

Instruction of Projeciton-Reconstruction NMR

By Wen-Jin Wu, 04-17-2007

This is the first modified version of the second prototype version for 3D Projection Reconstruction by Wolfgang Bermel from Bruker ("pr_readme"). It consists of:

AU programs (-> \$TOPSPINHOME/exp/stan/nmr/au/src)

pr_setup.be
pr_proc.be
pr_recos.be
pr_alpha.be

Pulse programs (-> \$TOPSPINHOME/exp/stan/nmr/lists/pp)

pr_hncogp3d.t1.be
pr_hncogp3dsc.ww (¹⁵N-semi constant time)
pr_hncagp3d.t1.be
pr_hncagp3dsc.ww (¹⁵N-semi constant time)
pr_hncocagp3d.ww
pr_hncocagp3dsc.ww (¹⁵N-semi constant time)
pr_hncacogp3d.ww
pr_hncacogp3dsc.ww (¹⁵N-semi constant time)
pr_hncacbgp3d_dp9.ww
pr_hncacbgp3dsc_dp9.ww (¹⁵N-semi constant time)
pr_hncbgp3d_dp9.ww
pr_hncbgp3dsc_dp9.ww (¹⁵N-semi constant time)
pr_cbcaconhgp3dsc.ww (¹⁵N-semi constant time)

The files need to be copied into the appropriate directories.

(1). Create a 3D dataset and set all parameters as if you were to run a normal 3D. Then start **pr_setup.be**. The program will create new expnos for the 2D projections. Change to the first 2D and acquire the data (e.g. multizg).

(2). Go back to the 3D dataset and start **pr_proc.be**. This program will rearrange the 2Ds and store them under a set of new expnos. Go to these new expnos, transform and phase correct the spectra.

(3). Go back to the 3D dataset and start **pr_recos.be** to reconstruct the 3D cube.

- The program **pr_recos.be** reconstructs the 3D cube, and calculates an F1F2 projection and counts the peaks therein. This number can be used to check how the reconstruction improves as the number of peaks should converge towards the end. (This part may be replaced by a 3d peak picking at some stage).
- The program **pr_alpha.be** calculates an F1F3 projection from the reconstructed cube and counts the peaks therein. It will do this for angles between -80o and +80o and will search for a maximum. The idea is that the best suited projection angle is the one with the largest number of peaks. So

the program will suggest the next projection angle to be recorded.

Additional note:

Under your 3D root directory you will find files:

“pr_setup”: this contains the number and the location of the 2D sub-spectra that you set up.

“pr_alpha”: this contains the prediction results from the macro pr_alpha.be

“pr_recos”: this contains the projection progress, number of cross peaks and tilted angles that have been used for reconstruction.

Step-by-step tutorial on PR-NMR

Getting ready

(a). Place the pulse sequences in the directory of “pr_pulprog” into your topspin pulse sequence

directory:
C:\Bruker\TOPSPIN\exp\stan\nmr
\lists\pp

(b). Place the au programs in the directory of “pr_au” into the following directory:

(C:\Bruker\TOPSPIN\exp\stan\nm
r\au\src
pr_setup.be
pr_proc.be
pr_recos.be
pr_alpha.be

(c). Copy the sample data set “workshop_hnco” into your topspin data directory:

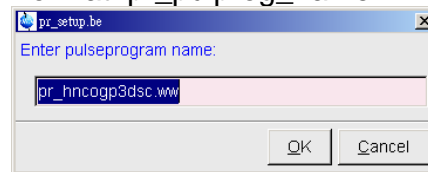
- C:\Bruker\TOPSPIN\data\your_name\nmr
- Or E:\data\your_name\nmr

(1). Setting up the experiments:

