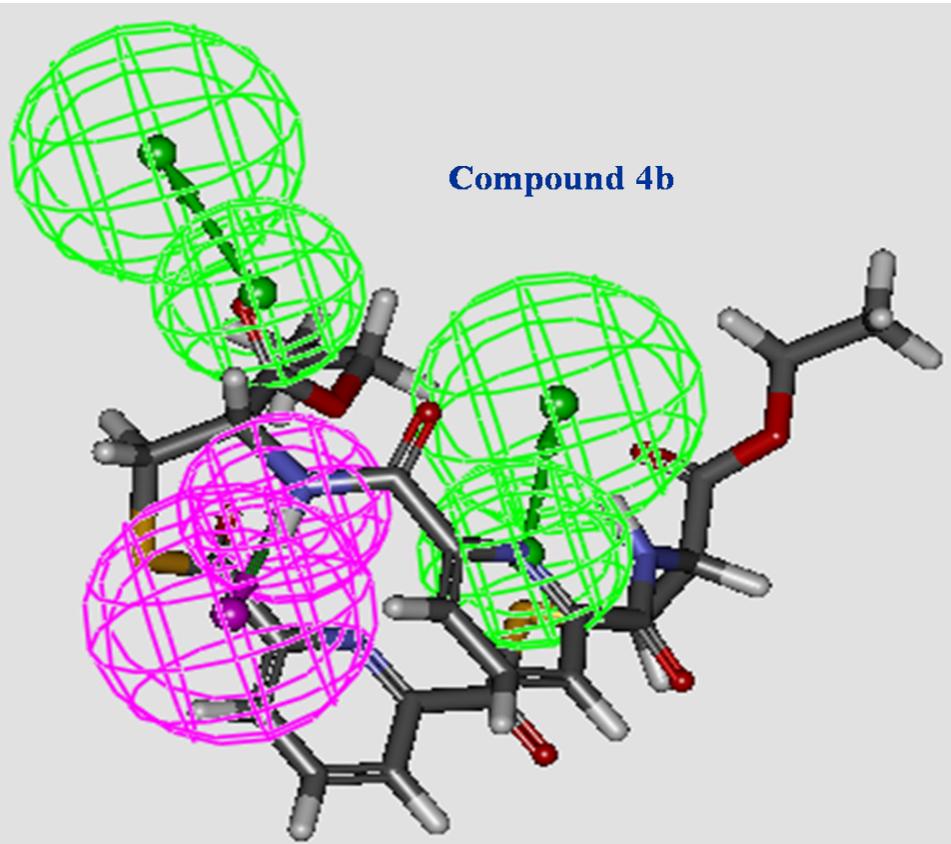


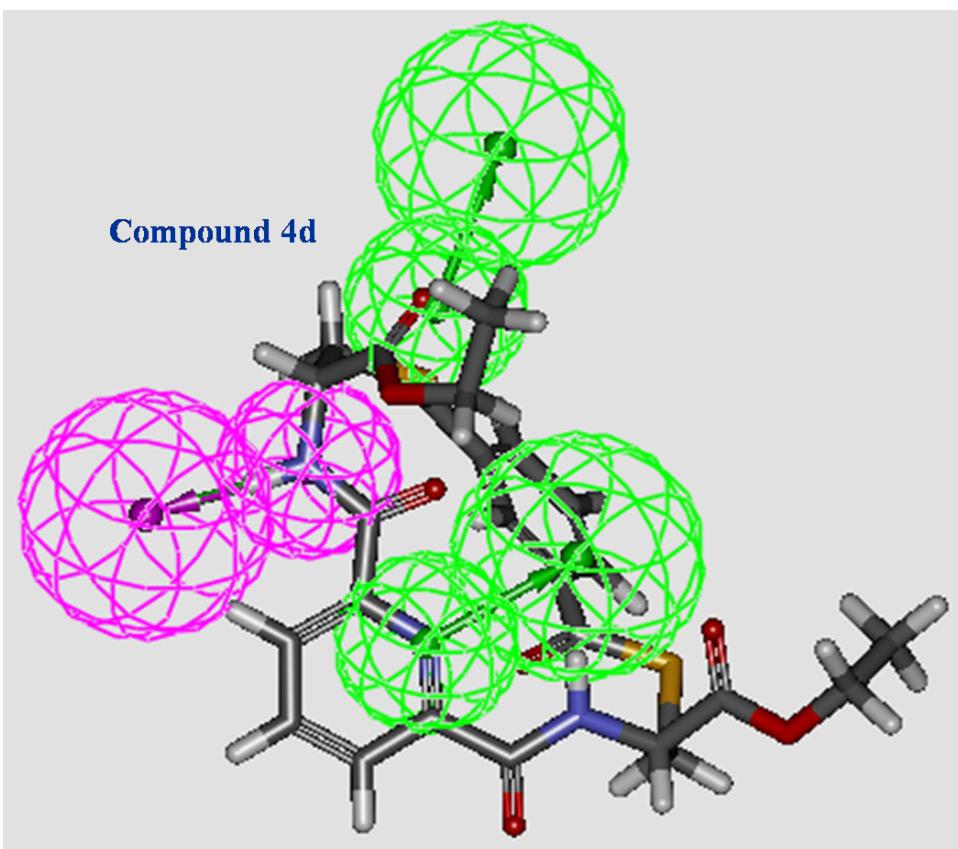
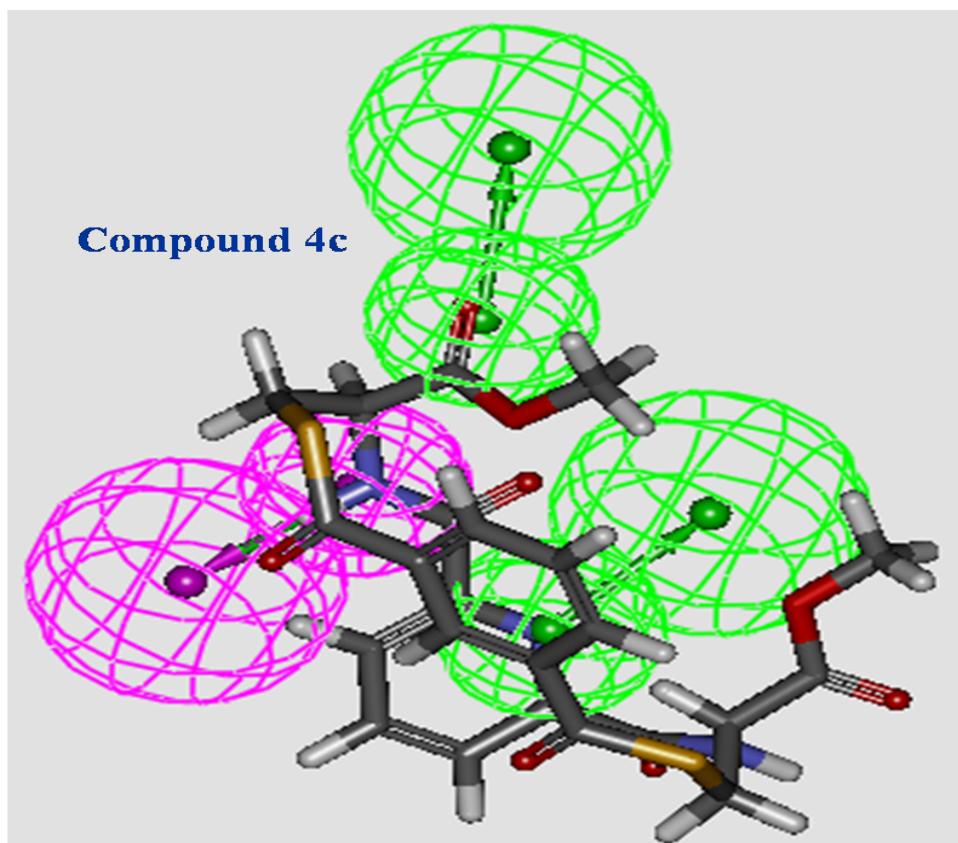
Figure S1. (A) Constraint distances, and (B) constraint angle of the generated 3D-pharmacophore for the antifungal bio-active compounds **4a-4l**, and **5-7** against *C. albicans* which contains two hydrogen bonding acceptor (HBA-1, HBA-2, green), and one hydrogen bonding donor (HBD, purple).

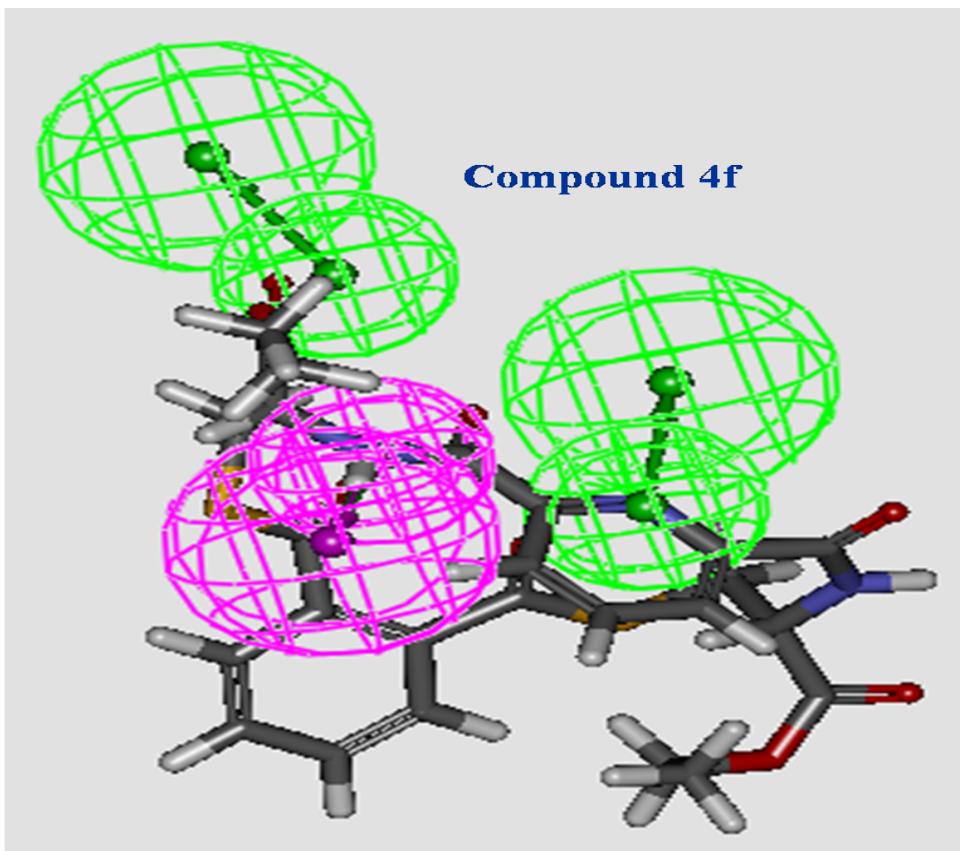
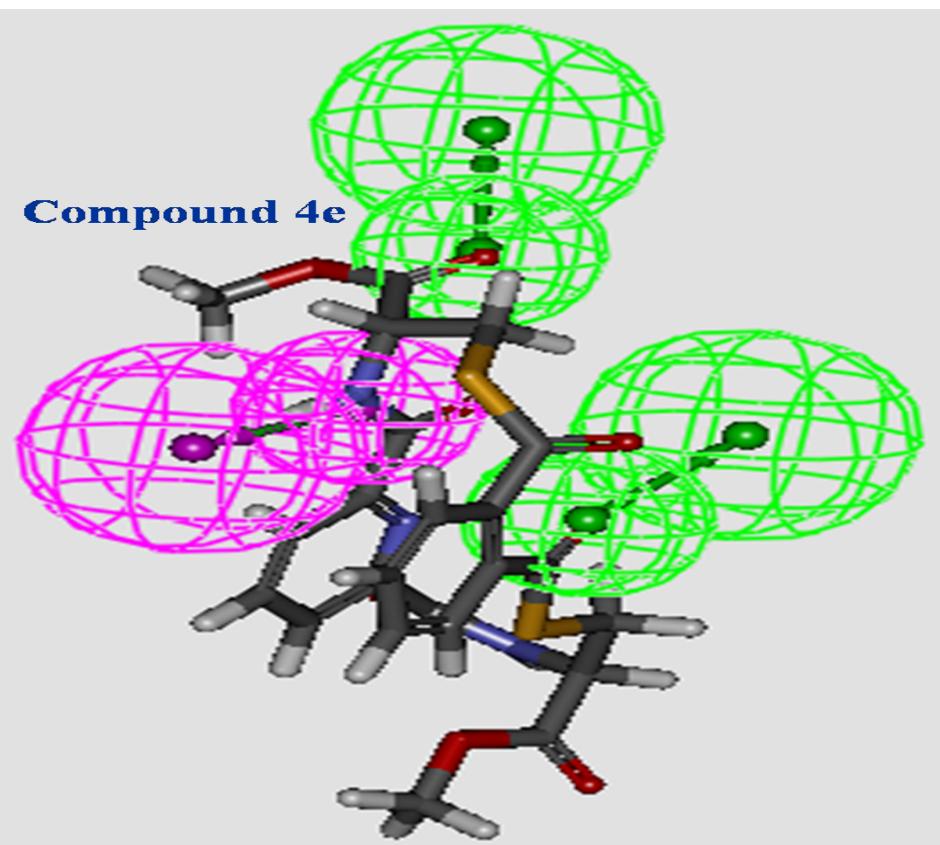
Compound 4a

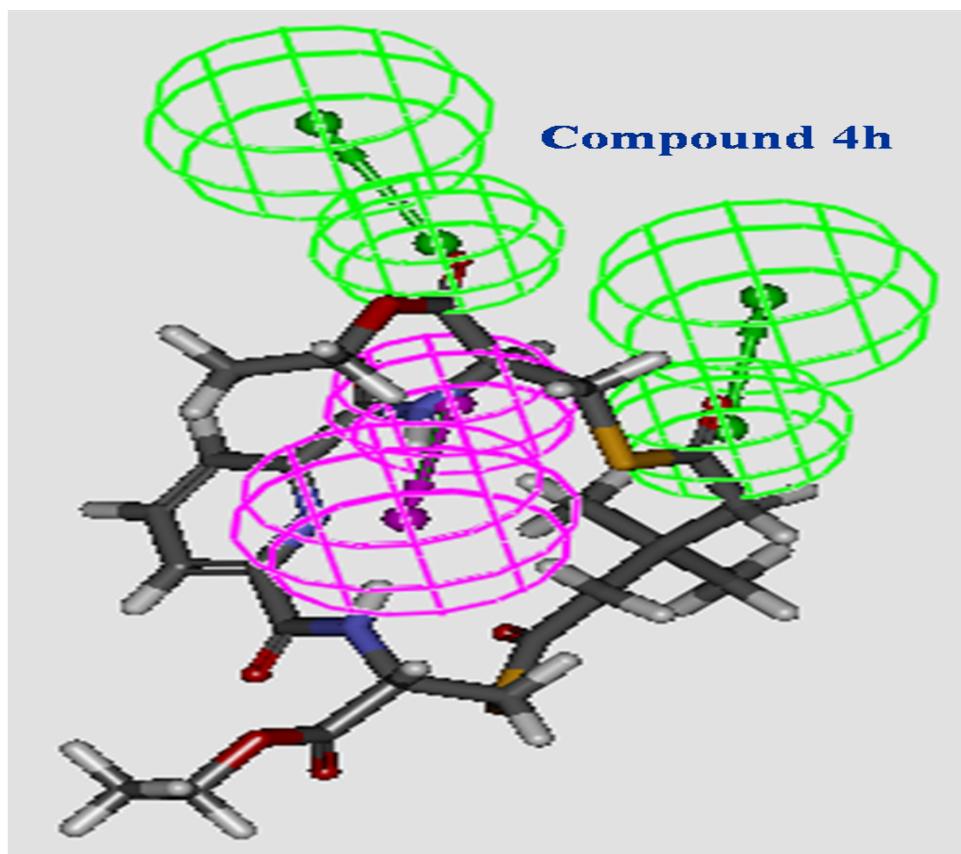
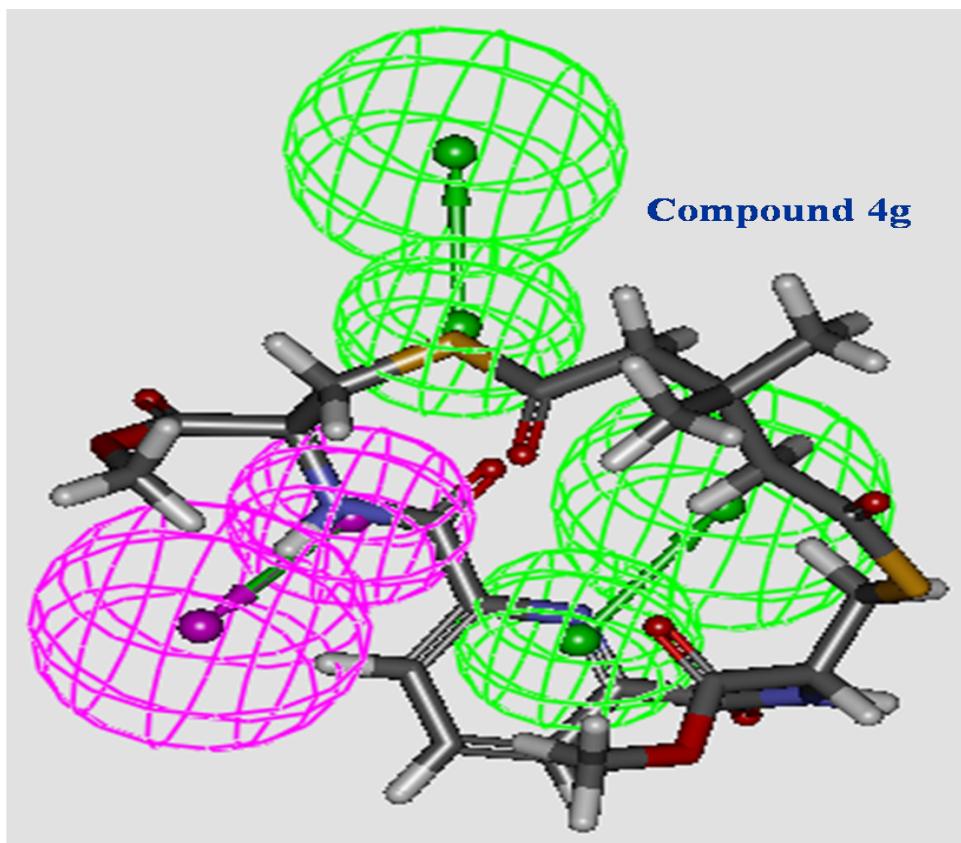


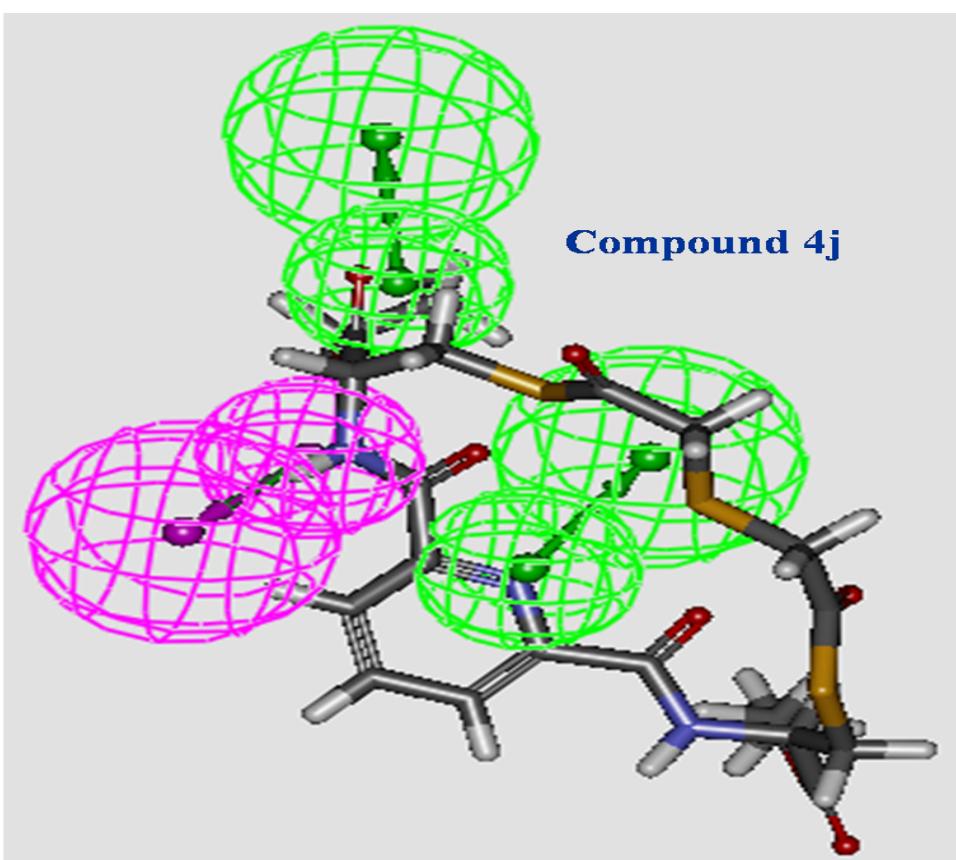
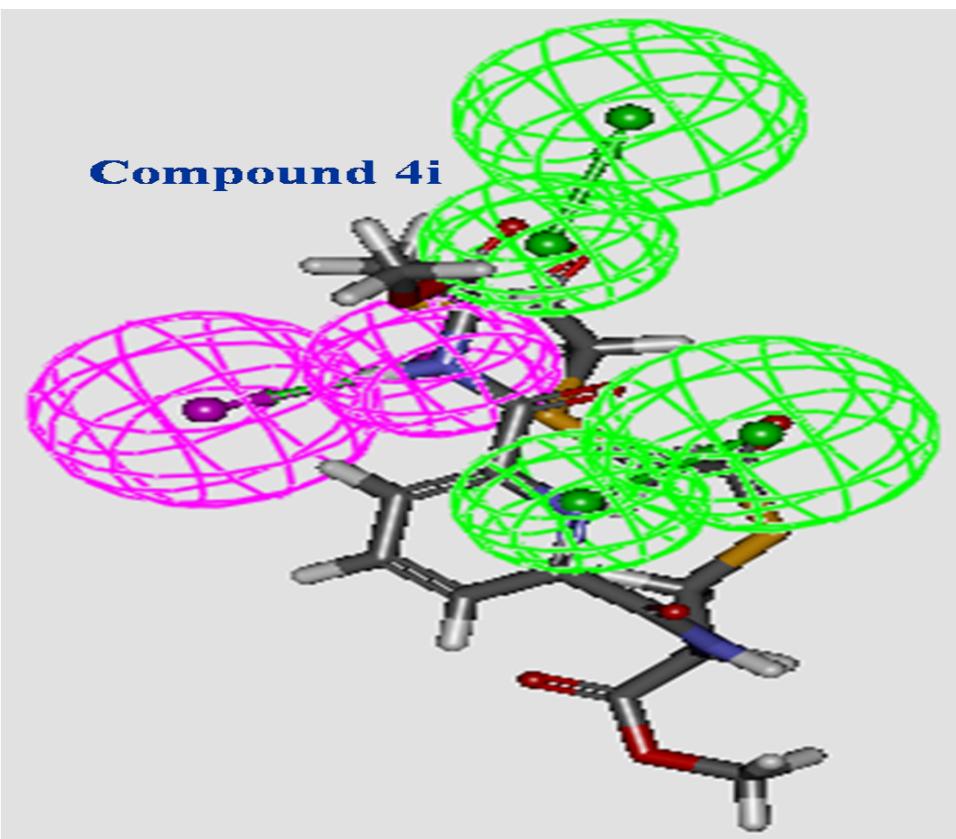
Compound 4b

