Instructions/Information for Remote Access:

Getting Started:

Once you have been informed that you will be running remotely, make sure that you have made contact with your host. Shipping information can be found on our web page:

http://www.gmca.anl.gov/userprogram/beforeyoucome.html#shipping

Your pucks must be clearly labeled and directions for the order in which they are loaded into the automounter dewar should be unambiguous (see below). You should be using ALS style pin bases and the lengths of the pins should be 18 mm. (refer to our web page if you have any questions.) We recommend that you provide a blank pin so that we are able to verify that everything is set up correctly. The F-puck position is reserved for tools, a pin (F1) and a YAG crystal (F2), that you can use if you need to.

http://www.gmca.anl.gov/facilities/automounter.html

You will need a spread sheet with your sample information. An example spreadsheet can be downloaded from the following site:

http://www.gmca.aps.anl.gov/sitefiles/

Choose the spread sheet that matches your puck type (Rigaku or ALS/Uni-puck). If you do not provide one, a generic one will be available in your home directory (Rigaku_template.xls or ALS_template.xls). Rows for all pucks must be in the template otherwise there will be errors in loading the templates. At the present time, you may either email the spread sheet to your host or email it to yourself and retrieve it on the machine that you will be working on.

At the start of your time, call the beamline and check with your host to get any last minute instructions or to clarify any remaining questions. (Beamline IDD (630)252-1823 or Beamline IDB (630)252-1723). Your time will be from 10:00 am to 8:00 am the next day. During the hours from 10 am to 10 pm (22:00) you can expect full support from your host. You may continue to run until your time ends in the morning the next day but there will be NO staff support after 10 pm. Your host can be contacted via phone, email, or chat.

Other information that will be needed from you are:

- IP addresses for the machines that you will be using during your time. These can be in the form 123.123.123.* or they can specify the entire address.
  Note: sometimes the IP address that you see within your institution is not what is

exposed to the outside world. To check the address as seen by our computers please browse to the following link:
http://www.gmca.anl.gov/remote/myip.html
- Shipping information (Account numbers and preference for the return of your dewars (wet or dry, Saturday delivery?))
- Send disks for backup (specify Windows or Linux backups).
- NOTE: Once you are onto the beamline computer, you can **ssh** to any of the other machines. This is of interest if you have ssh server at your institution and want to transfer your data back to it or reduce data. The machines that are recommended are:
     23ID-D: bl1ws5.gmca.aps.anl.gov (164.54.210.75)
     23ID-B: bl2ws5.gmca.aps.anl.gov (164.54.210.146)

   Besides that, one of the above two computers will also be open for you as an ssh server for two days after the end of your data collection time. You may **ssh, scp, or sftp** directly to the appropriate machine to continue to use this computer to finish up as well as transfer your data.

- Mapping of Robot position – pucks – dewar should be clearly indicated (example):

Robot dewar position	Puck ID	User Shipping Dewar
A	JS 3	Dewar 1
B	JS 6	Dewar 3
C	JS 2	Dewar 3
D	JS 1	Dewar 3
E	JS 4	Dewar 1
F	GMCA reference	

Connecting Computers for Remote Access

Minimum requirements:
- Linux, MacOSX or Windows
- 1280x1024 resolution on one monitor
- 100kB/sec internet connection

Recommended:
- Linux or MacOSX
- 1600x1200 resolution on each of two monitors
- 200kB/sec internet connection for data acquisition, 1+MB/sec for transferring data
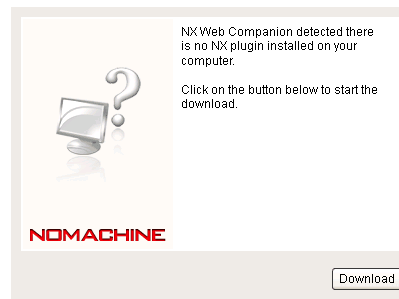
1.   Open your web browser

