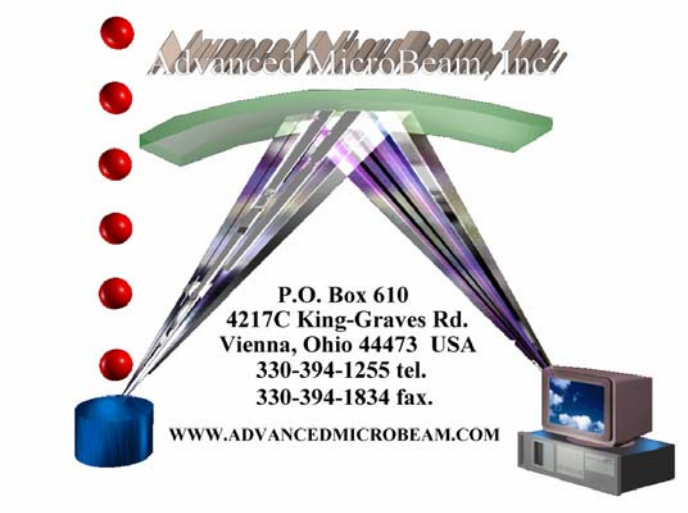


November 29, 2005

SIS Mosaic Imaging Manual

SEM Type: JEOL 6500, 7000, 7400

INSTRUCTIONS ARE SIMILAR FOR ARL SEMQ

Imaging System: Soft Imaging Systems GmbH

WDS System: Oxford Inca Wave

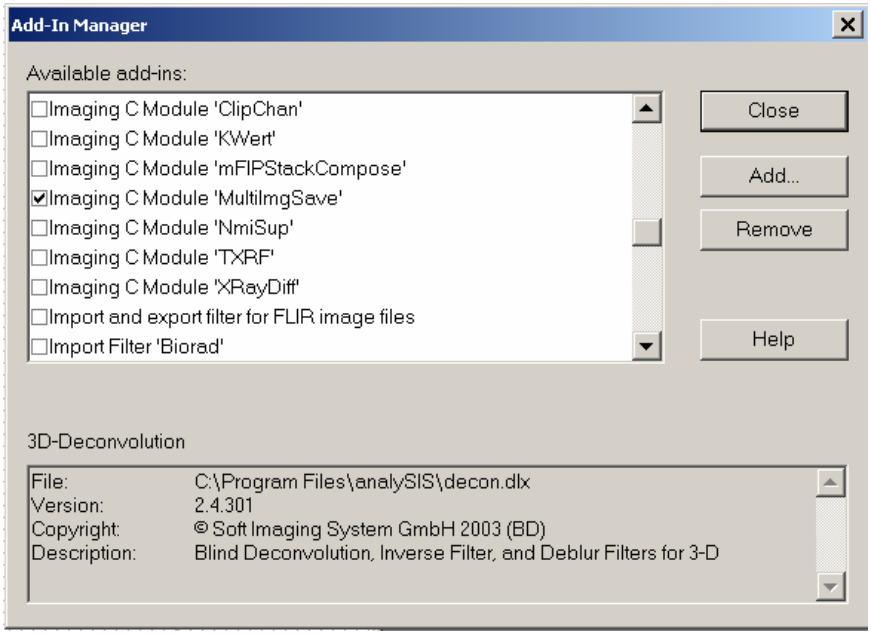
Fielname: JEOL650070007400MOSAICMANUALrev1.doc

Chapter Eight

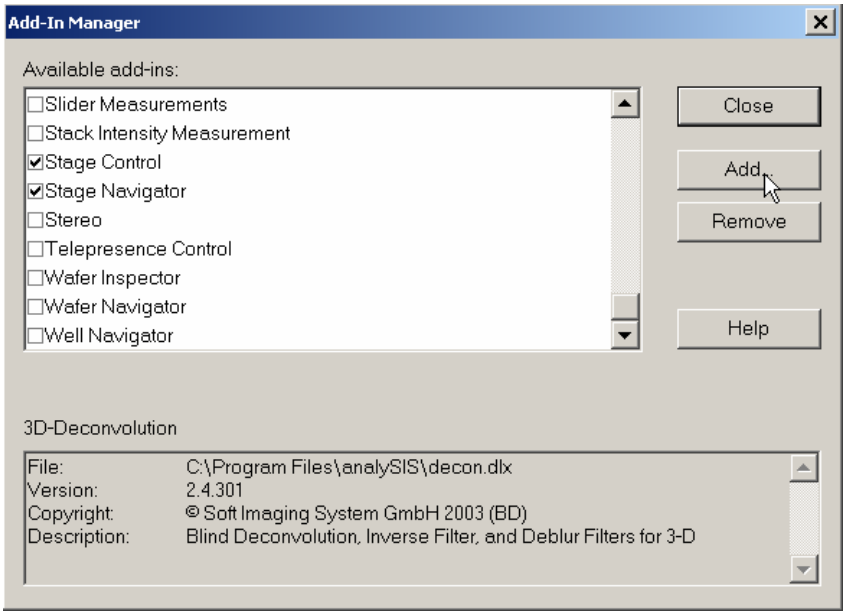
Installing Mosaic Imaging Software onto a JEOL 6500/7000/7400 SEM

Special Note: Steps 1 to 8 may already have been completed if you followed the manual.

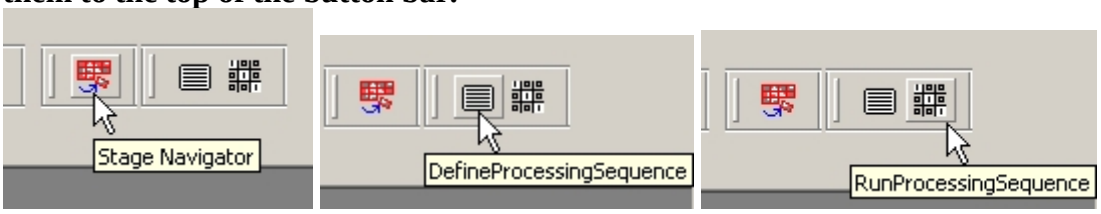
1. **Analysis Version 3.2 Build 8.31 or higher should be installed.**
2. **Copy the stage control DLL (STGJL7400.DLL) to the C:\Program Files\analysis folder.**
3. **Copy the stage control INI file (STGJL7400.INI) to the C:\Program Files\analysis folder.**
4. **Copy the 7400 remote control file (JL7400RM.DLL) to the C:\Program Files\analysis folder.**
5. **Add the following lines to the ANALYSIS.INI file in the [StageList] section.**
   Stage42=STGJL7400.DLL
   Ini42=STGJL7400.INI
   Load42=1
6. **Save the analysis.ini file after making these changes.**
7. **Create a folder called "MultiImageSave" in the C:\Program Files\Analysis\Module folder.**
8. **Copy the following files into this directory:**
   A. **AMUTIL.INI**
   B. **AMUTIL.SXU**
   C. **MultiImgSave.ini**
   D. **MultiImgSave.sxu**
9. **First Time Only: Load the Imaging C Module'MultiImageSave' using the Add-In Manager in the Special pull-down menu. Click the box so that a check-mark appears, then click the ADD button**



10.
11. **Repeat this procedure to load Stage Control and Stage Manager.**



12. The ICONS to start these modules may appear at the bottom of the display. Drag them to the top of the button bar.

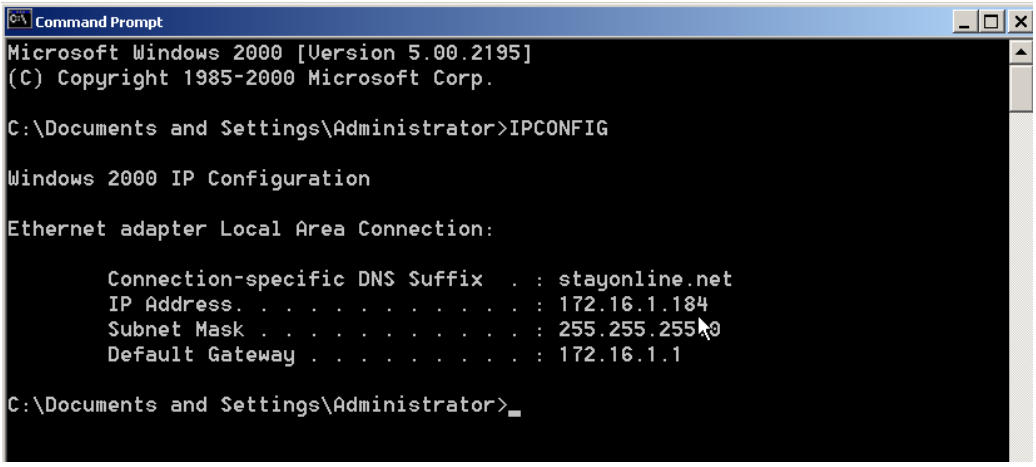
13. 

14. If the Analysis system is connected to a remote computer, instead of the JEOL computer, the IP ADDRESS of the JEOL SEM will have to be typed into the software.

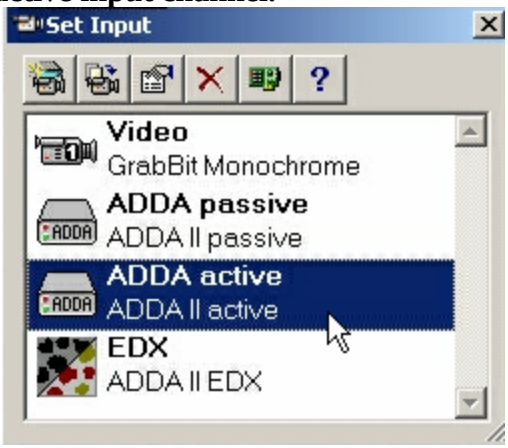
15. Click START, PROGRAMS, ACCESSORIES, COMMAND PROMPT. Type IPCONFIG, and make a note of the JEOL SEM IP address:

- **A. Server IP: 28.28.28.1 ??**
- **B. 208.196.228.18 ??**

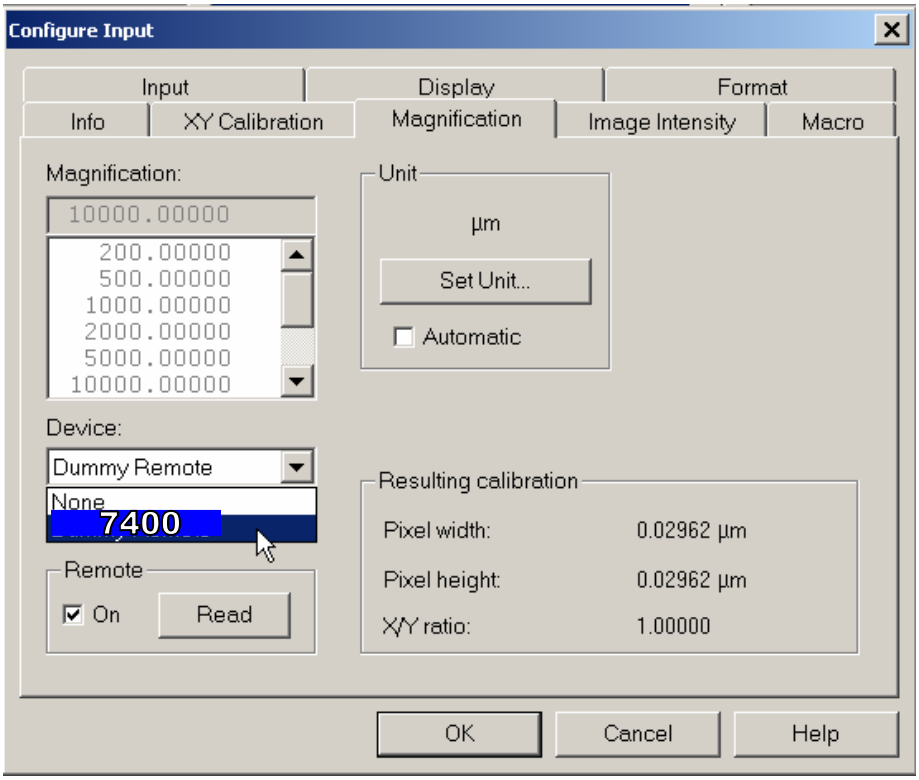
16. The Analysis software will prompt you to type in these addresses automatically.



17. Choose the ADDAII active input channel.



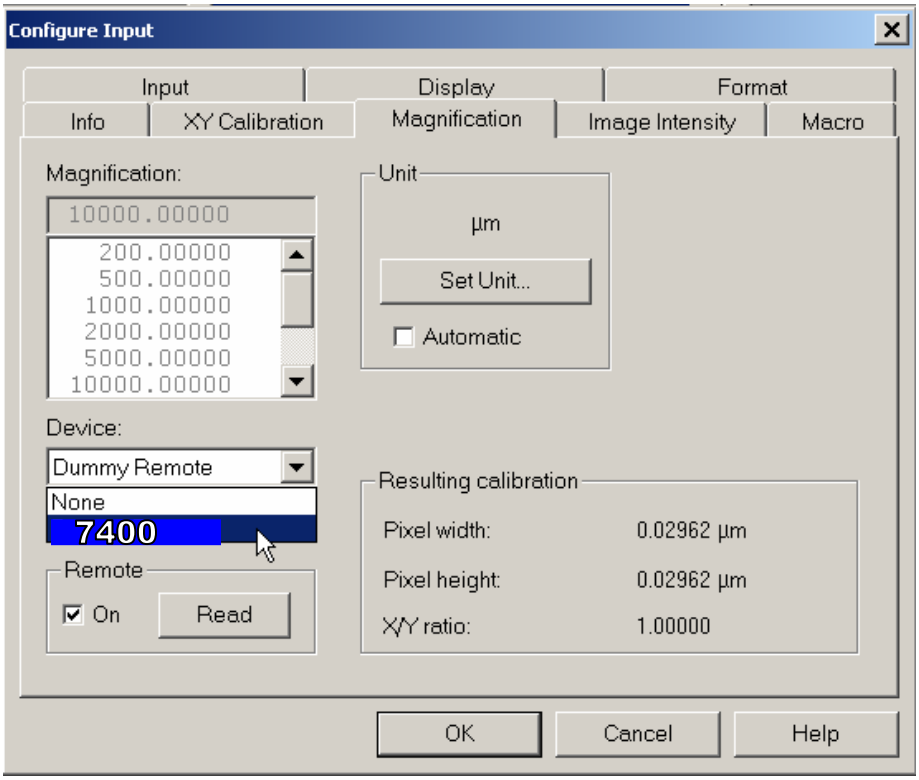
18. Go to the Configure Input window, and click the Magnification Tab.
19. Choose 7400 as the DEVICE.
20. In the REMOTE box, click the ON button box so that a check mark appears.

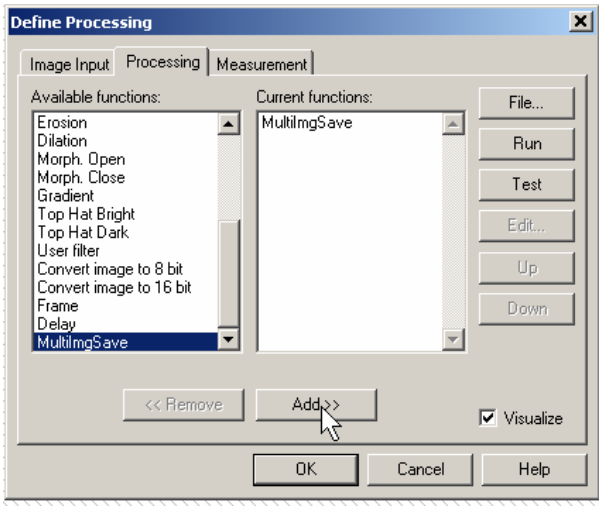


21. Calibrate the magnification of the electron beam using the XY Calibration tab.

22. Select the EDX logical input.

23. Go to the Configure Input window, and click the Magnification Tab.
24. Choose 7400 as the DEVICE.
25. In the REMOTE box, click the ON button box so that a check mark appears.



26. **Calibrate the magnification of the electron beam using the XY Calibration TAB.**
27. **Start analSIS and go to the Preferences pull-down menu.**
28. **Click the SPECIAL, PREFERENCES, STAGE tab, and select the 7400 driver. This driver reads the stage limits directly from the instrument without having to move and find the limit switches. Click the CONNECT button. The 7400-not initialized should then change to 7400, indicating that the stage is initialized.**
29. **Click STAGE, DEFINE PROCESSING, and PROCESSING TAB.**
30. **Select MULTIIMAGESAVE in the Available Functions window, then click the ADD button.**
31. **The MultiImgSave module should now appear in the Available Functions window in the Stage Manager, Define Processing window.**
32. 

