



KJM 9250

Proton T_1 Spectra on the DRX500 Spectrometer

Version 5.0

Topspin 1.3 Windows XP DRX 500



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1.0 Introduction

An **awprotont1** parameter set and linked **VDLIST** file have been set up on the DRX500 spectrometer running under **TS1.3**

The **awprotont1** parameter set has **D1 = 10 sec** and a linked **VDLIST** file with 8 x delays in the range 0.03 to 10 sec with the longest delay (10 sec) the first used VDLIST value and the shortest delay (0.03 sec) the last used value.

D1 and the longest (first) **VDLIST** value should be 3-5 times the longest T₁ in the sample compound.

T₁ data sets can be processed on the spectrometer terminal or off line using any version of Topspin provided a copy of the linked **VDLIST** file is resident in the experiment's top level folder (= default set up: see below) or a copy of the originally named **VDLIST** file is recreated in the offline terminal's *C:\Bruker\Topspin...\exp\stan\nmr\lists\vd* folder.

 uxnmr.info	2/01/2017 10:50 p...	INFO File	4 KB
 uxnmr.par	2/01/2017 10:50 p...	PAR File	24 KB
 vdlst	10/01/2018 8:49 a...	File	1 KB

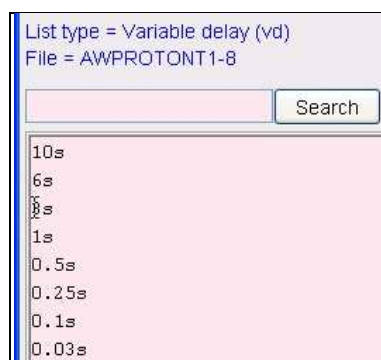
NB: The experimental copy of the variable delay file is named as **vdlst** irrespective of the name of the source vdlst file.

2.0 Experiment Set Up

- 1) Create an experiment and read in the **awprotont1** parameter set (+ **getprosol**).
Pulse programme = **t1ir**.

Two parameter sets with longer **30 or 60 sec d1 delays (awproton30t1 and awproton60t1)** and **12 or 16 VDLIST** values respectively have also been created..

- 2) Review default settings. These settings can be adjusted if required.
TD(F2) = 32K,
TD(F1) = 8 (or 12 or 16 for the 30 or 60 sec VDLIST files respectively)
SW = 14 ppm, O1P = 6.3 ppm.
D1 = 10 sec.
NS = multiple of 2, 4 or 8, DS = 0, 2 or 4.
- 3) Type **ased** (enter) and review other parameters used in the job including the linked **VDLIST** file = **AWPROTONT1-8**
- 4) The **VDLIST** file should have the entries shown below (next page). Values are in seconds. Do not alter the values in this file. An alternatively named **VDLIST** file should be created if different **VD** and **D1** values are required for a particular compound

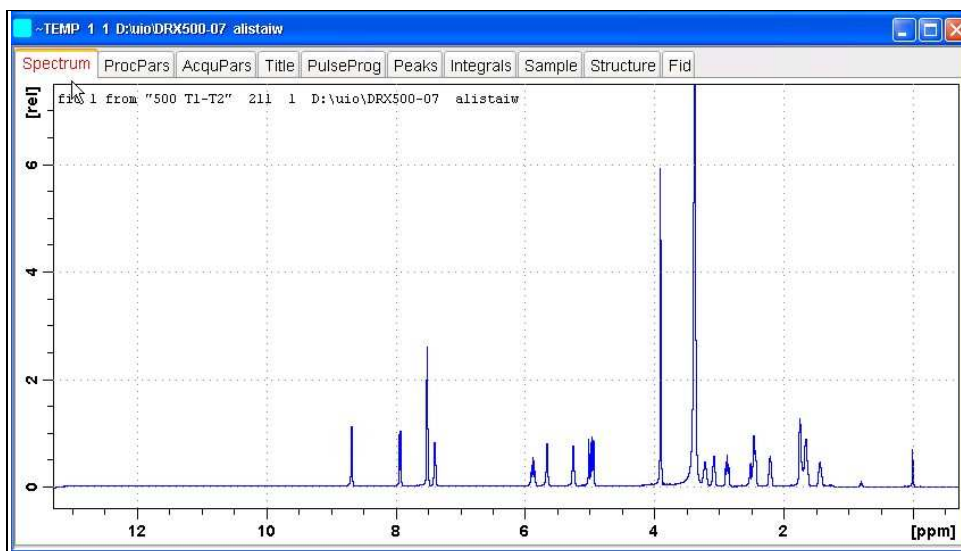


- 5) Set receiver gain using **RGA** (*important!*).
- 6) Type **edp** (enter) and check that **SI(F2) = 32K, SI(F1) = 8, WDW(F2) = EM, LB (F2) = 0.3-0.5 Hz** or other value of your choice.

