

# Electronic supporting information

## for

### Isothiazolones; thiol-reactive inhibitors of cysteine protease cathepsin B and histone acetyl transferase PCAF

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Haisma, Frank J. Dekker

#### Experimental section

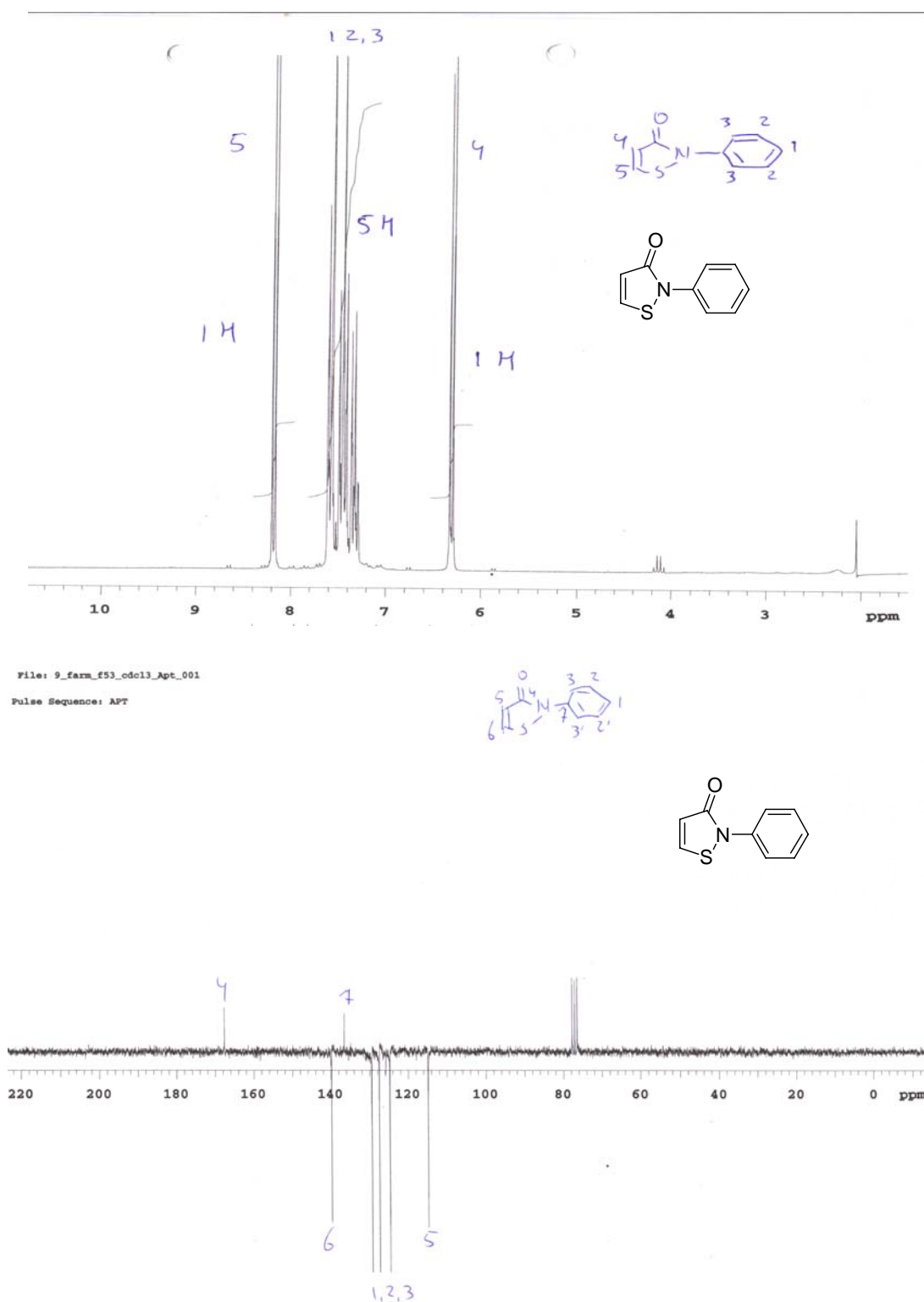
#### Chemistry

**Table S1.** Interatomic distances (Å) in the crystal structures for compounds **1** and **5**.

		2-phenyl- isothiazolo- lone <b>1</b>	5-chloro-2- phenyl-isothiazolo- lone <b>5</b>	Literature values sp <sup>2</sup> <sup>a</sup>	Literature values sp <sup>3</sup> <sup>a</sup>
Cl	C1		1.7084(18)		1.76
S	N	1.715(4)	1.7038(15)	1.56	1.78
S	C1	1.702(6)	1.7269(18)	1.70 (thiophene) <sup>b</sup> 1.61	1.81
O	C3	1.243(6)	1.231(2)	1.23-1.24 (amides)	1.42-1.44 (ethers)
N	C3	1.401(7)	1.396(2)	1.35 (imines)	1.46-1.48 (amines)
N	C4	1.433(7)	1.433(2)	1.35 (imines)	1.46-1.48 (amines)
C1	C2	1.345(7)	1.346(3)	1.31-1.34 (alkene)	
C2	C3	1.452(7)	1.454(3)	1.45-1.46 (single conjugated)	
C4	C5	1.399(7)	1.396(3)	1.38-1.40 (aromatic)	
C4	C9	1.408(7)	1.393(3)	1.38-1.40 (aromatic)	
C5	C6	1.383(7)	1.384(3)	1.38-1.40 (aromatic)	
C6	C7	1.391(8)	1.395(3)	1.38-1.40 (aromatic)	
C7	C8	1.402(8)	1.392(3)	1.38-1.40 (aromatic)	
C8	C9	1.374(9)	1.389(3)	1.38-1.40 (aromatic)	

