

## Supplemental Information

# Identification of the Molecular Targets of Disulfide Bond Disrupting Agents

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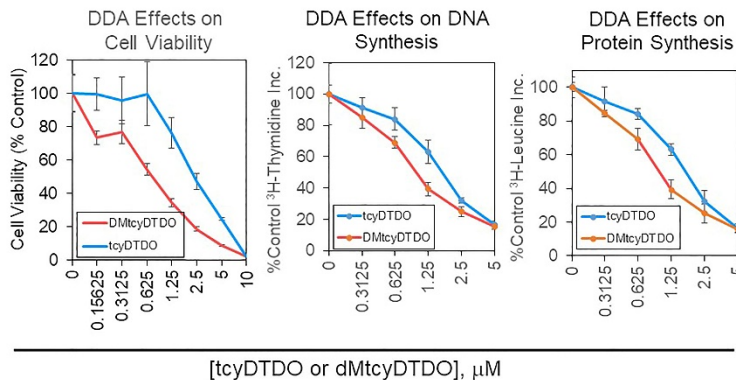
<sup>8</sup>Department of Pathology, Copenhagen University Hospital Herlev, DK-2730 Herlev, Denmark.

<sup>#</sup>Co-Contributing Corresponding Authors

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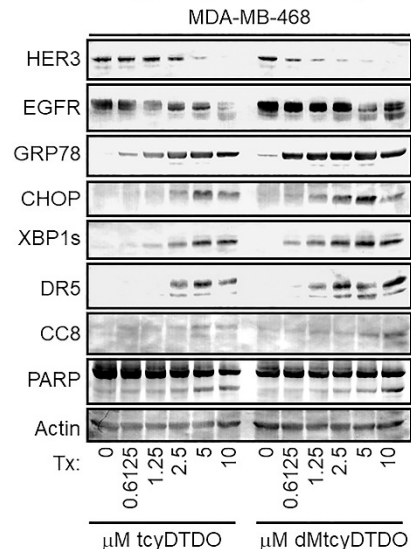
# S1A

DDA Effects on MDA-MB-468 Cells



# S1B

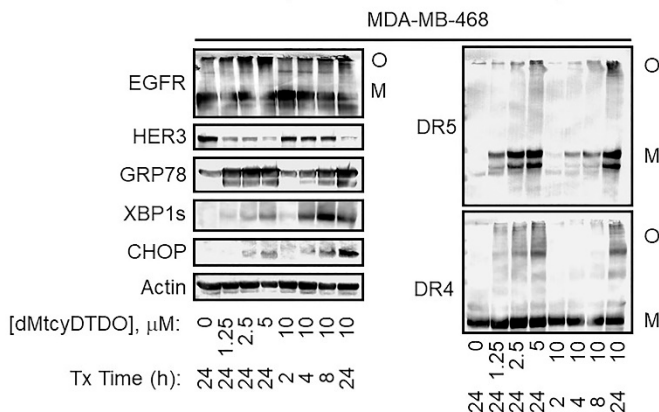
Reducing SDS-PAGE



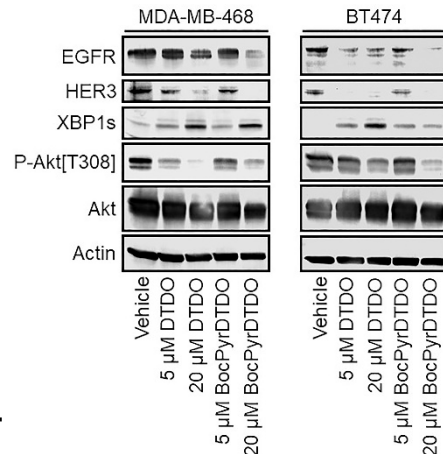
# S1C

Non-Reducing SDS-PAGE

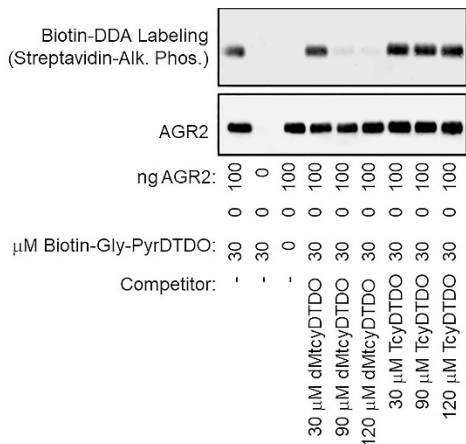
O: Oligomeric  
M: Monomeric



# S1D



# S1E



# S1F

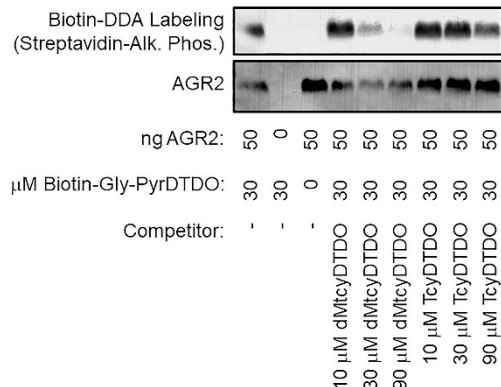


Fig. S1-Characterization of novel DDAs and an AGR2 DDA binding assay. S1A. MDA-MB-468 cells were treated for 24 h as indicated and assayed for viability, DNA synthesis, and protein synthesis in MTT assays, and tritiated thymidine and leucine incorporation assays, respectively. S1B. Reducing immunoblot analysis of MDA-MB-468 cells treated for 24 h as indicated. S1C. Non-reducing immunoblot analysis of MDA-MB-468 cells treated for 24 h as indicated. S1D. Immunoblot analysis of MDA-MB-468 and BT474 cells treated for 24 h as indicated. S1E. and S1F. AGR2 binding assays employing recombinant AGR2 and Biotin-GlyPyrDTDO under the indicated conditions followed by immunoblot analysis for AGR2 or blotting with Streptavidin-conjugated Alkaline Phosphatase.

Display Options: Total Spectrum Count    Req Mods: No Filter    Search: ERP

**Probability Legend:**

- over 95%
- 80% to 94%
- 50% to 79%
- 20% to 49%
- 0% to 19%

**Bio View:**  
214 Proteins in 197 Clusters  
With 213 Filtered Out

#	Visible?	Starred?	Accession Number	Molecular Weight	Protein Grouping Ambiguity	DDAT1	DDAT2
1	<input checked="" type="checkbox"/>	<input type="checkbox"/>	ERP44_HUMAN	47 kDa			2

Endoplasmic reticulum resident protein 44 O5=Homo sapiens OX=9606 GN=ERP44 PE=1 SV=1

## Unique Peptide Search: ERp44 (one peptide sequence; two peptides)



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Display Options: Total Unique Spectrum Count    Req Mods: No Filter    Search: PDI

Probability Legend:  
over 95%  
80% to 94%  
50% to 79%  
20% to 49%  
0% to 19%

Bio View:  
**214 Proteins in 197 Clusters**  
**With 212 Filtered Out**

#    Visible?    Starred?    Accession Number    Molecular Weight    Protein Grouping Ambiguity

1            H7B294\_HUMAN (+1)    53 kDa    3    DOAT1    DOAT2

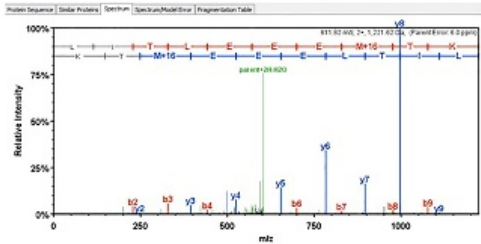
Protein disulfide-isomerase OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=2

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<input checked="" type="checkbox"/>	LVK	100%	49.7	30.6	36.1	2	Oxidation (+16)
<input checked="" type="checkbox"/>	LVK	100%	55.1	32.7	46.1	2	Oxidation (+16)
<input checked="" type="checkbox"/>	LVK	100%	68.1	32.5	46.0	2	Oxidation (+16)
<input checked="" type="checkbox"/>	LVK	100%	63.9	32.3	45.2	2	Oxidation (+16)
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<input checked="" type="checkbox"/>	LVK	100%	89.9	32.2	70.3	2	Oxidation (+16)
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Protein Sequence: M L R R A L L C L A V A A L V R A D A P E E E D H V L V L R K S N F A E A L A A H K Y L L V E F Y A P W C G H C K A L A P E Y A K A A G K L  
 K A E G S E I R L A K V D A T E E S D L A Q Q Y G V R G Y P T I K F F R N G D T A S P K E Y T G D V E S D S A K Q F L O A A E A I D D I P F  
 G I T S N S D V F S K Y Q L D K D G V L F K F F D E G R N N F E G S E V T K N L L D F I K H N Q L P L V I E F T Q T A P K I F G G E I K  
 I H I L L F L P K S V S Y D D K L S N F K T A A E S F R G K I L F I F I D S D H T D H G R I L E F F G L K E E D P A V R L I L E E E E  
 P K Y K P E S E E L T A E R I T E F C H R F L E G K I K P H L M S Q E L P E D W D H Q P K V L V L G K N F E D V A F D E K N V F E F Y A  
 P W C G H C K Q L A P I W D K L G E T Y K D H E I V I A K M D S T A N E V E A K K V H S F P T L K F P P A S A D R T V I D Y N G E R T L D  
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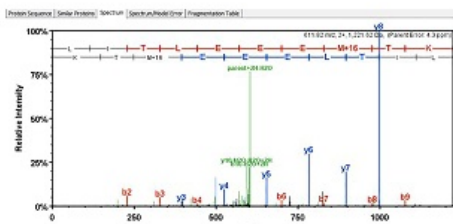
Protein Sequence	Similar Proteins	Spectrum	Spectrum/Model Error	Fragmentation Table						
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1	114.1	L	1,222.6	611.8	1,205.6	1,204.6	10			
2	227.2	I	1,109.5	555.3	1,092.5	1,091.5	9			
3	328.2	T	996.5	498.7	979.4	978.4	8			
4	441.3	L	895.4	448.2	878.4	877.4	7			
5	570.3	E	782.3	391.7	765.3	764.3	6			
6	699.4	350.2	681.4	E	653.3	636.3	5			
7	828.4	414.7	810.4	E	524.2	507.2	4			
8	975.5	488.2	957.5	H+16	395.2	378.2	3			
9	1,076.5	538.8	1,058.5	T	248.2	231.1	2			
10	1,222.6	611.8	1,205.6	1,204.6	K	147.1	130.1			1

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 K A E G S E I R L A K V D A T E E S D L A Q Q Y G V R G Y P T I K F F R N G D T A S P K E Y T G D V E S D S A K Q F L O A A E A I D D I P F  
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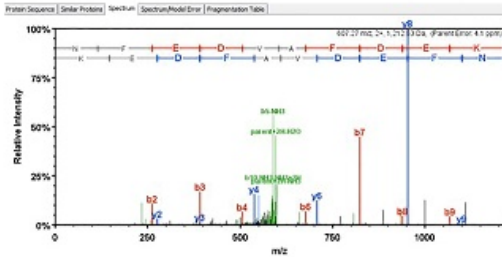
Protein disulfide-isomerase OS=Homo sapiens OX=960... All Biological Samples

Sequence Coverage	Protein	Accession	Category	Yield	Sequence	Prob	Mass...	Mass...	Mass...	MTT	Modifications
100%	Protein disulfide-isomerase OS=Homo sapiens OX=960...	P04114_HUMAN	Uncharacterized	100%	...K	100%	98.9	33.4	35.1	2	Oxidation (+16)
100%	Protein disulfide-isomerase OS=Homo sapiens OX=960...	P04114_HUMAN	Uncharacterized	100%	...K	100%	51.8	33.2	40.1	2	Oxidation (+16)
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100%	Protein disulfide-isomerase OS=Homo sapiens OX=960...	P04114_HUMAN	Uncharacterized	100%	...K	100%	63.1	32.7	46.3	2	Oxidation (+16)
100%	Protein disulfide-isomerase OS=Homo sapiens OX=960...	P04114_HUMAN	Uncharacterized	100%	...K	100%	63.9	32.3	45.3	2	Oxidation (+16)
100%	Protein disulfide-isomerase OS=Homo sapiens OX=960...	P04114_HUMAN	Uncharacterized	100%	...K	100%	42.1	33.3	42.0	2	Oxidation (+16)
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Protein Sequence: [Similar Proteins] [Spectrum] [Spectrum/Model Error] [Fragmentation Table]

**H7B2M\_HUMAN (100%), 52,560.8 Da**  
 Protein disulfide-isomerase OS=Homo sapiens OX=960 GN=PIH8 PE=1 SV=2  
 3 exclusive unique peptides, 3 exclusive unique spectra, 13 total spectra, 32464 amino acids (7% coverage)

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 KAEDSEIRLA KYDATEESDL AQQYGVRRGYP TIKFFRRNGDT ASPKEYTGDV ESDSAKQFLA AAEAIQDIPF  
 GITSNSDVFPS KYDLQDKDGV LFKKFDDEGRN NFEFGEVTKEN LLDPIKHNLD PLVIEFTBOT APKIFGGIEIL  
 THILLFLPKS VSDYDGLSN FKTAAESFKG KILFIIDSD HTDWRILEF FGLKKEICPA VRLITLLEEE  
**TKYKPESEEL TAERITFECH RFLGKIKPH LMSQELPEDW DKQPKVVLVG KRFEDVAFDE KKKLVVVEFYA**  
 PWCQGHCKQLA PIWDKLGSETY KDHENIVIAK **MDSTANEVEA VKVHSFPTLK FFPASADRTV IDYNGERTLD**  
 GPKKFLLESGG QDAGDDDDL EDLEEAEPD MEEDDQKAV KDEL



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1	115.1		98.0		N	1,213.5	607.3	1,196.5	1,195.5	10
2	262.1		245.1		F	1,099.5	550.3	1,082.5	1,081.5	9
3	391.2		374.1	373.2	E	852.4	476.7	935.4	934.4	8
4	506.2		489.2	488.2	D	823.4	412.2	806.4	805.4	7
5	605.3		588.2	587.2	V	708.4	354.7	691.3	690.3	6
6	676.3	338.7	659.3	658.3	A	609.3		592.3	591.3	5
7	823.4	412.2	806.3	805.4	F	538.3		521.2	520.2	4
8	938.4	469.7	921.4	920.4	D	391.2		374.2	373.2	3
9	1,067.4	534.2	1,050.4	1,049.4	E	276.2		259.1	258.1	2
10	1,213.5	607.3	1,196.5	1,195.5	K	147.1		130.1		1

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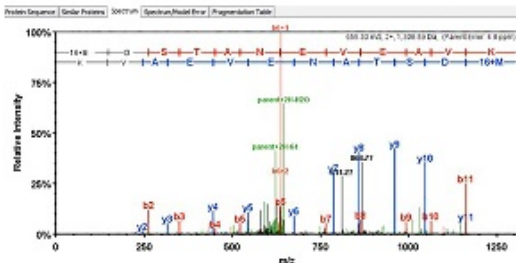
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 KAEDSEIRLA KYDATEESDL AQQYGVRRGYP TIKFFRRNGDT ASPKEYTGDV ESDSAKQFLA AAEAIQDIPF  
 GITSNSDVFPS KYDLQDKDGV LFKKFDDEGRN NFEFGEVTKEN LLDPIKHNLD PLVIEFTBOT APKIFGGIEIL  
 THILLFLPKS VSDYDGLSN FKTAAESFKG KILFIIDSD HTDWRILEF FGLKKEICPA VRLITLLEEE  
**TKYKPESEEL TAERITFECH RFLGKIKPH LMSQELPEDW DKQPKVVLVG KRFEDVAFDE KKKLVVVEFYA**  
 PWCQGHCKQLA PIWDKLGSETY KDHENIVIAK **MDSTANEVEA VKVHSFPTLK FFPASADRTV IDYNGERTLD**  
 GPKKFLLESGG QDAGDDDDL EDLEEAEPD MEEDDQKAV KDEL