2.   Go to http://www.gmca.aps.anl.gov/remote/

3.   Click on the data acquisition or data processing link for the beamline you will be using

4.   If Java is not installed, you will receive the following notice:
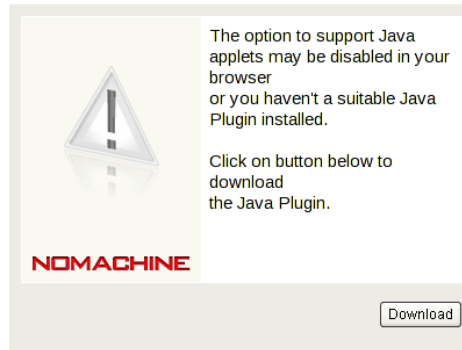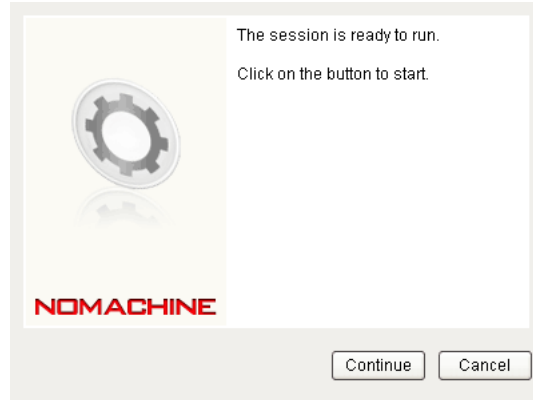

To install Java, browse to http://www.java.com/

5.   If NX has not been run before, click "Download"
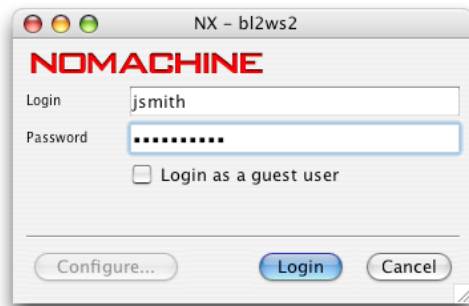

Allow the Java applet to run by clicking "Trust"

6.   If everything loads properly, you can click "**Continue**" to begin the session.

The session is ready to run.

Click on the button to start.
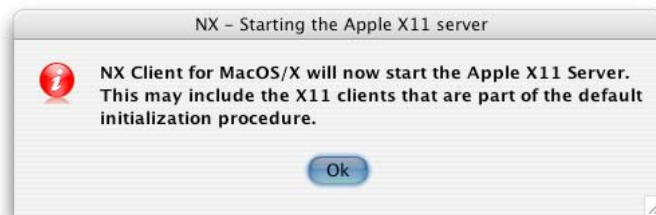
NOMACHINE

Continue   Cancel

Note: in case you already have NX client on your computer and do not want to install the second one via web browser, you can download and use preconfigured NX sessions to connect to the GMCA beamlines. The details are given at:

http://www.gmca.anl.gov/remote

7.   Login using the credentials given to you by your host

NX – bl2ws2

NOMACHINE

Login   jsmith

Password   ··········

☐ Login as a guest user

Configure...   Login   Cancel

8.   If you are using MacOSX and X11.app is not running, the NX client will start X11. Click "**Ok**" if asked.

NX – Starting the Apple X11 server

NX Client for MacOS/X will now start the Apple X11 Server.
This may include the X11 clients that are part of the default initialization procedure.

Ok

9. If this is your first connection attempt, you may receive a warning about authenticity. Please accept the RSA fingerprint and continue connecting by clicking "**Yes**"

10. You should now have a standard Linux desktop in a window. Expand the window across the two screens (**IMPORTANT**). To set up your remote data collection desktop efficiently, start the following:

Desktop One: Mar detector (This is to make sure that the detector program is running and you will be able to connect to BluIce). *To start, click on the marccd icon in the taskbar.*

This produces the window below. Select the "Yes, Connect to MAR desktop" button.

"
This is followed by request for your password and a verification. The "Alternative start for MAR" is used in cases when the other button does not work.

