

γ -Trifluoromethyl proline: Evaluation as a structural substitute of proline for solid state ^{19}F -NMR peptide studies

Vladimir Kubyshkin, Sergii Afonin, Sezgin Kara, Nediljko Budisa, Pavel K. Mykhailiuk and Anne S. Ulrich

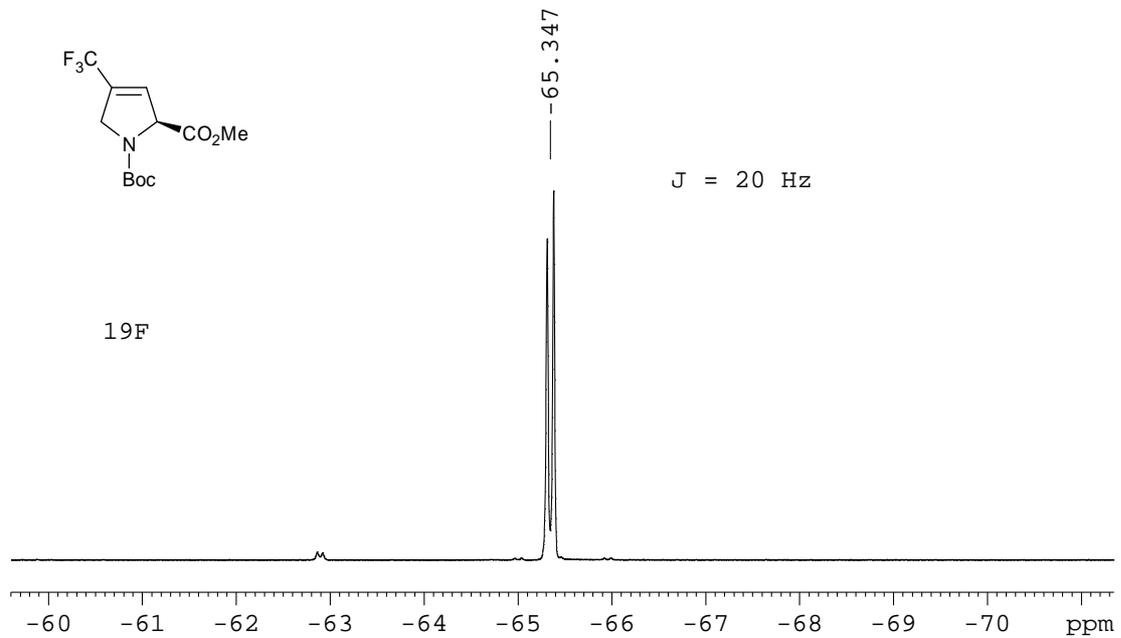
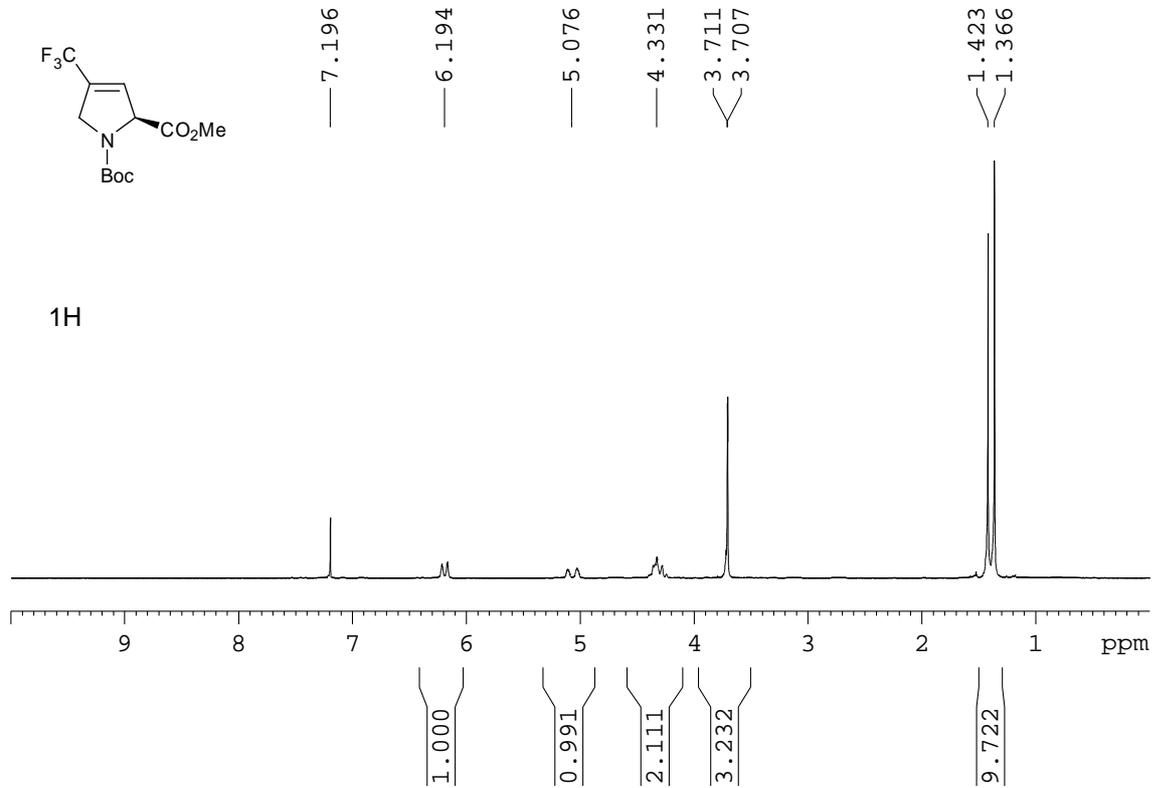
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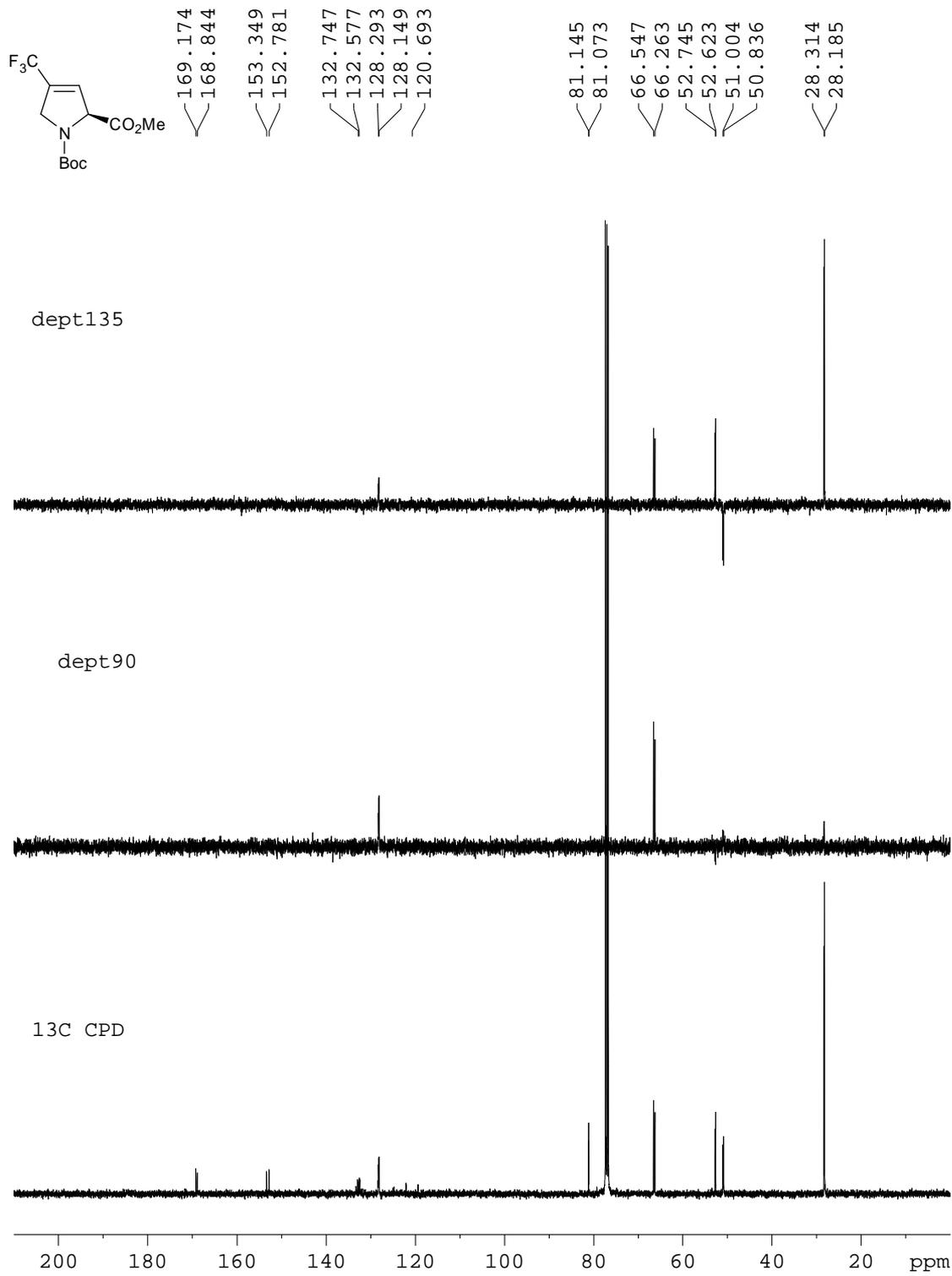
Copies of the NMR spectra for the compounds