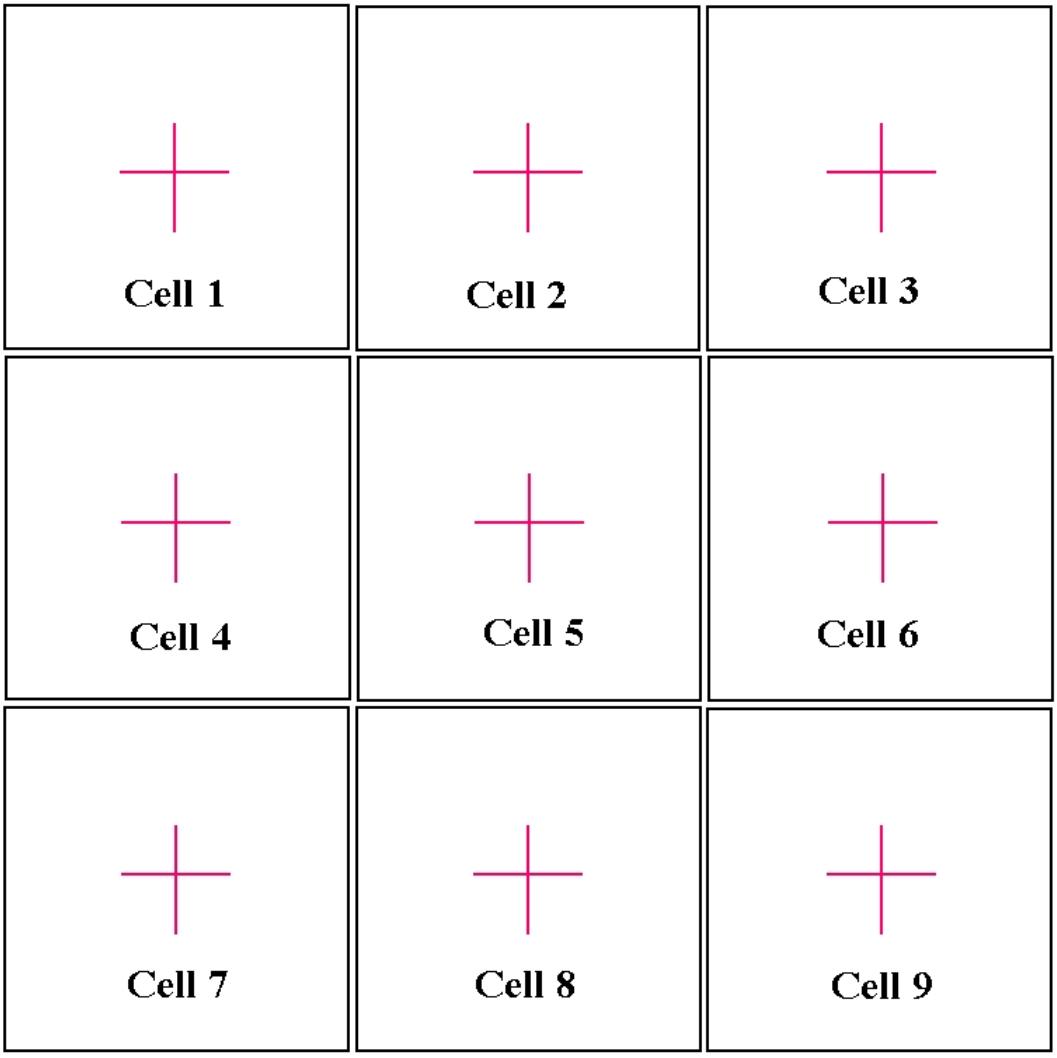
(End of Chapter 8)

Chapter 9

Large Area Mapping using Combined Beam and Stage Scanning
(Mosaic Mapping-Single Spectrometer Pass)

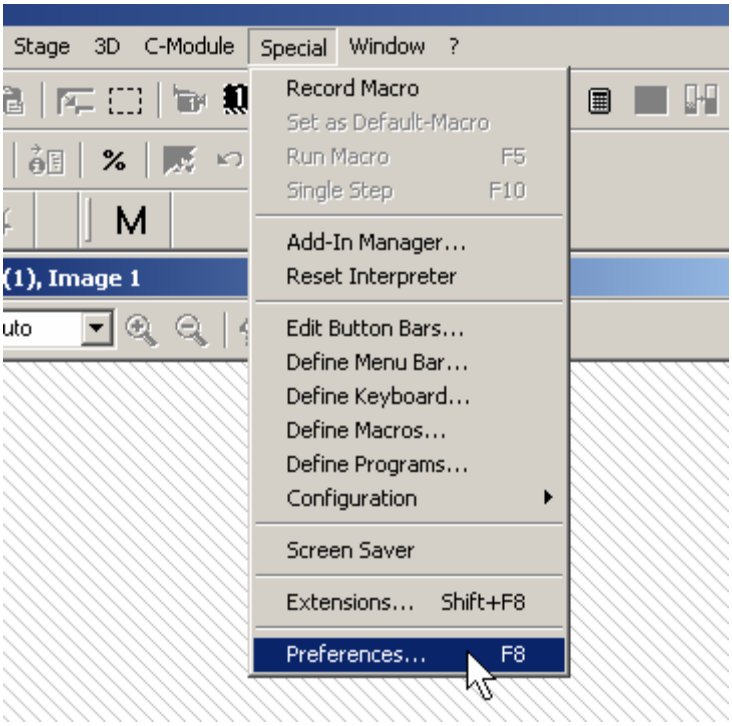
Mosaic Images and X-Ray maps are large images that are composed of a group of smaller images. The analysis program creates these images by moving the stage to the center of the first small cell and then scanning the electron beam over the entire cell. The stage then moves to the center of the next cell and repeats until finished.

3 X 3 Mosaic Image

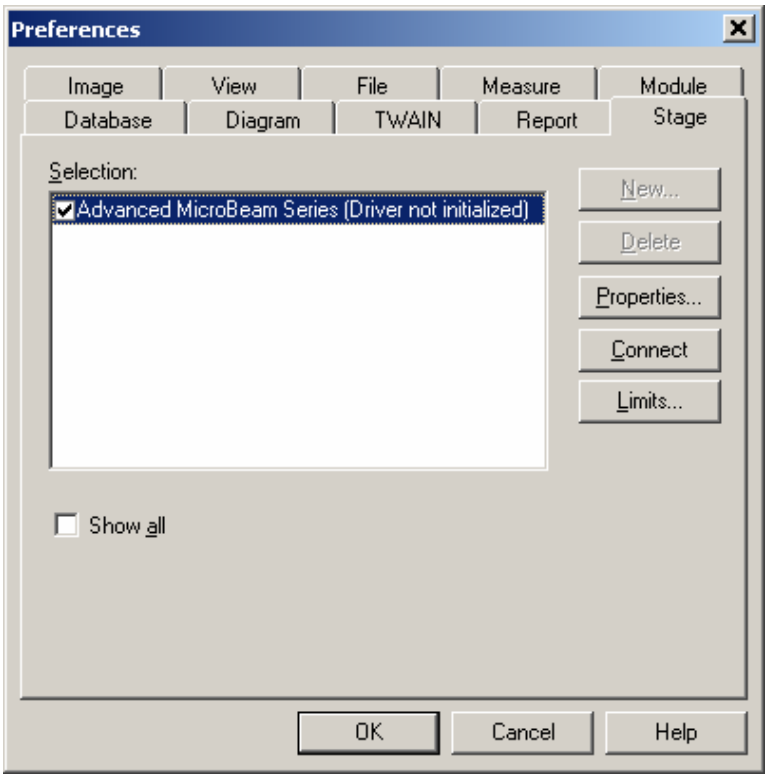


1. **Tune the wavelength spectrometers to the elements of interest. Move the stage to the area for mosaic mapping. Close all PFW programs, including Joywin, if applicable. JEOL 6500/7000/7400 users will not have these programs.**

2. **Open the analySIS program. Check that your Stage DLL is initialized. Select Special and then highlight the Preferences menu item.**

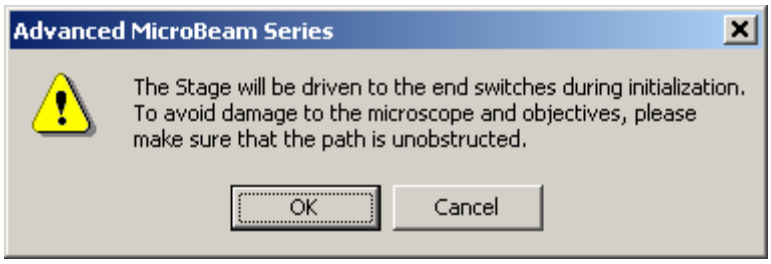


3. **This opens the Preferences window, select the Stage tab.**



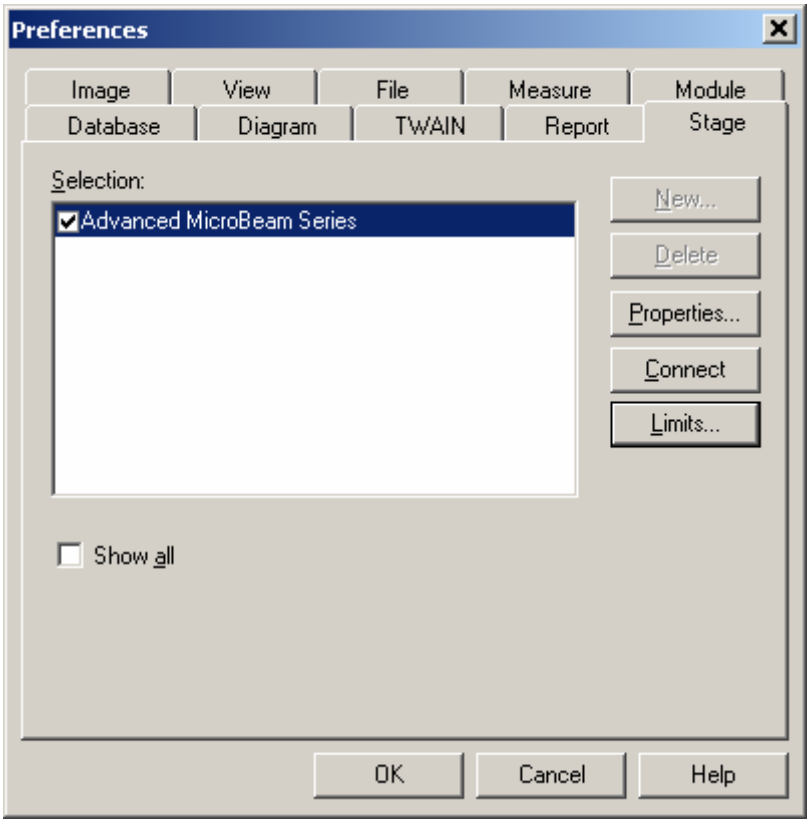
4. **The stage driver requires initialization. Click the Limits button. The Advanced MicroBeam Series driver window appears.**

5. ***Special Note: For a JEOL 6500/7000/7400, choose the JEOL 7400 driver, and click the CONNECT button. The stage initializes automatically and immediately, without going to the limit switches. Click OK and skip to step 9. "JEOL 7400 Series Initialized" will appear in the Selection Window.***



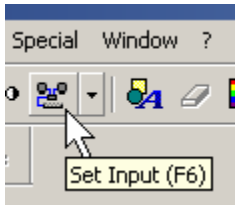
6. **Click its OK button. The stage drives to the lower limit switches, then reverses and drives to the upper limit switches, and finally the stage returns to the original coordinates.**

7. **The Preferences window indicates that the driver has been initialized.**

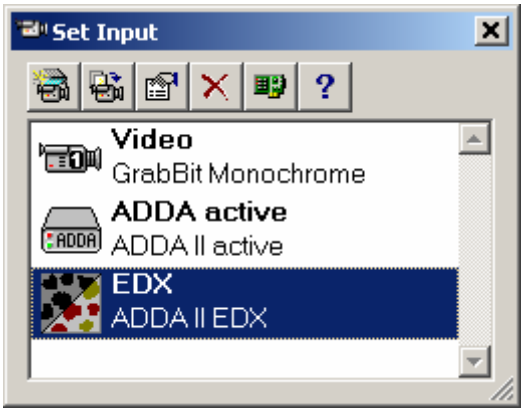


8. **Click the OK button to return to the main analySIS display.**

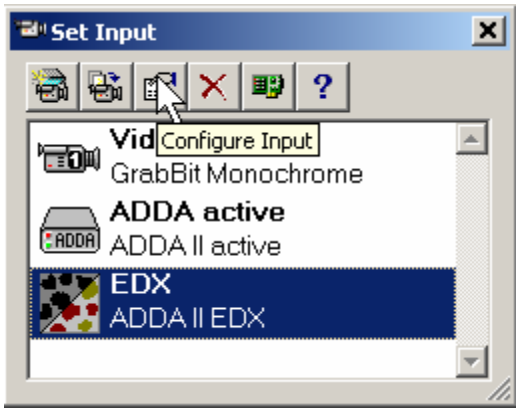
9. **The next step involves configuring the mapping input. Press the F6 key to open the SET INPUT dialog or click the SET INPUT icon.**



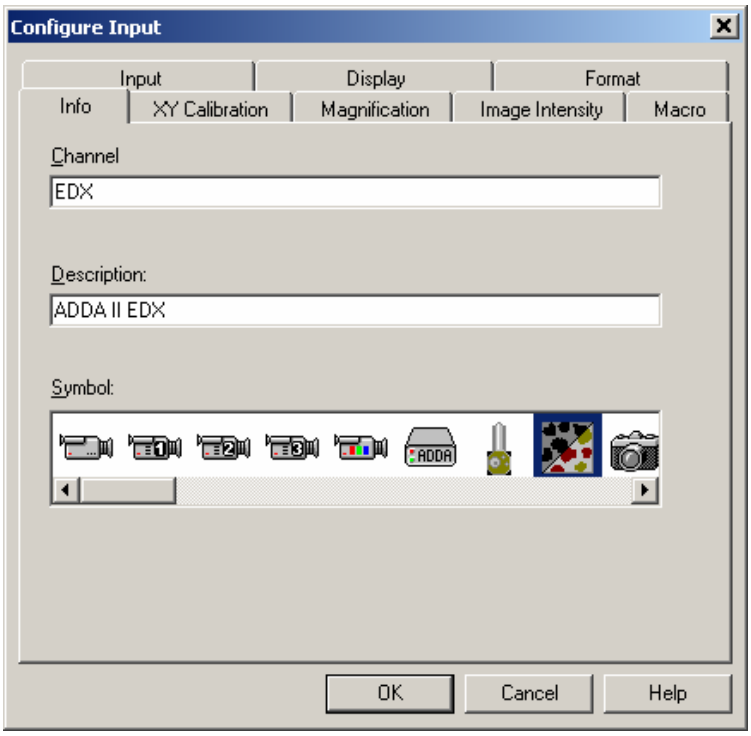
10. **Highlight EDX from the Set Input window as the logical input.**



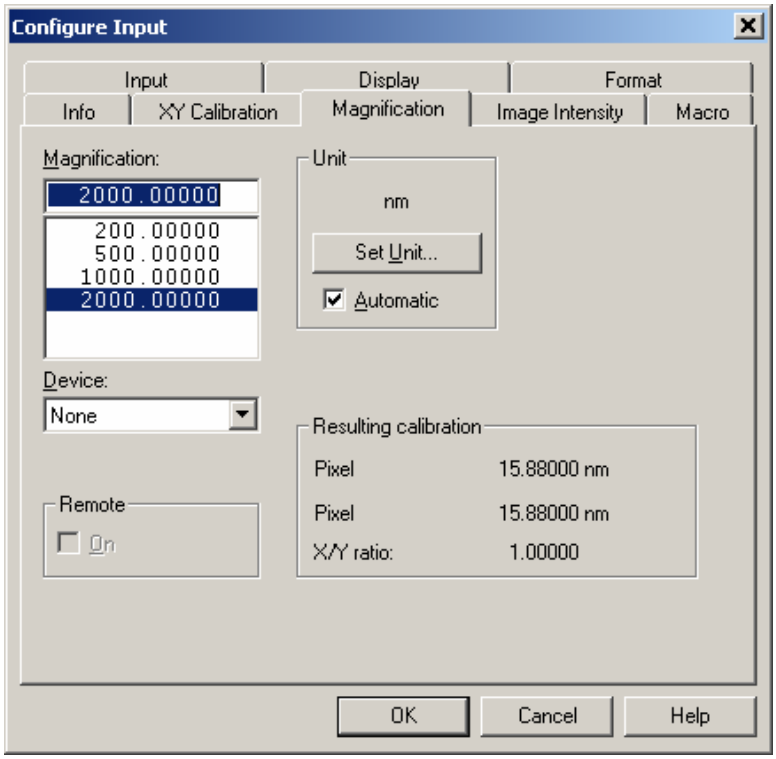
11. **Click the Configure Input button.**



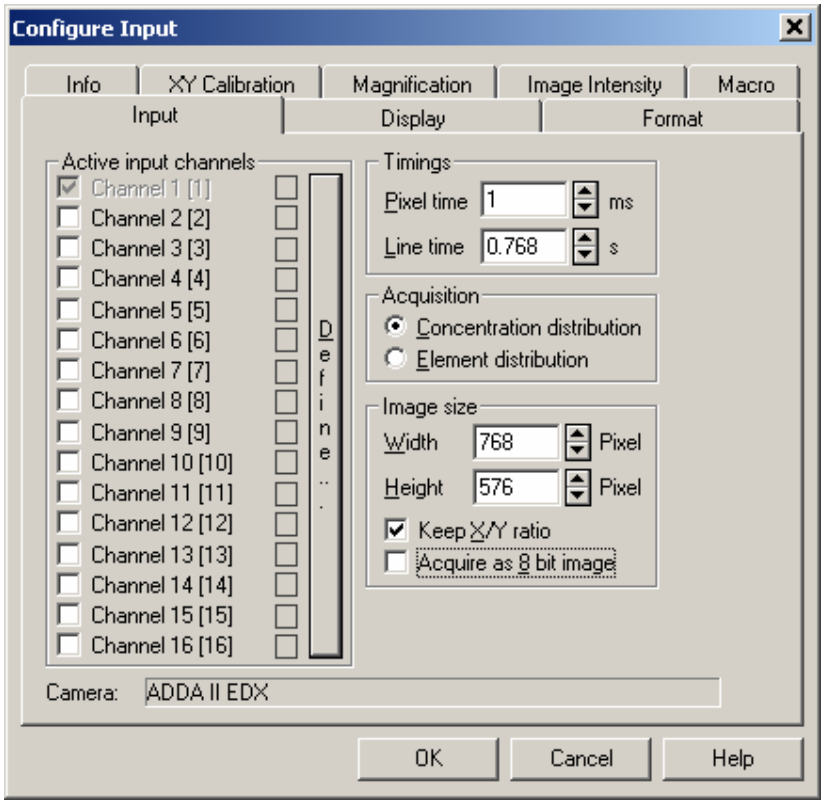
12. From the Configure Input window, first select the Magnification tab.