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2	263.1		245.1		D	1,162.6	581.8	1,145.5	1,144.5	11
3	350.1		332.1		S	1,047.5	524.3	1,030.5	1,029.5	10
4	451.1		433.1		T	960.5	480.8	943.5	942.5	9
5	522.2		504.2		A	858.5	430.2	842.4	841.4	8
6	636.2	318.6	619.2	618.2	N	788.4	394.7	771.4	770.4	7
7	765.3	383.1	748.2	747.3	E	674.4	337.7	657.3	656.4	6
8	864.3	432.7	847.3	846.3	V	545.3		528.3	527.3	5
9	993.4	497.2	976.4	975.4	E	446.3		429.2	428.3	4
10	1,066.4	532.7	1,047.4	1,046.4	A	317.2		300.2		3
11	1,163.5	582.2	1,146.5	1,145.5	V	246.2		229.2		2
12	1,309.6	655.3	1,292.6	1,291.6	K	147.1		130.1		1





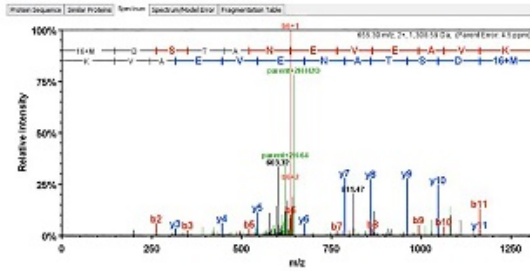
# Unique Peptide Search: PDIs (three peptide sequences; 13 peptides)

Protein: *Disulfide-isomerase OX-Homo sapiens OX-966...* (All Biological Samples)

Sequence Coverage	Protein	Accession	Category	Valid	Sequence	Prob	Mass	Mod.	Mod.	Mod.	HTT	Modifications
100%	<i>Disulfide-isomerase OX-Homo sapiens OX-966...</i>	P02411 (HUMAN)	Uncharacterized	✓	1.6 (K)LTLEEE(TYK)	100%	39.5	33.4	39.2	2	Oxidation (+16)	
100%	<i>Disulfide-isomerase OX-Homo sapiens OX-966...</i>	P02411 (HUMAN)	Uncharacterized	✓	1.6 (K)LTLEEE(TYK)	100%	55.5	33.2	41.1	2	Oxidation (+16)	
100%	<i>Disulfide-isomerase OX-Homo sapiens OX-966...</i>	P02411 (HUMAN)	Uncharacterized	✓	1.6 (K)MFAEALAA	100%	49.7	35.4	38.1	2	Oxidation (+16)	
100%	<i>Disulfide-isomerase OX-Homo sapiens OX-966...</i>	P02411 (HUMAN)	Uncharacterized	✓	1.6 (K)MFAEALAA	100%	59.8	35.5	46.6	2	Oxidation (+16)	
100%	<i>Disulfide-isomerase OX-Homo sapiens OX-966...</i>	P02411 (HUMAN)	Uncharacterized	✓	1.6 (K)MFAEALAA	100%	69.9	35.3	45.3	2	Oxidation (+16)	
100%	<i>Disulfide-isomerase OX-Homo sapiens OX-966...</i>	P02411 (HUMAN)	Uncharacterized	✓	1.6 (K)MFAEALAA	100%	79.7	35.5	46.6	2	Oxidation (+16)	
100%	<i>Disulfide-isomerase OX-Homo sapiens OX-966...</i>	P02411 (HUMAN)	Uncharacterized	✓	1.6 (K)MFAEALAA	100%	89.3	35.1	46.8	2	Oxidation (+16)	
100%	<i>Disulfide-isomerase OX-Homo sapiens OX-966...</i>	P02411 (HUMAN)	Uncharacterized	✓	1.6 (K)MFAEALAA	100%	99.2	35.5	38.6	2	Oxidation (+16)	
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100%	<i>Disulfide-isomerase OX-Homo sapiens OX-966...</i>	P02411 (HUMAN)	Uncharacterized	✓	1.6 (K)MFAEALAA	100%	128.8	35.4	31.4	2	Oxidation (+16)	
100%	<i>Disulfide-isomerase OX-Homo sapiens OX-966...</i>	P02411 (HUMAN)	Uncharacterized	✓	1.6 (K)MFAEALAA	100%	138.4	35.3	31.2	2	Oxidation (+16)	

Protein Sequence: *Disulfide-isomerase OX-Homo sapiens OX-966...* (100%), 82,593.8 Da  
 Protein disulfide-isomerase OX-Homo sapiens OX-966 G0M-P4H8 PD-1 SV-2  
 3 exclusive unique peptides, 3 exclusive unique spectra, 13 total spectra, 32,464 amino acids (7% coverage)

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 K A R G S E I R L A K V D A T E E S D L A G Q Y G V R G V P T I K F F R N G D T A S P K E Y T G D V E S S A R Q F L Q A A E A I D D I P F  
 G I T S N S D V F S K Y Q L D K G D V V L F N R P D E G R N L I P G E V T K E M L L D F I K W N Q L P L V Y E P F T Q T P N I F G C E I L K  
 T H I L L F L P K S V S D Y G K L S N F K T A A E S F R G K I L F I F I D S D H T D N R I L E F P G L K K E E C P A V R L I T L E E E K  
**Y K Y K P S E E L T A E R I T E F C H R F L E G K I K P H L S O E L P E D W D K O P V K V L V G K H F E D V A F D E K K N Y V F E F Y A**  
 P W G H C K G L A P I W A G L O S T Y K D H E N I V I A K **L D S T A N E V E A V K V H S F P T L K F P P A S A D R T V I D Y N G E R T L D**  
 S F K K F L E S G Q D G A G O D D D L E D L E A E E P D M E E D D Q K A V K D E L



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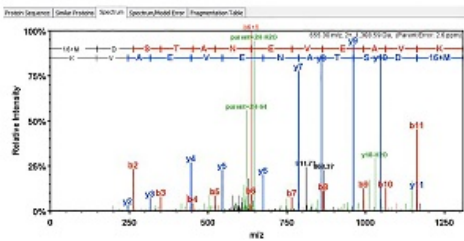
# Unique Peptide Search: PDIs (three peptide sequences; 13 peptides)

Protein: *Disulfide-isomerase OX-Homo sapiens OX-966...* (All Biological Samples)

Sequence Coverage	Protein	Accession	Category	Valid	Sequence	Prob	Mass	Mod.	Mod.	Mod.	HTT	Modifications
100%	<i>Disulfide-isomerase OX-Homo sapiens OX-966...</i>	P02411 (HUMAN)	Uncharacterized	✓	1.6 (K)LTLEEE(TYK)	100%	39.5	33.4	39.2	2	Oxidation (+16)	
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100%	<i>Disulfide-isomerase OX-Homo sapiens OX-966...</i>	P02411 (HUMAN)	Uncharacterized	✓	1.6 (K)MFAEALAA	100%	89.3	35.1	46.8	2	Oxidation (+16)	
100%	<i>Disulfide-isomerase OX-Homo sapiens OX-966...</i>	P02411 (HUMAN)	Uncharacterized	✓	1.6 (K)MFAEALAA	100%	99.2	35.5	38.6	2	Oxidation (+16)	
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 K A R G S E I R L A K V D A T E E S D L A G Q Y G V R G V P T I K F F R N G D T A S P K E Y T G D V E S S A R Q F L Q A A E A I D D I P F  
 G I T S N S D V F S K Y Q L D K G D V V L F N R P D E G R N L I P G E V T K E M L L D F I K W N Q L P L V Y E P F T Q T P N I F G C E I L K  
 T H I L L F L P K S V S D Y G K L S N F K T A A E S F R G K I L F I F I D S D H T D N R I L E F P G L K K E E C P A V R L I T L E E E K  
**Y K Y K P S E E L T A E R I T E F C H R F L E G K I K P H L S O E L P E D W D K O P V K V L V G K H F E D V A F D E K K N Y V F E F Y A**  
 P W G H C K G L A P I W A G L O S T Y K D H E N I V I A K **L D S T A N E V E A V K V H S F P T L K F P P A S A D R T V I D Y N G E R T L D**  
 S F K K F L E S G Q D G A G O D D D L E D L E A E E P D M E E D D Q K A V K D E L



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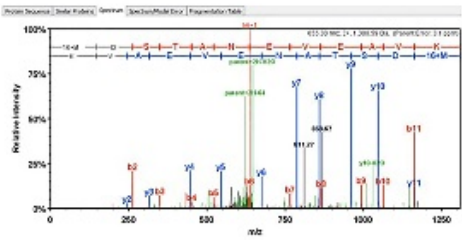
Unique Peptide Search: PDIs (three peptide sequences; 13 peptides)

Protein	Sequence	Prob	Mass <sub>1</sub>	Mass <sub>2</sub>	Mod	HTT	Modifications
1.6	QYVLEK	100%	314	314	2		Oxidation (+16)
1.6	QYVLEK	100%	315	312	40	2	Oxidation (+16)
1.6	QYVLEK	100%	417	304	36	2	Oxidation (+16)
1.6	QYVLEK	100%	315	317	46	2	Oxidation (+16)
1.6	QYVLEK	100%	315	315	48	2	Oxidation (+16)
1.6	QYVLEK	100%	315	313	45	2	Oxidation (+16)
1.6	QYVLEK	100%	315	312	41	2	Oxidation (+16)
1.6	QYVLEK	100%	307	316	33	2	Oxidation (+16)
1.6	QYVLEK	100%	312	313	34	2	Oxidation (+16)
1.6	QYVLEK	100%	313	312	30	2	Oxidation (+16)
1.6	QYVLEK	100%	313	313	31	2	Oxidation (+16)
1.6	QYVLEK	100%	313	314	31	2	Oxidation (+16)
1.6	QYVLEK	100%	414	313	31	2	Oxidation (+16)

Protein Sequence: Similar Proteins | Spectrum | Spectrum/Model Error | Fragmentation Table

**HT0294\_HUMAN (100%), 52,503.0 Da**  
**Protein disulfide-isomerase OS=Homo sapiens OX=9938 OMP=AHB PE=1 SV=2**  
**3 exclusive unique peptides, 3 exclusive unique spectra, 13 total spectra, 23444 amino acids (7% coverage)**

M L R R A L L C L A V A A L V R D A P E E E D H V L V L R K S F A E A L A A H Y L L V E F Y A P W G G H K K A L A P E Y A K A A G K L  
 K A E G S E I R L A K Y D A T E E S D L A D Q Y G V R D Y P T I K F P R N G D T A S P K E Y T G L V E S D A S A R D F L Q A A E A I D D I P P  
 G I T S N S D V F S K Y Q L Q K D G V V L F K F D E G R N N F E G E V T K E N L L D F I K H N Q L P L V I E F T E Q T A P K I F G G E I L L  
**T H I L L F L P K S V S D T Q D L S N F K T A A E S P F K D K I L F I F I Q S D H T D G R R I L E F F G L K E E S P C A V R L I F L K E E D E**  
**T K Y K P E S E L T A E R I T E F C H R F L E G K K P H L M S G E L P E D W D K G P V K V L F D E K N F E D Y A F D E K K R V E F Y E A**  
 P W C G H K K G L A P I W D K L G S T Y K H R E N I V I A K **L D S T A N E V C A Y K V H S P P T L K F P P S A S A D R T V I D Y N G E R T L D**  
 G F K K F L E S S G Q D G A G D D D L E D L E A E E P D M E E D D D G K A V K D E L



Protein Sequence	Similar Proteins	Spectrum	Spectrum/Model Error	Fragmentation Table						
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3	350.1			332.1	S	1,047.5	524.3	1,030.5	1,029.5	10
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5	522.2			504.2	A	859.5	430.2	842.4	841.4	8
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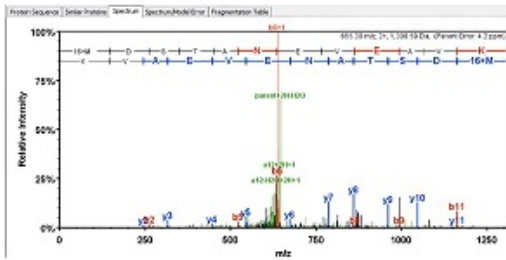
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1.6	QYVLEK	100%	315	313	45	2	Oxidation (+16)
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 G I T S N S D V F S K Y Q L Q K D G V V L F K F D E G R N N F E G E V T K E N L L D F I K H N Q L P L V I E F T E Q T A P K I F G G E I L L  
**T H I L L F L P K S V S D T Q D L S N F K T A A E S P F K D K I L F I F I Q S D H T D G R R I L E F F G L K E E S P C A V R L I F L K E E D E**  
**T K Y K P E S E L T A E R I T E F C H R F L E G K K P H L M S G E L P E D W D K G P V K V L F D E K N F E D Y A F D E K K R V E F Y E A**  
 P W C G H K K G L A P I W D K L G S T Y K H R E N I V I A K **L D S T A N E V C A Y K V H S P P T L K F P P S A S A D R T V I D Y N G E R T L D**  
 G F K K F L E S S G Q D G A G D D D L E D L E A E E P D M E E D D D G K A V K D E L



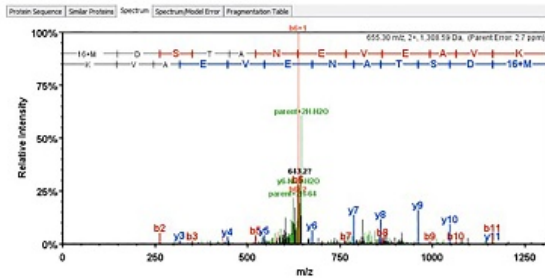
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Valid	Sequence	Prob	Misc...	Misc...	Misc...	NTT	Modifications
✓	1.0 [K]LLEEDN(EY)	100%	59.5	33.4	35.2	2	Oxidation (+16)
✓	1.0 [K]LLEEDN(EY)	100%	51.6	33.2	40.1	2	Oxidation (+16)
✓	1.0 [K]PPEHDAPEK(EY)	100%	47.7	30.6	36.1	2	
✓	1.0 [K]PPEHDAPEK(EY)	100%	65.1	32.7	46.1	2	Oxidation (+16)
✓	1.0 [K]PPEHDAPEK(EY)	100%	68.1	32.5	46.0	2	Oxidation (+16)
✓	1.0 [K]PPEHDAPEK(EY)	100%	63.9	32.3	45.3	2	Oxidation (+16)
✓	1.0 [K]PPEHDAPEK(EY)	100%	62.1	32.5	42.0	2	Oxidation (+16)
✓	1.0 [K]PPEHDAPEK(EY)	100%	76.7	32.6	53.0	2	Oxidation (+16)
✓	1.0 [K]PPEHDAPEK(EY)	100%	51.2	32.5	36.0	2	Oxidation (+16)
✓	1.0 [K]PPEHDAPEK(EY)	100%	83.8	32.2	58.7	2	Oxidation (+16)
✓	1.0 [K]PPEHDAPEK(EY)	100%	89.9	32.2	70.3	2	Oxidation (+16)
✓	1.0 [K]PPEHDAPEK(EY)	100%	32.8	32.4	32.4	2	Oxidation (+16)
✓	1.0 [K]PPEHDAPEK(EY)	100%	91.4	32.3	31.2	2	Oxidation (+16)