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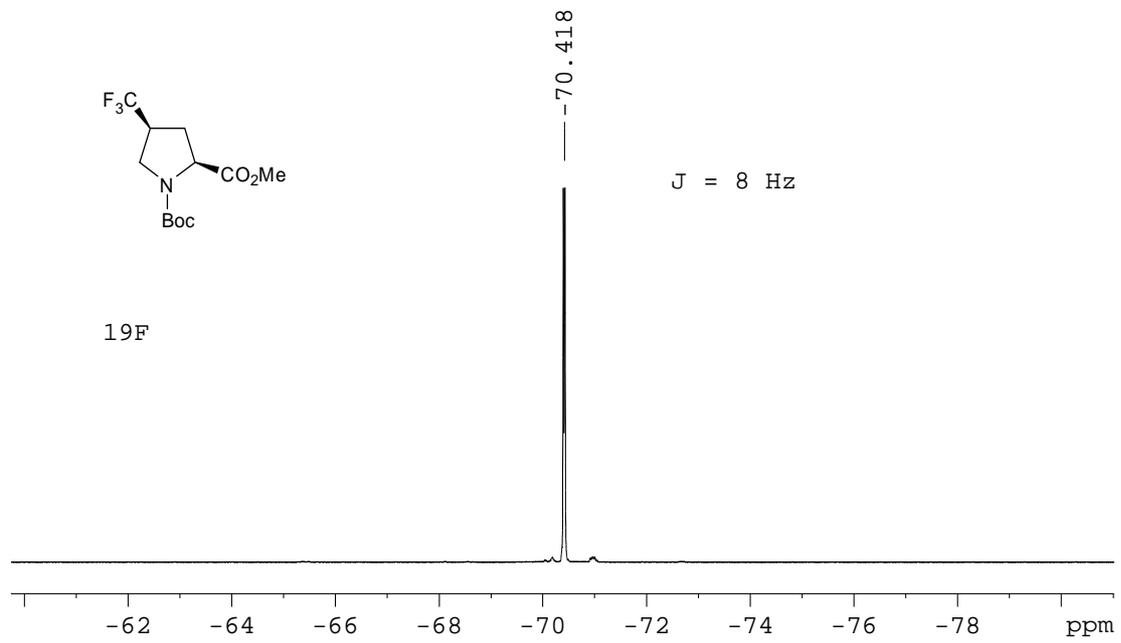
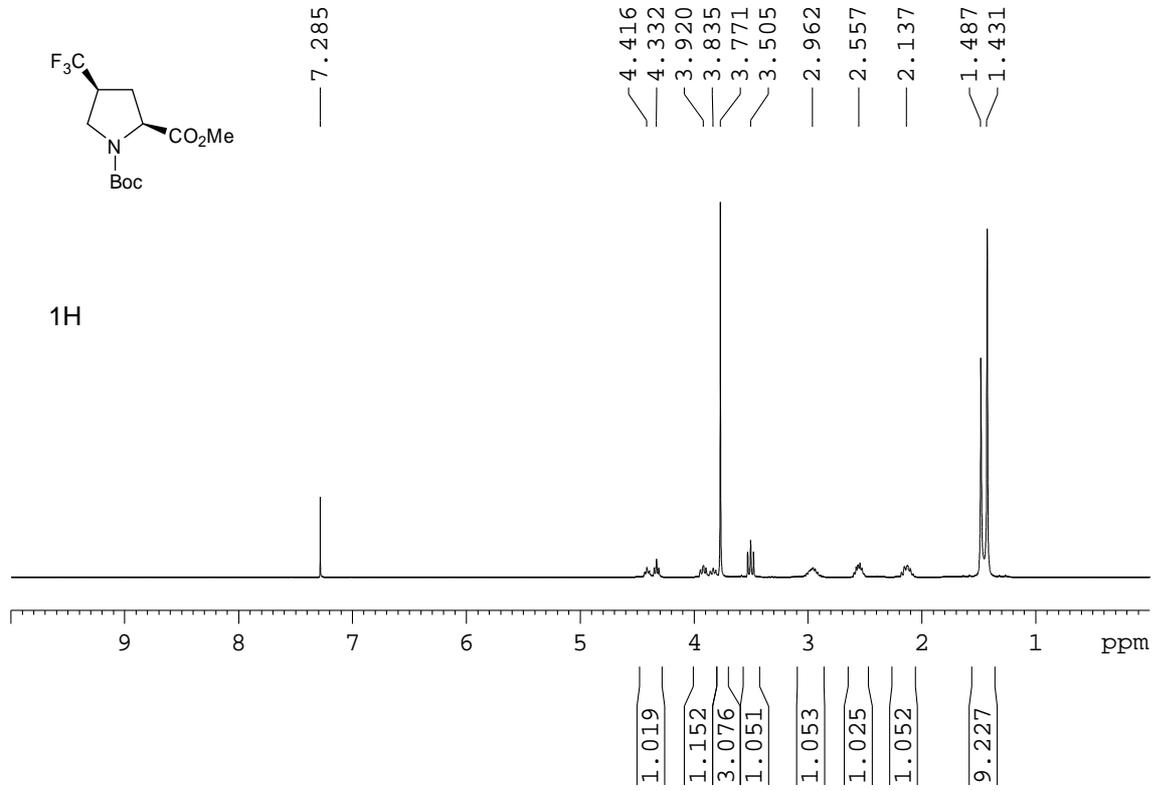
Copies of the NMR spectra for the compounds

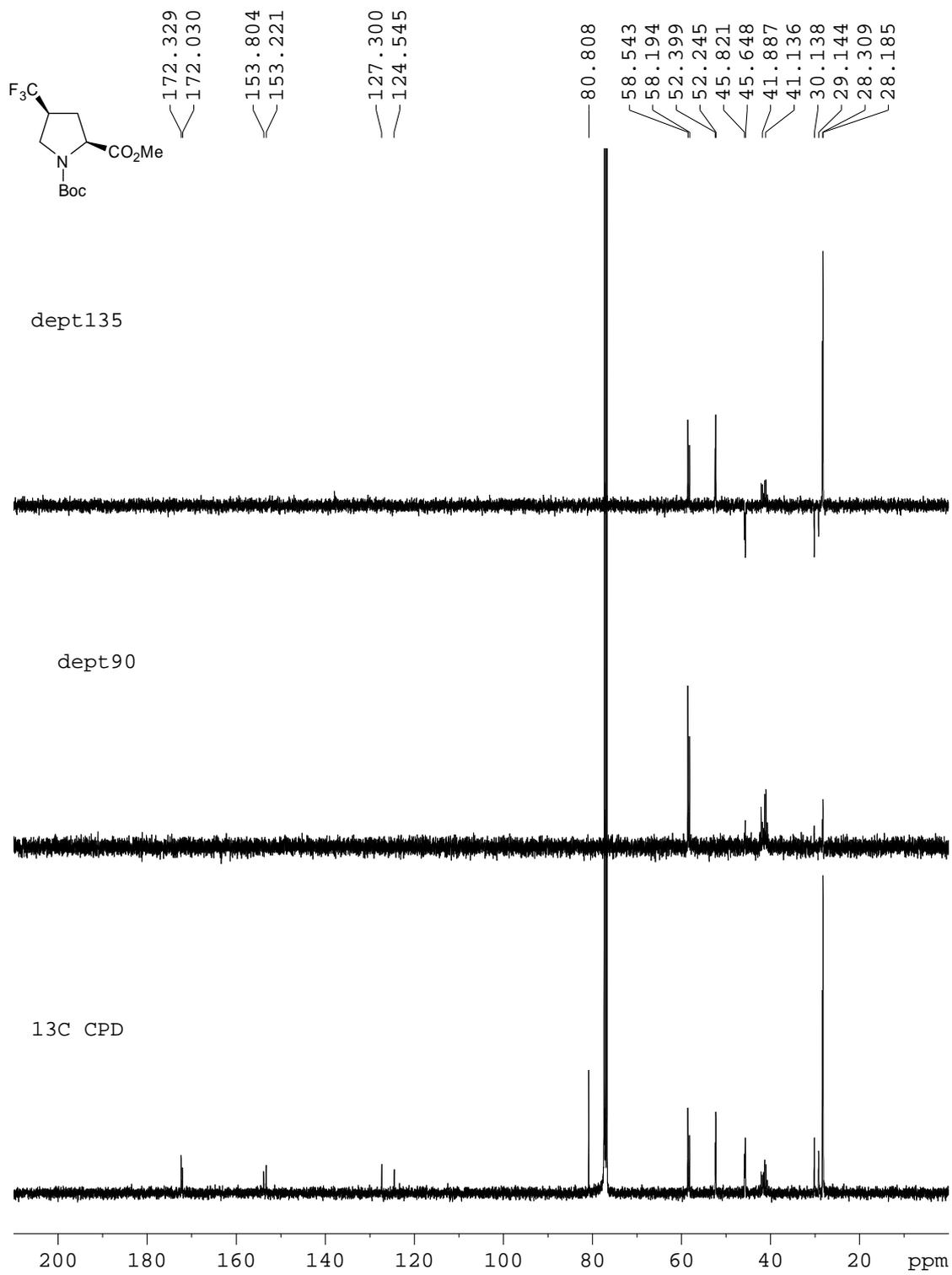
2-*tert*-butyl 2-methyl (2*S*)-4-trifluoromethyl-3-pyrrolin-1,2-dicarboxylate (**6**)