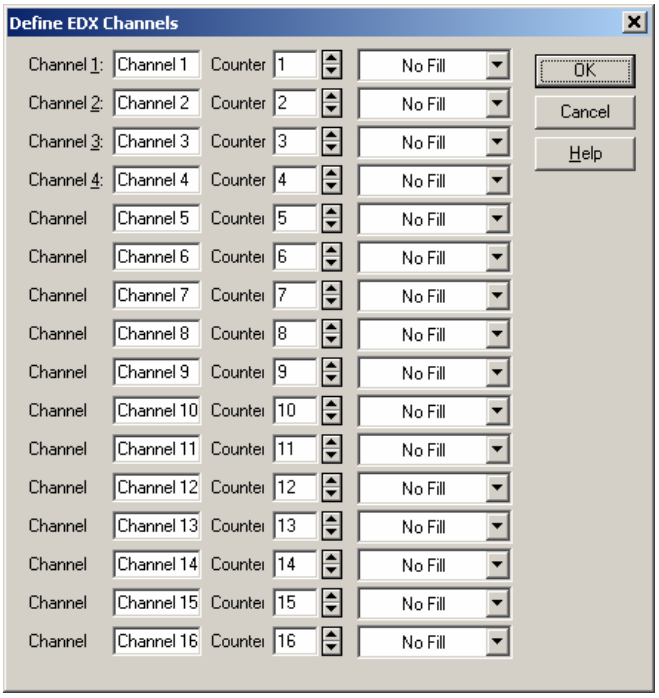
13. Highlight the appropriate magnification for your maps. Here, 2000x is selected to eliminate any Bragg defocusing issues. Also check that the instrument magnification is set to this same value. A magnification of 1000X is fine for the JEOL 7000 with Oxford Inca Wave spectrometer.



14. Select the Input tab.

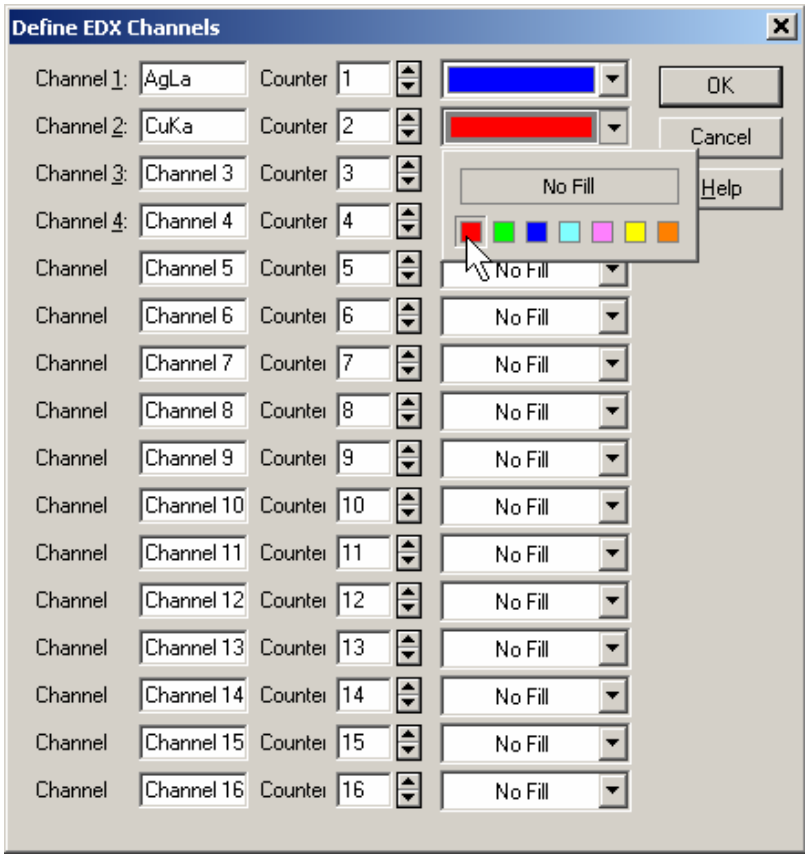


15. Check the correct number of Active Input channels (spectrometers for mapping) and click the Define bar to edit the label and color schemes in the Define EDX Channels window.



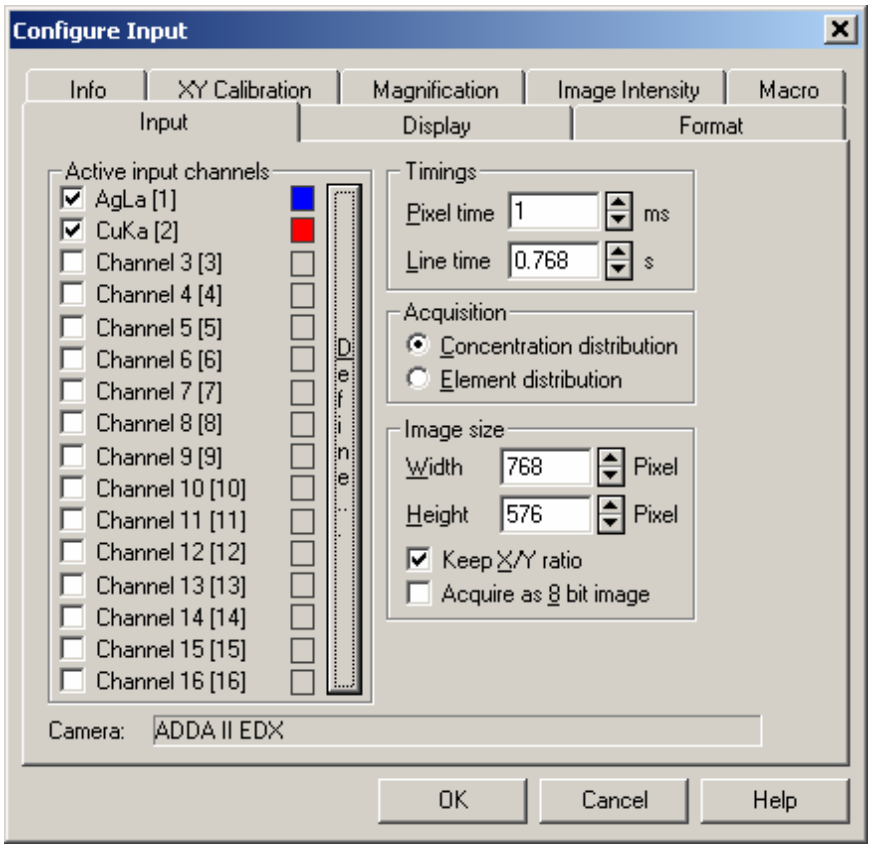
16. Type in the element designation in the Channel box, the Counter number indicates the spectrometer designation and finally click the down arrow by the No Fill box to modify the color displayed for each x-ray.

17. In this example, mosaic maps for both AgLa and CuKa x-rays will be collected on spectrometers 1 and 2, respectively.



18. Close this window by clicking the OK button.

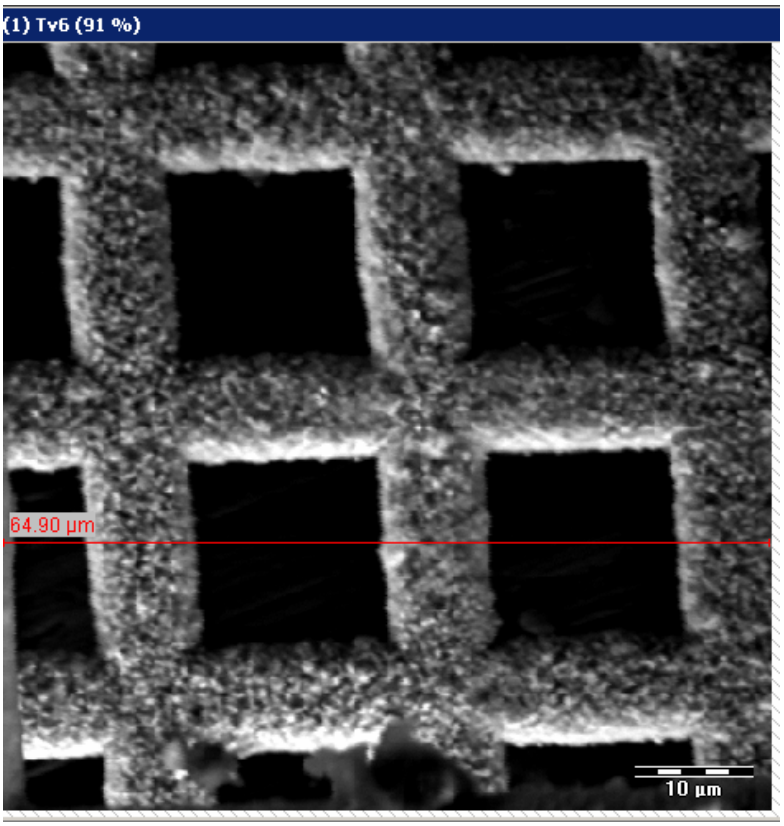
19. For an Oxford WDS spectrometer, only one WDS mapping output is available, and should be connected to Channel 1. For microprobes, choose up the total number of WDS spectrometers that are available. The remaining input channels can be connected to EDS mapping outputs.



20. Choose the Concentration distribution Acquisition button to create counter x-ray maps.

21. Next, choose an Image size, the following discussion illustrates how to calculate the cell width and height. In this example, a square raster/display is used (horizontal and vertical scan distances are equal) and the magnification is set to 2000 times.

22. First, determine the horizontal beam scan distance at 2000X on your instrument using the Horizontal Distance measurement feature in analySIS. In the figure below, the measurement indicates that the beam scans 65 microns.



23. Decide on the total size of image needed to cover your area of interest. In this example we will cover an area of 1mm x 1mm.

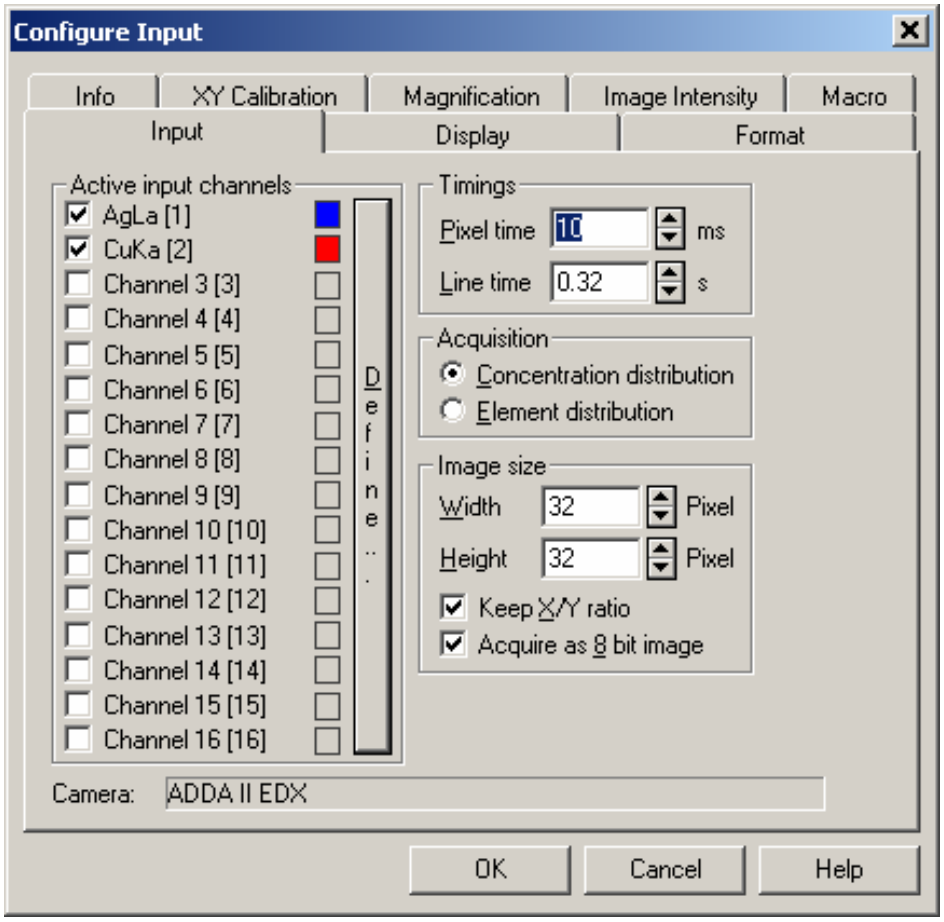
24. Choose how far you would like the beam to travel for each pixel. Here, the beam will travel 2 microns for each pixel.

25. Calculate the total mosaic resolution needed by dividing the total distance (1000 microns) by the stepping increment (2 microns) indicating 500 microns. It may be necessary to round up or down to the next available resolution, i.e., 512 x 512 resolution.

26. Next, determine the total number of cells to be acquired by dividing the total mosaic distance by the beam scan distance at the chosen magnification. For example, 1000 microns divided by 65 microns gives 15.4. This number is then rounded up to the next integer, 16. Thus, our original 1mm x 1mm square will be subdivided into 16 rows and 16 columns.

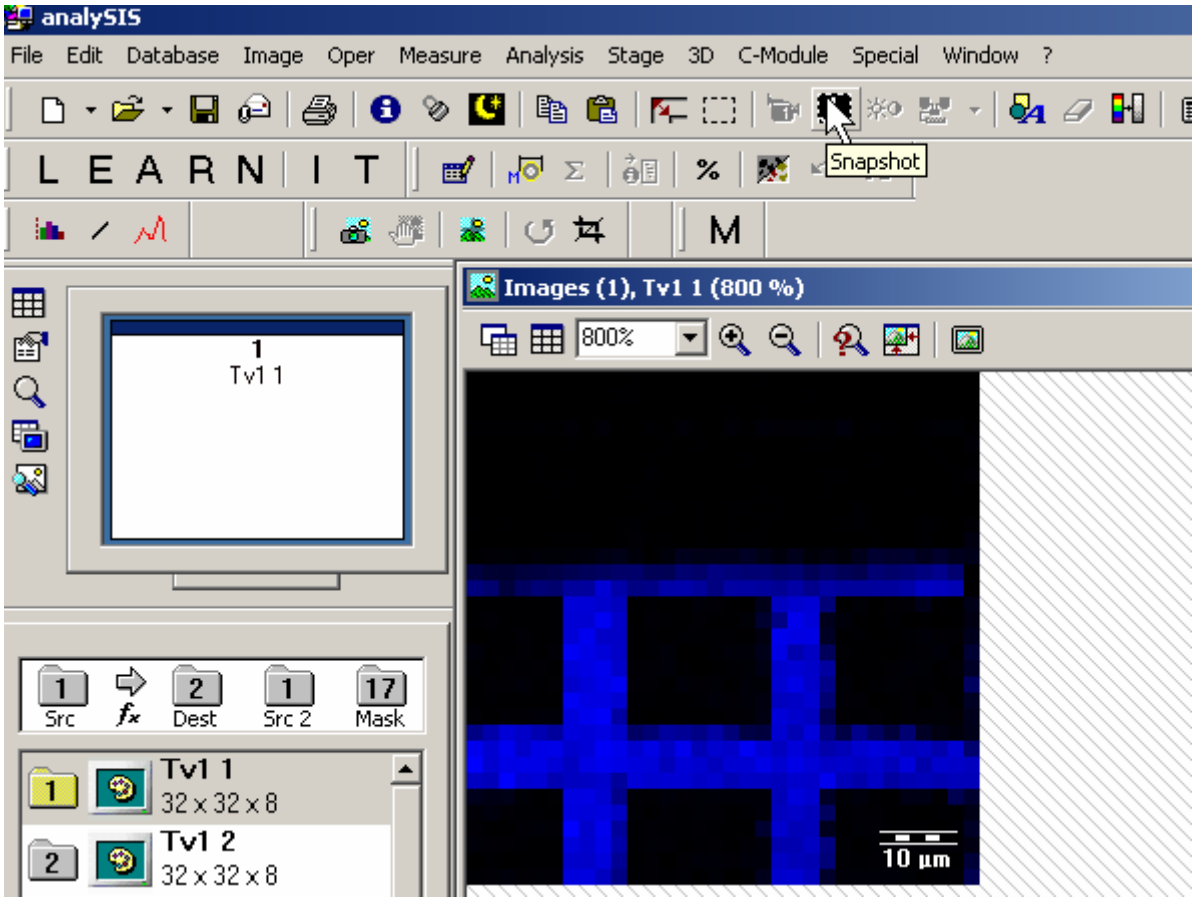
27. Finally, to determine each cell's size, (width and height), divide the total mosaic resolution by the number of cell rows. Here, 512 divided by 16 is equal to 32. Enter this number or use the up/down scroll buttons in the Image size section to set the cell pixel Width and Height. Only a certain number of fixed widths and heights are available: 16,32,48,64,80 and so on up to 4096.

28. Lastly, set your Pixel time. In this example 10 ms was chosen.



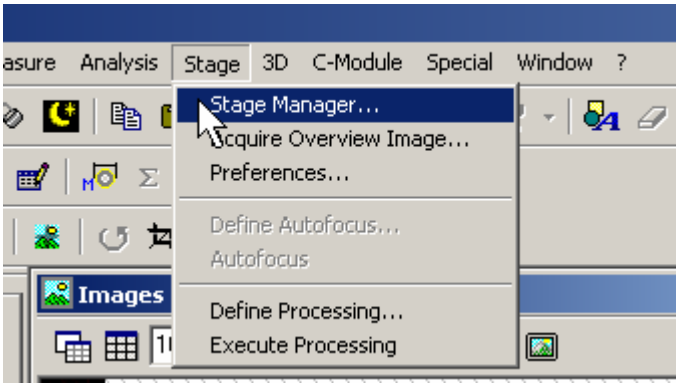
29. Click the OK button to complete this setup procedure.

30. Acquire a single scan x-ray map by clicking the Snapshot button, verify that an x-ray map is acquired in single-scan (snapshot) mode.