Desktop Two: Blu-ice & MEDM control screen
To start Blu-ice, click on the Blu-ice icon in the taskbar
To start the MEDM, click on the 23ID icon in the taskbar

Desktop Three: HKL2000
To start, open a terminal window and type:
HKL2000
HKL3000 *is available only on bl*ws1.*

Desktop Four: Ring status and other miscellaneous windows
> *To start the ring status, MEDM->Storage Ring Status*
> *To start shutter status,*
> *MEDM->APS->APS->EPS Status Beamline Status*

11.   Before collecting data, ask your host whether he/she has aligned the beam, collimator, and centered the goniometer using the YAG and centering pin.

12.   If you need help, the phone number is (630)252-1723 for GMCA 23-IDB (ID-out) and (630)252-1823 for GMCA 23-IDD (ID-in).

NOTE: Once you are onto the beamline computer, you can **ssh** to any of the other machines. This is of interest if you want to transfer your data back to your home institution. The machines that are recommended are:
IDD: bl1ws5.gmca.aps.anl.gov (164.54.210.75)
IDB: bl2ws5.gmca.aps.anl.gov (164.54.210.146)

New Features:

There are two new features (2/1/10) that you may want to try. The first is the Automated loop/crystal centering option in the JScreening tab (Figure below). It takes less than 30 seconds to complete a loop centering. If you will be running un-attended, click on the jpeg option so you could make sure that your sample was centered correctly.

The second new feature is annealing. The Annealing menu is located in the "Tools Tab" located in the "Sample" window. There are two different options for annealing, Flow and Motion. Control's with default values is shown in the figure below. More detail is available in the "Useful Features of the Sample Tab" section of this manual.
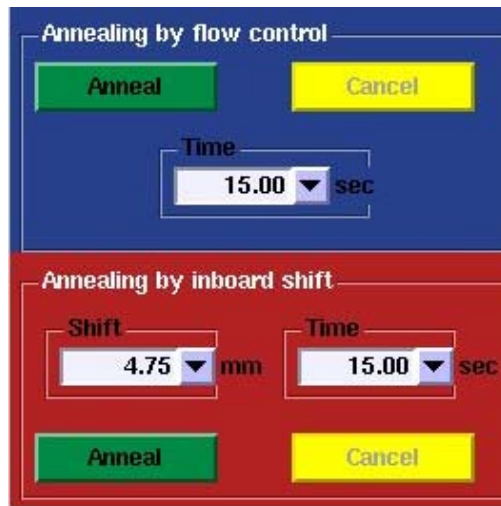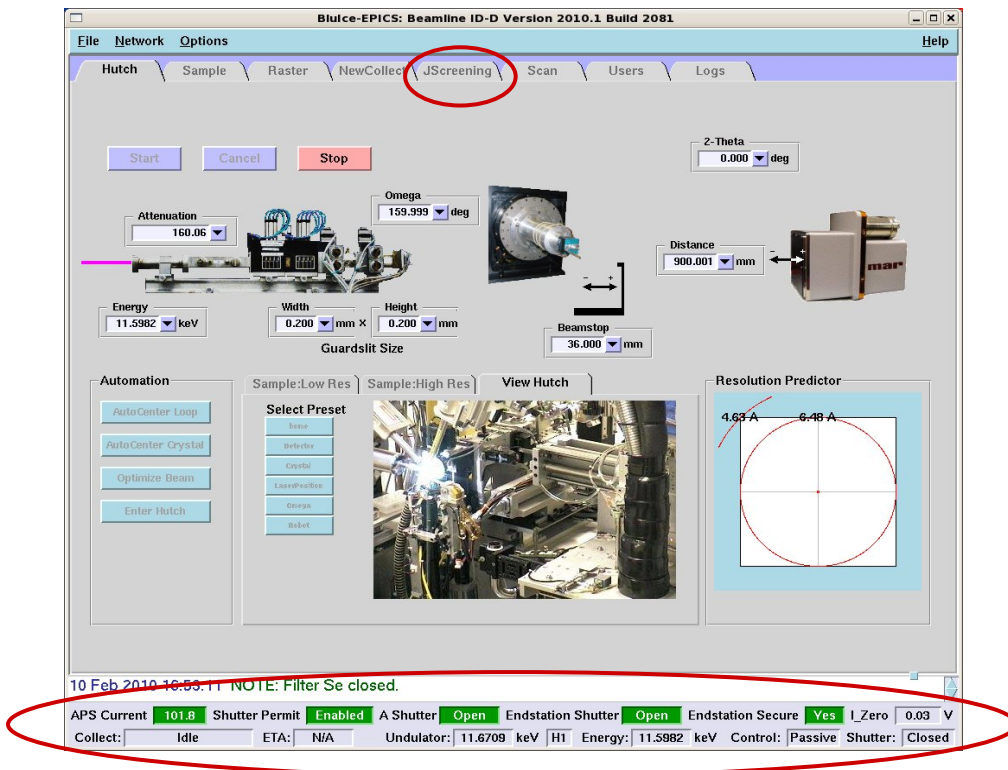
Features for Remote Users:

