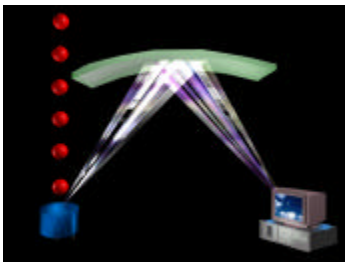
Probe for Windows 95/98/NT (32 bit) v. 4.52

User's Guide to Getting Started

By Daniel T. Kremser, Ph.D.



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Acknowledgements

The author would like to thank John Donovan, Don Lesher, and Dave Stanford for critical comments, technical assistance and their friendship over the years. Their expertise has made this manual better.

Disclaimer

Conventions Used in this Guide

The computer operating system employed here is Microsoft Windows NT (v. 4.0, service pack 4) running on a Pentium PC base. The software version of PROBE FOR WINDOWS (32 bit) is 4.52.

The following conventions are used in this document; **Menu Commands** and **Dialog Box (Windows) Names and buttons** are bold-faced whenever they occur in the text. *Dialog Box Options* are italicized and FILE NAMES are capitalized.

Several tips for saving time/steps include:

Context sensitive HELP is available in any window by pressing the F1 key.
Pressing <Enter> on the keyboard is identical to clicking the **OK** button.
Pressing the <Esc> key on the keyboard is identical to clicking the **Cancel** command.
To select a range of items in *Multi-Select* list boxes, click on the first item, move to the last and hold the <Shift> key down while clicking on the last item.
To select individual items in *Multi-Select* list boxes, hold down the <Ctrl> key down while clicking on the item.
De-select items in *Multi-Select* list boxes by holding the <Ctrl> key down and clicking the item.

Creating the Default Standard Database File

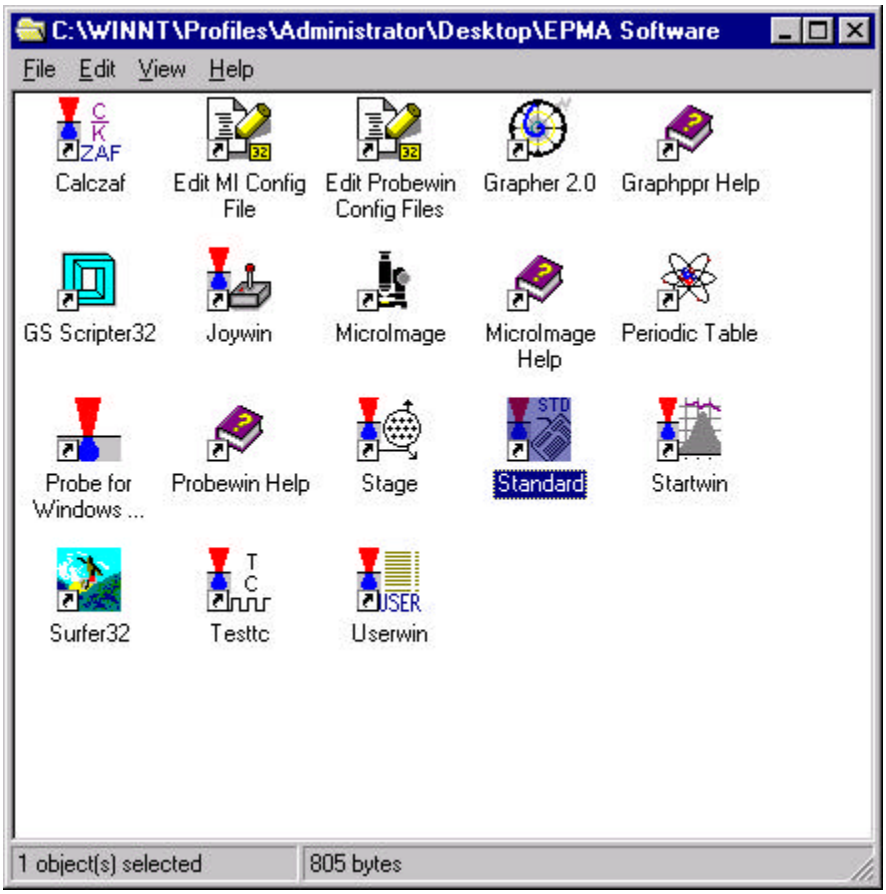
PROBE FOR WINDOWS requires a database of microprobe standards for use in quantitative analysis. This standard database can store up to 1000 standards each with up to 32 elements per standard. All standard information is stored in a file designated STANDARD.MDB. MDB is an abbreviation for Microsoft DataBase and represents a Microsoft Access v. 3.5 database file. In addition to the default standard database, three other standard databases are supplied as ASCII files. These are:

DHZ.DAT	Deer, Howie and Zussman
ORE.DAT	Dana's Mineralogy (Sulfides)
SRM.DAT	NIST standard reference alloys and glasses

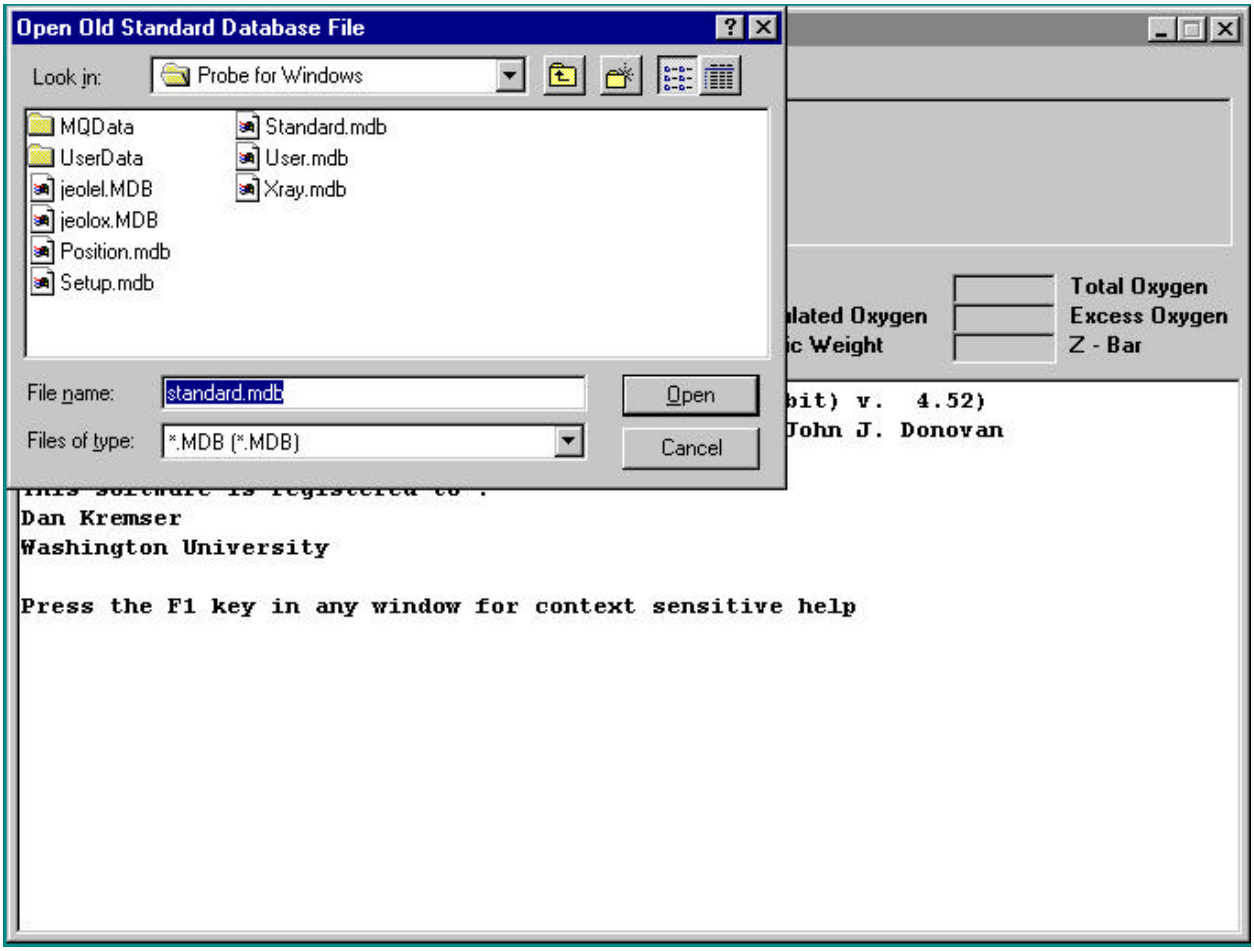
The DHZ.DAT file is a database of all of the analyses listed in the first edition of “Rock Forming Minerals” by Deer, Howie and Zussman. The ORE.DAT file is a database composed of sulfide minerals from Dana’s Mineralogy entered in ideal formulas. The SRM.DAT file is a database of SRM (Standard Reference Materials) alloys and glasses from the NIST SRM catalog. All of these database files can be used for reference and matching purposes but must first be imported into a PROBE FOR WINDOWS standard database file (see User’s Guide and Reference documentation) using the **File | Import** command.

The following procedure illustrates how to create a new default standard database and enter standard compositions into it. To import standard compositions from 16 bit PROBE FOR WINDOWS see the User's Guide and Reference documentation.

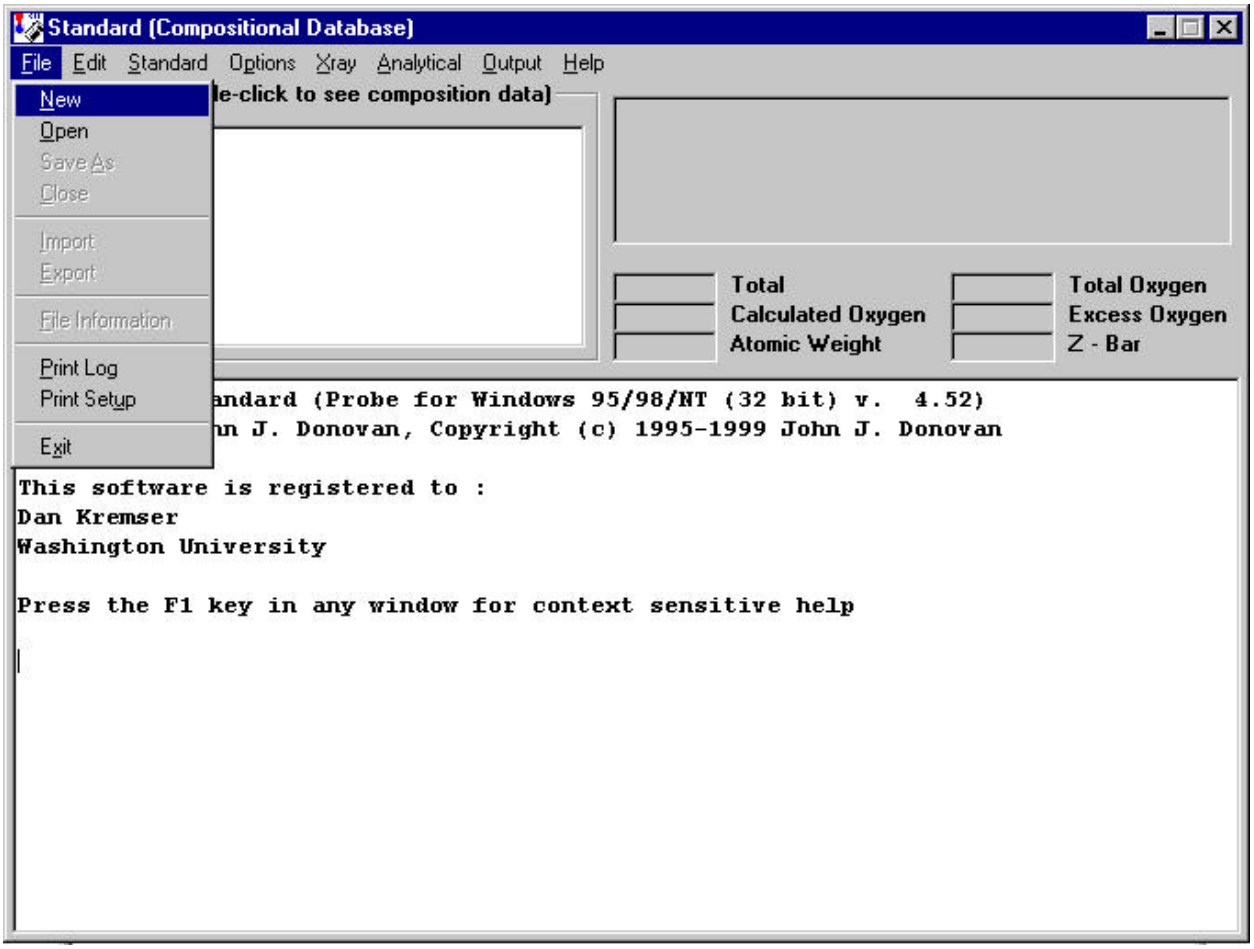
From the Desktop, double click on the yellow EPMA Software folder. Then double click on the **Standard** icon in the EPMA Software group.



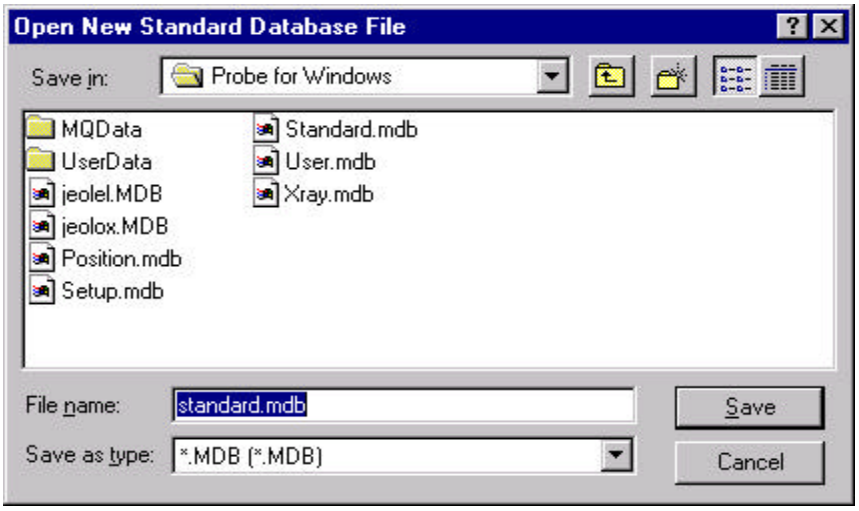
This action launches the STANDARD (Compositional Database) program and opens the **Open Old Standard Database File** dialog box. To create a new standard database, click on the **Cancel** button to close the **Open Old Standard Database File** dialog box.



Select **File** from the menu bar and then click on **New** from the menu.

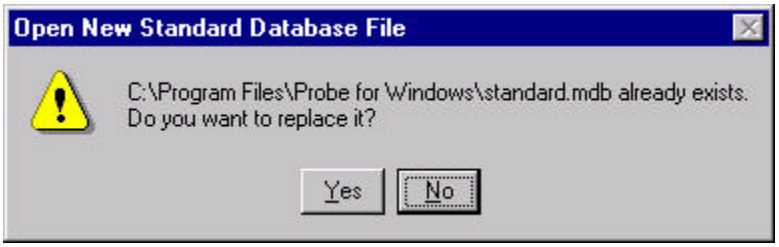


This opens the **Open New Standard Database File** dialog box.



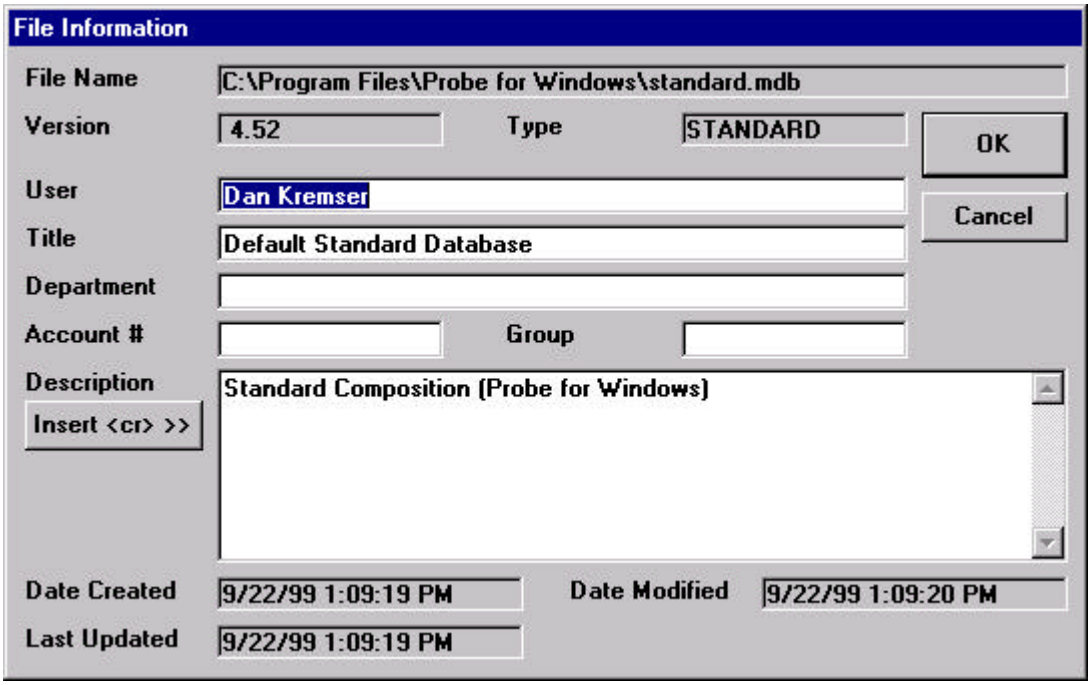
Click the **Save** button to open a new default standard database (STANDARD.MDB).

The **Open New Standard Database File** window appears.