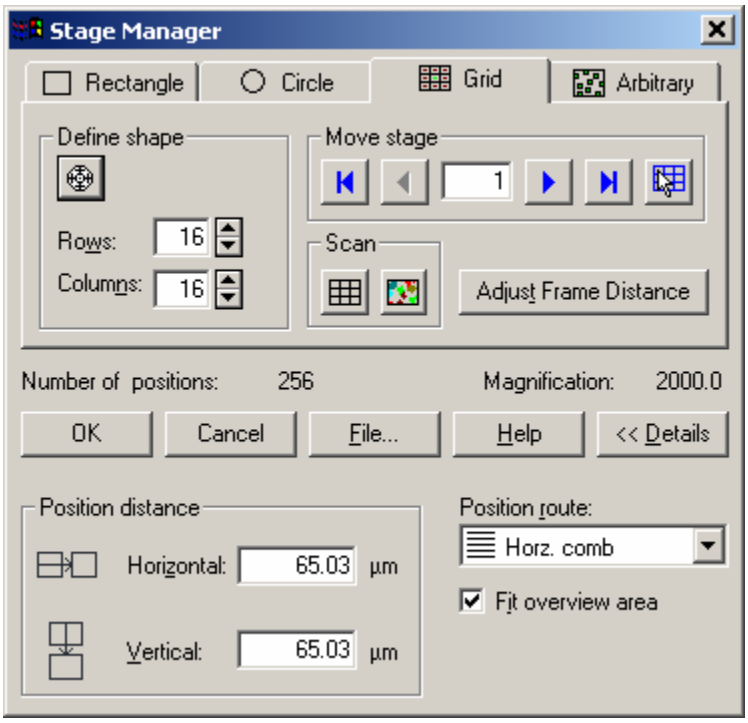


31. Next the operator will define the area to scan. In this example we will collect a 1mm x 1mm grid. Move the stage to the center point of the area of interest.

32. Open the Stage Manager by clicking the Stage menu and then Stage Manager.



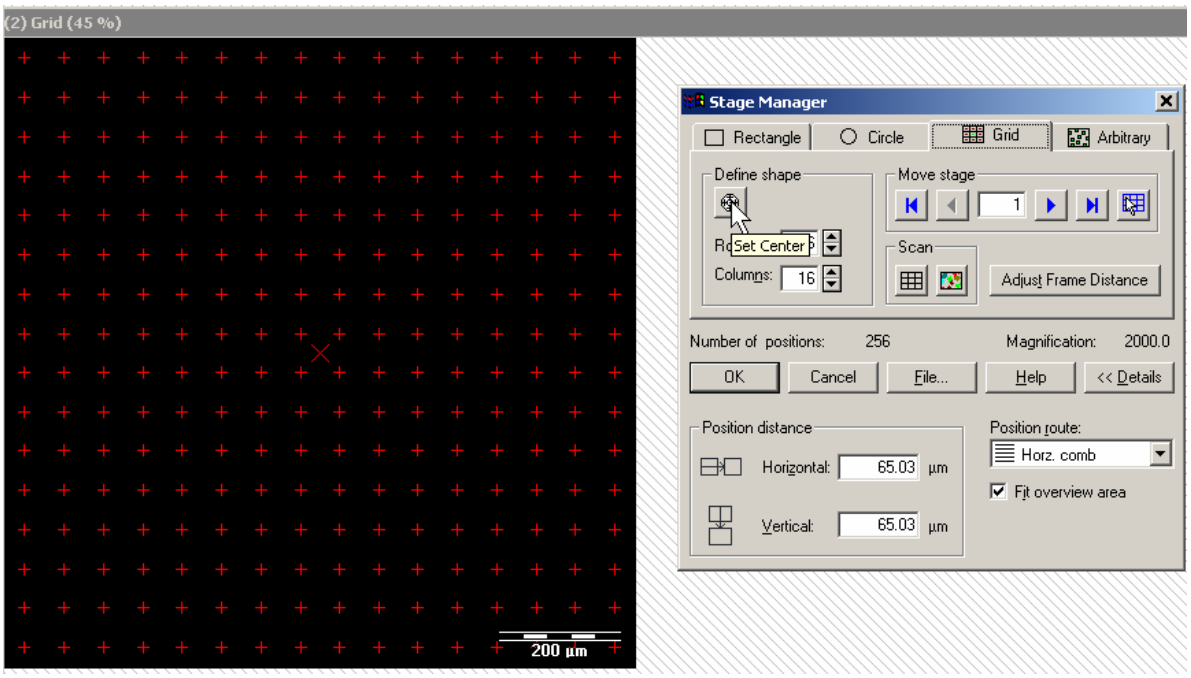
33. The Stage Manager dialog opens. Click the Grid tab and set the Rows and Columns to a value of 16.



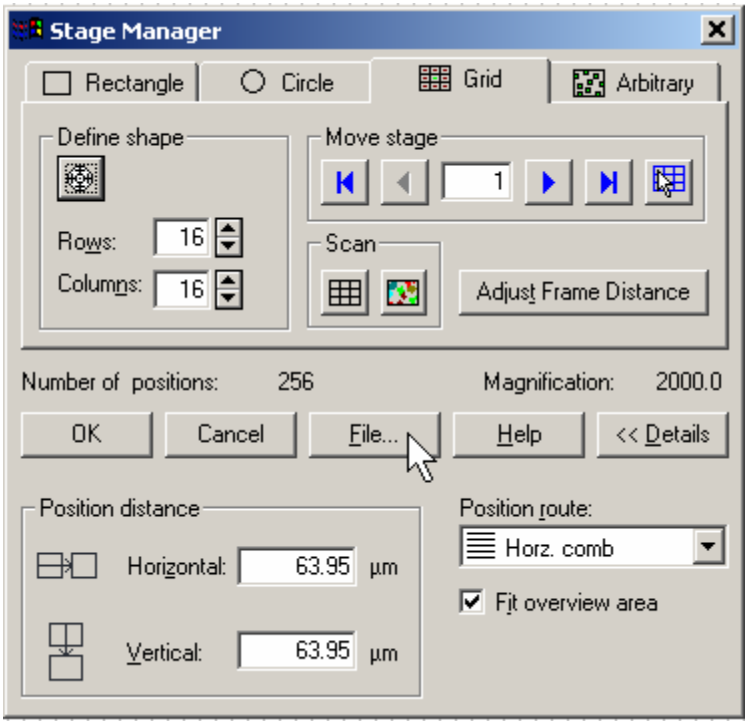
34. With the stage set in the center of the 1mm x 1mm area, click the Set Center button in the Define shape portion of the window.

35. Special Note:

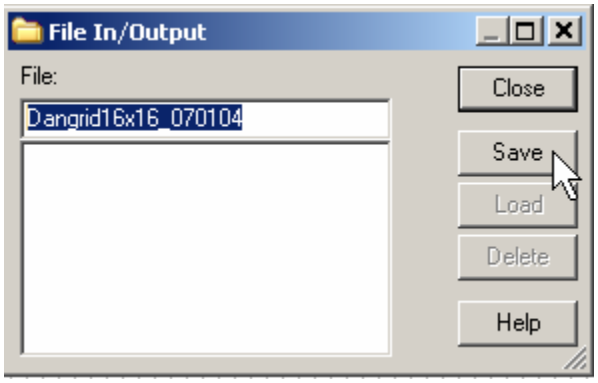
- **A. Also, click the ADJUST FRAME DISTANCE button. This forces the beam raster to beam the same size as the stage cell.**
- **B. If the cells do not align properly, this can mean that you have to use the Scan Rotation feature within the microscope to ensure that the X-Raster is perfectly parallel to the X-Stage movement. On the JEOL 7000 at JEOL-USA, a scan rotation setting of –5 degrees (via PCSEM) was used to align X-Raster to X-Stage. This number will not be the same on every instrument, but you will have to experiment with different scan rotation settings until the beam and stage are perfectly aligned.**
- **C. Choose Horizontal Comb in the Position Route window to minimize stage backlash.**



36. After setting the center point of the grid for the mosaic, the operator may store the coordinates for later use. To save these coordinates, click the File button.

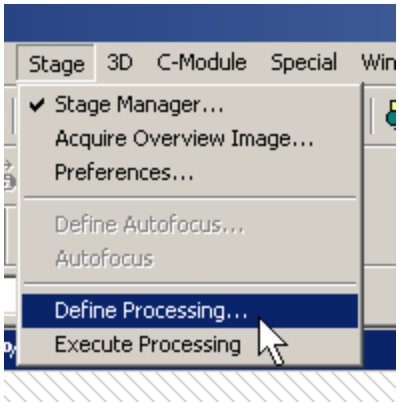


37. This opens the File In/Output window. Type in a name for the file, it will have a STB extension. The newly created file is located in the Stage subdirectory of analySIS.

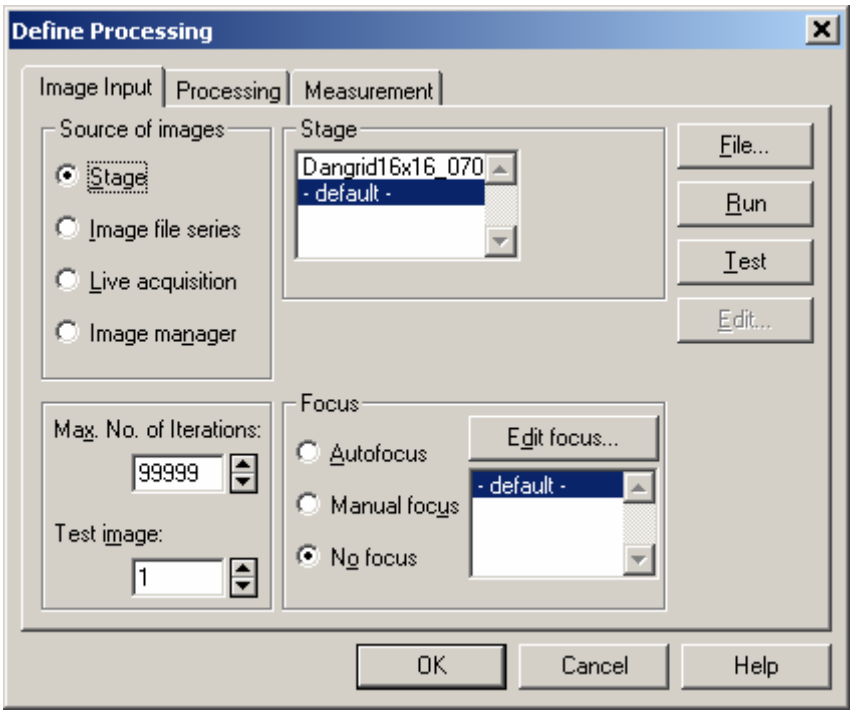


38. Click the Save button to complete the task. Then click the OK button of the Stage Manager window.

39. Click the Stage menu and Define Processing… item.

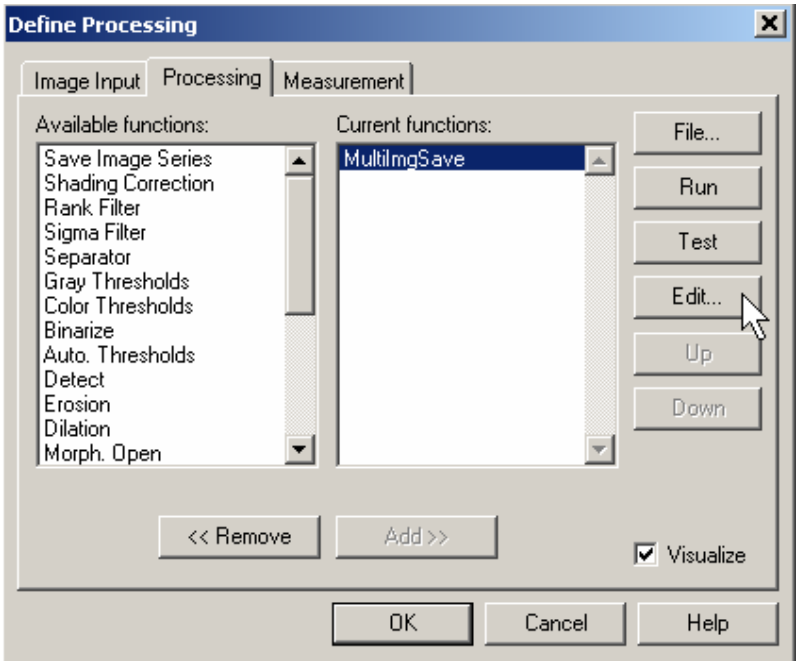


40. Opening the Define Processing window. Click the Image Input tab if it is not up.

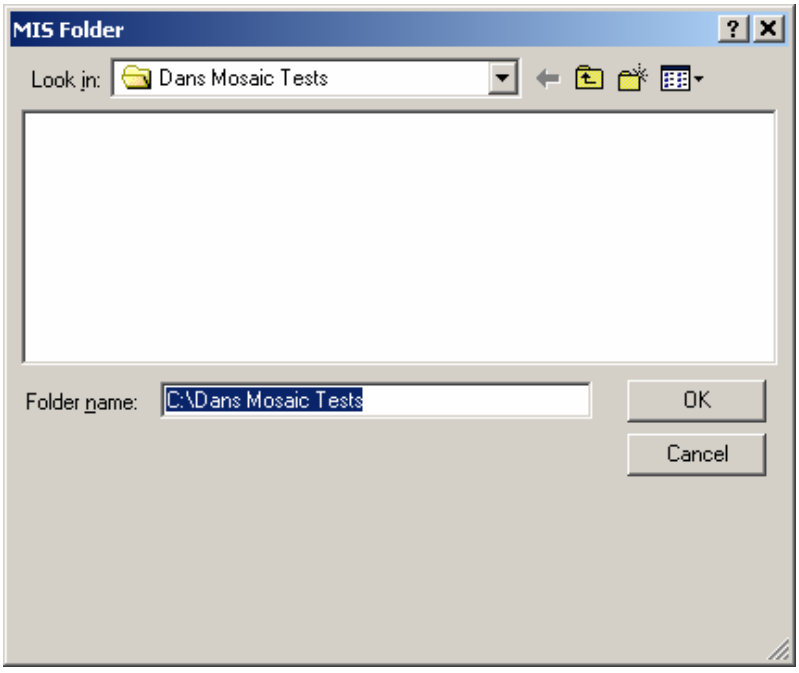


41. Highlight the Stage coordinate file to be used.

42. Select the Processing tab in the Define Processing window.

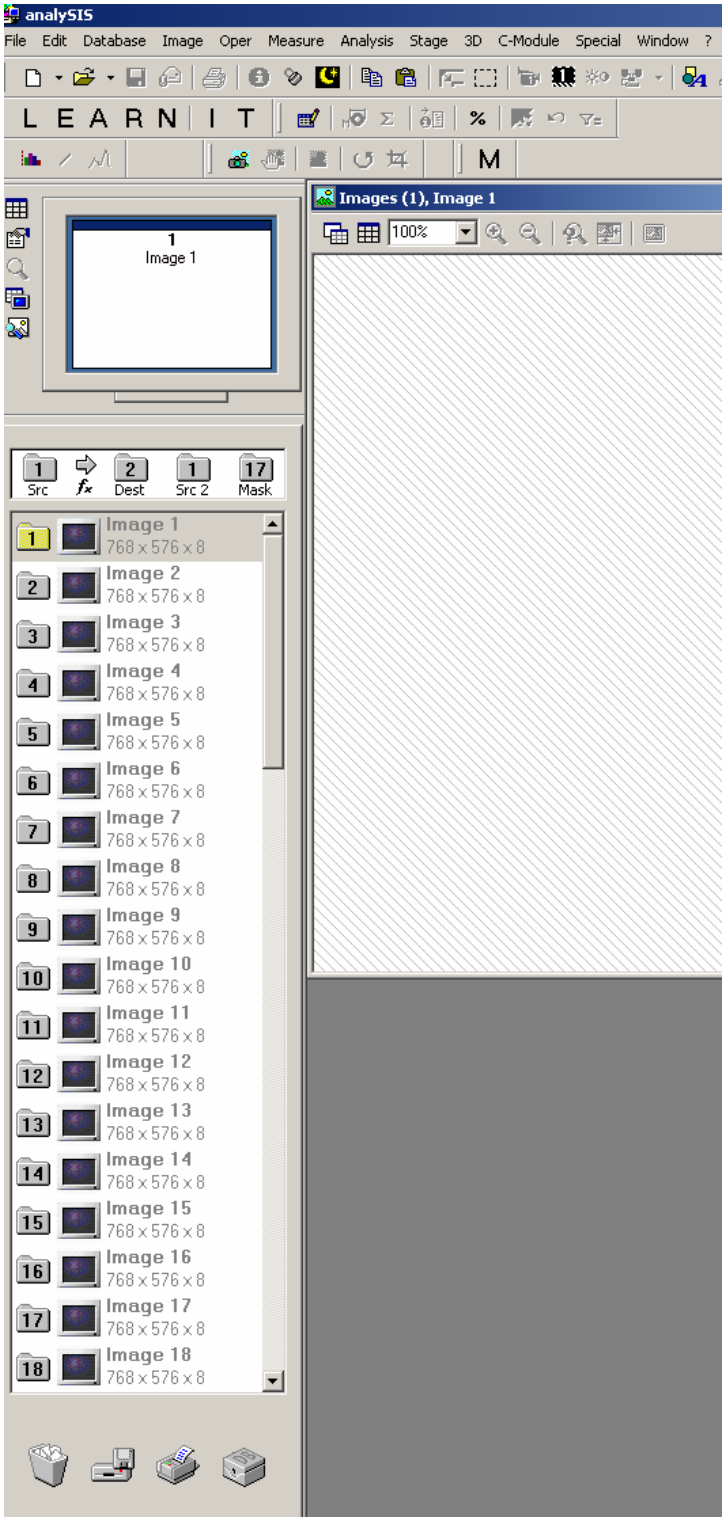


43. The MultiImgSave function should appear under current functions list. Click the MultiImgSave function and then click the Edit… button. This opens the MIS Folder dialog. Here the destination folder for your images is created or selected.

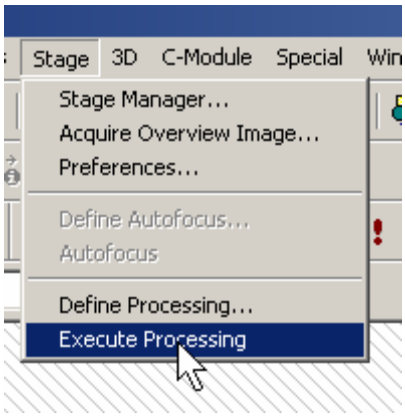


44. Click the OK button, returning to the Define Processing window. Click it's OK button.

45. In the example about to be collected a grid of 16 x 16 cells or 256 total will be collected. It is possible to start the cell numbering at 1 in order to keep track of the acquisition progress. Before starting the acquisition, click and drag any images located in the image manager to the trashcan below. Then highlight the first image buffer.