Standard uncertainty in the last decimal place is given in parentheses

a <sup>1</sup>, b CCDC 617103



**Figure S1.**  $^1\text{H}$  and  $^{13}\text{C}$  NMR spectra of **1**.

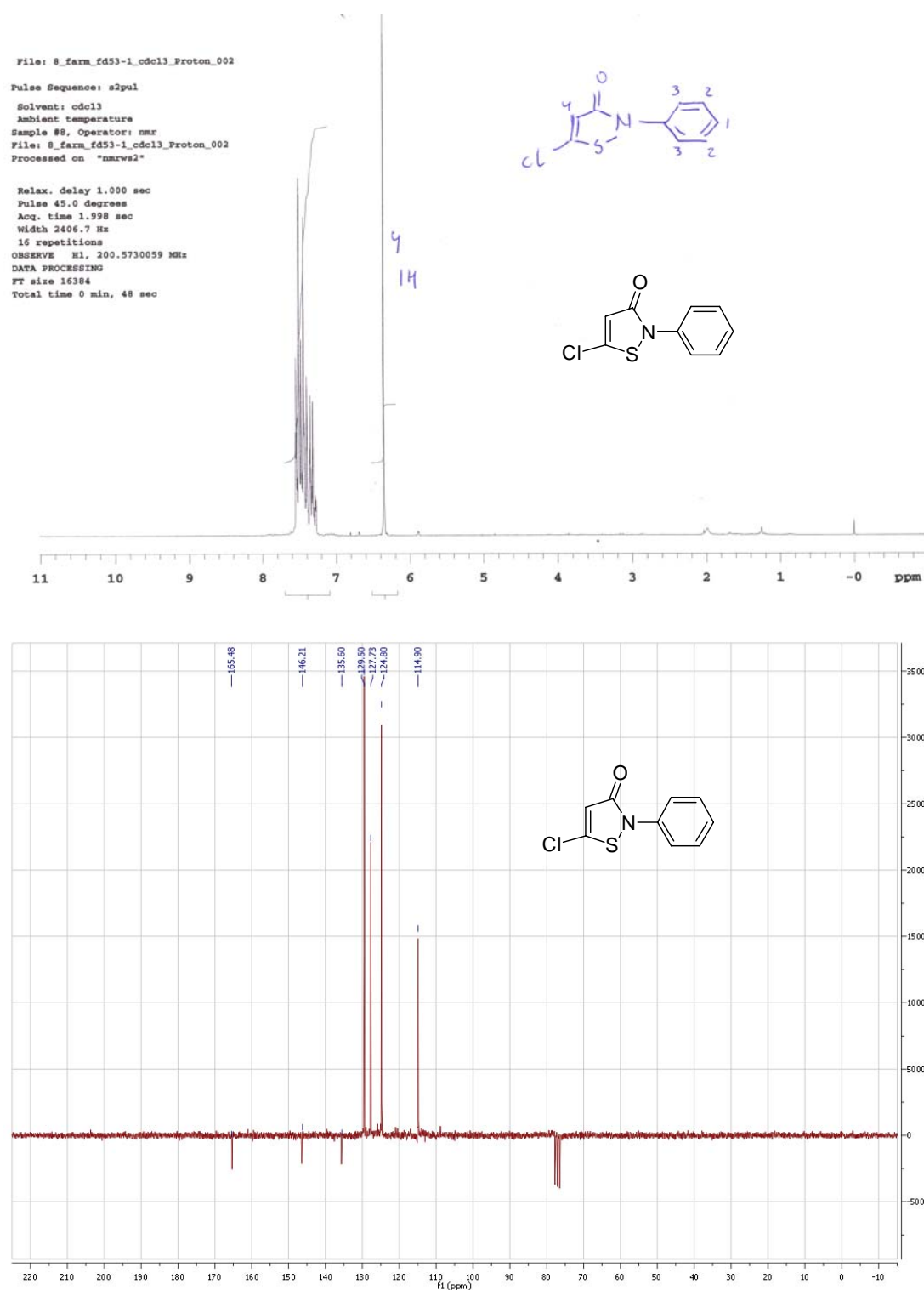
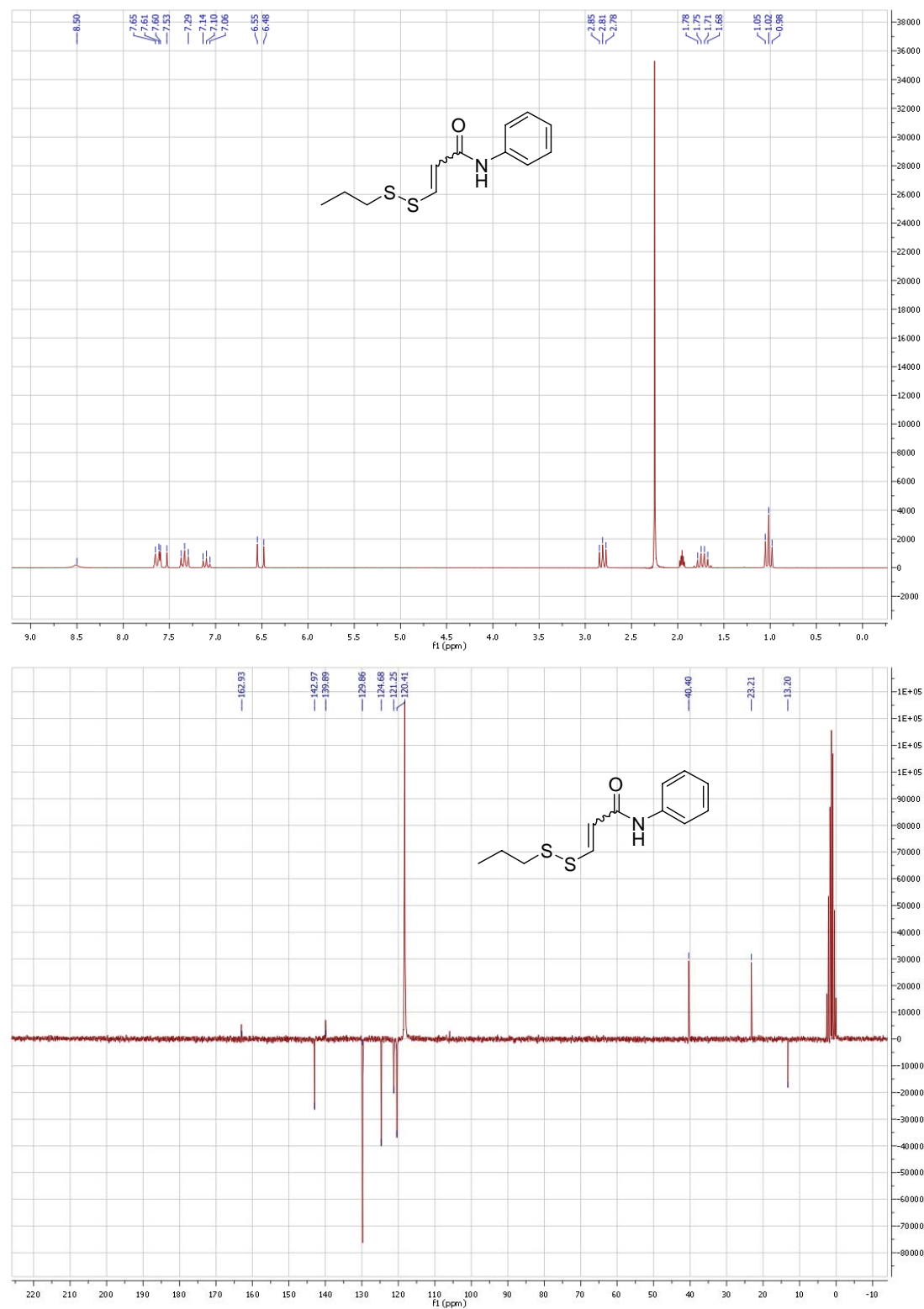
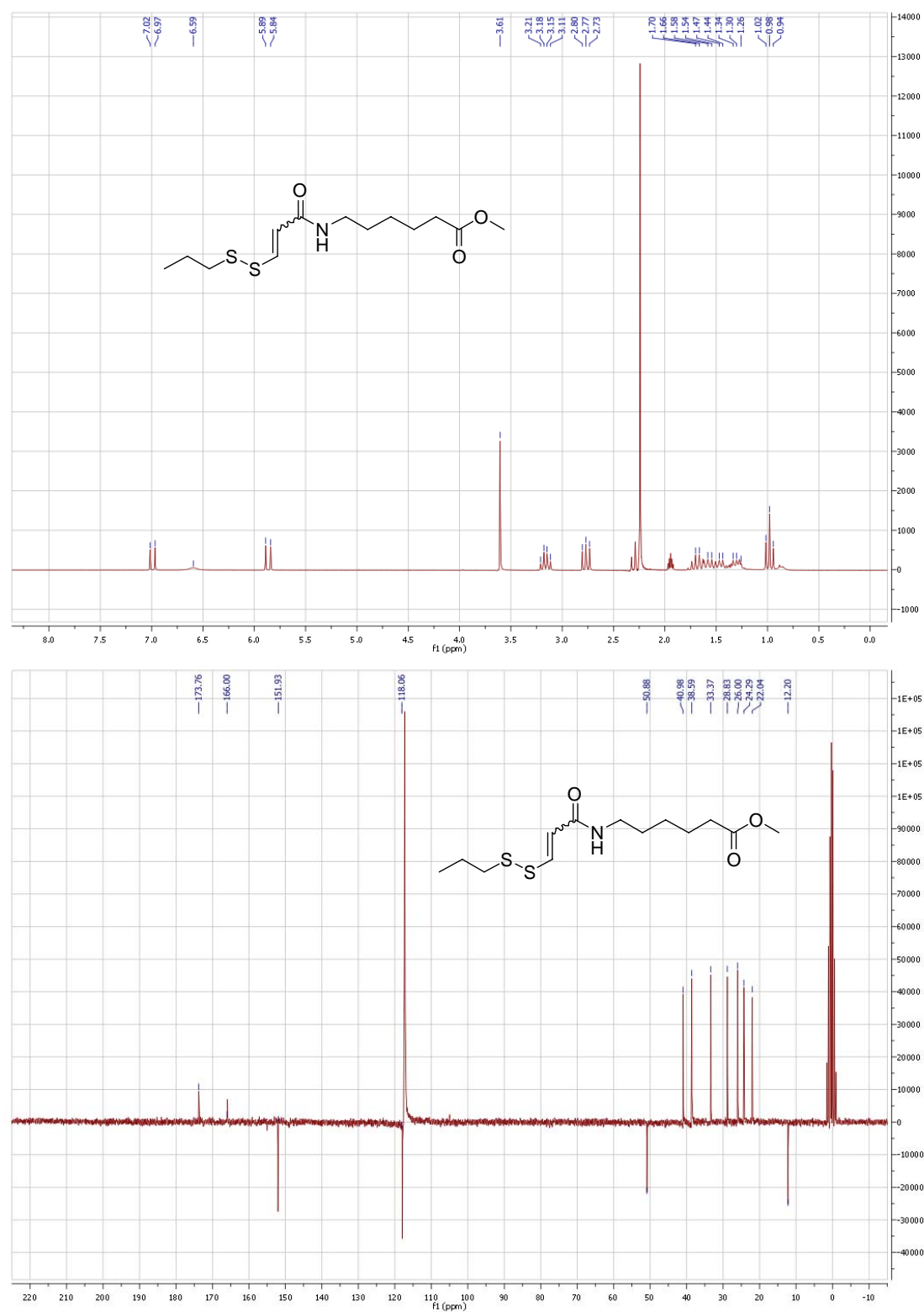