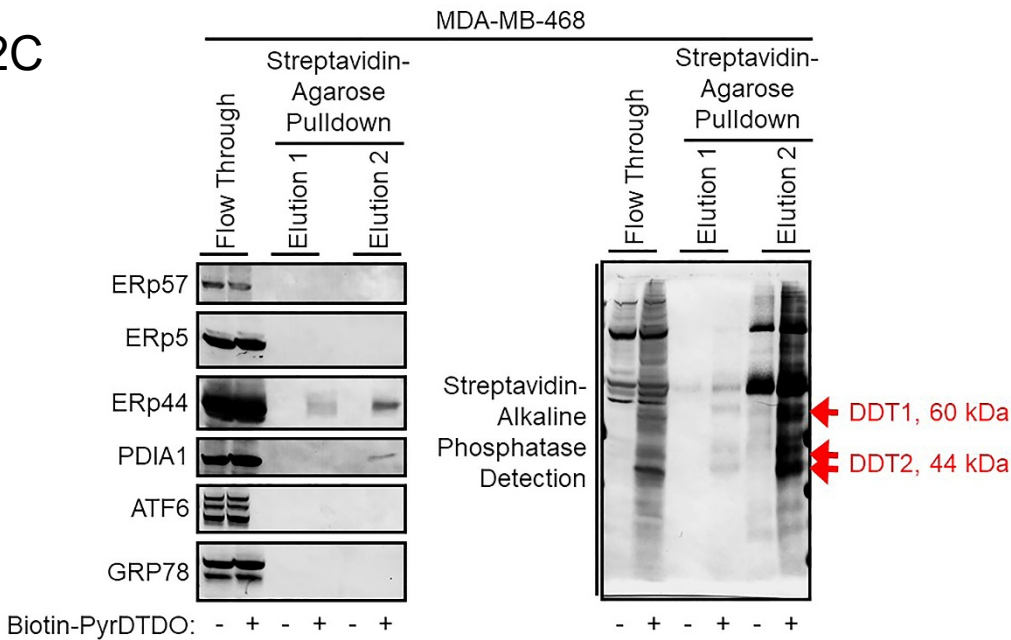
  

Protein Sequence	Similar Proteins	Spectrum	Spectrum/Model Error	Fragmentation Table
<b>H7B294_HUMAN (100%), 62,503.8 Da</b>				
<b>Protein disulfide-isomerase OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=2</b>				
<b>3 exclusive unique peptides, 3 exclusive unique spectra, 13 total spectra, 32/464 amino acids (7% coverage)</b>				
M L R R A L L C L A V A A L V R A D A P E E E D H V L V L R K S H F A E A L A A H K Y L L V E F Y A P W C G H C K A L A P E Y A K A A G K L K A E G S E I R L A K V D A T E E S D L A Q Q Y G V R G Y P T I K F F R N G D T A S P K E Y T G D V E S D S A K Q F L O A A E A I D D I P F G I T S N S D V F S K Y Q L D K D G V V L F K K F D E G R N N F E G E V T K E N L L D F I K H N Q L P L V I E F T E Q T A P K I F G G E I K T H I L L F L P K S V S D Y D G K L S N F K T A E S F K G K I L F I F I D S D H T D N Q R I L E F F G L K E E C P A V R L I T L E E E K <b>Y K Y K P E S E E L T A E R I T E F C N R F L E G K I K P H L M S Q E L P E D W D X Q P K V L V G K N F E D V A F D E K K N V F V E F F A A</b> P W G G H C K Q L A P I W D K L G E T Y K D H E N I V I A K <b>L D S T A N E V E A V X V H S P P T L K F F P A S A D R T V I D Y N G E R T L D</b> G F K K F L E S G G Q D G A G D D D D L E D L E E A E E P D M E E D D D Q K A V K D E L				



Protein Sequence	Similar Proteins	Spectrum	Spectrum/Model Error	Fragmentation Table						
B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.0				M+16	1,309.6	655.3	1,292.6	1,291.6	12
2	263.1			245.1	D	1,162.6	581.8	1,145.5	1,144.5	11
3	350.1			332.1	S	1,047.5	524.3	1,030.5	1,029.5	10
4	451.1			433.1	T	960.5	480.8	943.5	942.5	9
5	522.2			504.2	A	859.5	430.2	842.4	841.4	8
6	636.2	318.6	619.2	618.2	N	788.4	394.7	771.4	770.4	7
7	765.3	383.1	748.2	747.3	E	674.4	337.7	657.3	656.4	6
8	864.3	432.7	847.3	846.3	V	545.3		528.3	527.3	5
9	993.4	497.2	976.4	975.4	E	446.3		429.2	428.3	4
10	1,064.4	532.7	1,047.4	1,046.4	A	317.2		300.2		3
11	1,163.5	582.2	1,146.5	1,145.5	V	246.2		229.2		2
12	1,309.6	655.3	1,292.6	1,291.6	K	147.1		130.1		1

S2C



S2D

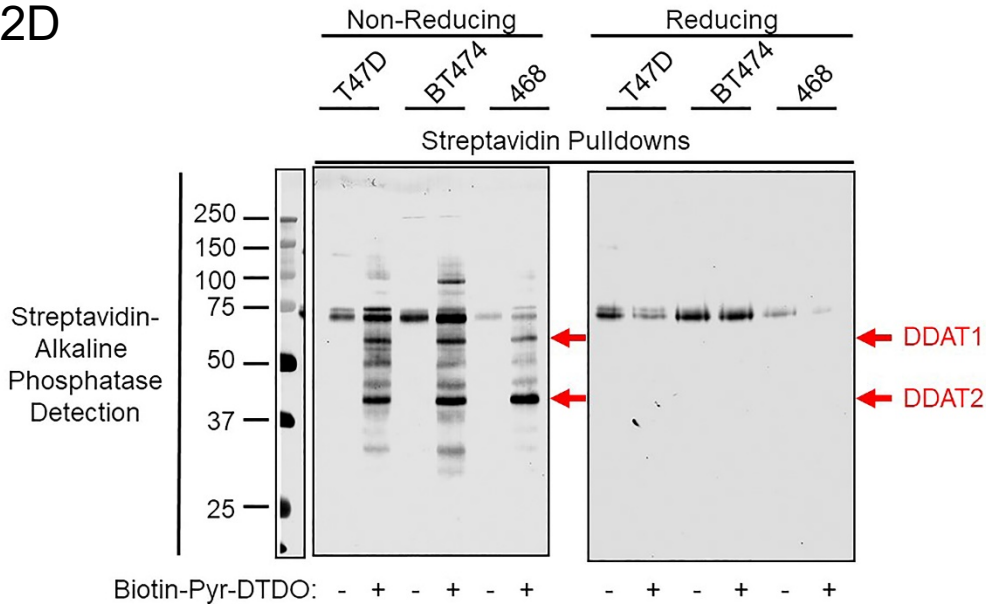
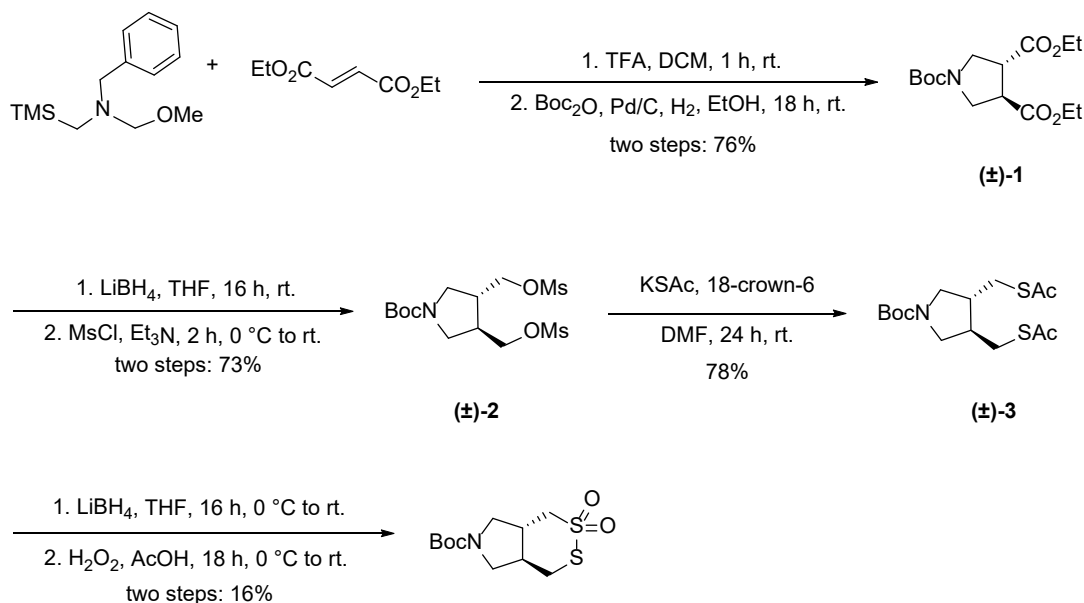


Fig. S2-Confirmation of ERp44 and PDIA1 as DDA targets. S2A. Peptide coverage of ERp44, and S2B. Peptide coverage of PDIA1 identified in Biotin-PyrDTDO/Streptavidin-Agarose pulldowns from MDA-MB-468 cells by tandem mass spectrometry. S2C. Streptavidin-Agarose pulldowns of Biotin-PyrDTDO treated cells in which the flow through, elution one (250  $\mu$ M dMtcyDTDO + 100  $\mu$ M 2-Mercaptoethanol), and elution 2 (2X SDS-PAGE Laemmli sample buffer + 2 mM Biotin) were analyzed by immunoblot and Streptavidin-Alkaline Phosphatase detection. S2D. Streptavidin-Agarose pulldowns of Biotin-PyrDTDO treated cells performed in the presence of 100 mM NEM. Half of each sample was brought to 1 M 2-mercaptoethanol and boiled for 20 minutes to generate reduction samples. These non-reducing (left panel) or reducing samples (right panel) were analyzed by blotting with Streptavidin-Alkaline Phosphatase. Molecular weight markers are indicated in kiloDaltons.

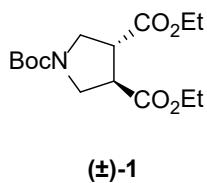
## General Methods

Reagents and solvents were purchased from commercial sources and used without further purification unless otherwise specified. Anhydrous solvents were obtained using a commercial solvent drying system (using activated alumina for THF, diethyl ether, dichloromethane; molecular sieves for DMF) and transferred via syringe to flame-dried glassware that had been cooled under an argon atmosphere.  $^1\text{H}$  and  $^{13}\text{C}$  NMR spectra were recorded using commercially-obtained deuterated solvents on Bruker-600 ( $^1\text{H}$  at 600 MHz;  $^{13}\text{C}$  at 151 MHz) and Varian Inova-500 ( $^1\text{H}$  at 500 MHz;  $^{13}\text{C}$  at 125 MHz) spectrometers. Chemical shifts ( $\delta$ ) are given in parts per million (ppm) relative to TMS and referenced to residual protonated solvent ( $\text{CDCl}_3$ :  $\delta_{\text{H}}$  7.26 ppm,  $\delta_{\text{C}}$  77.16 ppm;  $\text{CD}_3\text{OD}$ :  $\delta_{\text{H}}$  4.87 ppm,  $\delta_{\text{C}}$  49.00 ppm;  $\text{DMSO-}d_6$ :  $\delta_{\text{H}}$  2.50 ppm,  $\delta_{\text{C}}$  39.52 ppm;  $\text{D}_2\text{O}$ :  $\delta_{\text{H}}$  4.79 ppm). Coupling constants ( $J$ ) are reported in Hz. Spin multiplicities are presented by the following symbols: s (singlet), bs (broad singlet), d (doublet), t (triplet), q (quartet), p (pentet), and m (multiplet). Electrospray ionization (ESI) high-resolution mass spectra (HRMS) were recorded on an ESI-TOF instrument, operating in positive mode as stated, with methanol as the carrier solvent otherwise as mentioned.

### Synthesis of ( $\pm$ )-BocPyrDTDO:



### 1-(*tert*-Butyl)-3,4-diethyl-(3*S*,4*S*)- and (3*R*,4*R*)-pyrrolidine-1,3,4-tricarboxylate, ( $\pm$ )-1



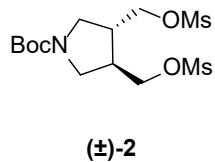
Intermediate ( $\pm$ )-1 was synthesized following a procedure described in a patent.<sup>1a</sup> To a stirred solution of diethyl fumarate (3.8 mL, 23 mmol) in DCM (50 mL) at 0 °C was added *N*-benzyl-1-methoxy-*N*-((trimethylsilyl)methyl)methanamine (5.4 mL, 21 mmol) followed by dropwise addition of a solution of TFA in DCM (0.1 mL of TFA in 1 mL of DCM) over 10 min. After completion of addition, the cold bath was removed, and the reaction mixture was stirred at rt for 1 h. The reaction mixture was diluted with DCM (20 mL), washed with a saturated solution of sodium bicarbonate (20 mL), and the organic layer was dried over

$\text{Na}_2\text{SO}_4$  and concentrated under reduced pressure. The residue was dissolved in ethyl acetate (25 mL) and to this was added  $\text{Boc}_2\text{O}$  (8.00 g, 36.6 mmol) followed by 10% palladium on carbon (1 g, wet). The resulting reaction mixture was subjected to catalytic hydrogenation using hydrogen gas for 18 h with stirring. The catalyst was filtered through a pad of celite, and the filtrate was concentrated. The residue was purified by flash silica gel column chromatography (0–25% EtOAc/hexanes) to provide the Boc-protected diester ( $\pm$ )-1 (5.1 g, 16 mmol, 76% yield) as a pale-yellow oil. The  $^1\text{H}$  NMR data matches the literature.<sup>1</sup>

**<sup>1</sup>H NMR** (CDCl<sub>3</sub>, 500 MHz): δ 4.16 (q, *J* = 7.1 Hz, 4H), 3.78–3.69 (m, 2H), 3.57–3.44 (m, 2H), 3.42–3.29 (m, 2H), 1.45 (s, 9H), 1.26 (t, *J* = 7.1 Hz, 6H).

**<sup>13</sup>C NMR** (CDCl<sub>3</sub>, 125 MHz): δ 171.81, 154.02, 80.02, 61.44, 48.12, 48.02, 46.12, 45.39, 28.54, 14.23.

***tert*-Butyl (3*S*,4*S*)- and (3*R*,4*R*)-3,4-bis(((methylsulfonyl)oxy)methyl)pyrrolidine-1-carboxylate, (±)-2**

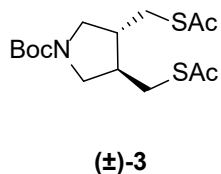


To an ice-cooled solution of the diester (±)-1 (5.0 g, 16 mmol) in anhydrous THF (135 mL) was added dropwise a solution of LiBH<sub>4</sub> in THF (16 mL of a 2.0 M LiBH<sub>4</sub> solution in THF diluted with an additional 20 mL of anhydrous THF). The reaction mixture was stirred overnight at rt and quenched with an aqueous 2 M NaOH solution. Ether was added, the layers were separated, and the aqueous phase was back extracted twice with ether. The combined organic extracts were dried over Na<sub>2</sub>SO<sub>4</sub>, filtered, and concentrated to give the diol which was used without further purification. To a stirred solution of the diol in DCM (110 mL) cooled to 0 °C was added triethylamine (11 mL, 80 mmol) followed by methanesulfonyl chloride (3.1 mL, 40 mmol). The reaction mixture was stirred at 0 °C for 15 min, then at rt for 1.5 h. The reaction mixture was poured into water (76 mL) and the phases were separated. The aqueous phase was extracted with DCM (2 × 76 mL). The combined organics were dried (MgSO<sub>4</sub>), filtered, and concentrated. The residue was purified by flash chromatography (0–100% EtOAc/DCM) to afford the desired dimesylate (±)-2 (4.5 g, 12 mmol, 73% yield) as a white solid.<sup>2</sup>

**<sup>1</sup>H NMR** (CDCl<sub>3</sub>, 500 MHz): δ 4.25 (m, 4H), 3.65 (m, 2H), 3.24 (m, 2H), 3.05 (s, 6H), 2.53 (m, 2H), 1.46 (s, 9H).

