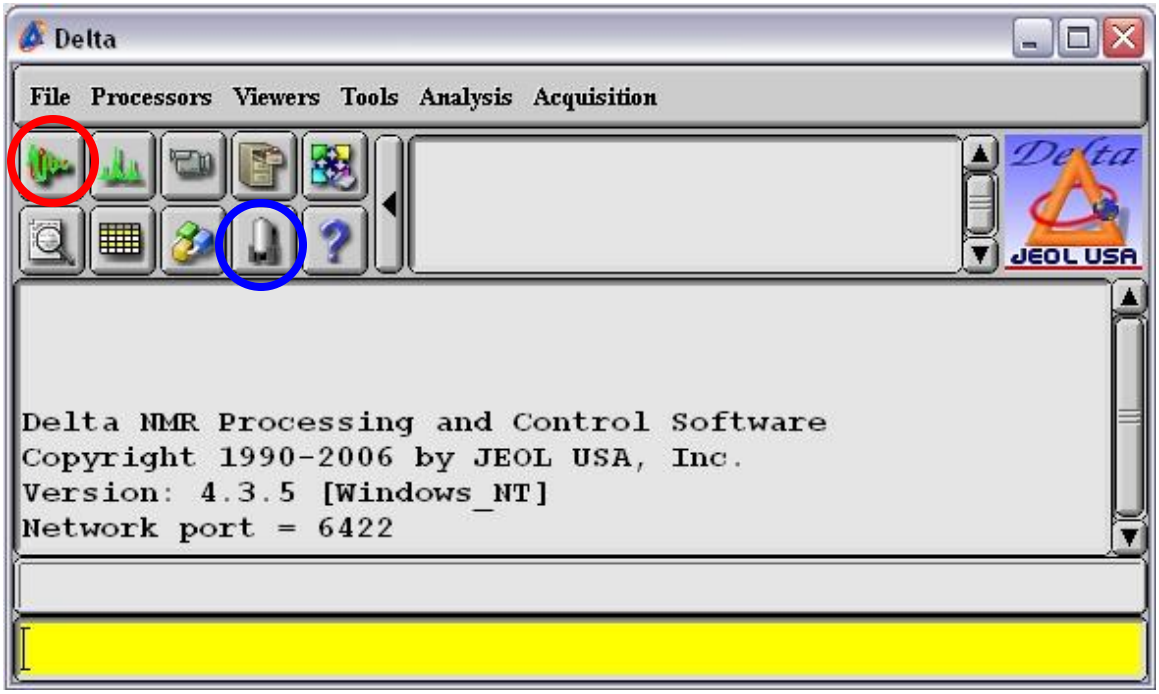
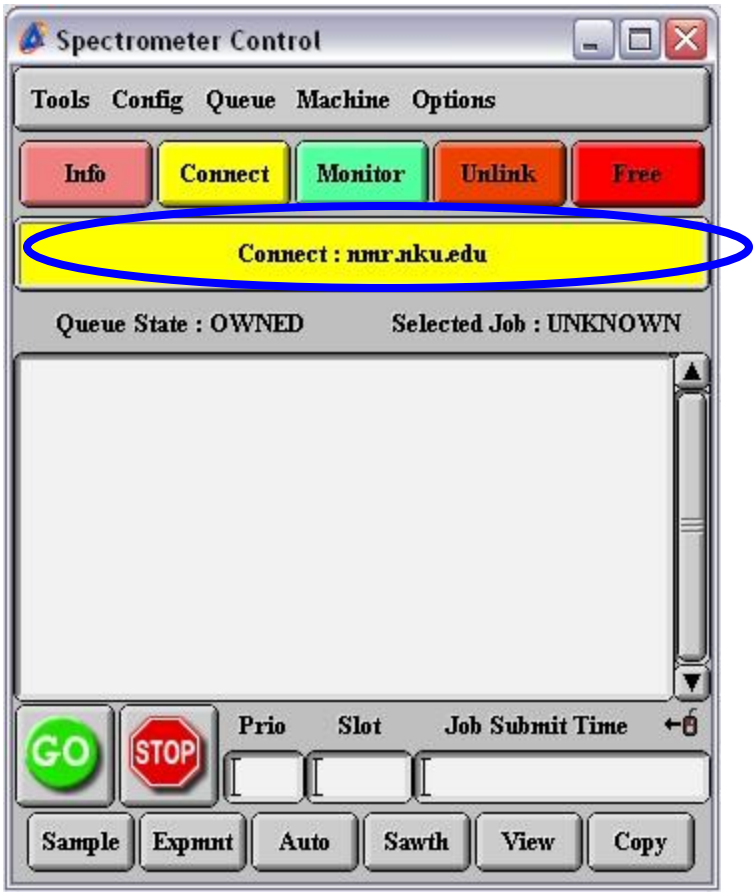
1. First start the Delta Software by clicking its icon 

found either on the Desktop or in the Start menu.
2. The window that appears is the main Delta window shown below. It will show important messages while you are running the software.



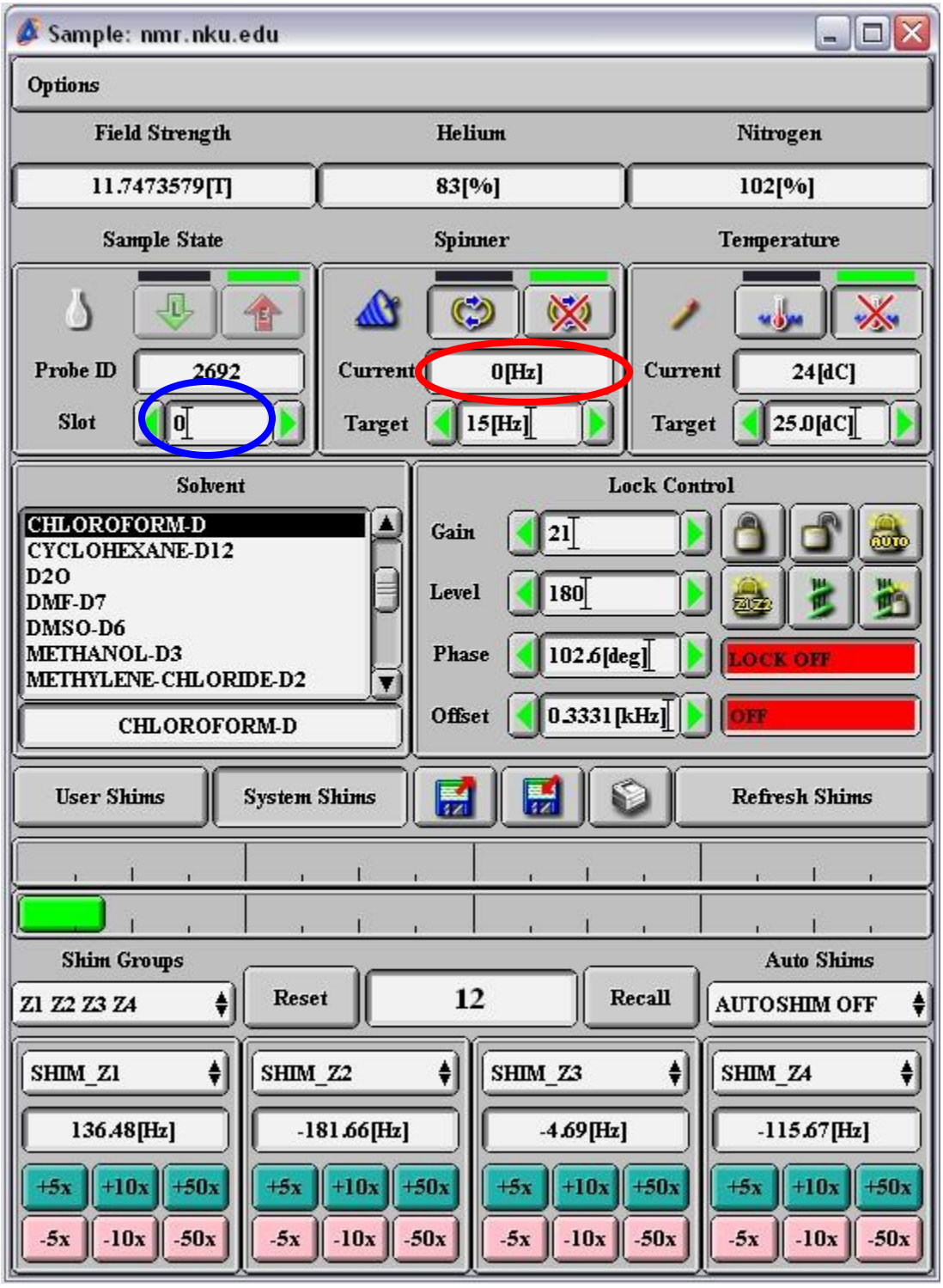
3. From this window you can connect to the magnet by clicking the magnet icon (blue circle, see step 4) or manipulate data files by clicking the Data Processor icon (red circle, see step 10).