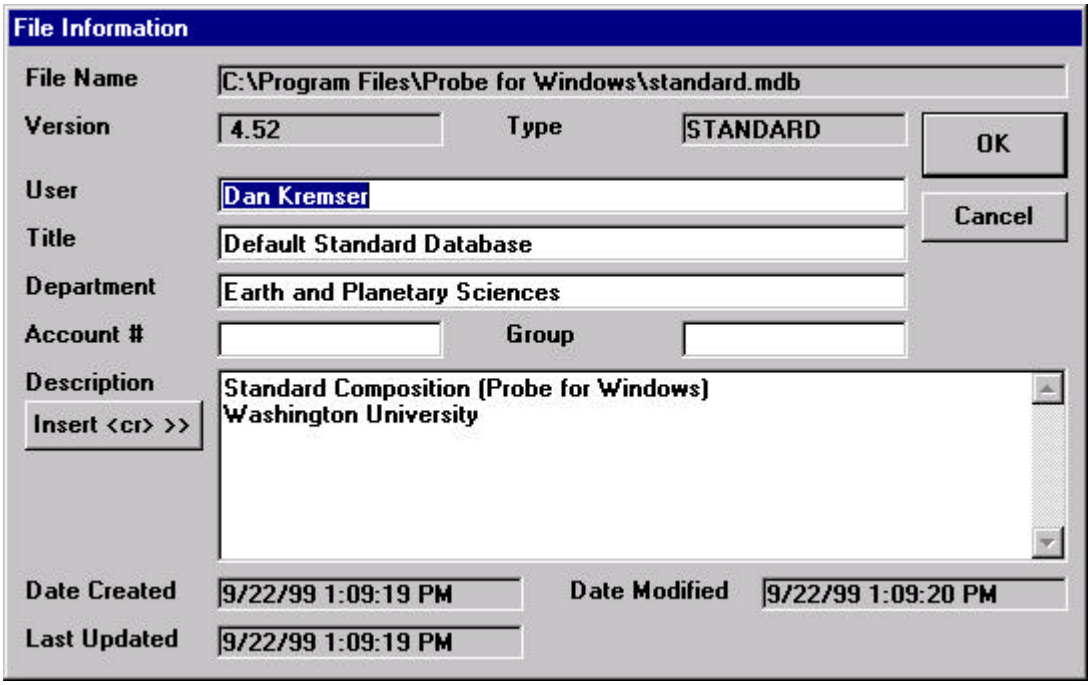


Click the **Yes** button to confirm overwriting the existing default database. Note: the supplied demonstration files JEOLEL.MDB and JEOLOX.MDB will no longer be usable after this operation.

The **File Information** window opens.

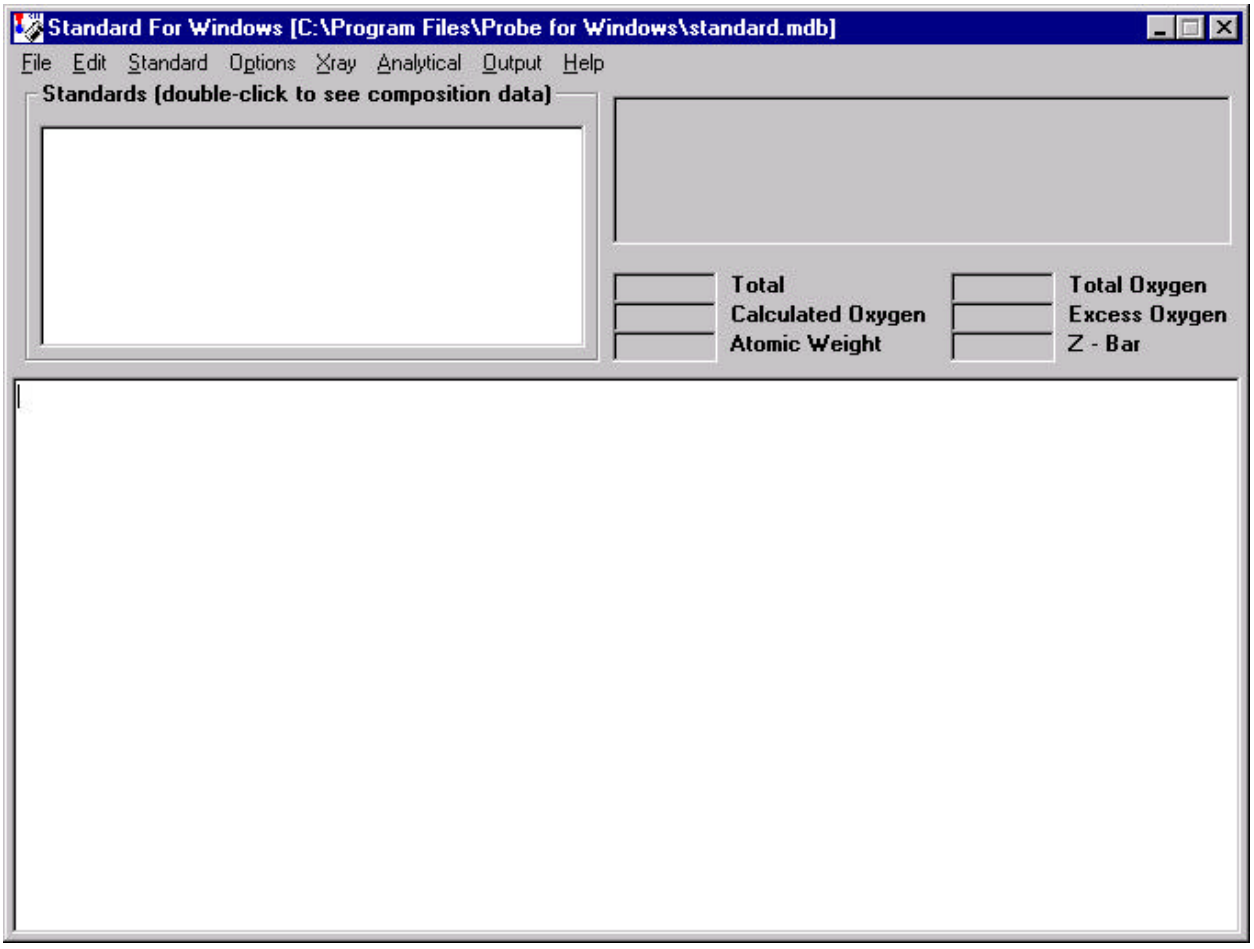


Enter the relevant information into the *User*, *Title*, and other *Description* text boxes shown in the **File Information** dialog box displayed below. Use the <tab> key to move between text boxes. Click the **Insert <cr> >>** button to insert a carriage return in the *Description* field text.

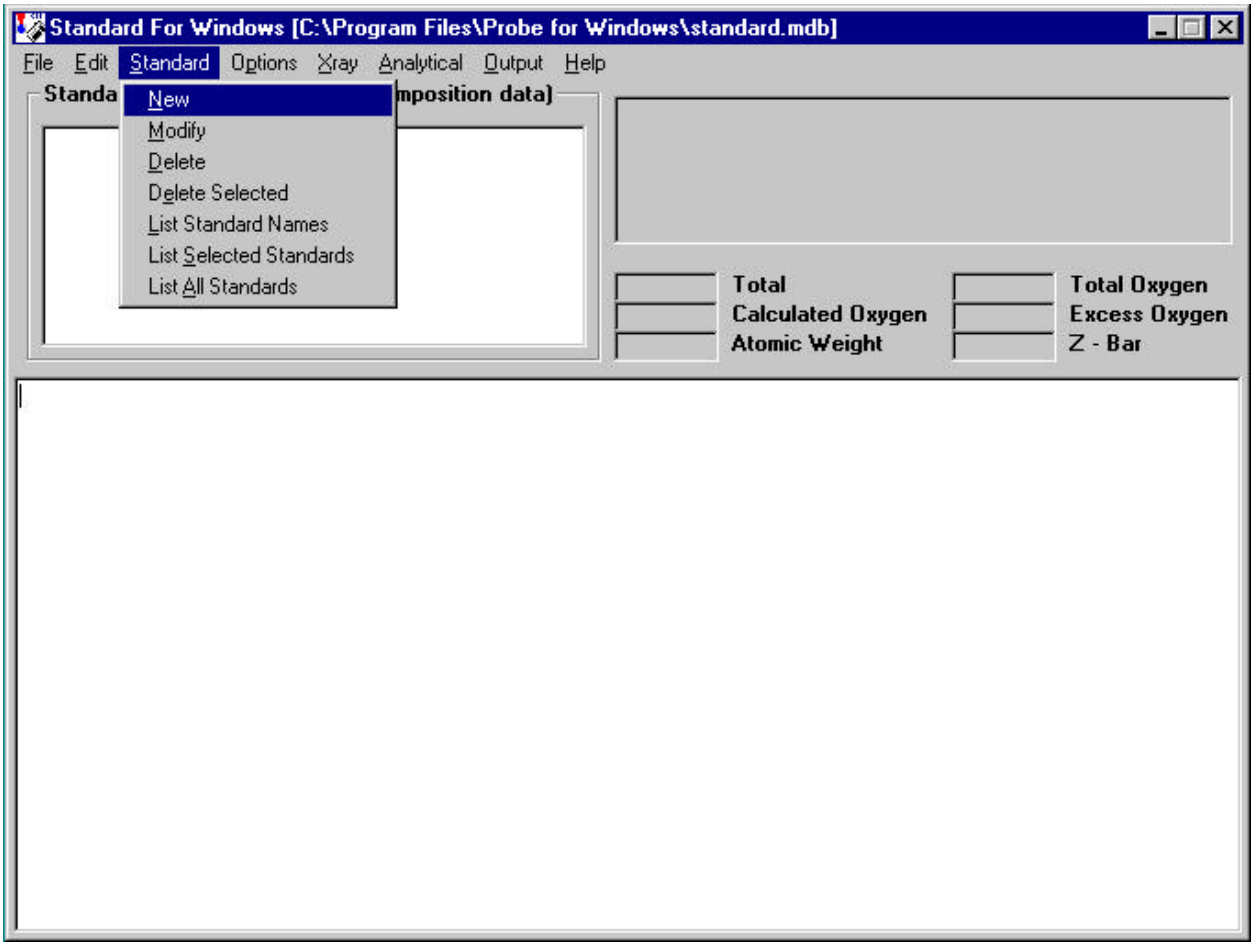


When finished, click the **OK** button.

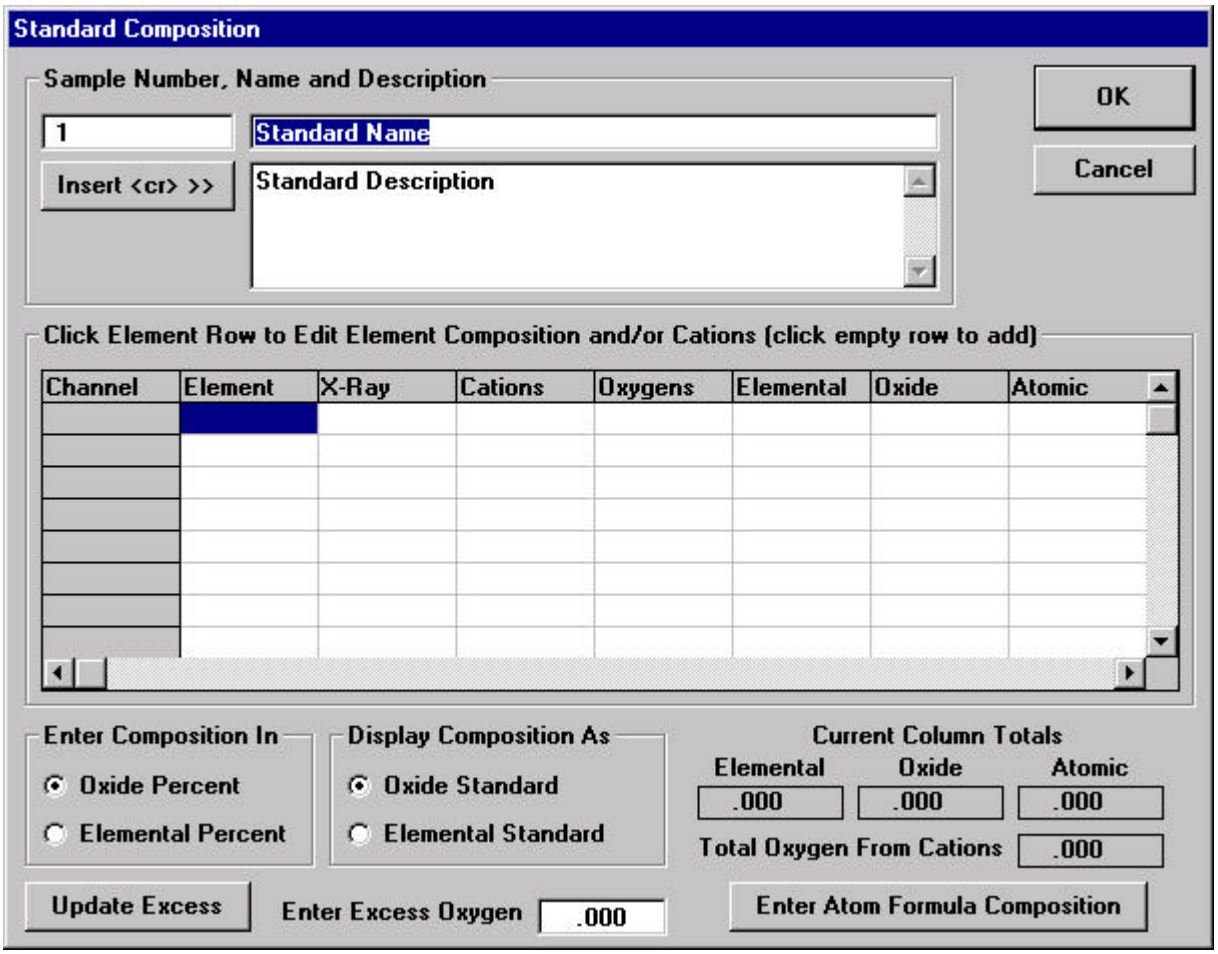
The user now has an empty database ready to accept standard composition data.



To enter standards into this database, select **Standard** from the menu bar and click on **New** from the menu.

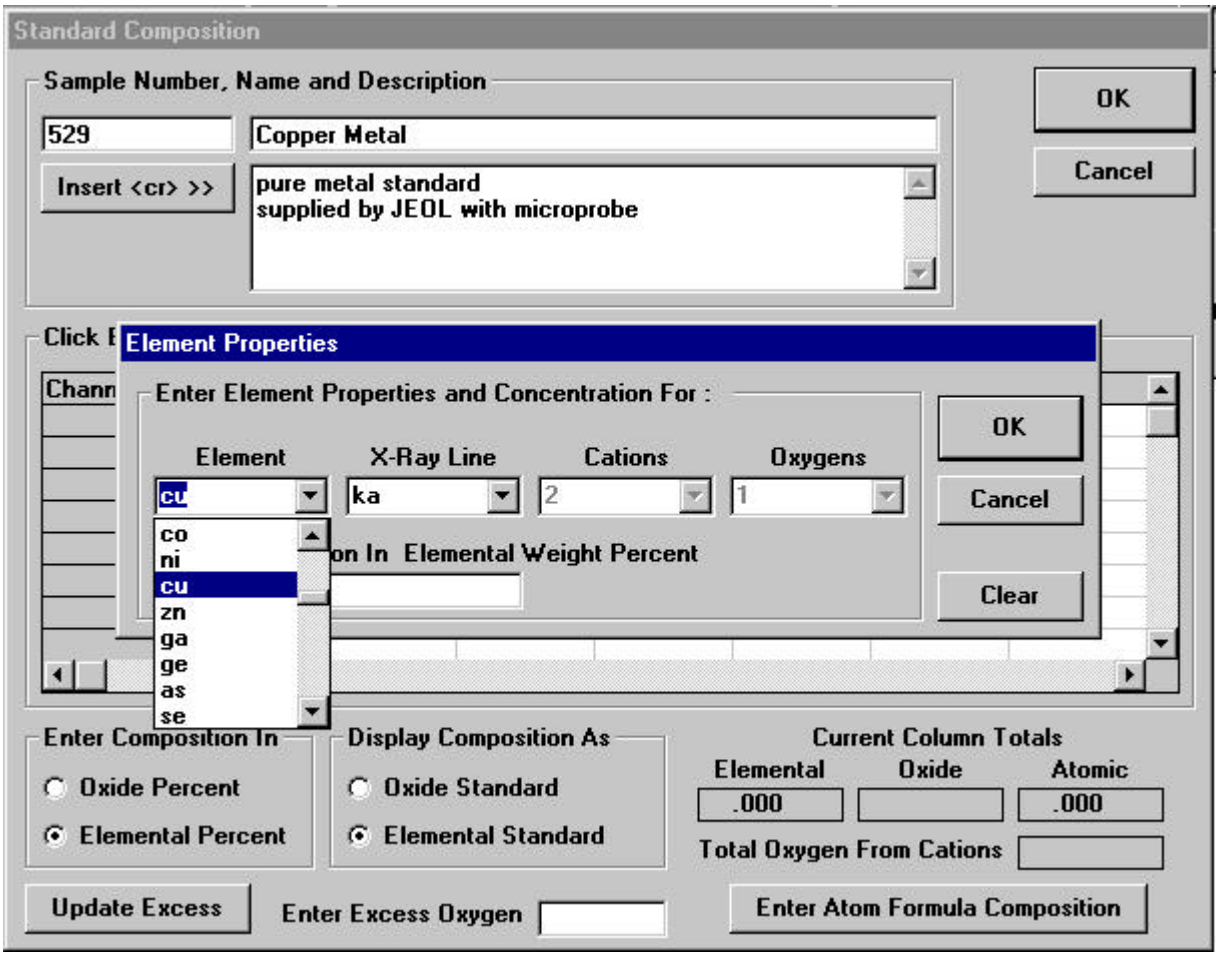


This action opens the **Standard Composition** dialog box. Type in the appropriate *Sample Number, Standard Name,* and *Standard Description* into the text boxes. The software automatically loads the next available number by default. Choose standard numbers that will allow grouping of standards into various functional sets. Standard numbers may range from 1 to 32768, however to avoid conflict with the supplied NIST SRM, DHZ, and Dana ORE sample databases select numbers below 2000.

