HHMI SCHEDULER- GETTING STARTED

1. Go to CMB website www.science.smith.edu/cmbs (bookmark this page - lots of great info).

2. Or from Smith home page, click "Science Center" from choices across the top. Under "Facilities /Resources' choose "Center for Molecular Biology." (again, bookmark this page - lots of great info).

3. From Quick Links on lower left, choose HHMI Scheduler

4. Sign in with your Novell user name and password (same as for your groupwise email).

5. Hit "Scheduling" on the left.

6. Choose a center from the drop down menu on the left, and equipment from the drop down menu on the right.

7. Click in the time slot you want to start, fill in all info and choose an end time. Click "Make Reservation."

8. After your sign out time has passed you will get an saying you need to log your use, every few days until you do it.

9. Hit the link in the email (this starts you at step 4 above), then for step 5, hit "Logging" on the left, choose your event and answer the few questions. All are defaulted to the usual answer, just enter the length of time that you used it in hours (like 0.5 for 30 minutes) and if anyone used it with you. **(If you have not been doing this, all of your scheduled uses are still there and we don't actually get credit for the use until you log it so please try to fill out this short survey for each use, just doing 10 a day til their done if necessary).

10. If you use a piece of equipment without scheduling the use, please please log the use. Sign in for "Logging" as on step 9. Then hit "click here" to log data for a non-reserved session. This can also be done if someone else is already scheduled where you used it. This happens often with the Apple Cart.

**For use of the HHMI scheduler email Louie at lbierwer@smith.edu with your name, lab name, and project name. You will be put into the database within a day or 2.
**You can also email me if you have any problems with the scheduler or need training on any of the equipment.
** If you don't get trained by me, it is appropriate to be trained by someone in your lab, especially if there is a specific protocol your lab uses. However, PLEASE READ THE GUIDELINES AT EACH INSTRUMENT. These highlight best practices and have helpful tips that often get lost in translation☺.