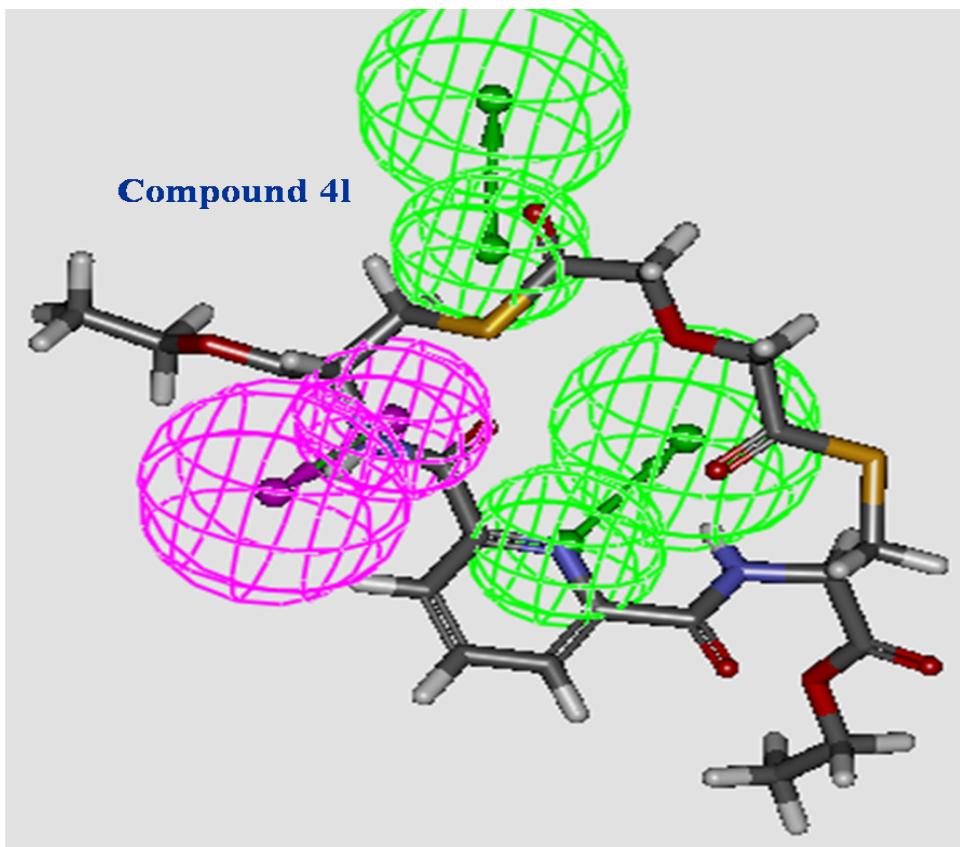
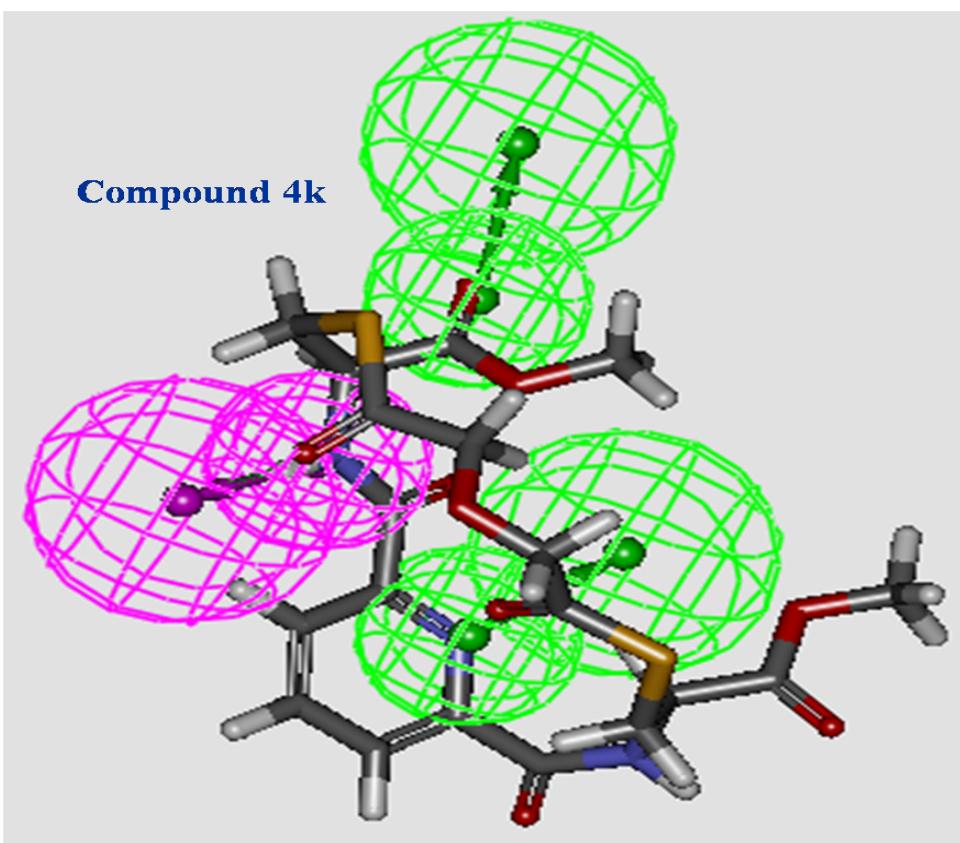




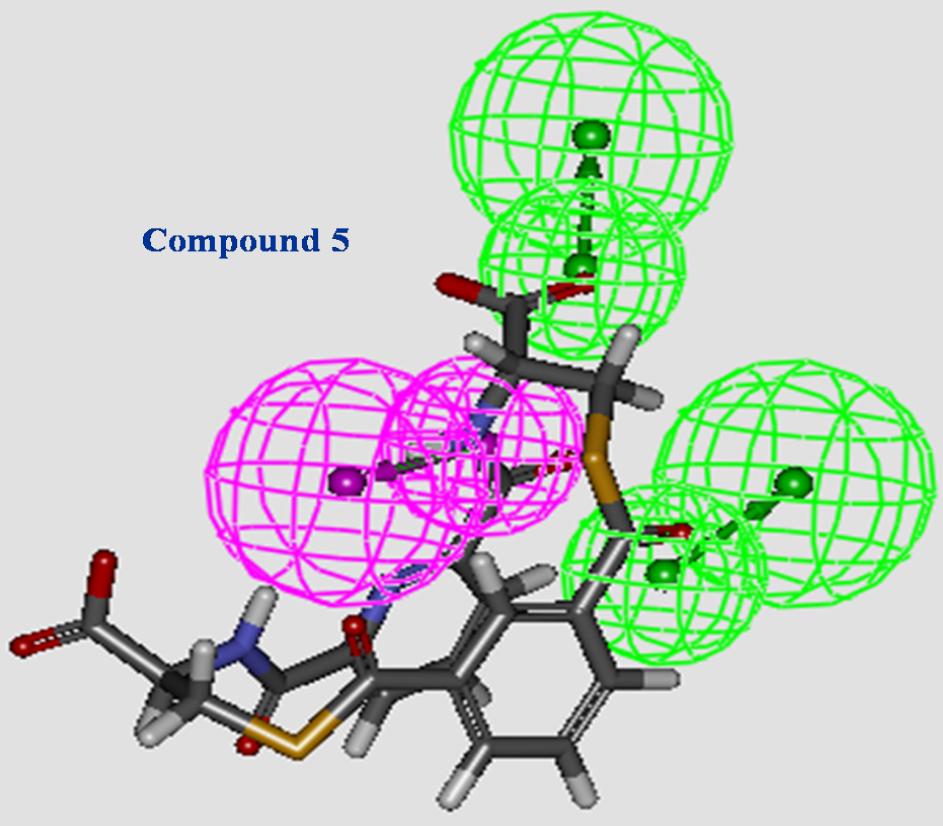




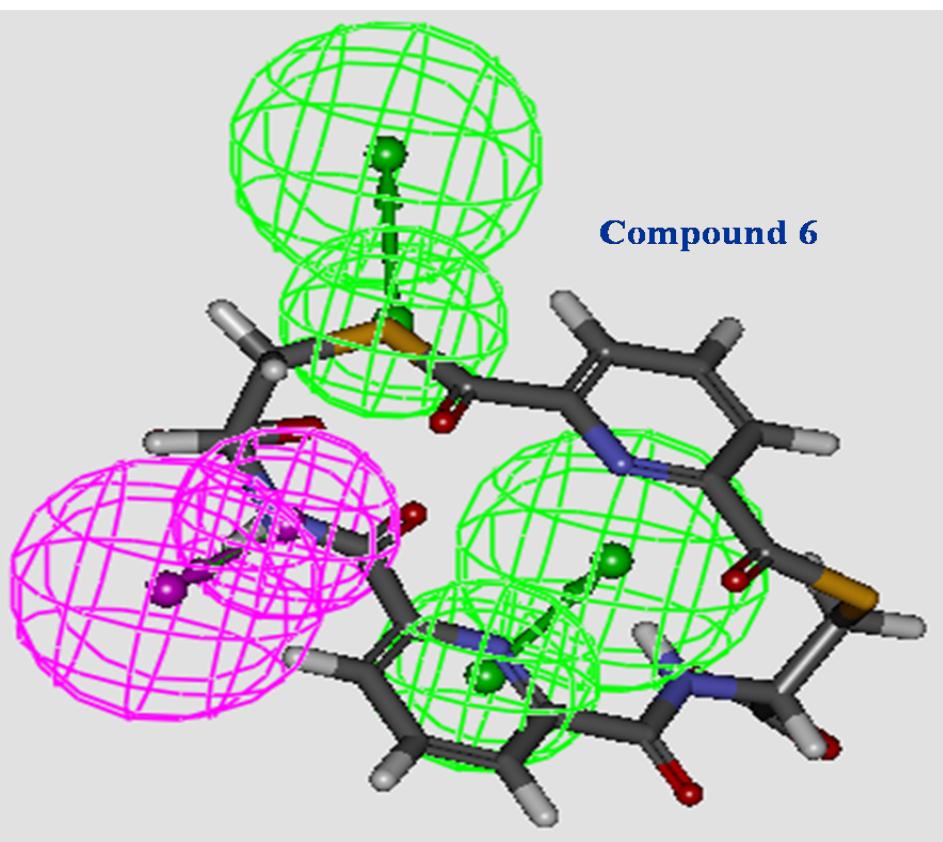




Compound 5



Compound 6



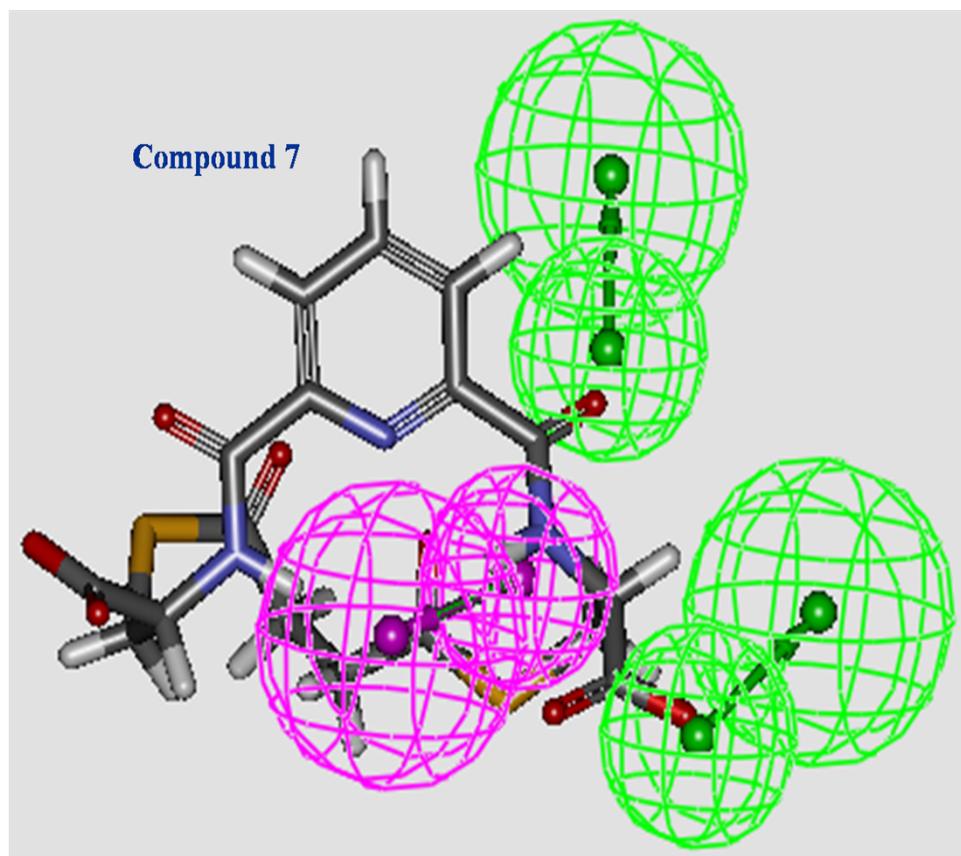
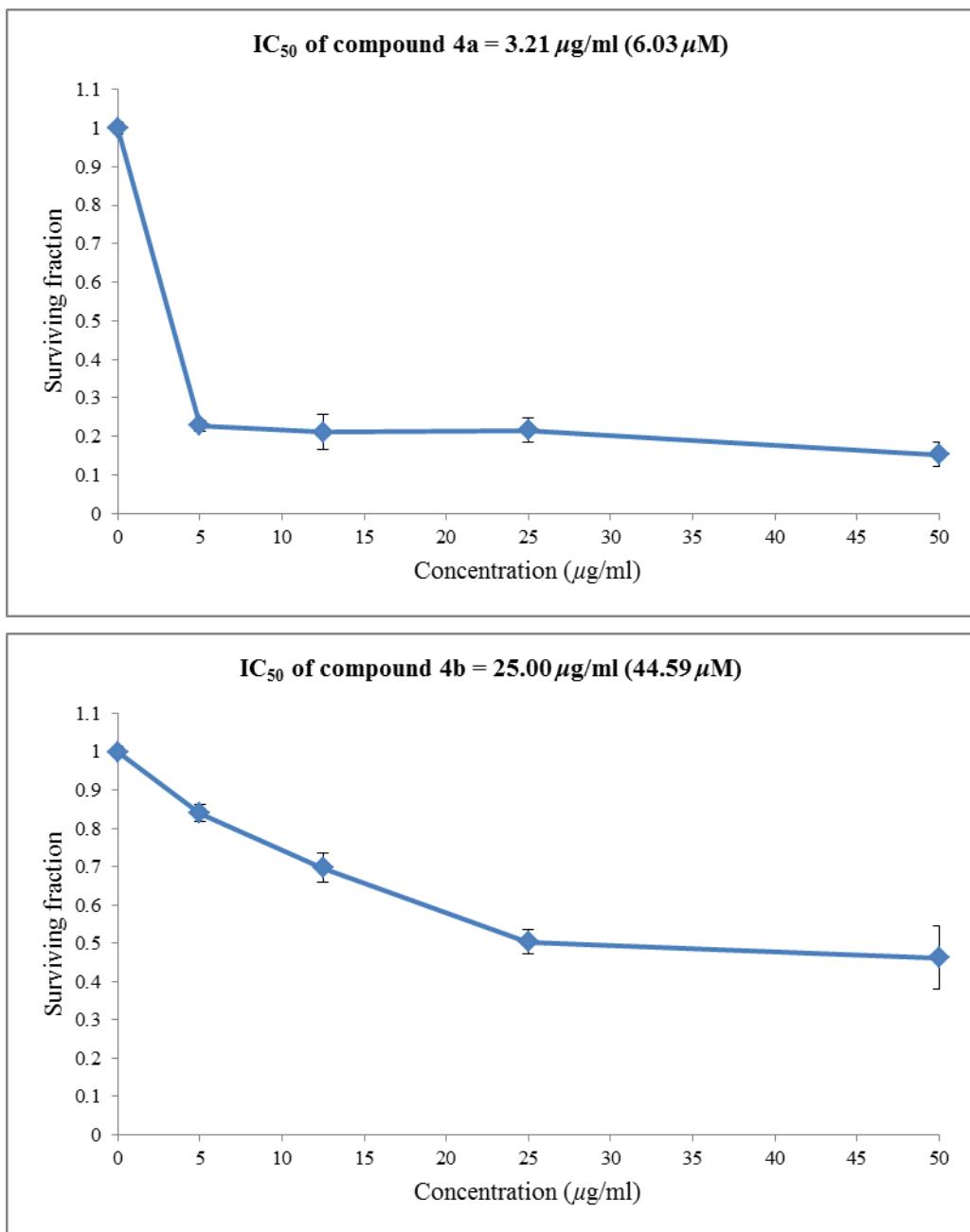
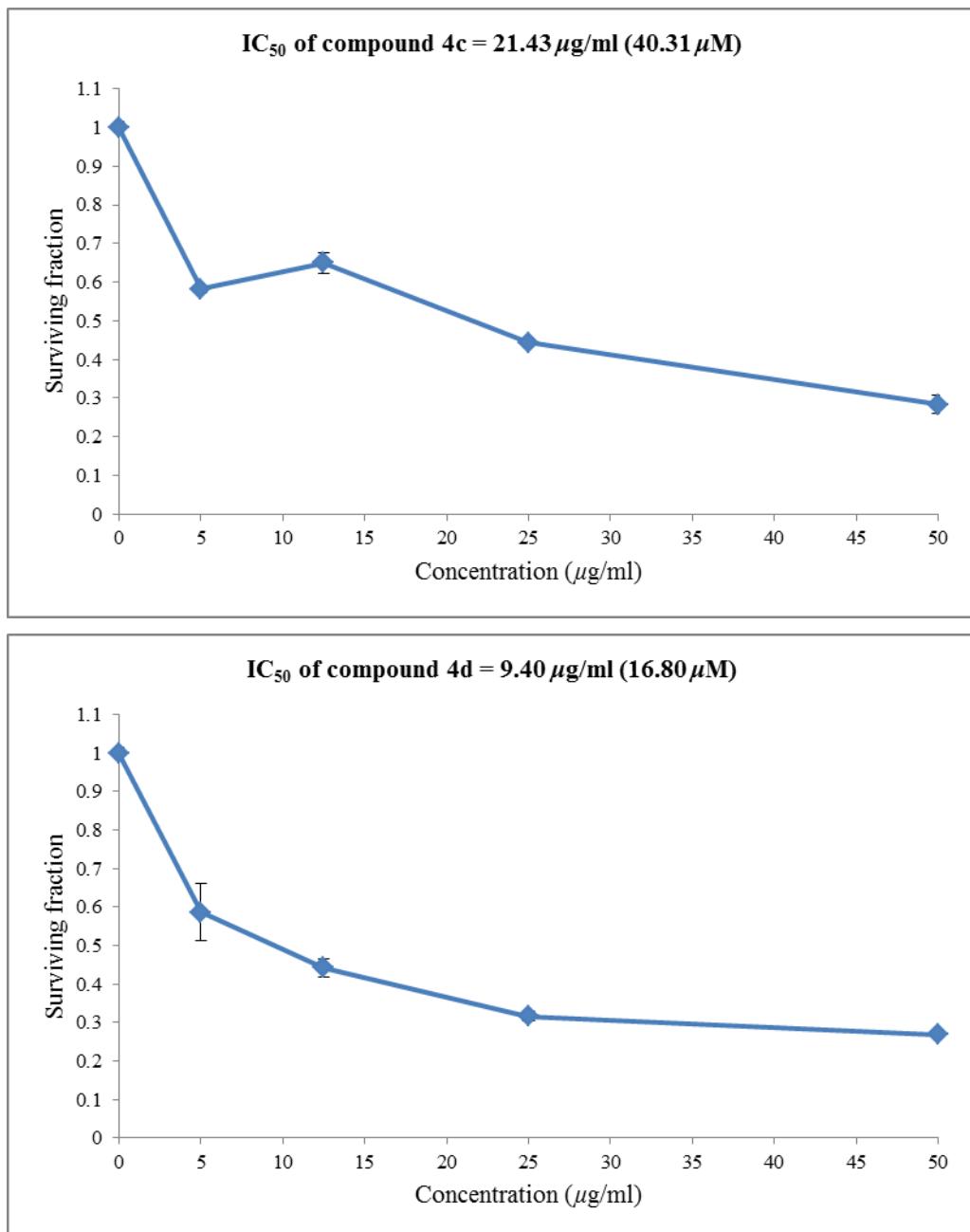
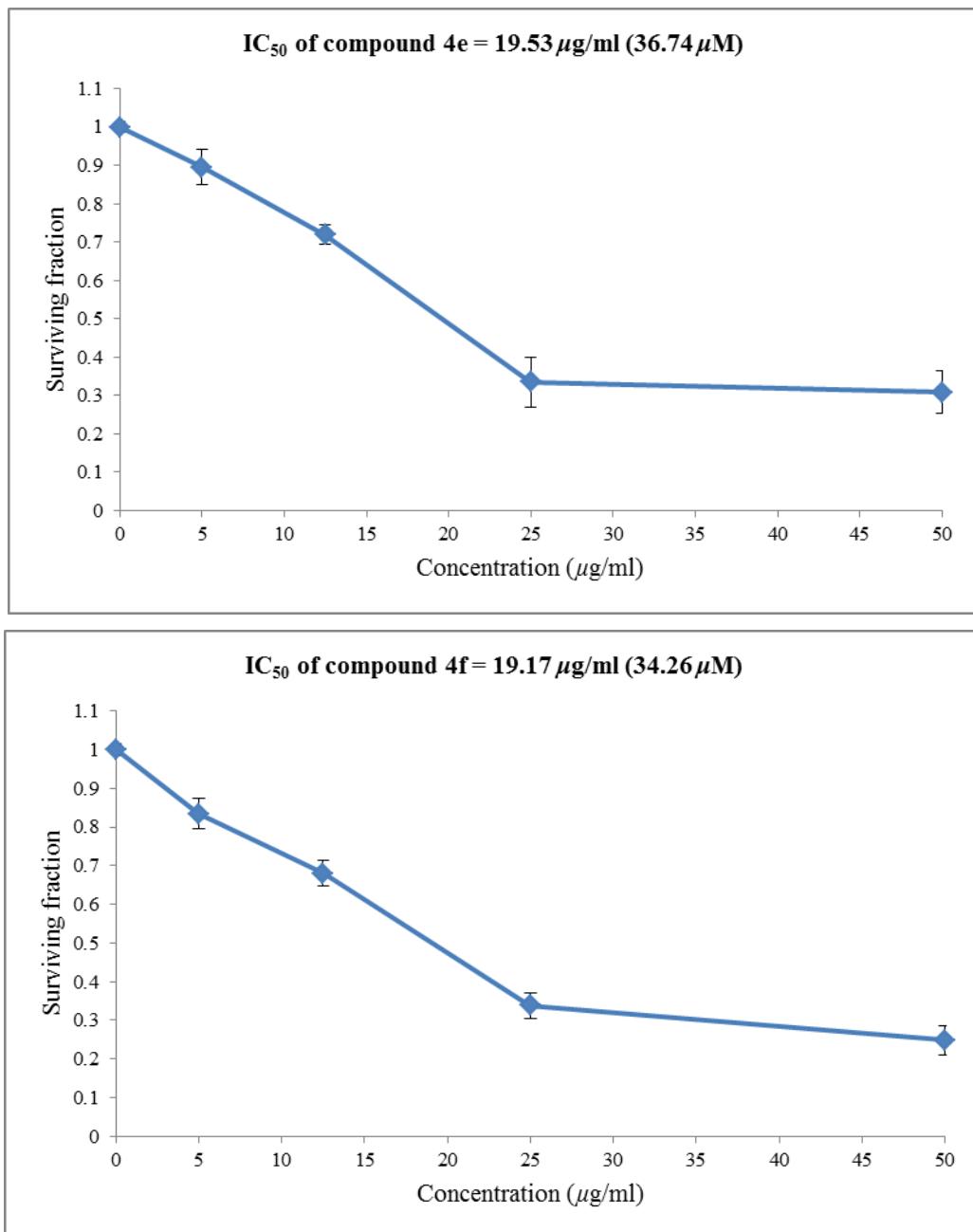
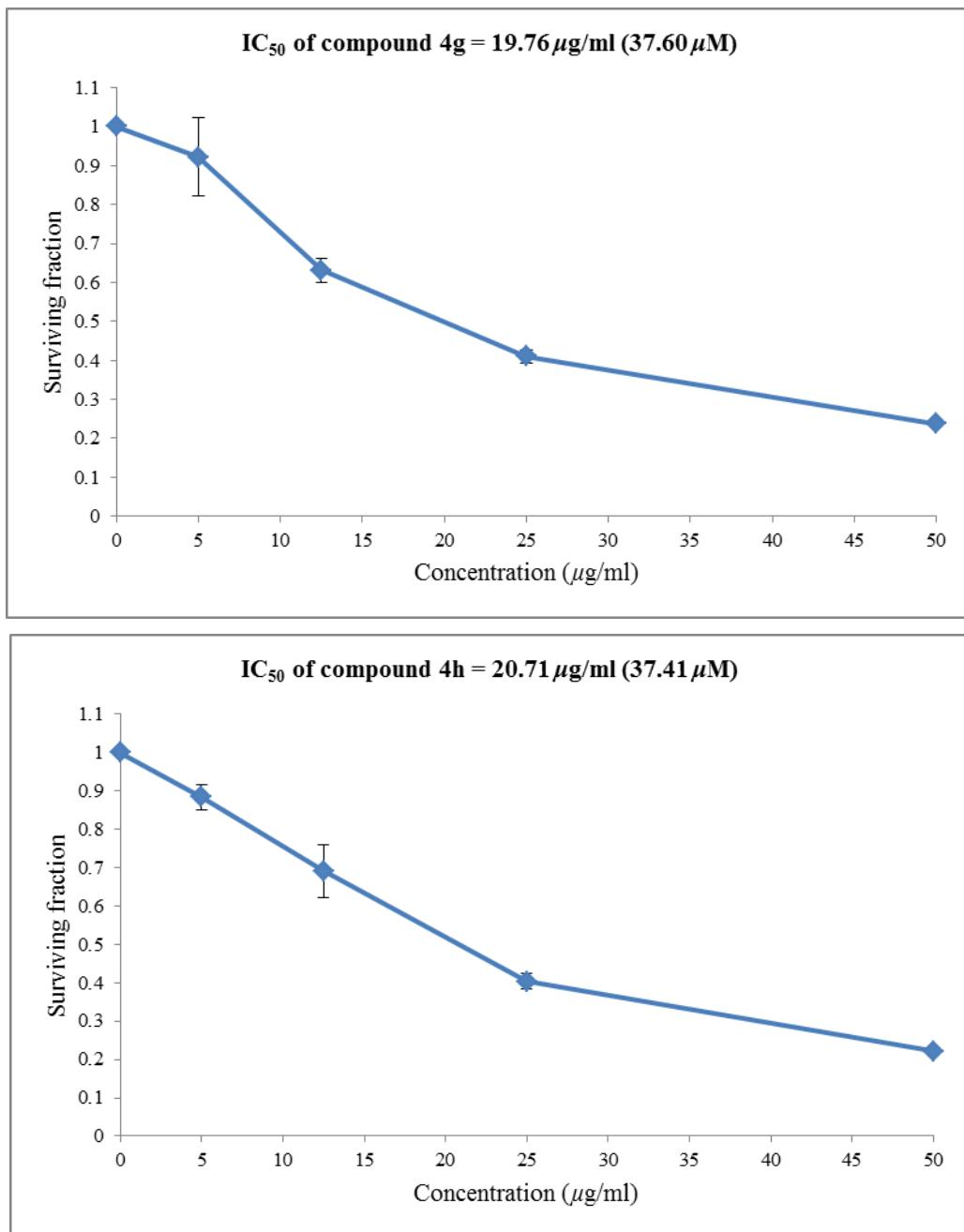