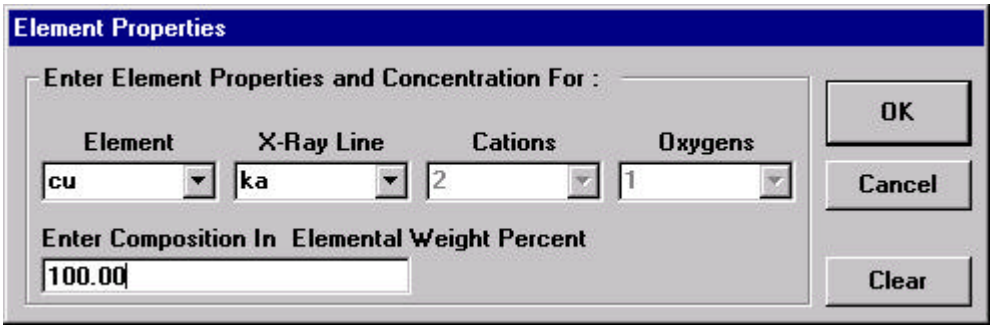


Click the *Elemental Percent* and *Elemental Standard* buttons under *Enter Composition In* and *Display Composition As* respectively, as necessary. All standard compositions are saved in the standard database as elemental concentrations. If oxygen is present in the standard then one must enter oxygen as an element and its concentration into the standard entry. See the silicate example in this manual for details.

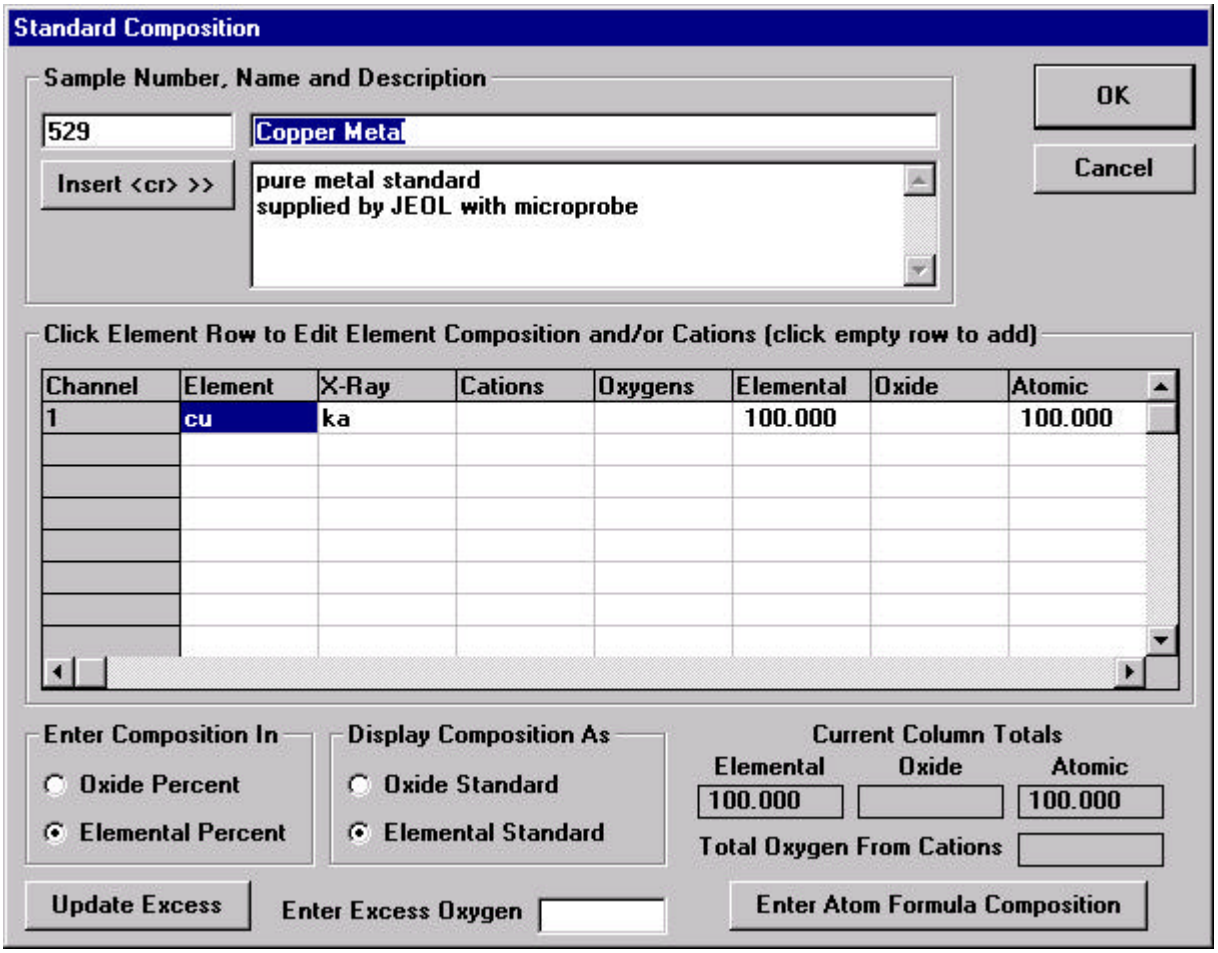
The first example will illustrate the entry of an elemental metal standard. Click on any empty row in the spreadsheet. This opens the **Element Properties** dialog box. In the *Element* field either type in the first element in the standard or use the drop-down list box to select the element symbol. Continue by choosing the correct *X-Ray Line*, *Cations*, and *Oxygens*. The *X-Ray Line* is used for modeling purposes only. When entering properties and concentrations for elements in elemental mode, the program grays out the *Cations* and *Oxygens* text boxes, no editing of these text boxes are necessary.



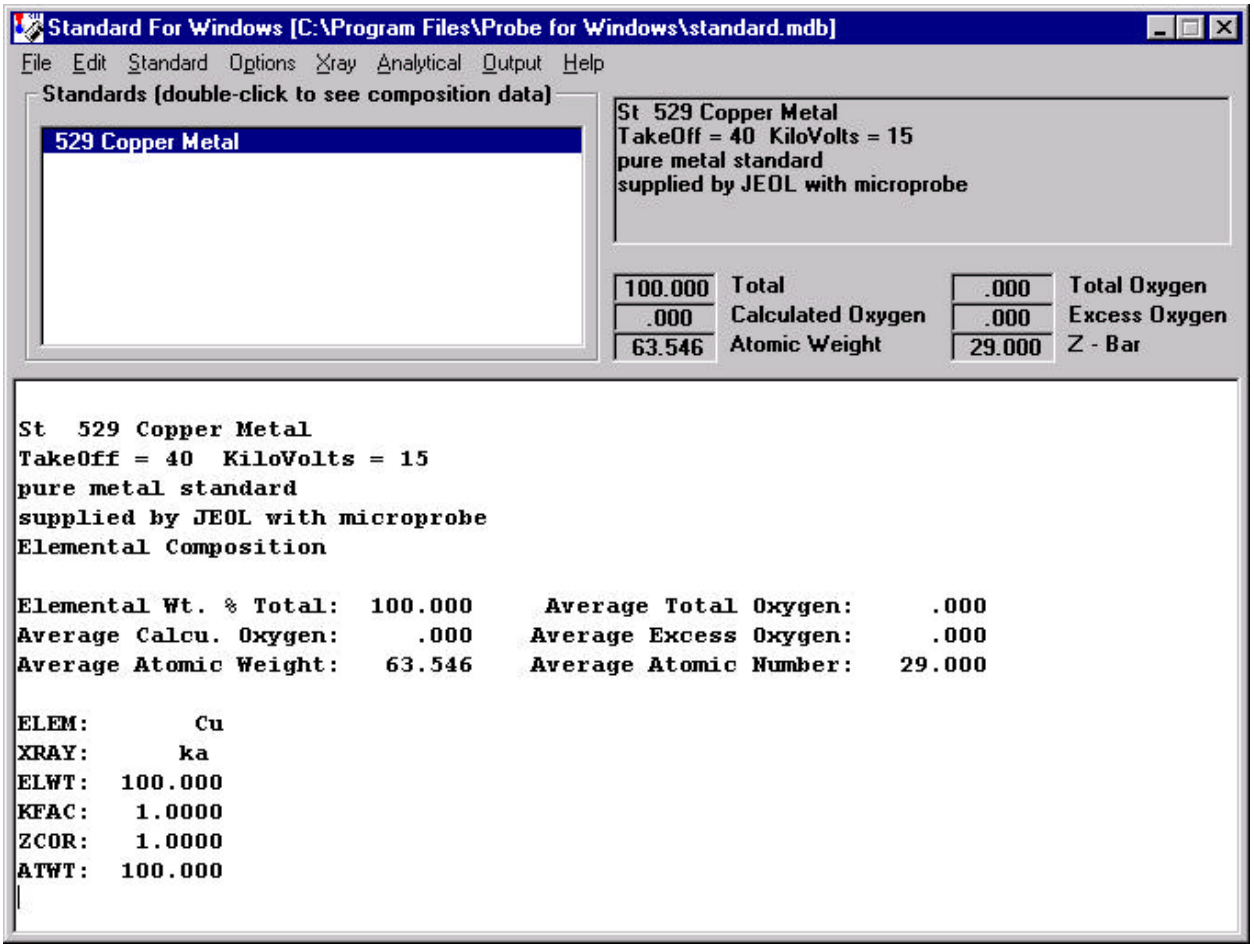
Enter the elemental weight percent for cu into the *Composition* text box. Finish by clicking the **OK** button of the **Element Properties** dialog box.



The program returns to the **Standard Composition** dialog box.

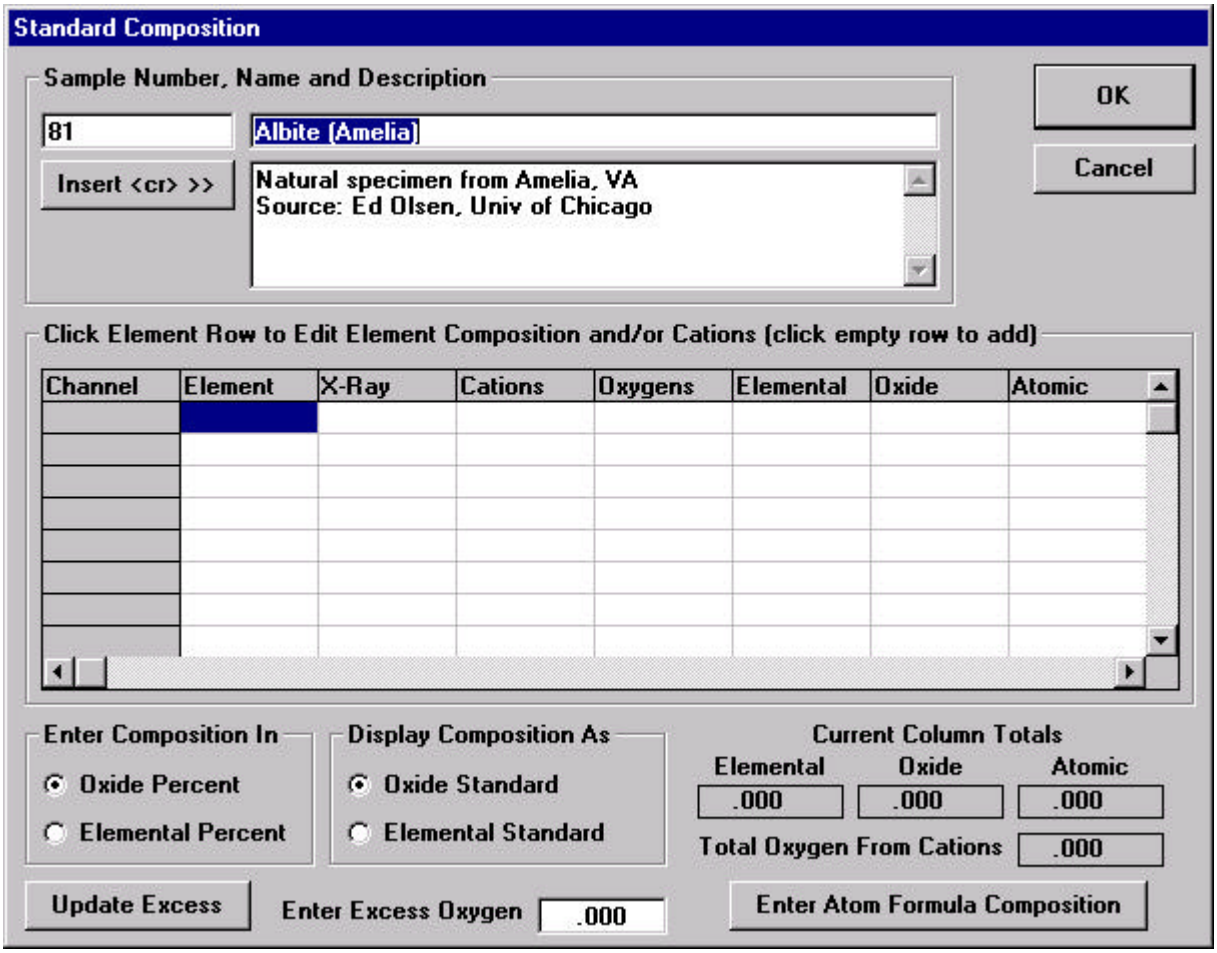


If there are more elements (compound standards) in the standard, click the next empty *Element* row and repeat the data entry process. When all elements are entered, click the **OK** button on the **Standard Composition** dialog box. This concludes the entry of a standard into the standard database and results in the following log window output.



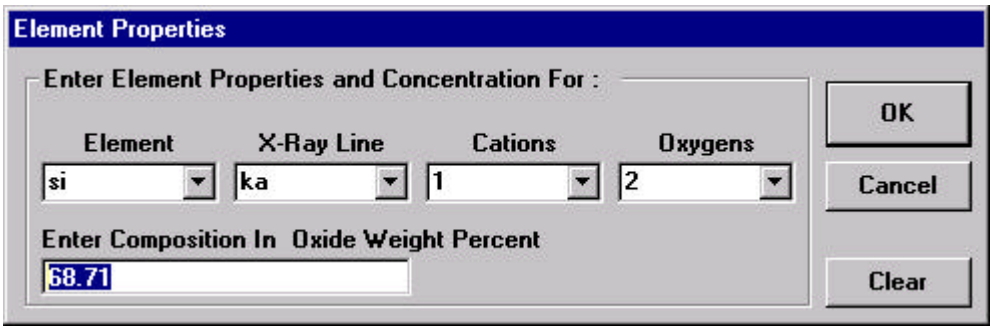
Many standards contain oxygen in their compositions. Since all standard compositions are saved to the standard database as elemental concentrations, it is necessary to enter the oxygen concentration if oxygen is present in the compound. This applies to all standards, even those which are entered and/or displayed as oxide concentrations. The following example illustrates a silicate (oxygen bearing) standard entry into the database.

From the main Standard log window, select **Standard** from the menu bar and click on **New** from the menu choices. This action opens the **Standard Composition** dialog box. Type in the appropriate *Sample Number, Standard Name,* and *Standard Description* into the text boxes. Click the *Oxide Percent* and *Oxide Standard* buttons under the *Enter Composition In* and *Display Composition As* boxes.

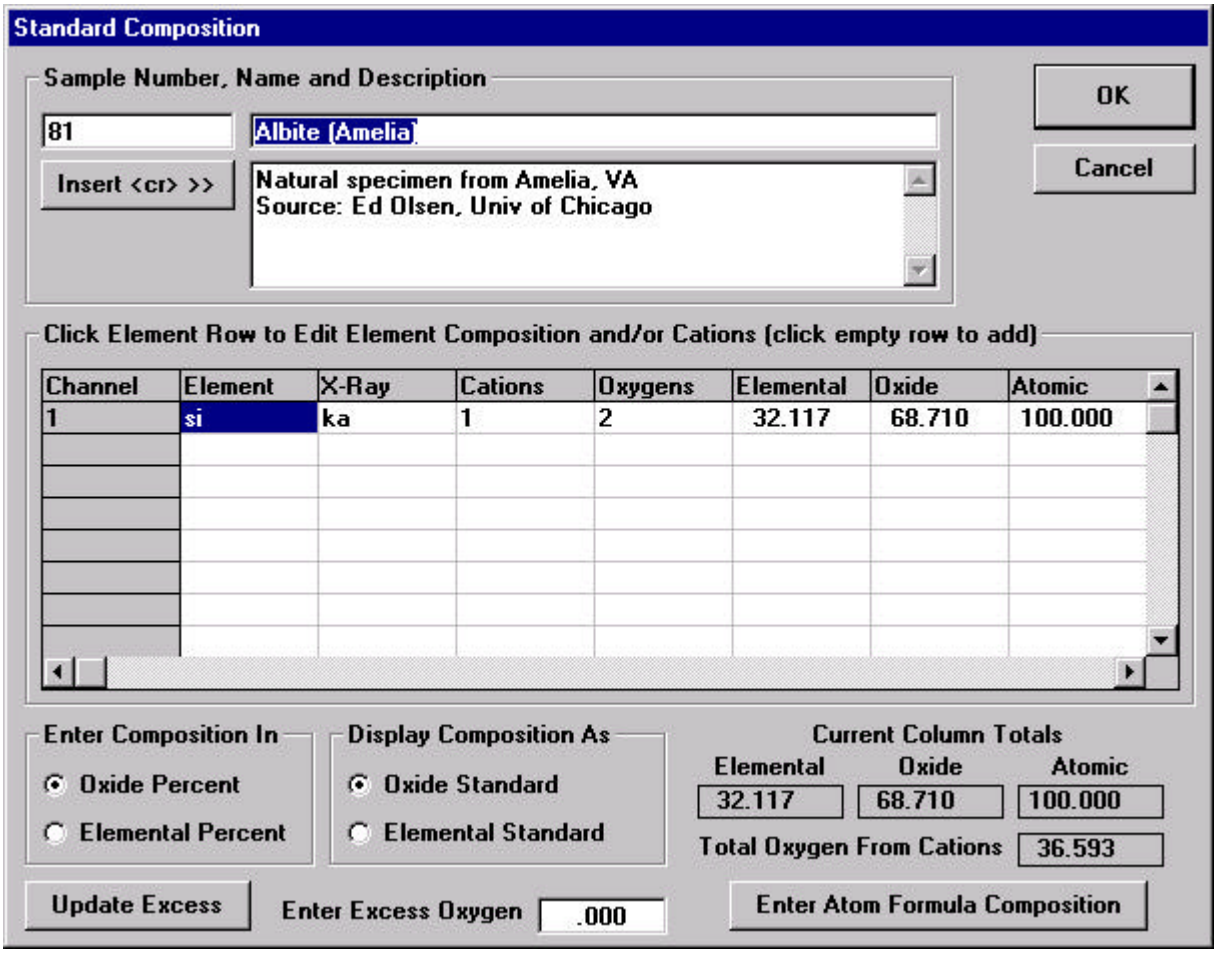


Click on any empty row in the spreadsheet.