Figure S2.  $^1\text{H}$  and  $^{13}\text{C}$  NMR spectra of **5**.



**Figure S3.** <sup>1</sup>H and <sup>13</sup>C NMR spectra of **3**.



**Figure S4.**  $^1\text{H}$  and  $^{13}\text{C}$  NMR spectra of **4** .

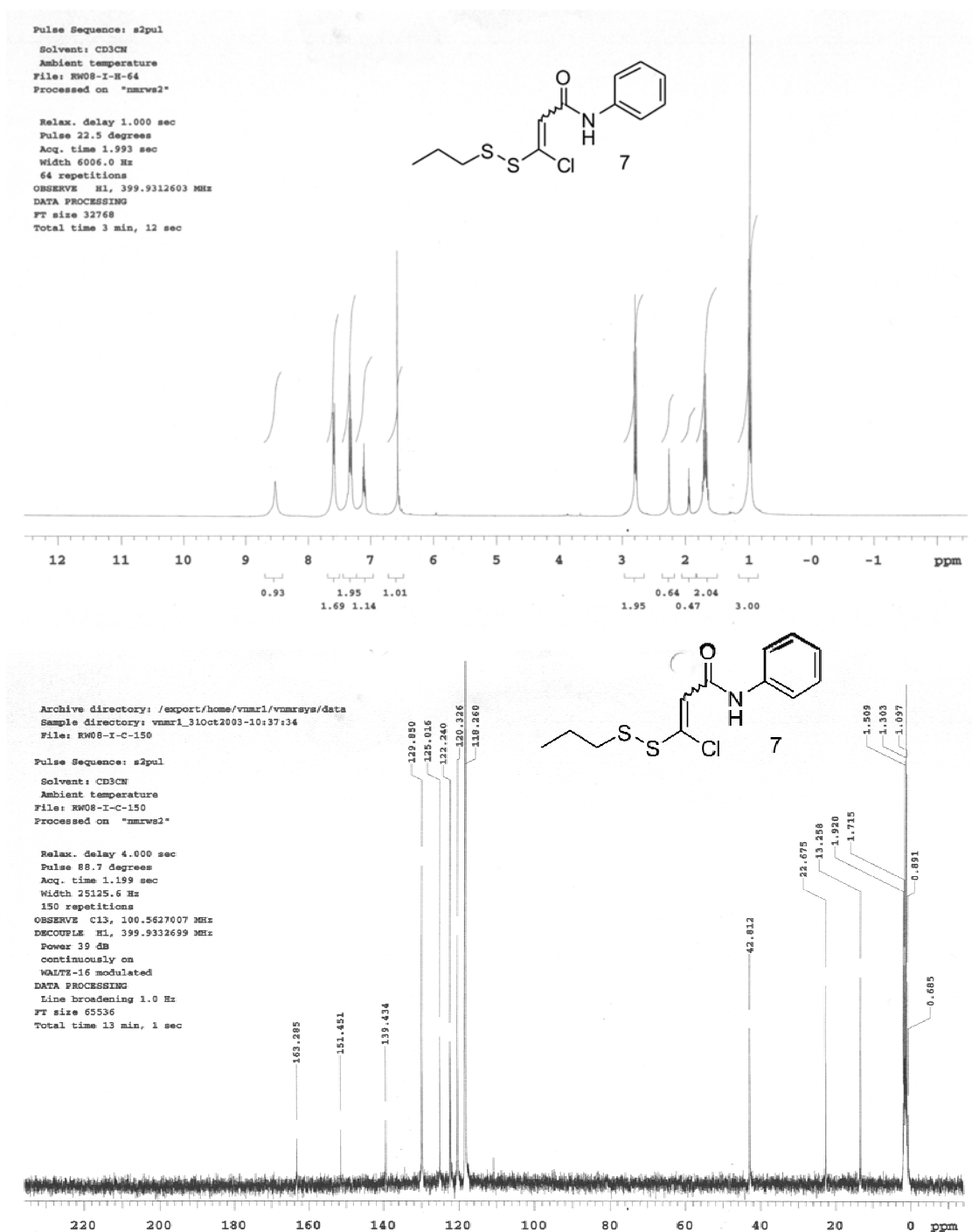


Figure S5.  $^1\text{H}$  and  $^{13}\text{C}$  NMR spectra of 7.

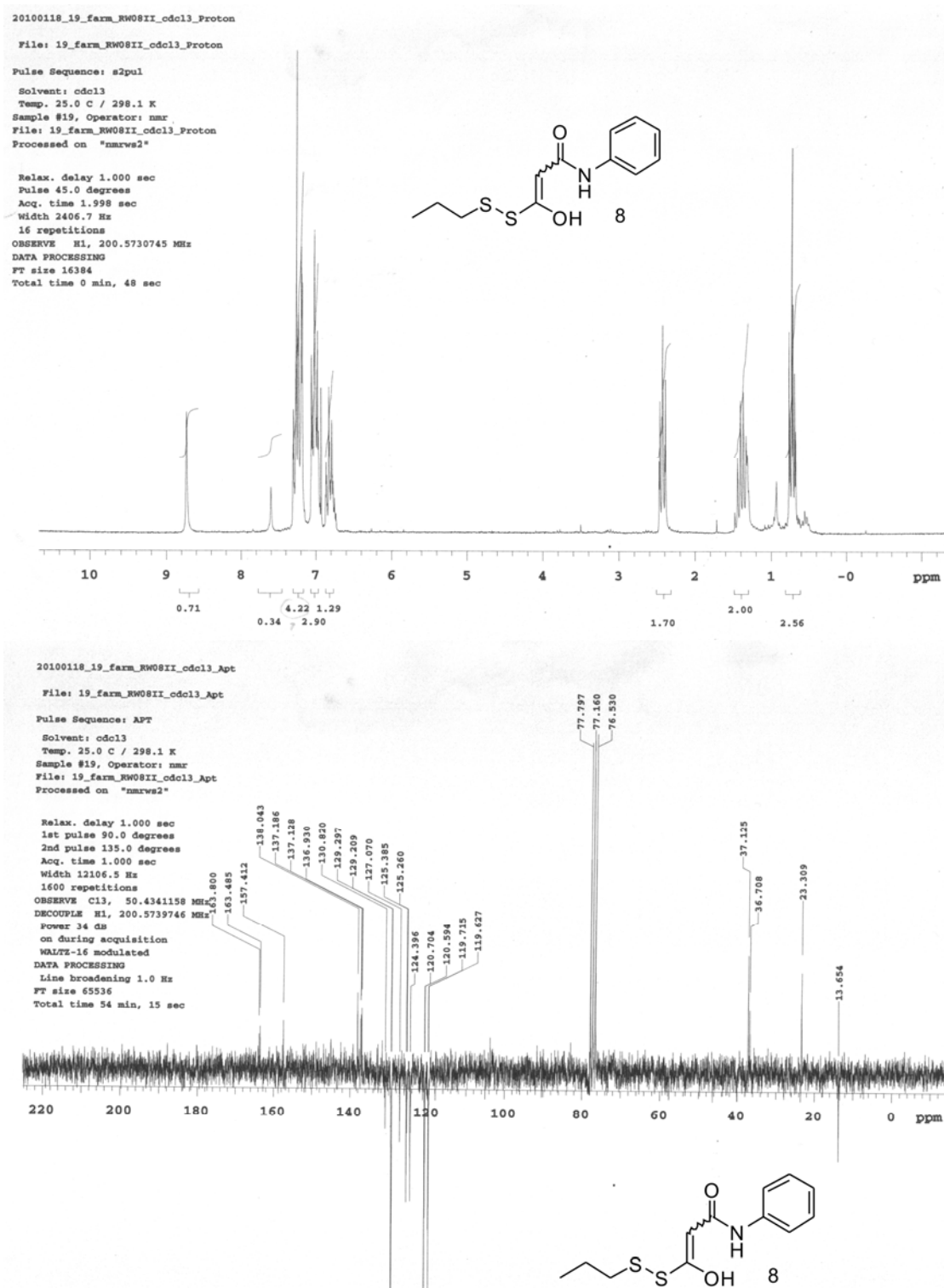
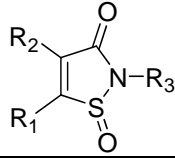


Figure S6. <sup>1</sup>H and <sup>13</sup>C NMR spectra of 8.