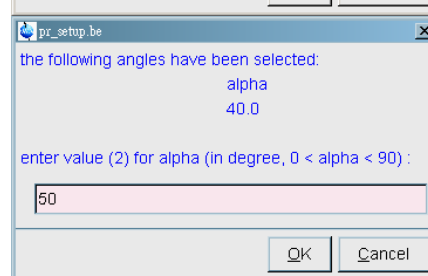
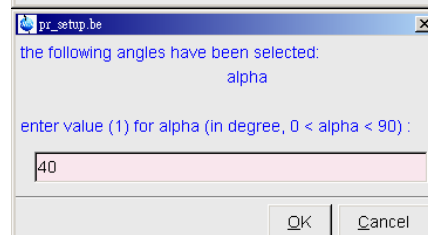
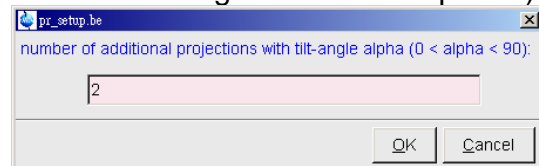
Under workshop_hnco 1/1, let’s practice setting up the experiments in PR-NMR mode. **(Note: for ¹⁵N semi-constant time experiment, set**

l0=td2 (¹⁵N).

- “pr_setup.be” ↵
- Enter pulse sequence name:
Format: pr_pulprog_name

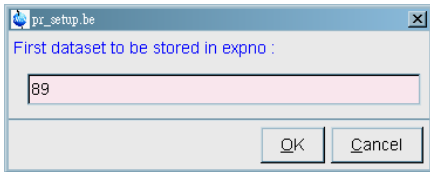


- Key in the number of additional projections with tilted-angle alpha (0<alpha<90) (besides the 0- and 90-degree two basic spectra)

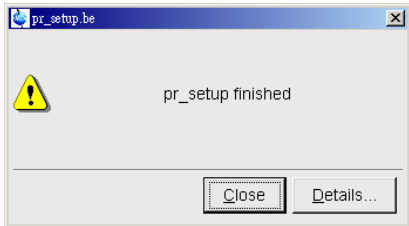


- Input the EXPNO for the first

dataset to be stored in:



- The PR-NMR set up is now finished

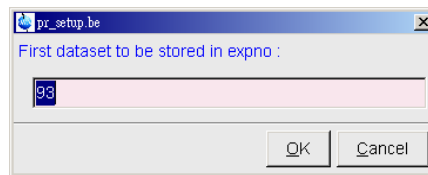
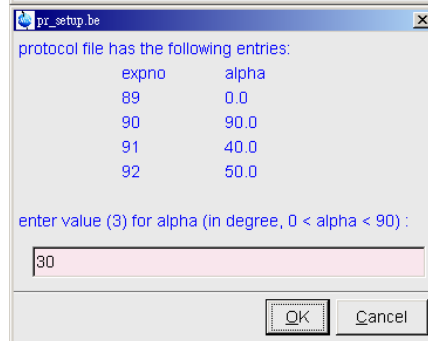
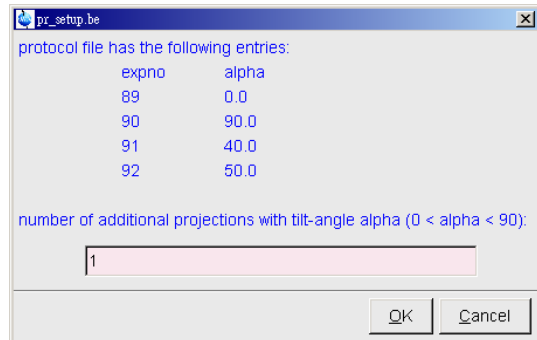
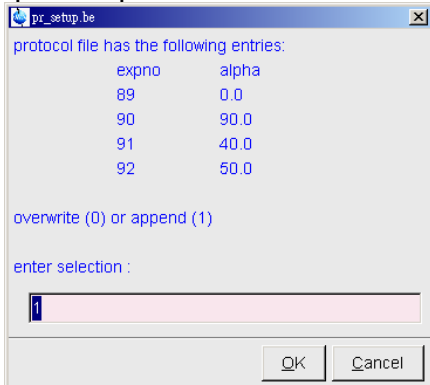