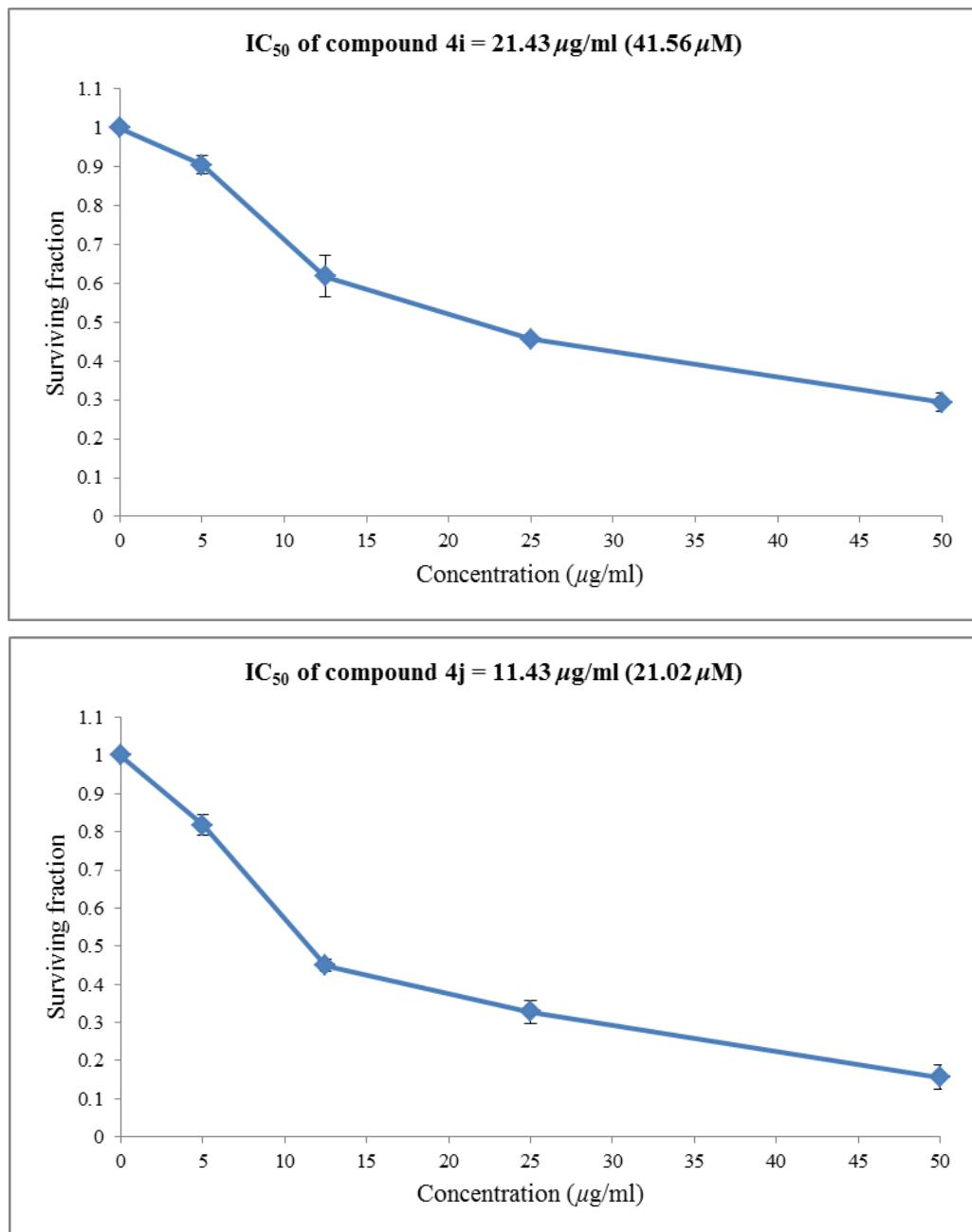
Figure S2. 3D-pharmacophore mapped on the antifungal macrocyclic peptidomimetics **4a-4l**, and **5-7**.