4. Clicking the magnet icon brings up the Spectrometer control window shown below. The software automatically connects to the magnet and the top portion of the window shows Connect: nmr.nku.edu and turns yellow (circled in blue). If it says anything else, you are not connected to the magnet typically because someone else is connected. You are not able to run experiments in this state.



This window also shows the experiment queue in the whitespace above the go and stop buttons, and gives you access to the Sample, Experiment, and Automation windows by the buttons along the bottom row. These windows will be discussed next.

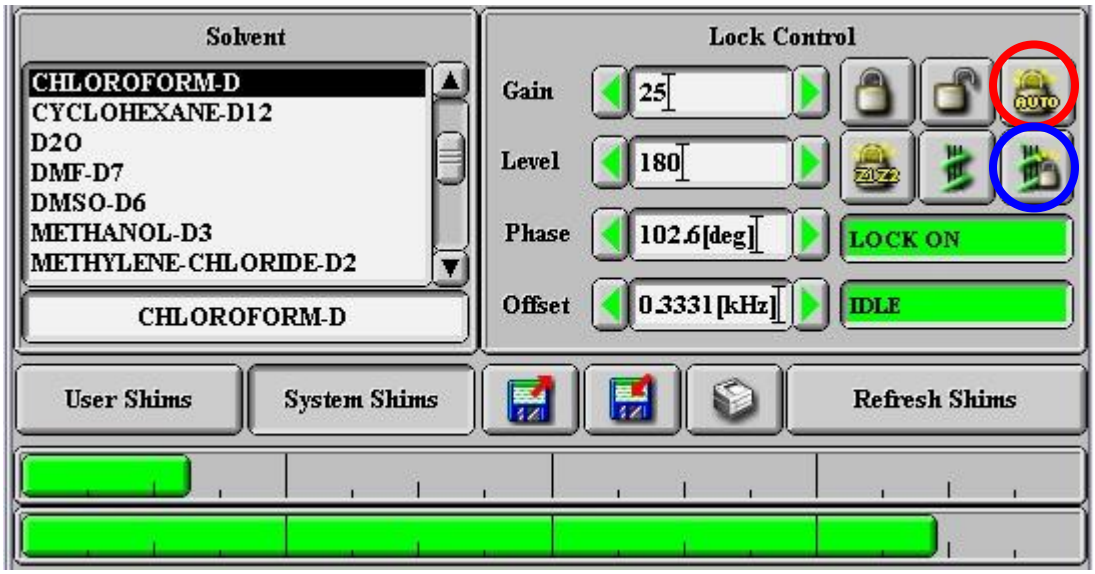
5. Open the Sample window (shown below). This window contains a wealth of information about the sample inside the magnet.



First, to load your sample put the slot number into the field under the

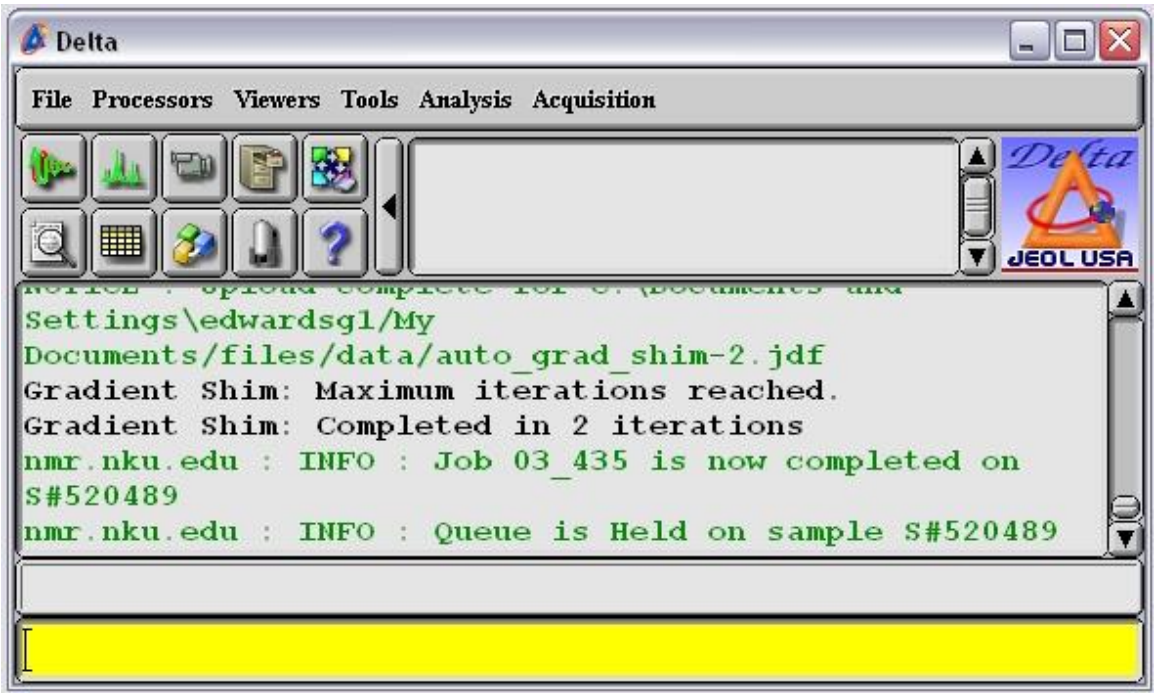
blue circle. The sample changer will automatically eject the sample that is inside the magnet (if there is one) and then pick up your sample/spinner combination and place it inside the magnet. While this is happening select the solvent that is inside your NMR tube. After your sample has loaded, watch the spin speed (red circle) to make sure the sample is spinning at the correct speed (someplace close to 15 Hz). *Trouble? Try ejecting your sample (by putting a zero in the sample slot) then reloading your sample. If this does not help try a different spinner, and then a different NMR tube.*

6. After the sample is spinning, select the solvent contained in your sample. We will lock onto the deuterated solvent signal by clicking the autolock button (red circle, as shown below) after a second or two the lock status will change to green and say lock on (just like the next picture).
   Trouble? If the spectrometer won't lock, make sure you have the correct deuterated solvent selected (you did use a deuterated solvent right)? If you are sure you are ok, load the system shims by pressing the button with the arrow pointing away from the disc. If this doesn't work find Dr. Edwards or your Advisor, we can fix it for you very quickly.