This opens the **Element Properties** dialog box. In the *Element* field either type in the first element in the standard or use the drop-down list box to select the element symbol. Continue by choosing the correct *X-Ray Line*, *Cations*, and *Oxygens*. Finally, enter the weight percent for SiO_2 into the *Enter Composition In Oxide Weight Percent* text box.

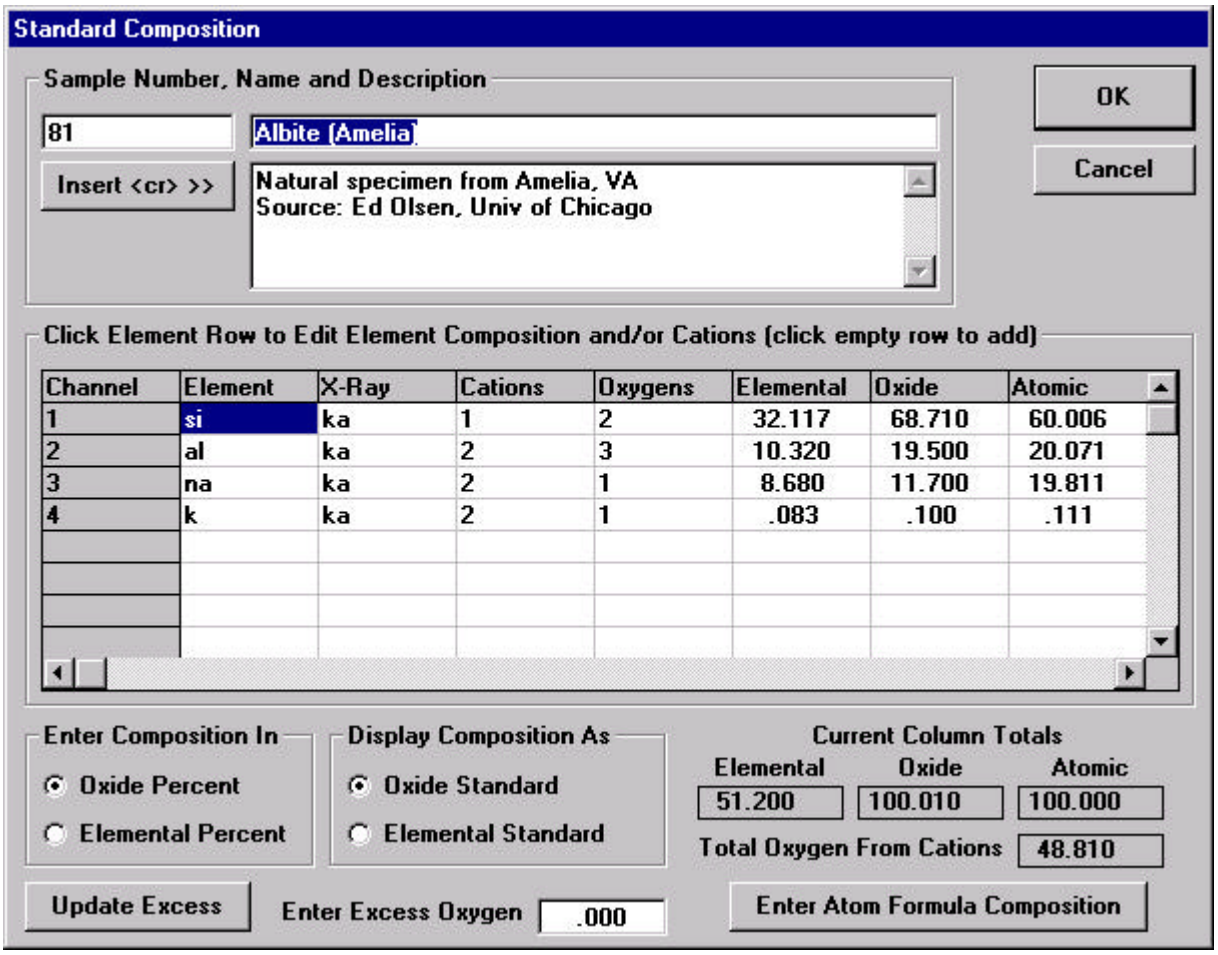


Finish by clicking the **OK** button of the **Element Properties** dialog box. This results in the following **Standard Composition** dialog box.

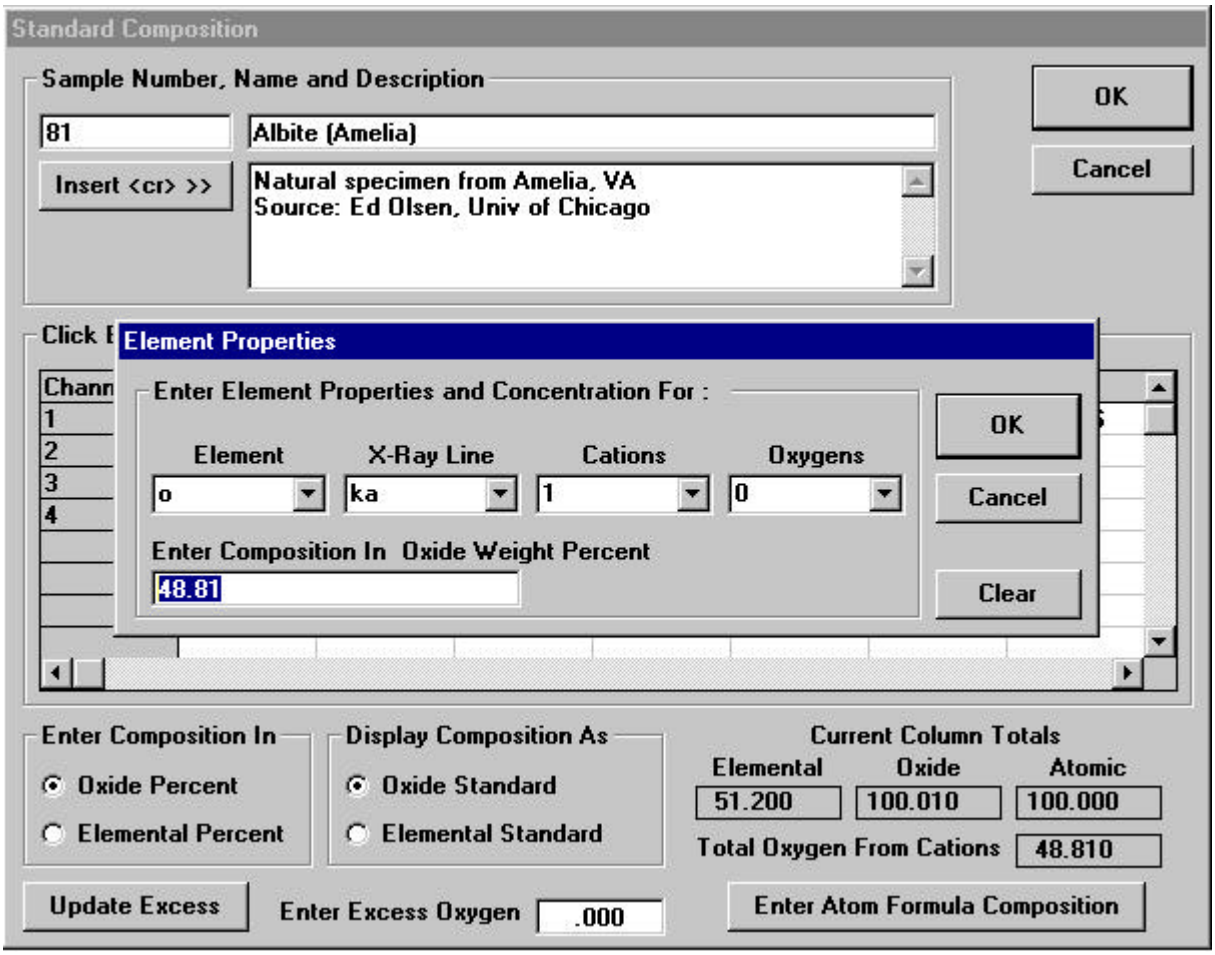


Note: to facilitate the data entry for the oxygen concentration of standard compositions which are entered as oxide concentrations, the program will display a running total in the text box designated *Total Oxygen From Cations.*

Continue the data entry process for the remaining elements (as oxides).

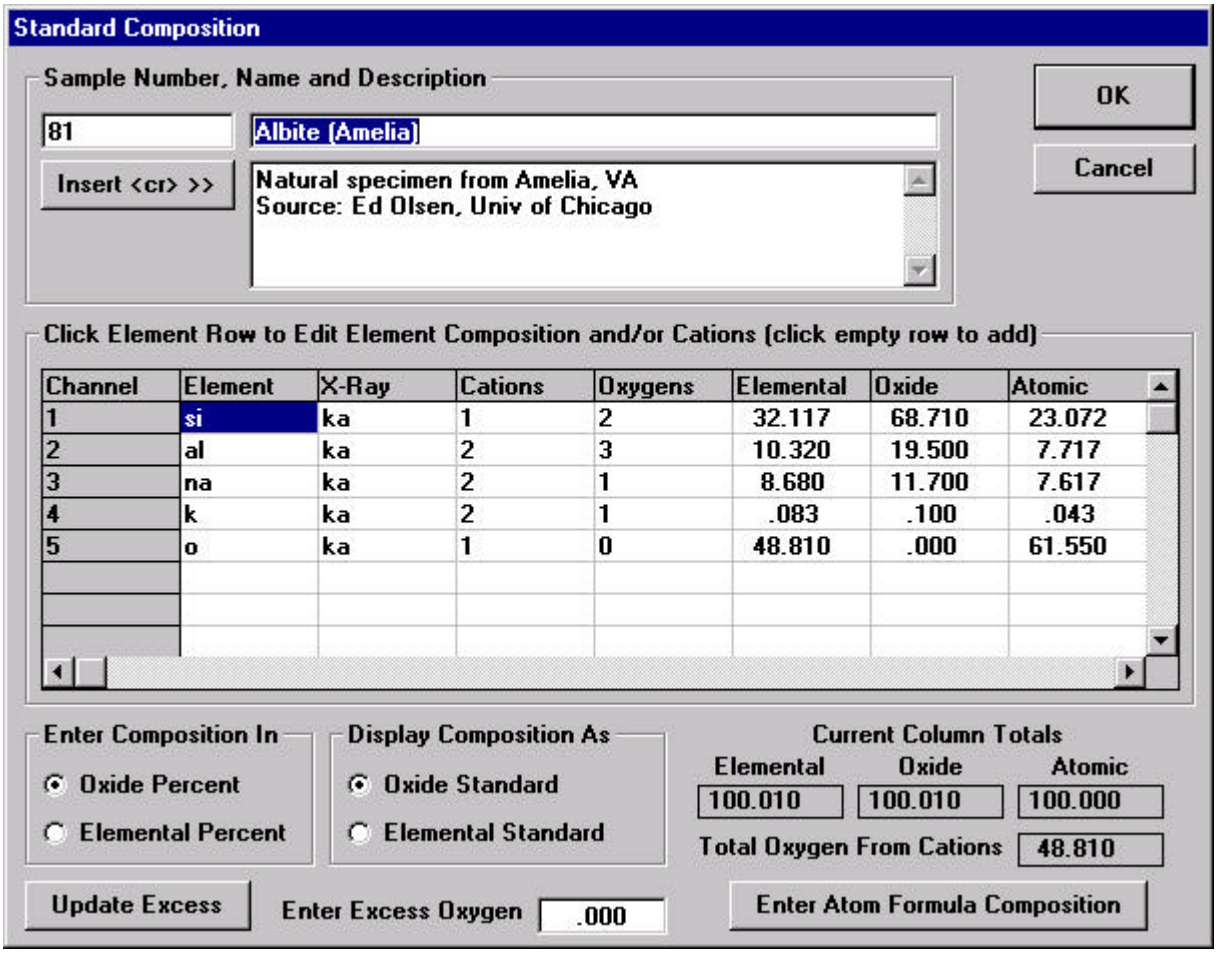


To complete the standard entry into the standard database, enter oxygen as the last element in the standard. Click on any empty row in the spreadsheet. This opens the **Element Properties** dialog box. In the *Element* field type in the element symbol for oxygen. Check for the appropriate *X-Ray Line*, *Cations*, and *Oxygens*. Finally, enter the running total from the *Total Oxygen From Cations* text box into the *Enter Composition in Oxide Weight Percent* text box.

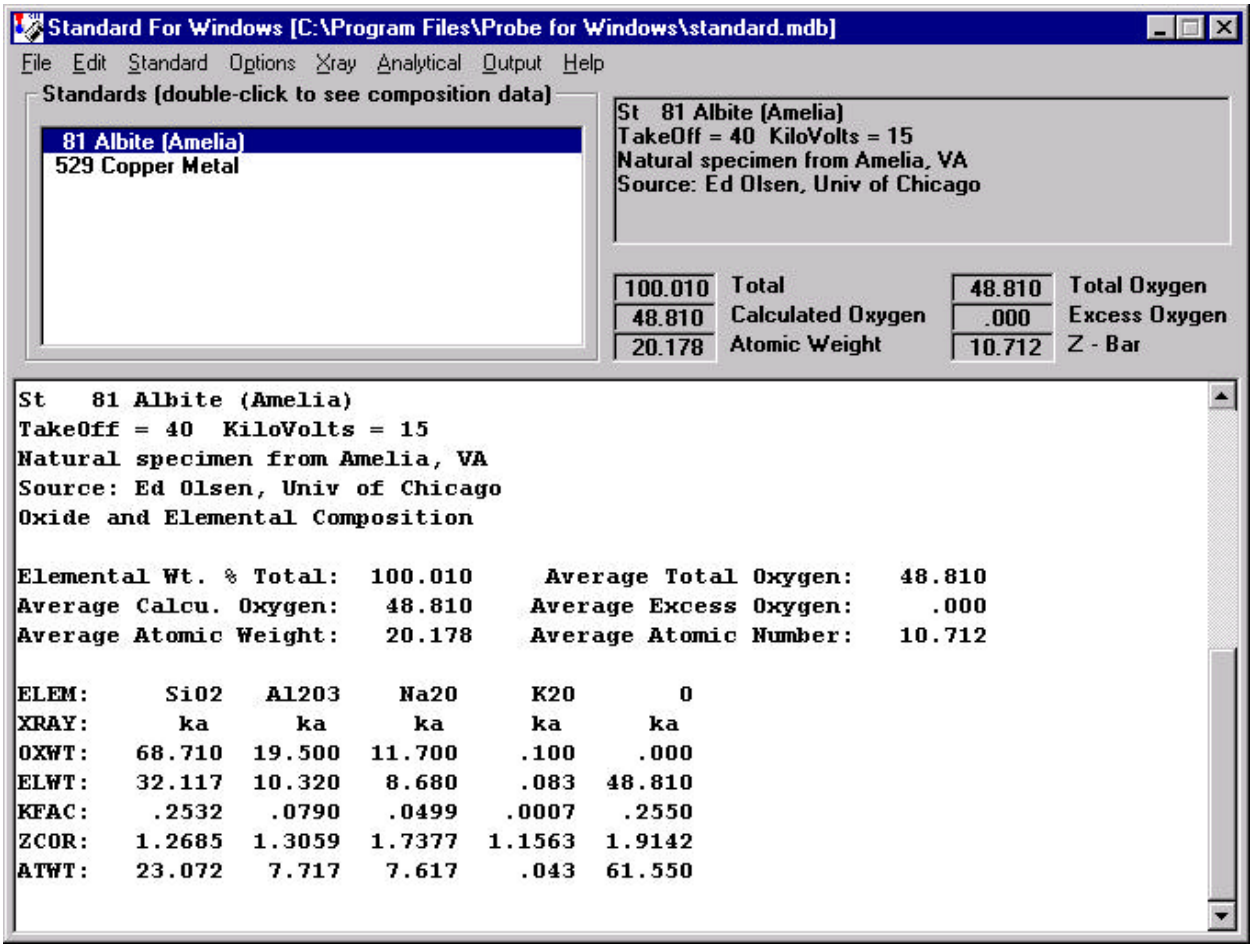


Click the **OK** button of the **Element Properties** dialog box.

The following **Standard Composition** dialog box illustrates the completed five element silicate standard, Albite.



The compositional data of any standard entered into the standard database may be reviewed by simply double-clicking on the standard of interest from the scrollable *Standards* list box. The following window contains two standards with the compositional data of Albite displayed in the log window in oxide form.



To modify a particular standard, select the standard in the *Standards* list box. Click **Standard** from the menu bar and select **Modify** from the menu. Edit the appropriate fields in the **Standard Composition** window as described previously.

After entering all of the standard compositions in your standard collection, save this important file (STANDARD.MDB) to another directory on the hard disk and likewise to a floppy for archival purposes.

Note: the takeoff, kilovolt, x-ray and cation ratio parameters displayed here are used only for nominal calculations of the k-factors and ZAF corrections within the program STANDARD. The PROBE FOR WINDOWS quantitative analysis will calculate the quantitative standard k-factors based on the actual conditions.