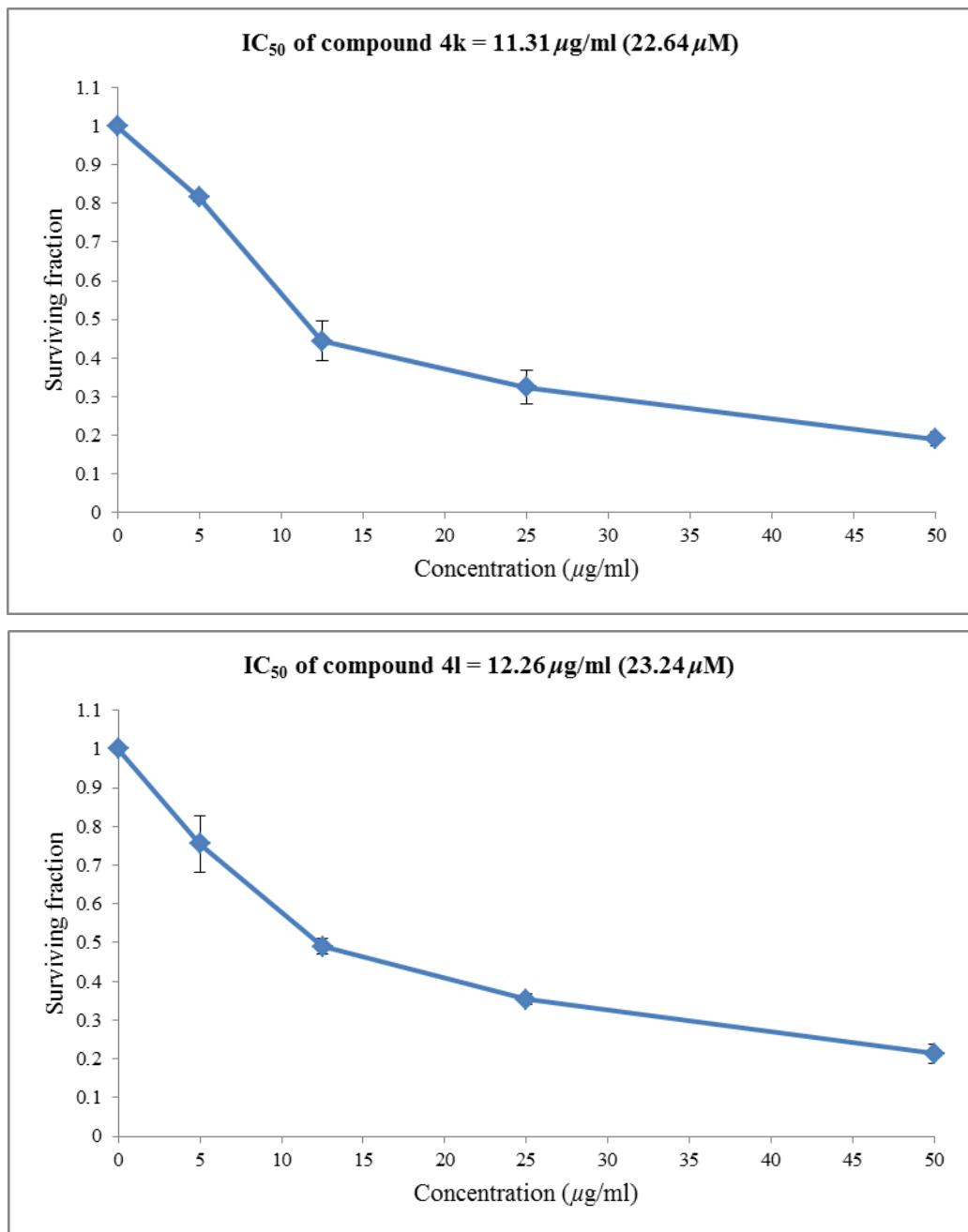


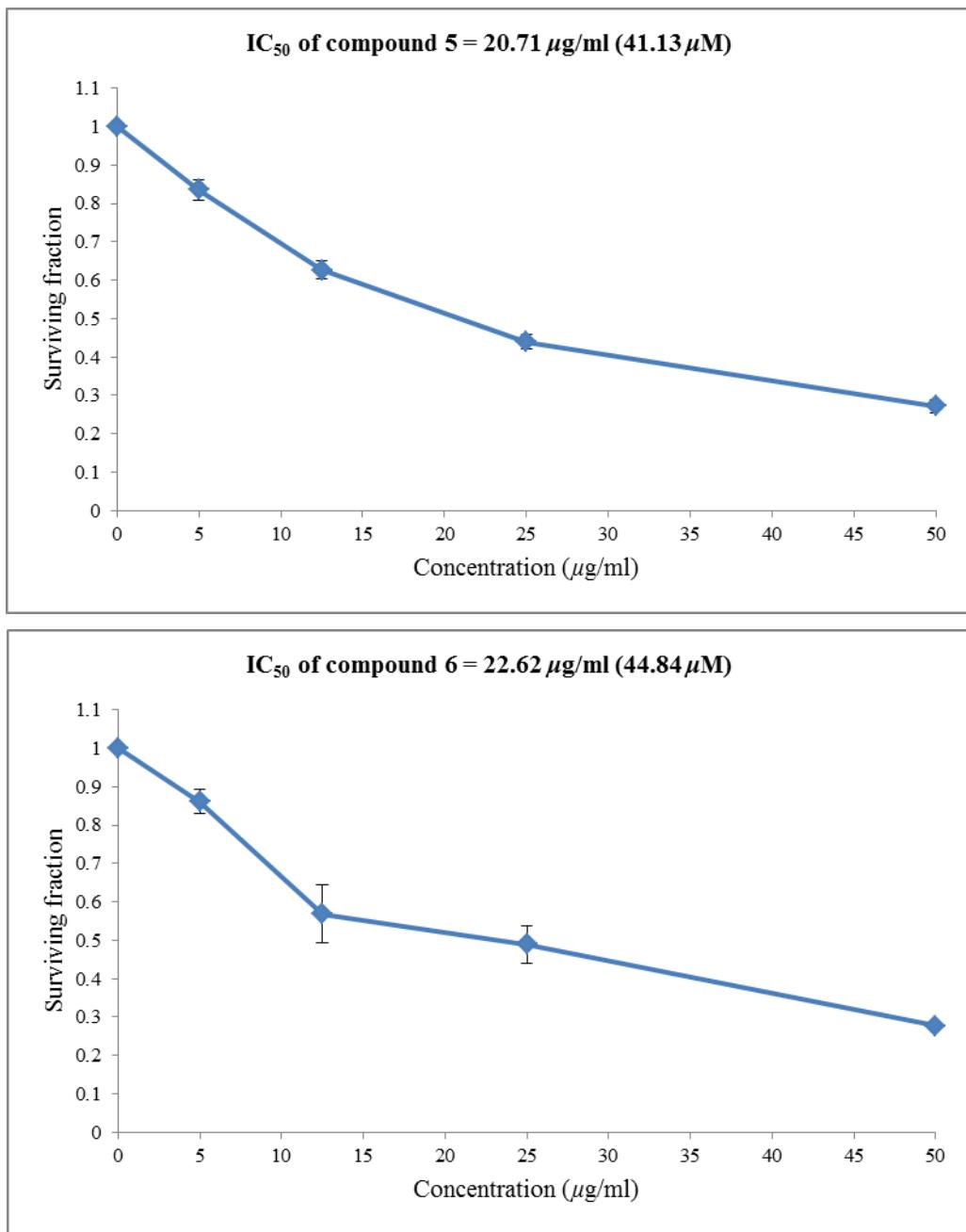












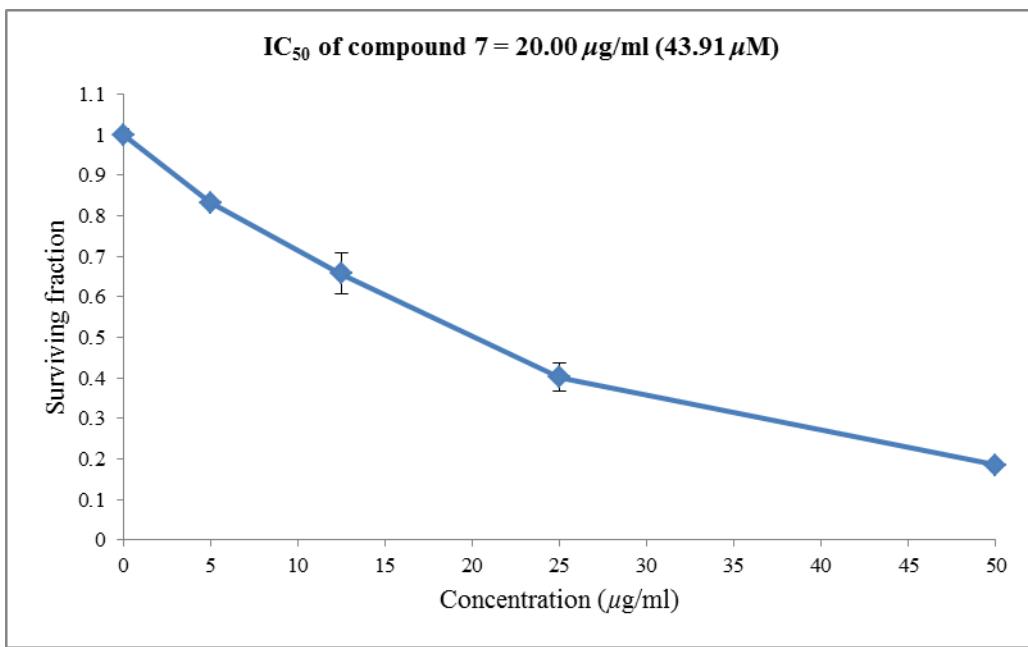
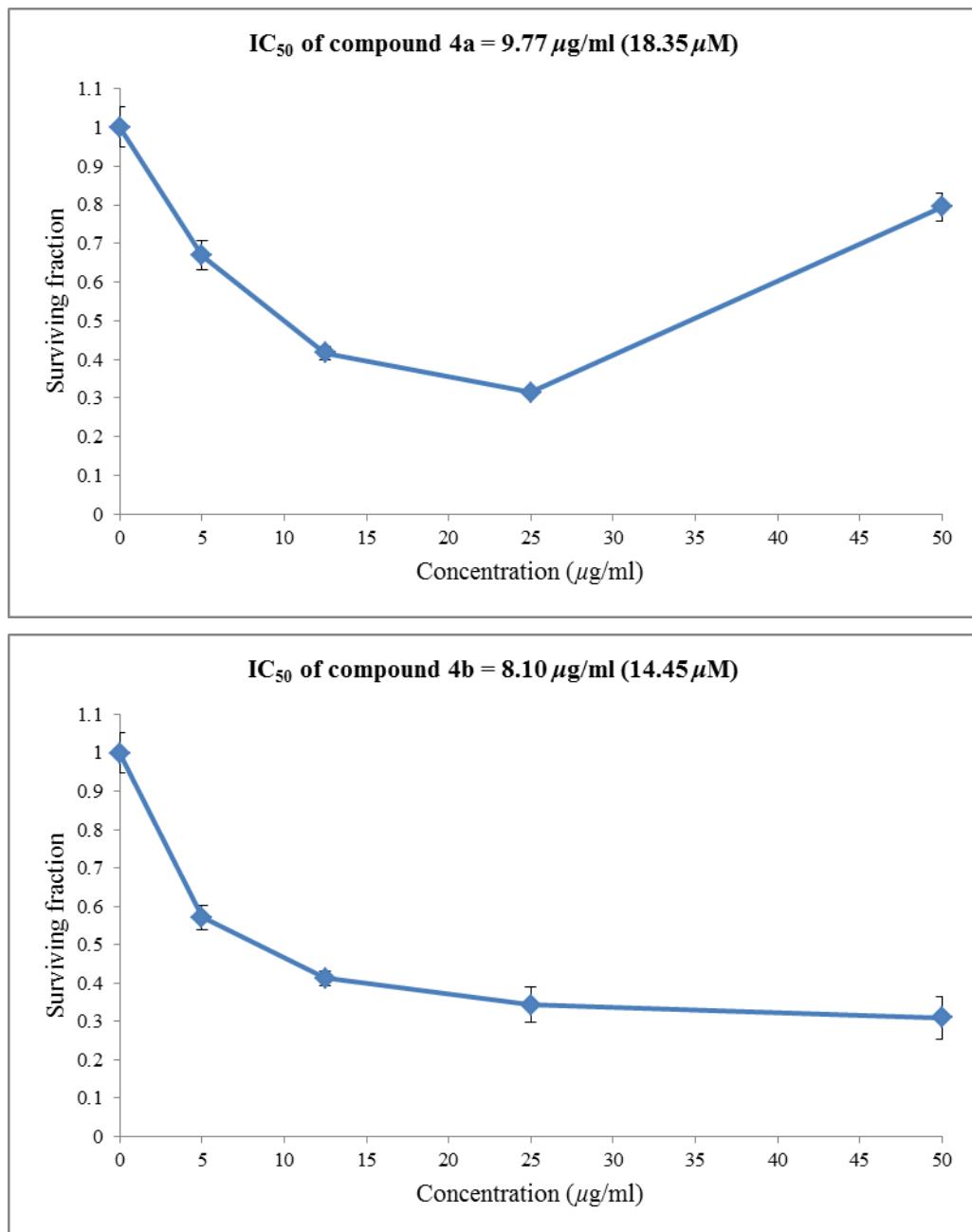
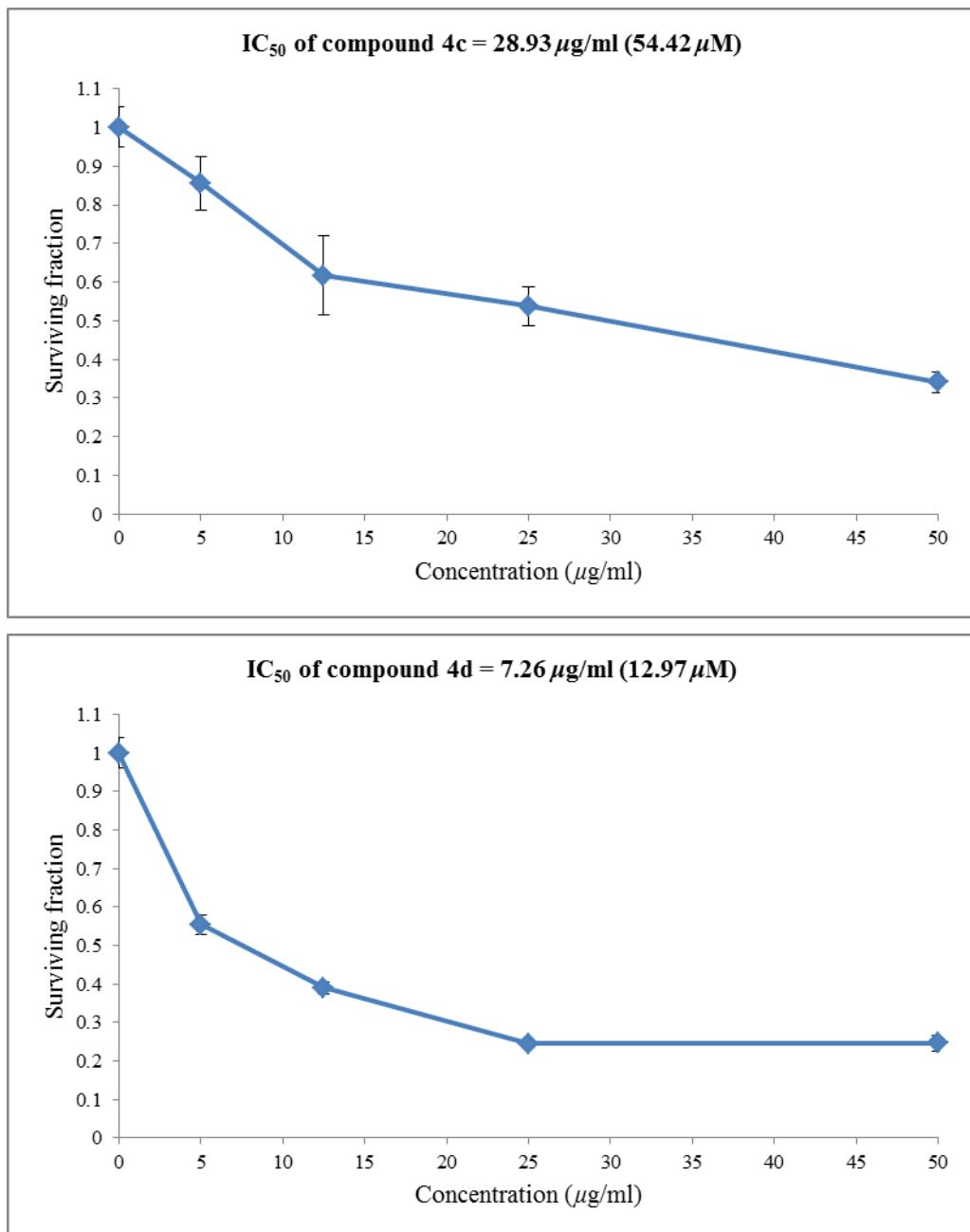
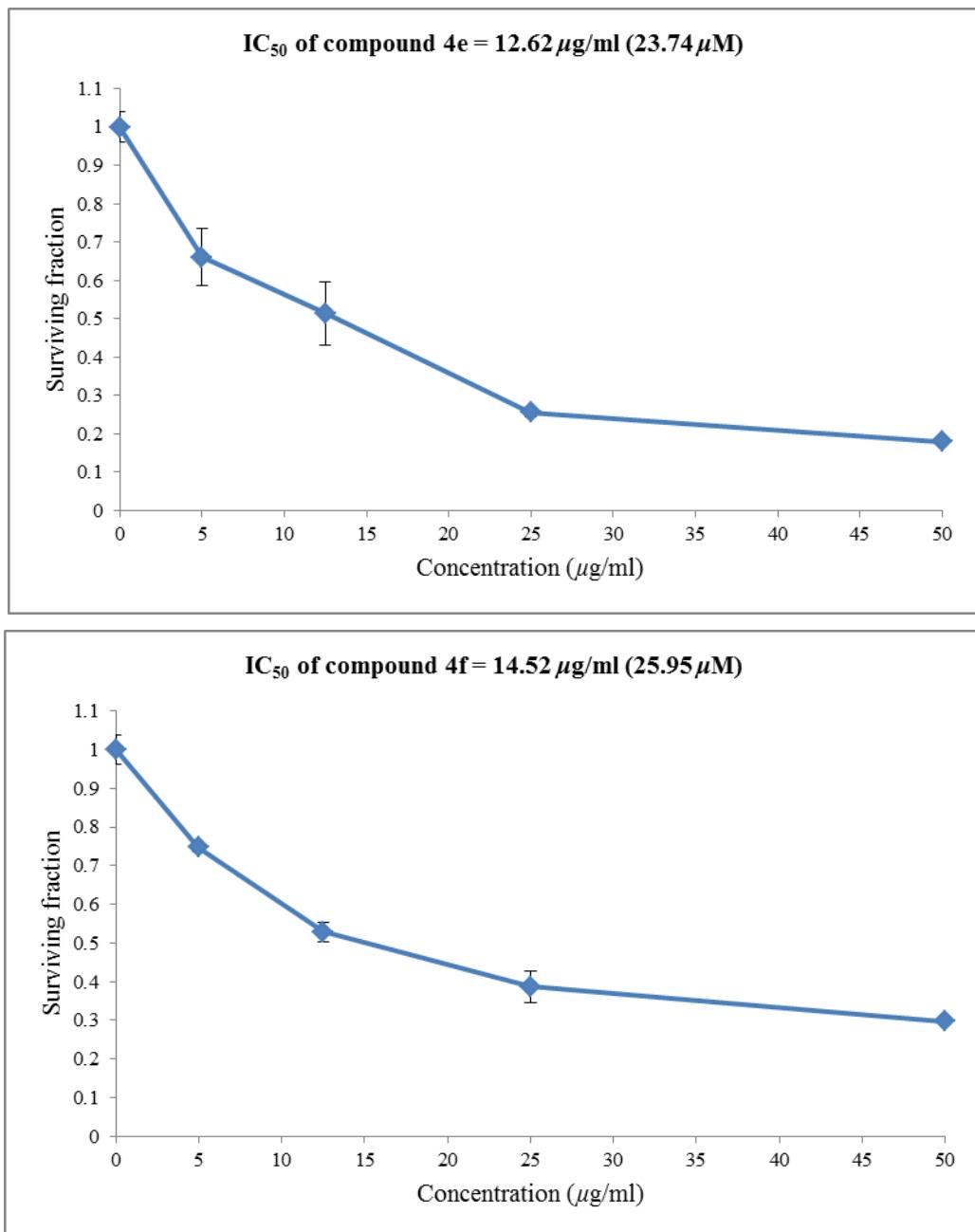
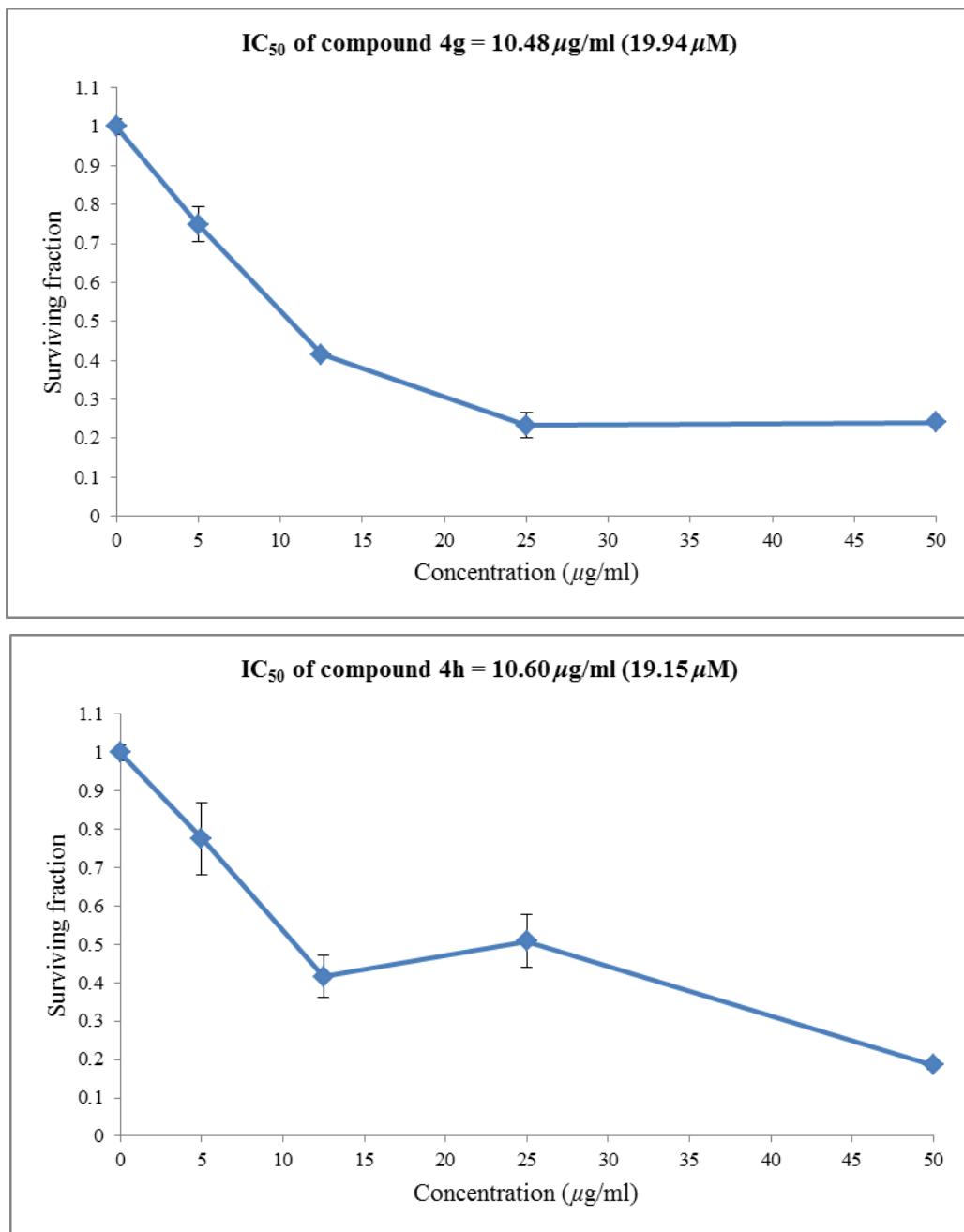


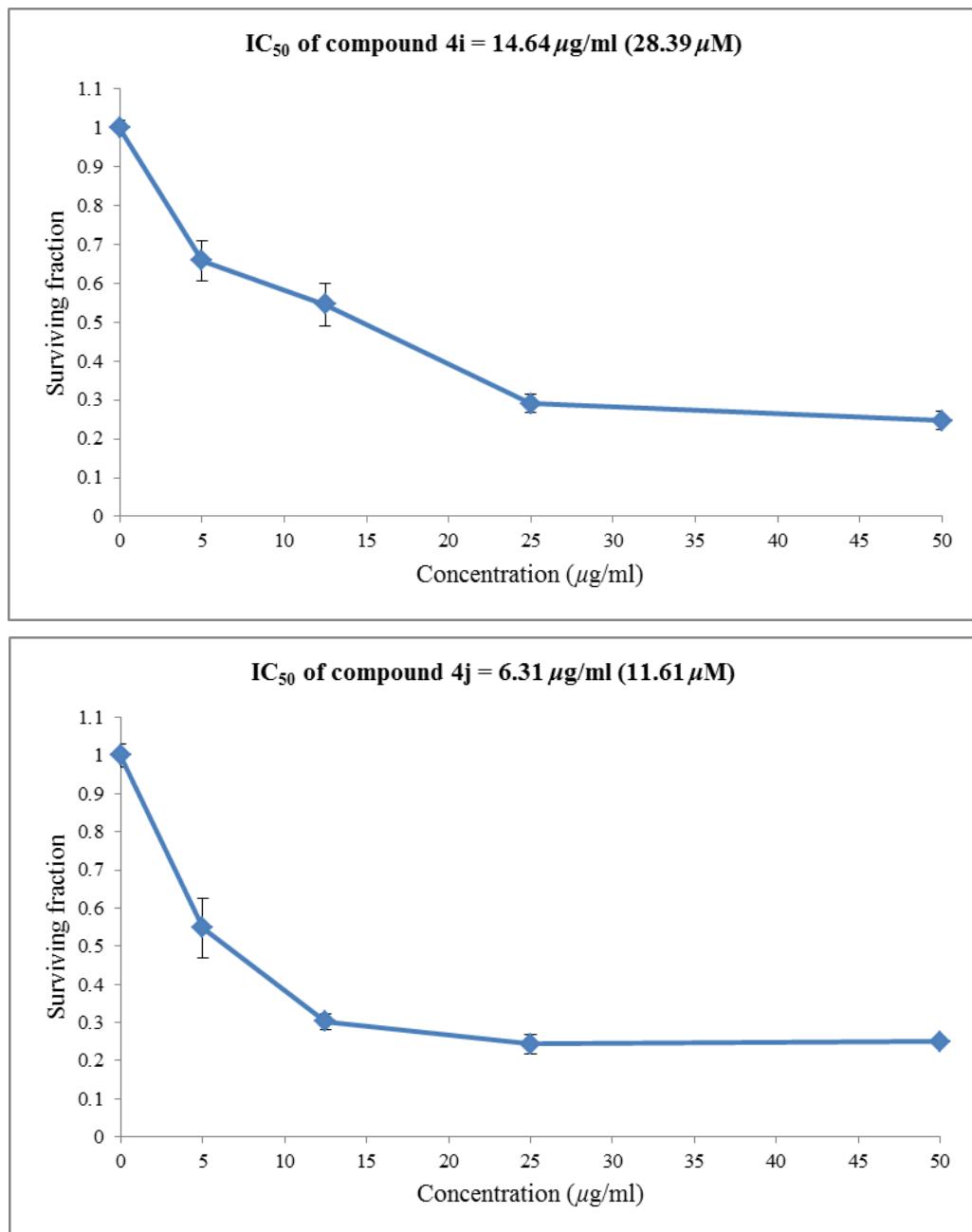
Figure S3. Dose-response curves of the macrocyclic peptidomimetics **4a-l**, and **5-7** against HepG2 (liver) human tumor cell line.