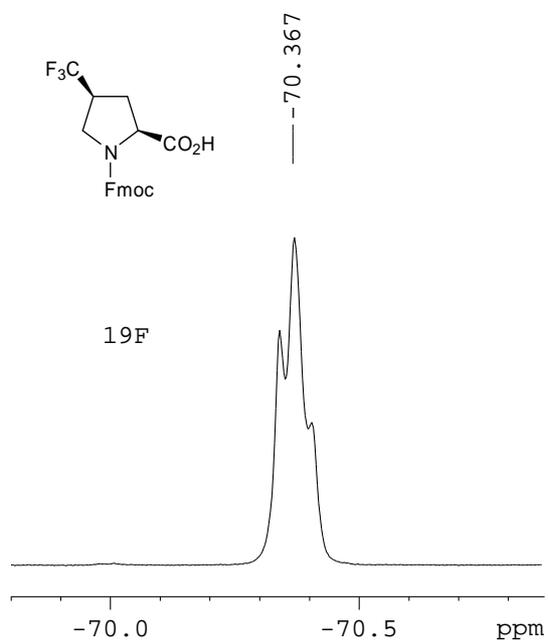
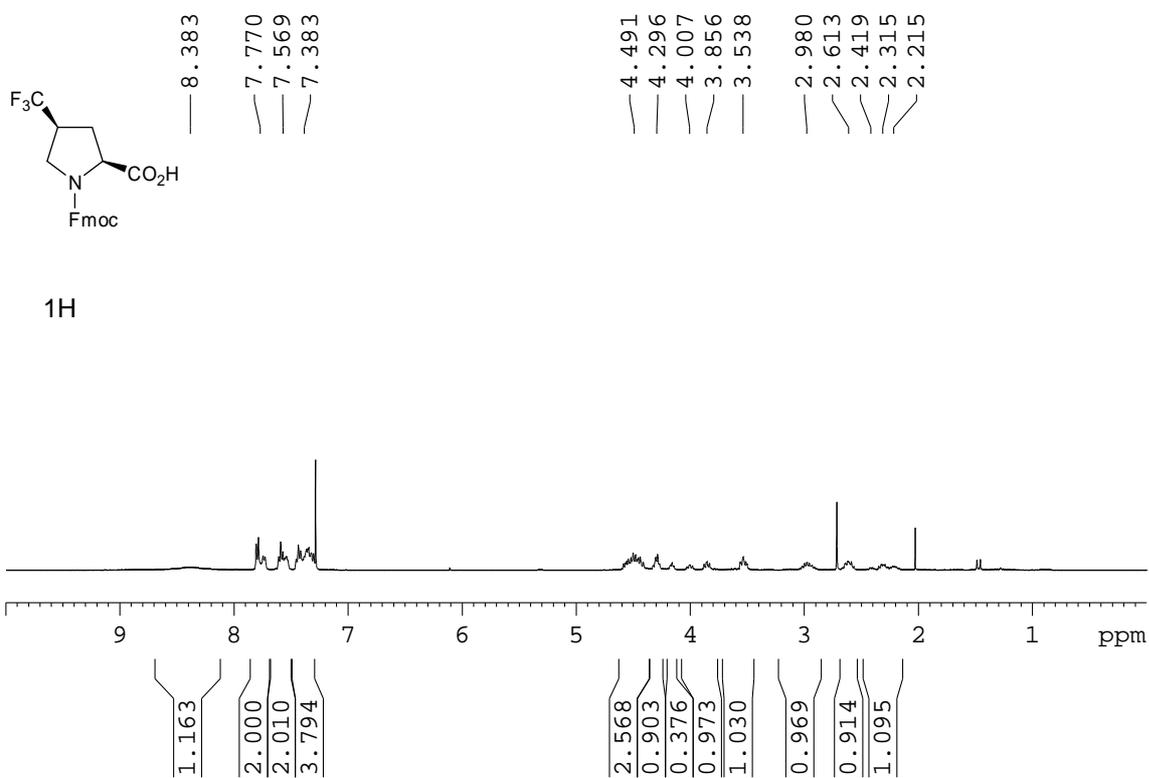


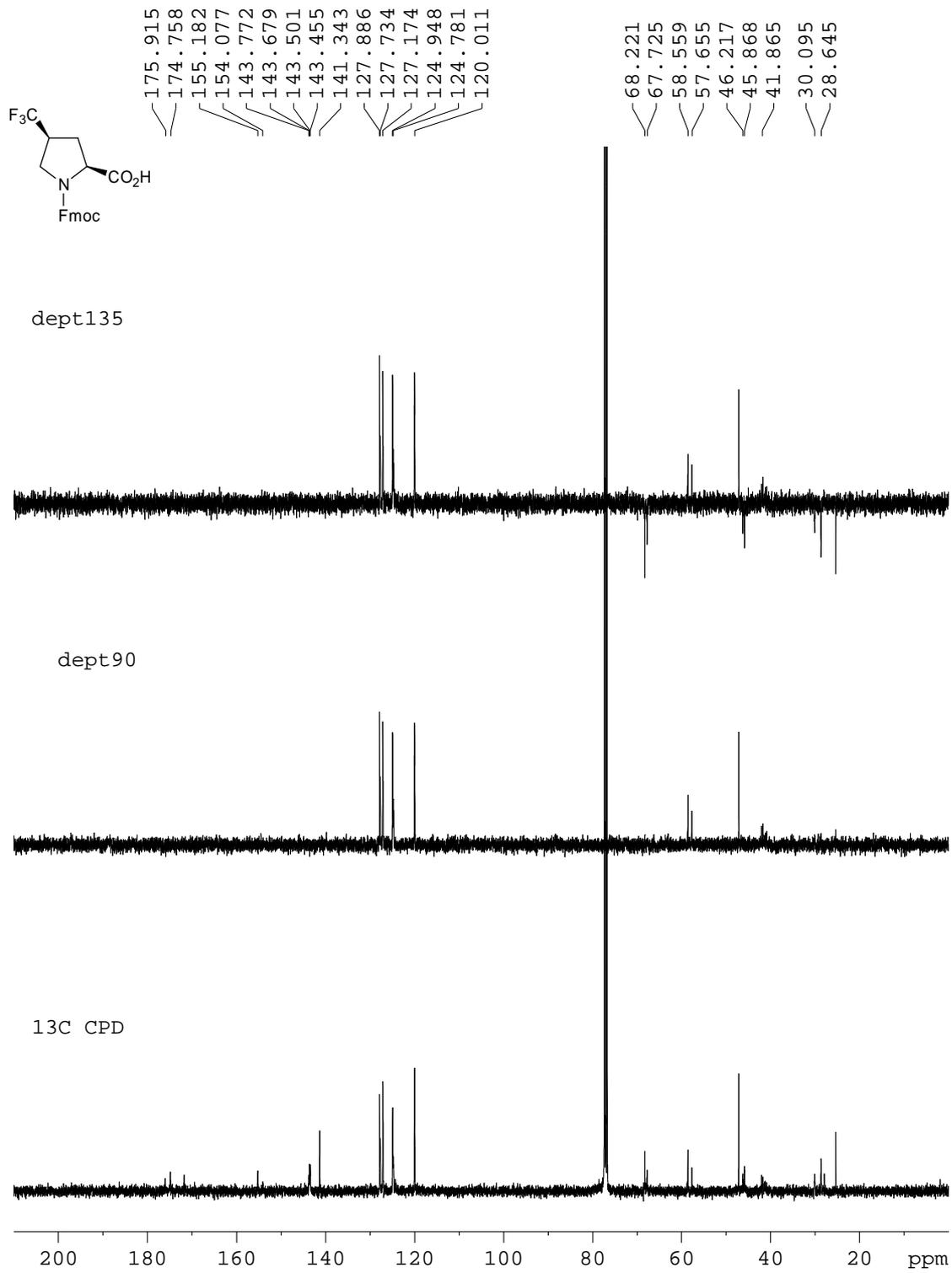
Methyl (2S,4S)-N-tert-butoxycarbonyl-4-trifluoromethylprolinate (**7**)



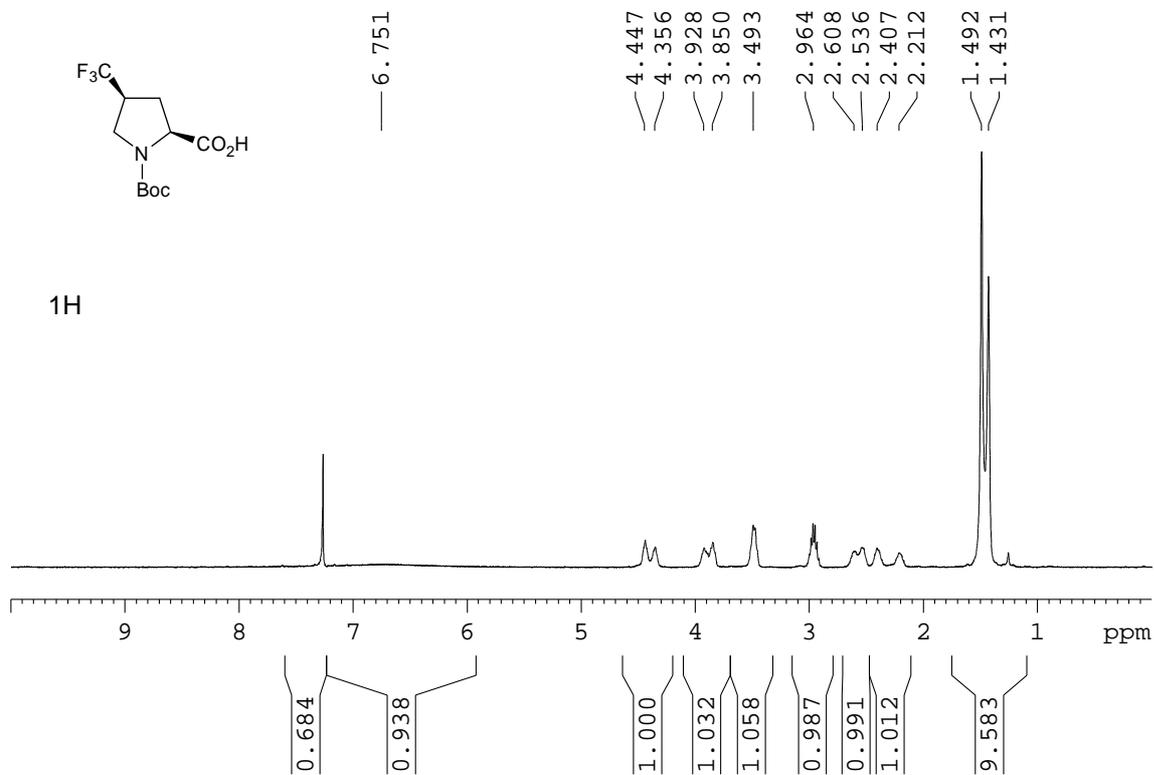


(2S,4S)-N-(9-fluorenylmethoxycarbonyl)-4-trifluoromethylproline (**9**)