Reference			
SI =	32768	8	Size of real spectrum
SF [MHz] =	500.1300000	500.1300000	Spectrometer frequency
OFFSET [ppm] =	13.301	12.308	Low field limit of spectrum
SR [Hz] =	0.00	0.00	Spectrum reference frequency
HZpPT [Hz] =	0.213709	751.201904	Spectral resolution
Window function			
WDW =	EM	no	Window functions for trf, xfb,...
LB [Hz] =	0.3	0.30	Line broadening for em

Experiments with 12 or 16 VDLIST points are processed with SI(FI) = 16.

- 7) Start the acquisition using the **ZG** command.
- 8) When the experiment has run type **rser 1** (enter) to read in the first serial file which will appear in a TEMP screen display window.
- 9) Type **EFP** (return) to transform it and phase it as per a normal proton spectrum.



- 10) Type **edp** (enter) and note the phase constants for this spectrum.

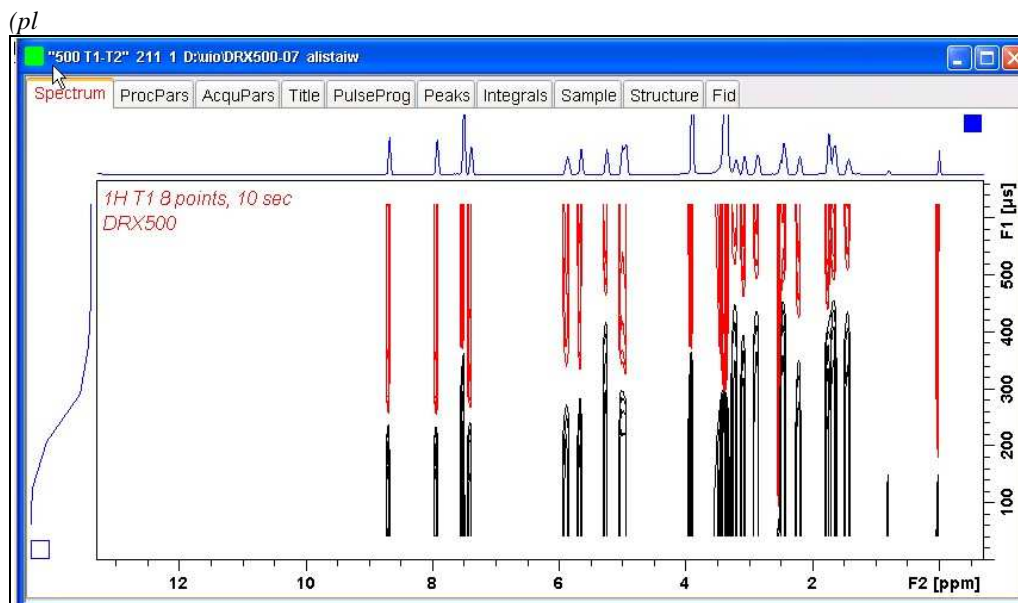
Phase correction	
PHC0 [degree] =	185.998
PHC1 [degree] =	0.019
PH_mod =	pk

- 11) Close the **TEMP** window and reload the T₁ data set file.
- 12) Type **edp** (enter) and enter the phase constants noted in step 10 above into the **F2 PHC0** and **PHC1** cells and check **PH_MOD = pk**. **F1** cell info is not used.

Phase correction			
PHC0 [degree] =	185.998	0.000	0th order correction for pk
PHC1 [degree] =	0.019	0.000	1st order correction for pk
PH_mod =	pk	mc	Phasing modes for trf, xfb, ...

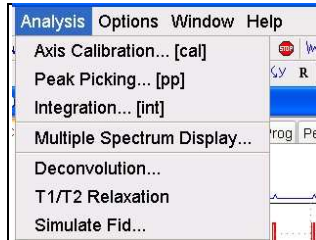
- 13) Type **xf2** (return) to transform the 2D data set followed by **abs2** (return) to baseline smooth it.