The "Common Problems and Solutions" section are at the end of this manual.

There are certain features that will aid you in running remote. These are features that have been implemented into BluIce but you may not have noticed when you visited the beamlines.

Status Bar:

The status bar near the bottom of the BluIce window (highlighted within the long red ellipsoid) will give you most of the necessary information as to the status of the beamline. The APS current is the ring current, in top-off mode it is ~102 mA. **All shutter status indicators are also control buttons.** The APS Shutter (A Shutter) status is the front end status. This shutter closes automatically if the beam in the storage ring is lost or there are problems in the beamline. When beam is restored or the problem is cleared it can be opened by pressing on this button. The Endstatsion Secured indicator signals whether the hutch has been searched and enabled. The Endstation Shutter button serves as an indicator of the status of the shutter as well as opening and closing this shutter. It allows beam into the experimental hutch. The I_zero (I0) window displays, in volts, the I0 monitor that is downstream of the data collection shutter. The "Shutter" button will toggle open and close during data collection. If this is open, your sample is being exposed to radiation. If any of the indicators are red, you will not be able to bring x-rays to your sample.

A second smaller ellipsoid can be seen in the top middle of the window. In the fall of 2009, a new screening tab was launched and has now completely replaced the older "Screening tab". Many new features have been introduced, see section below.

Summary:

All the Shutter buttons (A-Shutter, Endstation Shutter, and Shutter (experimental)) serve as both status and control.

APS Current – Ring current, 102 mA in top-off mode.
Shutter Permit – Displays the APS "A shutter" status. If it is enabled, beam can be brought into the beamline.
A Shutter – Shutter that separates ring from beamline. It can be used to toggle open this shutter. (Only opens, it does not close.)
**Endstation Secured** – Experimental hutch is searched and safety interlocked.
Endstation Shutter – Shutter that allows beam into the endstation (experimental hutch). This is not to be confused with the shutter that controls the data collection.
I_Zero – I0 monitor value in volts. This is downstream of the data collection shutter.
Shutter - This is used for data collection. Normally it is automatically controlled but it can be toggled open/close manually. When this is open, beam is hitting your sample.