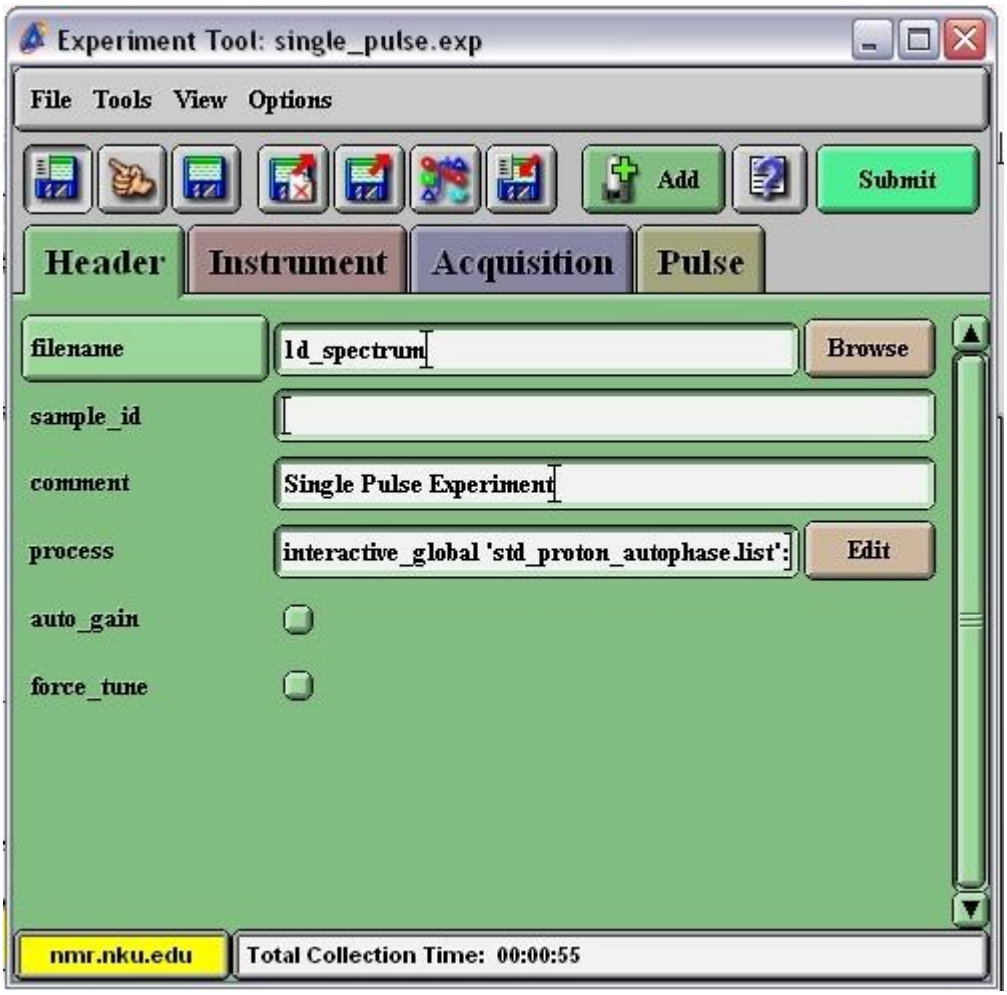
7. Next click the gradient shim button (blue circle above). This will shim the magnet so that you achieve the best possible line width and shape in your resulting spectra. It takes a couple of minutes. When it is done, the main Delta window will show a message about being done in two iterations as shown below.

   Trouble? Did you see an error message? Note it in the instrument log.



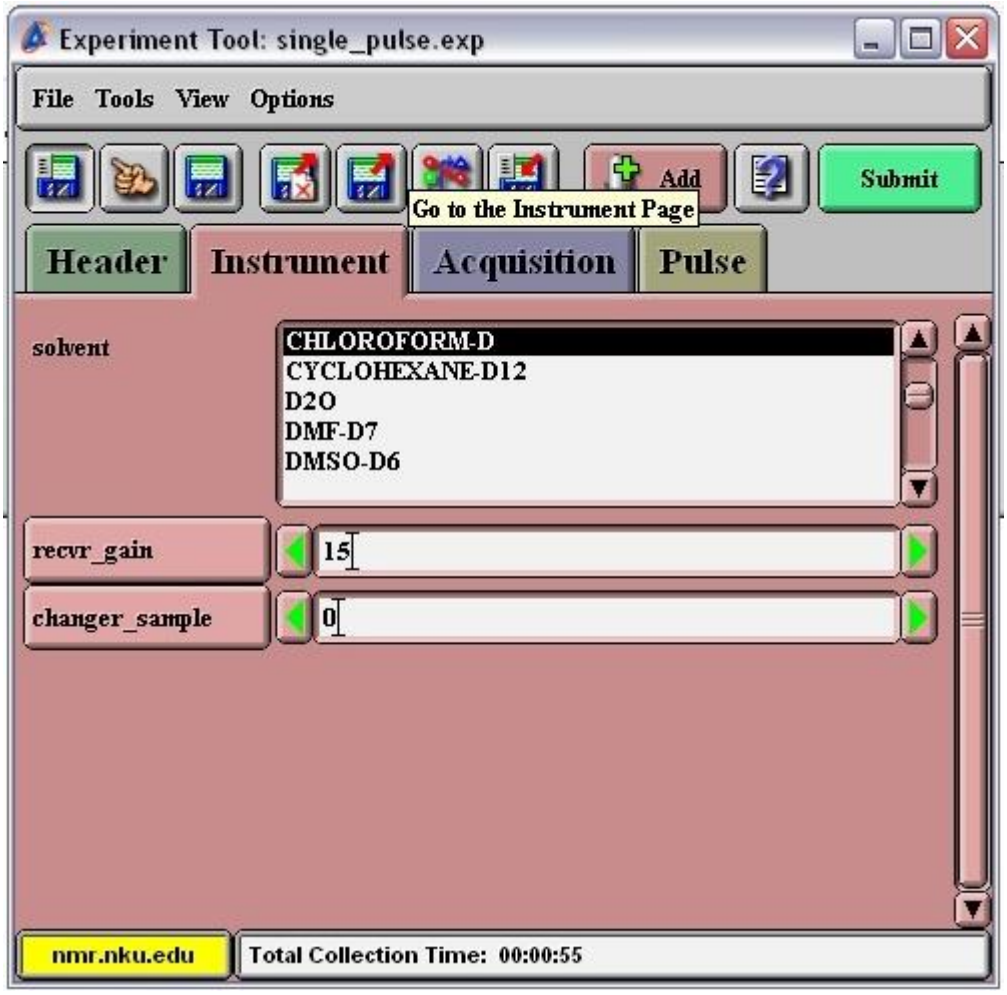
8. Now that the sample is loaded, locked, and shimmed. You are ready to run your experiments. Load the open experiment window (shown below) by clicking on the EXPMNT button in the spectrometer control window. You will now select the experiment of interest. (click on the global directory button in Red, then select your experiment single_pulse.exp for proton and single_pulse_dec.exp for carbon).