**<sup>13</sup>C NMR** (CDCl<sub>3</sub>, 125 MHz): δ 154.24, 80.23, 68.86, 47.95, 47.46, 40.52, 39.42, 37.70, 28.58.

***tert*-Butyl-(3*S*,4*S*)- and (3*R*,4*R*)-3,4-bis((acetylthio)methyl)pyrrolidine-1-carboxylate, (±)-3**



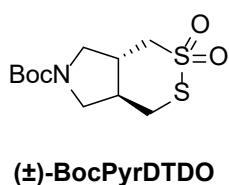
A mixture of the dimesylate (±)-2 (7.8 g, 20 mmol), KSAc (4.6 g, 40 mmol), and 18-crown-6 (1.3 g, 5.0 mmol) in anhydrous DMF (392 mL) was stirred for 24 h at rt. After completion of the reaction, water (392 mL) was added and the mixture was extracted with EtOAc (3 × 392 mL). The combined organic phases were washed with water (392 mL) and brine (392 mL), dried (Na<sub>2</sub>SO<sub>4</sub>), concentrated, and purified by column chromatography (0–10% DCM/EtOAc) to afford the dithioacetate (±)-3 (5.4 g, 16 mmol, 78% yield) as a colorless oil.

**<sup>1</sup>H NMR** (CDCl<sub>3</sub>, 500 MHz): δ 3.69–3.50 (m, 2H), 3.20–3.09 (m, 2H), 3.09–2.93 (m, 2H), 2.85 (dd, *J* = 13.7, 7.3 Hz, 2H), 2.34 (s, 6H), 2.22–2.05 (m, 2H), 1.44 (s, 9H).

**<sup>13</sup>C NMR** (CDCl<sub>3</sub>, 125 MHz): δ 195.26, 154.37, 79.63, 50.64, 50.29, 43.13, 42.40, 30.74, 30.65, 28.60.

**HRMS** (ESI-TOF): Calculated for [C<sub>15</sub>H<sub>25</sub>NO<sub>4</sub>S<sub>2</sub> + Na]<sup>+</sup>: 370.1117; found: 370.1104.

***tert*-Butyl-(4*aS*,7*aS*)- and (4*aR*,7*aR*)-tetrahydro-1*H*-[1,2]dithiino[4,5-*c*]pyrrole-6(4*H*)-carboxylate 2,2-dioxide, (±)-BocPyrDTDO**



To an ice-cooled solution of the dithioacetate (±)-3 (5.42 g, 15.6 mmol) in anhydrous THF (132 mL) was added dropwise a solution of LiBH<sub>4</sub> in THF (7.8 mL of 4.0 M LiBH<sub>4</sub> in THF diluted with additional 27 mL of anhydrous THF). The reaction mixture was stirred overnight at rt and quenched with an aqueous 2 M NaOH solution. Ether (25 mL) was added, the layers were separated, and the aqueous phase was back extracted with ether (2 × 25 mL). The combined organic extracts were dried over Na<sub>2</sub>SO<sub>4</sub>, filtered, and

concentrated to give the crude dithiol (3.81 g, 14.5 mmol, 93% yield), which was used without further purification for the next step. A solution of the crude dithiol (1.91 g, 7.23 mmol) in AcOH (9.0 mL) was cooled in an ice bath and a solution of H<sub>2</sub>O<sub>2</sub> in water/AcOH (2.59 mL of 30% H<sub>2</sub>O<sub>2</sub> in water diluted with 3.0 mL of AcOH) was added slowly such that the reaction temperature did not rise above 35 °C. After stirring for 18 h, the solvent was removed under vacuum, and the residue was diluted with water (15 mL), neutralized with NaHCO<sub>3</sub>, and extracted with EtOAc (3 × 50 mL). The organic extract was dried with Na<sub>2</sub>SO<sub>4</sub>, filtered, and concentrated under vacuum. The crude material was purified by column chromatography (0–100% EtOAc/DCM) to afford the desired (**±**)-**BocPyrDTDO** (0.66 g, 2.25 mmol, 16% yield).

**<sup>1</sup>H NMR** (CDCl<sub>3</sub>, 500 MHz): δ 3.75 (m, 1H), 3.67 (m, 1H), 3.52 (m, 1H), 3.41 (t, *J* = 12.6 Hz, 1H), 3.33 (t, *J* = 12.6, 1H), 3.14 (m, 1H), 3.07 (t, *J* = 10.8 Hz, 1H), 3.01 (t, *J* = 10.8 Hz, 1H), 2.8–2.67 (m, 1H), 2.40–2.28 (m, 1H), 1.45 (s, 9H).

**<sup>13</sup>C NMR** (CDCl<sub>3</sub>, 125 MHz): δ 154.09, 80.27, 62.62, 62.50, 50.16, 49.76, 49.63, 49.19, 43.14, 43.01, 42.44, 42.36, 35.43, 35.30, 28.55.

**HRMS** (ESI-TOF): Calculated for [C<sub>11</sub>H<sub>19</sub>NO<sub>4</sub>S<sub>2</sub> + Na]<sup>+</sup>: 316.0648; found: 316.0646.

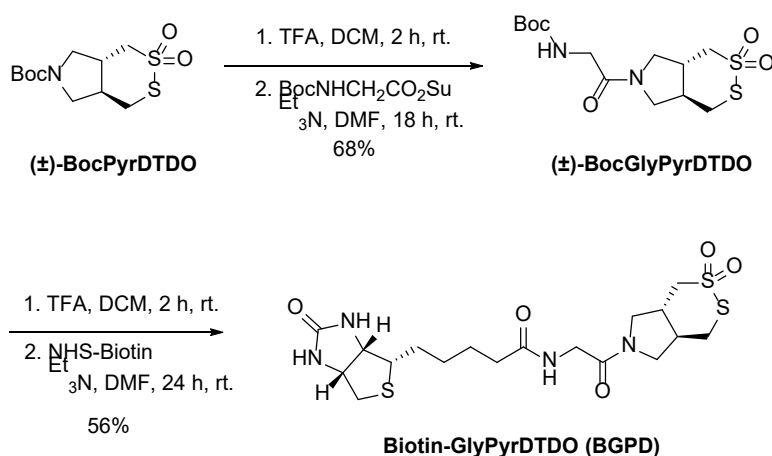
Slow *s*-cis/*s*-trans interconversion with respect to the *N*-acylpyrrolidine ring<sup>3</sup> produces two conformational diastereomers and additional NMR signals at room temperature.

The interconversion is fast on the NMR timescale at 75 °C in DMSO-*d*<sub>6</sub>:

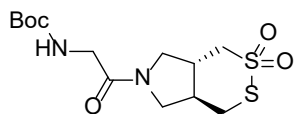
**<sup>1</sup>H NMR** (DMSO-*d*<sub>6</sub>, 500 MHz) at 75 °C: δ 3.80 (dd, *J* = 13.1, 2.8 Hz, 1H), 3.63–3.53 (m, 3H), 3.43 (dd, *J* = 13.5, 2.9 Hz, 1H), 3.32 (dd, *J* = 13.5, 11.4 Hz, 1H), 3.03 (t, *J* = 10.6 Hz, 1H), 2.97 (t, *J* = 10.6 Hz, 1H), 2.65–2.53 (m, 1H), 2.41–2.31 (m, 1H), 1.43 (s, 9H).

**<sup>13</sup>C NMR** (DMSO-*d*<sub>6</sub>, 125 MHz) at 75 °C: δ 153.87, 79.12, 62.83, 50.04, 49.58, 42.78, 42.01, 35.55, 28.70. High temperature 1D and 2D NMR spectra for this compound are included.

### Synthesis of BioGlyPyrDTDO (BGPD):



***tert*-Butyl-(2-((4*aS*,7*aS*)- and (4*aR*,7*aR*)-2,2-dioxidotetrahydro-1*H*-[1,2]dithiino[4,5-*c*]pyrrol-6(4*H*)-yl)-2-oxoethyl)carbamate, (**±**)-**BocGlyPyrDTDO****



**BocPyrDTDO**

A solution of (**±**)-**BocPyrDTDO** (0.10 g, 0.34 mmol) was stirred in TFA:DCM (3.4 mL, 1:1) for 2 h, at rt. The reaction mixture was then concentrated under vacuum to provide the deprotected ammonium trifluoroacetate salt **HPyrDTDO.TFA** as a brown solid, which was used in the next step without further purification.

**<sup>1</sup>H NMR** (DMSO-*d*<sub>6</sub>, 500 MHz): δ 9.25 (bs, 2H), 3.91 (dd, *J* = 13.0, 2.9 Hz, 1H), 3.68 (t, *J* = 12.6 Hz, 1H), 3.53–3.42 (m, 3H), 3.33 (dd, *J* = 13.6, 11.5 Hz, 1H), 2.95 (tq, *J* = 13.4, 6.6 Hz, 2H), 2.62–2.53 (m, 1H), 2.40–2.30 (m, 1H).

**<sup>13</sup>C NMR** (DMSO-*d*<sub>6</sub>, 125 MHz): δ 60.97, 47.55, 47.30, 41.98, 40.64, 33.97.

To the solution of the resulting solid in DMF (4.8 mL) was added Et<sub>3</sub>N (0.10 mL, 0.68 mmol) and 2,5-dioxopyrrolidin-1-yl (*tert*-butoxycarbonyl)glycinate (0.09 g, 0.34 mmol), respectively, and the reaction mixture was stirred at rt for 24 h. After this time the solvent was evaporated, and the crude product was purified by flash chromatography (0–1% MeOH/DCM) to afford (**±**)-**BocGlyPyrDTDO** (0.08 g, 0.23 mmol 68%) as a viscous white solid.

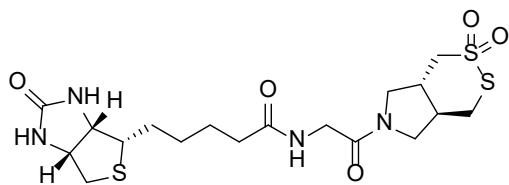
**<sup>1</sup>H NMR** (CDCl<sub>3</sub>, 500 MHz): δ 5.38 (s, 1H), 4.01–3.95 (m, 1H), 3.93–3.79 (m, 2H), 3.74 (dt, *J* = 16.0, 8.5 Hz, 1H), 3.58 (t, *J* = 13.9 Hz, 1H), 3.48–3.34 (m, 2H), 3.26–3.04 (m, 3H), 2.9–2.7 (m, 1H), 2.53–2.29 (m, 1H), 1.44 (s, 9H).

**<sup>13</sup>C NMR** (CDCl<sub>3</sub>, 125 MHz): δ 167.38, 155.92, 80.06, 62.42, 62.14, 49.89, 49.38, 48.94, 43.39, 43.14, 42.96, 42.88, 41.72, 41.60, 35.18, 34.95, 28.46.

**HRMS** (ESI-TOF): Calculated for [C<sub>13</sub>H<sub>22</sub>N<sub>2</sub>O<sub>5</sub>S<sub>2</sub> + Na]<sup>+</sup>: 373.0862; found: 373.0863.

Slow *s*-cis/*s*-trans interconversion with respect to the *N*-acylpyrrolidine ring<sup>3</sup> produces two diastereomers and additional NMR signals (e.g., PyrDTDO ring peak doubling) at room and even elevated (in DMSO-*d*<sub>6</sub>) temperature.

***N*-(2-((4a*S*,7a*S*)- and (4a*R*,7a*R*)-2,2-Dioxidotetrahydro-1*H*-[1,2]dithiino[4,5-*c*]pyrrol-6(4*H*)-yl)-2-oxoethyl)-5-((3a*S*,4*S*,6a*R*)-2-oxohexahydro-1*H*-thieno[3,4-*d*]imidazol-4-yl)pentanamide, Biotin-GlyPyrDTDO (BGPD)**



**Biotin-GlyPyrDTDO (BGPD)**

A solution of (**±**)-**BocGlyPyrDTDO** (0.08 g, 0.23 mmol) was stirred in TFA:DCM (6 mL, 1:2) for 2 h at rt. After this time the reaction was concentrated under vacuum to provide the deprotected ammonium trifluoroacetate salt as a brown oily solid, which was used in the next step without further purification. To a solution of the resulting solid and (+)-biotin *N*-succinimidyl ester (0.08 g, 0.23 mmol) in DMF was added Et<sub>3</sub>N (0.06 mL, 0.46 mmol) and the reaction mixture was stirred at rt for 24 h. Then the solvent was evaporated and the crude product was purified by flash chromatography (0–10% MeOH/DCM) to afford **Biotin-GlyPyrDTDO** (0.06 g, 0.13 mmol, 56%) as a white solid.

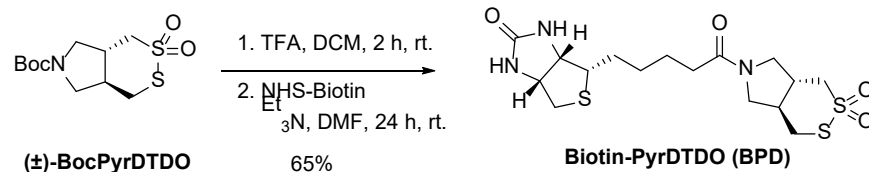
**<sup>1</sup>H NMR** (DMSO-*d*<sub>6</sub>, 500 MHz) δ 7.94 (s, 1H), 6.41 (s, 1H), 6.35 (s, 1H), 4.33–4.27 (m, 1H), 4.14–4.11 (m, 1H), 3.90–3.68 (m, 5H), 3.64 (td, *J* = 12.9, 2.0 Hz, 1H), 3.46 (ddd, *J* = 13.5, 6.4, 2.8 Hz, 1H), 3.35–3.30 (m, 1H), 3.24–3.17 (m, 1H), 3.11–3.05 (m, 1H), 3.02–2.91 (m, 1H), 2.82 (dd, *J* = 12.4, 5.1 Hz, 1H), 2.69–2.47 (m, 2H), 2.46–2.25 (m, 1H), 2.14 (t, *J* = 7.0 Hz, 2H), 1.65–1.58 (m, 1H), 1.55–1.42 (m, 3H), 1.39–1.25 (m, 2H).

**<sup>13</sup>C NMR** (DMSO-*d*<sub>6</sub>, 125 MHz): δ 172.31, 166.93, 166.86, 162.68, 61.79, 61.65, 61.00, 59.18, 55.41, 49.25, 48.76, 48.31, 42.72, 41.67, 41.05, 40.87, 40.78, 40.11, 34.94, 34.85, 34.80, 28.14, 28.02, 25.23.

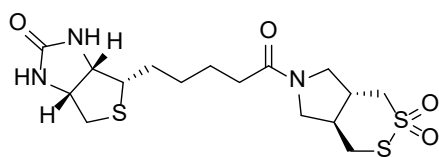
**HRMS** (ESI-TOF): Calculated for [C<sub>18</sub>H<sub>28</sub>N<sub>4</sub>O<sub>5</sub>S<sub>3</sub> + H]<sup>+</sup>: 477.1295; found: 477.1287.

Slow *s-cis/s-trans* interconversion with respect to the *N*-acylpyrrolidine ring<sup>3</sup> produces two diastereomers and additional NMR signals (e.g., PyrDTDO ring peak doubling).

### Synthesis of Biotin-PyrDTDO (BPD):



### (3aS,4S,6aR)-4-(5-((4aR,7aR) and (4aS,7aS)-2,2-dioxidotetrahydro-1H-[1,2]dithiino[4,5-c]pyrrol-6(4H)-yl)-5-oxopentyl)tetrahydro-1H-thieno[3,4-d]imidazol-2(3H)-one, Biotin-PyrDTDO (BPD)



**Biotin-PyrDTDO (BPD)**

A solution of **(±)-BocPyrDTDO** (0.20 g, 0.68 mmol) was stirred in TFA:DCM (6 mL, 1:1) for 2 h at rt, monitoring by TLC. After reaction completion, the mixture was concentrated under vacuum to provide the deprotected ammonium trifluoroacetate salt as a brown solid, which was used in the next step without further purification. To a solution of the resulting solid and (+)-biotin *N*-succinimidyl ester in DMF was added Et<sub>3</sub>N (0.20 mL, 1.40 mmol) and the reaction mixture was stirred at rt for 24 h.

Then the solvent was evaporated and the crude product was purified by flash chromatography (0–10% MeOH/DCM) to afford **Biotin-PyrDTDO** (0.19 g, 0.45 mmol, 65%) as a white solid.