All of the manuals that you have used on the beamline can be accessed by pressing **Help**, located in the top right of the BluIce screen (Figure below). **Except for the Jscreening tab. The help is indicated in the figure of the JScreening tab (as of 2/10/10).**
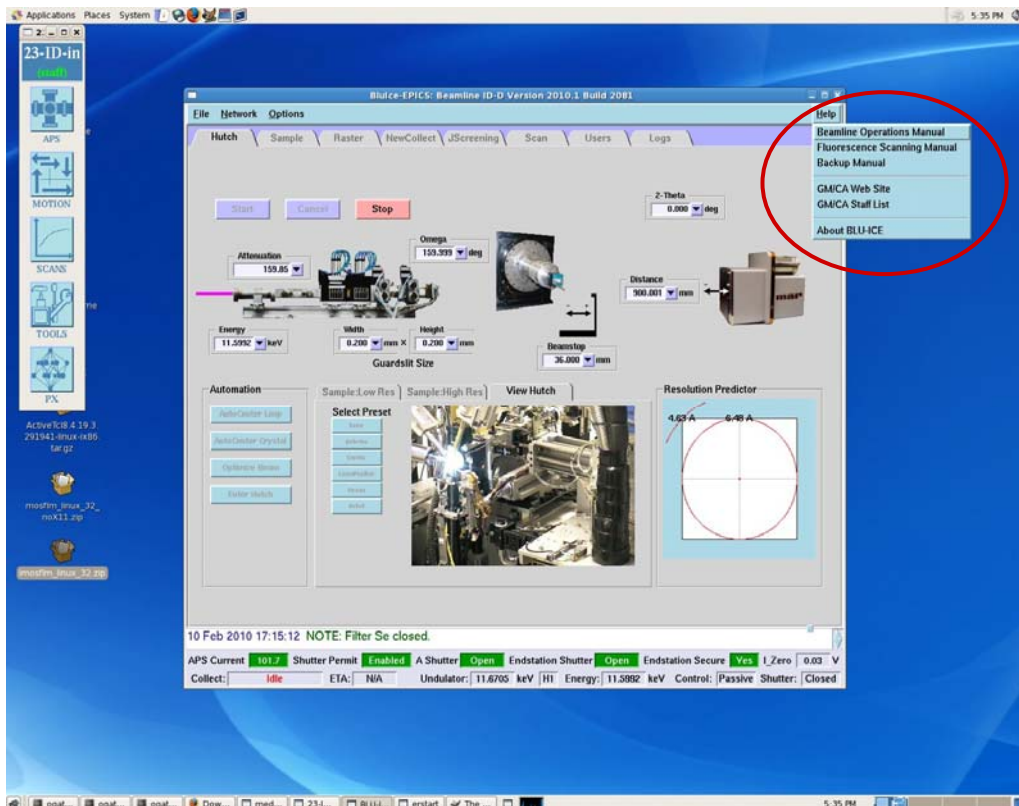
In order to view into the hutch, remember that in addition to the "Sample_Low Res" and "Sample High Res" tabs there is the "View Hutch" tab. Open the Sample Window and choose the "View Hutch" tab. The Sample window is shown in the Figure below. The Laser Position and Robot view are highlighted as possible views to check for robot operations.

There are six selected presets that you may choose to check on things in the hutch.

Home – overall view of the sample area

Detector - view to the downstream side of the home view, to view the normal detector positions.

Crystal – A closeup view of the sample area from this camera.

Laser Position – You can check to see the robot sample detection laser in case there is an error.

Omega – This will point toward the Omega axis. You may have to move the detector back if you want to see this axis.