Open the “pr_setup” file under the current data directory
You will see the following:

- 4
- | | |
|----|------|
| 89 | 0.0 |
| 90 | 90.0 |
| 91 | 40.0 |
| 92 | 50.0 |
- multizg 89-92

-
- (after analyzing the data, if you need to acquire more tilted angles, repeat “pr_setup.be”, and use “append” instead of “overwrite” to add more angles, and store the first data set in a new expno)

“pr_setup.be”



- The “pr_setup” file is then updated
- 5
- | | |
|----|------|
| 89 | 0.0 |
| 90 | 90.0 |
| 91 | 40.0 |
| 92 | 50.0 |
| 93 | 30.0 |

“zg” the new experiment of 93/1

- Alternatively, you can add the new tilted angle experiment to any new experiment number. For example in 130/1 instead of 93/1 as suggested (you may have other experiments queued up in 93/1 for acquisition).

The “pr_setup” file is then updated

5
 89 0.0
 90 90.0
 91 40.0
 92 50.0
 130 30.0

(2). Processing the PR-NMR data

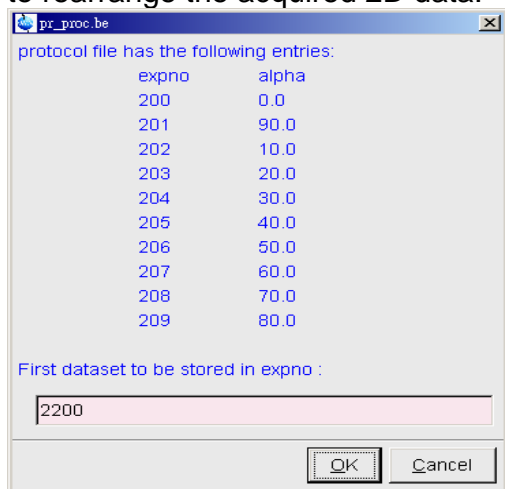
(2a). rearrange the 2D-projection spectra, and process them.

Sample data set: “workshop_hnco/31” is the processed PR-NMR 3D HNCO 32/1 is for you to practice.

(1). The 2D-projeciton spectra are from 200/1 to 209/1 (written to the file “pr_setup”).

(2). Under the root directory 32/1: change the file size under EDP. Use 1H=1K, 15N=256, 13C=256, use your usually processing parameter for all other parameters: i.e. ssb=3, linear prediction (LPFc, NCOEF=32 for a

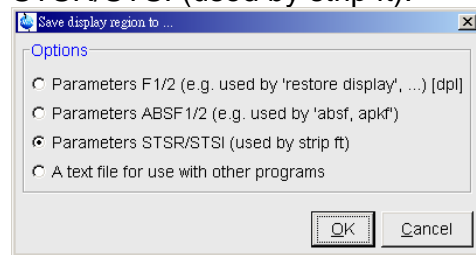
(3). Type in the command “pr_proc.be” to rearrange the acquired 2D data.



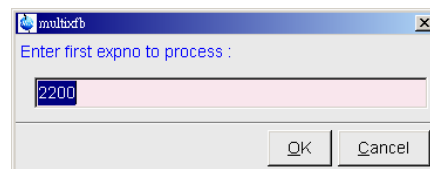
(4). Open the file “pr_proc”, the rearranged data location is

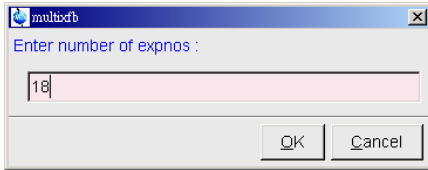
reported here.
 18
 2200 0.0
 2201 90.0
 2202 10.0
 2203 -10.0
 2204 20.0
 2205 -20.0
 2206 30.0
 2207 -30.0
 2208 40.0
 2209 -40.0
 2210 50.0
 2211 -50.0
 2212 60.0
 2213 -60.0
 2214 70.0
 2215 -70.0
 2216 80.0
 2217 -80.0

