## **External Referencing of Samples** on the U400

There are several ways to reference the chemical shifts of a given sample.

1. Reference to the solvent. This method is most commonly used for <sup>1</sup>H and <sup>13</sup>C NMR where an organic solvent such as CDCl<sub>3</sub> is used which has residual protons and carbon-13 at natural abundance.

2. Reference to an added standard. Tetramethylsilane (TMS) is the standard reference for <sup>1</sup>H, <sup>13</sup>C and <sup>29</sup>Si NMR.

3. Reference to a compound in a capillary tube which is placed in the research sample. In this case, the standard might be insoluble in the lock solvent chosen or it might be reactive with the solvent or research sample.

4. Reference to an "external" standard. This usually means that a standard sample is inserted in the spectrometer, a frequency measurement taken, the standard removed, the research sample inserted, a spectrum obtained and the frequency calibration applied to the spectrum.

This fourth method of referencing is the focus of this handout. Three possible cases exist and are given in order of preference for accuracy of the reference.

1. The standard sample and the research sample are both in the same lock solvent at similar concentration and ionic strenghth

- 2. The standard sample is in a different lock solvent than the research sample.
- 3. The standard sample is not in a lock solvent, or the research sample is not in a lock solvent.

Three examples are given below.

**Example One:** The standard sample has a lock solvent.

<sup>19</sup>F research sample in CDCl<sub>3</sub> and CF<sub>3</sub>C<sub>6</sub>H<sub>5</sub> standard in C<sub>6</sub>D<sub>6</sub>. (Note that CDCl<sub>3</sub> at 7.26 ppm and C<sub>6</sub>D<sub>6</sub> at 7.24 ppm are close enough in lock frequency that this will work.)

insert the research sample

	use the standard setup for F19	
jexp1 <>	join experiment 1	
LC Main Menu	activate main menu display	
LC Setup	activate setup menu	
LC Nucleus,Solvent	select nucleus, solvent menu	
LC F19	select nucleus	
LC CDC13	select solvent	
rts('current shim library') <>	retrieve shims	
su <>	perform experiment set up	

When set up is complete:

load='n' <>dg <>

set load shim values to no display acquisition parameters

lock the sample and crudely shim Z1 and Z2 and disconnect the VNMR Acquistion window set nt to some reasonable number that will allow the peak(s) to be visible start acquisition (will wft when complete) ga <>

when acquisition is complete:

f full <>	display full sweep width to screen		
aph <>	autophase		
make sure that the peak(s) are visible at this sweep width and number of transients			
LC Connect (in the VNMR acquisition window)	IMPORTANT:		
LC Lock	If you do not turn the lock off before		
LC Lock off	ejecting the sample, your reference		
eject the research sample	will not be correct.		
insert the standard sample			
do not change any parameters			
lock on the standard by			
LC Lock off	turn lock off		
LC Lock on	turn lock on		
do not change Z0			
it might be necessary to increase lockpower and/or lockgain to lock on the standard			
once locked, crudely shim Z1 and Z2 and disconnect the VI	NMR Acquisition Window		
nt=4 <>	set number of transients		
ga <>	start acquisition (will wft when complete)		
when acquisition is complete:			
f full <>	display full sweep width to screen		
aph <>	autophase		
LC HOLD, then release	move first cursor to the left of reference line		
RC HOLD, then release	move second cursor to the right of reference line		
LC Expand	expand region inside cursors		
LC HOLD, then release	move first cursor to center of line		
nl <>	select nearest line		
rl(-63.73p) <>	set reference (in ppm)		
f full <>	display full sweep width to screen		
LC HOLD, then release	move first cursor far right of spectrum, to the last		
	data point on the screen		
LC Mark	request frequency		
cr =	write down the frequency (which is in hertz)		

cr = \_\_\_\_\_

### It is a good idea at this time to save the reference FID.

LC Connect (in the VNMR acquisition window)	IMPORTANT:	
LC Lock	If you do not turn the lock off before	
LC Lock off	ejecting the sample, your reference	
eject the standard sample	will not be correct.	
insert the research sample		
lock on the research sample without changing Z0		
the research sample should now be shimmed as normal and the VNMR Acquisition window disconnected		
do not change any other parameters		
set nt so that the peak(s) will be visible		
ga <>	start acquisition (will wft when complete)	

When acquisition is complete:

f full <>	display full sweep width to screen
aph <>	autophase
LC HOLD, then release	move first cursor far right of spectrum, to the last data point on the screen
rl(cr value in hertz) <>	set reference (in hertz)
f full <>	display full sweep width to screen