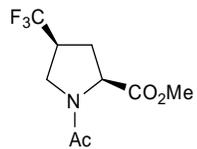




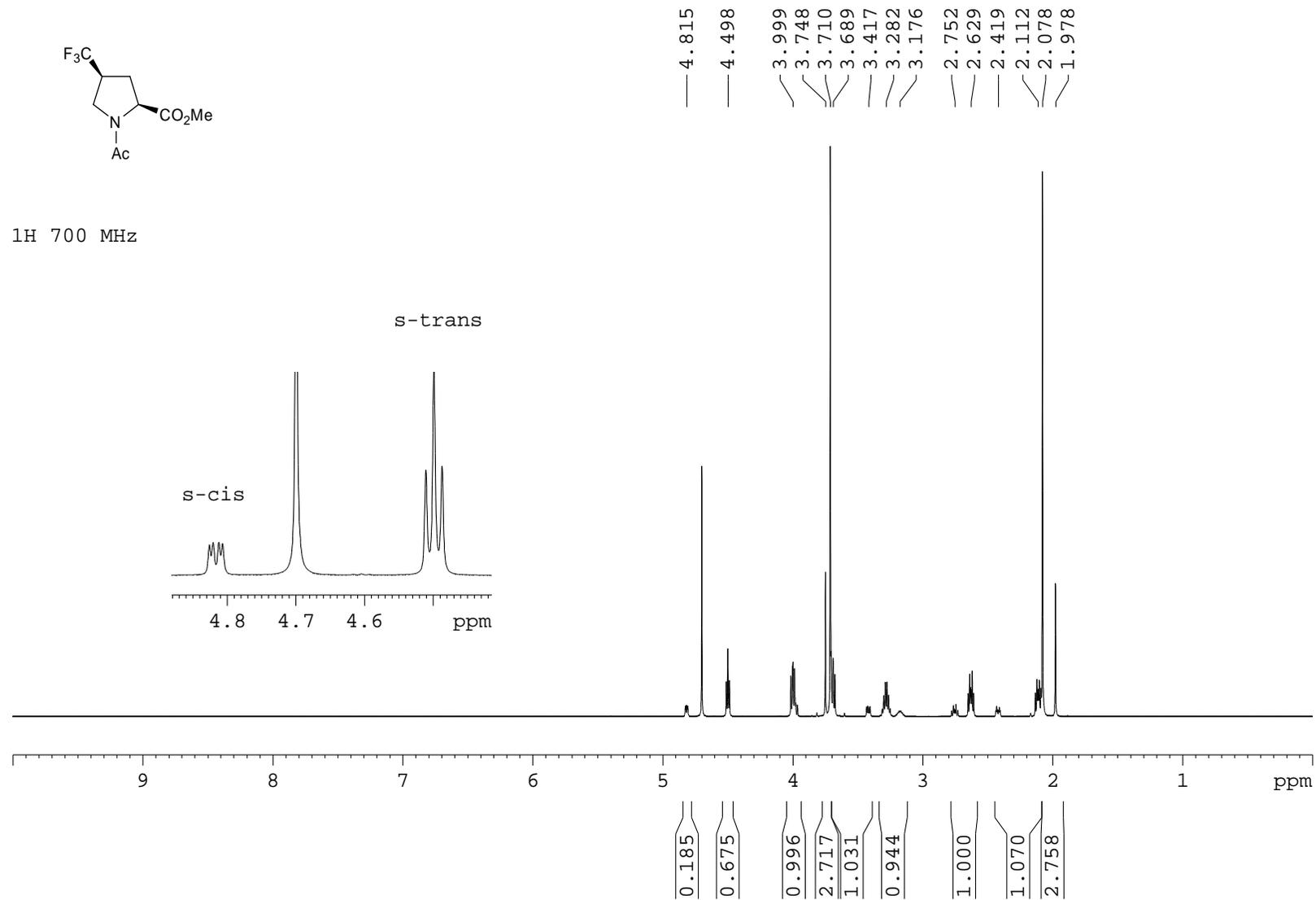
(2S,4S)-N-(*tert*-butoxycarbonyl)-4-trifluoromethylproline (**1**)

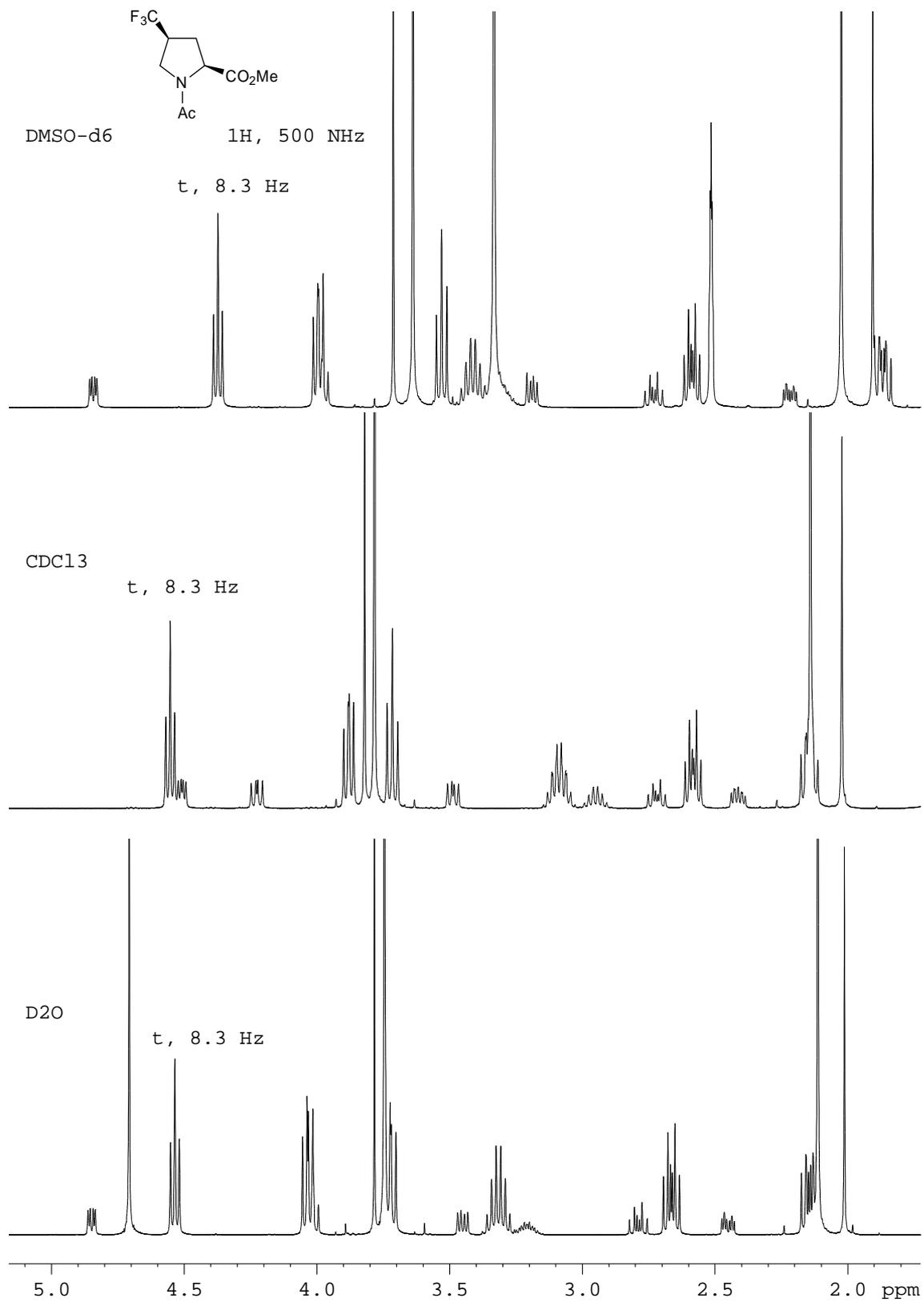


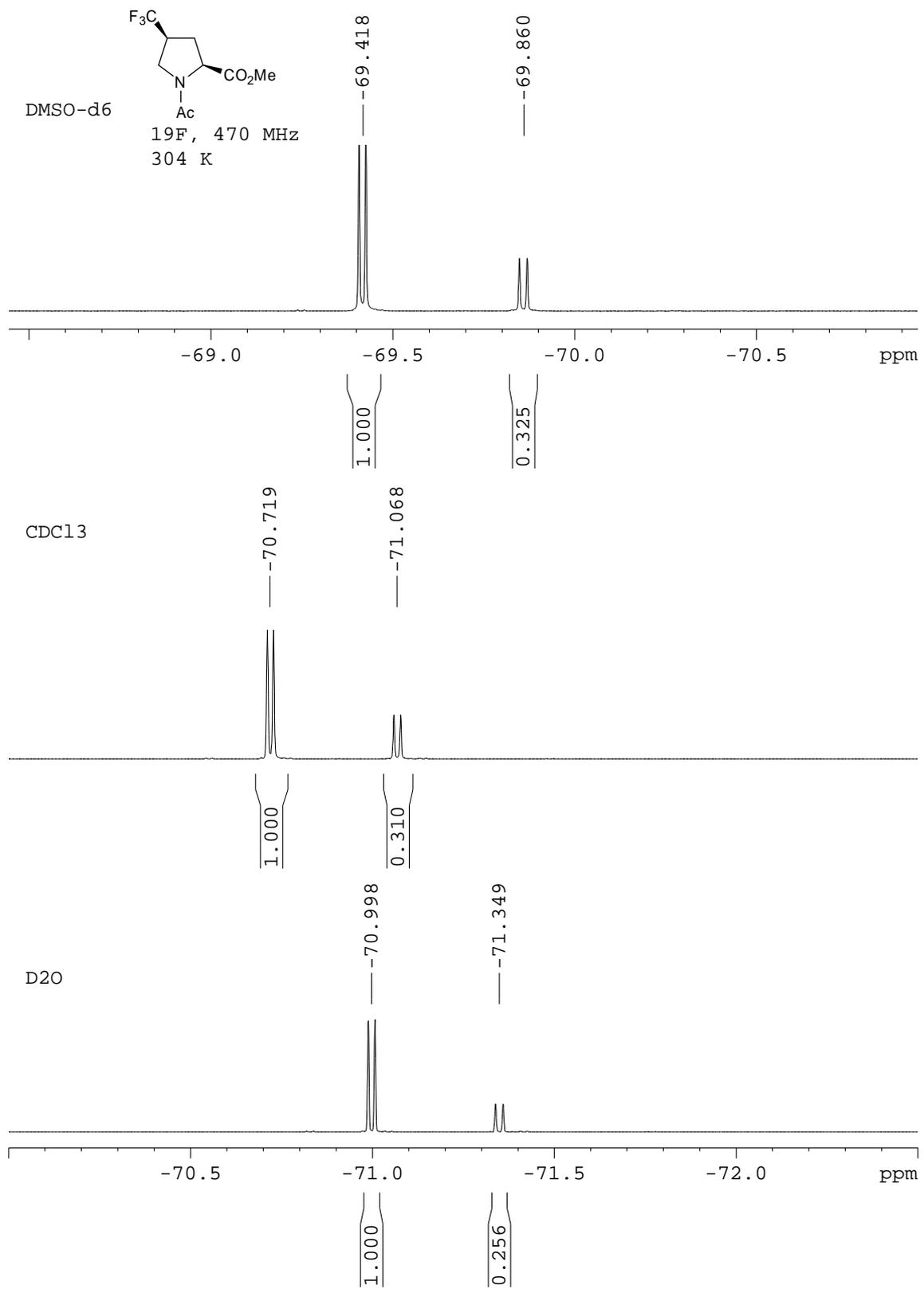
Methyl (2S,4S)-N-acetyl-4-trifluoromethylprolinate (**8**)