(5). Go to 2200/1, use “xfb” to FT this first 2D spectrum, phase the spectrum, and expand only the region that contains peaks (left-bottom to drag the defined the region (exclude water), and use the right-bottom to save the display region to “parameters STSR/STSI (used by strip ft).



(6). Now use the command “multixfb” to phase all of the spectra

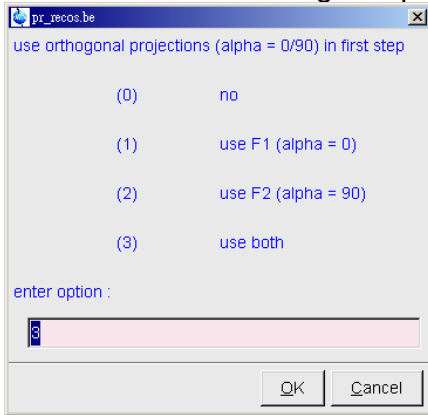




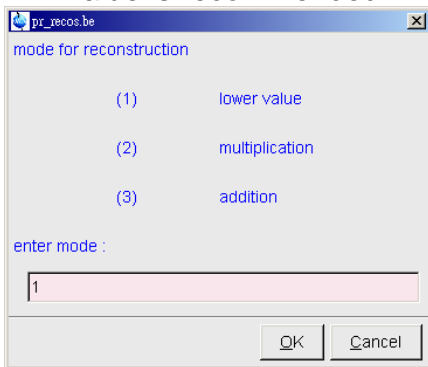
Now we are ready to reconstruct the 3D spectrum

(2b). Reconstruction of the 3D spectrum

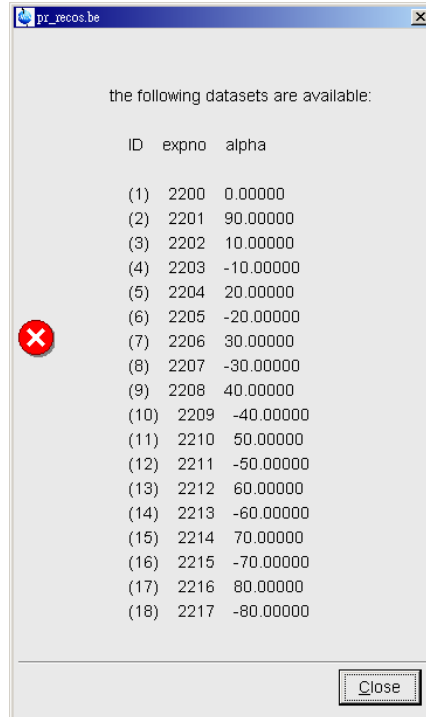
(7). Go back to the 3D root directory 32/1, key in the command "pr_recos.be", and the following window will pop up. Choose "(3) use both" for using both of the C-H and N-H orthogonal planes



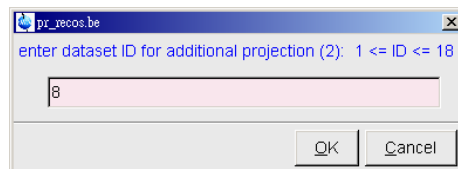
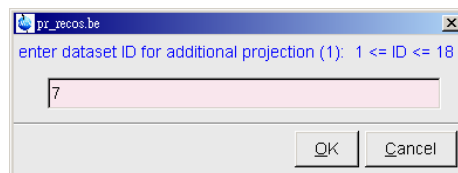
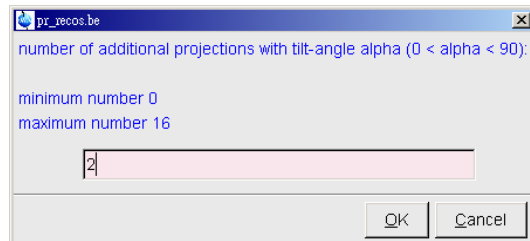
- Mode for reconstruction: lower value is recommended



- Available 2D-tilted experiments are listed:



(8). Input the number of additional projections with tilted-angle alpha ($0 < \alpha < 90$): Let's use two additional projections for now.