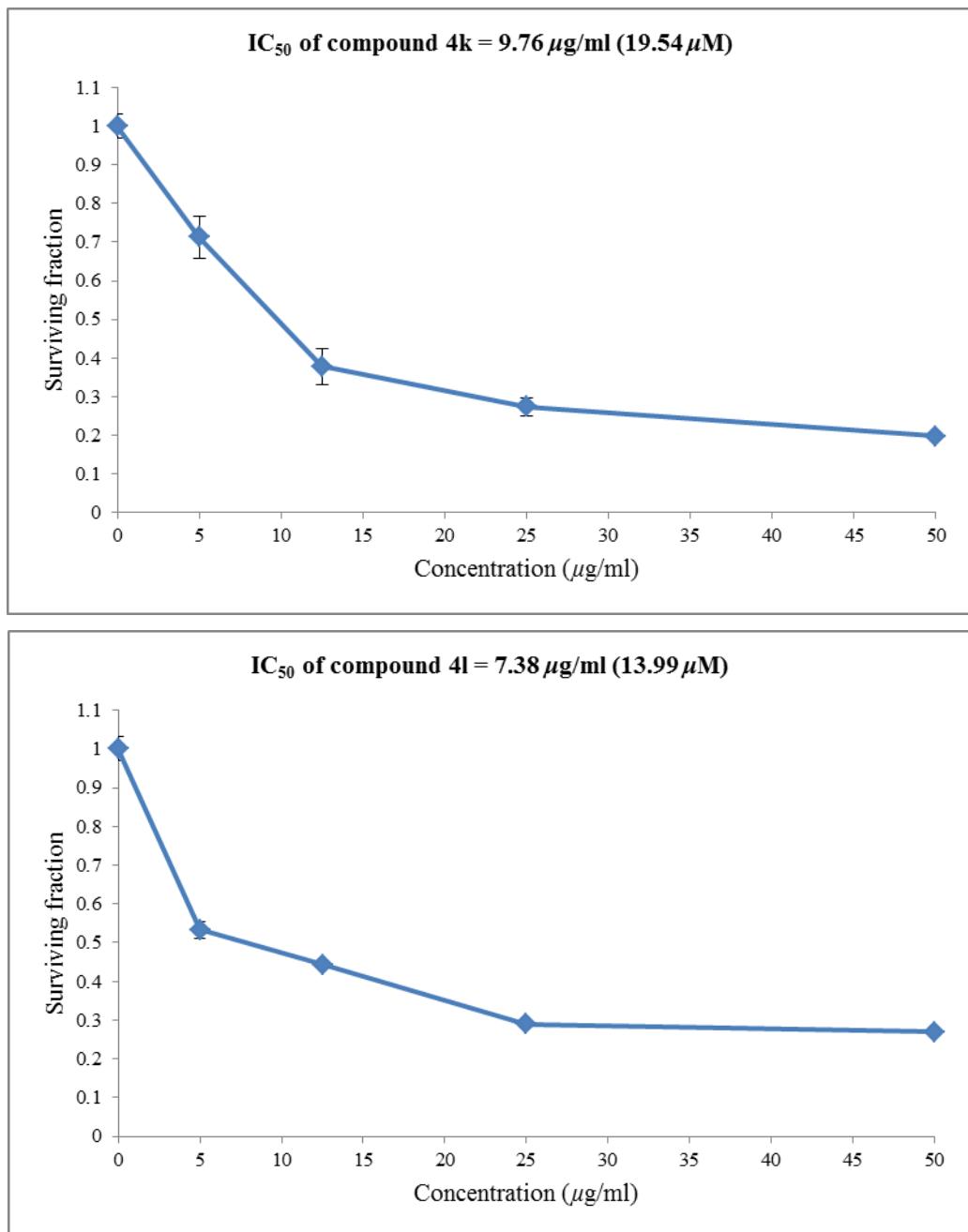


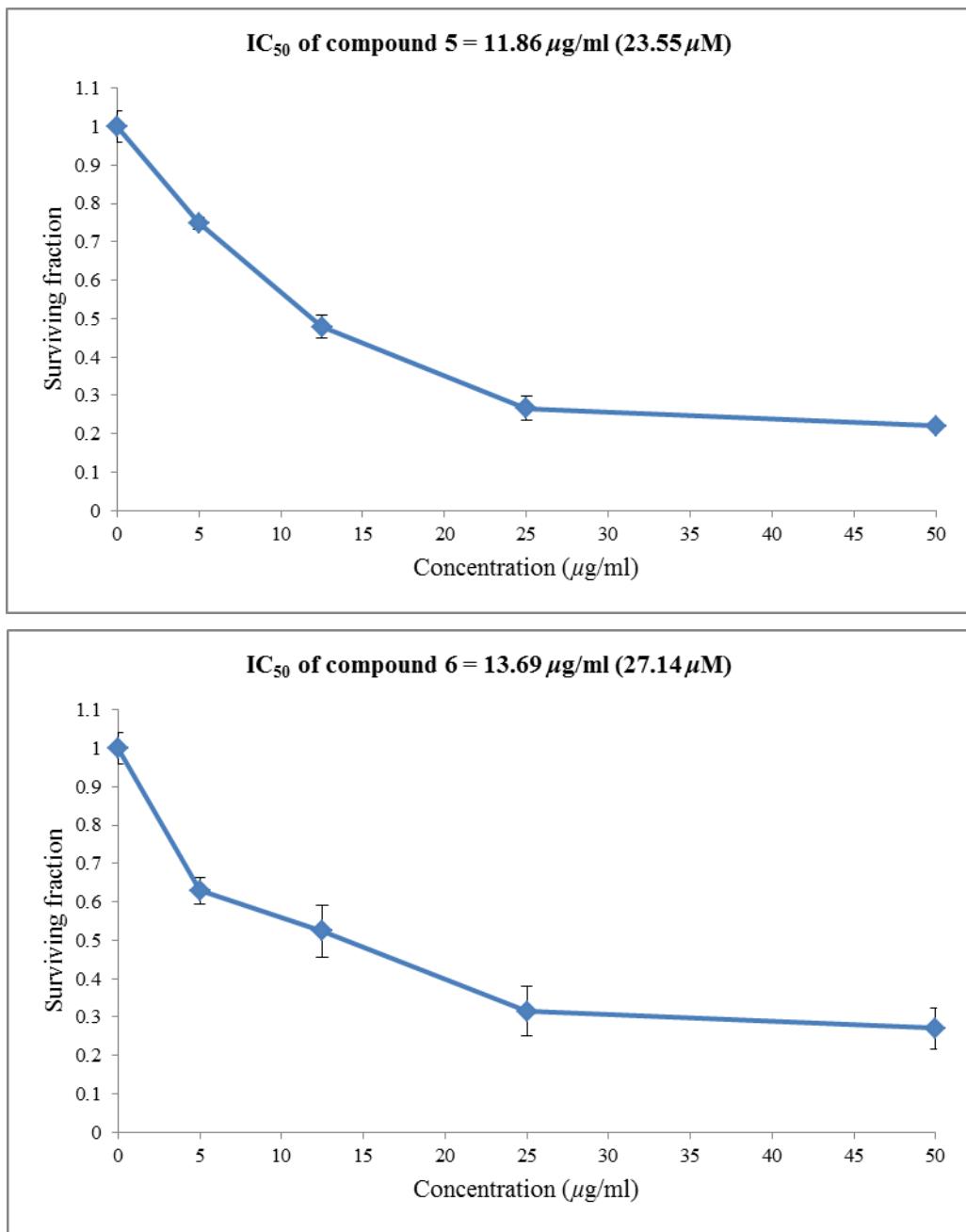












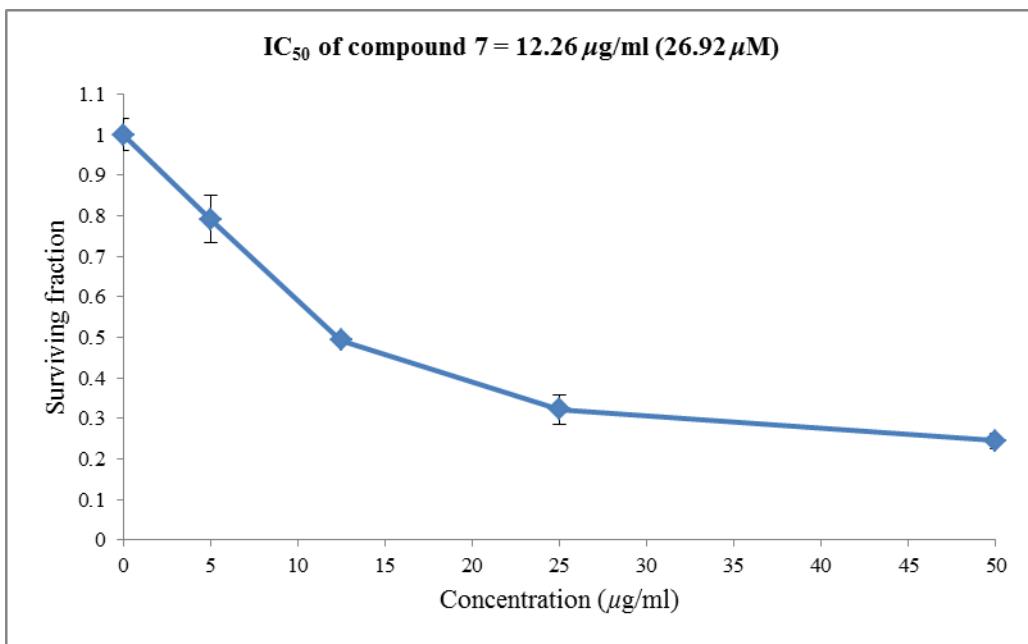
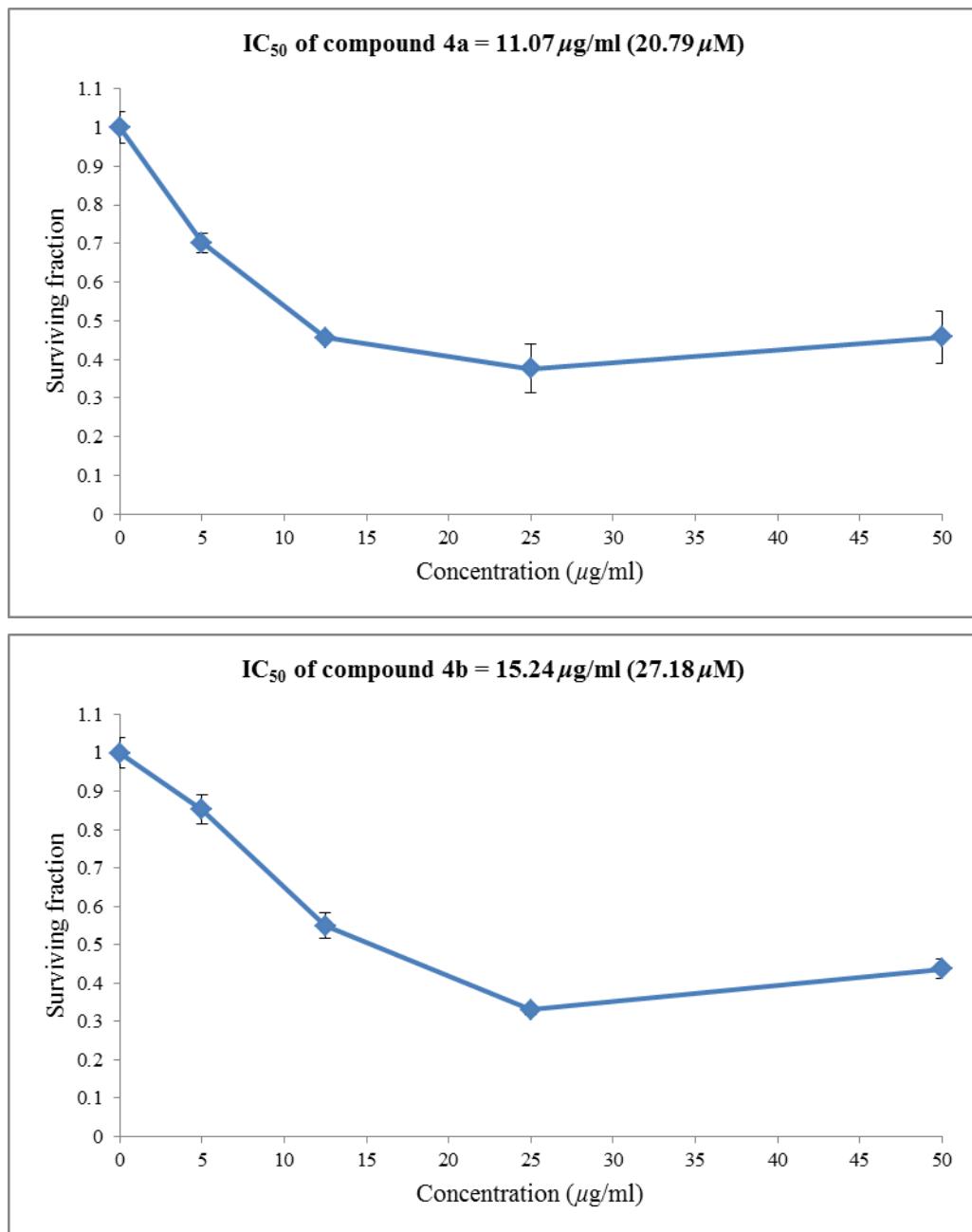
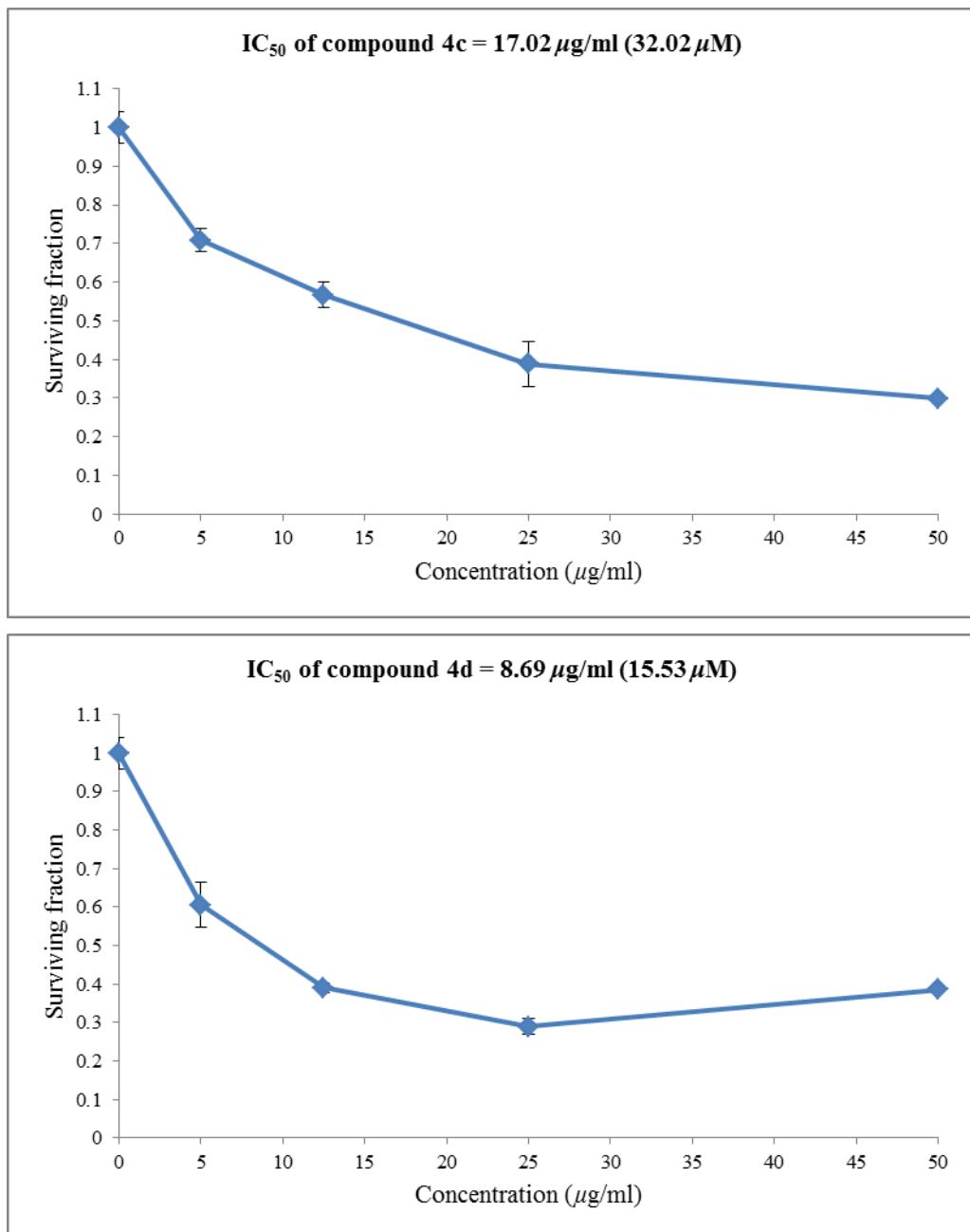
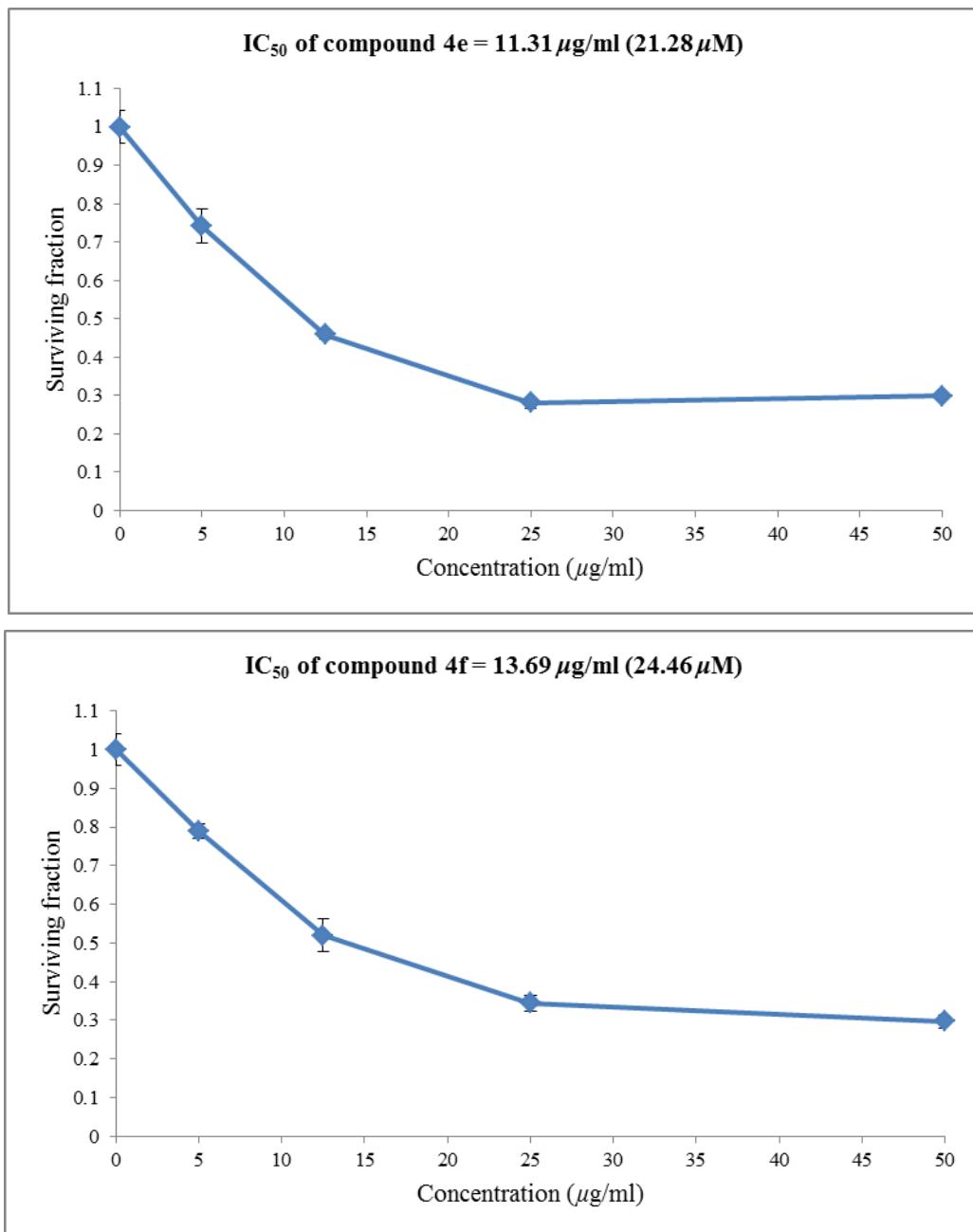
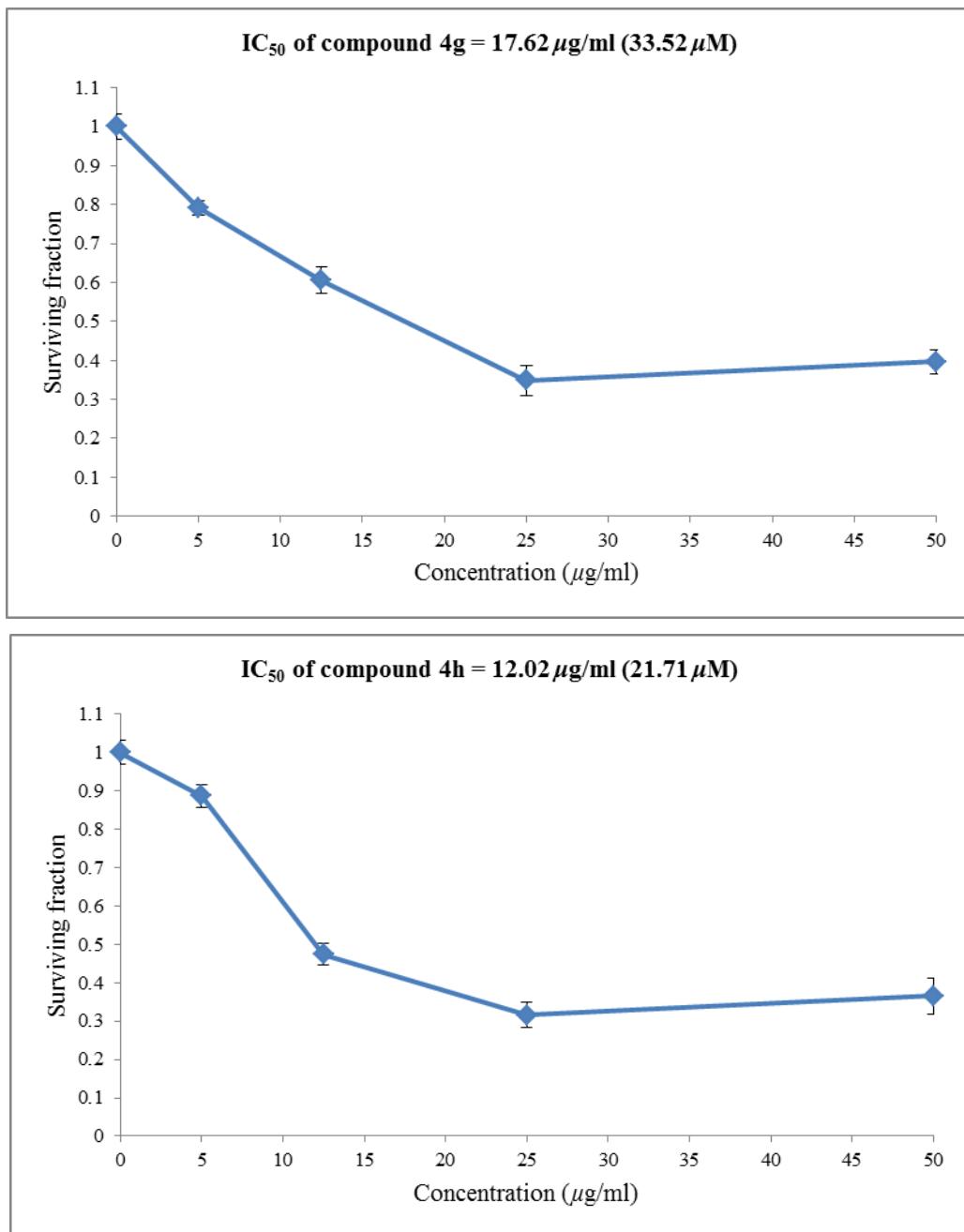


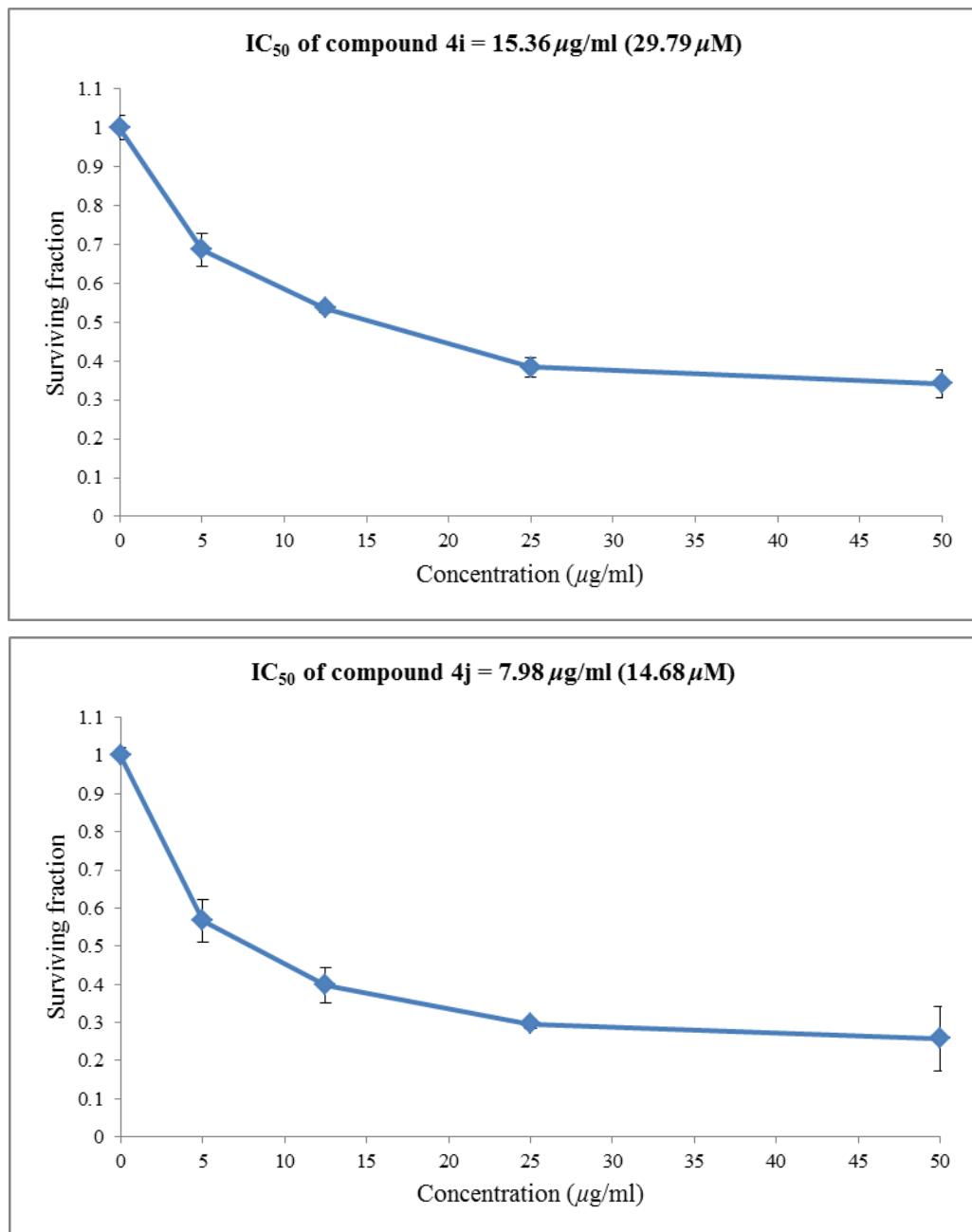
Figure S4. Dose-response curves of the macrocyclic peptidomimetics **4a-l**, and **5-7** against HeLa (cervical) human tumor cell line.