¹H 700 MHz







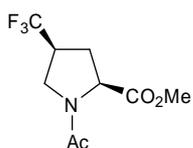
(only the major rotamer labelled)

173.622
172.913

126.063

58.563
53.056
47.188
41.322

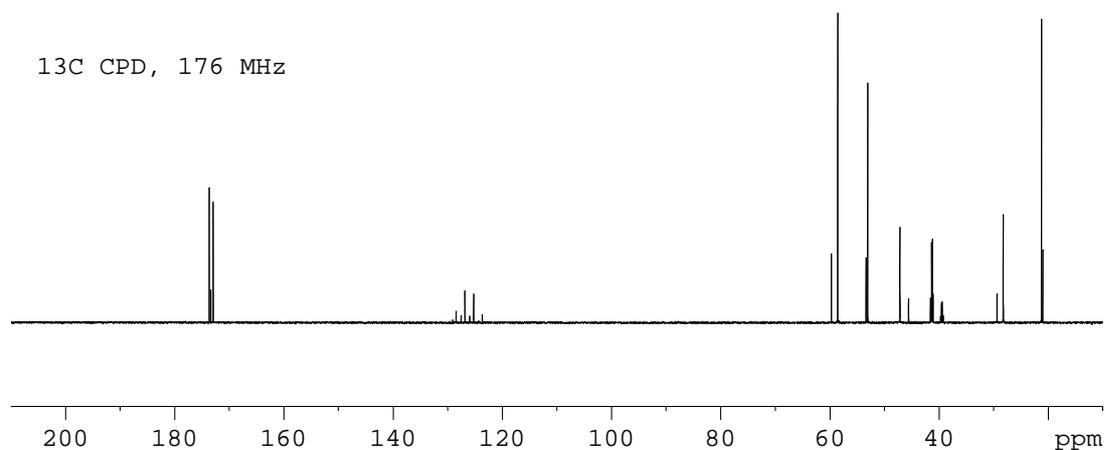
28.272
21.226

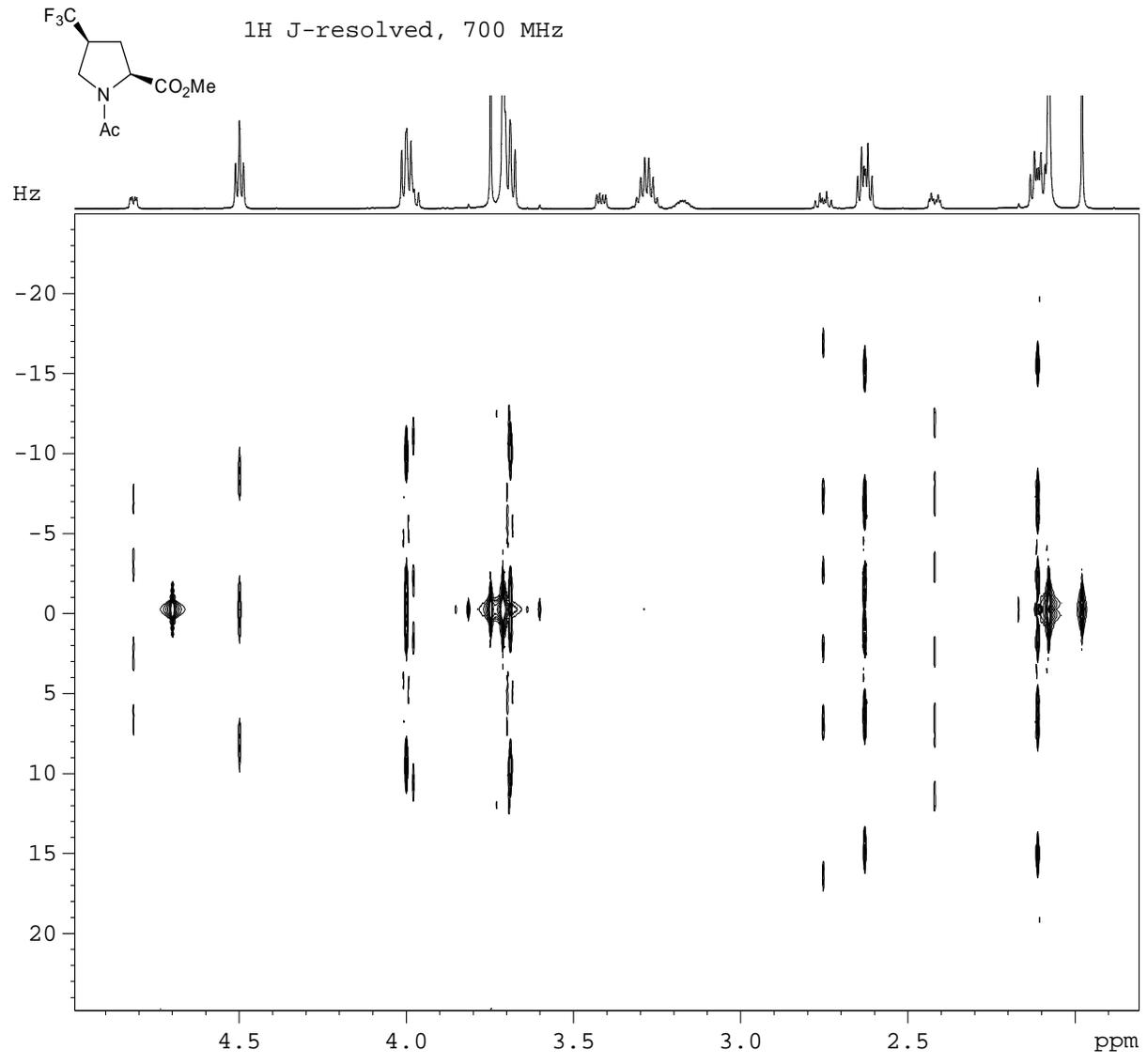


dept135

dept90

dept45





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PROCNO   1

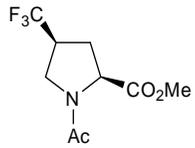
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SOLVENT  D2O
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DS       16
SWH      2230.152 Hz
FIDRES   0.544471 Hz
AQ       0.9183232 sec
RG       33.06
DW       224.200 usec
DE       10.00 usec
TE       297.8 K
DQ       0.0000300 sec
D1       2.0000000 sec
IN0      0.0100000 sec

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P2      34.00 usec
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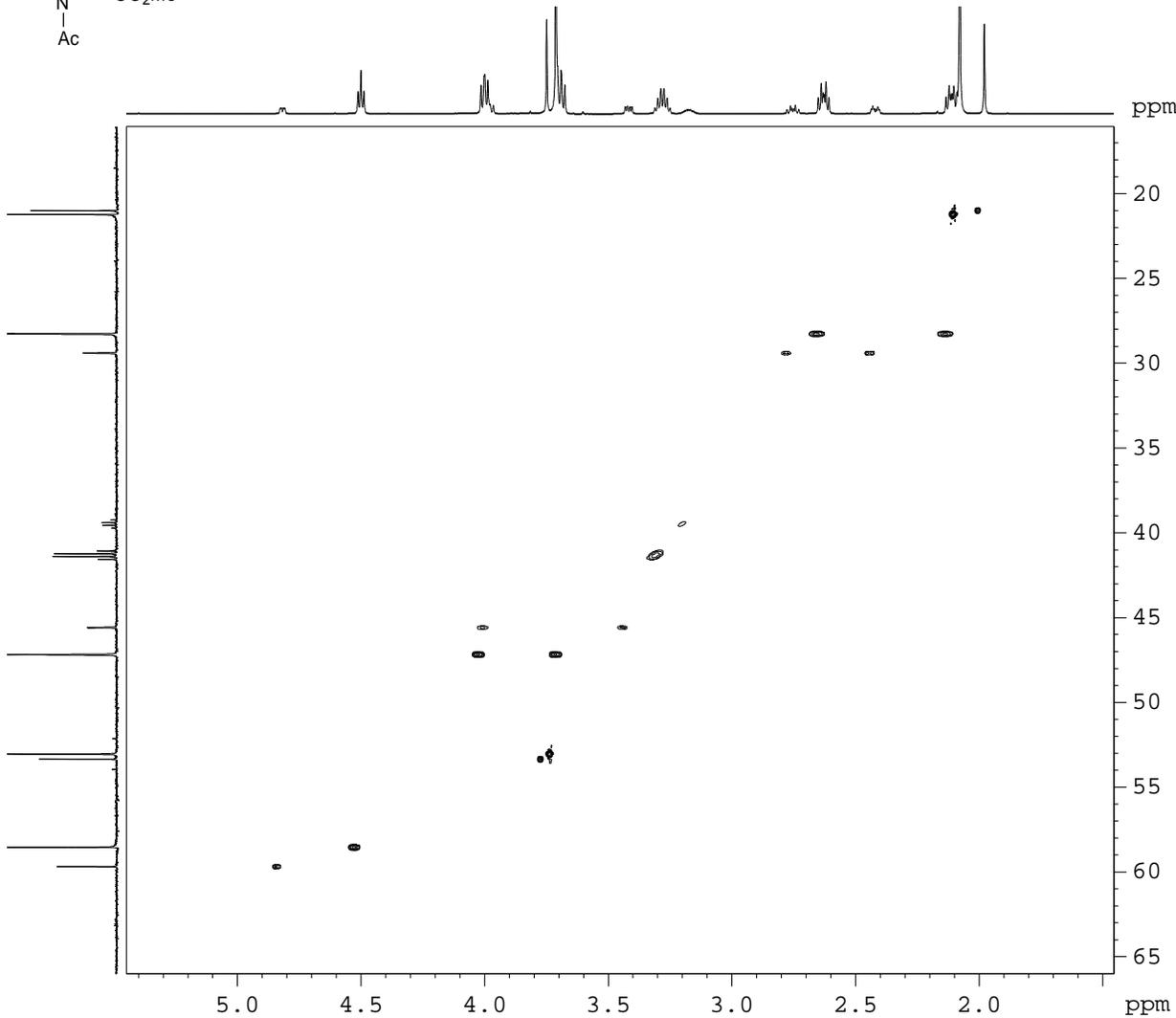
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LB       0 Hz
GB       0
PC       10.00