It will then perform the 3D

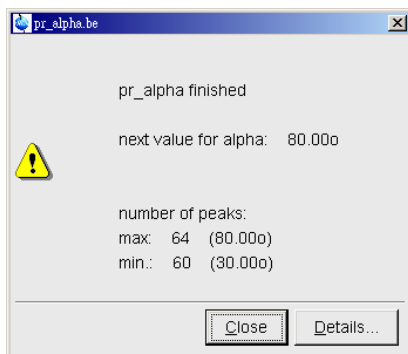
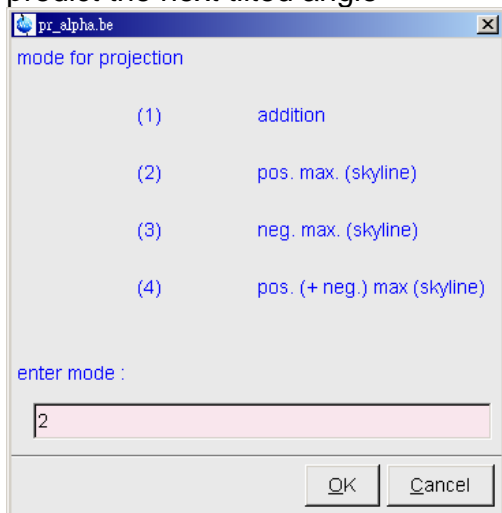
reconstruction



(9). When it is done, under the current directory, open the file “pr_recos” to view the reconstruction result. You can also look at the 3D cube now.

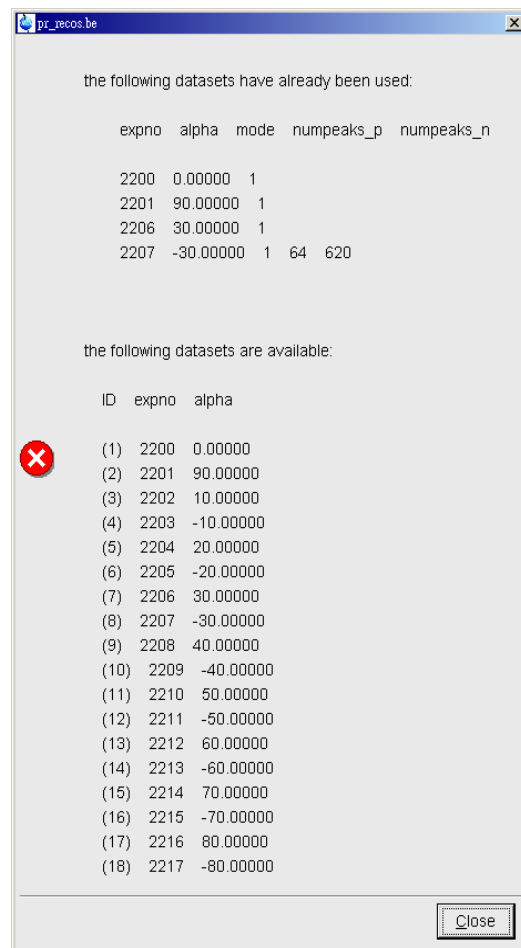
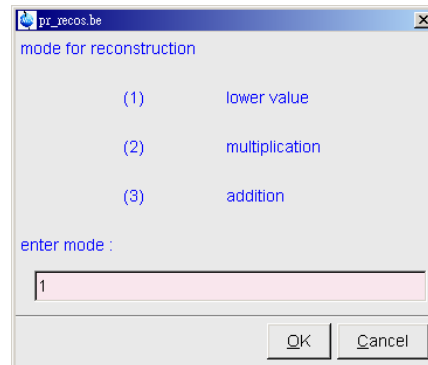
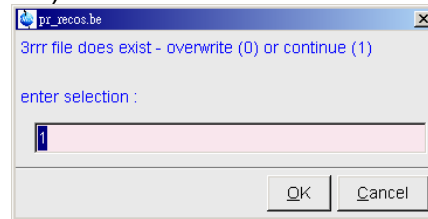
(c). Predict the next tilted plane to acquire