This will bring up the Experiment Tool window for the specific experiment. I have shown the proton experiment below.

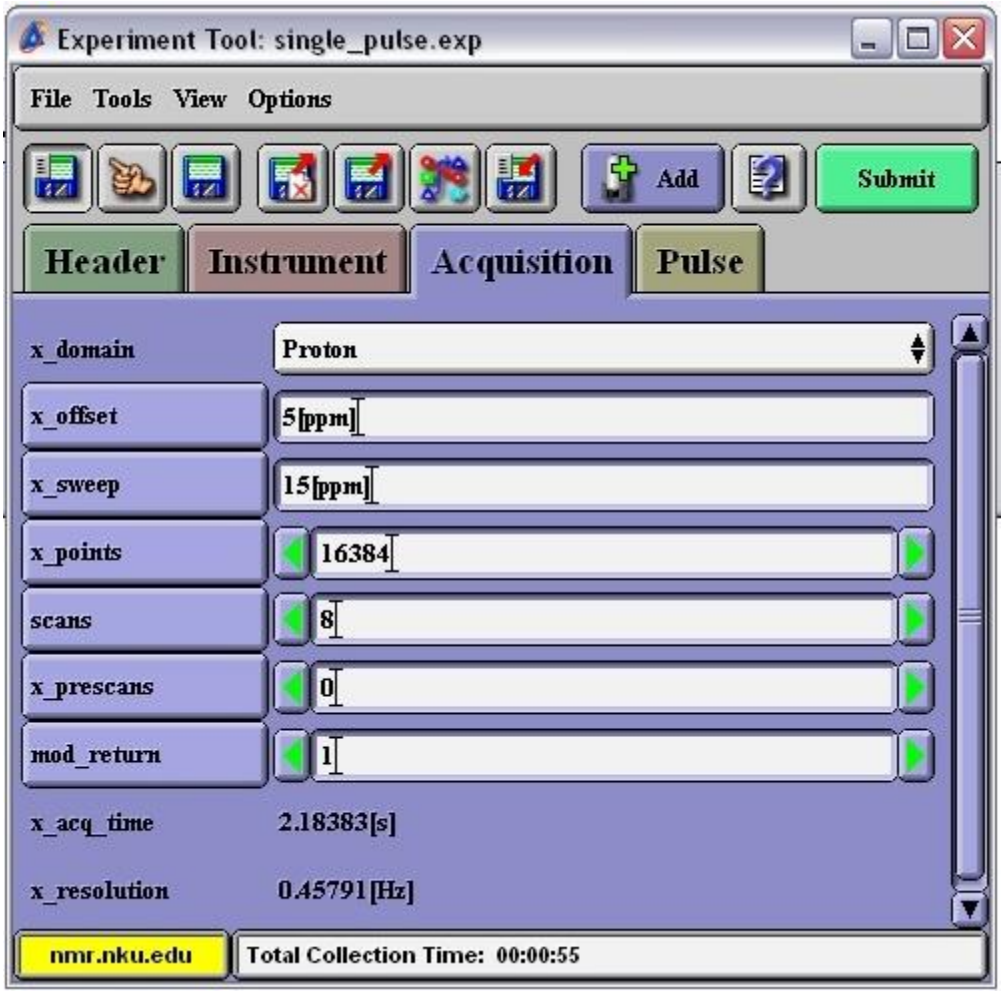


Under the Header tab, you can change your filename and put in a sample identifier. I also suggest your click the auto_gain check box.

Under the Instrument tab, check to make sure the right solvent is selected, and changer_sample corresponds to the slot your sample was in. the recvr_gain will be set by the auto_gain routine later.