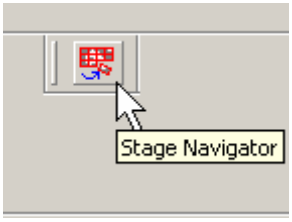


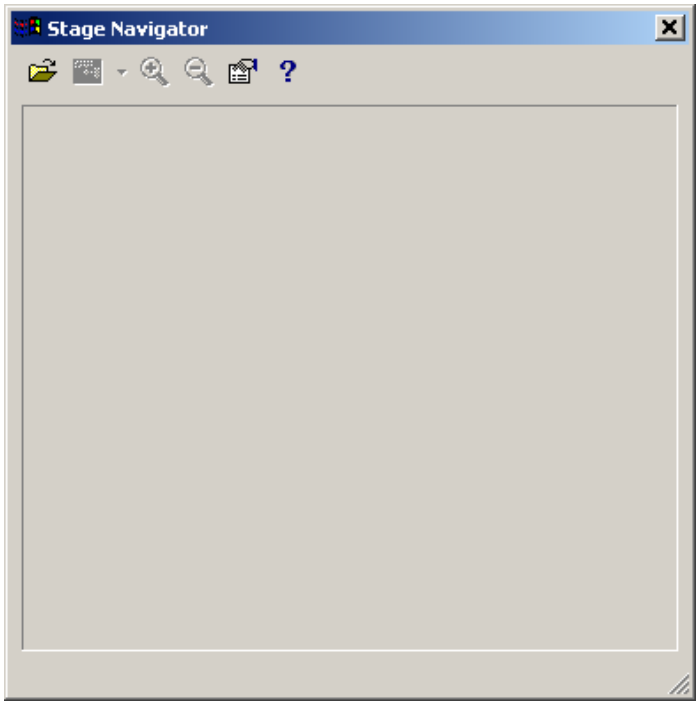
46. Click the Stage menu and then select the Execute Processing… item to start the mosaic acquisition sequence.



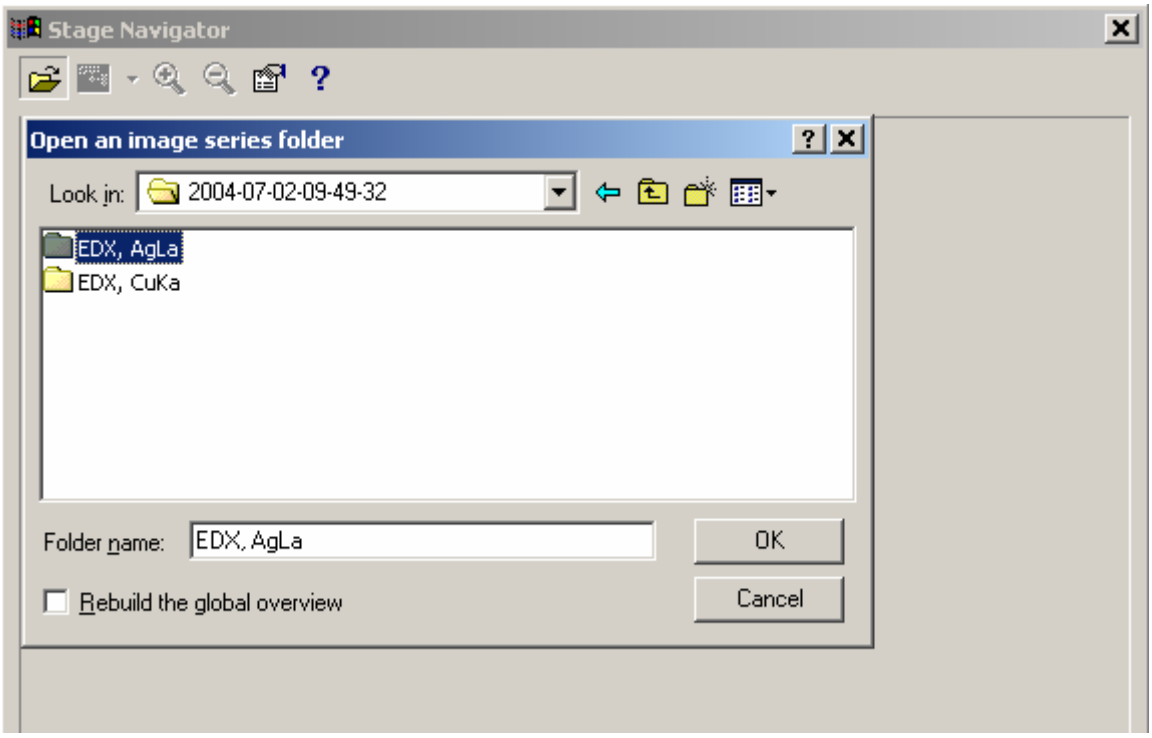
47. All of the x-ray images will be collected as defined above and stored in.

48. Use the Stage Navigator to piece the entire mosaic image together. Open the Stage Navigator by clicking its icon.

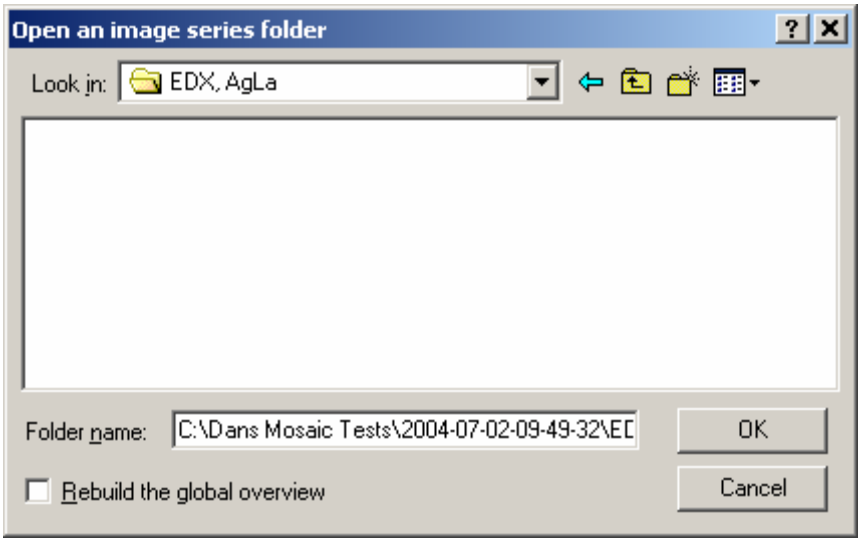




49. Click the Open Folder icon and find the location of the current sample. Highlight the X-ray element of interest.

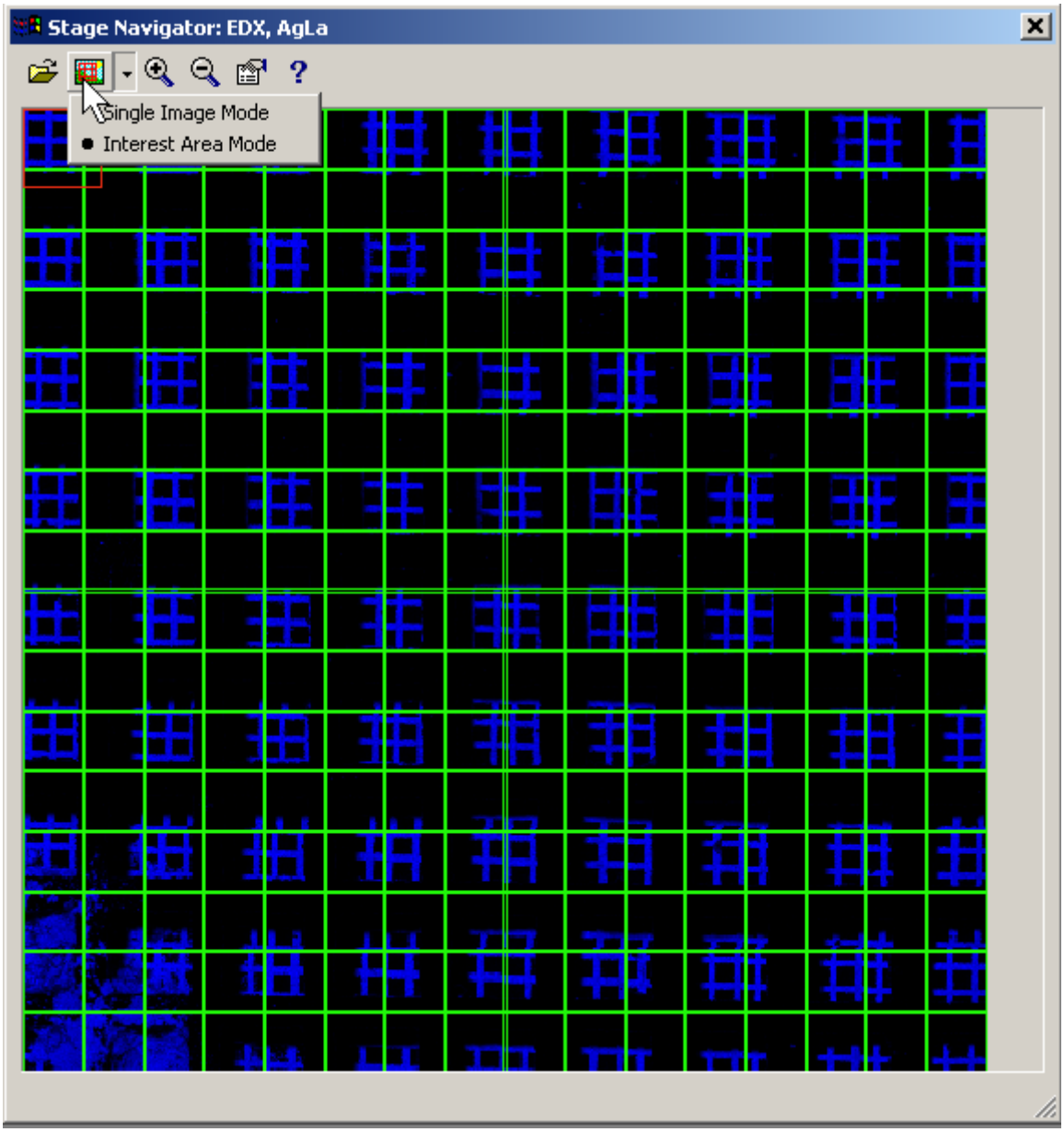


50. Each folder under the main storage directory is coded by date and time of acquisition. Double click on the EDX, AgLa folder.



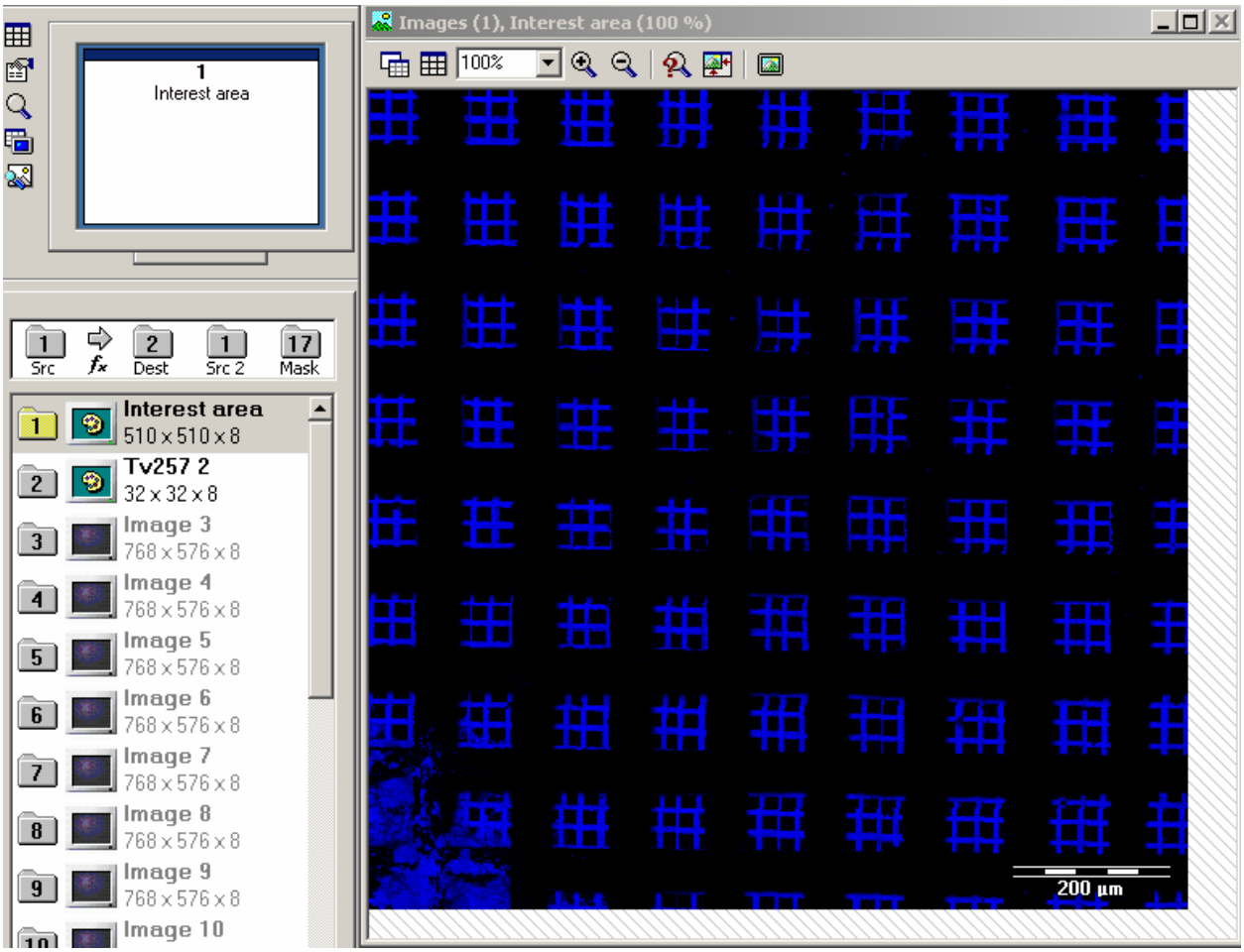
51. Click the OK button, initializing the loading of all 256 cells for AgLa into the Stage Navigator.

52. Next, from the Image Mode icon, select the Interest Area Mode menu item. This highlights a colored single frame box (red) that may be dragged across all of the AgLa cells to group them into one image.



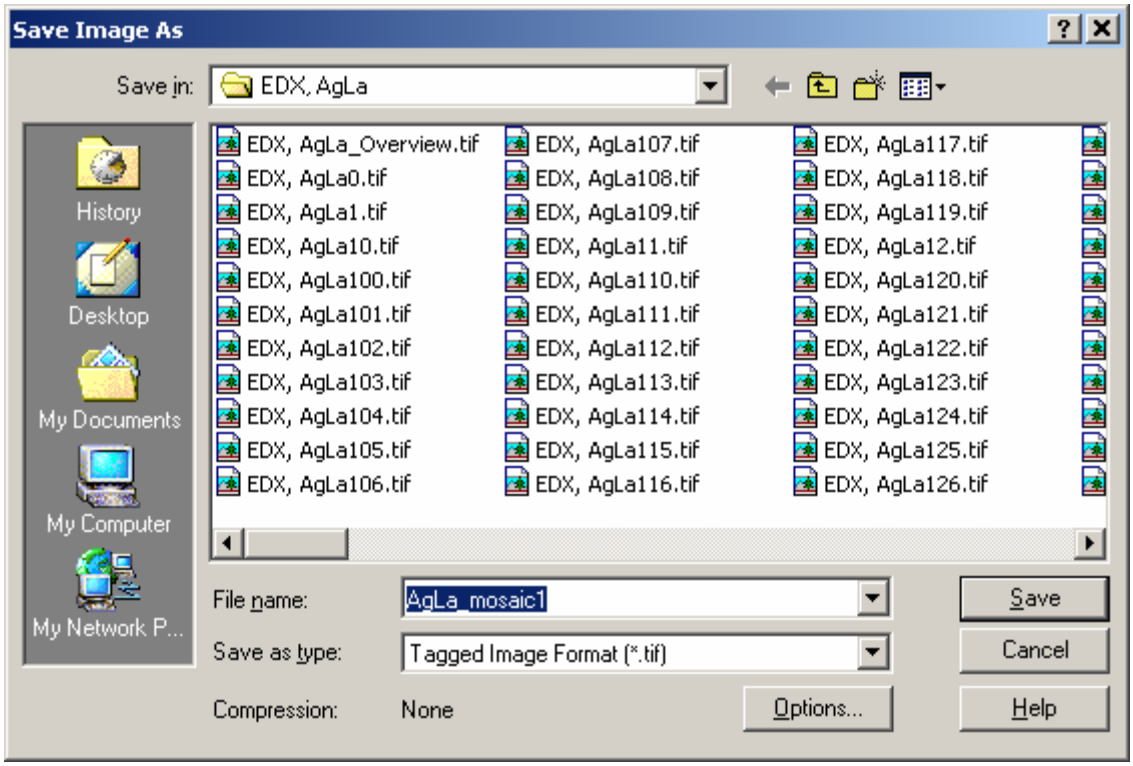
53. Drag this box to the lower right hand corner and release mouse, creating a new image called Interest area in the Image Manager.

54. The Image Manager and combined image are shown below. Note it is 510 x 510 x 8bits in size.



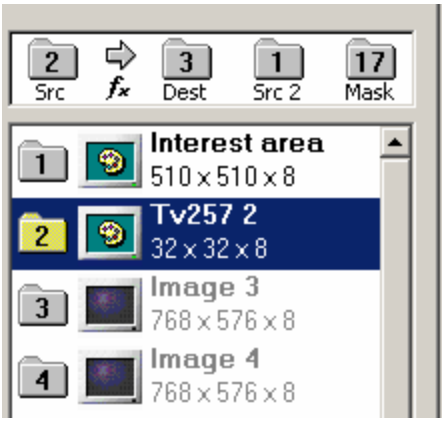
55. Highlight this image and go to the File and Save As menu to store this mosaic. All of the individual cells are stored in this directory as well.