Robot – Overall view of the robot. You can see the robot going through its motions. This view is similar to the Home view.
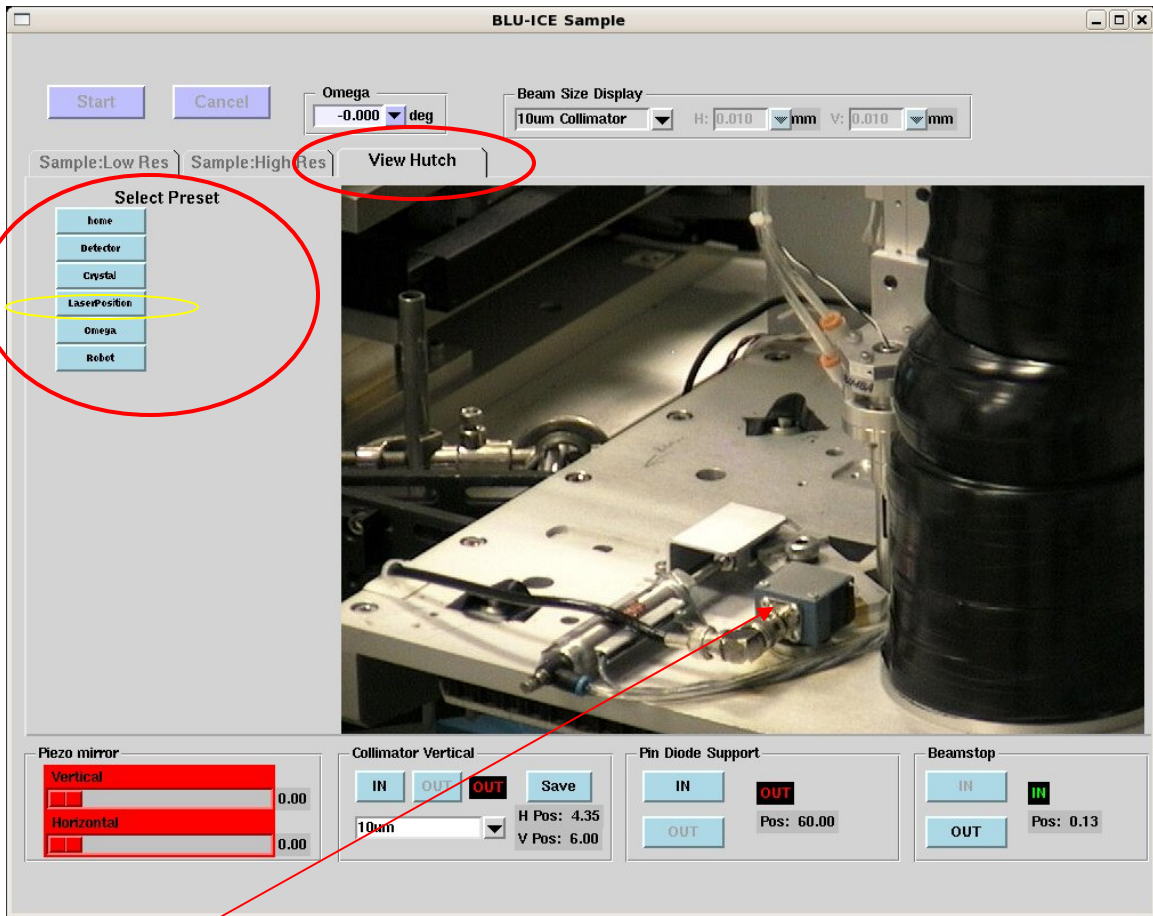
Laser Readout box in its correct orientation, the laser is hidden behind the black taped fill reservoir.

Figure. This is the Sample tab window showing the "Select Preset" tab selection, with the "Laser Position" selected. The laser is used for pin detection in the gripper after mounting and unmounting the sample. You may be able to see if the Readout box has turned away from the laser.

JScreening Tab –

There are two areas that display useful diagnostic information. These are circled in red in the figure of the JScreening Tab below. One appears at the bottom of all of the windows (lower left red ellipsoid). This updates the "Overall Status" of the operations that are being carried out. You can read the status while paying special attention to any text that appears in RED. The other is the text in the "Robot Status" section of the JScreening Tab window that is circled in red, located at the lower right in the figure below. You will be able to follow the steps in the robot operation and read any of the error messages that occur, i.e. ERR:recover:pin@gonio. When communicating with the host, you will be able to report the status or problems with the robot by reading these messages. You or your host will then be able to focus in and resolve the problem.