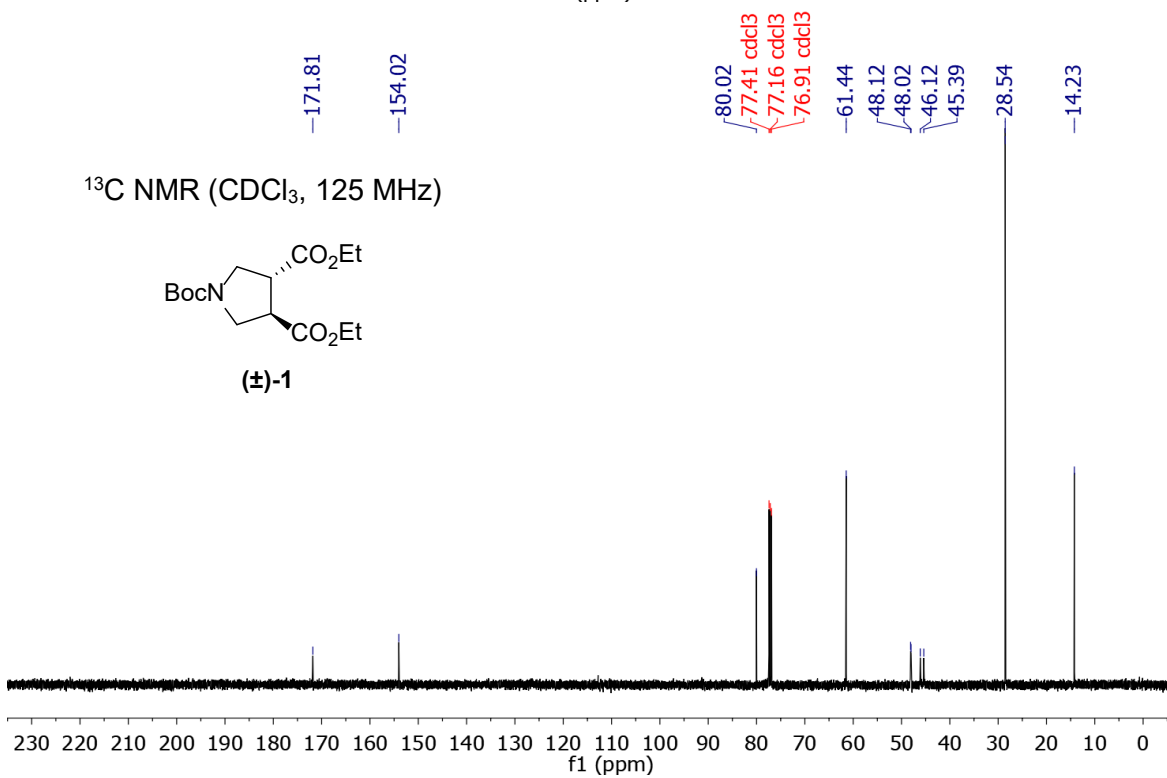
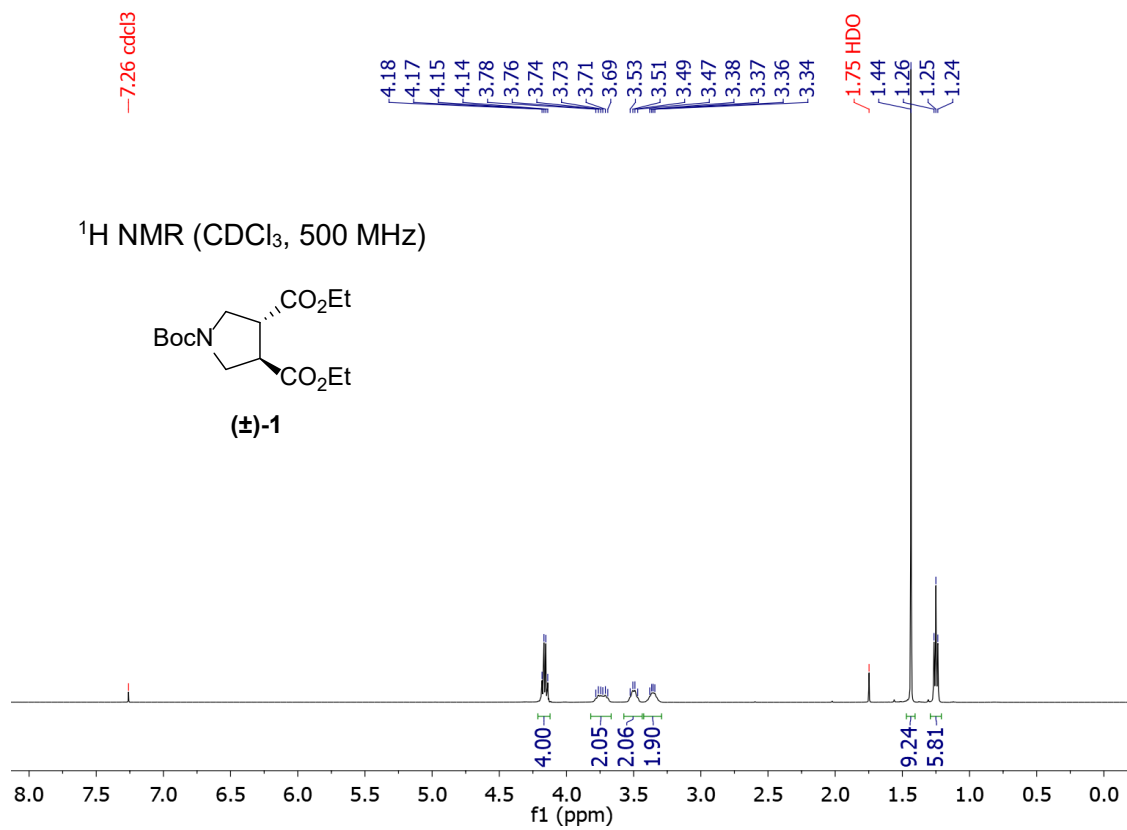
**<sup>1</sup>H NMR** (DMSO-*d*<sub>6</sub>, 600 MHz)  $\delta$  6.44 (s, 1H), 6.36 (s, 1H), 4.31 (dd, *J* = 7.8, 5.0 Hz, 1H), 4.14 (ddd, *J* = 7.1, 4.5, 1.8 Hz, 1H), 3.88–3.82 (m, 1H), 3.76–3.66 (m, 3H), 3.65–3.60 (m, 1H), 3.49–3.40 (m, 1H), 3.28–3.35 (m, 1H), 3.23–3.13 (m, 1H), 3.13–3.07 (m, 1H), 2.99–2.87 (m, 1H), 2.83 (dd, *J* = 12.4, 5.1 Hz, 1H), 2.58 (d, *J* = 12.4 Hz, 1H), 2.67–2.47 (m, 1H), 2.45–2.28 (m, 1H), 2.26–2.13 (m, 2H), 1.68–1.57 (m, 1H), 1.56–1.42 (m, 3H), 1.40–1.27 (m, 2H).

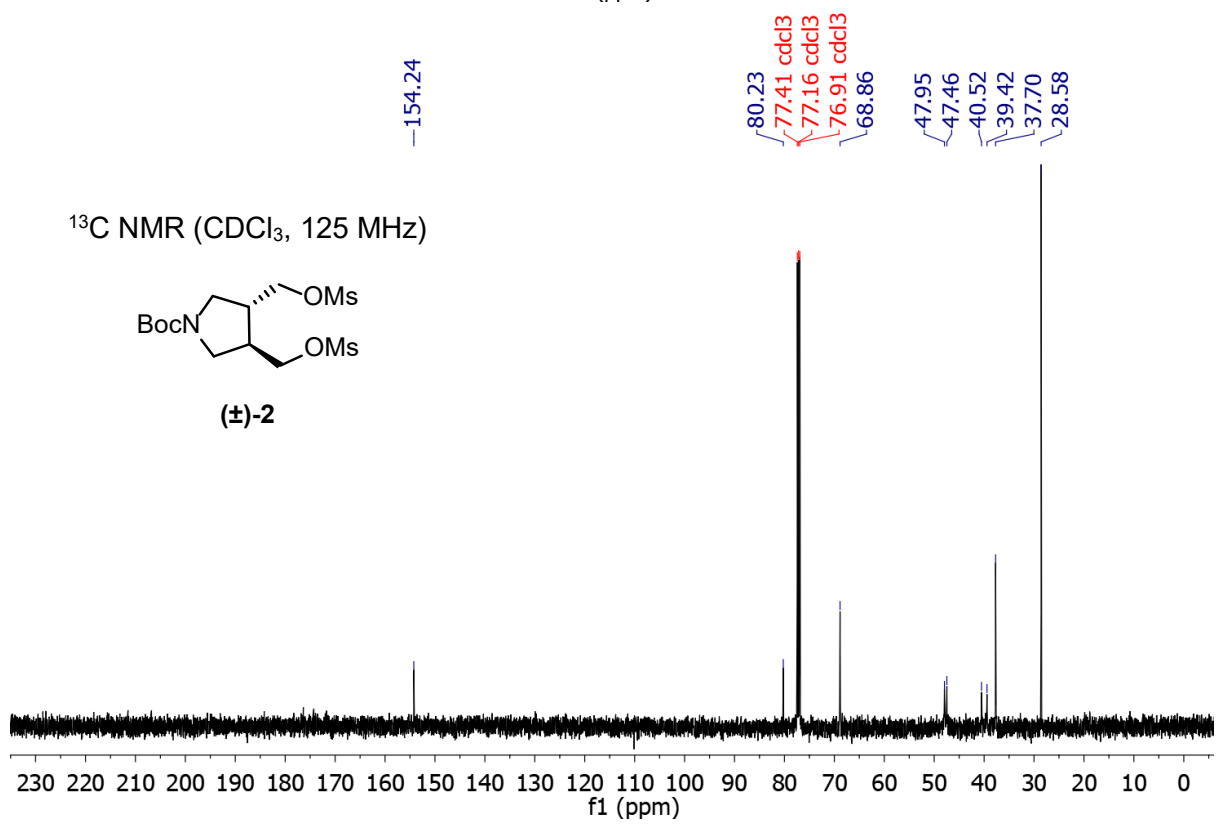
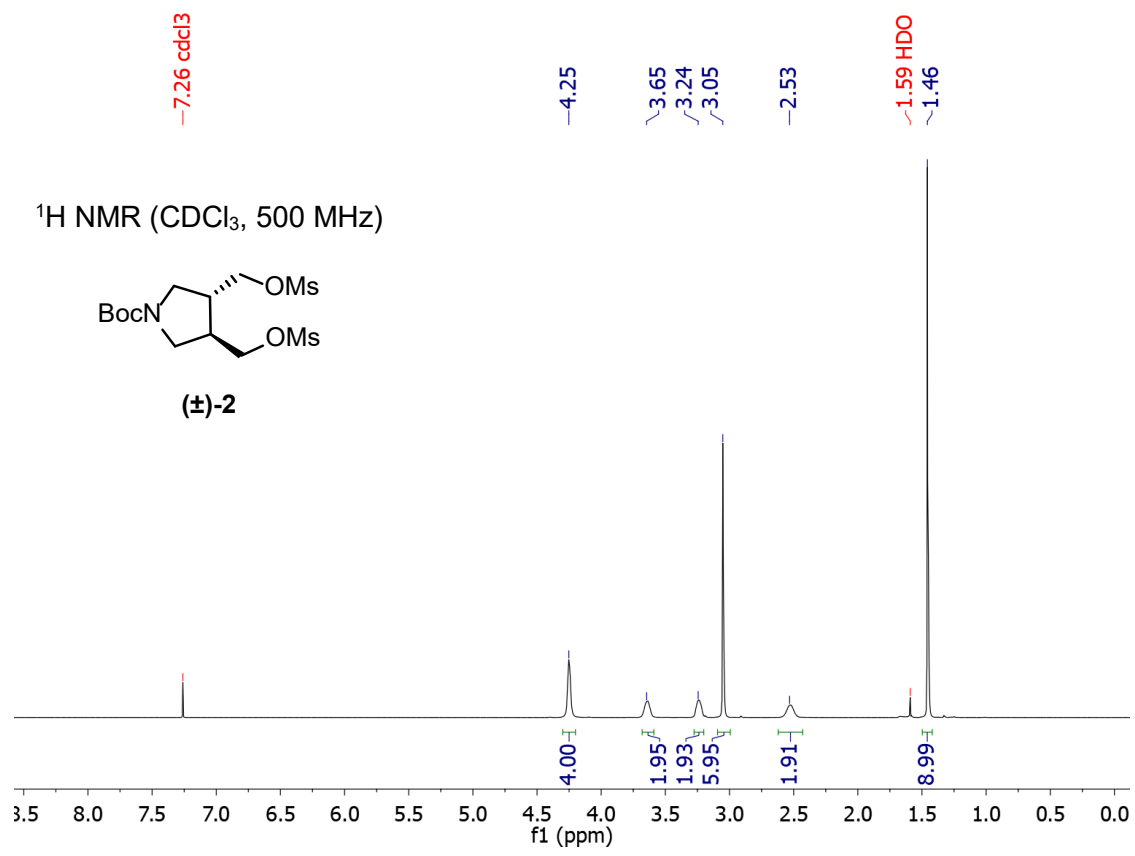
**<sup>13</sup>C NMR** (DMSO-*d*<sub>6</sub>, 151 MHz):  $\delta$  170.42, 170.35, 162.71, 61.89, 61.69, 61.05, 59.18, 55.45, 49.67, 49.22, 49.02, 48.52, 42.70, 41.71, 41.23, 40.34, 39.87, 35.06, 34.86, 33.18, 33.11, 28.29, 28.11, 24.27.