F1 - Processing parameters
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1H13C HSQC, 700/176 MHz



```

Current Data Parameters
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EXPNO         26
PROCNO        1

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FIDRES        1.366969 Hz
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TE            298.3 K
CNST2         145.0000000
D0            0.00000300 sec
D1            2.00000000 sec
D4            0.00172414 sec
D11           0.03000000 sec
D16           0.00020000 sec
D24           0.00086207 sec
INO           0.00005680 sec
ZGOP1NS

===== CHANNEL f1 =====
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NUC1           1H
P1             17.00 usec
P2             34.00 usec
P28            1000.00 usec
PLW1           22.00000000 W

===== CHANNEL f2 =====
SF02          176.0651054 MHz
NUC2           13C
CPDPRG[2]     garp
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PLW2           67.00000000 W
PLW12          2.92919993 W

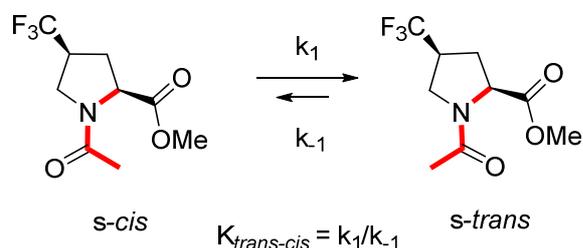
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GPNAM[2]      SMSQ10.100
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GPZ1          80.00 %
GPZ2          20.10 %
GPZ3          11.00 %
GPZ4          -5.00 %
P16           1000.00 usec
P19           600.00 usec

F1 - Acquisition parameters
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SF01          176.0651 MHz
FIDRES        34.386005 Hz
SW            49.998 ppm
PnMODE        Echo-Antiecho

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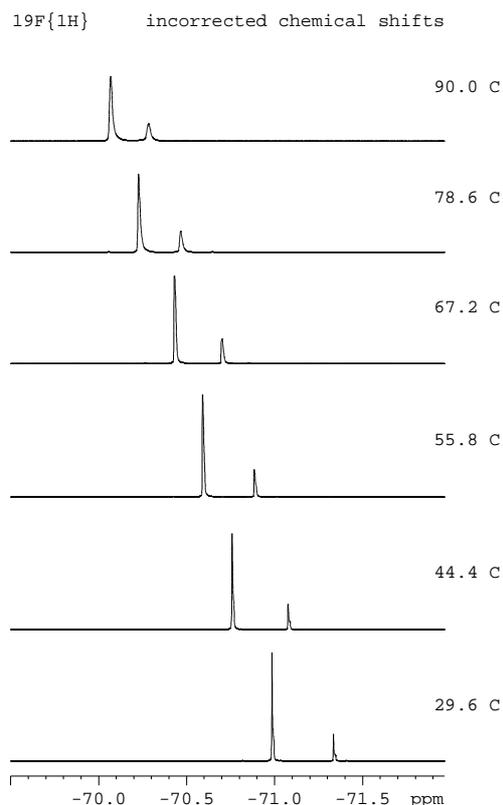
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```

Thermodynamic parameters of the *trans-cis* rotation in 8



Basic experimental procedure is described in the main text. ^{19}F NMR 30-deg flip angle spectra were collected on 471 MHz resonance frequency without or with ^1H decoupling (inverse gated, no NOE enhancement).

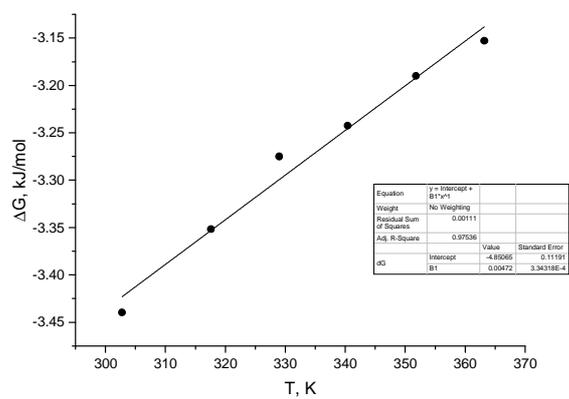
The 1D time domain contained 131072 data-points making 2.8 s acquisition time. Recycling delay was 1 s. The spectra were collected from 4 steady state and 32 recorded transients. Time domain spectra were processed with Gaussian windowing (gb = 0.05, lb = -1 Hz) in a phase sensitive fashion, baseline corrected and integrated. The K values were calculated directly from the integrals and converted into ΔG for plotting.



- measured in deuterium oxide. The shift due to the lock (water) resonance temperature shift was not corrected.

$T_{\text{calibrated}}$, K	T , °C	K_{fc}	ΔG , kJ/mol
302.8	29.6	3.92	-3.44
317.6	44.4	3.56	-3.35
329.0	55.8	3.31	-3.27