(10). Use the macro “pr_alpha.be” to predict the next tilted angle



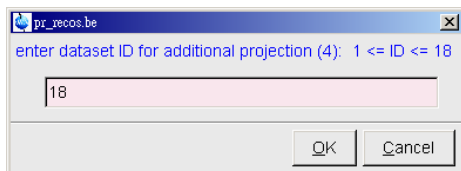
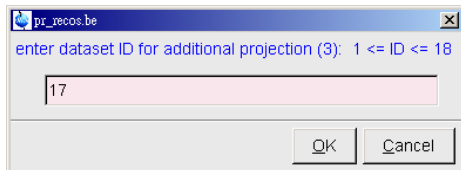
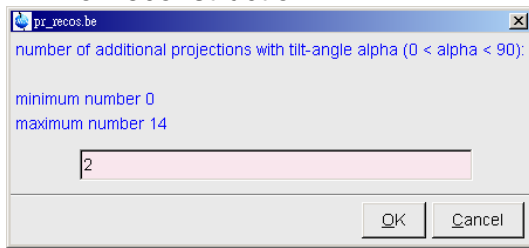
(11). continue to reconstruct the 3D spectrum by adding the 80 and -80 tilted spectra (not to overwrite the 3rrr

file)



● And add #17 (80) and #18 (-80)

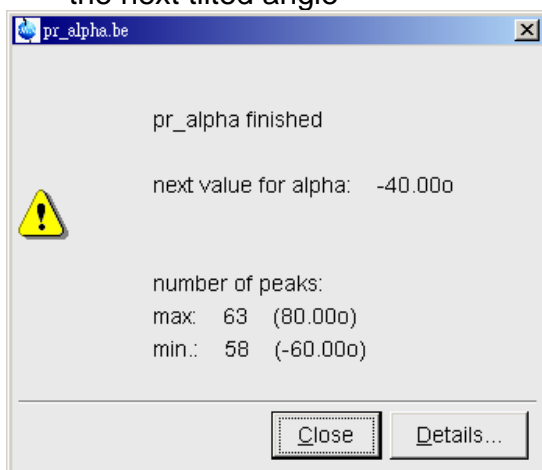
for reconstruction.



