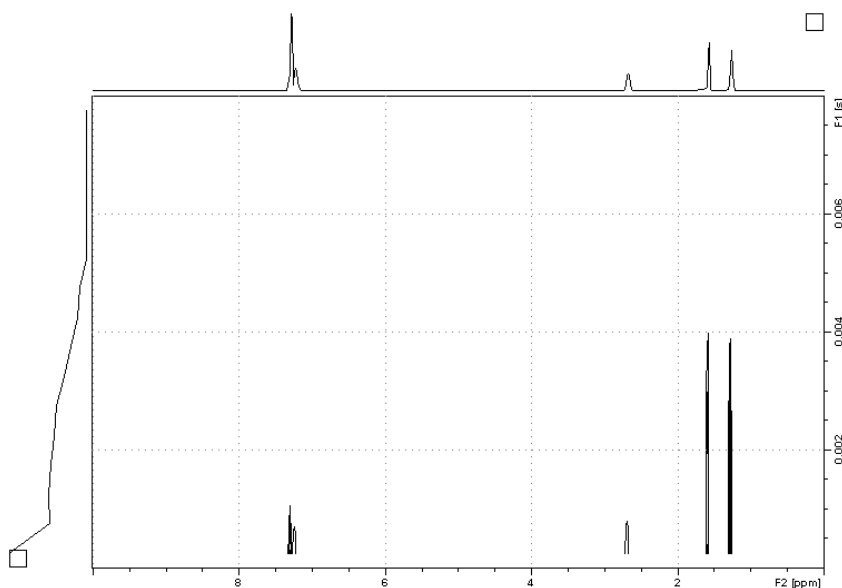


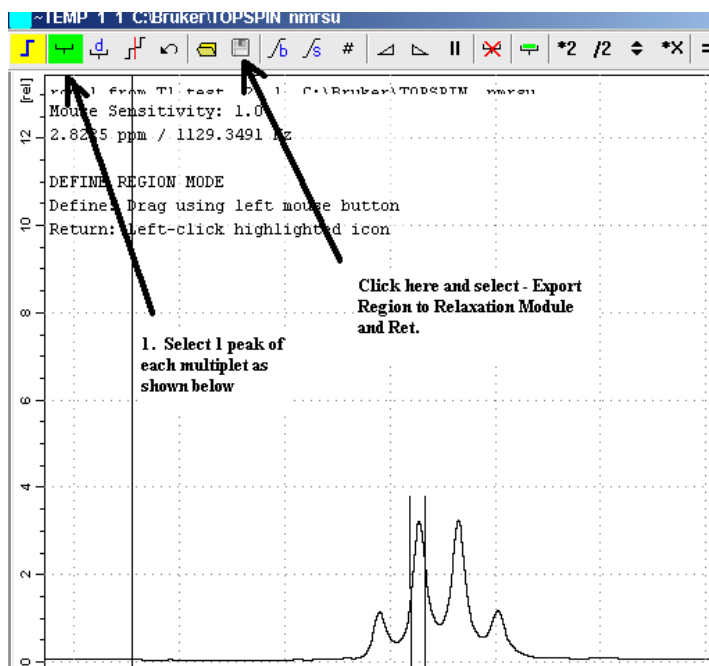



T1 Inversion Recovery - Quick Reference

1. Setup and obtain an optimized 1-D proton spectrum on your sample of interest.
2. To obtain a quick T1 estimate follow these steps. For a more accurate T1 measurements go to step 3. Type **'iexpno'** [enter]. Type **'eda'** [enter] and change the pulse program to **t1ir1d**. Type **'d7 0'** [enter]. Type **'phmod pk'** [enter]. Type **'ns'** [enter] and type **'1'** [enter]. Type **'zz'** [enter]. Phase your spectrum so all the peaks are negative if they are not that way. Now, type **'iexpno'** [enter]. Type **'d7 1'** [enter]. Type **'zz'** [enter]. Some of your peaks may still be negative, some may be positive, some may be null. Your goal is find the null point of your peaks of interest by changing **d7**. If your peaks vary greatly, you may want to run the longer pseudo-2D version described below. T1 is approximately = **d7** for null*1.443].
3. It is a good idea to do the quick estimate described in #2 prior to running this extended version so you can set an appropriate D1 value. D1 for this experiment should be no less than 3 X longest T1 from #2. Type **edc** [enter] and change the experiment number to **2** (or type **iexpno** [enter]). Type **rpar** [enter] and select **T1_BROWN, copy all**. Type **'eda'** [enter] and make sure the values of **sw** and **o1p** and **aq** are the same as those you recorded from **exp 1**. Select the proper solvent and click the little blue test tube 'prosol' button. This is not a 2-D experiment, but it is set up in 2-D mode it is an array of 10 different experiments. Each experiment uses a different variable delay, read from the default **vdlist**, **t1delay**. To view the default values, type **'vdlist'** [enter] and select **ok** and the values of the default list will be displayed. If you change them, click the 'save as' button and give it a name specific to you. You may need to generate your own vdlist if the default list does not afford you a reasonable fit when calculating T1. Be sure to write down how many entries are in your list, and realize that the default values are seconds so use the following format when making your own list – 0.001, 0.01, 0.1, 1 for 1ms, 10ms, 100ms, or 1s. In the 'ased' window, you will need to put your filename in the **vdlist** window, and the number of entries in your vd list is the value that goes in the td box of F1. Type **rga** [enter] and then **zg** [enter] when rga is finished. Default is set to 1 scan to get an idea of how well experiment will run. Once curve looks good, repeat experiment with 8 scans.