340.4	67.2	3.14	-3.24
351.8	78.6	2.98	-3.19
363.2	90.0	2.84	-3.15

linearization:

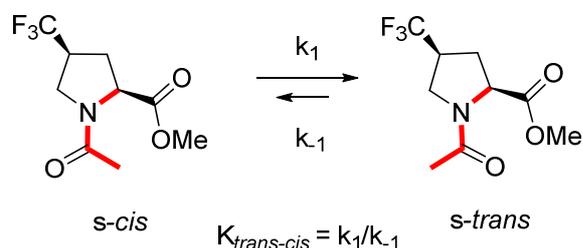


Determined parameters of the rotation:

$$\Delta H = -4.85 \pm 0.11 \text{ kJ/mol}$$

$$\Delta S = -4.72 \pm 0.33 \text{ J/mol}\cdot\text{K}$$

Kinetic parameters of the *trans-cis* rotation in 8

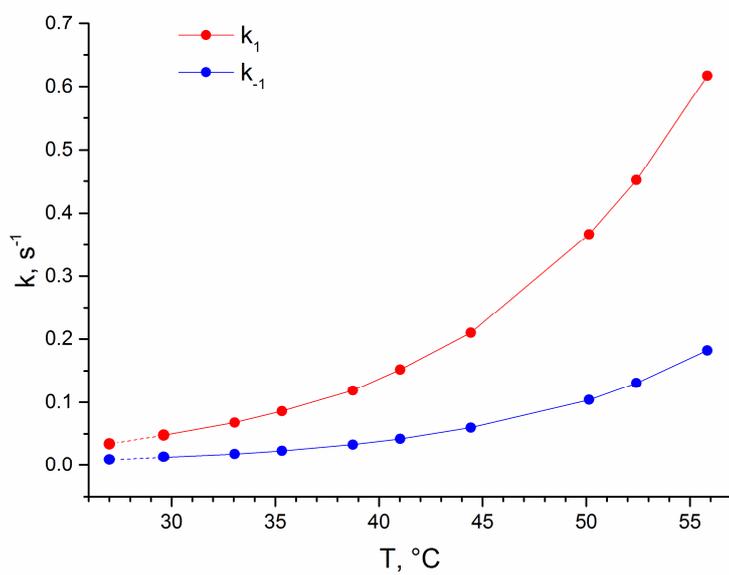


Basic experimental procedure is described in the main text. The ^{19}F EXSY spectra were collected on 471 MHz resonance frequency without decoupling.

The spectral width was 2.0x2.0 ppm, time domain array 2048x512 data-points, making acquisition times of 1.11x0.26 s. Recycling delay was 1 s, number of scans 2. The spectra were processed with sinc squared windowing on both dimensions in a phase sensitive mode, baseline corrected and integrated. 128 data-points were linearly predicted in the indirect dimension. The difference to a standard NOESY processing setup was the use of squared sinc function instead of conventional squared sine bell. This change was done in order to make additional smoothing of the peaks for integration and reduce truncation noise.

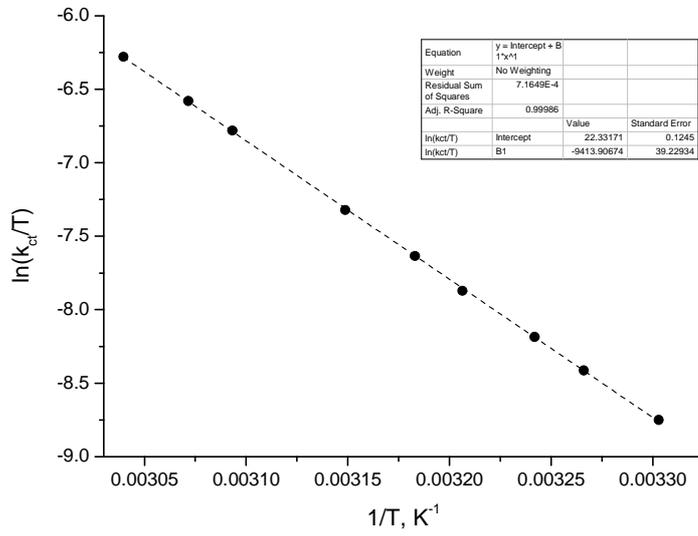
Exchange rate matrices calculations were performed in EXSYCalc® (Mestrec), where EXSY integral values were inset. Secondary diagonal elements were the k values given in the table below:

$T_{\text{calibrated}}, \text{K}$	$T, \text{°C}$	k_1, s^{-1}	k_{-1}, s^{-1}
302.8	29.6	0.048	0.013
306.2	33.0	0.068	0.018
308.5	35.3	0.086	0.023
311.9	38.7	0.119	0.033
314.2	41.0	0.152	0.042
317.6	44.4	0.21	0.06
323.3	50.1	0.367	0.104
325.6	52.4	0.452	0.131
329.0	55.8	0.617	0.182

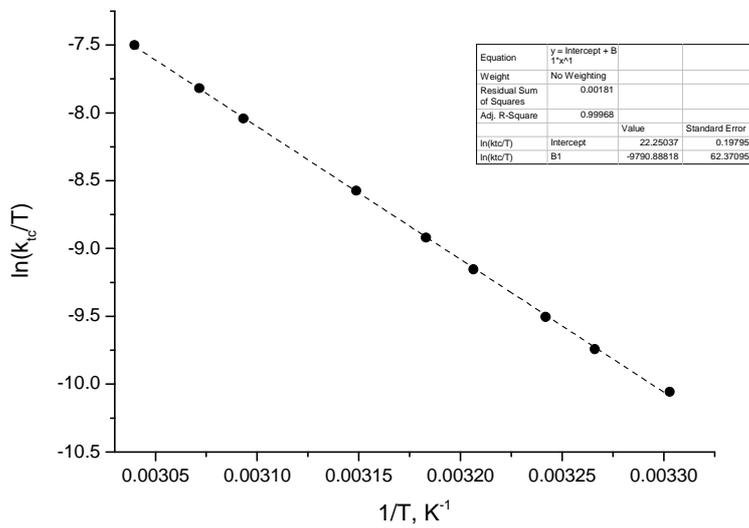


Eyring plots:

for the k_1



for the k_{-1}



Determined parameters of the process:

for k_1 :

$$\Delta H = 78.3 \pm 0.3 \text{ kJ/mol}$$

$$\Delta S = -11.9 \pm 1.0 \text{ J/mol}\cdot\text{K}$$

$$\text{For } 300 \text{ K } E_a = 81.9 \pm 0.6 \text{ kJ/mol}$$

for k_{-1} :

$$\Delta H = 81.4 \pm 0.5 \text{ kJ/mol}$$

$$\Delta S = -12.6 \pm 1.6 \text{ J/mol}\cdot\text{K}$$

$$\text{For } 300 \text{ K } E_a = 85.2 \pm 1.0 \text{ kJ/mol}$$

$$\Delta E_a (\text{cis/trans} - \text{trans/cis}) = -3.4 \text{ kJ/mol}$$

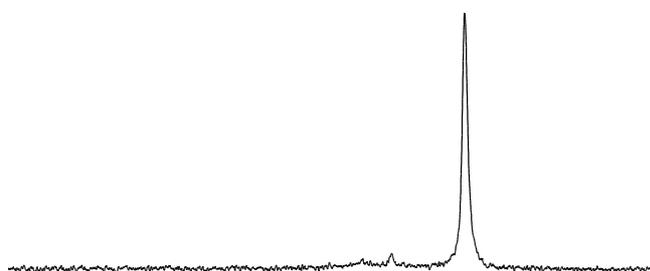
Solution NMR spectra of the peptides

^{19}F NMR spectra of **2TfmPro-GS** in different media (at 298 K):

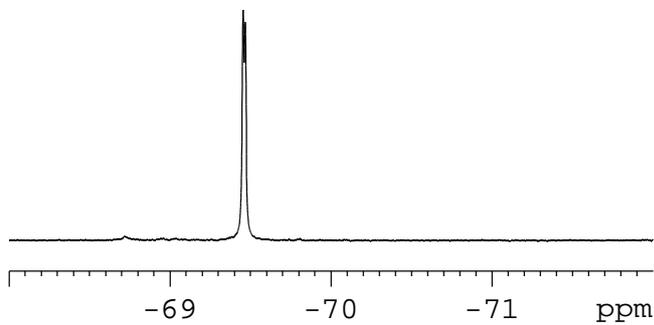
^{19}F W5 (centered -77.2 ppm)
in PB-TFE



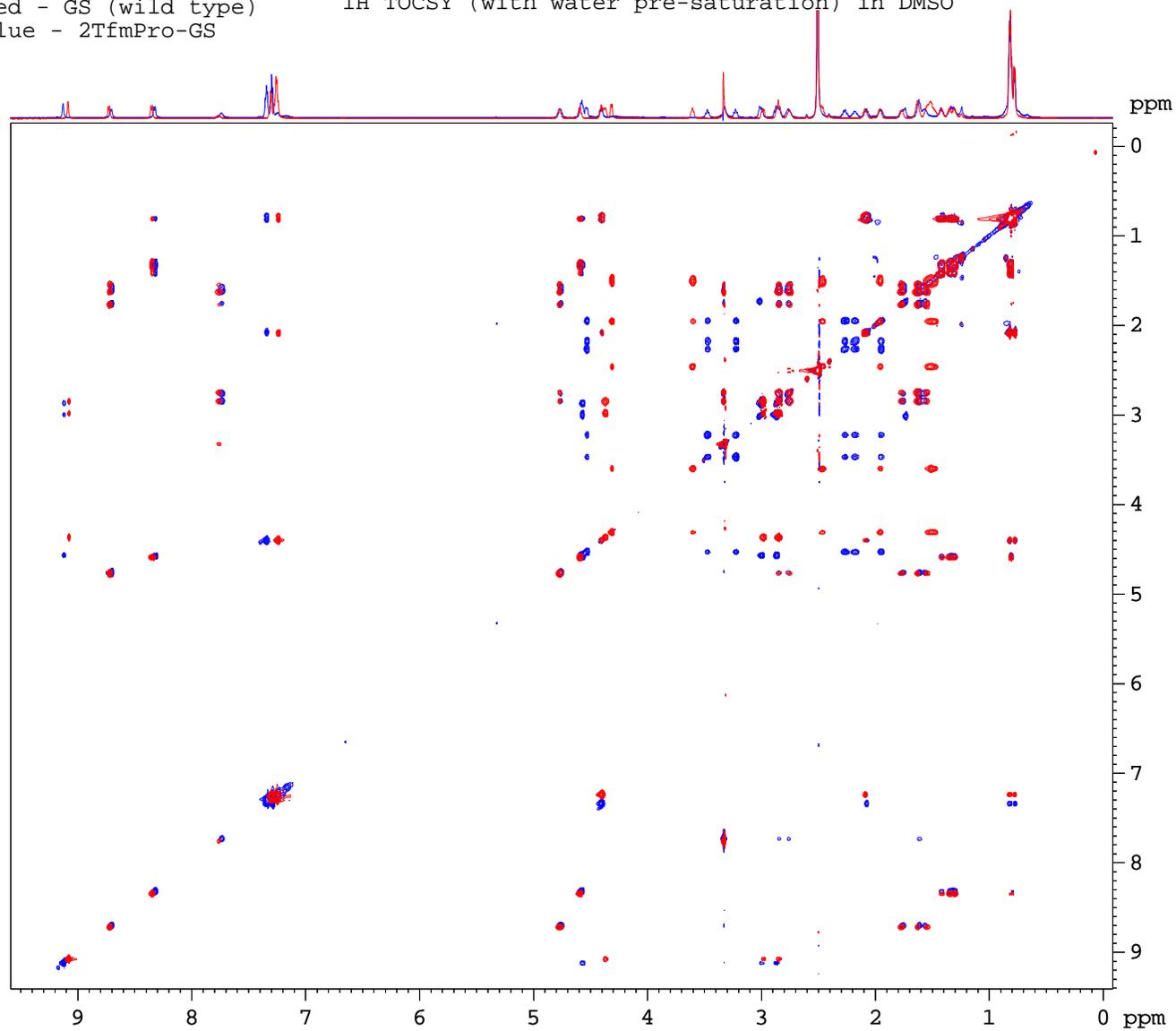
^{19}F in PB / SDS micelles



^{19}F in DMSO-d₆

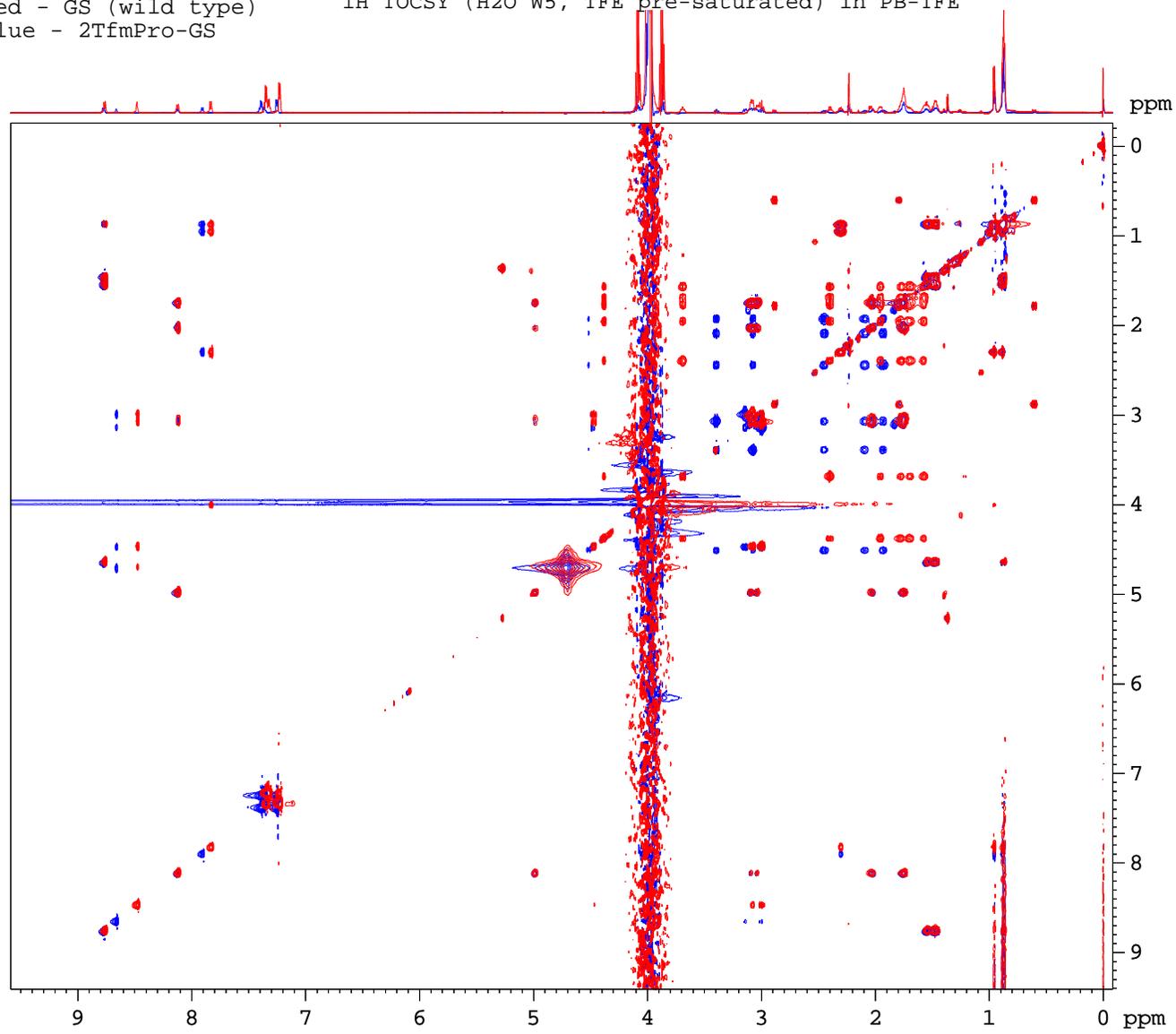


red - GS (wild type) 1H TOCSY (with water pre-saturation) in DMSO