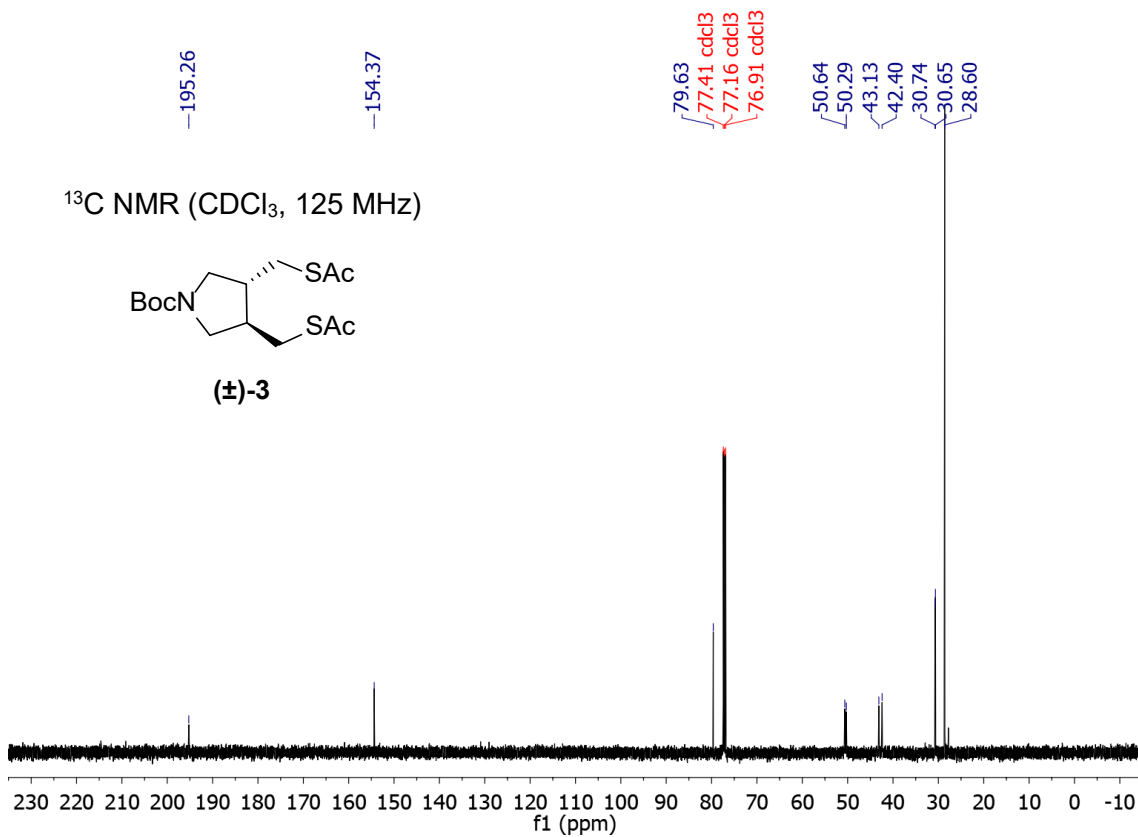
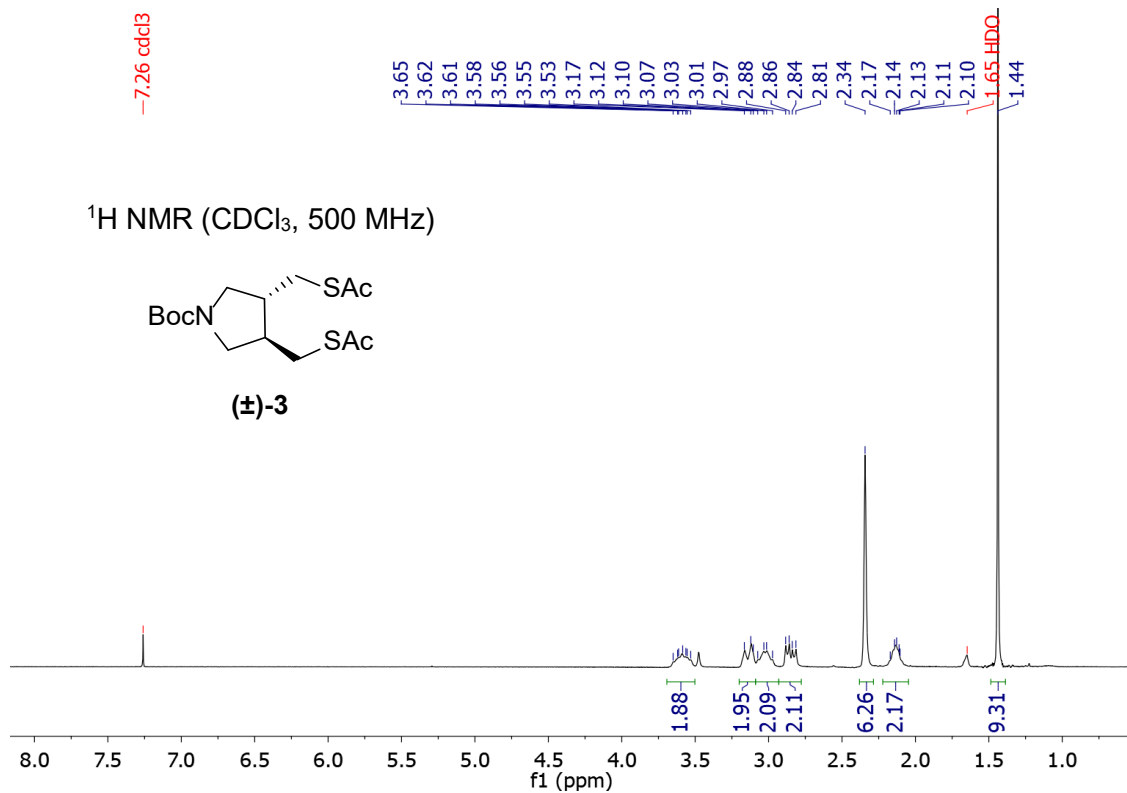
**HRMS** (ESI-TOF): Calculated for [C<sub>16</sub>H<sub>25</sub>N<sub>3</sub>O<sub>4</sub>S<sub>3</sub> + Na]<sup>+</sup>: 442.0899; found: 442.0899.

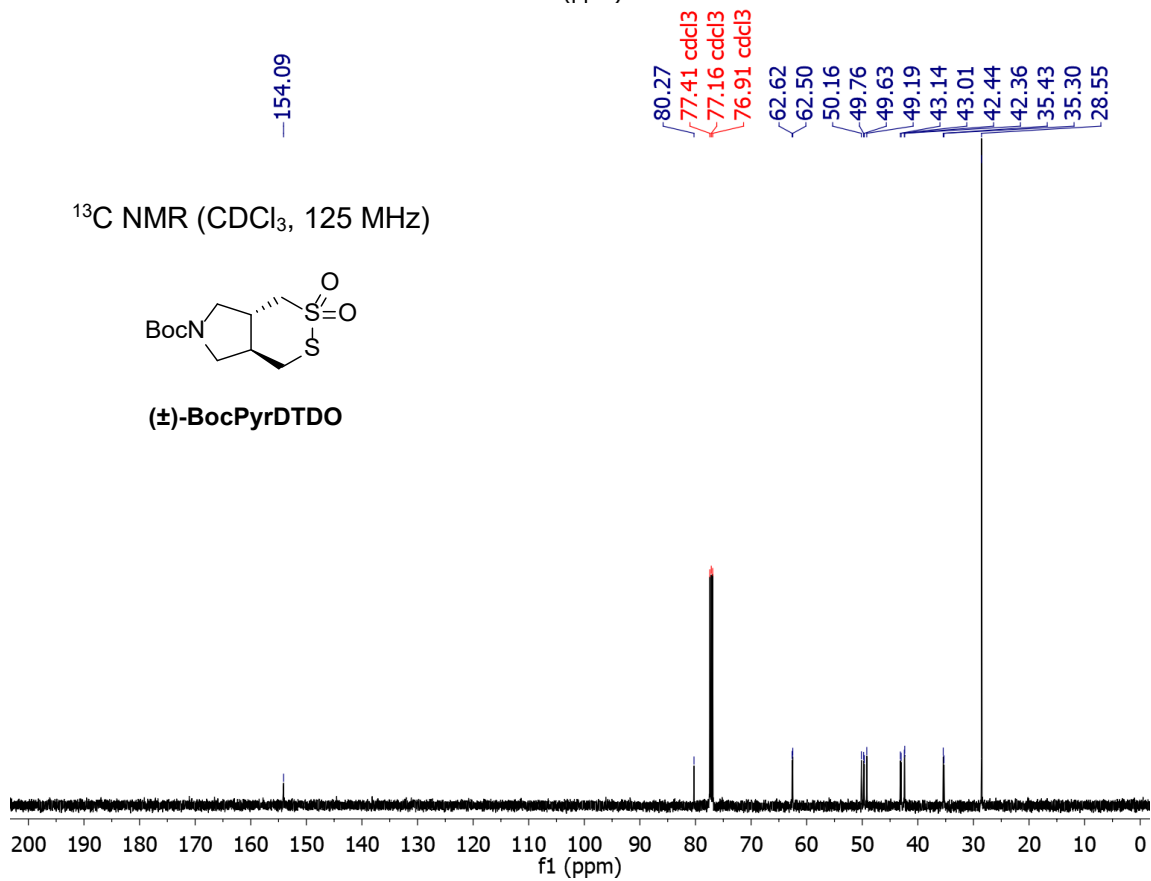
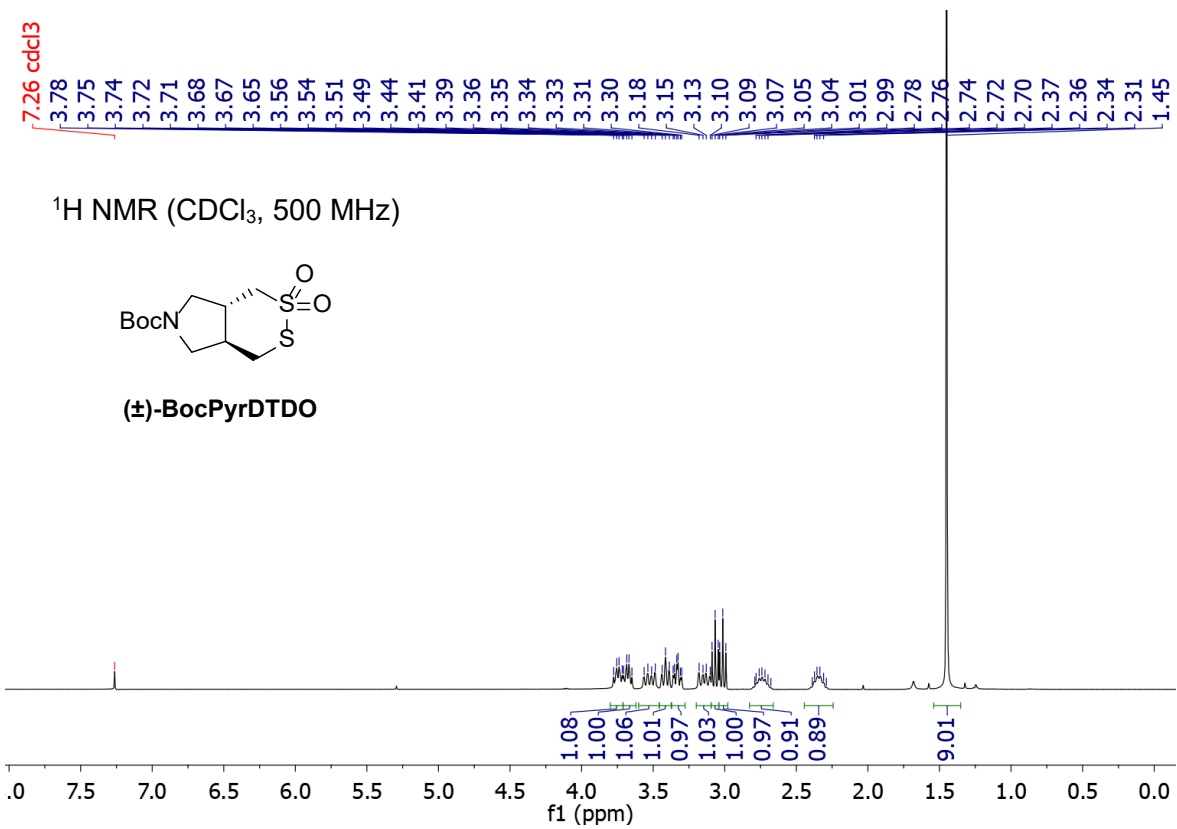
Slow *s-cis/s-trans* interconversion with respect to the *N*-acylpyrrolidine ring<sup>3</sup> produces two diastereomers and additional NMR signals (e.g., PyrDTDO ring peak doubling).

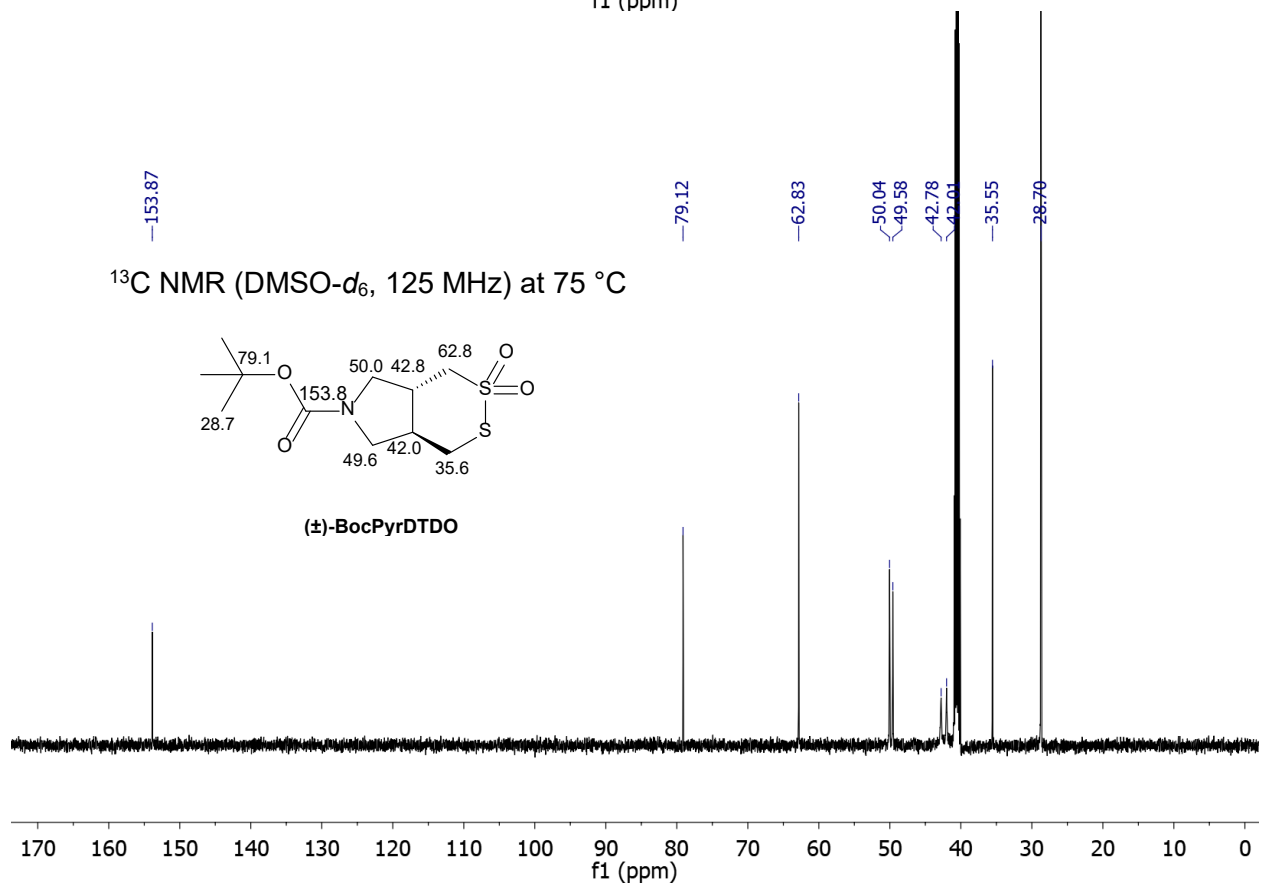
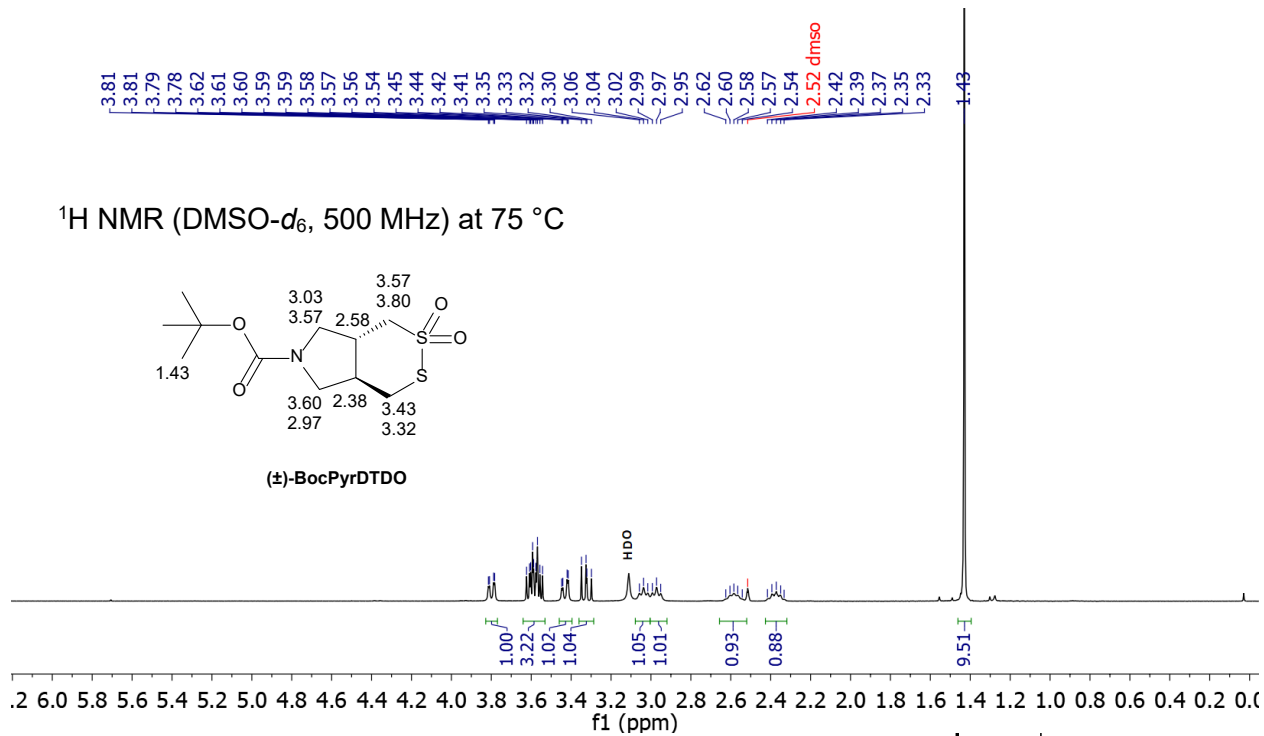