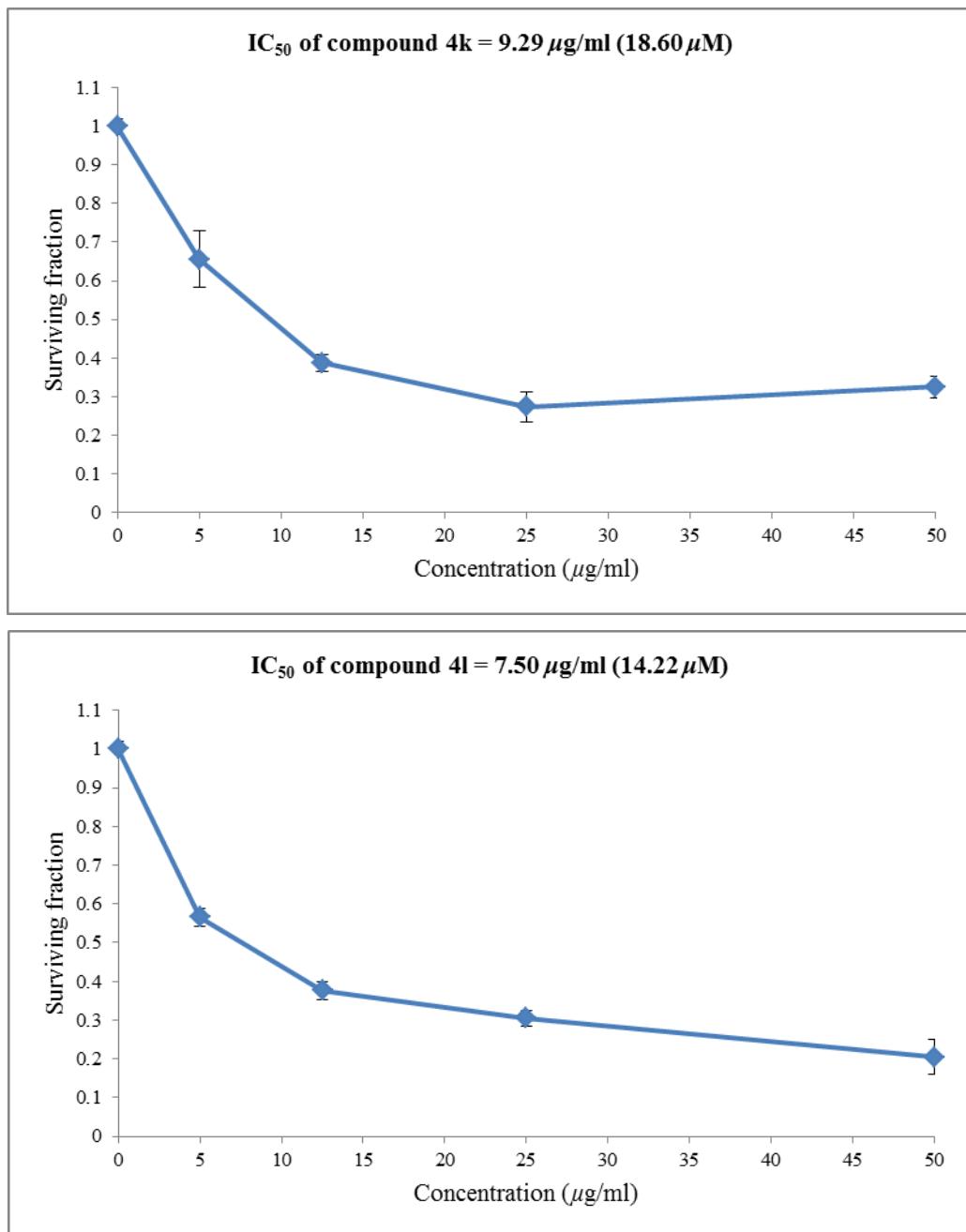


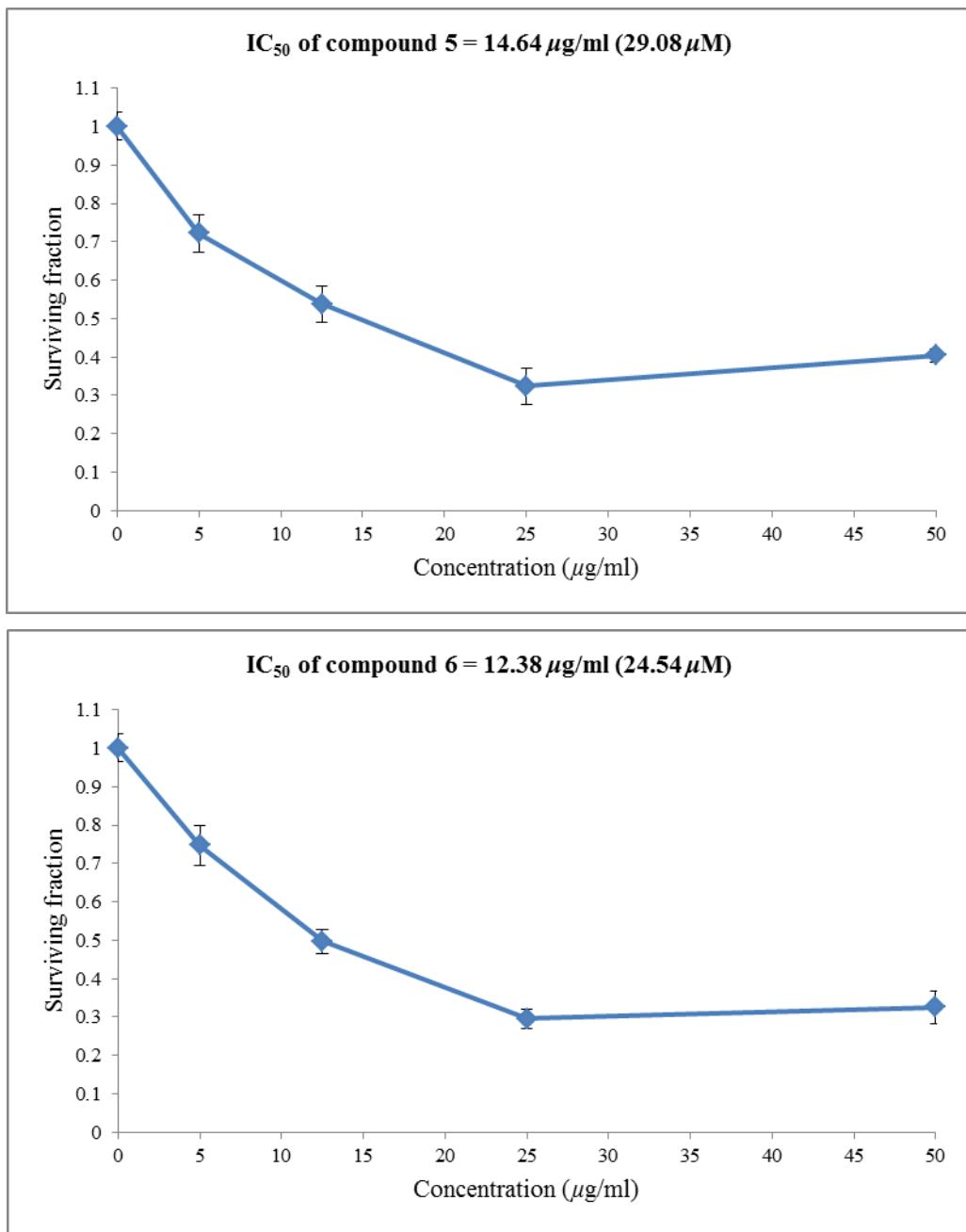












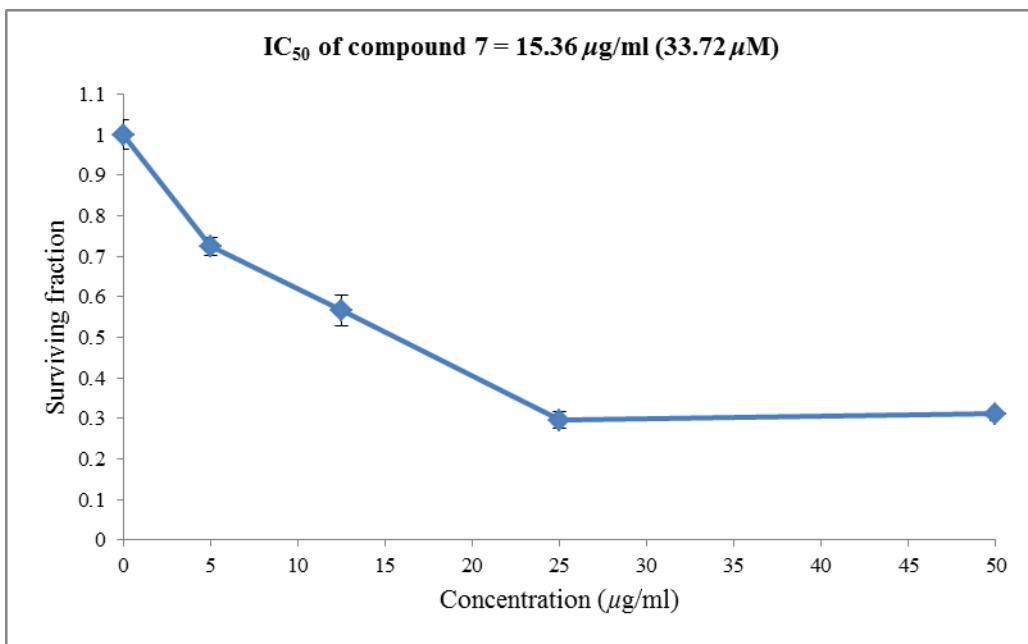
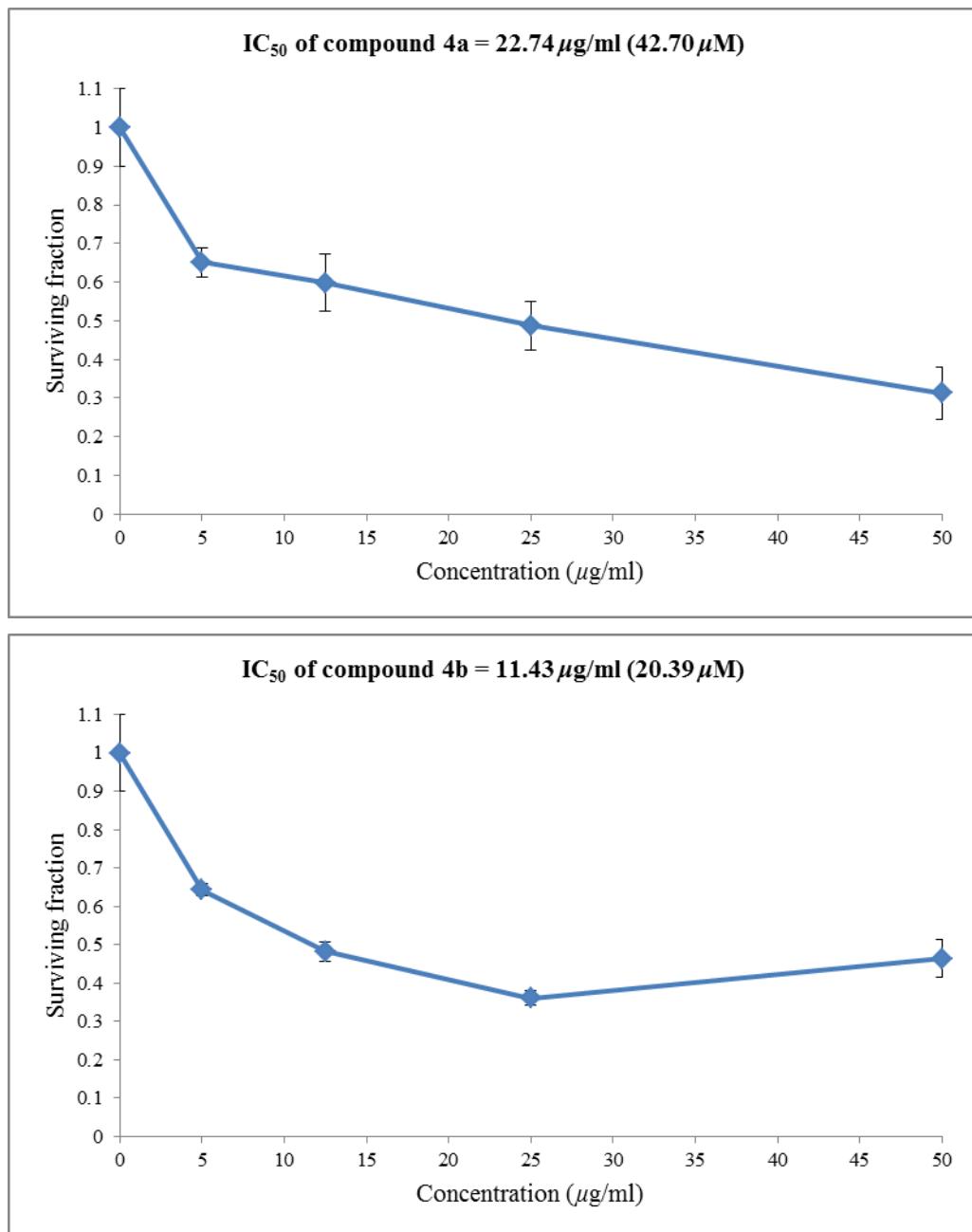
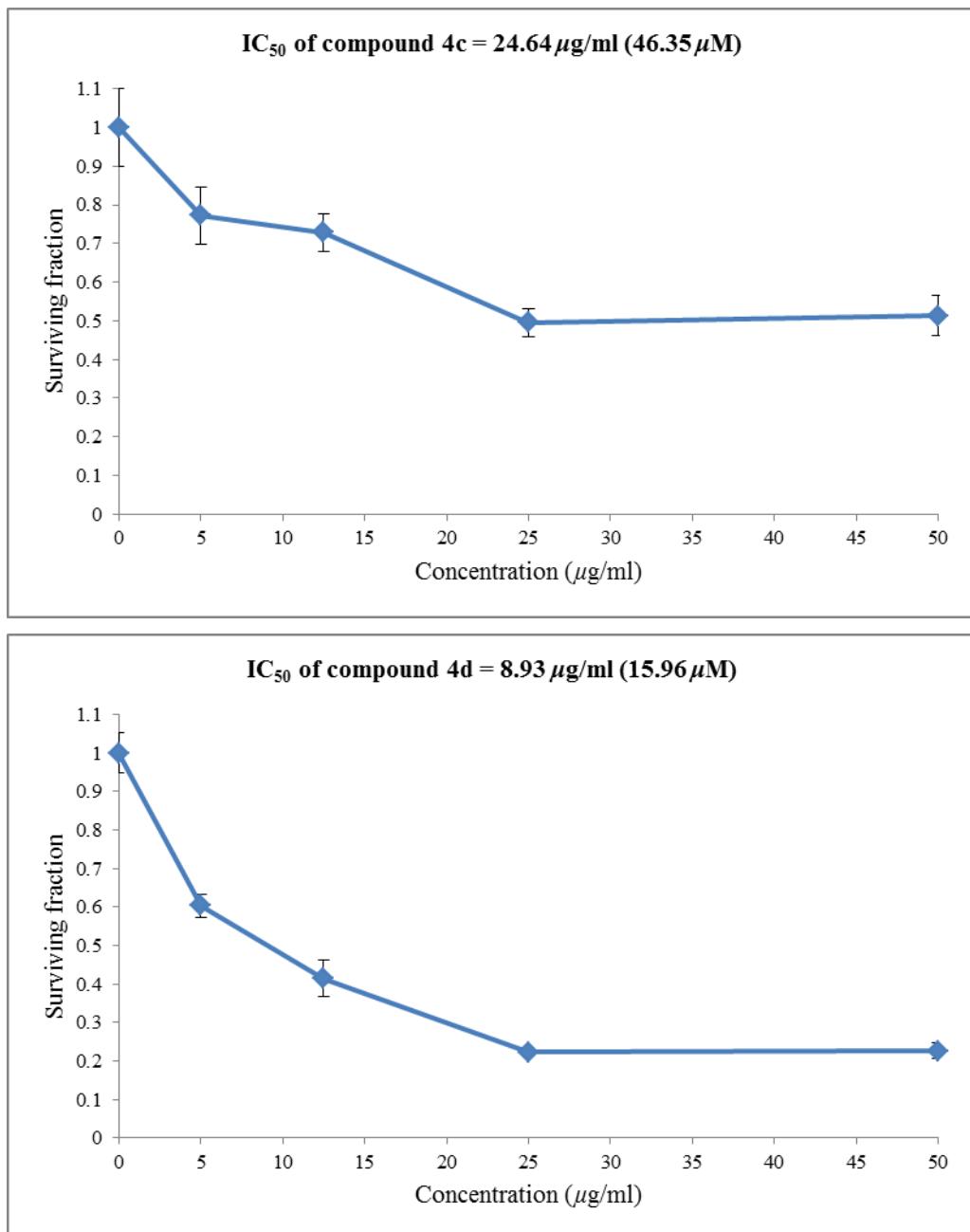
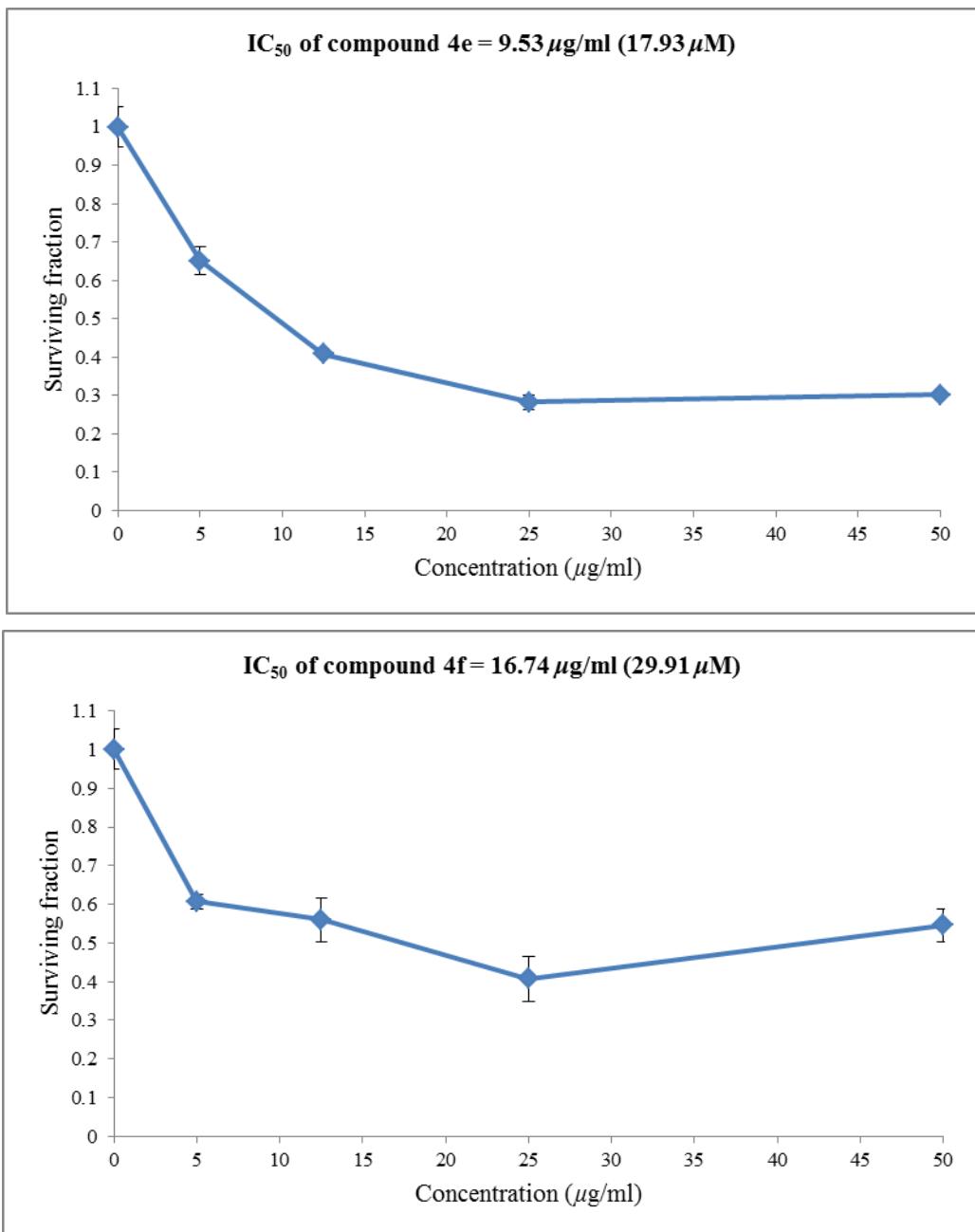
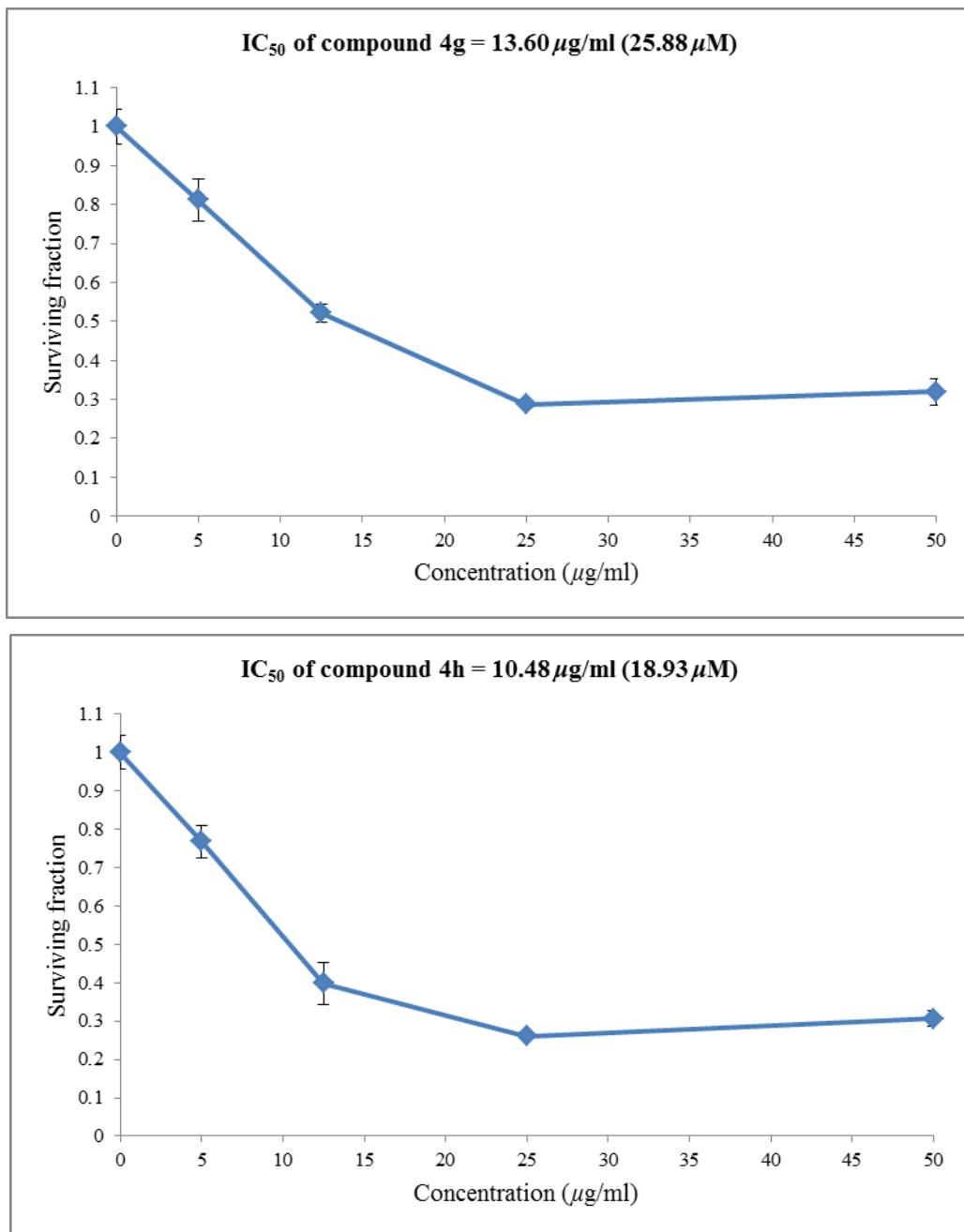