- Exam the “pr_recos” file for status 6

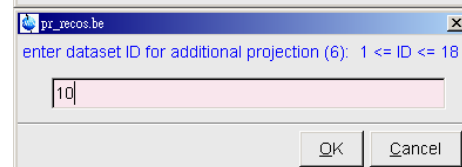
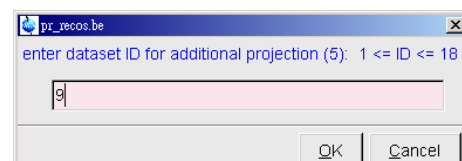
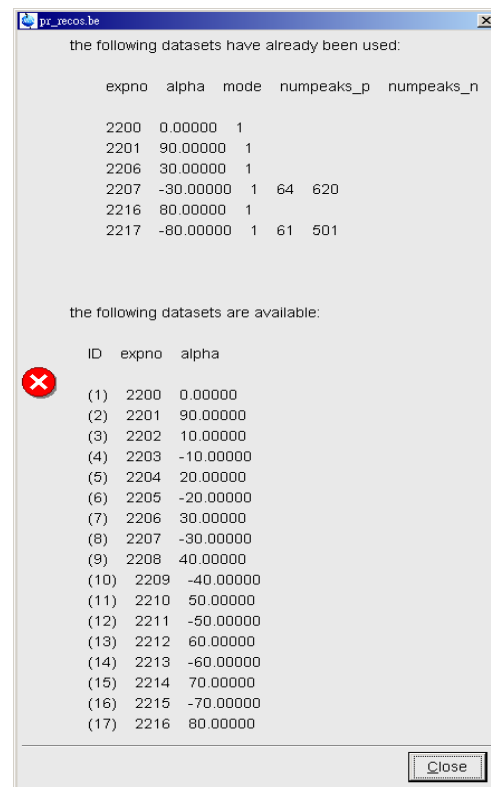
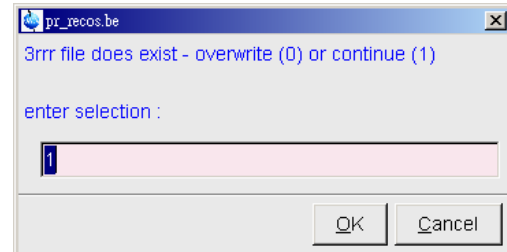
2200	0.0	1		
2201	90.0	1		
2206	30.0	1		
2207	-30.0	1	64	620
2216	80.0	1		
2217	-80.0	1	61	501

- Again use “pr_alpha.be” to predict the next tilted angle



(Pretend that we have continue to acquire the 40-degree angle data)

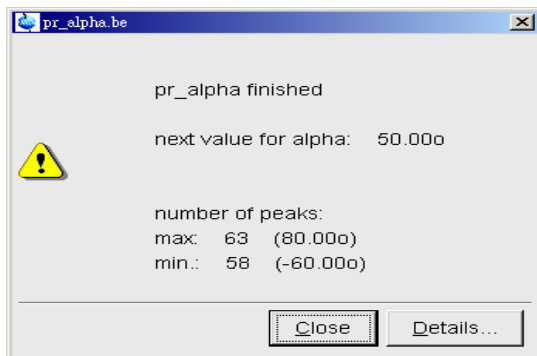
Now reconstruct the spectrum by adding the data of 40 and -40-degree data



- Now, let's check the “pr_recos” again.

8				
2200	0.0	1		
2201	90.0	1		
2206	30.0	1		
2207	-30.0	1	64	620
2216	80.01			
2217	-80.0	1	61	501
2208	40.01			
2209	-40.0	1	61	541

18				
1200	0.0	1		
1201	90.0	1		
1206	30.0	1		
1207	-30.0	1	64	600
1216	80.01			
1217	-80.0	1	61	517
1208	40.01			
1209	-40.0	1	61	541
1210	50.01			
1211	-50.0	1	60	594
1204	20.01			
1205	-20.0	1	60	586
1214	70.01			
1215	-70.0	1	60	547
1212	60.01			
1213	-60.0	1	60	
1202	10.01			
1203	-10.0	1	60	



- Add 50 and -50 (#11 and #12) for reconstruction

..... Check the the "pr_recos" file again.

10				
2200	0.0	1		
2201	90.0	1		
2206	30.0	1		
2207	-30.0	1	64	620
2216	80.01			
2217	-80.0	1	61	501
2208	40.01			
2209	-40.0	1	61	541
2210	50.01			
2211	-50.0	1	60	580

- Eventually, with using all 8 angle, it shows that only one-extra tilted angle (30-dgree) is sufficient for reconstructing a 3D HNCO for the 62 a.a. protein since no improvement in the number of cross peaks can be achieved with more tilted angles.

"pr_recos" using all tilted angles