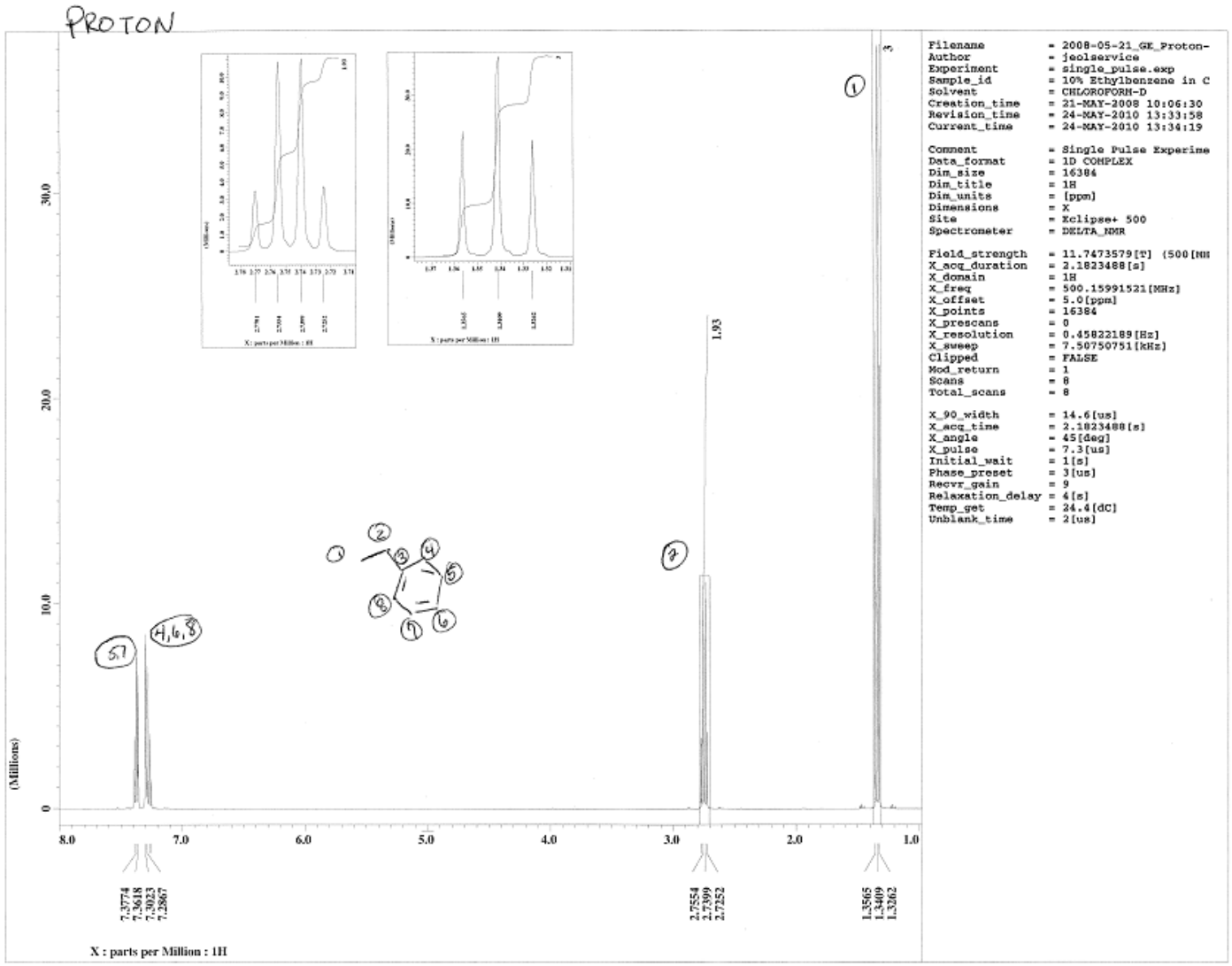


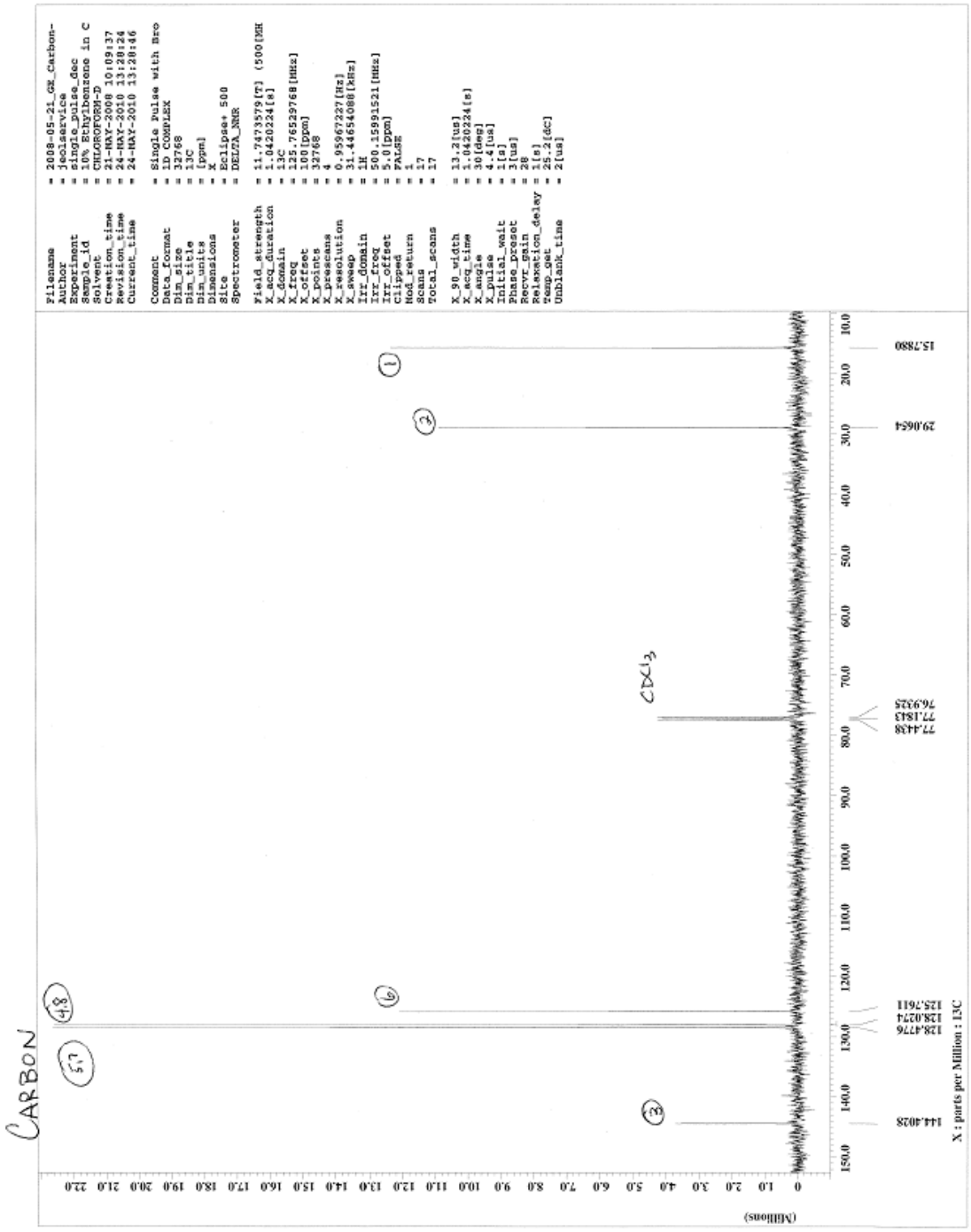
The acquisition tab has a number of instrumental features that you can change, but you really only need to be concerned with the number of scans. You can set this to any number you wish, larger scans will typically increase your signal to noise ratio, but also increase acquisition time.