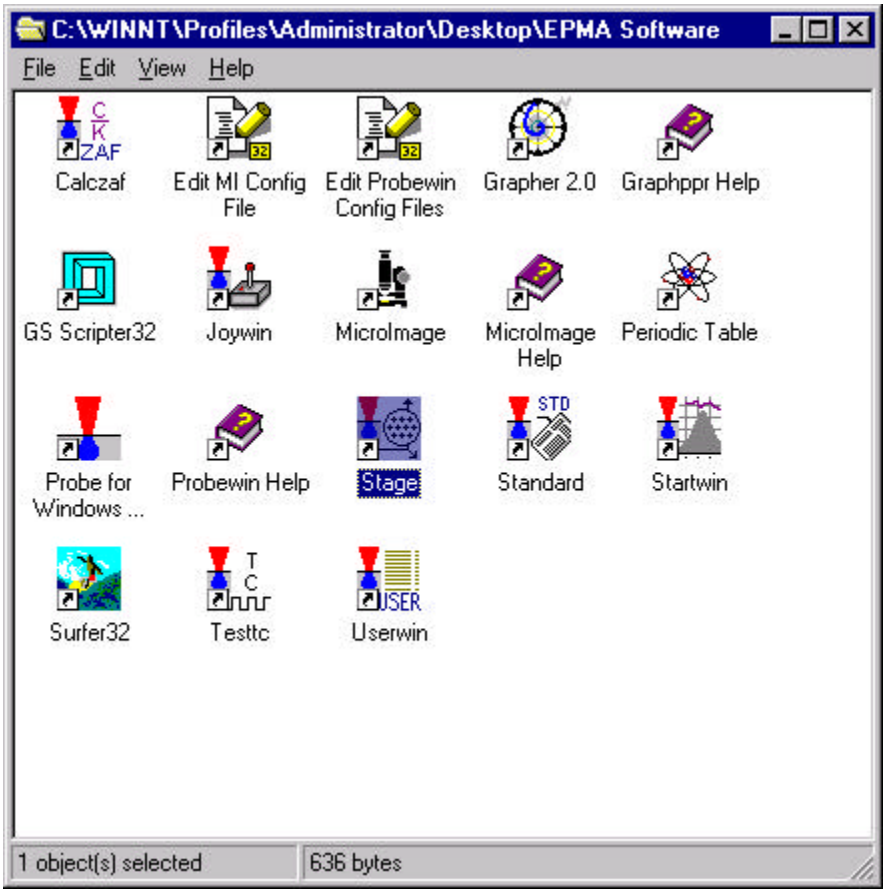
Creating Standard Position Files

Program STAGE.EXE is used to digitize your standard mounts to create pre-digitized standard coordinate files. These files are necessary for automated acquisition and standardization. The standard coordinates are digitized in three dimensions (X, Y, and Z) as well as the W stage position (multi-position specimen stages only) and are typically referenced to three physical fiducial marks on the standard mount surface. These coordinate files should be digitized with the standard mount located in the position where it is typically found.

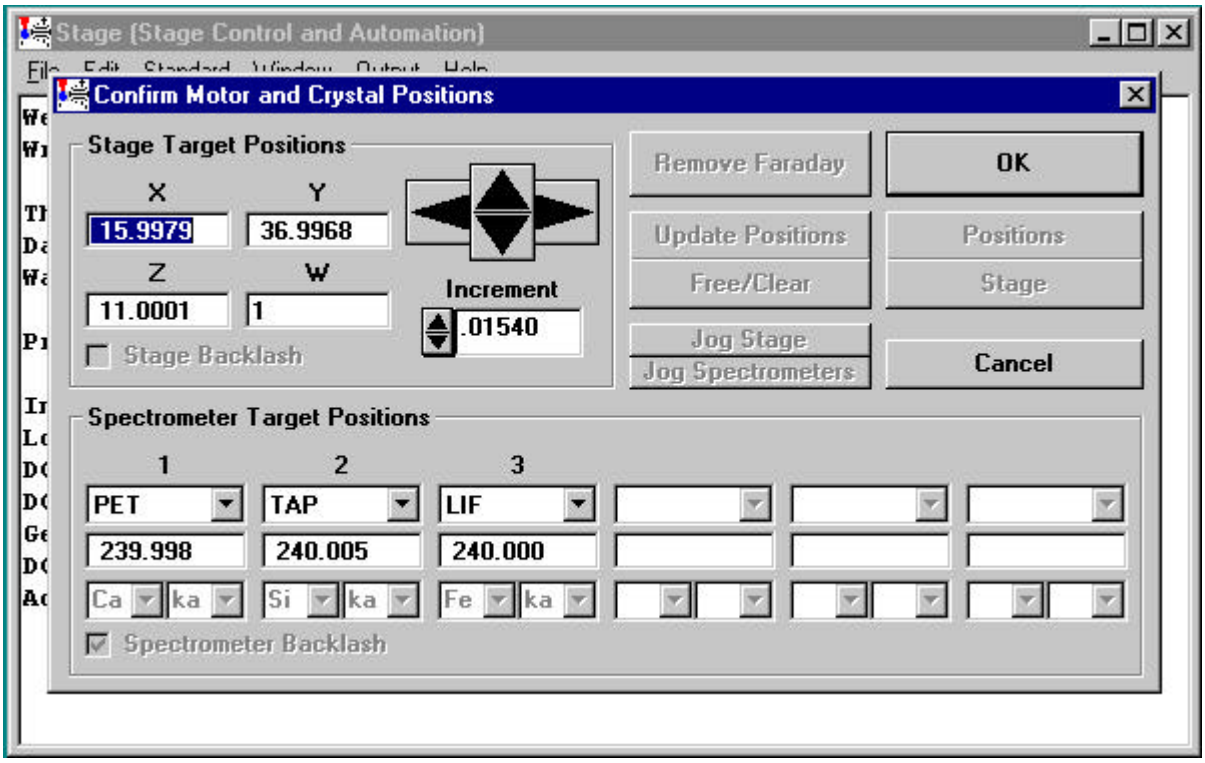
The following procedure illustrates how to create a new standard position file. In this example, four carbonate standards will be digitized. These standards must already be entered into the standard database using program STANDARD.

When creating digitized standard files for standard mounts containing more than 42 standards, a slightly different procedure than outlined below must be followed. Concise instructions on how to bypass the current 42 standard limit in the STAGE digitize feature are outlined in the reference documentation. To find these instructions, open the PROBEWIN.HLP program from the EPMA Software folder. Click the **Search** button and type in digitize in the text box. Highlight the topic entitled *Digitizing Standard Mounts with More Than 42 Standards* and click the **Display** button.

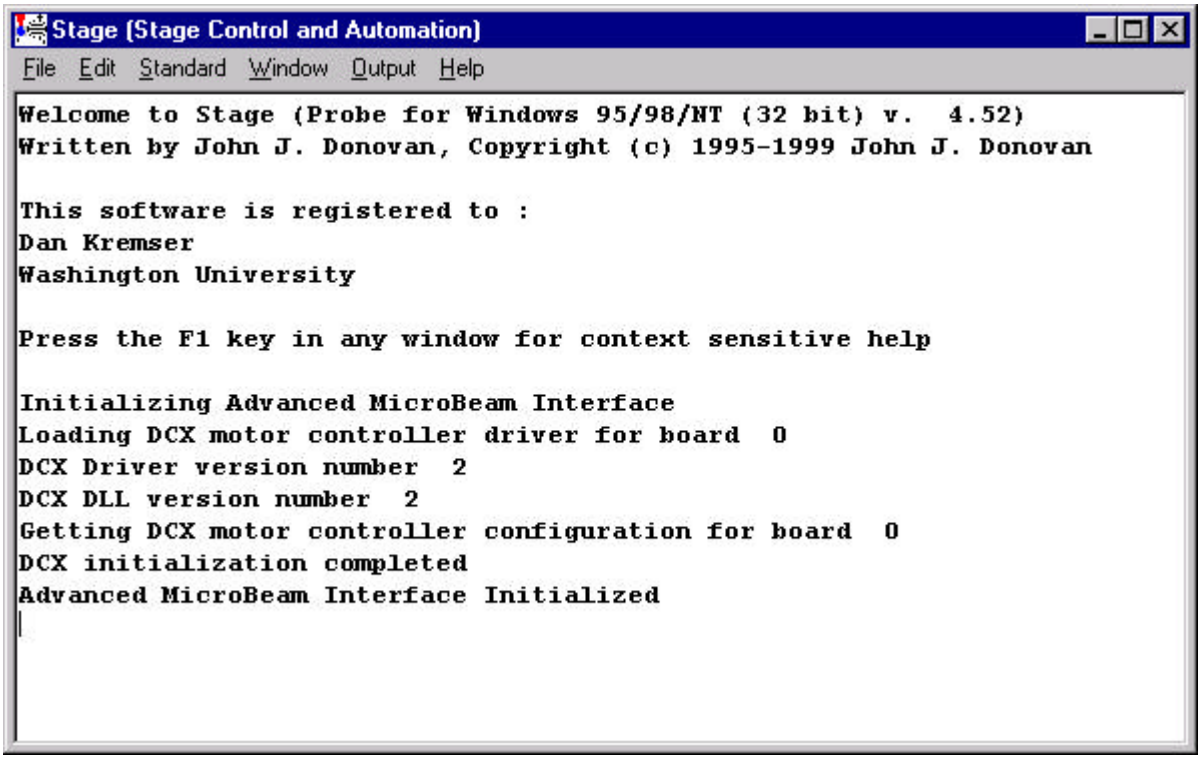
Open STAGE (Stage Control and Automation) by double clicking on the **Stage** icon in the EPMA Software group.



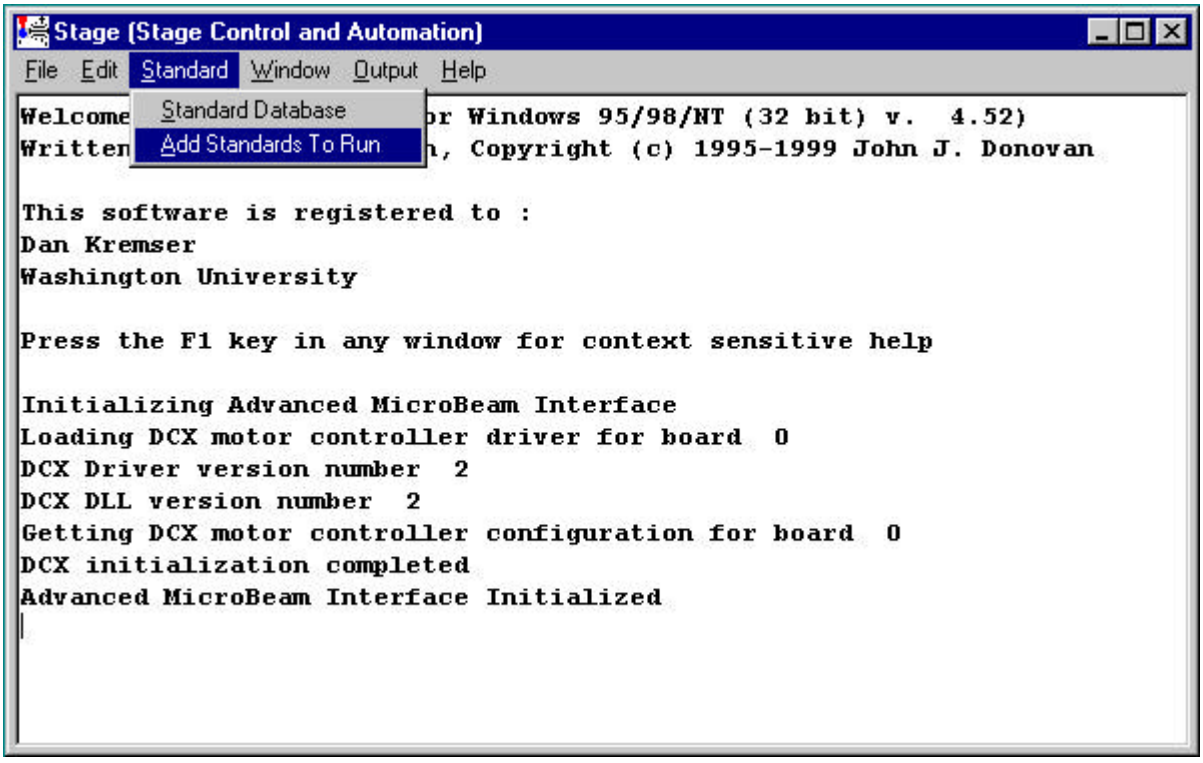
This starts the STAGE program and brings up the **Confirm Motor and Crystal Positions** dialog box. Confirm that all of the motors (stage and spectrometer positions) and crystal designations are correctly calibrated. If there is disagreement between the mechanical positions (actual) and the software values, adjust the software values. Use the <tab> key to move between the *Target Positions* text boxes. Click the **OK** button to close the **Confirm Motor and Crystal Positions** dialog box when done.



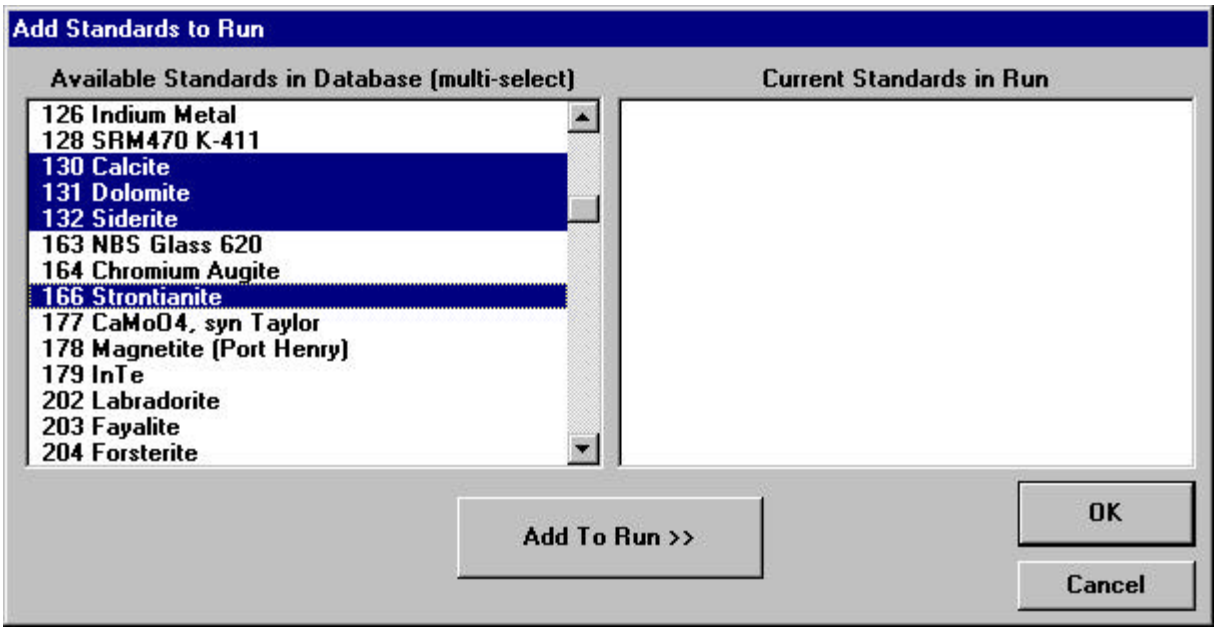
The following display illustrates the STAGE log window.



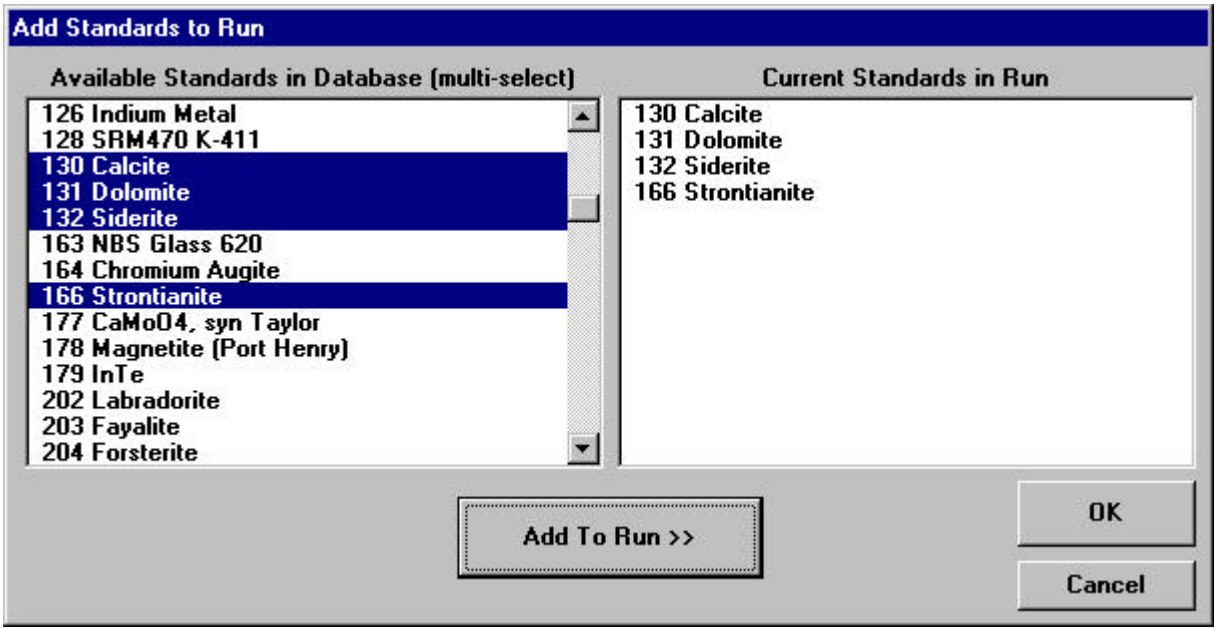
Select **Standard** from the menu bar and click on **Add Standards to Run** from the menu choices.



This action opens the **Add Standards to Run** dialog box. Click on the name of each of the standards in the standard block to be digitized from the *Available Standards in Database* list box.

