

Quick Guide on BRUKER NMR Systems

Princeton University – Chemistry - NMR Laboratory

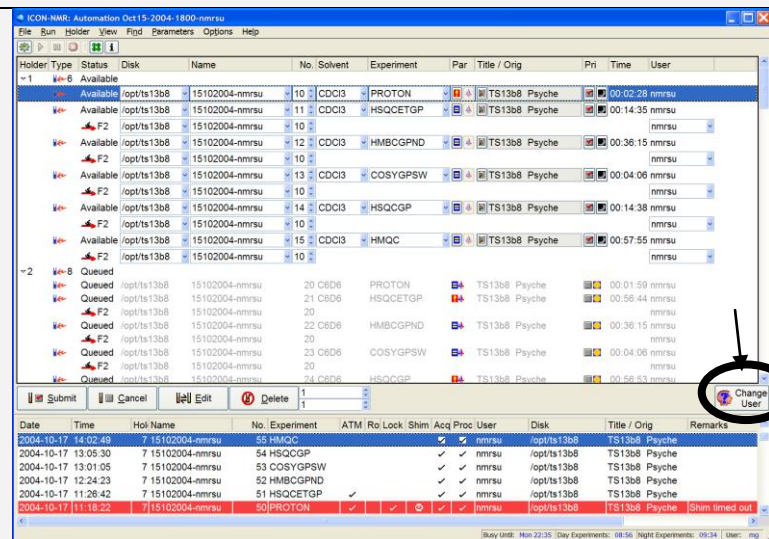
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Differences of each spectrometer hardware:

- Bruker-500, **A1**: cryo- ^1H optimized, Excellent for 1D ^1H experiments, such as acquiring 1D ^1H NMR data; optimum for ^1H detected experiments, such as 2D's ^1H - ^{13}C (X): HMQC(HSQC), HMBC, etc.
- Bruker-500, **A2**: cryo- ^{13}C optimized, excellent for 1D ^{13}C experiments.
- Bruker-500, **A3**: cryo-QNP optimized, excellent for 1D ^1H , ^{13}C , ^{31}P , and ^{15}N direct detection experiments.

- 1) **Inserting the sample**
- Insert the sample in the 5-mm *Bruker* spinner.
 - Adjust the sample height with the *Bruker* gauge (prepare your sample always with 45-50 mm length, approx. 500 uL volume).
 - Wipe clean the sample.
 - Find an empty holder in the carousel and insert the sample (**BIGGER** numbers are **OUTSIDE** holders and *small* numbers are **INSIDE** holders).
- The carousel has 120 holders.

- 2) **Login using ICON-NMR interface** (see right column)
- At the workstation, click on the Change User button, and type inside the next 2 input windows:
- Your NMR username
<ENTER>
- Your NMR password
<ENTER>
- ICON interface will then be available for you to specify the experiment at the holder # where your sample was **PREVIOUSLY INSERTED.**



- 3) **Removing sample from the carousel**
- Make it sure that you **never** pick a sample up from below the arm of the autosampler (This procedure leads to various errors, some serious).
 - To remove your sample from the carousel, use the two buttons on the front panel labeled with arrows (forward and backward).
 - Move the carousel **only when the autosampler is not in action, handling another sample.** Remove your sample from its holder, returning the *Bruker* spinner to the shelf.