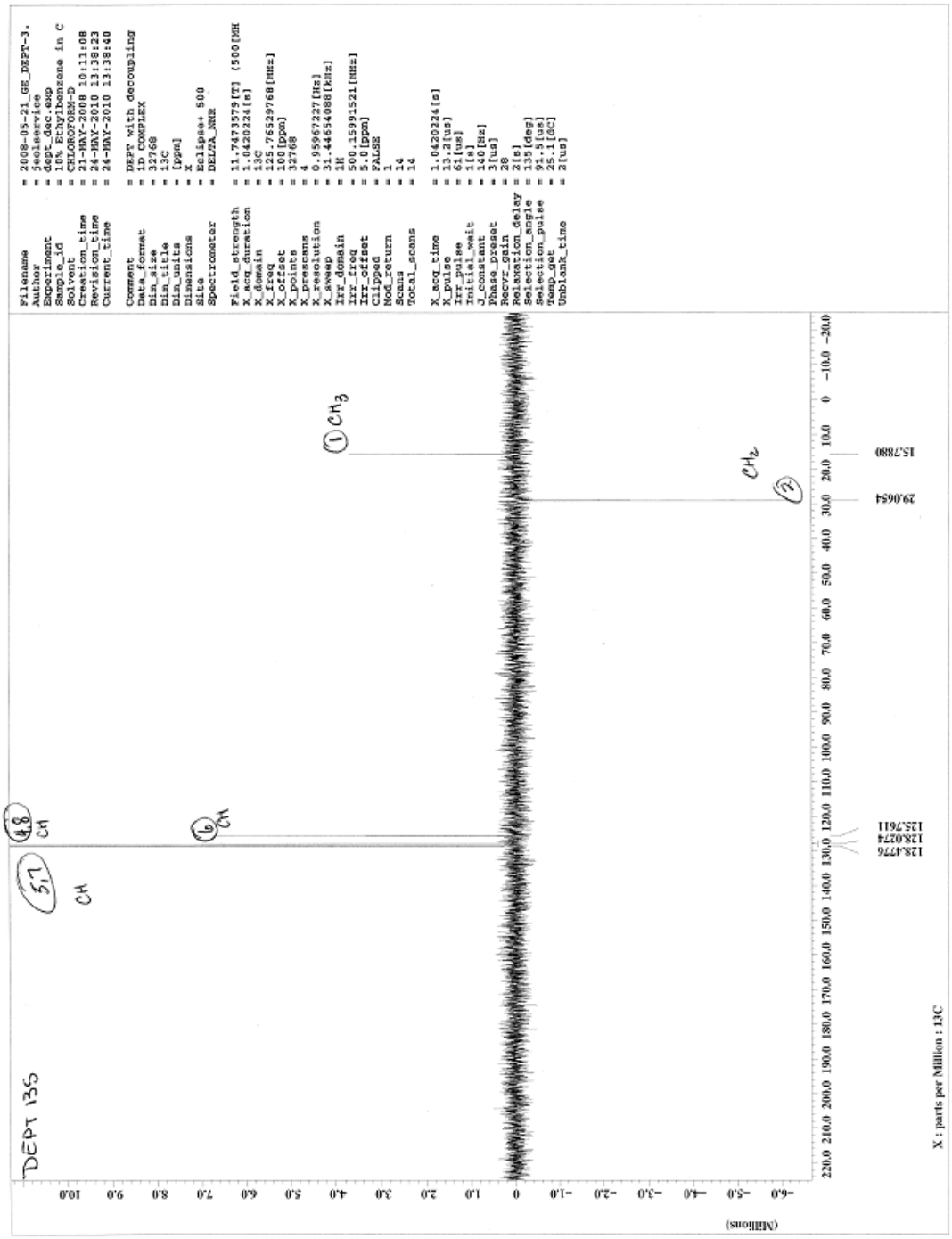


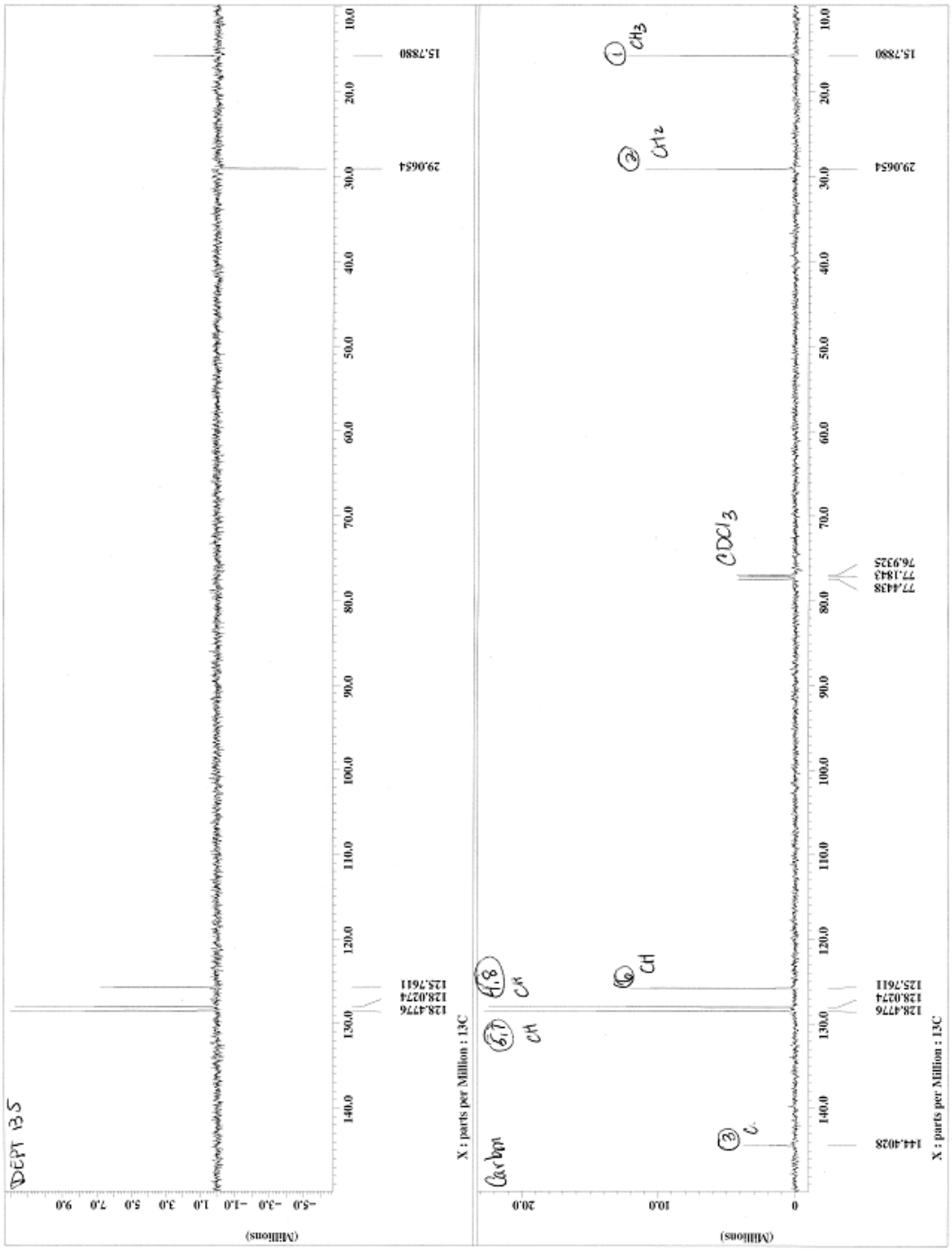
You do not need to mess with anything on the Pulse tab.

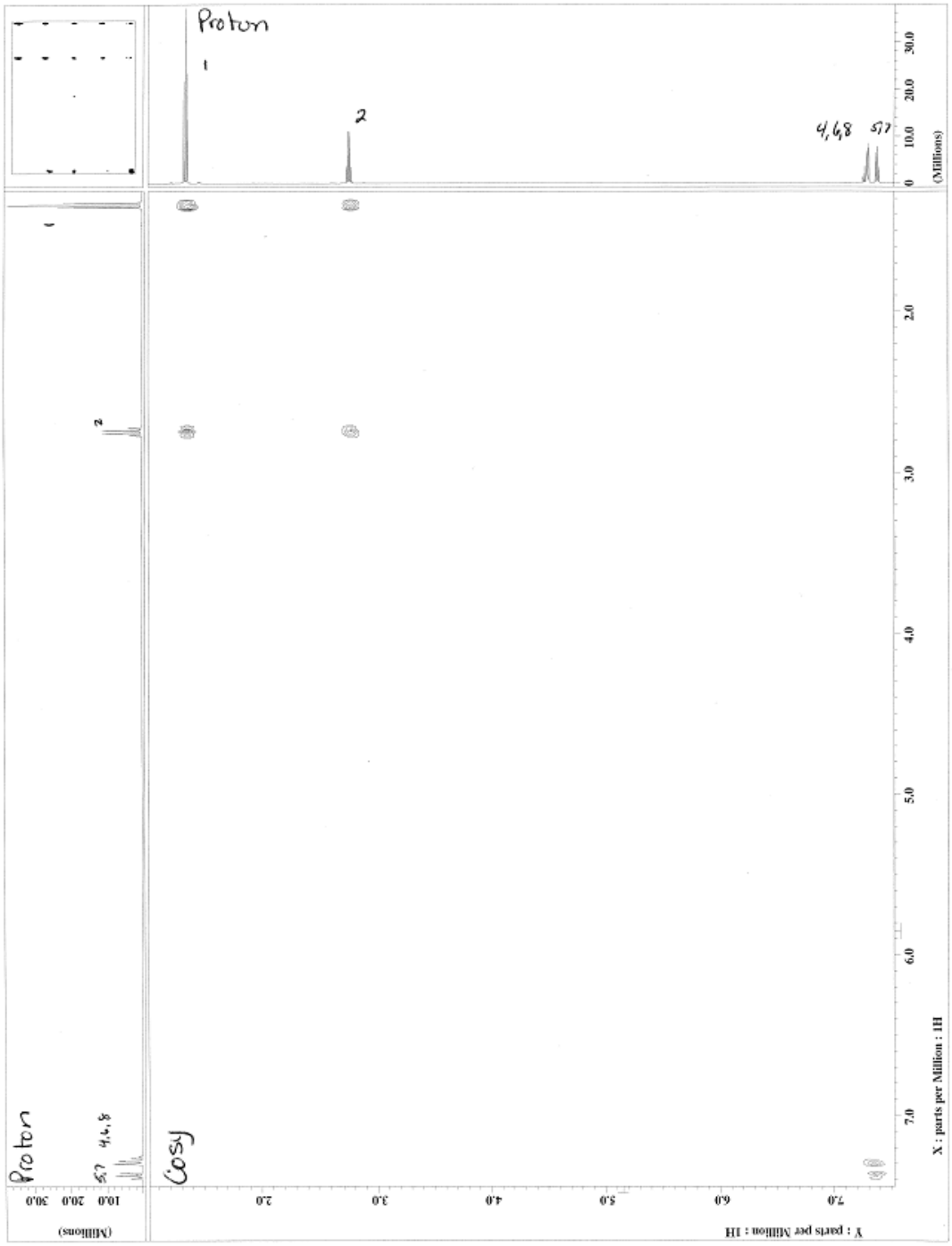
9. When you are done you can press submit and your job will be loaded into the Spectrometer Control window and the experiment will be executed. Once the job is complete, the data should appear on your screen. You can now eject your sample by putting a zero in the slot number of the sample window.