## Biochemistry

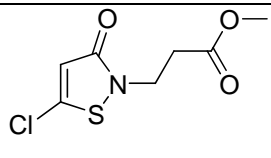
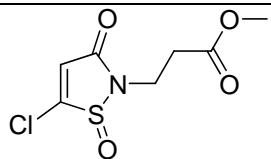
**Table S2.** IC<sub>50</sub> values for inhibition of Cathepsin B and PCAF

	R <sub>1</sub>	R <sub>2</sub>	R <sub>3</sub>	Cat B <sup>a</sup> IC <sub>50</sub> (μM)	PCAF <sup>b</sup> IC <sub>50</sub> (μM)
<b>19</b>	Cl	H	-Ethyl	27.4 ± 1.1	>10
<b>20</b>	Cl	Cl	-Ethyl	39.0 ± 0.5	>10
<b>21</b>	Cl	Methyl	-Ethyl	17.4 ± 1.3	>10
<b>22</b>	Cl	H	-(CH <sub>2</sub> ) <sub>2</sub> CO <sub>2</sub> Me	21.3 ± 1.5	5.6 ± 0.2
<b>23</b>	Cl	Cl	-(CH <sub>2</sub> ) <sub>2</sub> CO <sub>2</sub> Me	34.5 ± 1.2	>10
<b>24</b>	Cl	Methyl	-(CH <sub>2</sub> ) <sub>2</sub> CO <sub>2</sub> Me	23.1 ± 3.1	>10
<b>25</b>	-S(CH <sub>2</sub> ) <sub>11</sub> CH <sub>3</sub>	H	-(CH <sub>2</sub> ) <sub>2</sub> CO <sub>2</sub> Me	>100	>10
<b>26</b>	-S(CH <sub>2</sub> ) <sub>11</sub> CH <sub>3</sub>	Cl	-(CH <sub>2</sub> ) <sub>2</sub> CO <sub>2</sub> Me	>100	>10

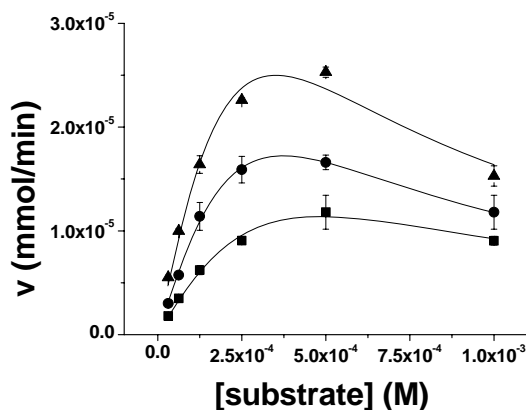
<sup>a</sup> maximal concentration in the assay 100 μM.

<sup>b</sup> data reported previously.<sup>2,3</sup> maximal concentration in the assays 10 μM

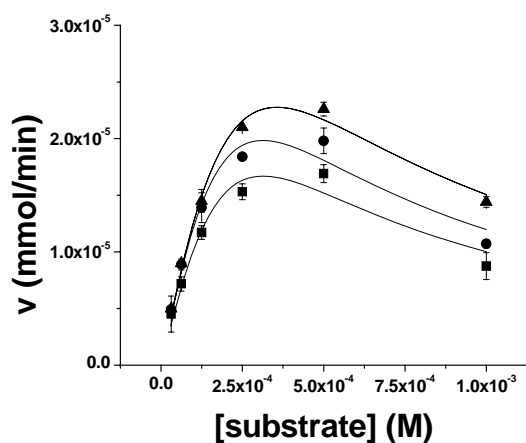
**Table S3.** Enzyme kinetics parameters for Cathepsin B inhibition (n = 3)

	Conc inhibitor (μM)	V <sub>max</sub> (nmol/s)	K <sub>m</sub> (mM)	K <sub>S</sub> (mM)	R <sup>2</sup>
 <b>14</b>	0	0.65 ± 0.66	1.2 ± 1.3	0.10 ± 0.11	0.989
	6	0.51 ± 0.24	1.4 ± 0.7	0.10 ± 0.051	0.998
	12	0.23 ± 0.13	1.2 ± 0.7	0.20 ± 0.13	0.995
 <b>22</b>	0	0.56 ± 0.67	1.1 ± 1.4	0.098 ± 0.13	0.982
	11	0.52 ± 0.59	1.1 ± 1.2	0.11 ± 0.15	0.972
	22	0.50 ± 0.70	1.1 ± 1.9	0.090 ± 0.15	0.972





**Figure S7.** Conversion of the substrate Cbz-Arg-Arg-AMC by the enzyme Cathepsin B with no inhibitor present ( $\blacktriangle$ ) shows substrate inhibition at high substrate concentrations. The same is observed for the enzyme activity after preincubation with 6  $\mu$ M inhibitor **14** ( $\bullet$ ) and the enzyme activity after preincubation with 12  $\mu$ M inhibitor **14** ( $\blacksquare$ ). The data were fitted to equation 1 and the parameters are shown in table S3.



**Figure S8.** Conversion of the substrate Cbz-Arg-Arg-AMC by the enzyme Cathepsin B with no inhibitor present ( $\blacktriangle$ ) shows substrate inhibition at high substrate concentrations. The same is observed for the enzyme activity after preincubation with 11  $\mu$ M inhibitor **22** ( $\bullet$ ) and the enzyme activity after preincubation with 22  $\mu$ M inhibitor **22** ( $\blacksquare$ ). The data were fitted to equation 1 and the parameters are shown in table S3. The data represented by the blocks ( $\blacksquare$ ) and circles ( $\bullet$ ) did not fit well to equation 1.

**Table S4.** Time dependent inhibition of Cathepsin B by **5**. The IC<sub>50</sub> of the residual enzyme activity was determined after 1, 15, 40 or 120 minutes pre-incubation of the enzyme with the inhibitor (n = 3).