- 14) Provided phase constants have been correctly set up the transformed data set plot should resemble that shown below. Black = a positively phased signal, red = a negatively phased signal.

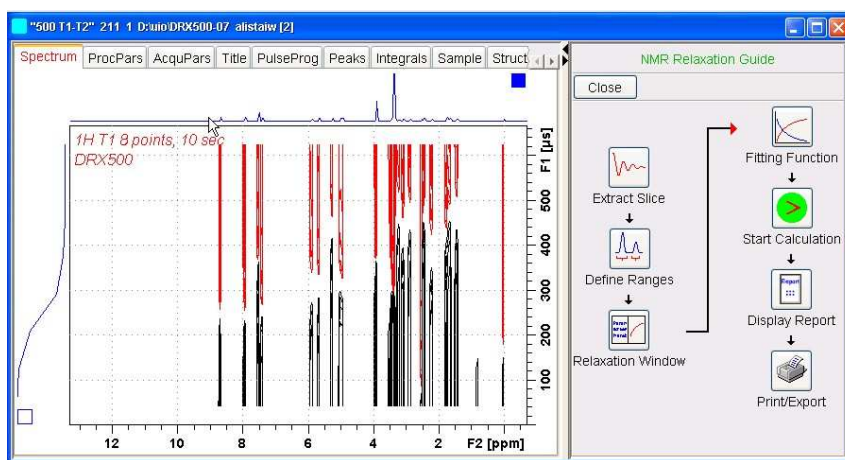


3.0 T₁ Data Set Processing

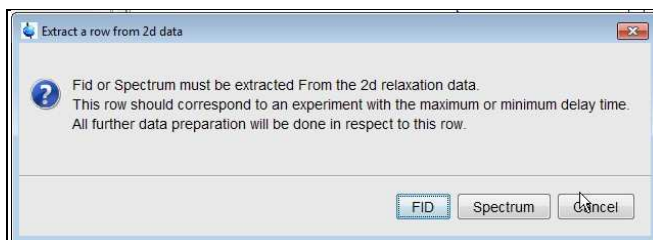
15) Open Topspin's **Analysis** menu and click its **T1/T2 Relaxation** tab.



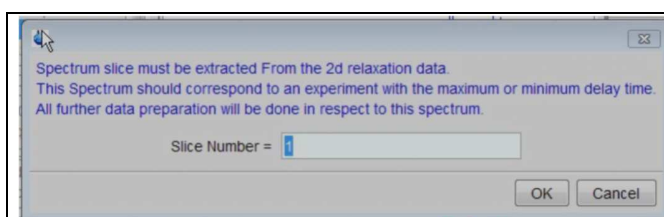
This will open up the screen display shown below.



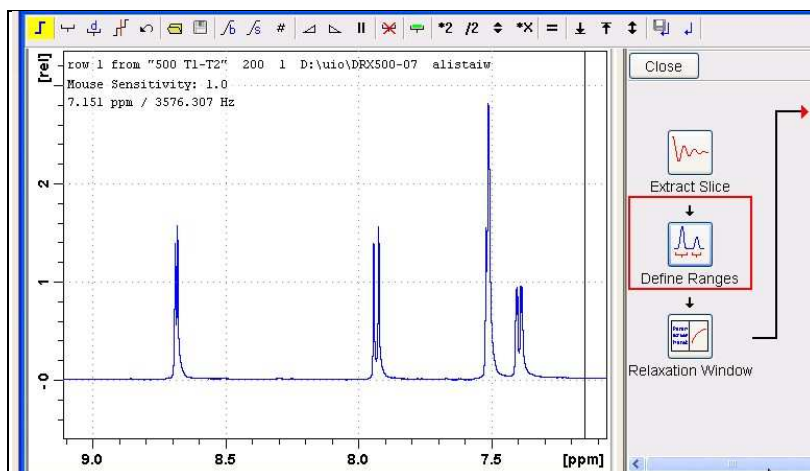
16) Click the **Extract Slice** button and then click the **Spectrum** button in the panel that appears.