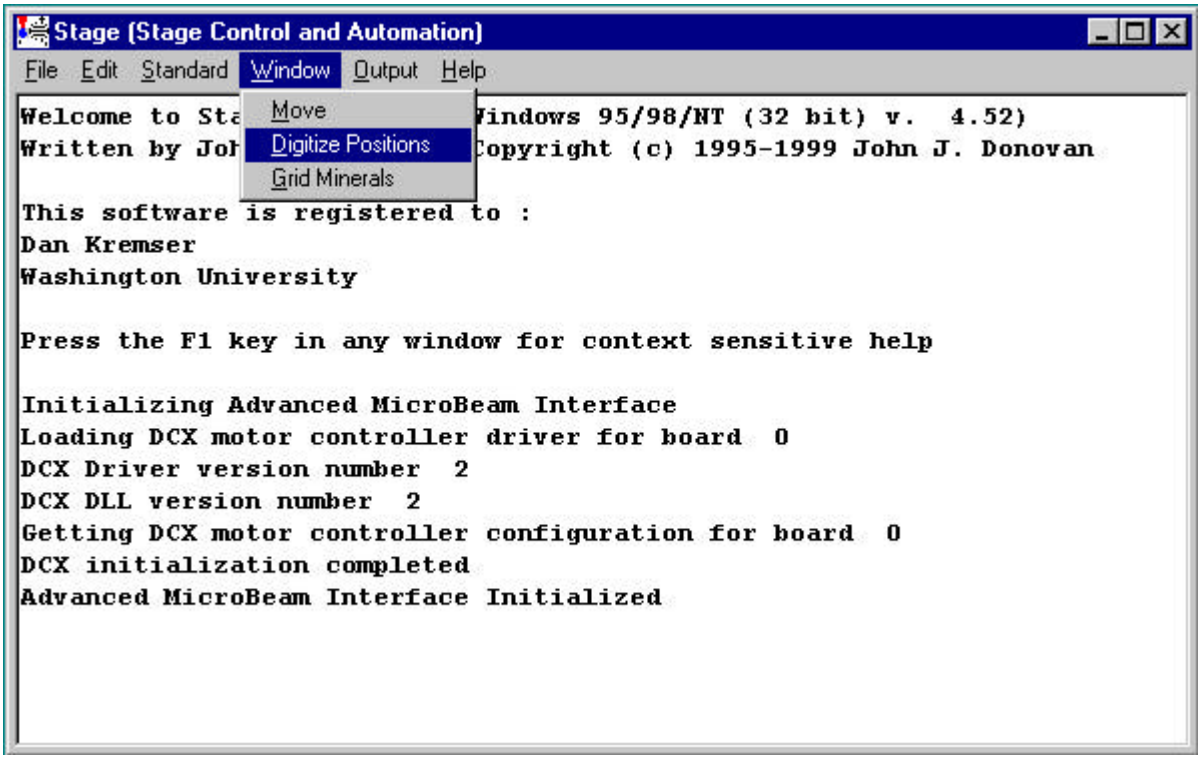


Click the **Add to Run >>** button to add these standards to be digitized. Standards maybe added one at a time or one may multi-select standards by holding down the <Ctrl> button on the keyboard as standards are selected.

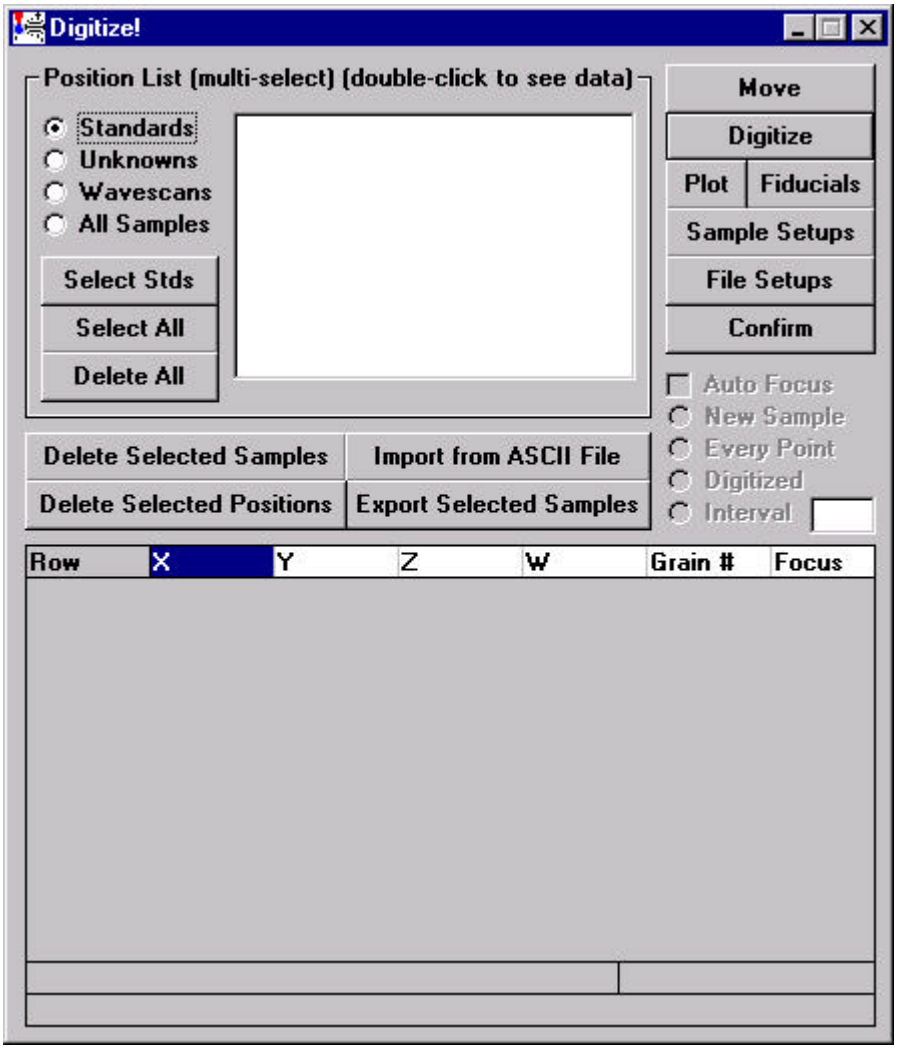


Click the **OK** button of the **Add Standards to Run** dialog box when finished.

Select **Window** from the menu bar and choose **Digitize Positions** from the menu choices.

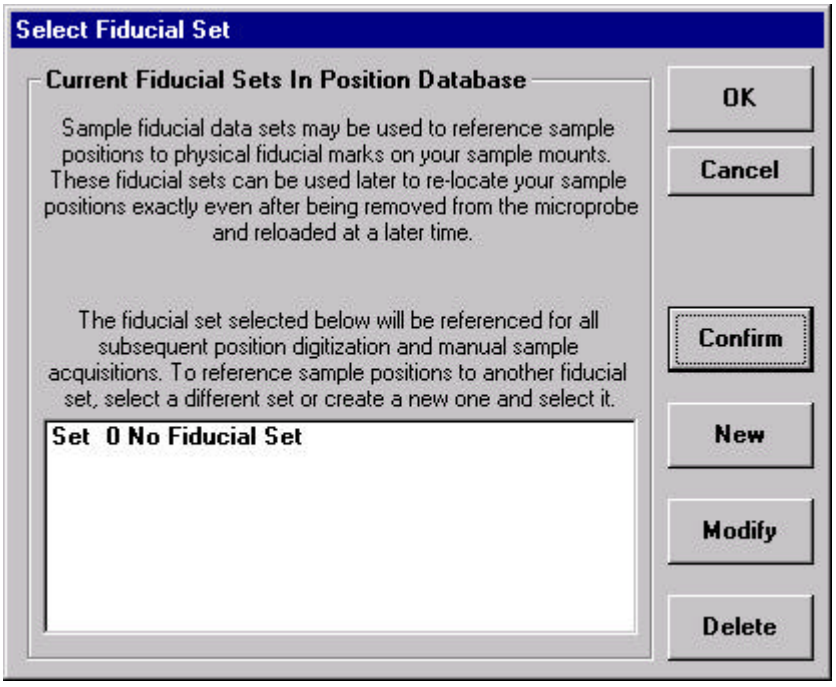


This action opens the **Digitize!** dialog box.

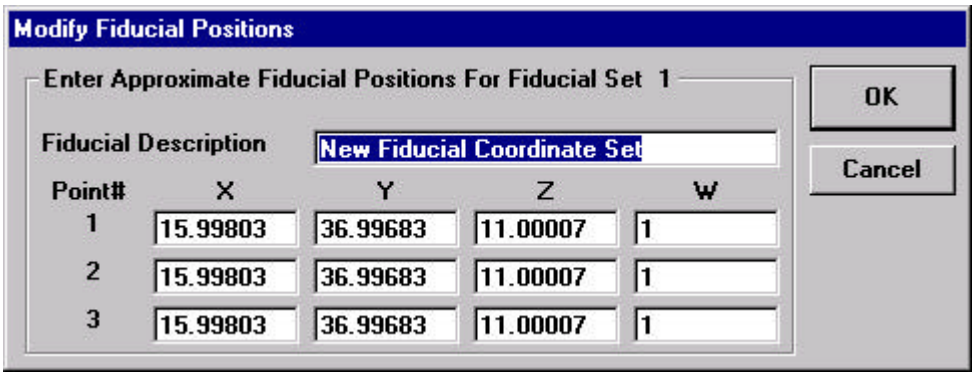


Click the **Fiducials** button.

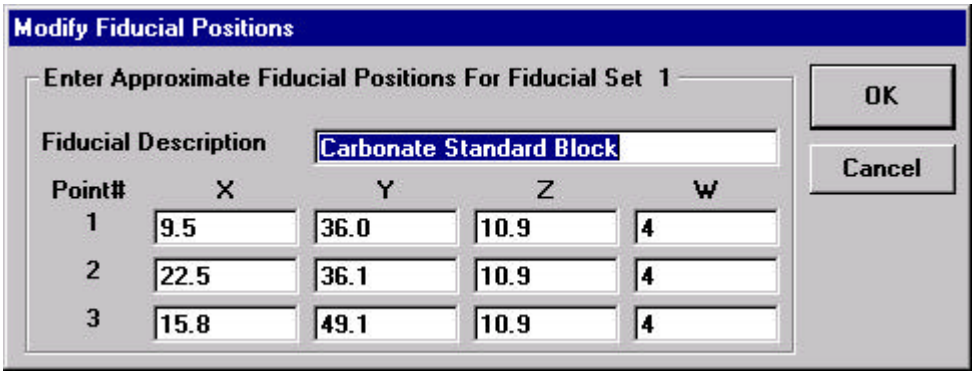
This opens the **Select Fiducial Set** window.



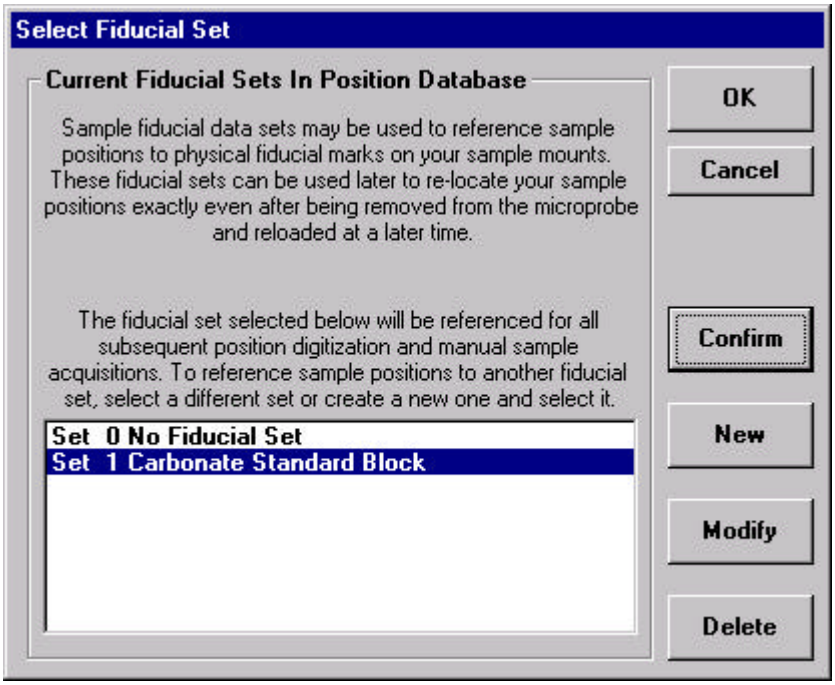
Click the **New** button. This opens the **Modify Fiducial Positions** window. The current stage coordinates are loaded by default.



Type in a *Fiducial Description.* Enter the nominal coordinates or move to each of the three fiducial marks on the standard mount, determining their approximate coordinates, and enter those values into the appropriate fields. On JEOL 733 microprobes, the W stage position needs to be recorded as well. The following window results.

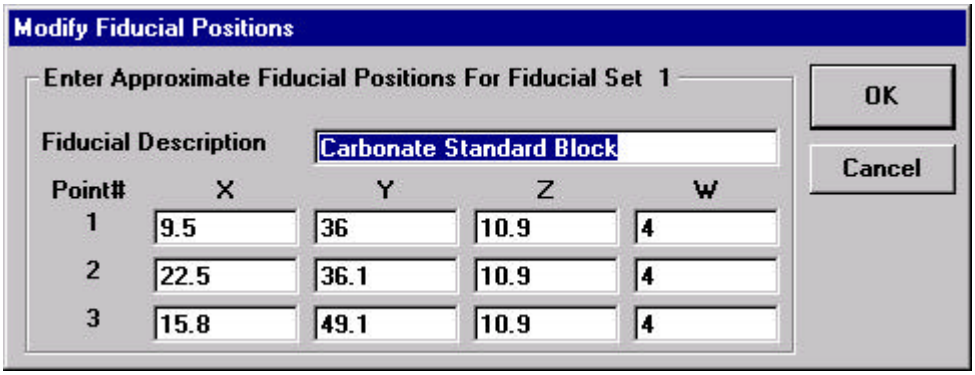


Click the **OK** button when done. This creates a new entry in the **Select Fiducial Set** list box as shown below.



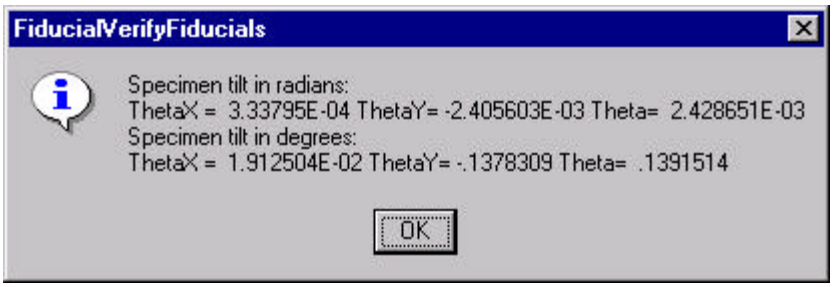
Select (highlight) the new fiducial set and click the **Confirm** button to initiate a precise centering of the three fiducial marks.

The **Modify Fiducial Positions** window opens displaying the originally entered fiducial coordinates. Click the **OK** button to confirm.

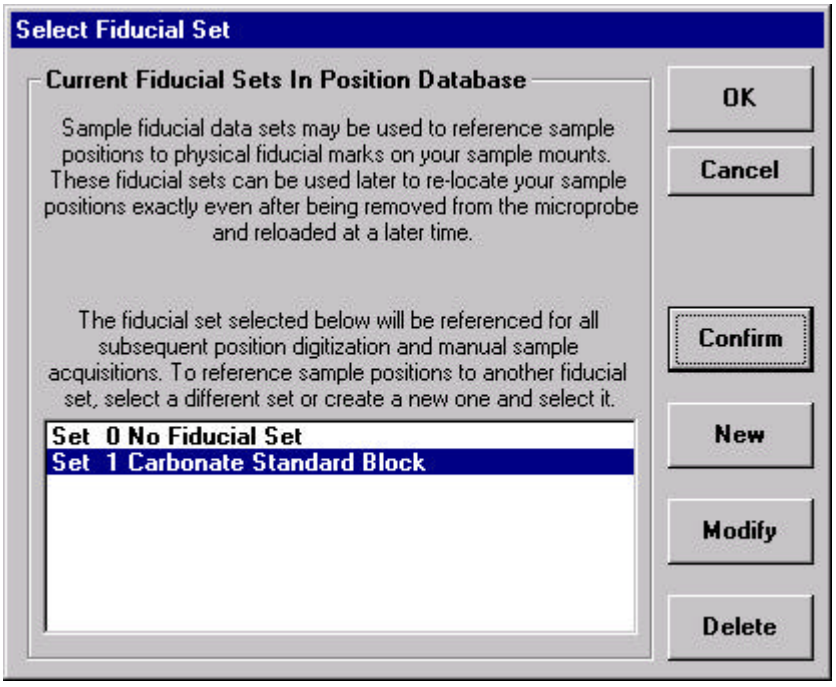


The computer then drives to each fiducial mark and displays the **FiducialVerifyFiducial** window. Adjust the stage position to center the fiducial mark and click the **OK** button.

After centering the third fiducial mark and clicking the **OK** button, the **FiducialVerifyFiducials** window opens to display the specimen tilt in radians and degrees. A warning will be given if the sample is tilted at more than 0.5 degrees. Click this **OK** button.