Time (min)	IC <sub>50</sub> (μM)
1	13.6 ± 1.5
15	12.7 ± 1.3
40	9.3 ± 1.1
120	8.1 ± 1.0

**Table S5.** Dilution experiments after pre-incubation of Cathepsin B (20 nM) and inhibitor **5** (17 μM) with a substrate solution (100 μM) demonstrates a reduction of activity that is proportional to the dilution. This demonstrates covalent binding of the enzyme to the inhibitor (n = 3) <sup>6</sup>.

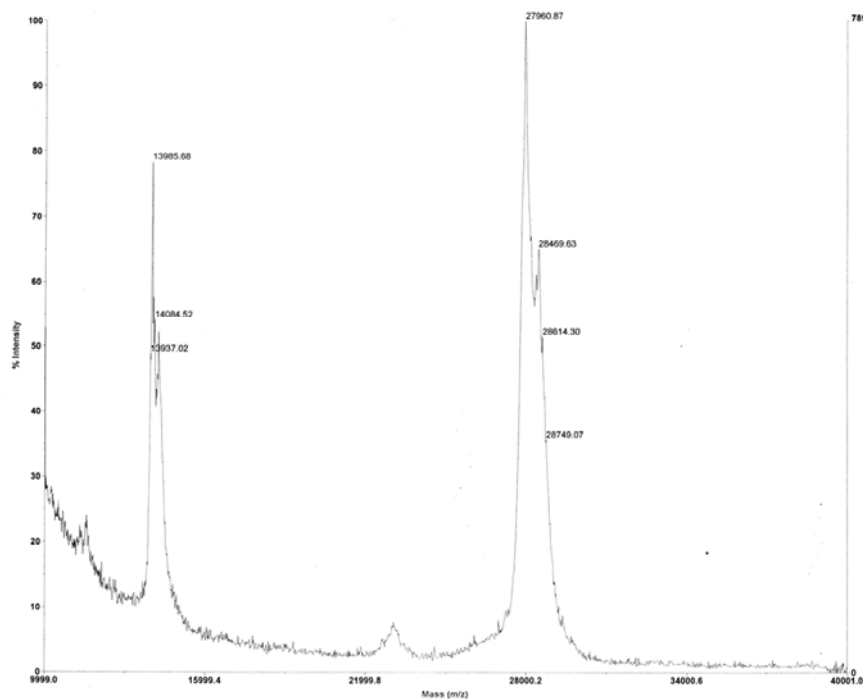
Dilution	v (fluorescence units/min)	Reduction in activity
1	13.3 ± 0.5	1.00
2	6.9 ± 0.1	1.93
5	2.7 ± 0.1	4.93

**Table S6.** Reduction rate of cathepsin B by **5**. The initial rate of cathepsin B (1.5 nM) activity with or without inhibitor **5** (14 μM) were determine after 20 second reaction of the enzyme with the substrate (33.3 μM). (n = 3) The result shows a very quick reduction of the enzyme activity in presence of the inhibitor.

Inhibitor	V (fluorescence units/s)
No Inhibitor	25.3 ± 1.2
<b>5</b> (14 μM)	11.9 ± 5.0

### Applied Biosystems Voyager System 6363

Voyager Spec #1=>NF0.7=>SM19=>NR(2.00)[BP = 27959.7, 789]



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Extraction mode: Delayed  
Polarity: Positive  
Acquisition control: Manual

Accelerating voltage: 25000 V  
Grid voltage: 92.2%  
Guide wire 0: 0.15%  
Extraction delay time: 350 nsec

Acquisition mass range: 10000 – 40000 Da  
Number of laser shots: 100/spectrum  
Laser intensity: 1712  
Laser Rep Rate: 20.0 Hz  
Calibration type: Default  
Calibration matrix: Sinapinic acid  
Low mass gate: 5000 Da

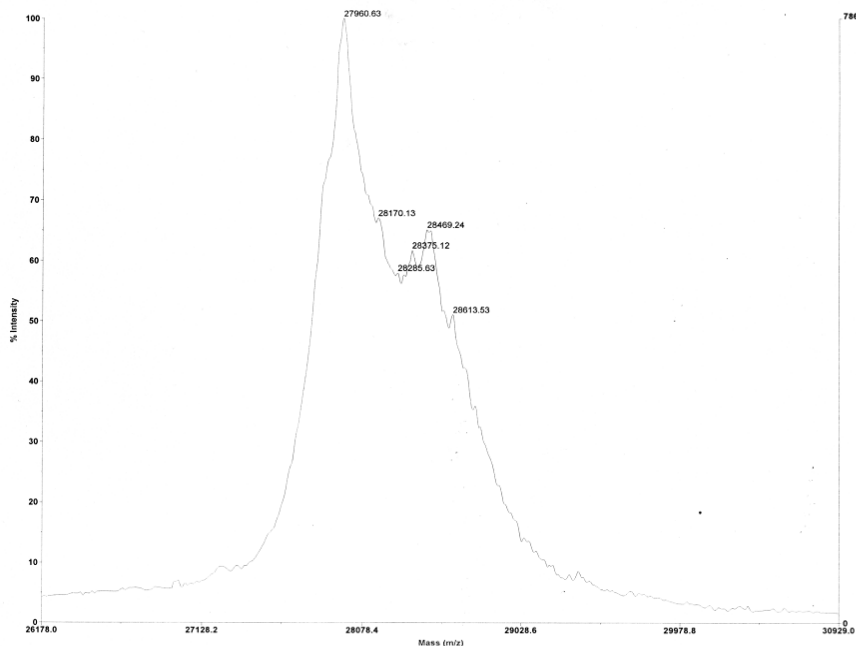
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Plate type filename: C:\VOYAGER\100 well plate.plt  
Lab name: PE Biosystems

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Absolute y-position: 32111.4  
Relative x-position: -808.102  
Relative y-position: 43.8993  
Shots in spectrum: 600  
Source pressure: 3.63e-007  
Mirror pressure: 1.112e-007  
TC2 pressure: 0.001  
TIS gate width: 8  
TIS flight length: 689.45

### Applied Biosystems Voyager System 6363

Voyager Spec #1=>NR(2.00)=>SM19=>NF0.7[BP = 27959.7, 787]



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Extraction mode: Delayed  
Polarity: Positive  
Acquisition control: Manual