#### At this point, it is a good idea to save the standard sweep width FID.

LC Next	access the next display menu
LC Thres	select threshold
LC HOLD, then release	move threshold line to include the peak(s)
axis='p' <>	set axis to ppm
pll page <>	print peak frequencies in Hz and ppm

The written record of the referenced chemical shifts is necessary if the sweep width and/or transmitter offset need to be changed. If the sweep width needs to be made larger or smaller, the spectrometer will not keep a record of the reference position and the peak references will be wrong in the next spectrum. However, using the prinout, the peaks can be easily re-referenced.

**Example Two:** The standard sample and the research sample have lock solvents with very different chemical shifts. The user will not be able to lock on the reference and should treat this like example three below.

**Example Three:** The standard sample has no lock solvent. <sup>31</sup>P research sample in CDCl<sub>3</sub> and 85% H<sub>3</sub>PO<sub>4</sub> standard.

insert the research sample

use the standard s	etup for P31
jexp1 <>	join experiment 1
LC Main Menu	activate main menu display
LC Setup	activate setup menu
LC Nucleus,Solvent	select nucleus, solvent menu
LC P31	select nucleus
LC CDCI3	select solvent
rts('current shim library') <>	retrieve shims
su <>	perform experiment set up
when set up is complete:	
load='n' <>	set load shim values to no
dg <>	display acquisition parameters
lock the sample and crudely shim Z1 and Z2 and disconnect set nt to some reasonable number that will allow the peak(s	t the VNMR Acquistion window ) to be visible start acquisition (will wft when complete)
ga 💙	start acquisition (will wit when complete)
When acquisition is complete:	
f full <>	display full sweep width to screen
aph <>	autophase
make sure that the peak(s) are visible at this sweep width an	nd number of transients
LC Connect (in the VNMR acquisition window)	<u>IMPORTANT</u> :
LC Lock	If you do not turn the lock off before
LC Lock off	ejecting the sample, your reference
eject the research sample	will not be correct.
insert the standard sample	
do not change any parameters	
nt=4 <>	set number of transients
ga <>	start acquisition (will wft when complete)

When acquisition is complete:

f full <>	display full sweep width to screen
aph <>	autophase
LC HOLD, then release	move first cursor to the left of reference line
RC HOLD, then release	move second cursor to the right of reference line
LC Expand	expand region inside cursors
LC HOLD, then release	move first cursor to center of line
nl <>	select nearest line
rl(0p) <>	set reference (in ppm)
f full <>	display full sweep width to screen
LC HOLD, then release	move first cursor far right of spectrum, to the last
	data point on the screen
LC Mark	request frequency
cr =	write down the frequency (which is in hertz)

# It is a good idea at this time to save the reference FID.

LC Connect (in the VNMR acquisition window) LC Lock LC Lock off eject the standard sample	<u>IMPORTANT</u> : If you do not turn the lock off before ejecting the sample, your reference will not be correct.
insert the research sample	
lock on the research sample without changing Z0 the research sample should now be shimmed as normal an <i>do not change any other parameters</i> set nt so that the peak(s) will be visible ga <>	d the VNMR Acquisition window disconnected start acquisition (will wft when complete)
when acquisition is complete:	
f full <> aph <> LC HOLD, then release	display full sweep width to screen autophase move first cursor far right of spectrum, to the la

rl(cr value in hertz) <> f full <> display full sweep width to screen autophase move first cursor far right of spectrum, to the last data point on the screen set reference (in hertz) display full sweep width to screen

#### At this point, it is a good idea to save the standard sweep width FID.

LC Next LC Thres LC HOLD, then release axis='p' <> pll page <>

access the next display menu select threshold move threshold line to include the peak(s) set axis to ppm print peak frequencies in ppm

The written record of the referenced chemical shifts is necessary if the sweep width and/or transmitter offset need to be changed. If the sweep width needs to be made larger or smaller, the spectrometer will not keep a record of the reference position and the peak references will be wrong in the next spectrum. However, using the prinout, the peaks can be easily re-referenced.

NOTE: If vt is used for the research sample, the standard should be run at the same temperature, if possible. Under no circumstances should samples in  $D_20$  or 85%  $H_3PO_4$  be run below 0°C. If the reference sample can not be run at the same temperature as the research sample, note the conditions of the reference sample and the research sample and report these in appropriate experimental sections.