

## Short user instructions

### Sample preparation

Samples should be more concentrated than samples for "normal" NMR. For example, 3 drops of monomer/polymer solution in 0.6 ml deuterated chloroform (around 3 times than usually).

### Preheating samples

Samples can be preheated in heating station to measurement temperature before introduced to spectrometer.

### Setting up the analysis

Touchscreen can be used with or without gloves. Choose Standby for disabling standby mode. Set-up the experiment:

- Observe Nucleus: e.g.  $^1\text{H}$
- Lock Nucleus: e.g.  $^2\text{H}$
- Solvent: e.g. Chloroform-D
- Experiment: e.g. 1D
- Number of Scans: e.g. 16

Remove the "blue sample". Blue sample is pure deuterated chloroform. This sample can be used to check the status of the spectrometer, if desired. Insert sample tube into to the spectrometer all the way to the bottom of the spectrometer. DO NOT drop the sample tube (it breaks easily). Choose GO to start measurement. After measurement, save the spectrum by choosing local (diskette icon). Name the spectrum and save. Measure the next sample.

### After last sample

Choose Standby and insert the "blue sample". Confirm, when blue sample is inserted. The Standby mode initiates automated shimming routines. Thus, the spectrometer should ALWAYS be kept on Standby mode, when not in use.

### Collecting data

Use USB memory stick to collect your data from Results. Spectra is recorded as JCAMP-DX files. Convert data into DX files using an external software, e.g. TopSpin. Notice that the solvent peak is automatically subtracted from the sample spectrum by the spectrometer.