56. Edit the Save Image As window as appropriate.



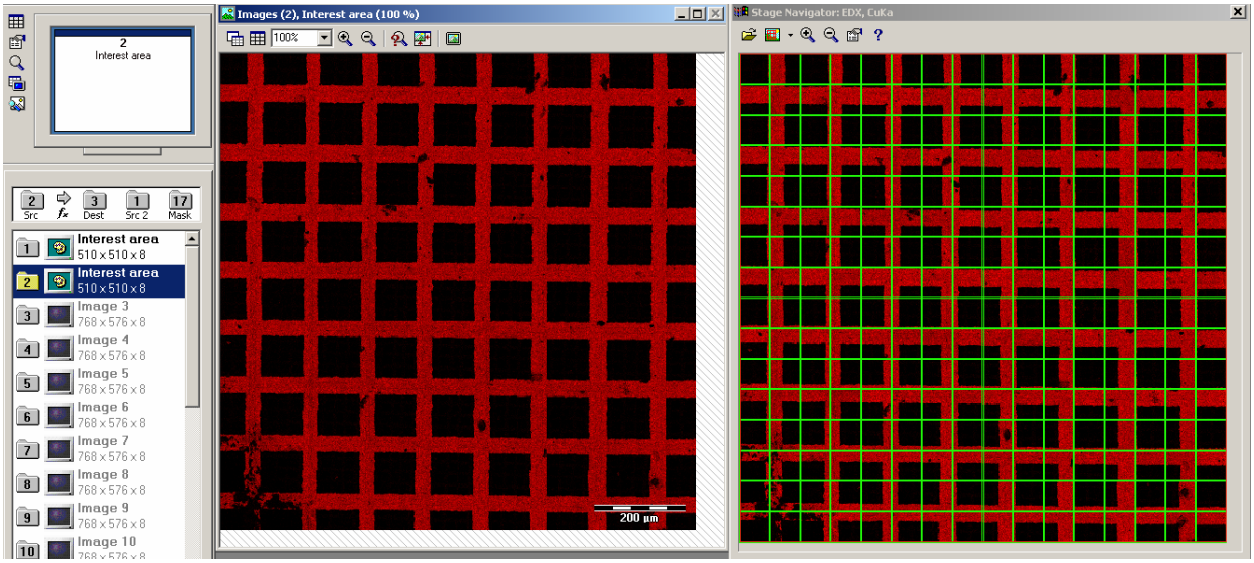
57. Click the Save button.

58. **Return to the Image Manager and click on the second buffer (CuKa).**

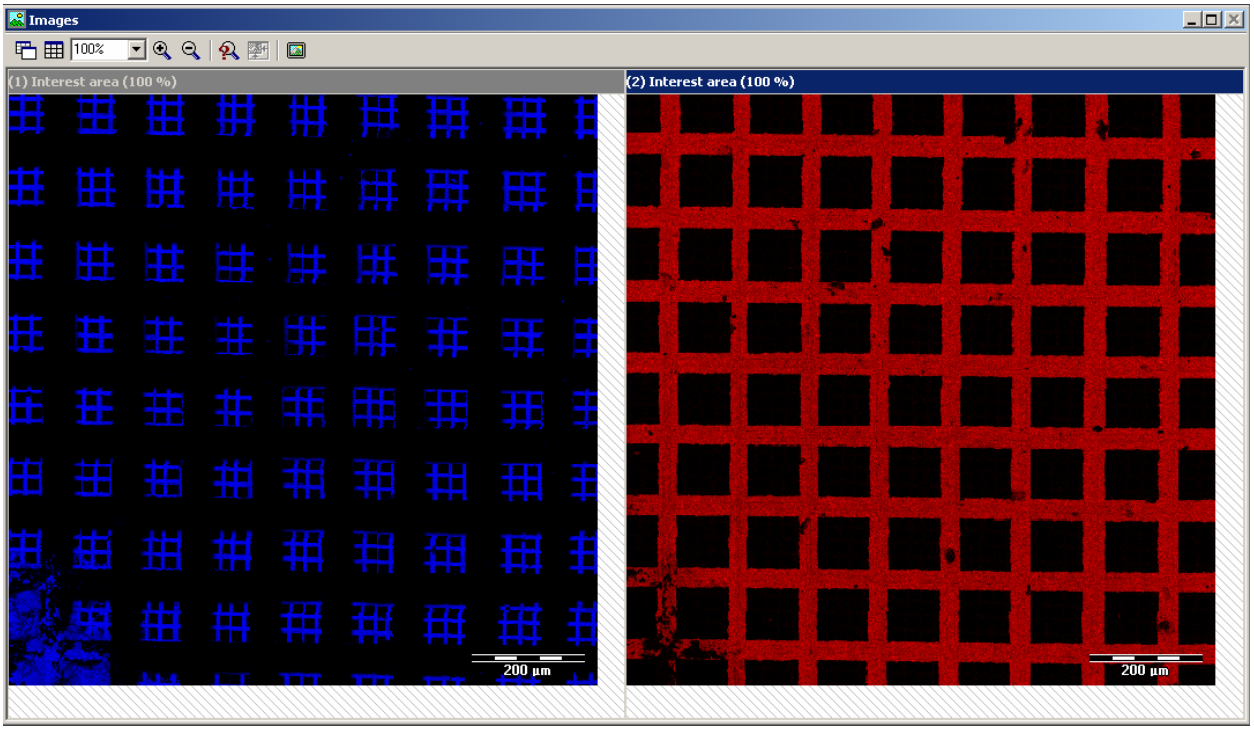


59. **Go to the Stage Navigator, find the corresponding image storage location and open the image**.

60. Drag the Interest Area box to cover the entire mosaic and then save the grouped mosaic as described above.



61. **Both collected mosaics are displayed below**.



(End of Chapter 9)

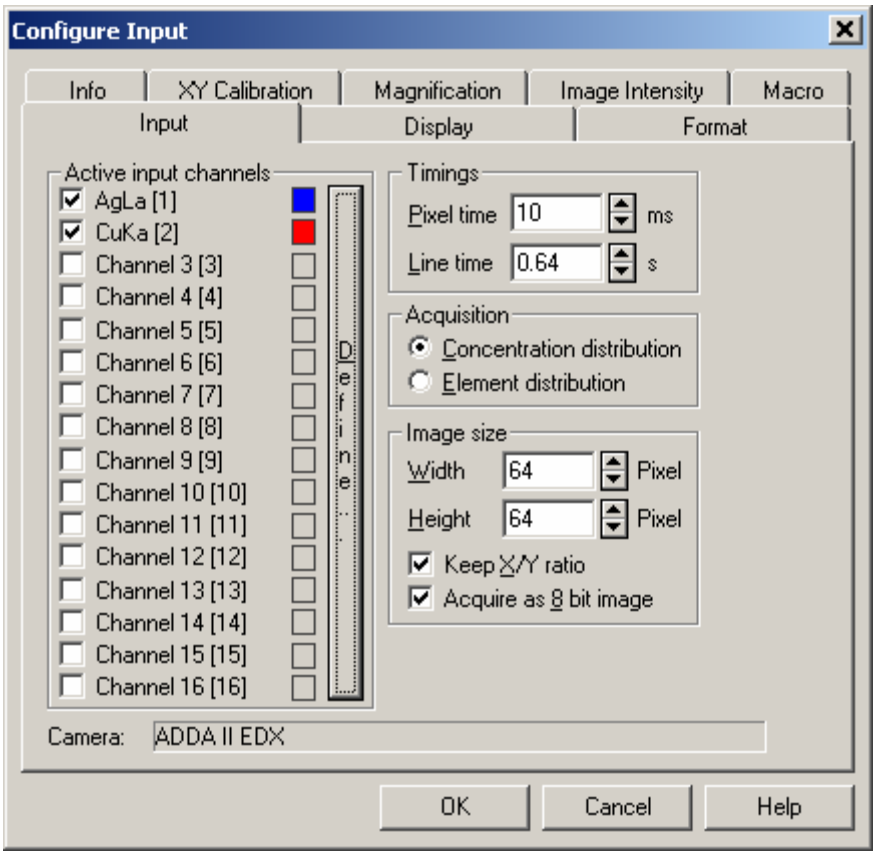
Chapter 10

How to Acquire Mosaic X-Ray Maps at Multiple Stage Locations

This example will illustrate the procedure to set up two different stage locations on a mount, at which x-ray mosaics will then be acquired.

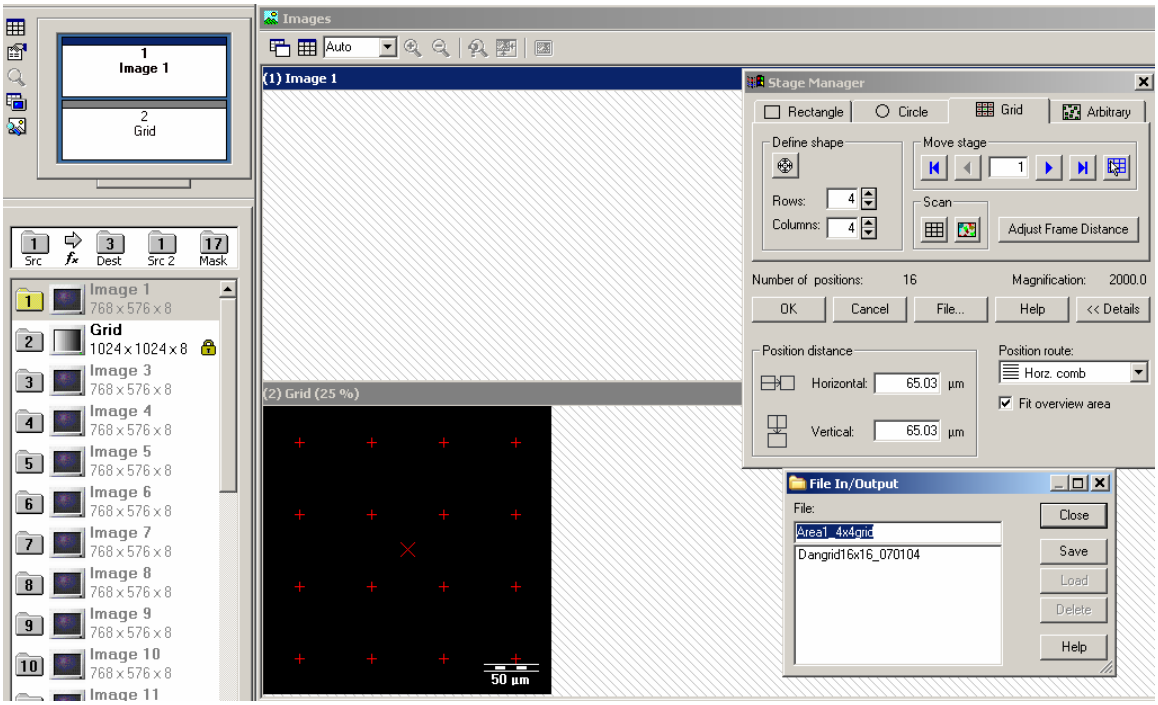
The initial set up follows closely the Mosaic Mapping-Single Spectrometer Pass document. Check that the Stage Driver is initialized. Configure the mapping inputs for the elements of interest, in this example Cu and Ag. Check the magnification settings.

The two areas will cover a 500micron x 500micron square area, stepping and collecting every 2microns. The overall resolution will be 256 x 256 and we will collect 16 cells in a 4 x 4 pattern, with each cell having 64-pixel width and height. The pixel time will be set at 10ms.



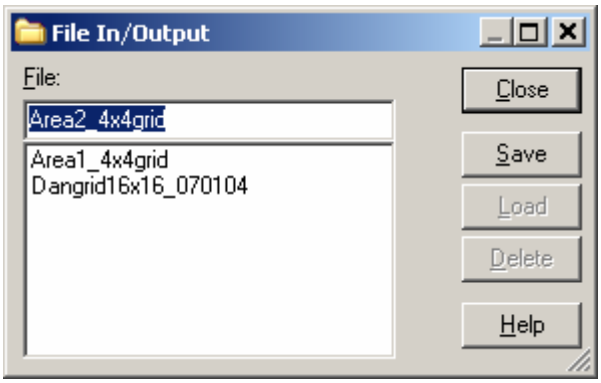
Next, the operator will establish the areas for each mosaic. Move to the first area.

Open the Stage Manager dialog. Select the Rows and Columns, Define the center of the mosaic. Store the coordinate locations, click the File button.



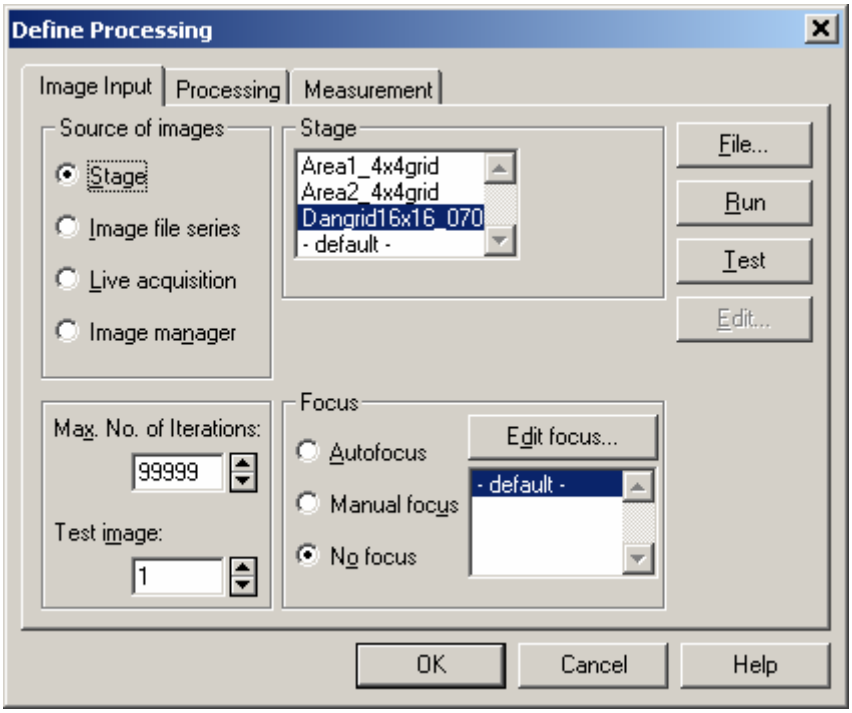
Enter the name of the first area in the File In/Output dialog. Click Save button.

Move to the second area to collect, find it's center, then click the Set center button under Define shape. Store the second set of coordinates, under the File button. Save Area 2 coordinates.

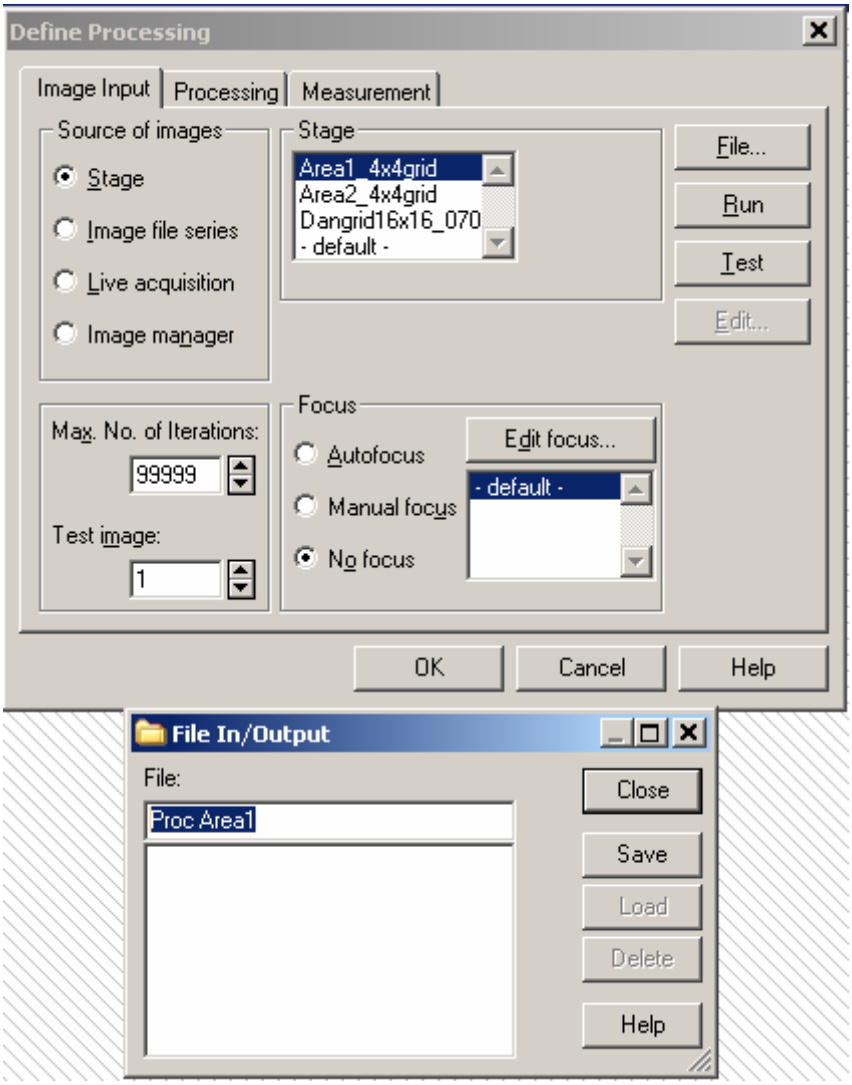


Click the OK button to close the Stage Manager.

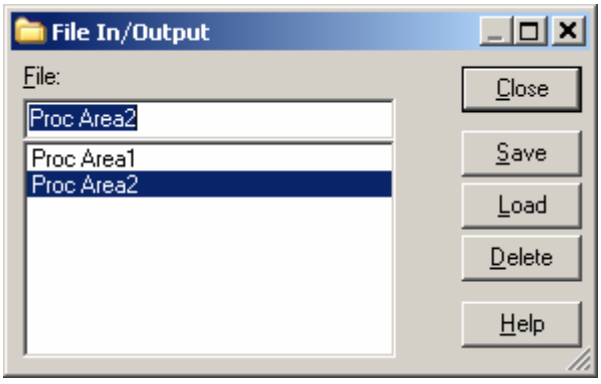
Next, open the Define Processing window and select the Image Input tab.



Highlight the first area to run and click the File button.