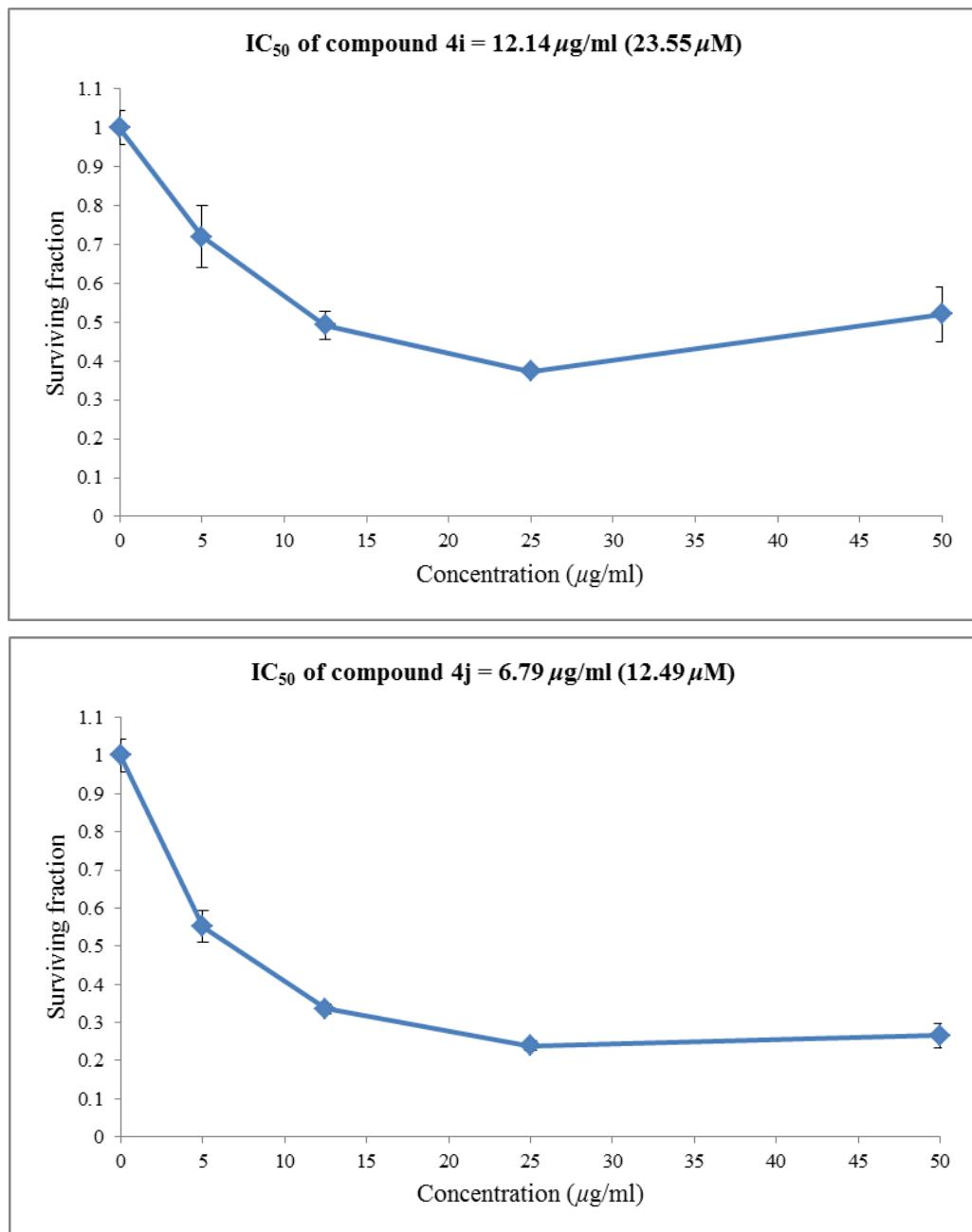
Figure S5. Dose-response curves of the macrocyclic peptidomimetics **4a-l**, and **5-7** against HCT116 (colon) human tumor cell line.