blue - 2TfmPro-GS



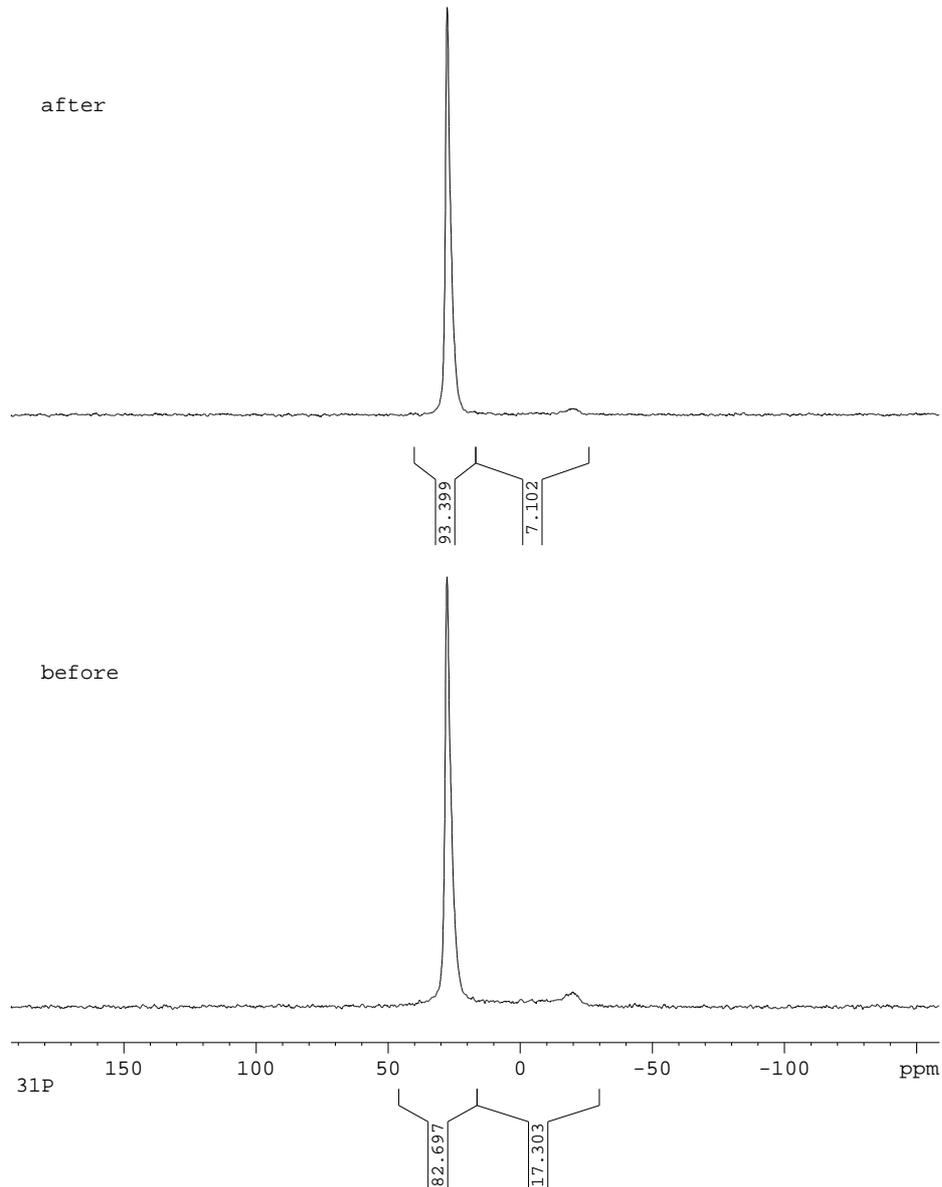
red - GS (wild type)
blue - 2TfmPro-GS

¹H TOCSY (H₂O W5, TFE pre-saturated) in PB-TFE

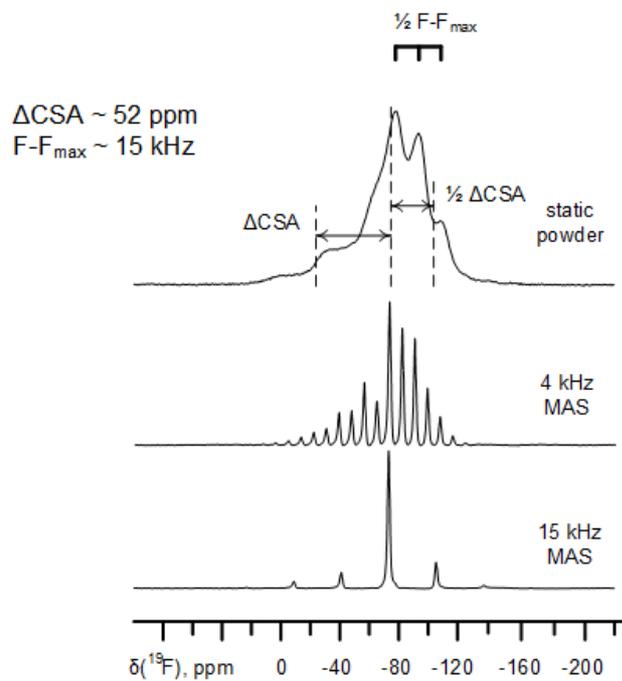


Supporting solid state NMR spectra

^{31}P NMR of the **2TfmPro-GS/DLPC** oriented sample before and after the ^{19}F NMR temperature series reported in the main text. The spectra were measured well above the phase transition of DLPC – at 303 K. Sample macroscopic placement was such that the membrane normal was parallel to the magnetic field. The percentage of the desired macroscopic alignment was found to be higher than 80 %.



^{19}F NMR powder static and magic angle spinning (MAS) spectra of **2TfmPro-GS** for estimation of the maximal anisotropic parameters. The spectra were taken at 298 K and 470.5 MHz. The isotropic chemical shift was found to be -70.4 ppm.



pK_a determination for the amino group of TfmPro

25 mg of **1** was dissolved in 1 ml dichloromethane and 0.5 ml trifluoroacetic was added. The solution was stirred at the room temperature for an hour and the volatiles were blown off by excessive nitrogen current. The rest was dissolved in 50 μ l of water and resulting solution was aliquotized 2 μ l in the NMR tubes containing 550 μ l of 150 mM sodium phosphate buffer. The final concentration of TfmPro in the buffered systems was therefore \sim 6 mM. The last data-point at pH 13 was measured in 0.1 M NaOH.

¹⁹F NMR spectra were measured in inverse gated decoupled 30-degree flip angle experiments at 471 MHz frequency and 298 K. The residual TFA signal was observed at -75.39 ± 0.01 ppm in all samples and the ratio between TfmPro and TFA was found as 1.3. From these measurements several points deviated from the sigmoidal behavior in the range 8.5 – 10.1. In this range the buffer capacity of phosphate buffer is too low to quench 16 mM acidic additive.

Therefore we collected additional dataset with diluted TfmPro*⁺TFA. Such that the final concentration was 0.6 and 0.16 mM.

All datapoints were collected together except of the ones rejected where preference was given to the more diluted samples. The found ¹⁹F chemical shifts of TfmPro were plotted against pH as depicted, fitted according to the Boltzman fit (OrifinPro 9.1, alternatively logistic fit with similar outcome) and the first derivative of the fit delivered the maximum point 8.5. Apparent standard error was 0.1 (electrode).

³¹P NMR chemical shifts were used for control. Two series showed after all a good consistency to one another. The bending point for the second ionization constant was found at 6.8 in both series.