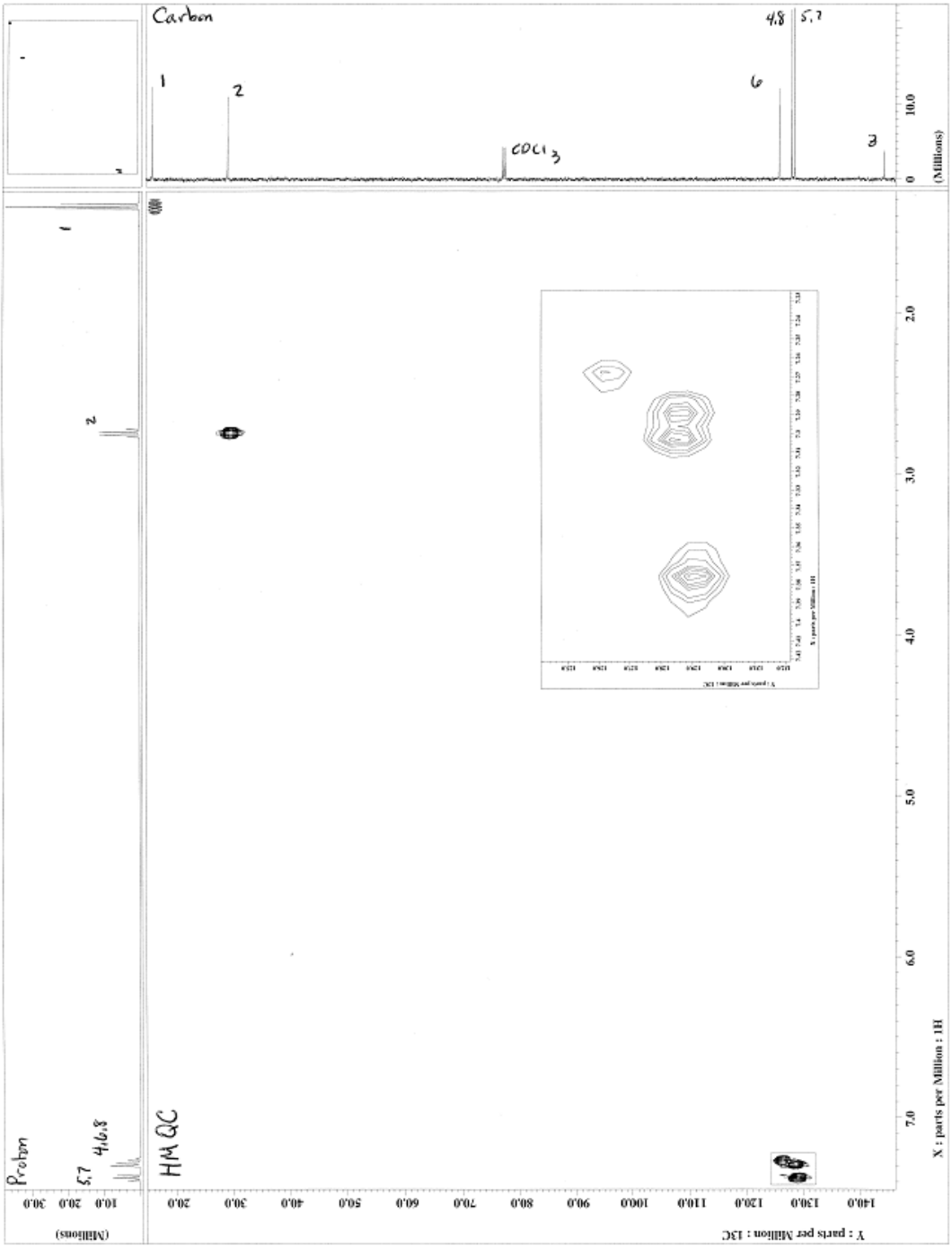

PROTON
1.93
(Millions)
30.0
20.0
10.0
0
8.0
7.0
6.0
5.0
4.0
3.0
2.0
1.0
7.3774
7.3618
7.3023
7.2867
2.7554
2.7399
2.7252
1.3565
1.3409
1.3262
X : parts per Million : 1H
Filename = 2008-05-21_GE_Proton-
Author = jeolservice
Experiment = single_pulse.exp
Sample_id = 10% Ethylbenzene in C
Solvent = CHLOROFORM-D
Creation_time = 21-MAY-2008 10:06:30
Revision_time = 24-MAY-2010 13:33:58
Current_time = 24-MAY-2010 13:34:19
Comment = Single Pulse Experime
Data_format = 1D COMPLEX
Dim_size = 16384
Dim_title = 1H
Dim_units = [ppm]
Dimensions = X
Site = Eclipse+ 500
Spectrometer = DELTA_NMR
Field_strength = 11.7473579[T] (500[MH
X_acq_duration = 2.1823488[s]
X_domain = 1H
X_freq = 500.15991521[MHz]
X_offset = 5.0[ppm]
X_points = 16384
X_prescans = 0
X_resolution = 0.45822189[Hz]
X_sweep = 7.50750751[kHz]
Clipped = FALSE
Mod_return = 1
Scans = 8
Total_scans = 8
X_90_width = 14.6[us]
X_acq_time = 2.1823488[s]
X_angle = 45[deg]
X_pulse = 7.3[us]
Initial_wait = 1[s]
Phase_preset = 3[us]
Recvr_gain = 9
Relaxation_delay = 4[s]
Temp_get = 24.4[dC]
Unblank_time = 2[us]