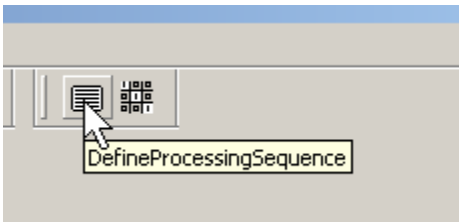


Type in a label, here, Proc Area1 and click the Save button. Repeat for Area 2.

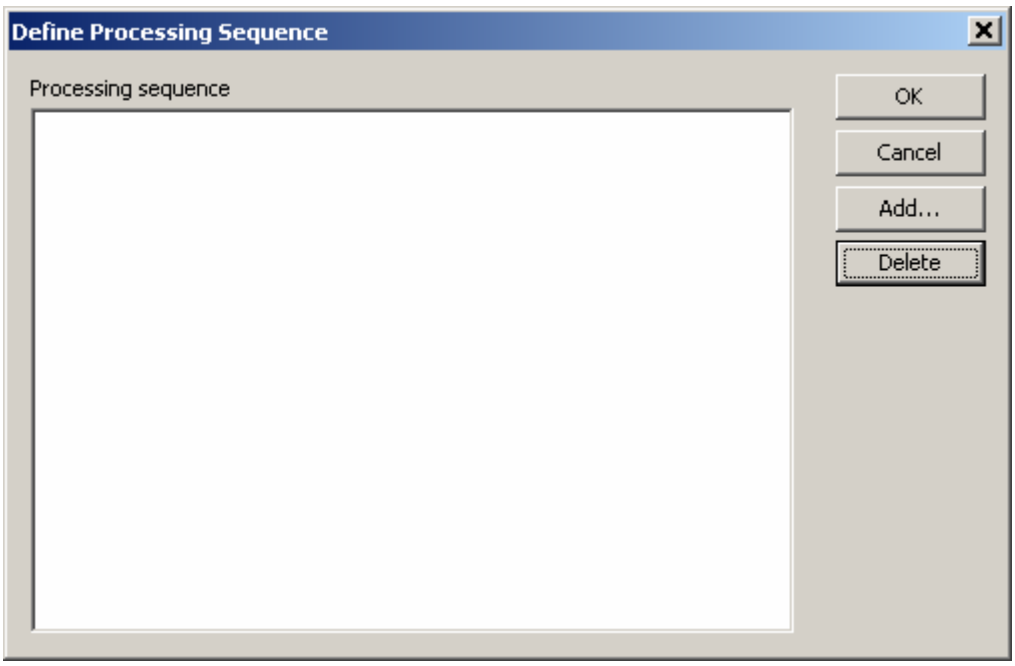


The location for storage of all cells and mosaic information is set in the Processing tab of the Define Processing window. Click Edit and select the appropriate location from the MIS Folder window. The Processing Sequence name is appended to the sub-directory name (date and time indicators).

The next step is to define the processing sequence, click the Define Processing Sequence icon.

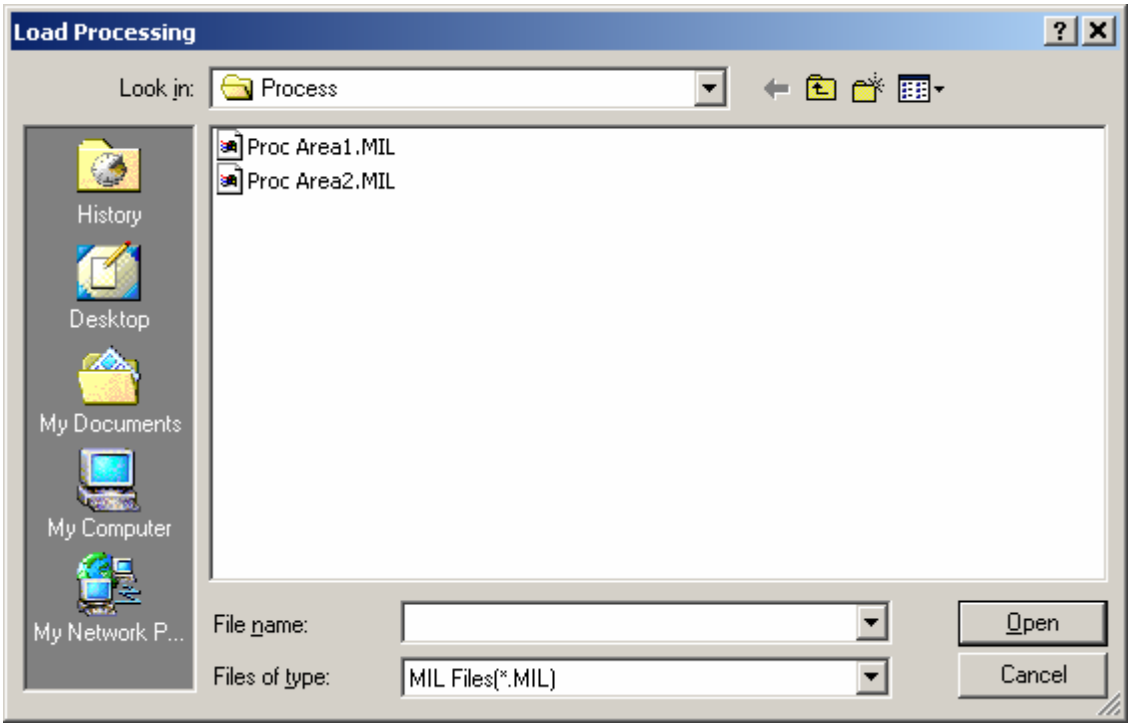


This opens the Define Processing Sequence dialog

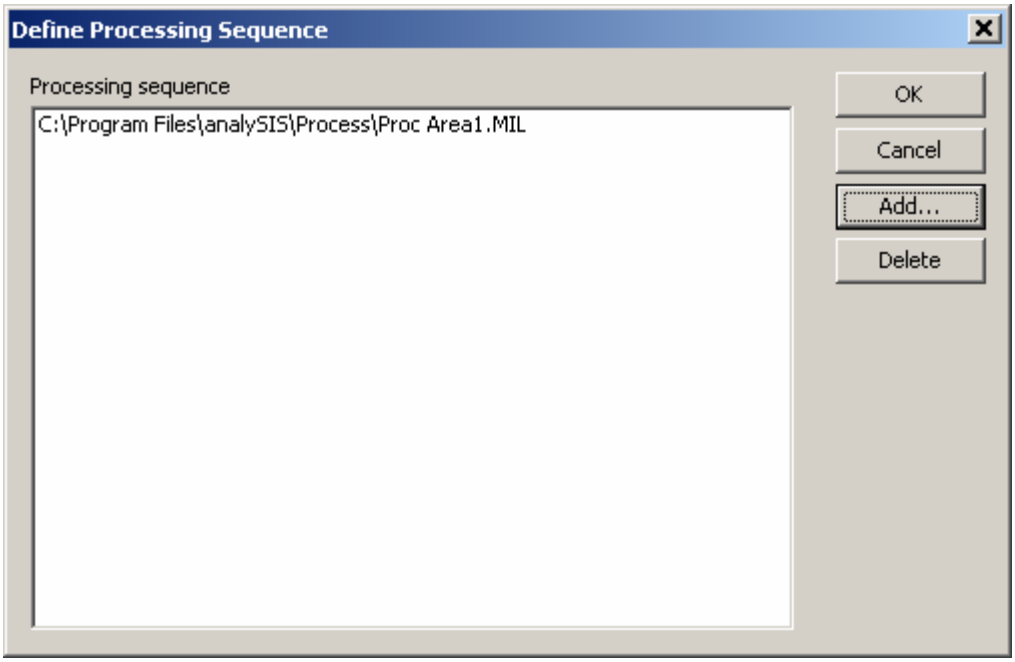


If there are any old Processing sequence listings shown, delete them now, unless you wish to rerun them. Add the relevant tasks, click the Add button. The Load Processing window appears.

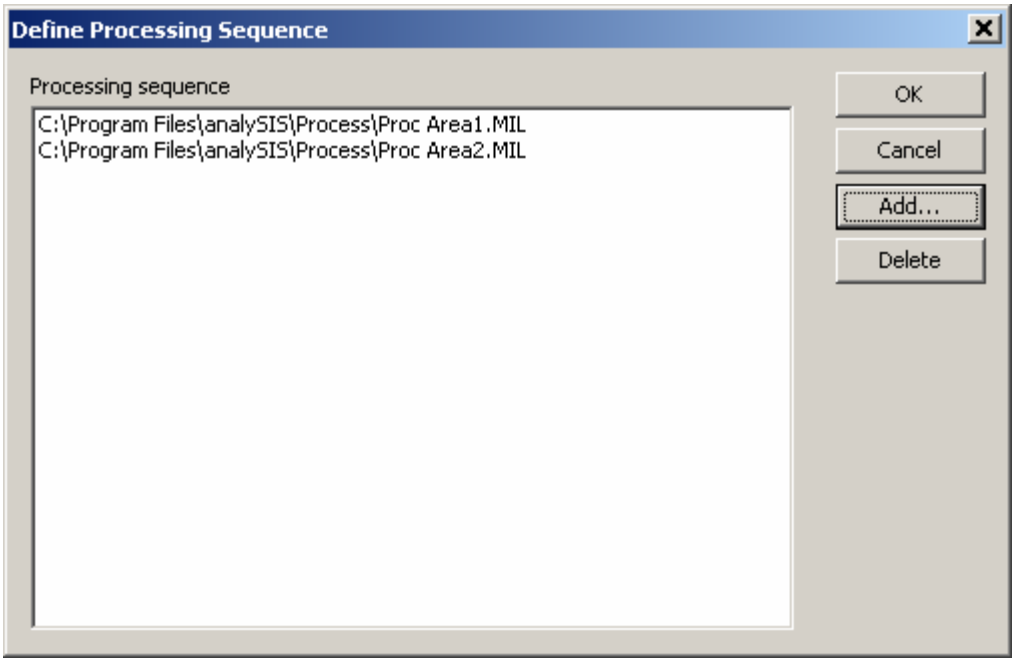
Select the first area to be run. We have designated it Area1.



Highlight Proc Area1.MIL and click Open. This loads the first Processing sequence.

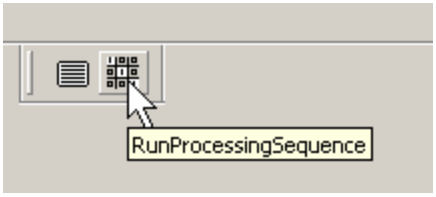


Add the next one, Area2 in this example.



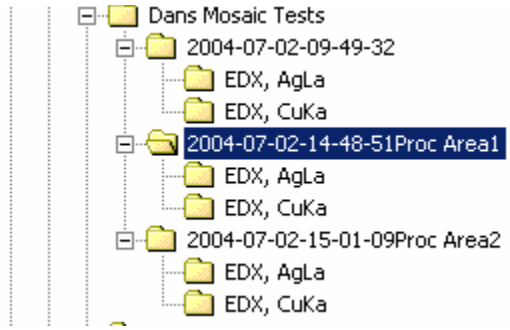
When done entering the sequences you wish to run, click the OK button.

From the main analySIS program, click the Run Processing Sequence icon.

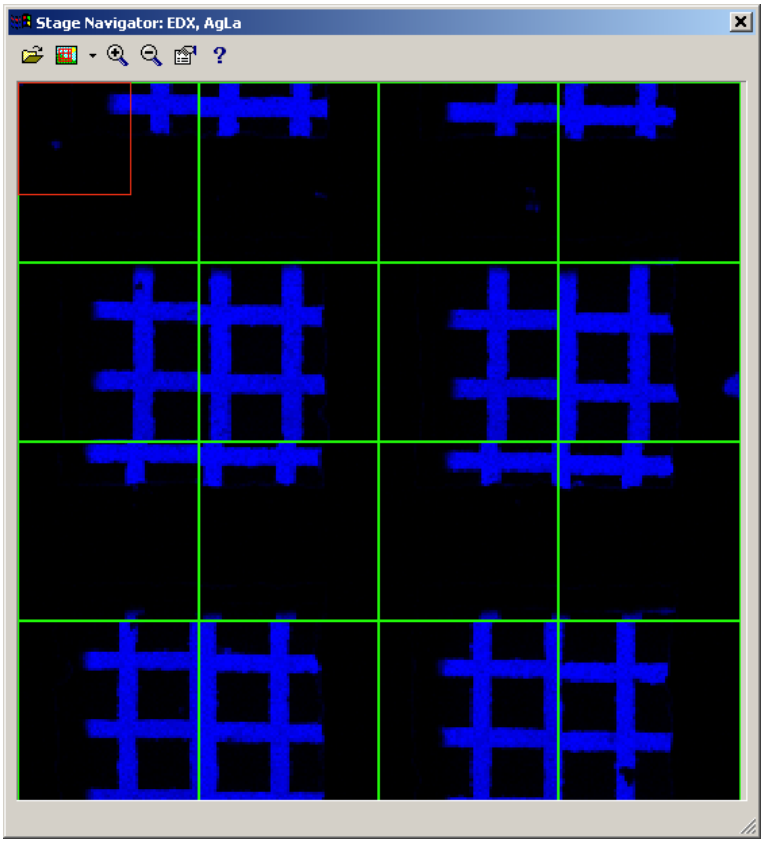


This executes the processing sequence, allowing the x-ray mosaics at various locations to be acquired.

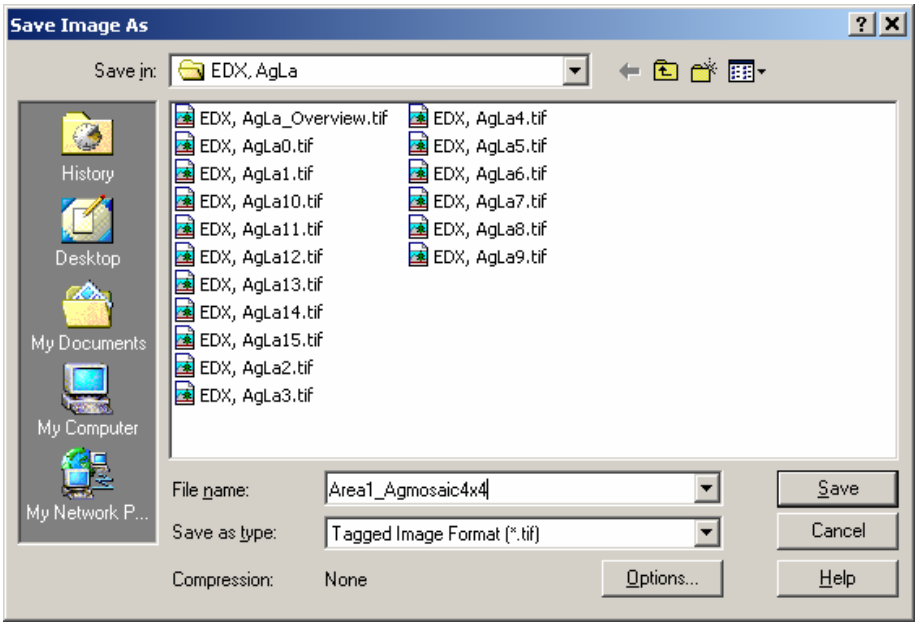
The file structure is similar to earlier described.



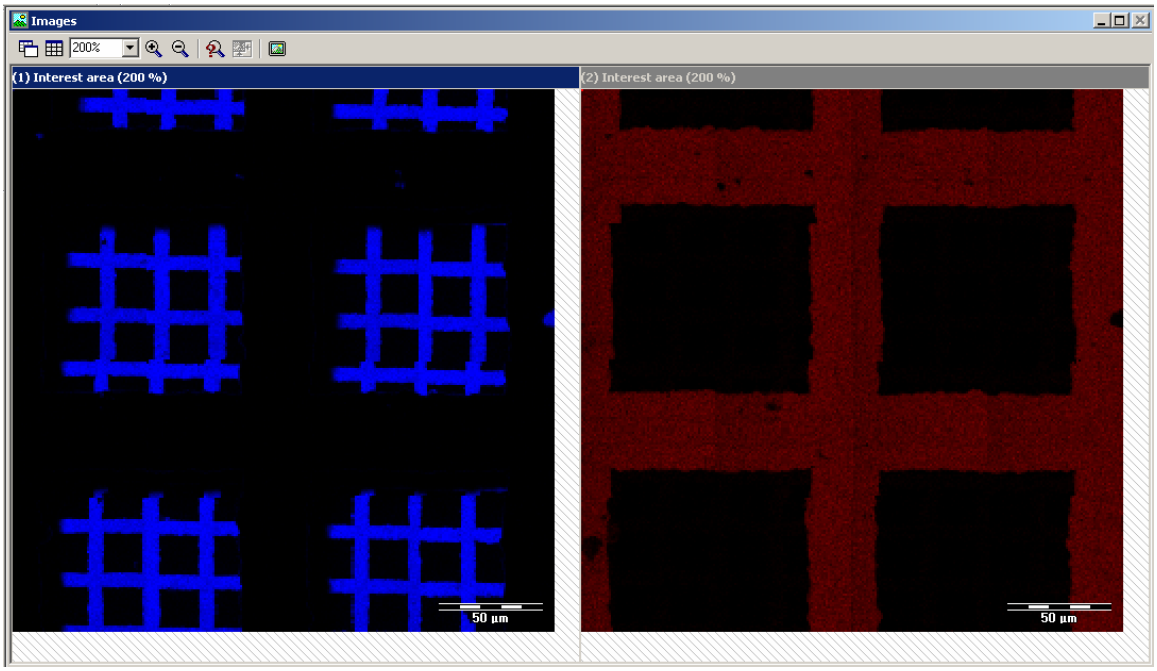
At the conclusion of the mosaic collection, the data is processed as described previously. The Stage Navigator is opened, all of the cells are loaded, and then combined into one image.