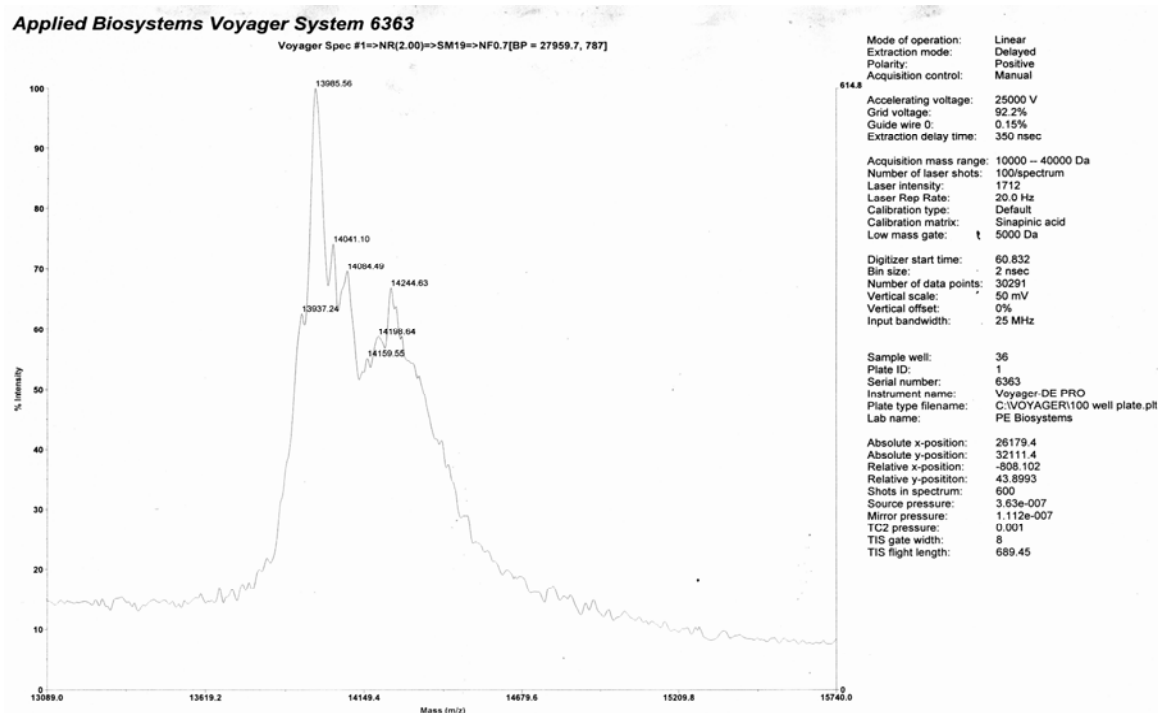
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Extraction delay time: 350 nsec

Acquisition mass range: 10000 – 40000 Da  
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Laser intensity: 1712  
Laser Rep Rate: 20.0 Hz  
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Calibration matrix: Sinapinic acid  
Low mass gate: 5000 Da

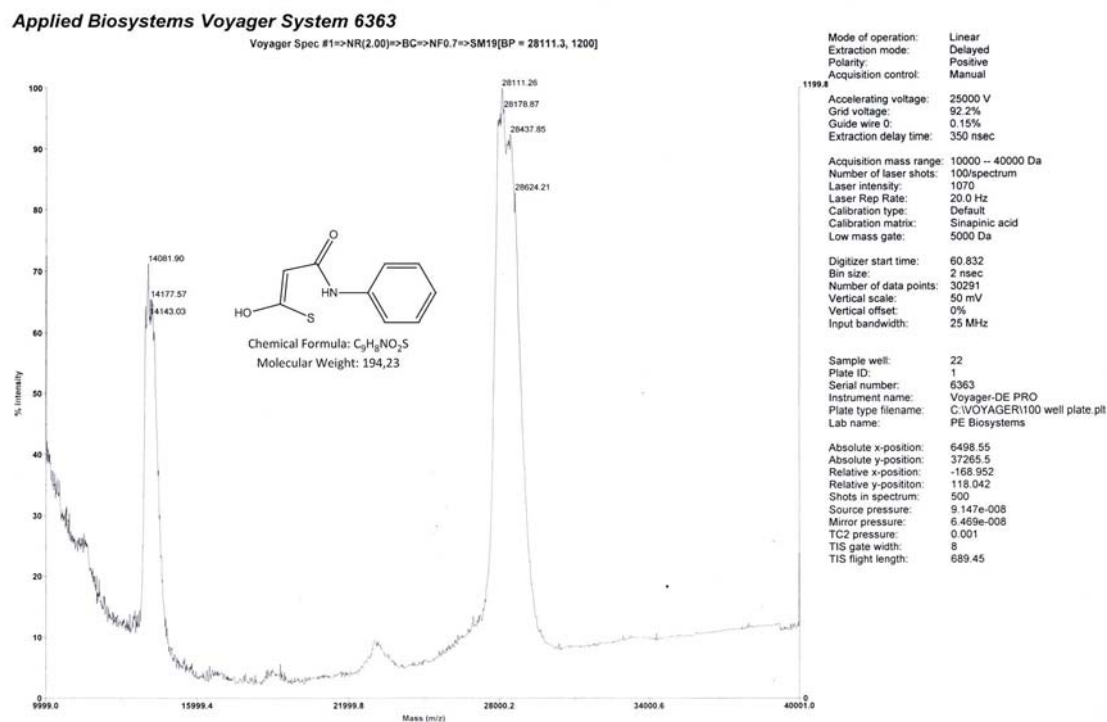
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Bin size: 2 nsec  
Number of data points: 30291  
Vertical scale: 50 mV  
Vertical offset: 0%  
Input bandwidth: 25 MHz

Sample well: 36  
Plate ID: 1  
Serial number: 6363  
Instrument name: Voyager-DE PRO  
Plate type filename: C:\VOYAGER\100 well plate.plt  
Lab name: PE Biosystems

Absolute x-position: 26179.4  
Absolute y-position: 32111.4  
Relative x-position: -808.102  
Relative y-position: 43.8993  
Shots in spectrum: 600  
Source pressure: 3.63e-007  
Mirror pressure: 1.112e-007  
TC2 pressure: 0.001  
TIS gate width: 8  
TIS flight length: 689.45