Manual for screening

Overall status

Sample centering

Robot status
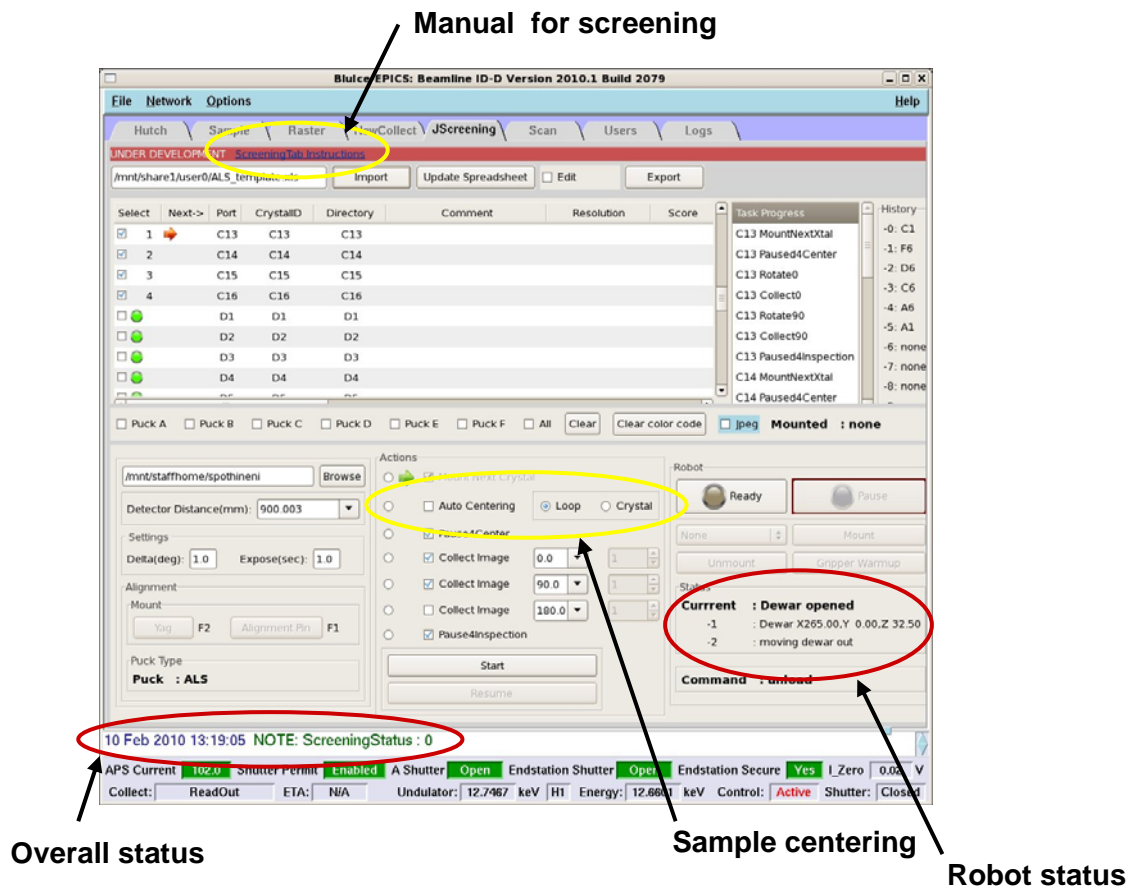
In the figure above, the yellow circle at the top of the window indicates the location of the JScreening Manual, as of this time (2/11/10) it it not located under **Help**, but it will appear soon. The second yellow ellipsoid in the middle of the window is a new feature for the Winter 2010 run (2/1 – 5/1/10). It allows the choice of either loop or crystal centering. It takes less than 30 seconds to automatically center the loop.

Useful features in the Sample Tab:

Another feature that may be useful to you is the +/- n button in the Sample tab. This is useful for aligning the YAG crystal or in moving your sample crystal in order to get a better view. The "Rotate +-n" window sets the step size and the +n/-n buttons next to the +90/-90 buttons will rotate the sample accordingly (red ellipsoids). See figure below.
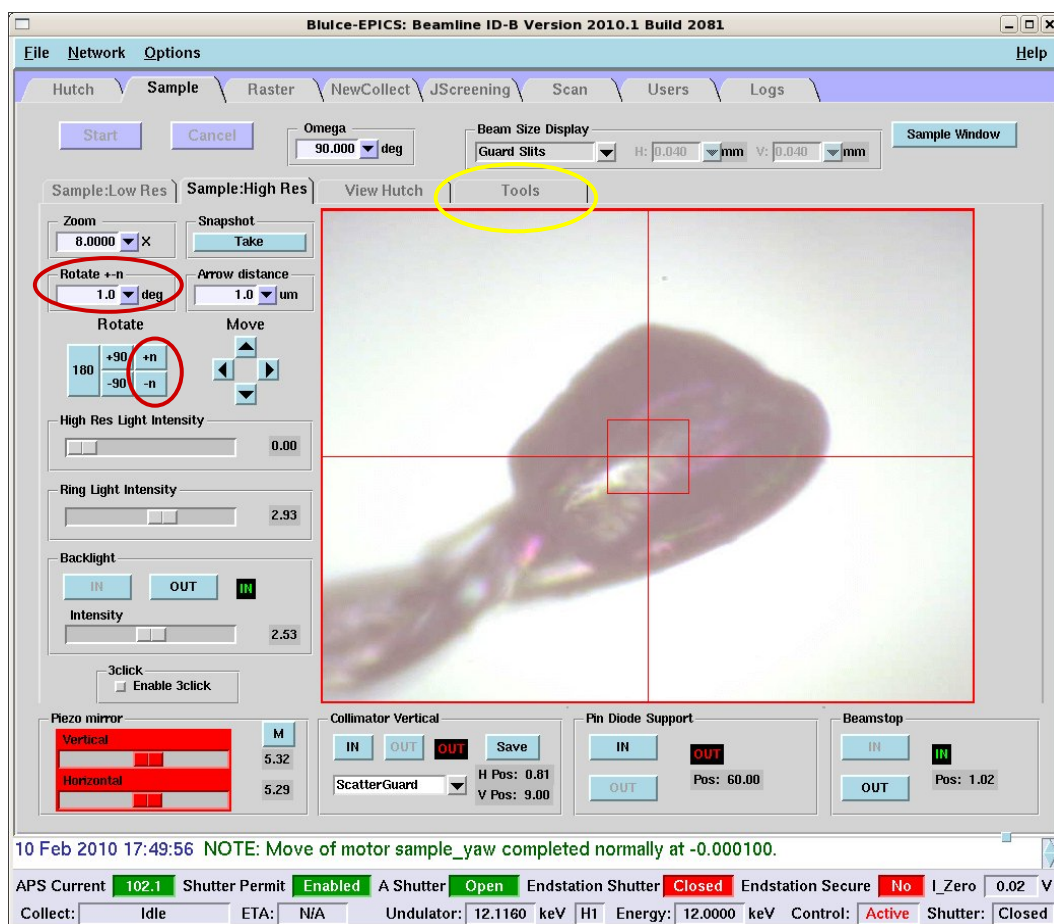
Figure. The Rotate +-n sets the angular step size and the +n/-n buttons will rotate the sample in the specific direction. The Tools Tab, in the yellow ellipsoid will bring up the annealing tools.

A new feature as of 2/1/10 are the annealing buttons. They are located under the "Tools" Tab in the "Sample" window, (yellow ellipsoids in figure above and below). There are two different ways to anneal a sample. One is by controlling the flow of the cryostream to the sample. The advantage of this method is that you can watch your crystal in the "Sample High Res" camera. Remember to put in the back light, set the annealing time, and press the "Anneal" button in the Flow control. If you do not know what time to set, you could set the timer to 30 -60 seconds, watch your crystal, and press the "Cancel" button. The other method is by moving the crystal out of the coldstream. You will not be able to see effects as it is happening. The suggested value is 4.75 mm. This will keep the sample in the dry nitrogen shield gas stream during the annealing process.

Common Problems and Solutions:

1) Problem: The robot stops working and goes to pause.
   Solution: Try switching from Pause to Ready by pressing the Ready button. Often times this resolves simple problems.

2) Problem: Robot consistently has problems in mounting or dismounting the bases into the dewar.
   Solution: Inform your host of this problem. Ask him to check to see if the pucks were loaded correctly and that you are using the correct pin bases.

3) Problem: Gripper repeatedly fails to unmount the sample on the Goniostat.
   Solution: Contact host and notify him of this problem. He will adjust the gripper warm-up parameters.

4) Problem: The gripper does not cool down to the temperature that it is supposed to or it is taking a long time to cool. (You've been waiting too long for the robot to proceed.)
   Solution: Contact your host immediately, describe the problem. It could be that one of the temperature probe wires is loose or the dewar is not filling correctly.

5) Problem: I have ice on my crystal, what shall I do?
  Solution: The only solution that we have at this time is to un-mount then re-mount the
   sample. This sometimes works.

6) Problem: Can I anneal my sample?
  Solution: As of 2/1/10 you can. Go to the sample tab, under the tools menu tab (see
   above). There are two ways to anneal. Take your pick.