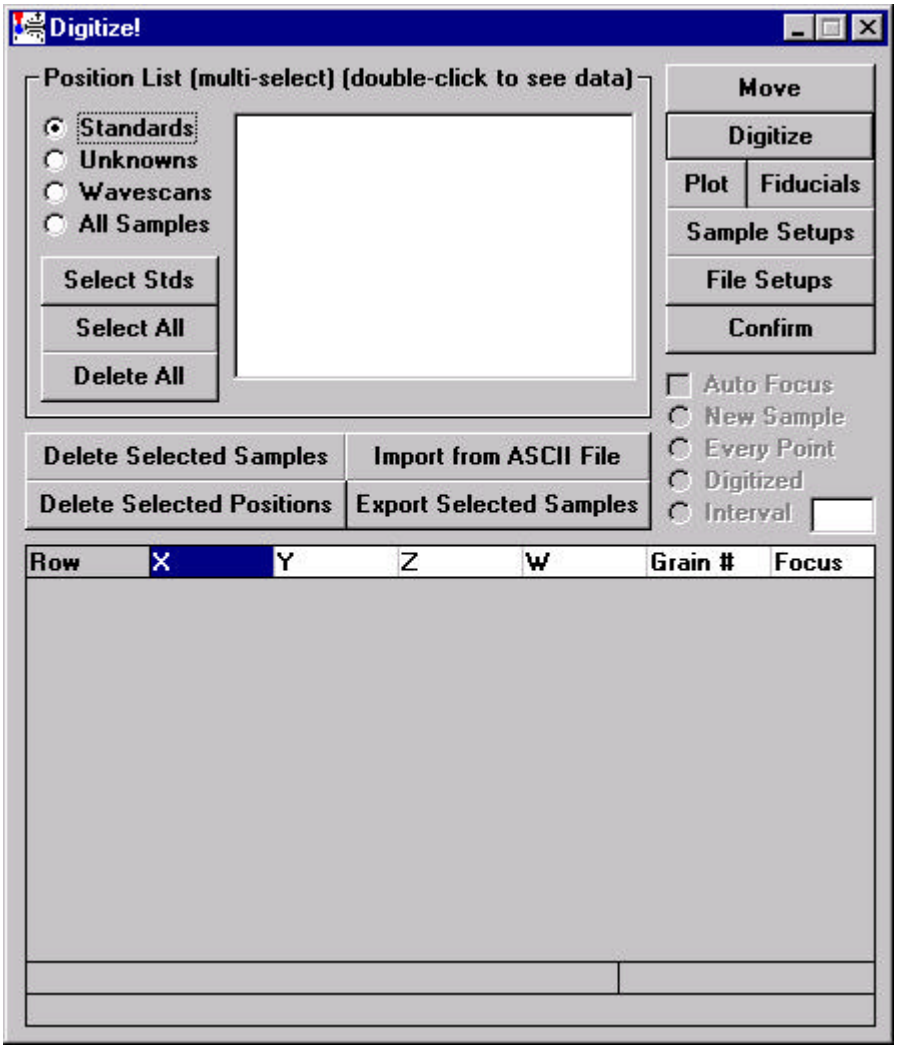
Closing the **FiducialVerifyFiducials** window returns to the **Select Fiducial Set** dialog box.



Finally, click the **OK** button on the **Select Fiducial Set** dialog box. This opens the **FiducialSaveSelect** window to confirm the currently selected fiducial set.

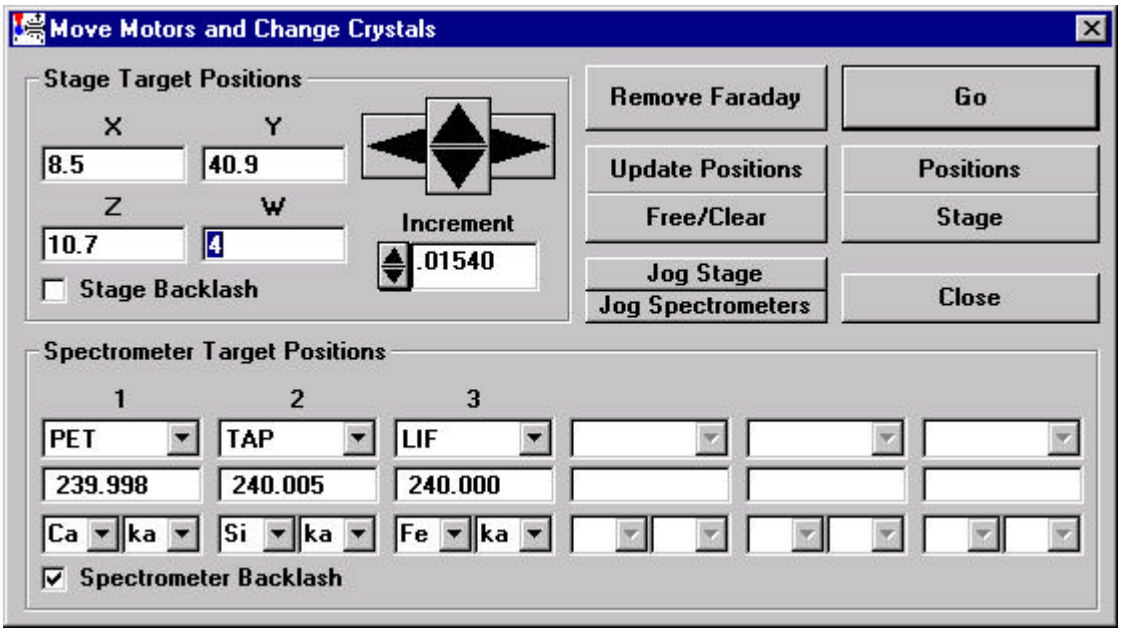
Click the **OK** button of the **FiducialSaveSelect** window.

The fiducial coordinate positions are recorded to disk and the **Digitize!** dialog box returns.



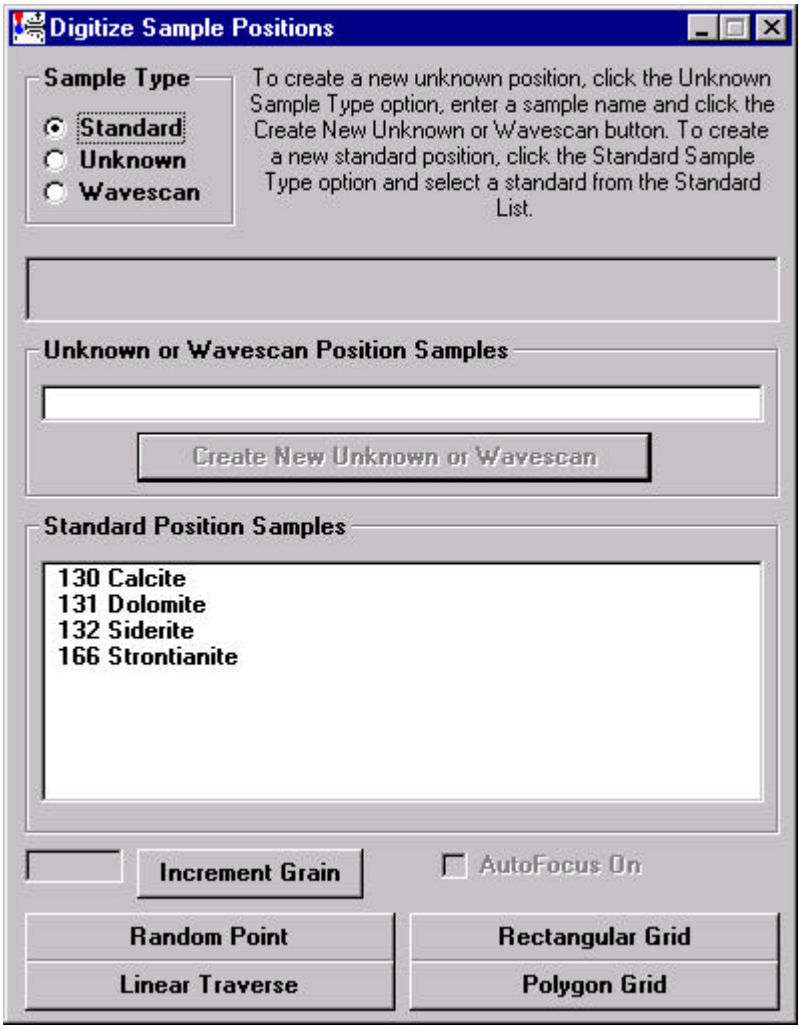
The position of each of the standards in this standard mount must now be digitized. Move to the first standard; either by turning the motor controls manually or using the joystick via the JOYWIN (Joystick Control for Stage and Spectrometers) program or use the **Move** button in the **Digitize!** window. Clicking the **Move** button opens the **Move Motors and Change Crystals** dialog box.

Type in the appropriate target coordinates in the *Stage Target Positions* boxes for the first standard. Use the <tab> key to move between entries.

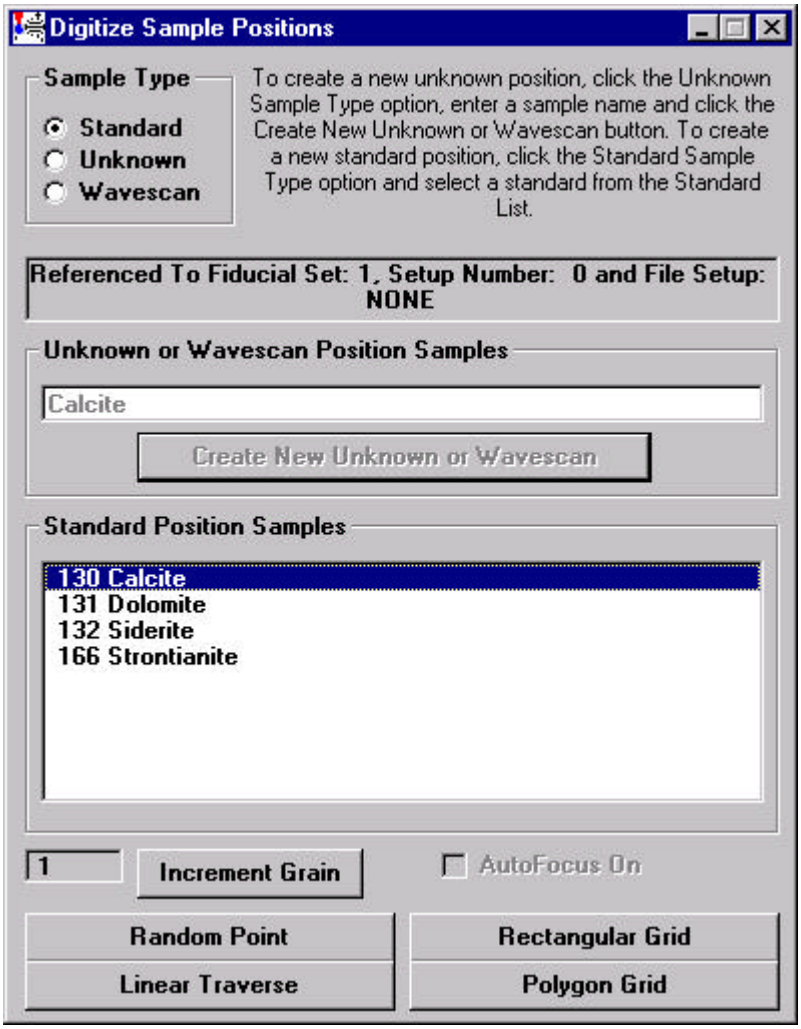


Click **Go** or press <Enter> on the keyboard, this will drive the stage to the target positions. Check the position and optical focus.

Click the **Digitize** button of the **Digitize!** dialog box. This activates the **Digitize Sample Positions** dialog box. The *Standard Position Samples* list box contains the standards already added to the run.

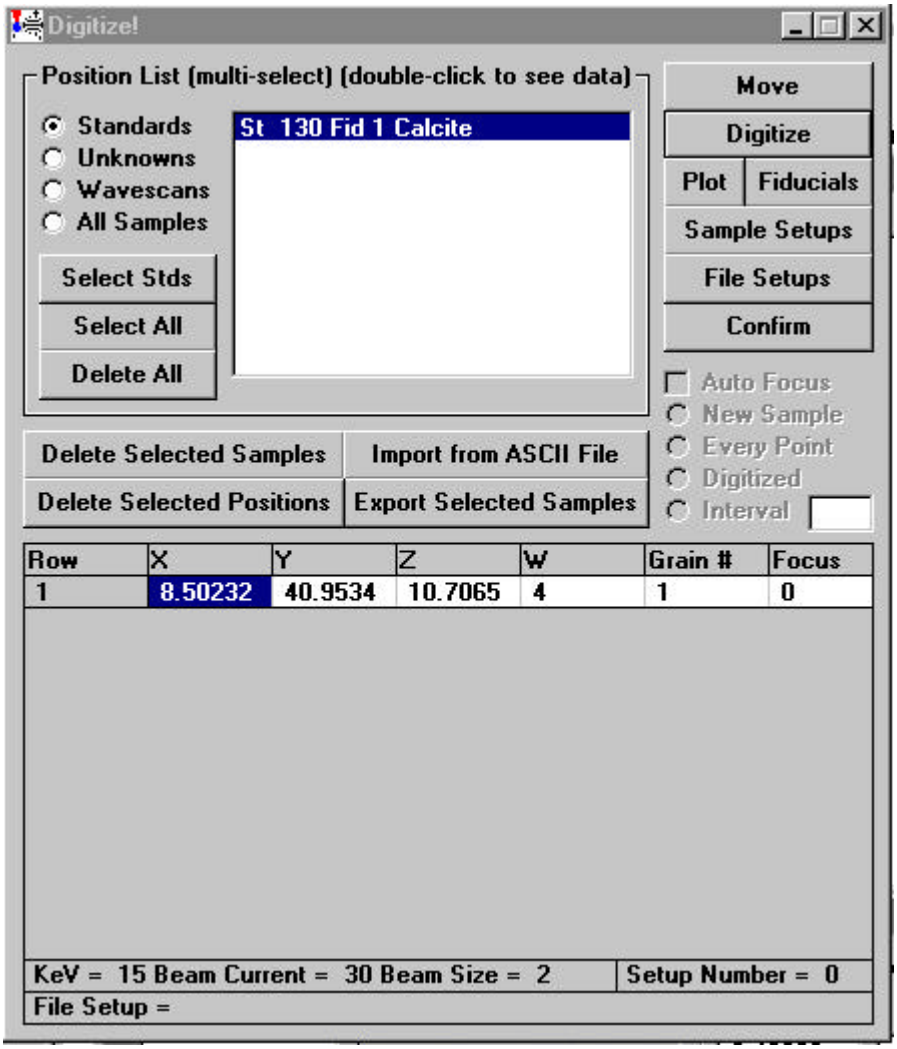


Select (highlight) the first standard to digitize from the *Standard Position Samples* list box. The standard will be added automatically to the **Digitize!** *Position List*.



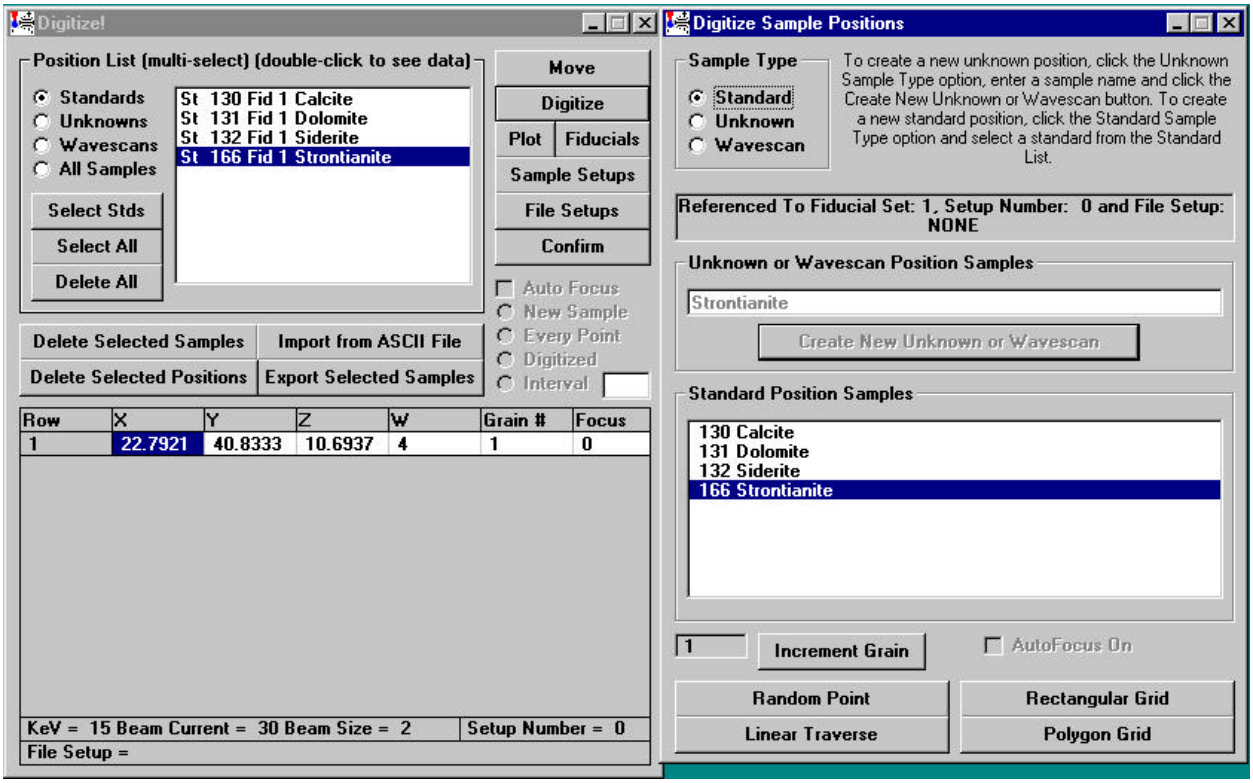
To digitize a random point on this standard, click the **Random Point** button of the **Digitize Sample Positions** dialog box to record the current coordinates (X, Y, Z, and W) for this grain.

The coordinates of this standard in the **Digitize!** dialog box, are seen below.