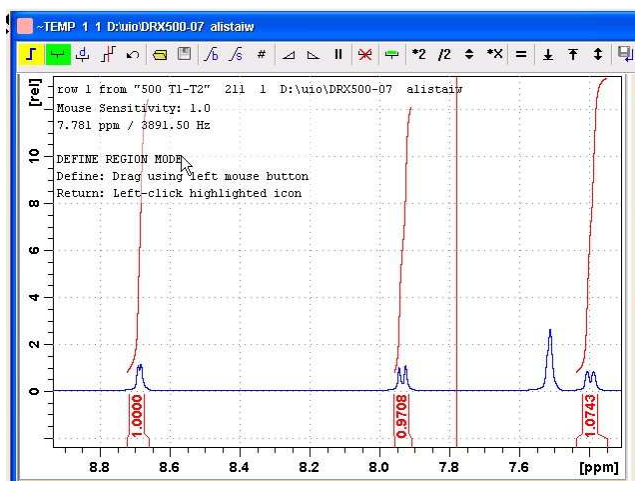
17) Enter **1** in the **Slice Number** cell and click the **OK** button. This will display the transformed spectrum ex the first (longest) **VDLIST** value = the one that was phased via the **rser 1** routine in steps 8 and 9.



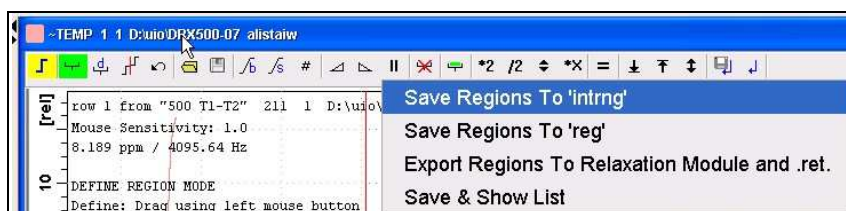
18) Close the screen message that appears and click the **Define Ranges** button.



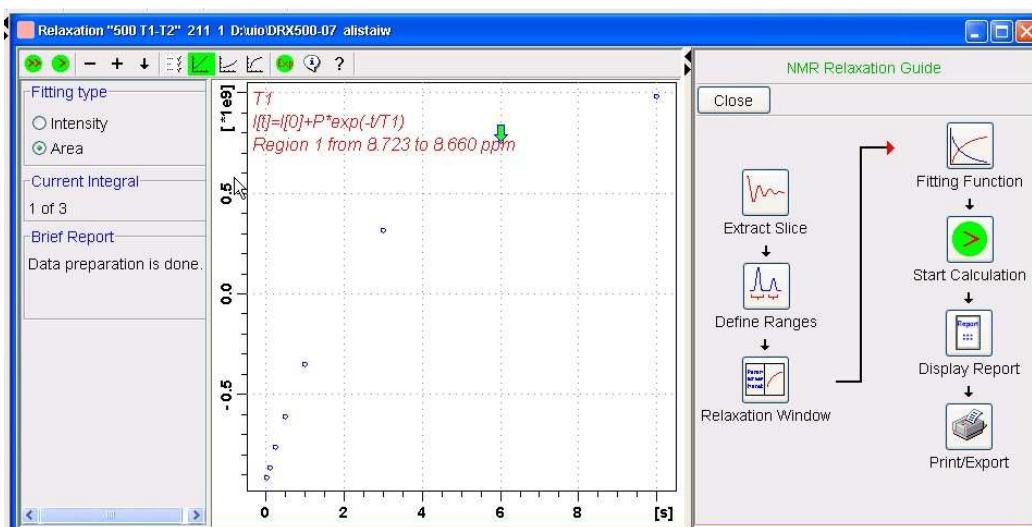
19) Expand the spectrum that appears in the usual way and integrate selected peaks in it. Integrals should start and terminate as close as possible to the edge of a peak.



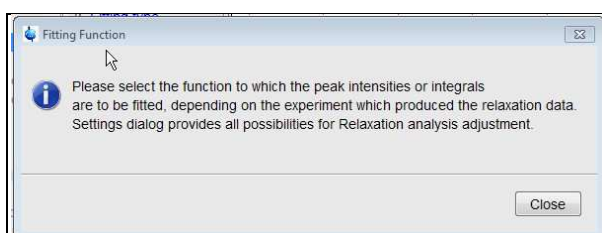
20) Click the Floppy Disk icon button (7th from the left hand side of the menu bar in TS1.3) and select its **Export Regions to Relaxation Module and .ret.** tab.