2. When the acquisition is finished, type **'xf2'** [enter]. Increase the intensity until you see intensity form at the bottom of the screen at the chemical shifts of your



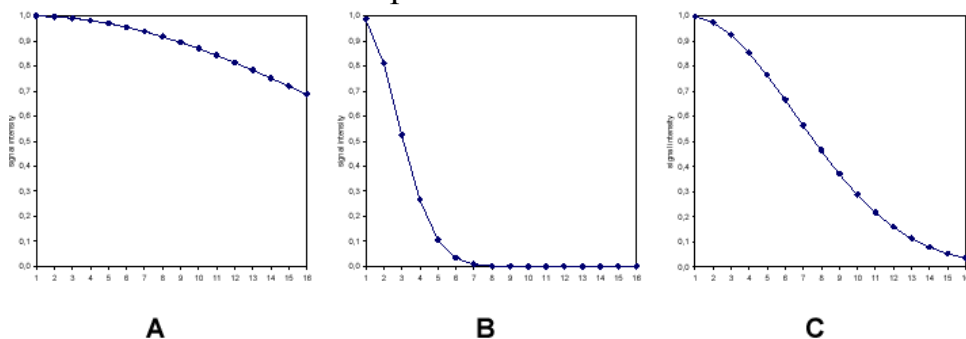
spectrum (see figure). Click the phase button . Right mouse click on one of the signals in your spectrum and select 'add'. Next click on the  horizontal arrow with the R over it. Your spectrum should appear. Phase it and save it. Type 'abs2' [enter]. Select 'T1/T2 Relaxation' from the 'Analyse/Dynmaics' pull down menu at the top of the screen. Select 'Extract Slice' [enter], 'Spectrum' [enter], 'Slice #1' [OK]. Your spectrum should appear and it should be phased. Select 'Define Ranges' in the relaxation module and click [OK] to the pop-up box. Use the normal expansion tool to expand around each of the peaks you wish to analyze. Next, click the little bracket tool to select a region in each of your resonances of interest. NOTE: This routine does not work well if there are baseline artifacts so if you have negative intensity on the edges of your resonances, select a narrow region as shown in the figure. When all of your resonances are selected, click the disc button and choose 'Export ...' (See Figure).



3. Click the Relaxation window icon. Click 'OK'. Click the  icon to calculate the T1 of all the resonances you selected. The default mode is 'area'. You can try 'intensity' as well. The data should be close either way. Click the + or - to scroll through the different curves. You want the curves to look like a smooth decay. Click the 'Display Report' icon and you will see a tabulated data table for each of your resonances that you can print if you wish. Obviously if your curves look bad, you will need to run the experiment again with an edited vdlst.

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Examples of good curves and bad curves. NOTE: Depending on phasing, your curves may be opposite of these curves. It's not the slope that matters, but that you make it from one extreme to the other with the data points in the middle.



- A – Delays would not be long enough
- B – Delays would be too long.
- C – Delays would ideal.