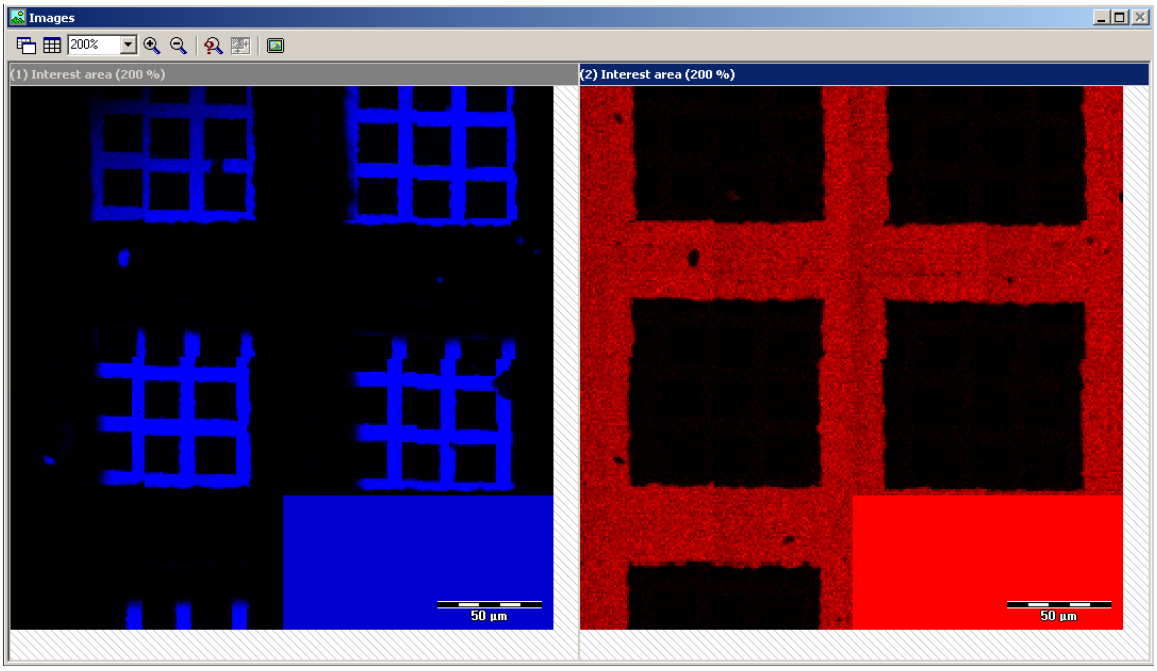
The final image is then saved.



Area1



Area2



(End of Chapter 10)

Chapter 11

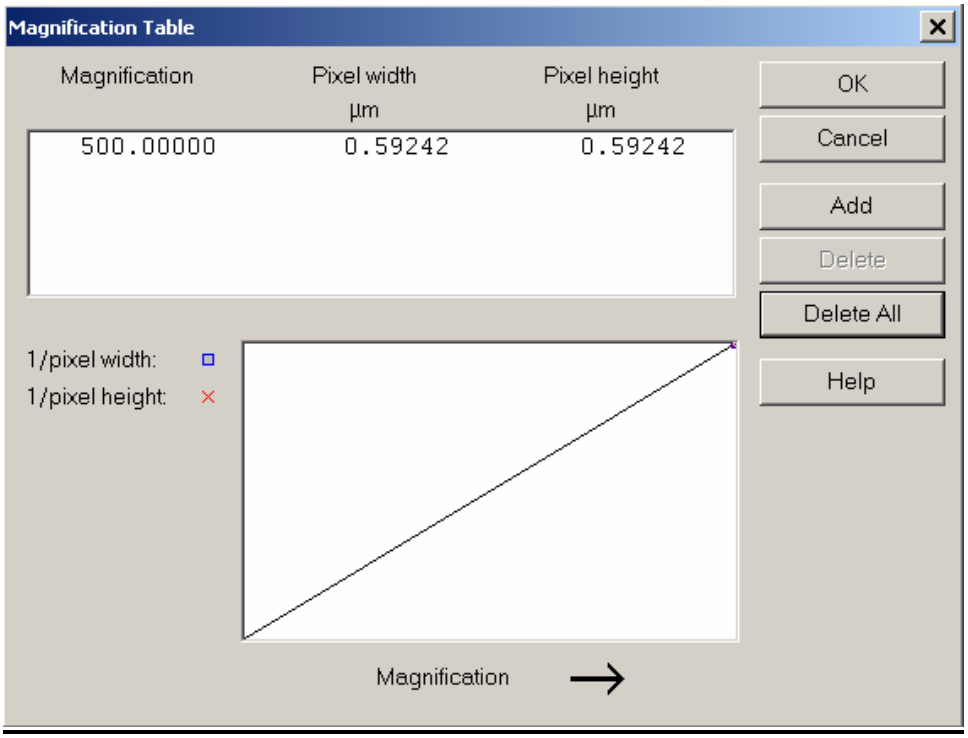
Acquiring X, Y, Rotation X-Ray Maps

To Be Continued

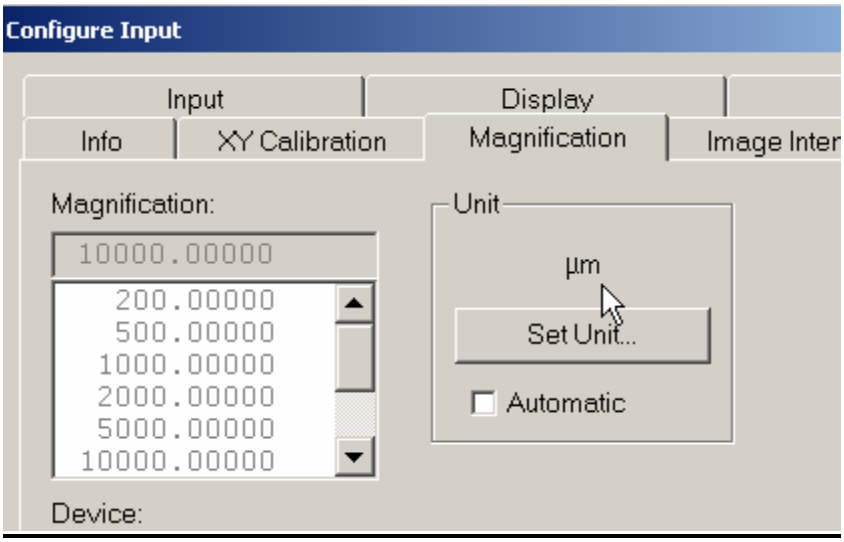
(End of Chapter 11)

Chapter 12

Magnification



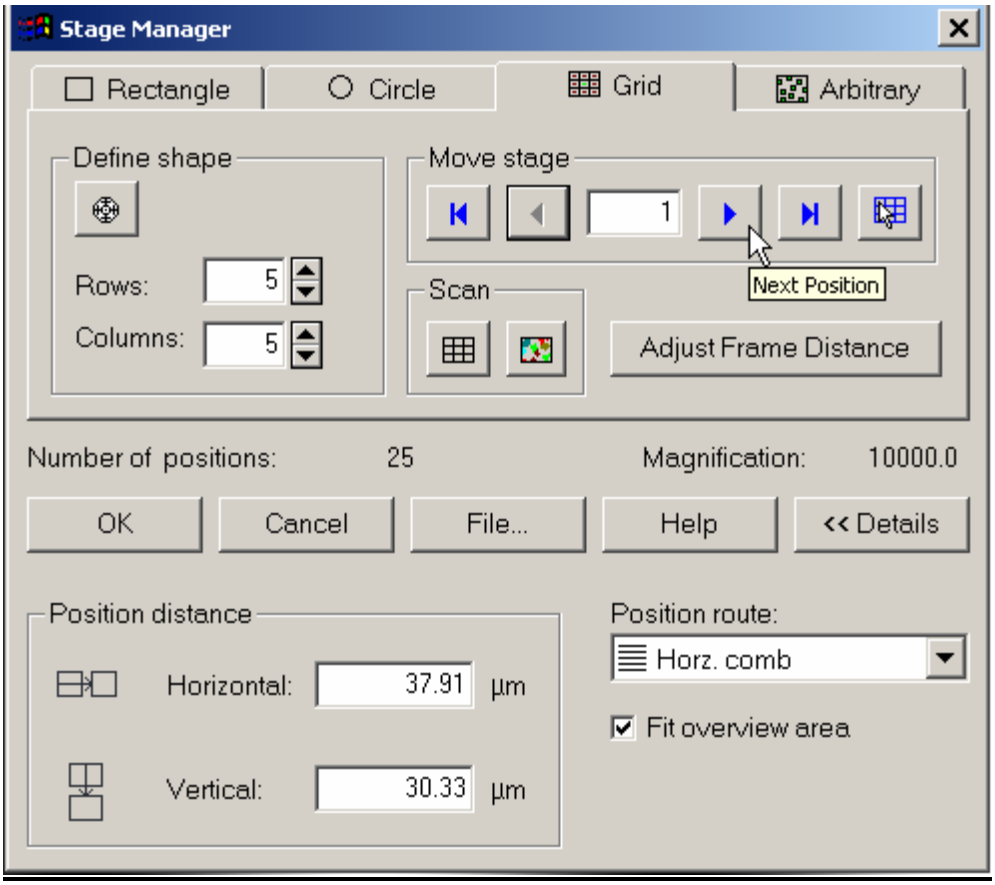
A proper Magnification calibration should create a linear graph.



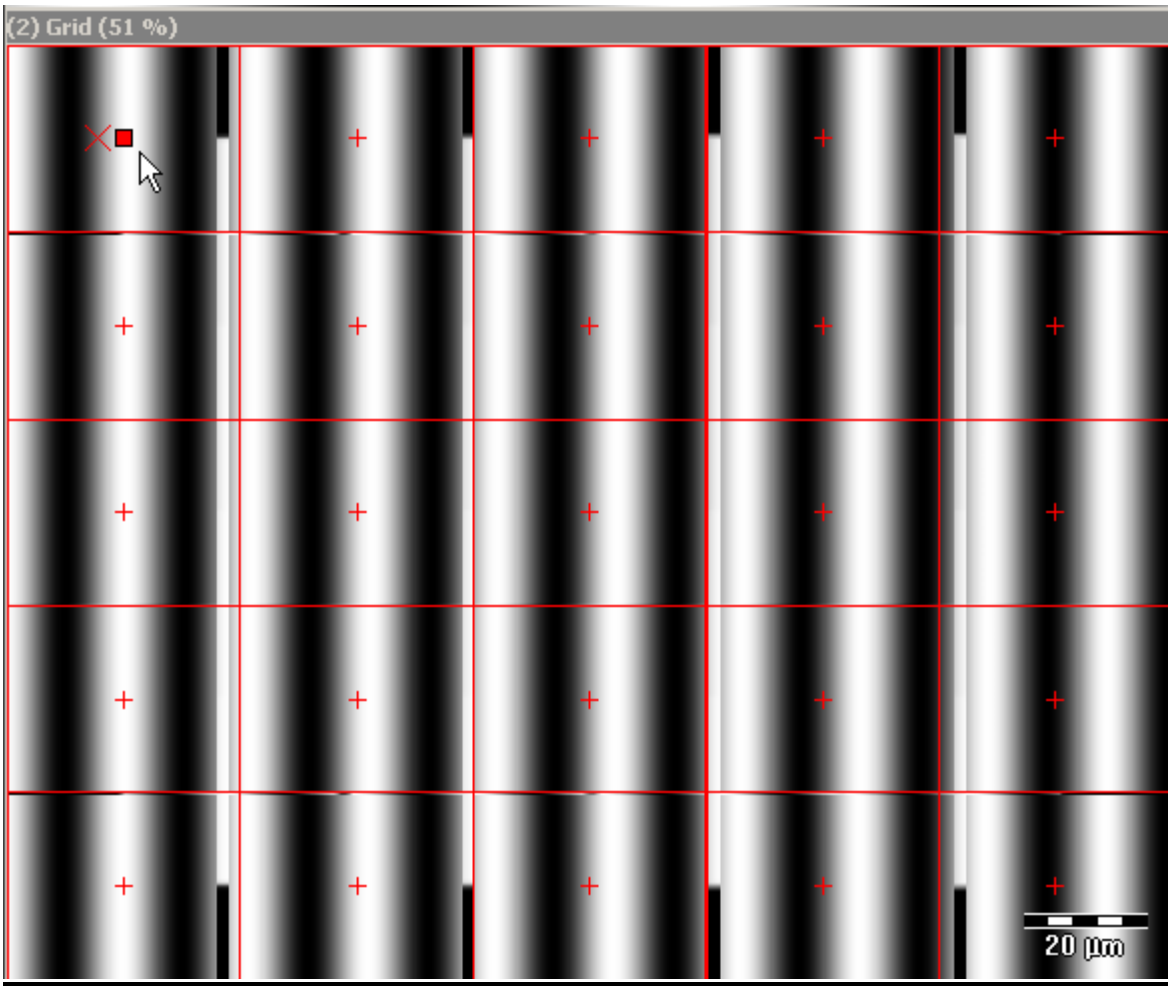
Set Units to Microns

Chapter 13

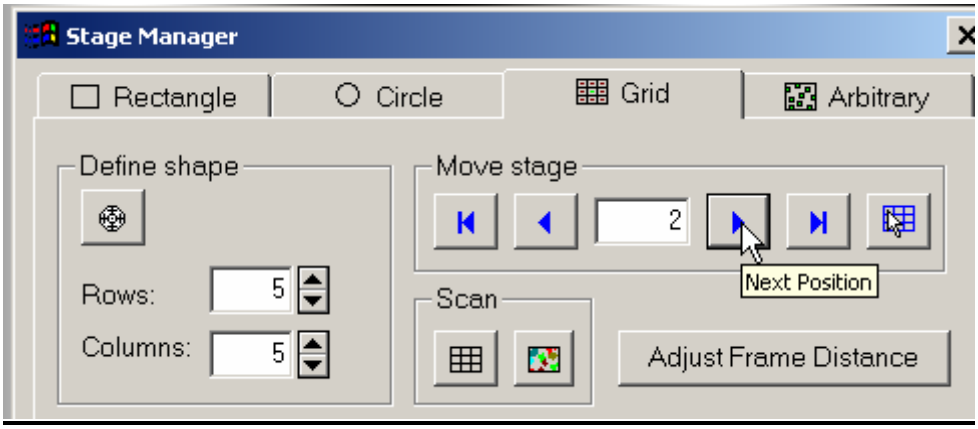
Testing Stage Movement



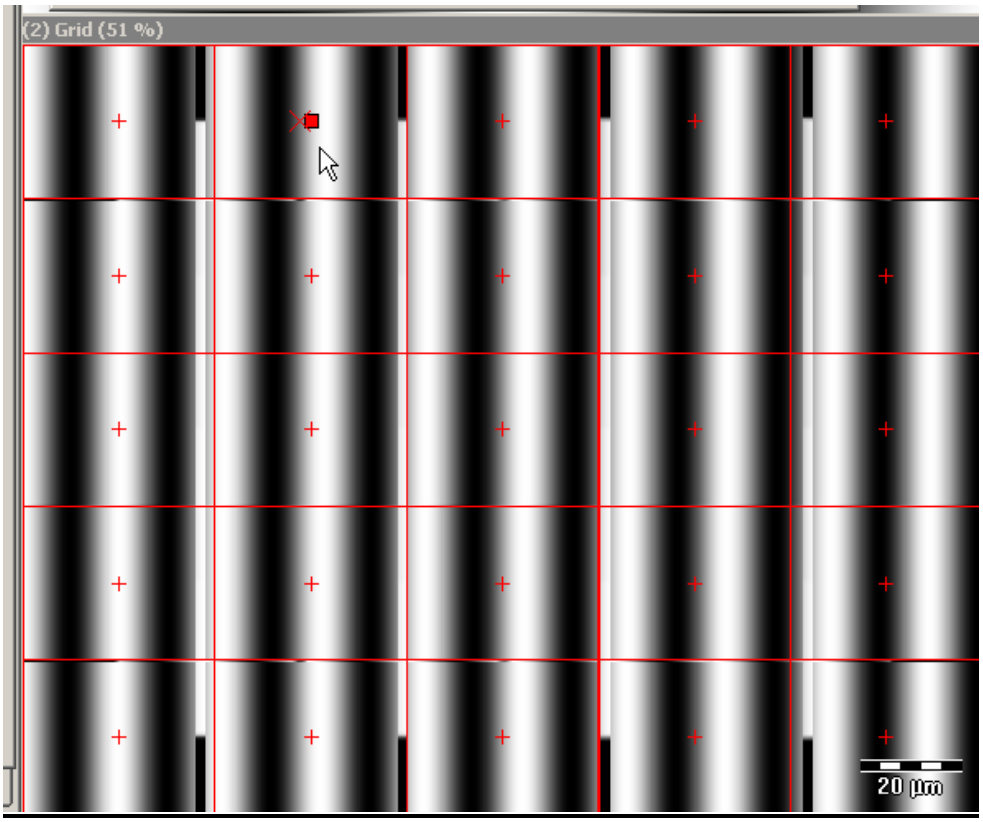
1. **Click the Next Position Button to move the beam to the center of cell 1.**



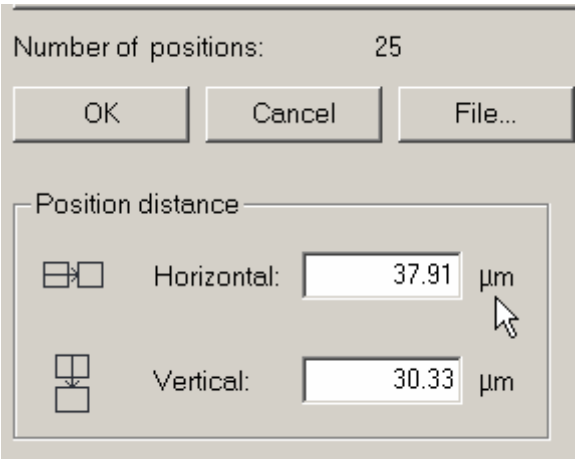
2. **The beam will move to the center of cell 1.**
3. **Record the X stage position of the JEOL 7000 using PCSEM.**



4. Click the Next Position button to move the stage to the center of cell 2.



4. **The beam should move to the center of cell 2.**
5. **Record the X stage position of the JEOL 7000 using PCSEM.**



6. **Subtract the two X positions. <u>X1 – X2 = Horizontal Position Distance.</u>**
   The sum of those two numbers should be the same as the number that appears in the horizontal Position Position Distance box above.

<u>End of Document</u>