Welcome everyone!

Today's Experiment **NMR Analysis**

We will begin at 12:10pm.

Please add your group number to the beginning of your name.

Use this time to ask questions and chat!



Common Solvent Residual Peaks

CHEM 12A Section 311 Laboratory October 21st, 2020

Chloroform



deuterated

H₃C

Dimethyl Sulfoxide (DMSO)

CH₃ CD₃ D_3C

deuterated





Stepwise NMR Spectra Processing

1. Set CHEM 12A Template Defaults

Open the file available on bCourses entitled "Chem 12A MNova layout template".

2. Open Sample FID (Free Induction Decay)

Open the FID file provided for the given sample.

3. Apply Processing Corrections

Select the Processing tab on the top of the page in MNova. Click on "Auto Baseline Correction" and "Auto Phase Correction".

4. Select a Reference Peak

Press "R" on your keyboard and select the reference peak (usually near 0 ppm). Reassign this peak to 0.00 ppm.

5. Integrate Each Peak

Press "I" on your keyboard and click and drag over each peak. Note that the first peak you integrate will automatically normalize to 1.00.

6. Normalize Integrals

Select an peak of known proticity (proton count) and right click it's integration value. Select "edit integral" and reassign its normalized value to the known proton count.

7. Pick through peaks

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Press "command K" on OS X or "control K" on Windows and pick through each peak.

8. Zoom in on spectrum and export

Press "Z" once to highlight across an entire horizontal region. Zoom in from the leftmost peak to the rightmost peak. Press "Z" again to highlight across an entire vertical region. Zoom in from the tip of the largest peak to just below the baseline.

You are now ready to export the document as a **PDF** for submission.