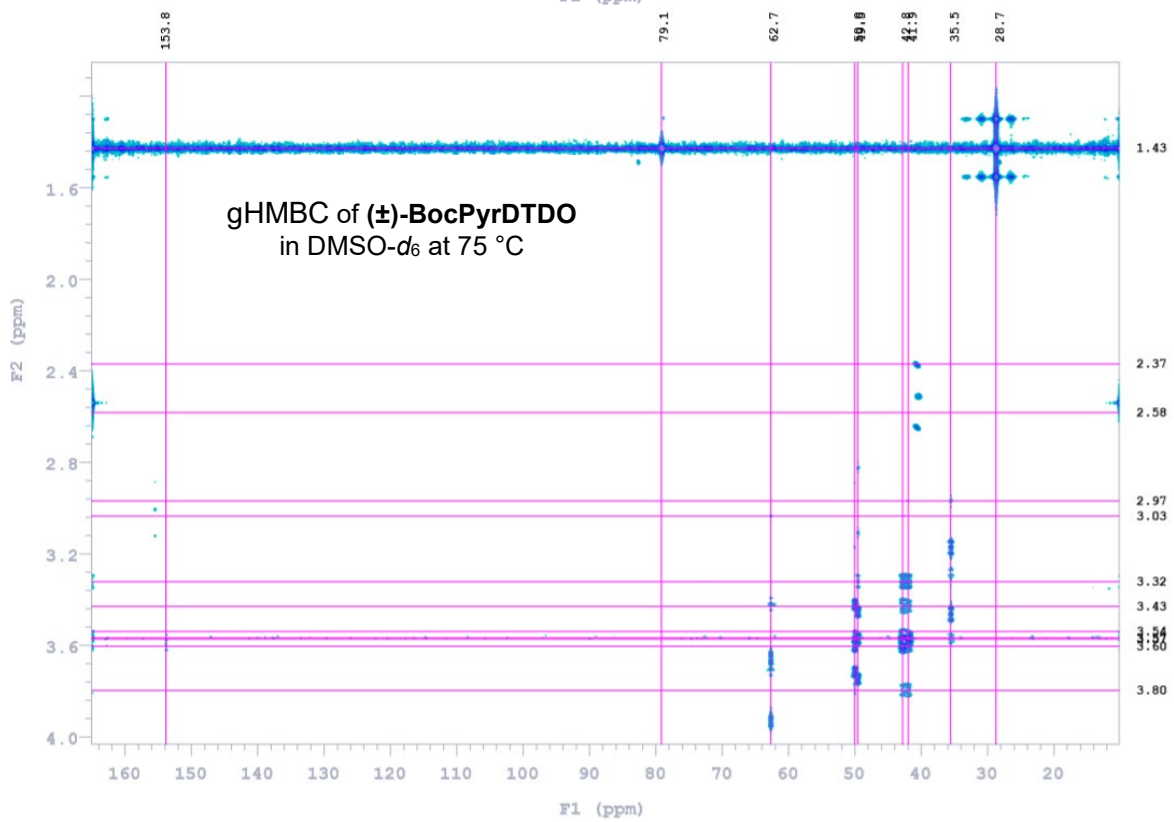
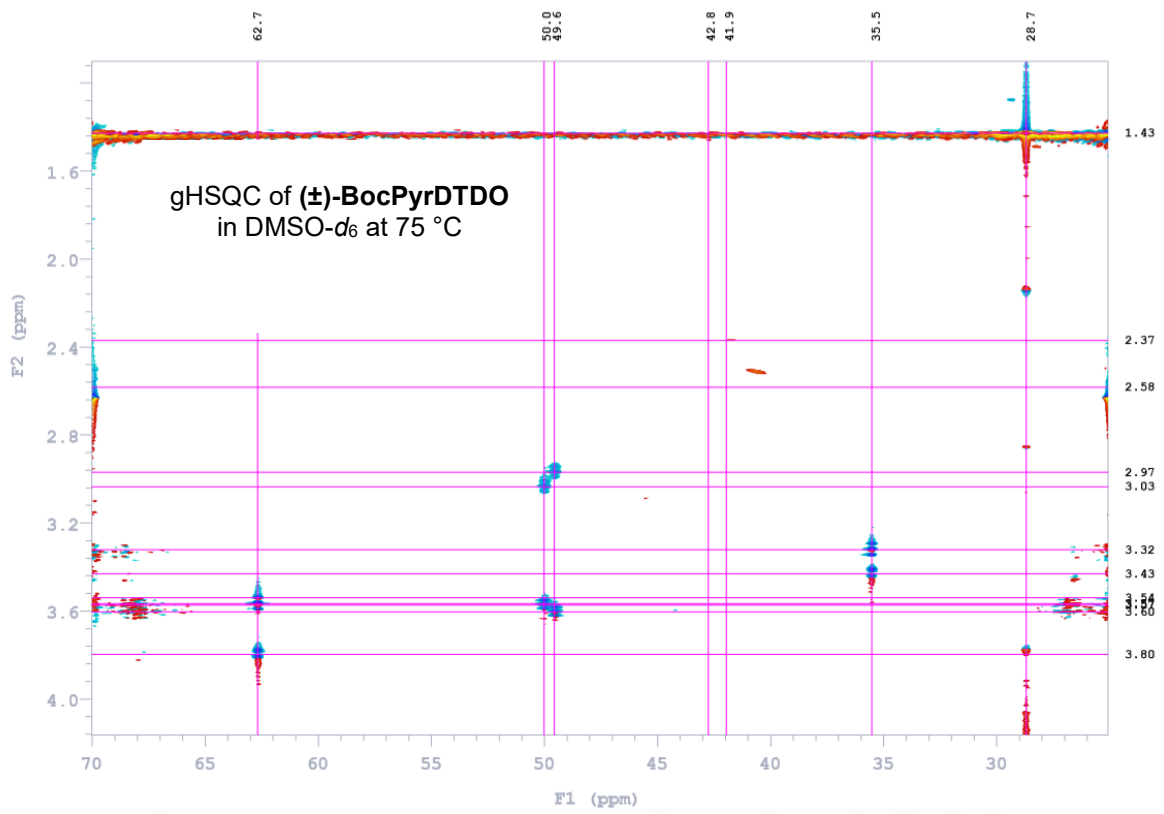


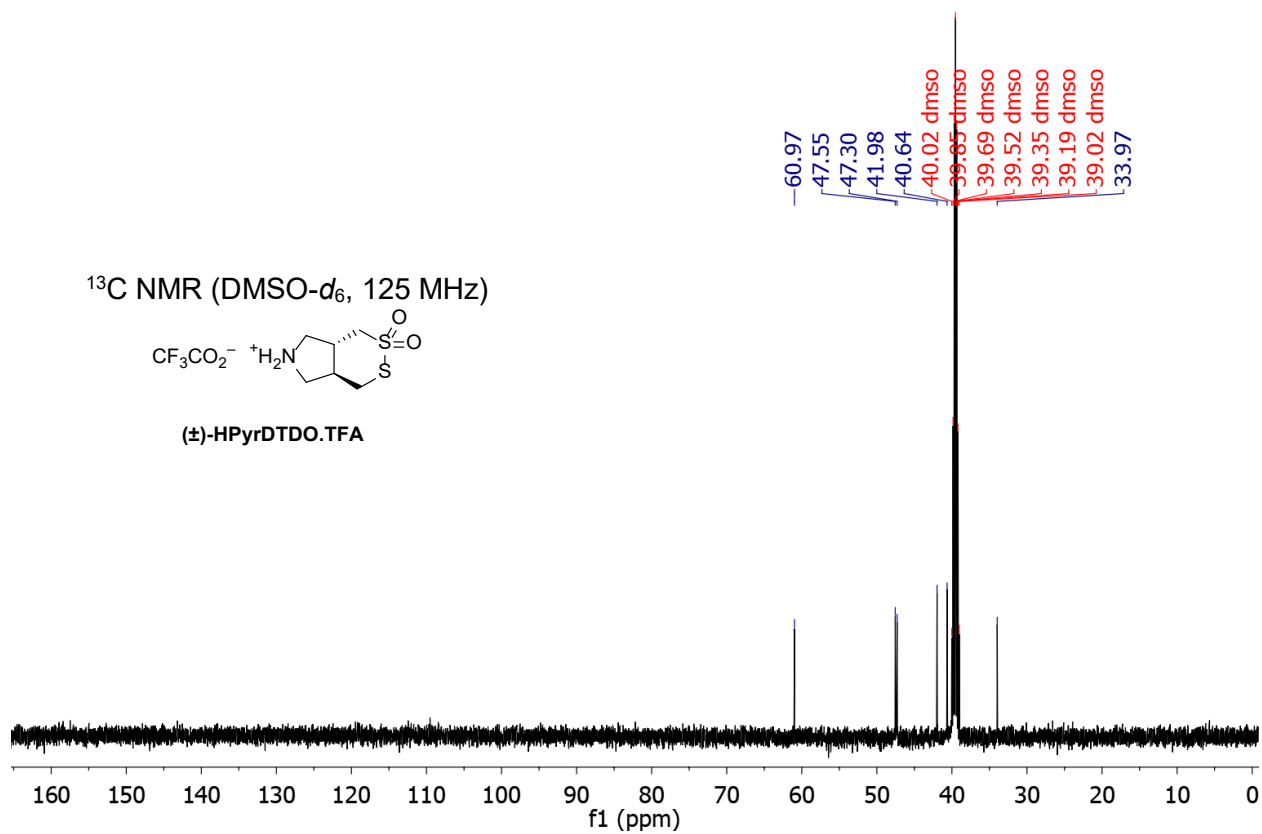
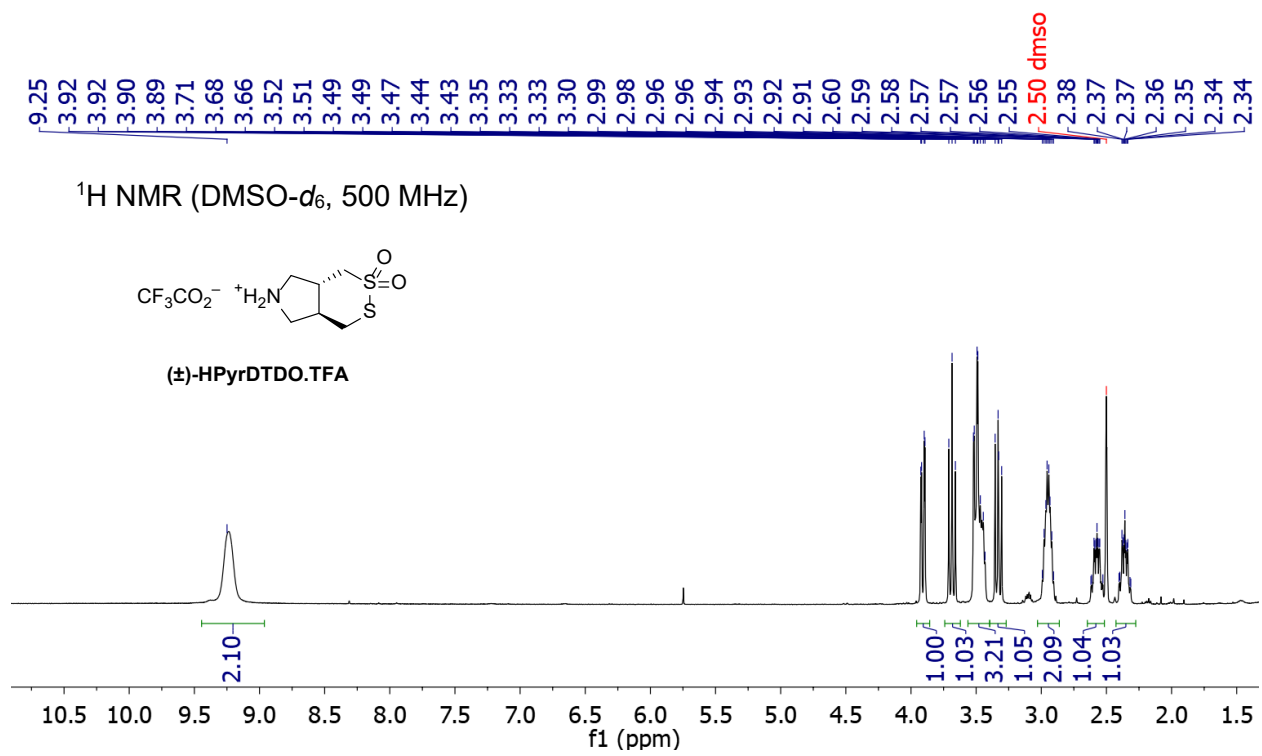