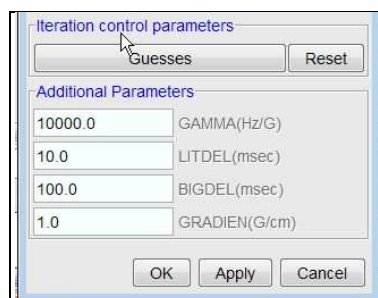
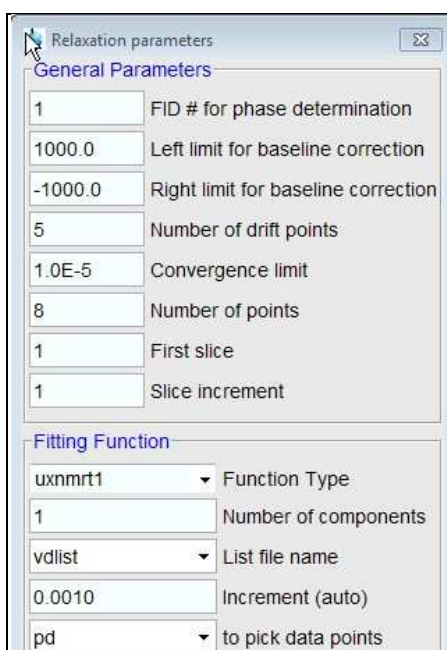
- 21) Click the **Relaxation Window** button, note any screen messages that may appear and close them. Select **Intensity** or **Area** in the plot window that appears. **Area** is invariably the better choice.



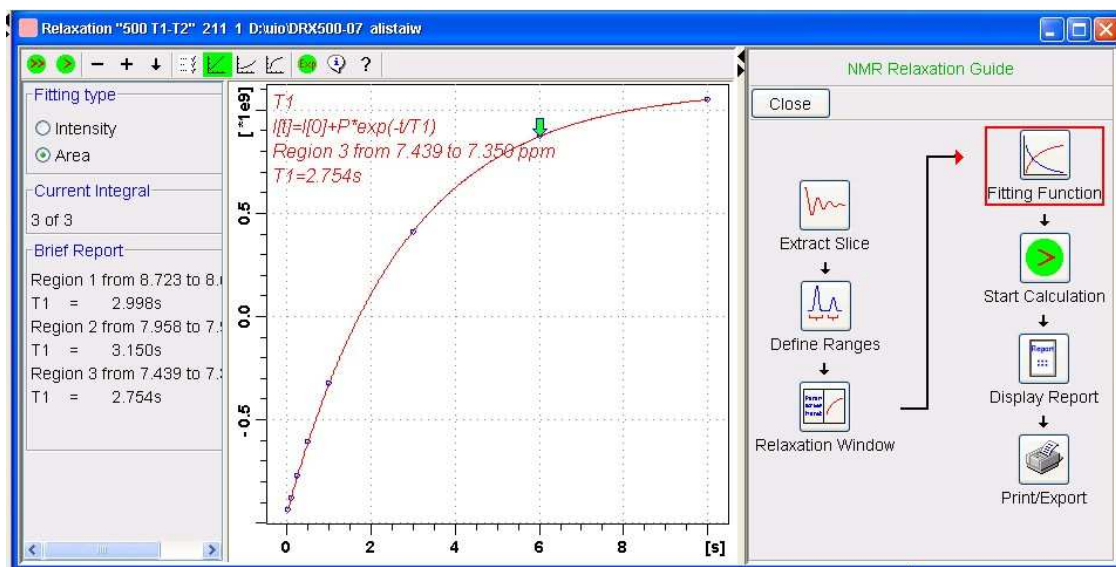
- 22) Click the **Fitting Function** button and note the comments about **intensity** or **area** options in the screen display that appears and close it.



- 23) When the Fitting Function message screen is closed a panel with relaxation parameters (split into two screen will appear).



- 24) Check **Function Type = uxnmrt1** and **List file name = vdlst**.
Other cells/values can be left as they are (= default settings)
- 25) Click the **double red arrow** in the menu bar at the *top left* of the plot window and **NOT** the single red arrow button in the NMR Relaxation Guide menu below the Fitting Function button.



- 26) The + and - buttons in the upper menu bar can be used to advance (or reverse) the individual T₁ plots.
- 27) Fitting type (**Intensity** or **Area**) can be changed in the plot display. If this is done clicking the **double red arrow** will recalculate the T₁ results and update their plots.
- 27) The NMR Relaxation Guide has buttons which can be used to display and/or print T₁ results. A sample report for one signal is shown below.