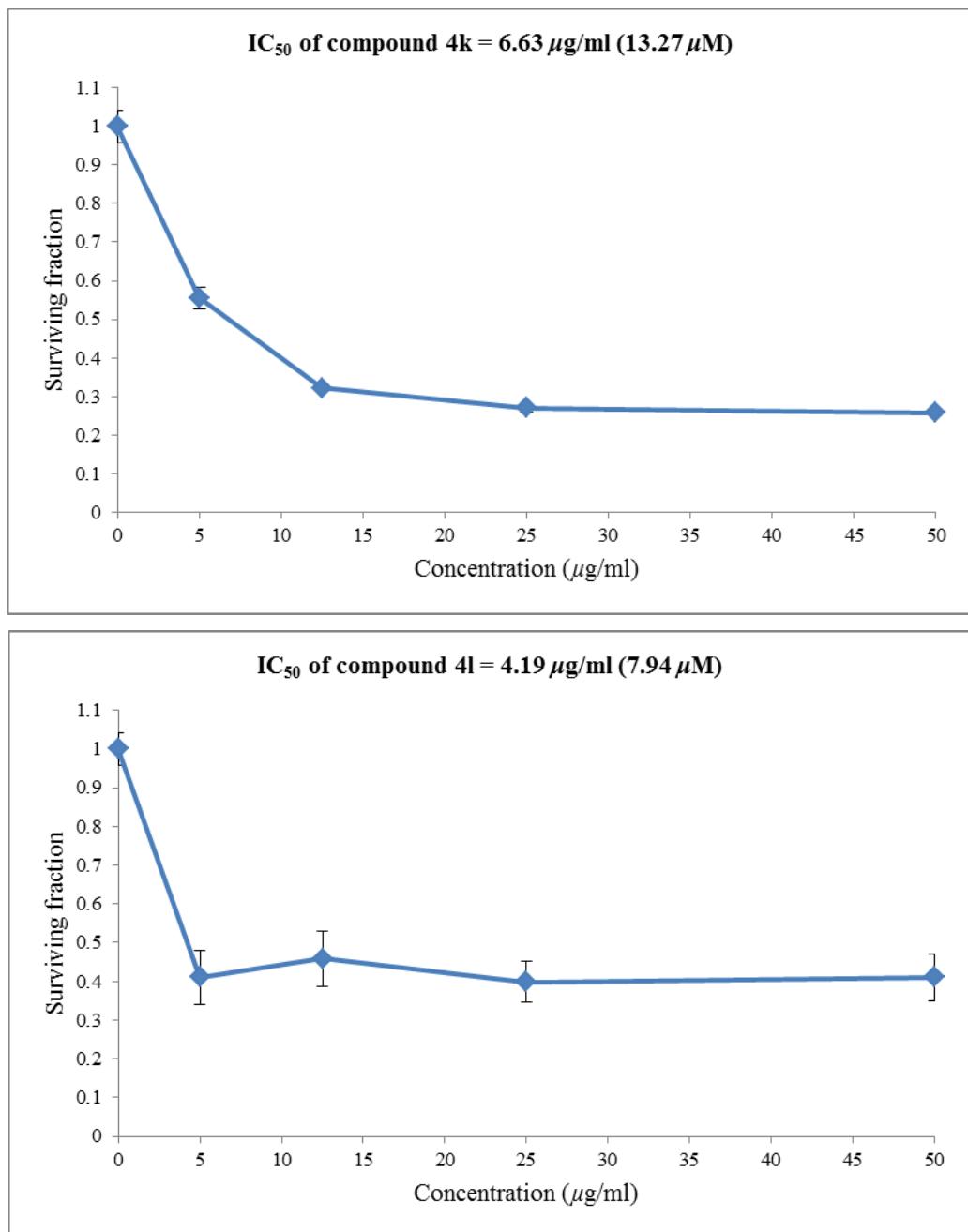


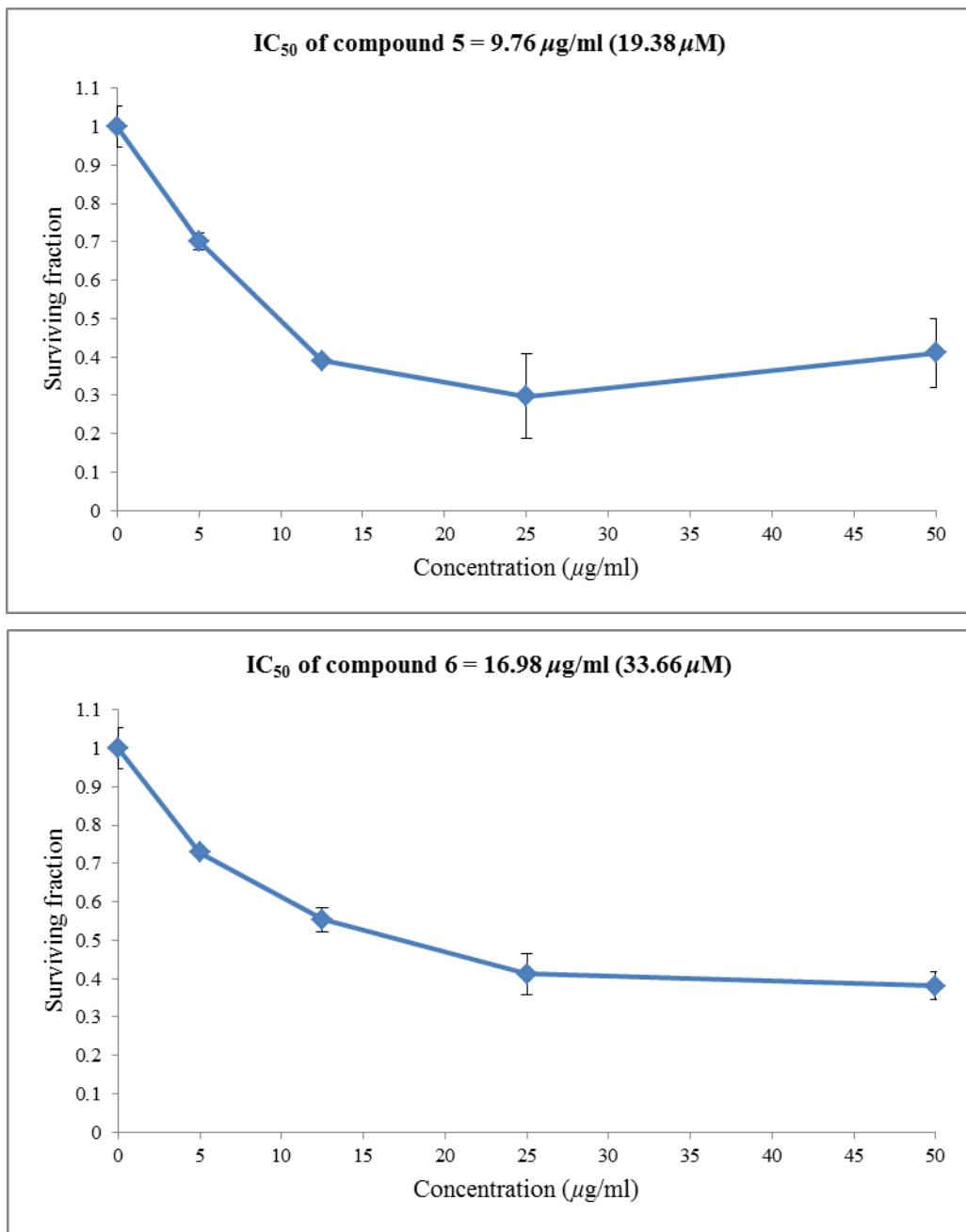












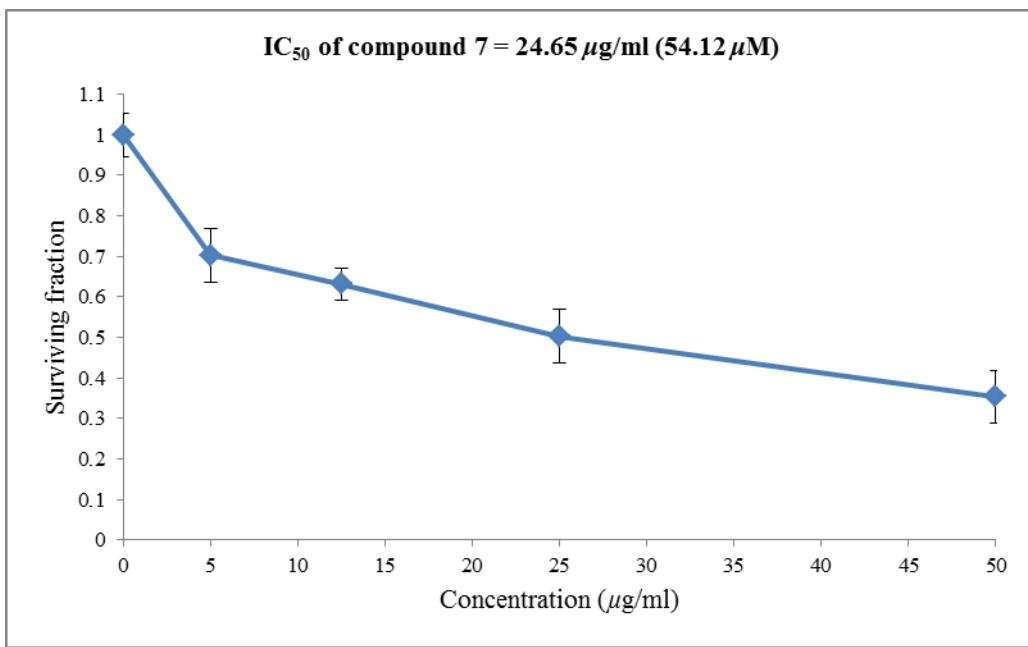
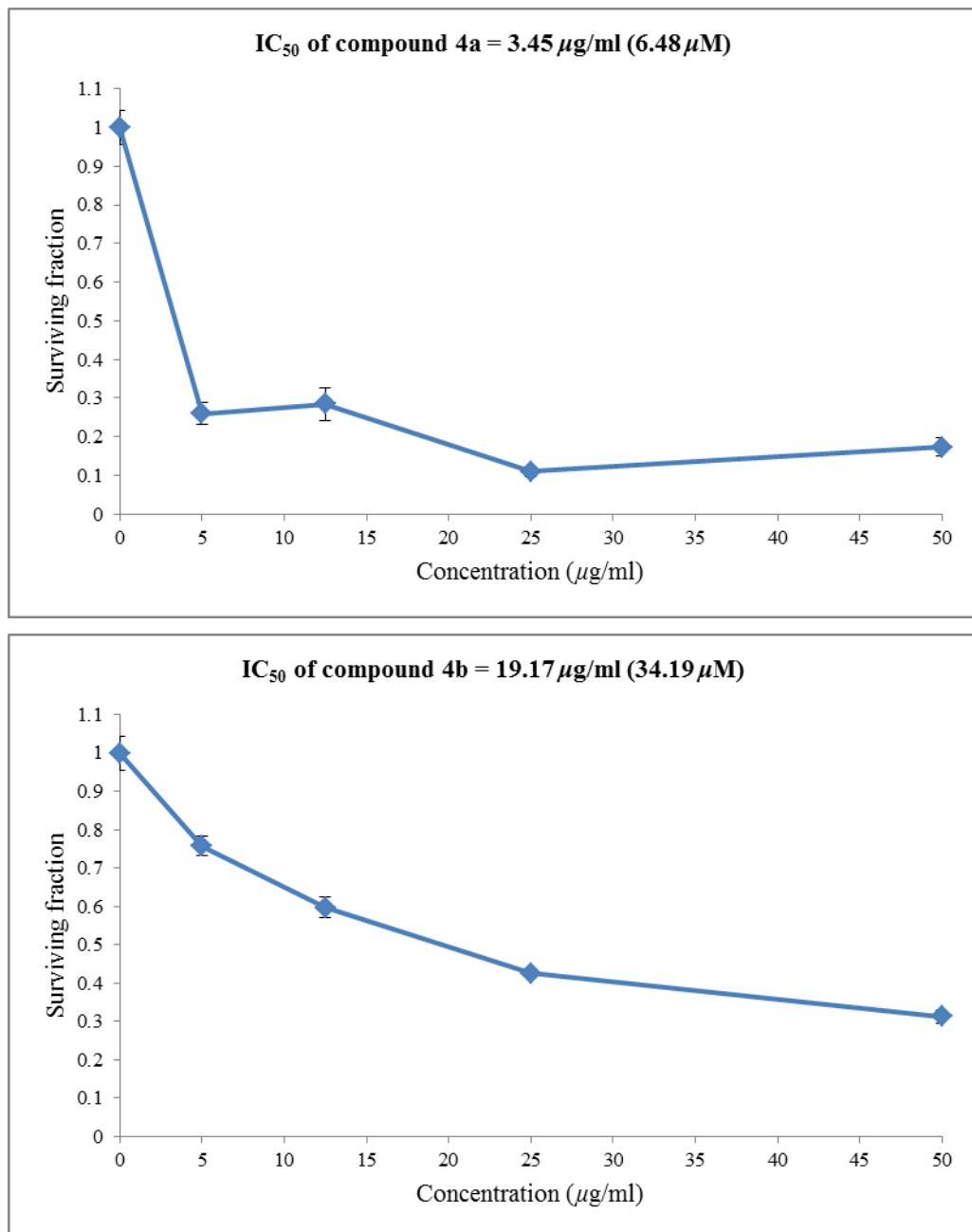
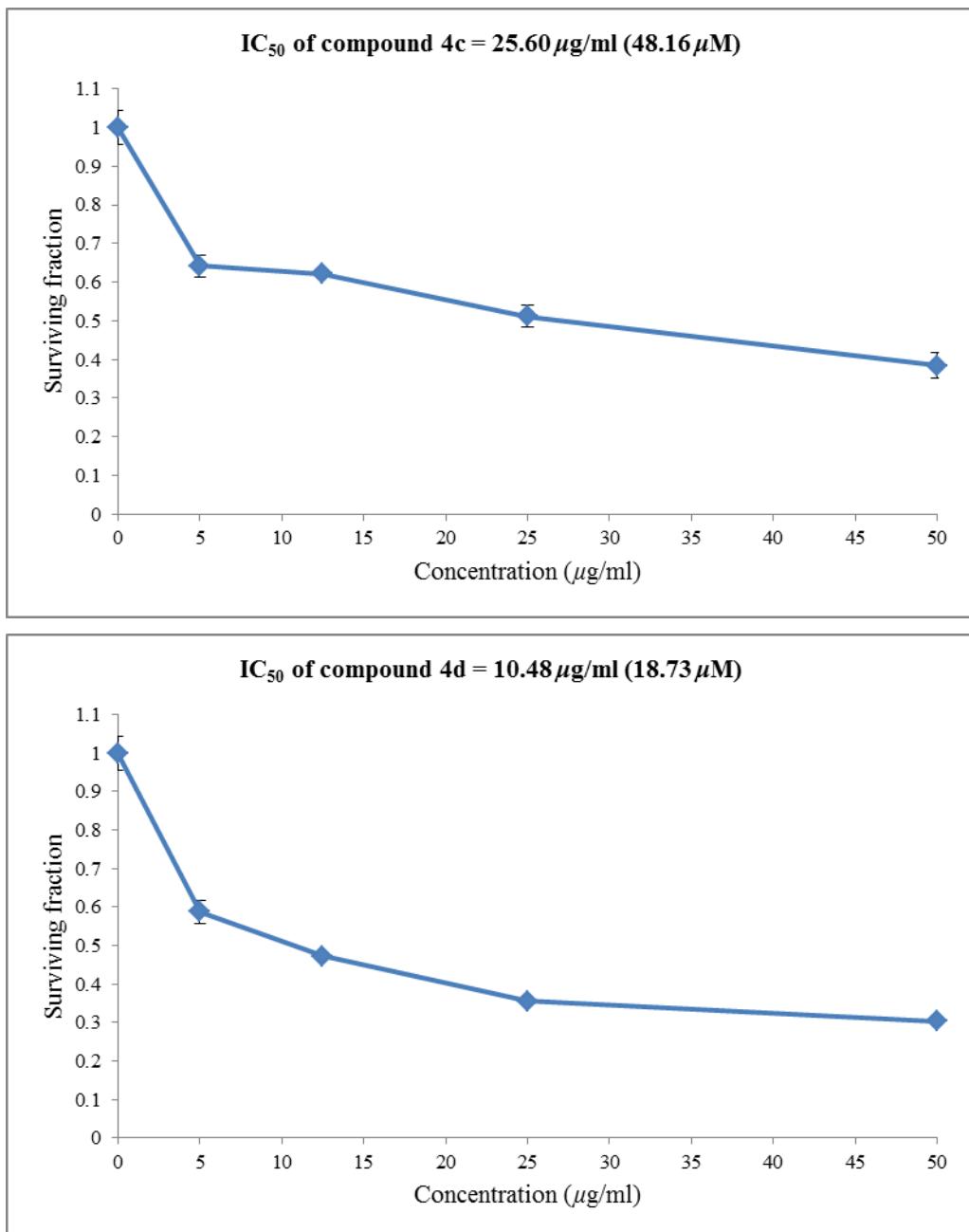
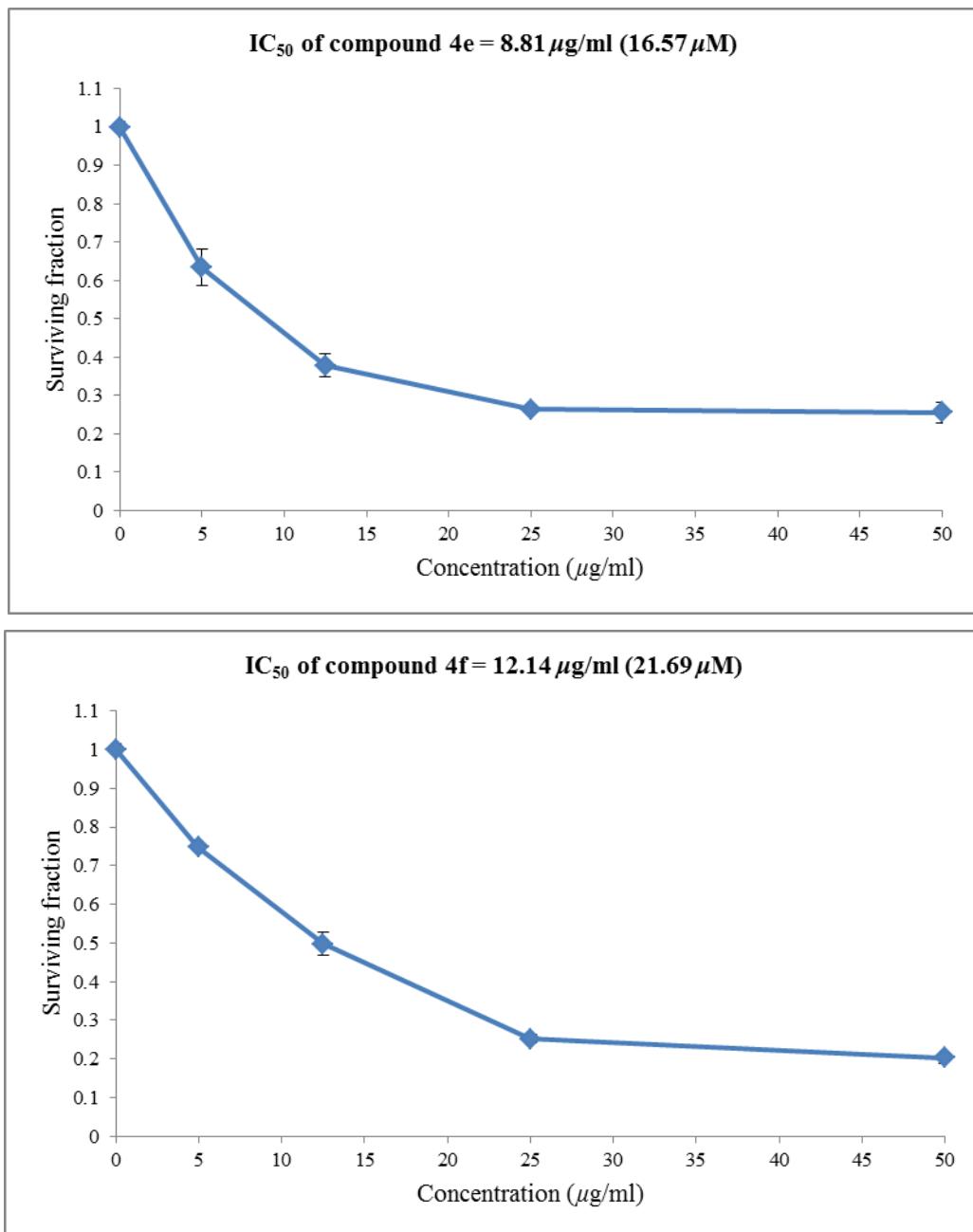
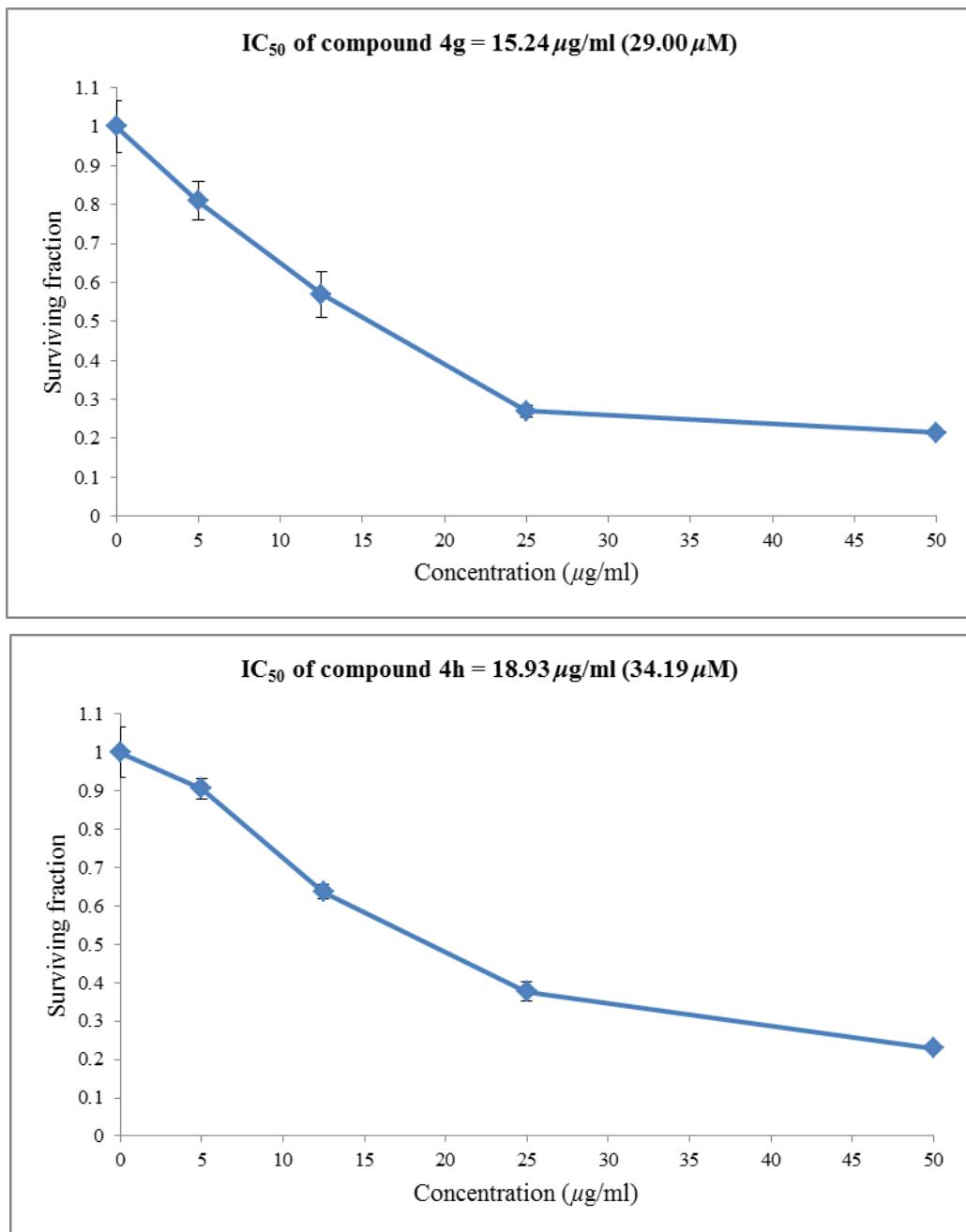


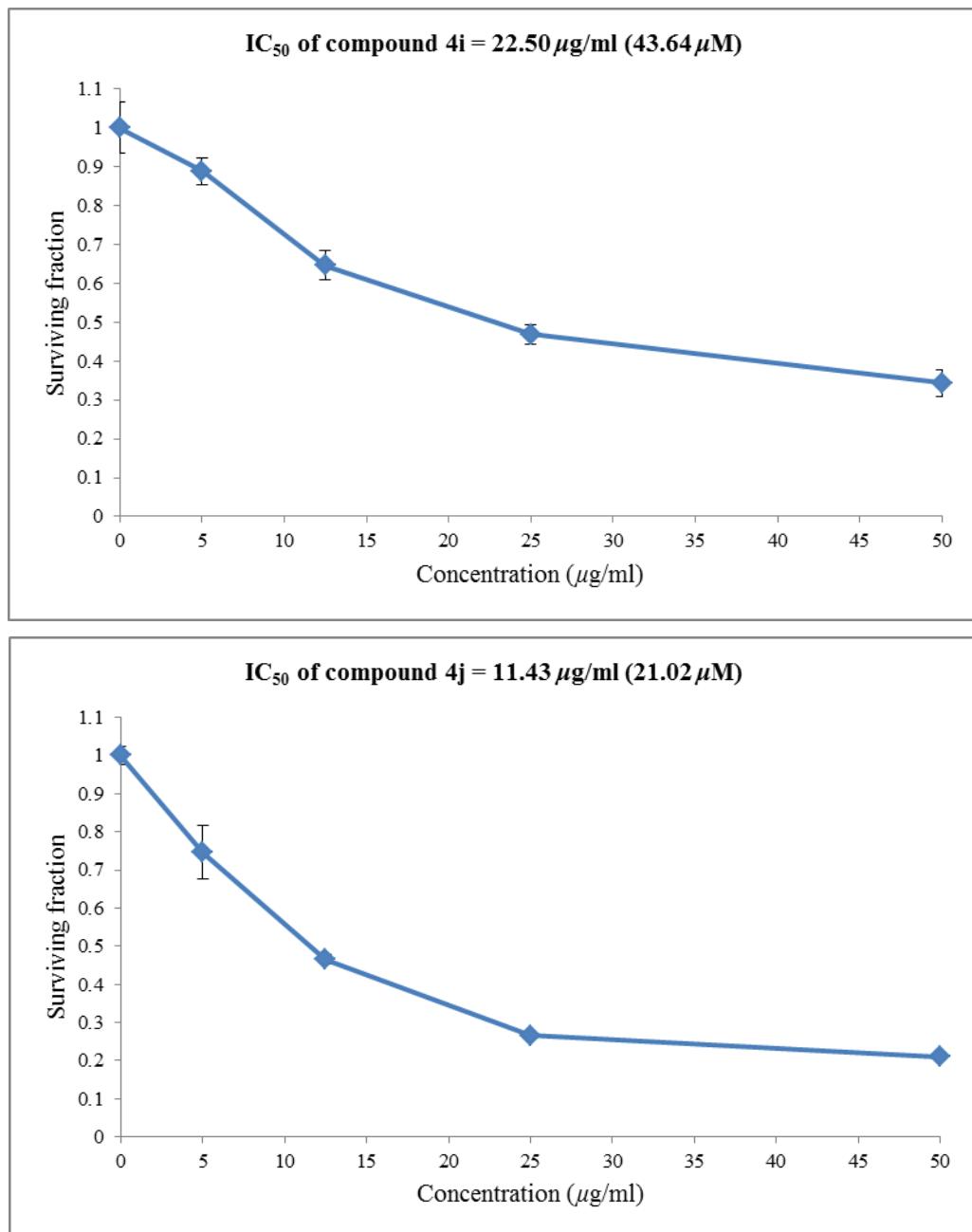
Figure S6. Dose-response curves of the macrocyclic peptidomimetics **4a-l**, and **5-7** against PC3 (prostate) human tumor cell line.

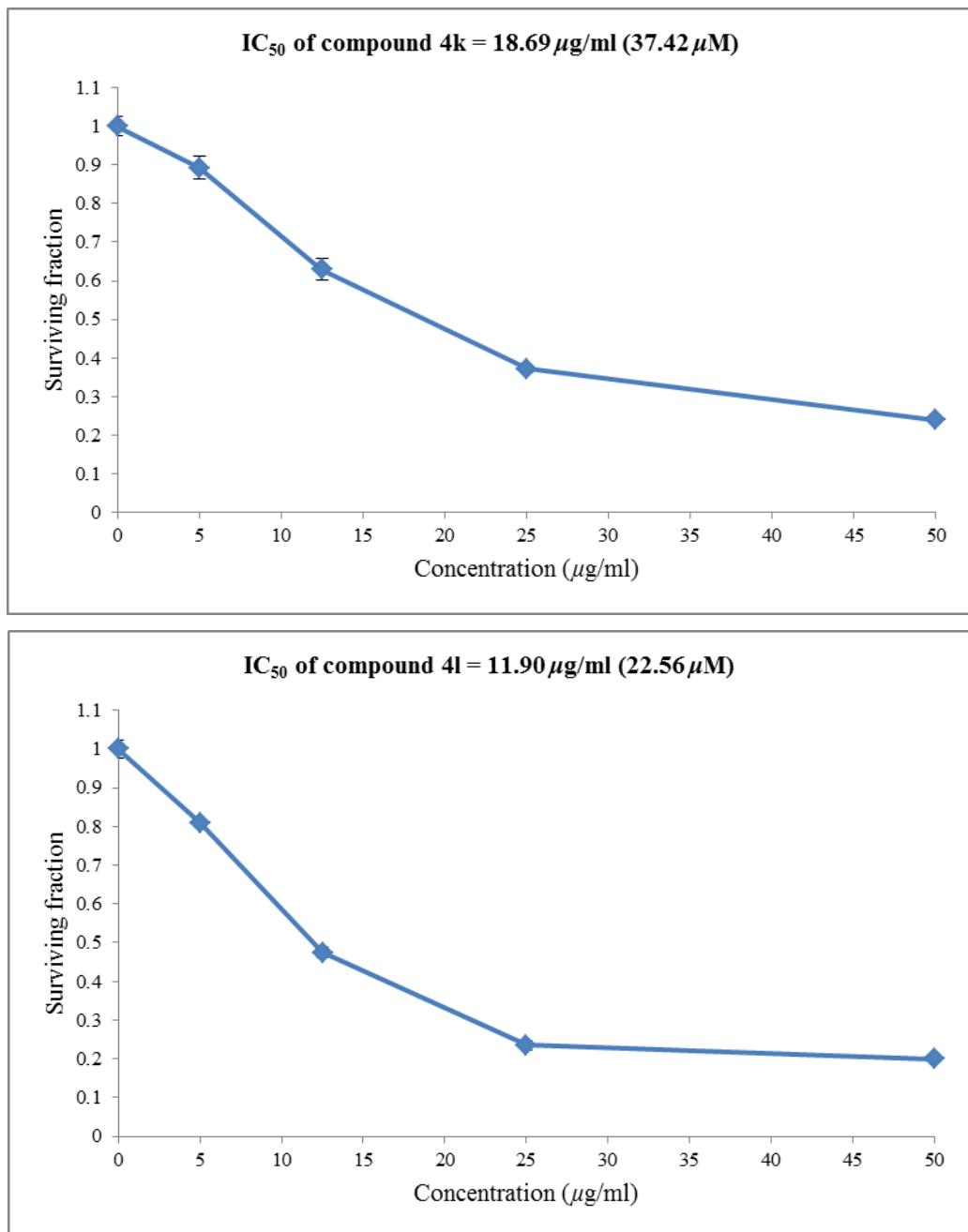


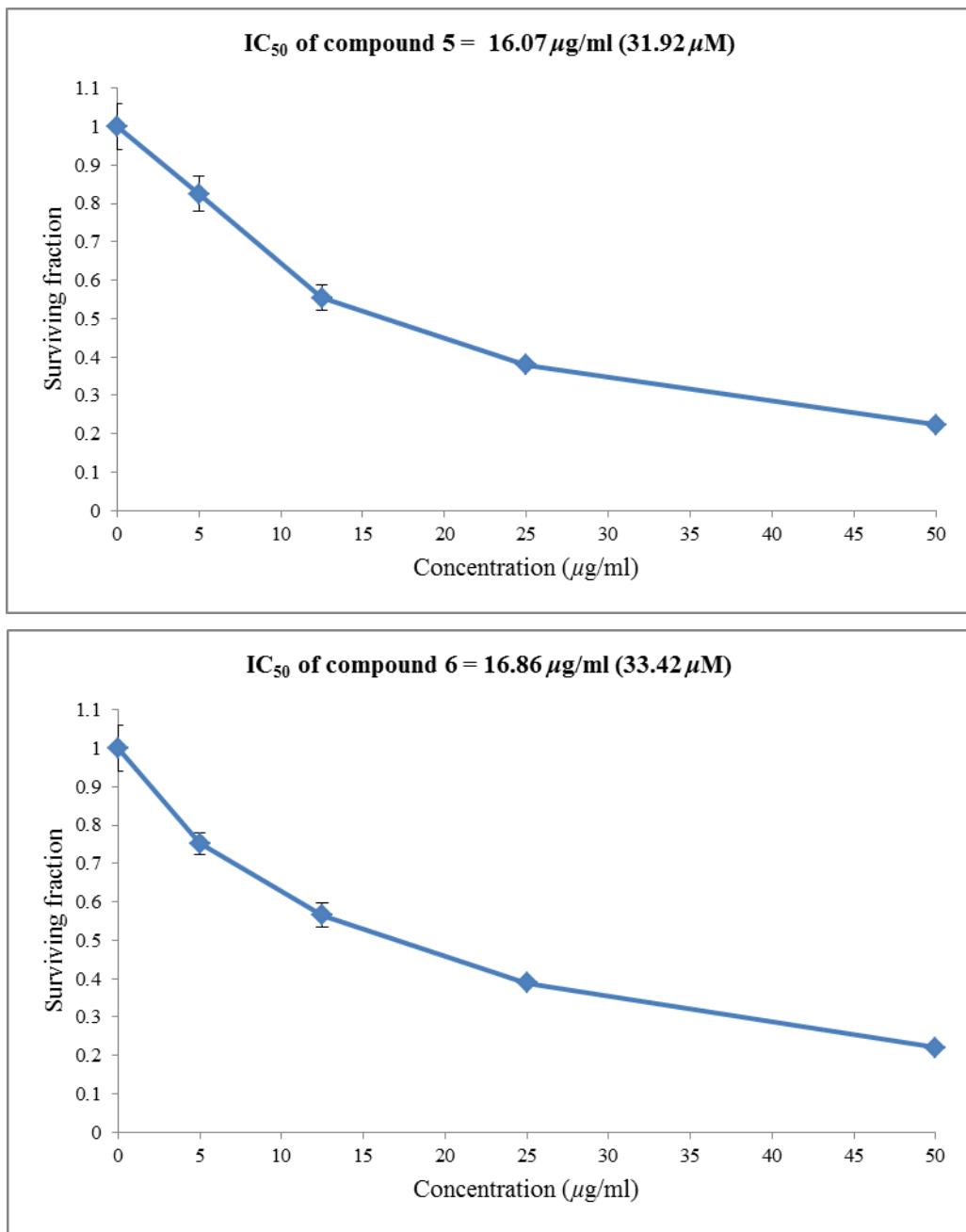












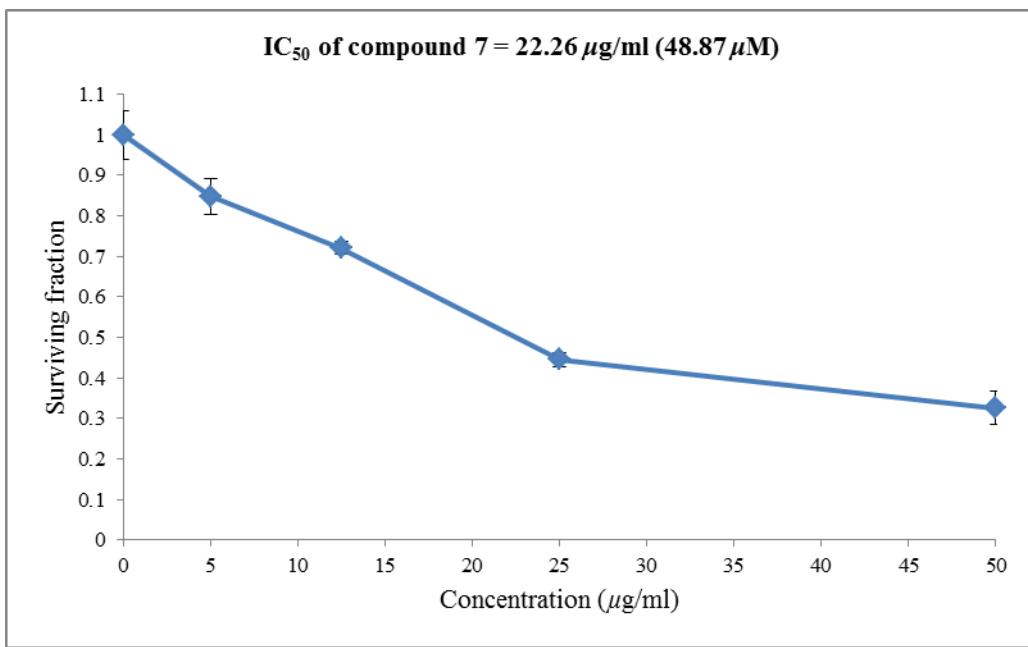


Figure S7. Dose-response curves of the macrocyclic peptidomimetics **4a-l**, and **5-7** against MCF7 (breast) human tumor cell line.