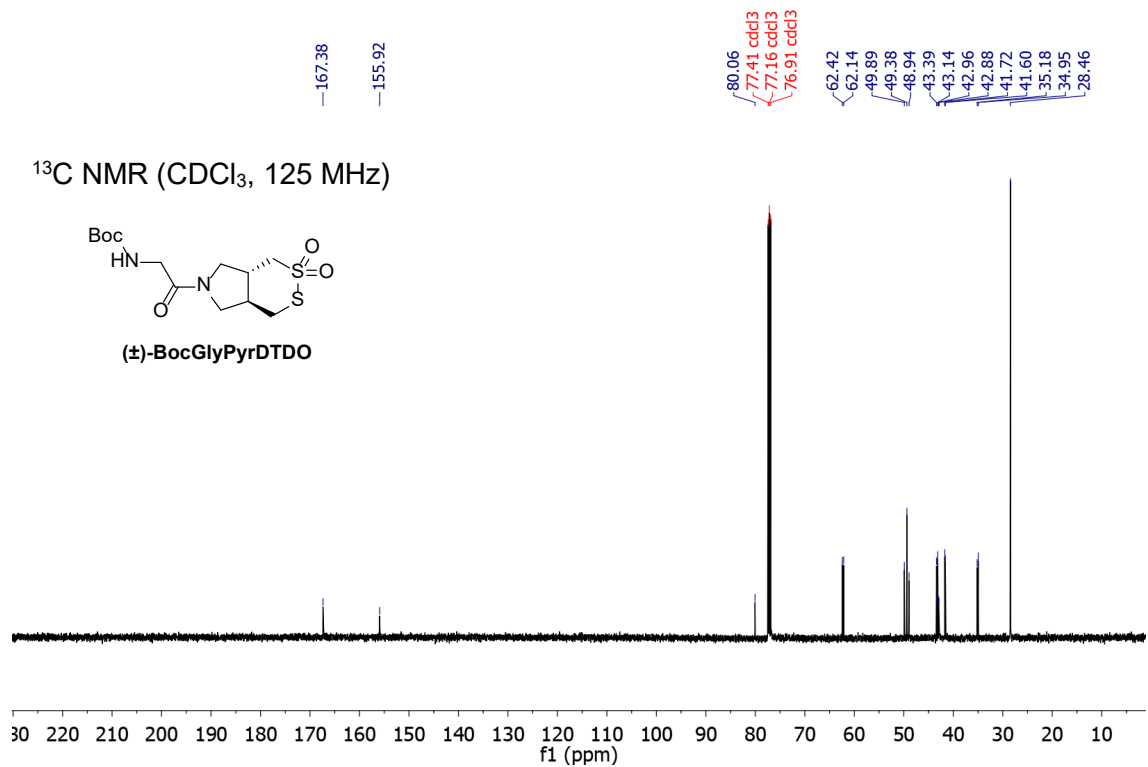
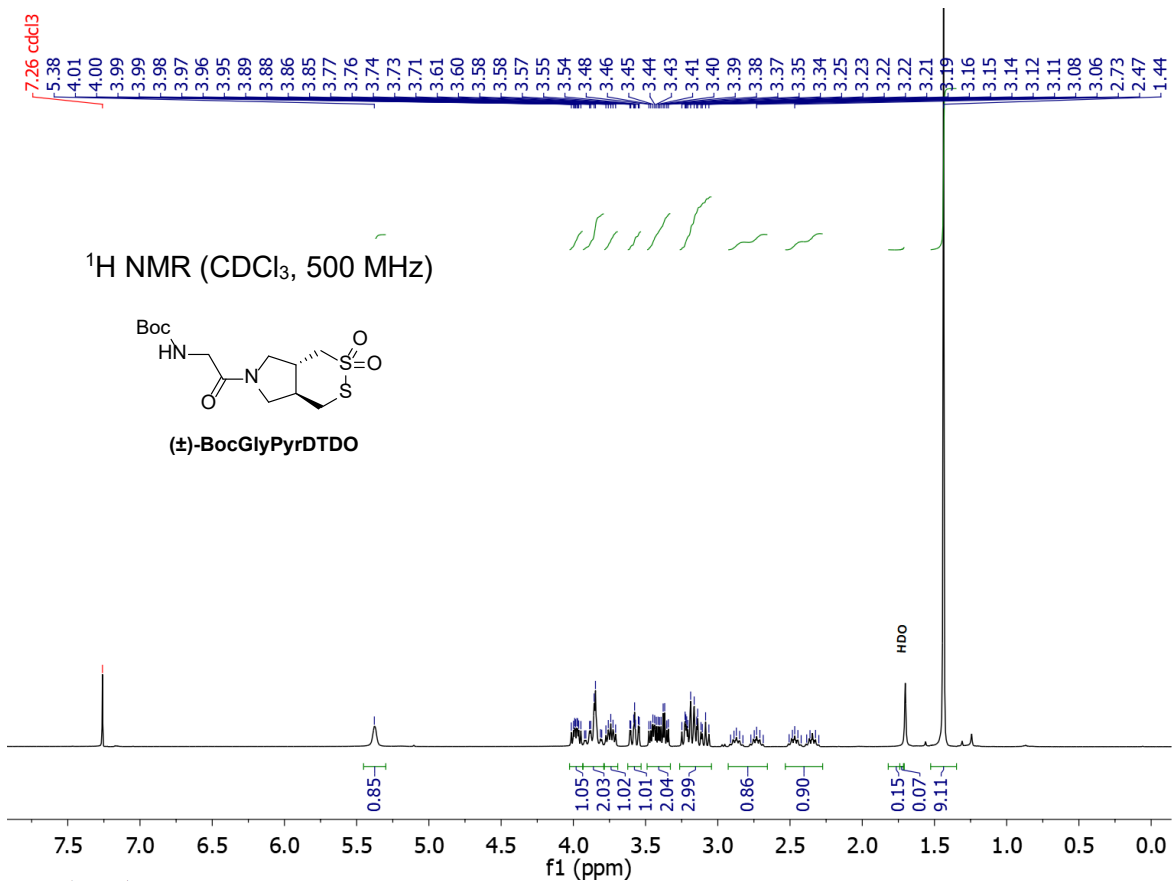




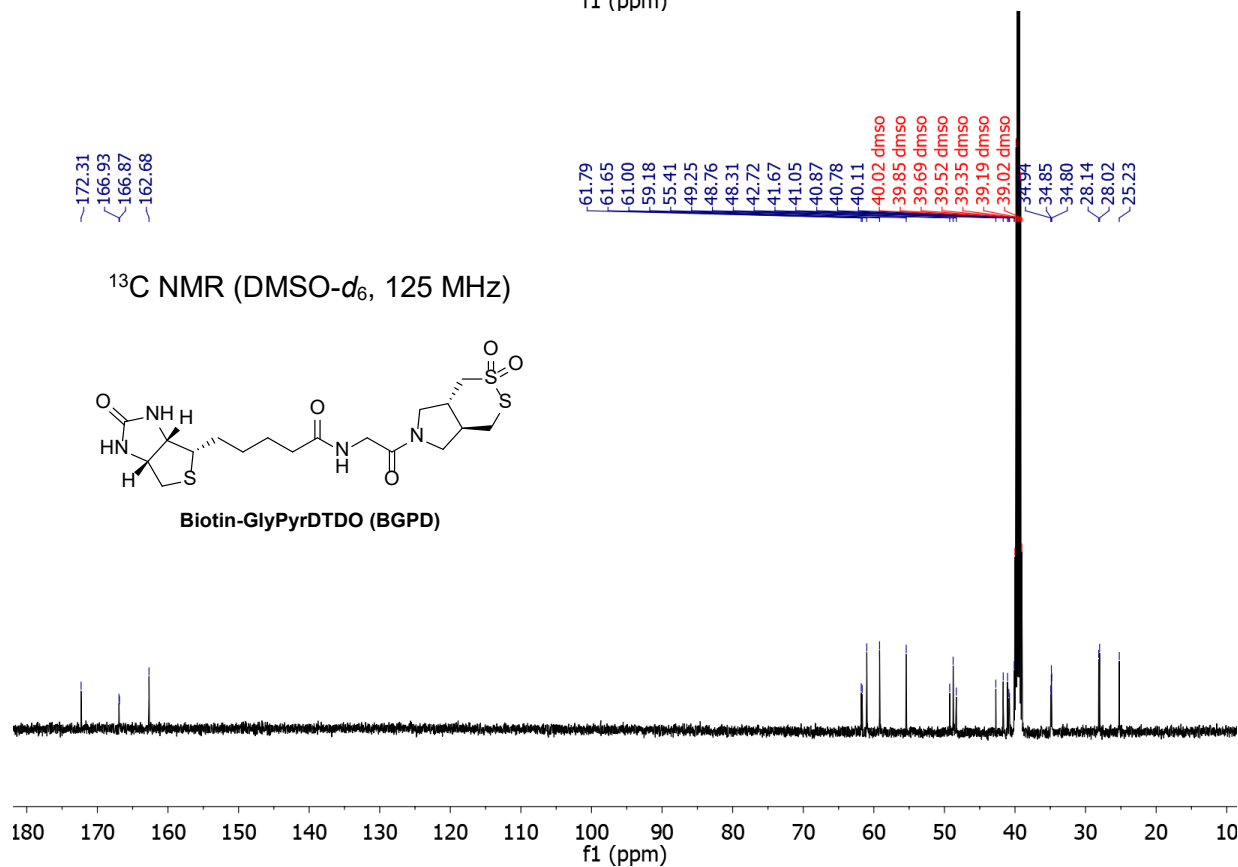
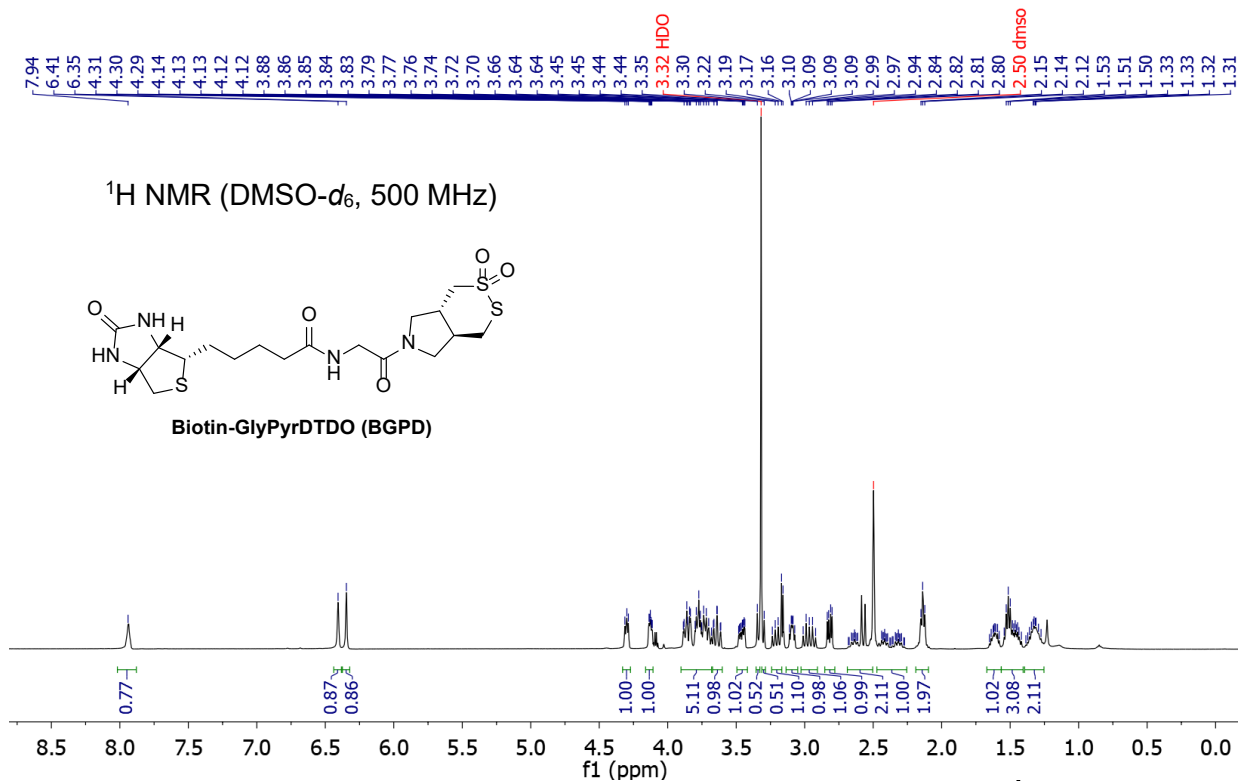






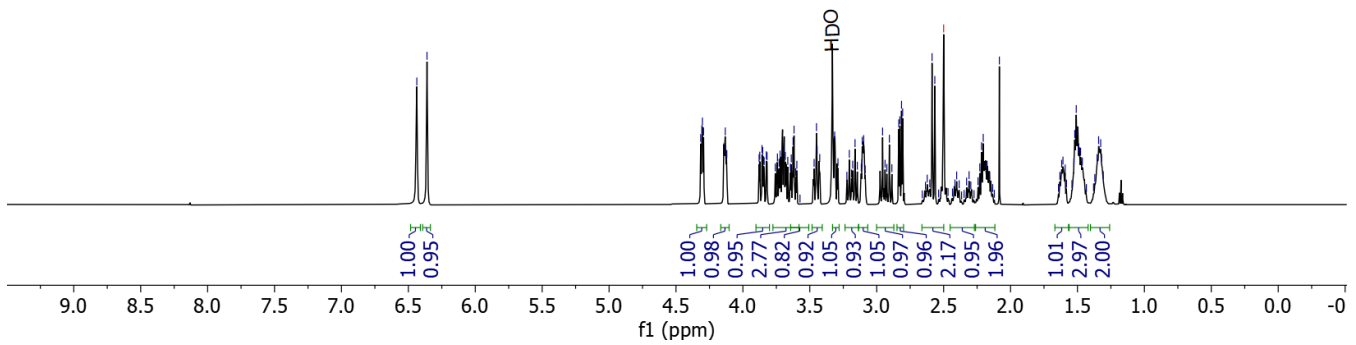
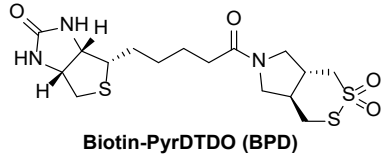






6.44  
6.36  
4.32  
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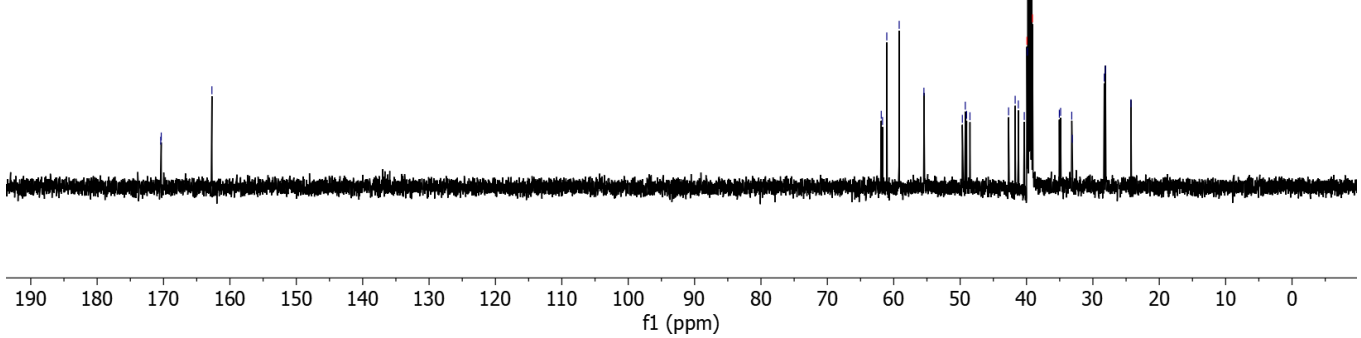
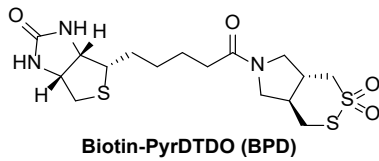
<sup>1</sup>H NMR (DMSO-*d*<sub>6</sub>, 600 MHz)



170.42  
170.35  
-162.71

61.89  
61.69  
61.05  
59.18  
55.45  
49.67  
49.22  
49.02  
48.52  
42.70  
41.71  
41.23  
40.34  
39.94 DMSO  
39.87  
39.80 DMSO  
39.66 DMSO  
39.52 DMSO  
39.38 DMSO  
39.24 DMSO  
39.10 DMSO  
35.06  
34.86  
33.18  
33.11  
28.29  
28.11  
24.27

<sup>13</sup>C NMR (DMSO-*d*<sub>6</sub>, 151 MHz)



## References

1. a) Gohimukkula, D. R.; Jones, D.; Qabaja, G.; Zhu, J. J.; Cooper, J. T.; Banner, W. K.; Sundermann, K.; Bondlela, M.; Rao, M.; Wang, P.; Gowda, R. B.; Andrews, R. C.; Gupta, S.; Hari, A. Preparation of phenyl-heteroaryl derivatives as inhibitors of advanced glycosylation end product receptors (RAGE). Assignee: TransTech Pharma, Inc.; WO 2011103091 (A1) August 25, **2011**. b) Rodríguez Sarmiento, R. M. a.; Wirz, B.; Iding, H., Chemoenzymatic preparation of non-racemic N-Boc-pyrrolidine-3,4-dicarboxylic acid 3-ethyl esters and their 4-hydroxymethyl derivatives. *Tetrahedron: Asymmetry* **2003**, *14* (11), 1547.
2. J.; Hunziker, D.; Mattei, P.; Mauser, H.; Tang, G.; Wang, L. Preparation of bicyclic derivatives as autotaxin inhibitors for therapy. Assignee: F. Hoffmann-La Roche AG, Switz.; Hoffmann-La Roche Inc. WO 20144048865 (A1), April 3, **2014**.
3. For some case studies of N-acyl-prolyl isomerization please see: a) Kubyshkin, V.; Durkin, P.; Budisa, N., Energetic contribution to both acidity and conformational stability in peptide models. *New J. Chem.*, **2016**, *40* (6), 5209. b) Kubyshkin, V.; Budisa, N., Amide rotation trajectories probed by symmetry. *Org. Biomol. Chem.*, **2017**, *15* (32), 6764.