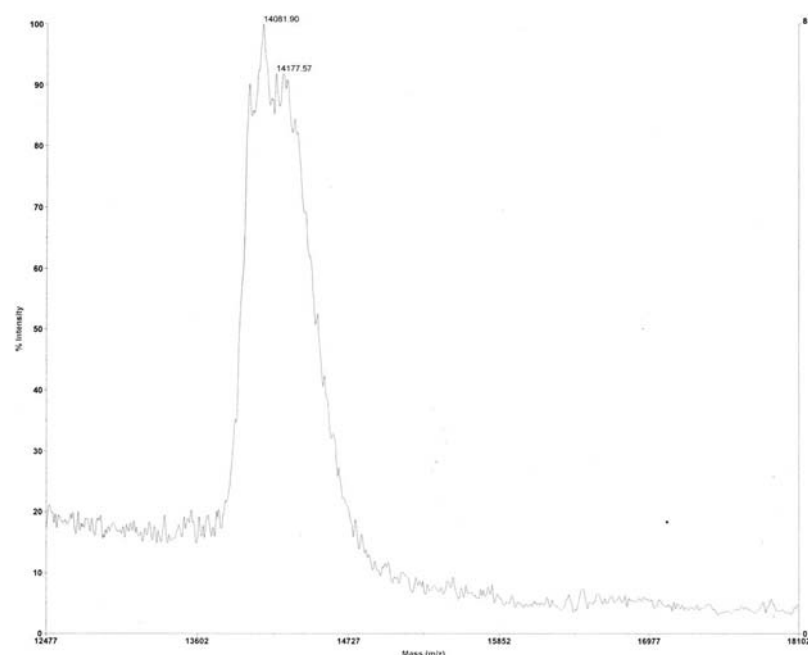


**Figure S9.** MALDI – TOF mass spectrum of Cathepsin B.



**Applied Biosystems Voyager System 6363**

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Mode of operation: Linear  
Extraction mode: Delayed  
Polarity: Positive  
Acquisition control: Manual

Accelerating voltage: 25000 V  
Grid voltage: 92.2%  
Guide wire 0: 0.15%  
Extraction delay time: 350 nsec

Acquisition mass range: 10000 – 40000 Da  
Number of laser shots: 100/spectrum  
Laser intensity: 1070  
Laser Rep Rate: 20.0 Hz  
Calibration type: Default  
Calibration matrix: Sinapinic acid  
Low mass gate: 5000 Da

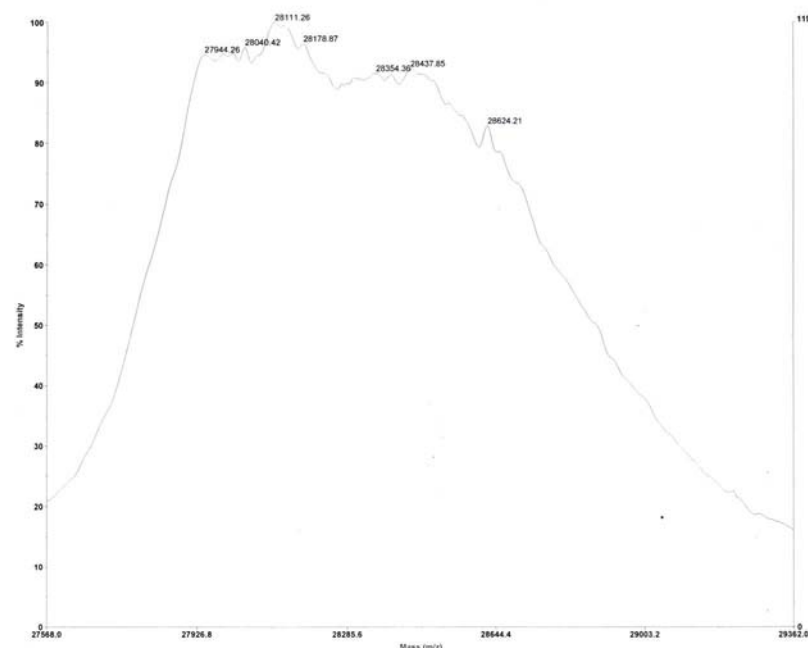
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Vertical scale: 50 mV  
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Sample well: 22  
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Serial number: 6363  
Instrument name: Voyager-DE PRO  
Plate type filename: C:\VOYAGER\100 well plate.plt  
Lab name: PE Biosystems

Absolute x-position: 6498.55  
Absolute y-position: 37265.5  
Relative x-position: -168.952  
Relative y-position: 118.042  
Shots in spectrum: 500  
Source pressure: 9.147e-008  
Mirror pressure: 6.469e-008  
TC2 pressure: 0.001  
TIS gate width: 8  
TIS flight length: 689.45

**Applied Biosystems Voyager System 6363**

<<Cath B +FD531\_0001>> Voyager Spec #1=>NR(2.00)=>BC=>NF0.7=>SM19[BP = 28111.3, 1200]



Mode of operation: Linear  
Extraction mode: Delayed  
Polarity: Positive  
Acquisition control: Manual

Accelerating voltage: 25000 V  
Grid voltage: 92.2%  
Guide wire 0: 0.15%  
Extraction delay time: 350 nsec

Acquisition mass range: 10000 – 40000 Da  
Number of laser shots: 100/spectrum  
Laser intensity: 1070  
Laser Rep Rate: 20.0 Hz  
Calibration type: Default  
Calibration matrix: Sinapinic acid  
Low mass gate: 5000 Da

Digitizer start time: 60.832  
Bin size: 2 nsec  
Number of data points: 30291  
Vertical scale: 50 mV  
Vertical offset: 0%  
Input bandwidth: 25 MHz

Sample well: 22  
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Serial number: 6363  
Instrument name: Voyager-DE PRO  
Plate type filename: C:\VOYAGER\100 well plate.plt  
Lab name: PE Biosystems

Absolute x-position: 6498.55  
Absolute y-position: 37265.5  
Relative x-position: -168.952  
Relative y-position: 118.042  
Shots in spectrum: 500  
Source pressure: 9.147e-008  
Mirror pressure: 6.469e-008  
TC2 pressure: 0.001  
TIS gate width: 8  
TIS flight length: 689.45

**Figure S10.** MALDI – TOF mass spectrum of Cathepsin B that was pre-incubated with inhibitor 5.

## References

1. E. V. Anslyn and D. A. Dougherty, *University Science Books*, 2006, 22.
2. F. J. Dekker, M. Ghizzoni, N. Van der Meer, R. Wisastra and H. J. Haisma, *Bioorg. Med. Chem.*, 2009, **17**, 460-466.
3. M. Ghizzoni, H. J. Haisma and F. J. Dekker, *Eur J Med Chem*, 2009, **44**, 4855-4861.