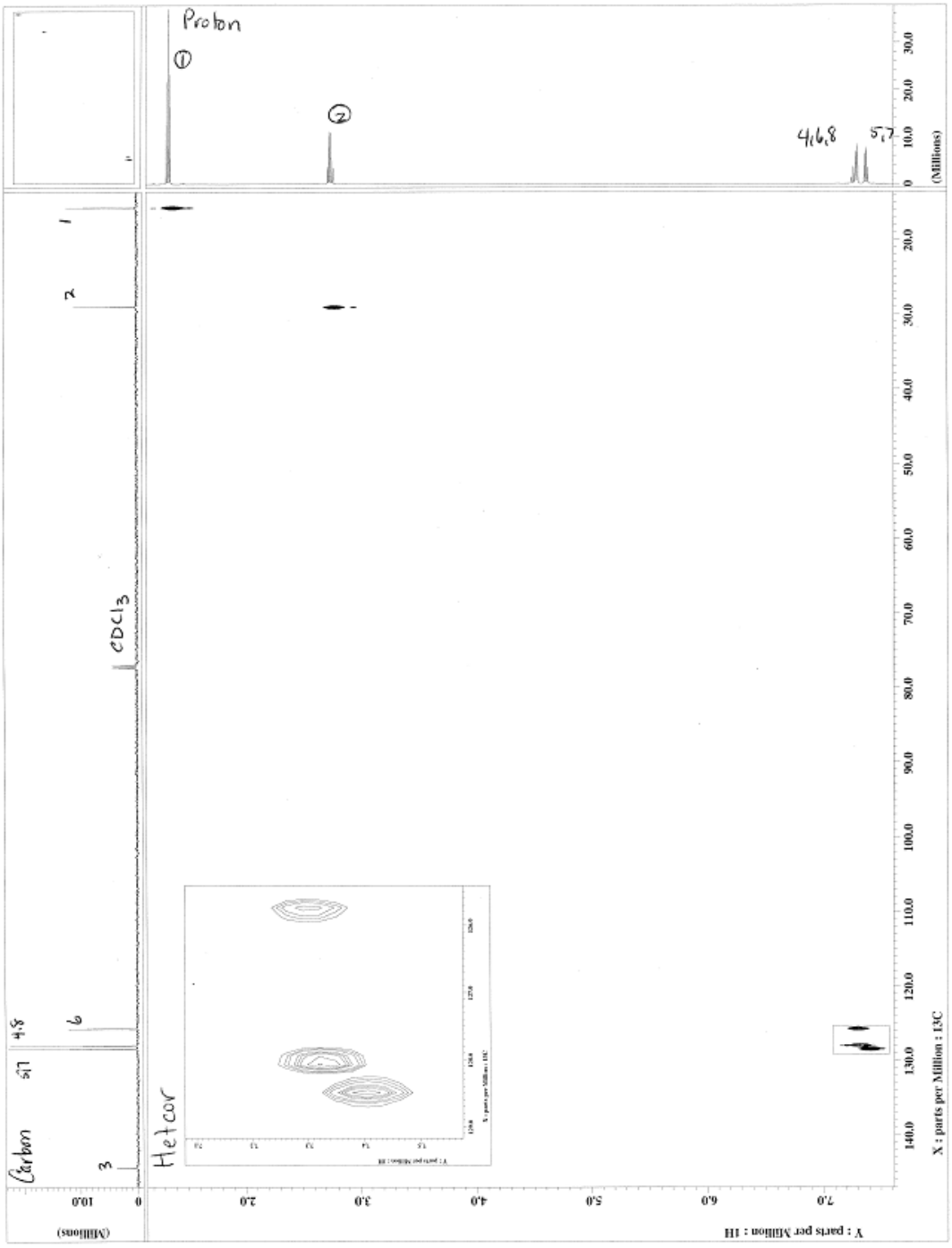

CARBON
48
57
6
3
1
3
CDCl3
Filename = 2008-05-21_GX_Carbon-
Author = jeolservice
Experiment = single_pulse_dec
Sample_id = 10% Ethylbenzene in C
Solvent = CHLOROFORM-D
Creation_time = 21-MAY-2008 10:09:37
Revision_time = 24-MAY-2010 13:28:24
Current_time = 24-MAY-2010 13:28:46
Comment = Single Pulse with Bro
Data_format = 1D COMPLEX
Dim_size = 32768
Dim_title = 13C
Dim_units = [ppm]
Dimensions = X
Site = Eclipse+ 500
Spectrometer = DELTA_NMR
Field_strength = 11.74735579[T] (500[MH
Acq_duration = 1.04202224[s]
X_domain = 13C
X_freq = 125.76529768[MHz]
X_offset = 100[ppm]
X_points = 32768
X_prescans = 4
X_resolution = 0.959672237[Hz]
X_sweep = 31.446554080[kHz]
Irr_domain = 1H
Irr_freq = 500.15991521[MHz]
Irr_offset = 5.0[ppm]
Clipped = FALSE
Mod_return = 1
Scans = 17
Total_scans = 17
X_90_width = 13.2[us]
X_acq_time = 1.04202224[s]
X_angle = 30[deg]
X_pulse = 4.4[us]
Initial_wait = 1[s]
Phase_preset = 3[us]
Recvr_gain = 28
Relaxation_delay = 1[s]
Temp_get = 25.2[dc]
Unblank_time = 2[us]
144.4028
128.4776
128.0274
125.7611
77.4438
77.1843
76.9325
29.0664
15.7880
(Millions)
X : parts per Million : 13C


DEPT 135
5,7
CH
4,8
CH
6
CH
① CH3
② CH2
15.7880
29.0654
128.4776
128.0274
125.7611
X : parts per Million : 13C
(Millions)
Filename = 2008-05-21_GE_DEPT-3.
Author = lwolleservice
Experiment = dept.dac:exp
Sample_id = 10% Benzene in C
Solvent = CHLOROFORM-D
Creation_time = 21-MAY-2008 10:11:08
Revision_time = 24-MAY-2010 13:38:23
Current_time = 24-MAY-2010 13:38:40
Comment = DEPT with decoupling
Data_format = 1D COMPLEX
Dim_size = 32768
Dim_title = 13C
Dim_units = [ppm]
Dimensions = X
Site = Eclipse+ 500
Spectrometer = DELTA2_NMR
Field_strength = 11.74735791[T] (500[MH
Acq_duration = 1.04202241[s]
X_domain = 13C
X_freq = 125.76529768[MHz]
X_offset = 100[ppm]
X_points = 32768
X_prescans = 4
X_resolution = 0.95967227[Hz]
X_sweep = 31.44654088[kHz]
Irr_domain = 1H
Irr_freq = 500.15991521[MHz]
Irr_offset = 5.0[ppm]
Clipped = FALSE
Mod_return = 1
Scans = 14
Total_scans = 14
X_acq_time = 1.04202241[s]
X_pulse = 13.72[us]
X_90_pulse = 61[us]
Initial_wait = 1[s]
J_constant = 140[Hz]
Phase_preset = 3[us]
Recvr_gain = 28
Relaxation_delay = 2[s]
Selection_angle = 135[deg]
Selection_pulse = 91.5[us]
Temp_get = 25.1[dC]
Unblank_time = 2[us]


DEPT 135
(Millions)
X : parts per Million : 13C
15.7880
29.0654
77.4438
77.1843
76.9325
128.4776
128.0274
125.7611
144.4028
CDCl3
Carbon
CH3
CH2
CH
C
1
2
3
6
7
8


Proton
1
2
4,6,8
5,7
(Millions)
X : parts per Million : 1H
Y : parts per Million : 1H
Proton
cosy


Carbon
4.8
5.7
1
2
6
3
CDCl3
10.0
0
(Millions)
HMQC
Proton
5.7
4.6.8
X : parts per Million : 1H
Y : parts per Million : 13C


Proton
1
2
4.6.8
5.7
(Millions)
Carbon
5.7
4.8
6
3
CDCl3
Hetcor
(Millions)
Y : parts per Million : 1H
X : parts per Million : 13C