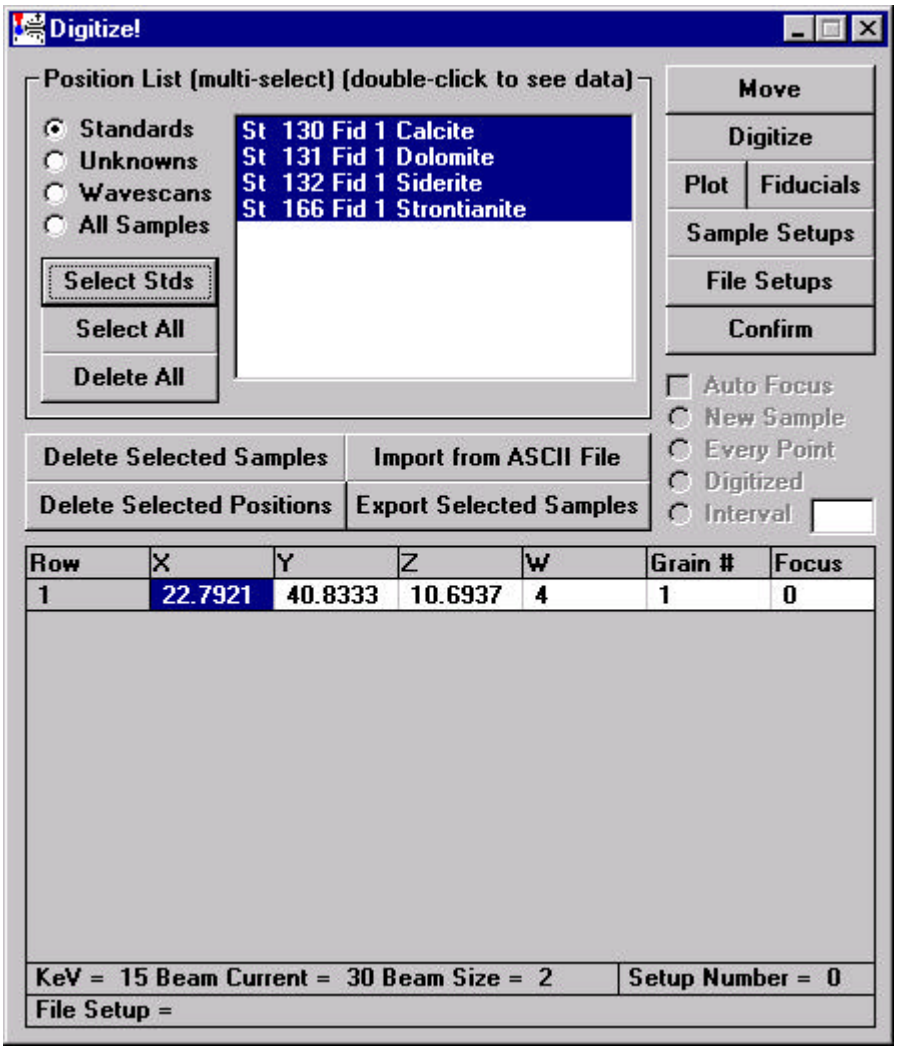
Note, that although only one position per standard need be digitized, if additional points are digitized, PROBE FOR WINDOWS will automatically utilize them. Otherwise, PROBE FOR WINDOWS will simply increment the stage X position for each additional acquisition required.

Move to the next standard, select the standard from the list box in the **Digitize Sample Position** window and click the **Random Point** button again. The standard position will be digitized. Continue until all of the remaining standards in the standard block are digitized. In this example the **Digitize!** and **Digitize Sample Positions** dialog boxes would appear as follows.



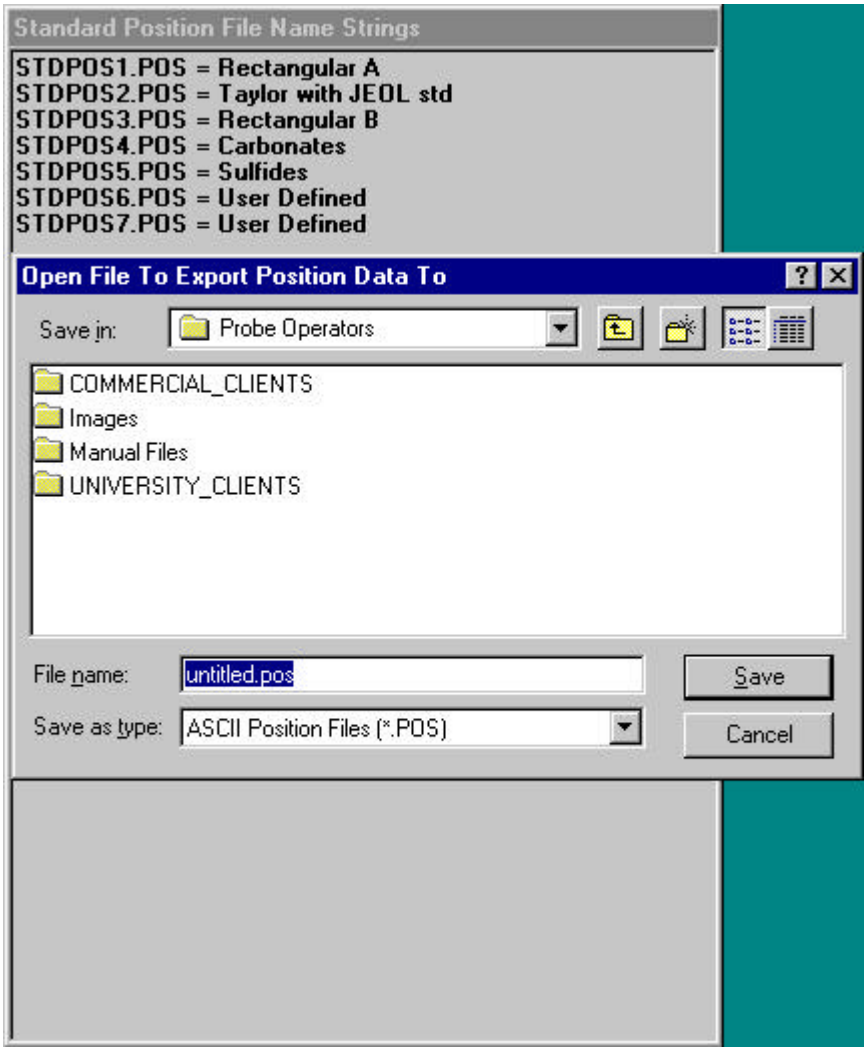
Close the **Digitize Sample Positions** dialog box by clicking the **Close** button in the upper right corner.

Finally, store the new pre-digitized standard coordinates to disk as an ASCII position file (.POS). Select all of the standards using the **Select Stds** button of the **Digitize!** dialog box.



Click the **Export Selected Samples** button.

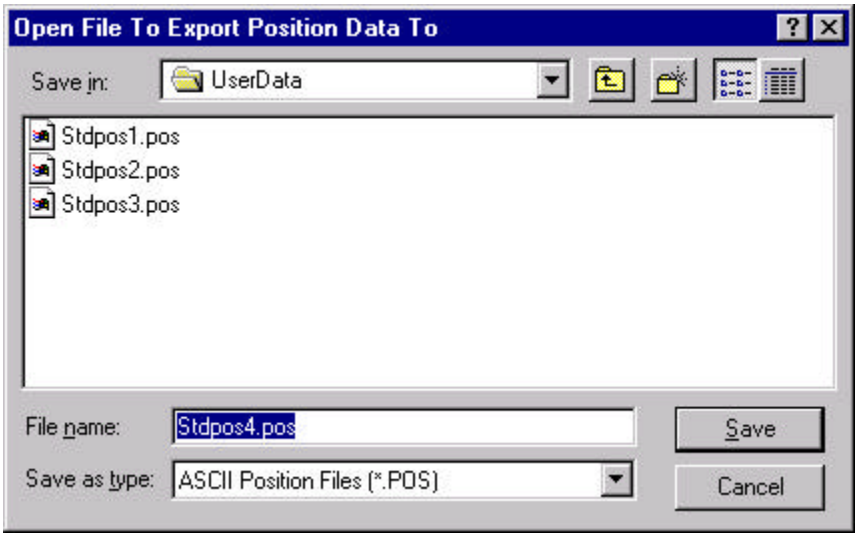
This action opens both the **Standard Position File Name Strings** and the **Open File To Export Position Data To** windows. The **Standard Position File Name Strings** listing is from the PROBEWIN.INI file. In this example the Carbonate Standard Block is designated as STDPOS4.POS.



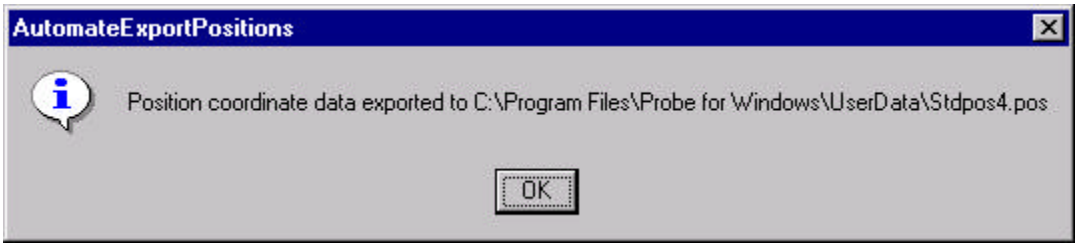
The default directory (set by Advanced MicroBeam Inc.) for the *Save in:* location is C:\Program Files\Probe for Windows\UserData. This is the normal location for *.POS files. The default *Save in:* location is specified by the UserDataDirectory keyword in the PROBEWIN.INI file.

At Washington University the default directory path was changed for convenience. For the export of position data files, edit the path to C:\Program Files\Probe for Windows\UserData.

Type in the appropriate *File name:* as designated in the **Standard Position File Name Strings** (from the PROBEWIN.INI file). Click the **Save** button of the **Open File To Export Position Data To** window.

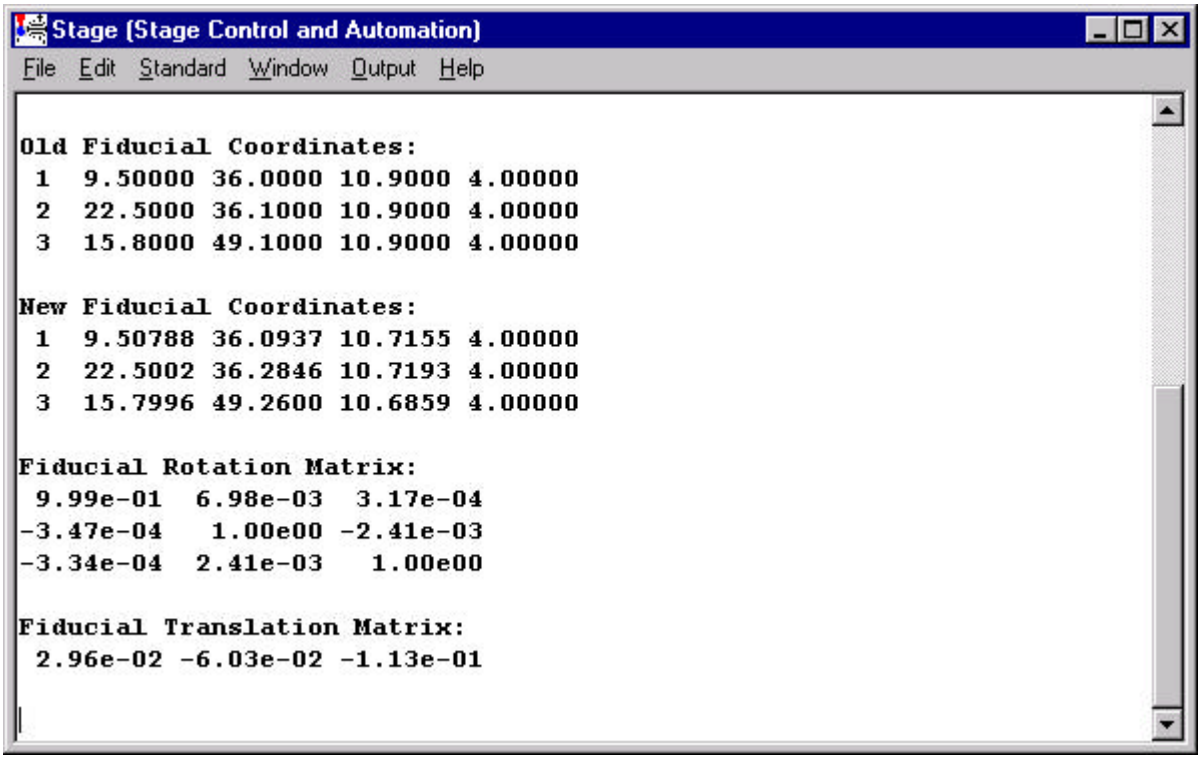


After the positions are written to disk, click the **OK** button to confirm the exported position coordinate data to disk in the **AutomateExportPositions** window.



Close the **Digitize!** dialog box by clicking the **Close** button.

Close STAGE by clicking the **File | Exit** menu.

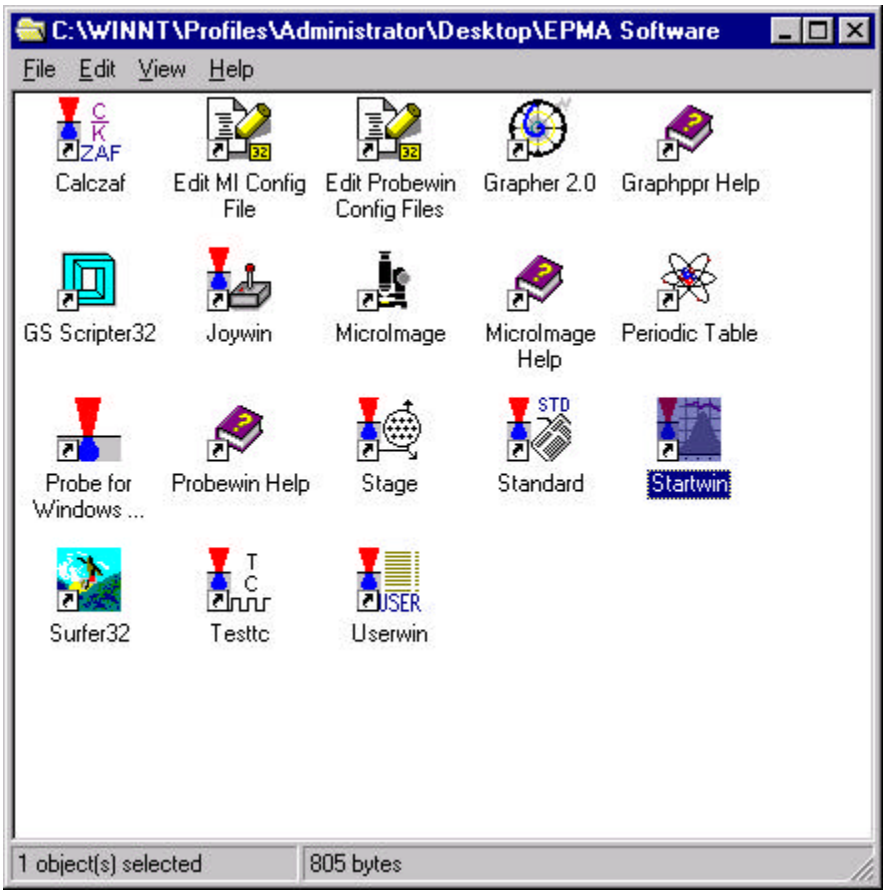


After digitizing all of the standards on the standard mounts and creating various STDPOSx.POS files, save these files to another directory and to a backup floppy.

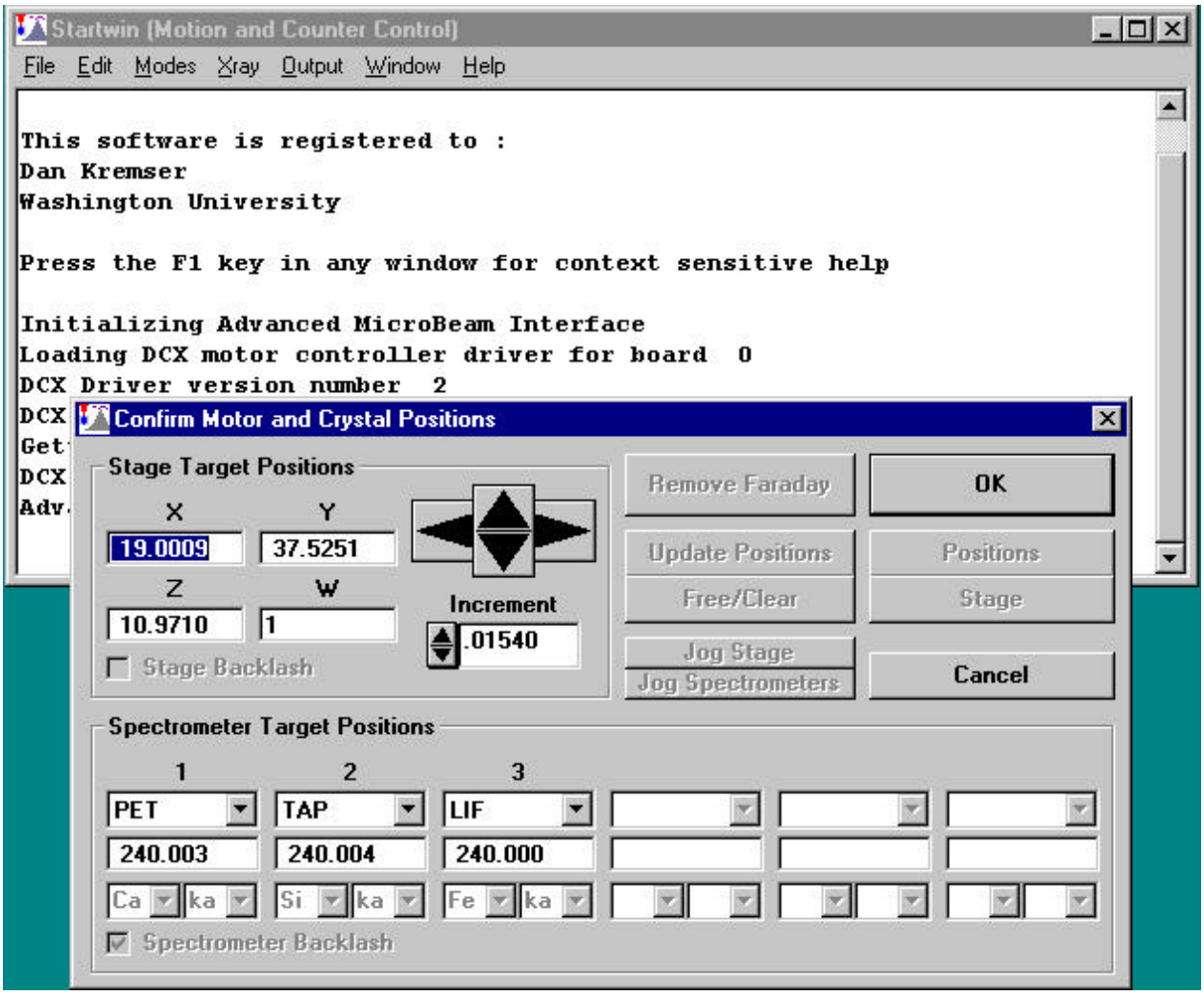
Beam and Detector Stability

Testing beam (drift) stability is an important step prior to acquiring any quantitative data. The following step-by-step procedure illustrates how to monitor and plot beam current with time.

From the Desktop, double click on the yellow EPMA Software folder. Then, double click on the **Startwin** icon in the EPMA Software group.

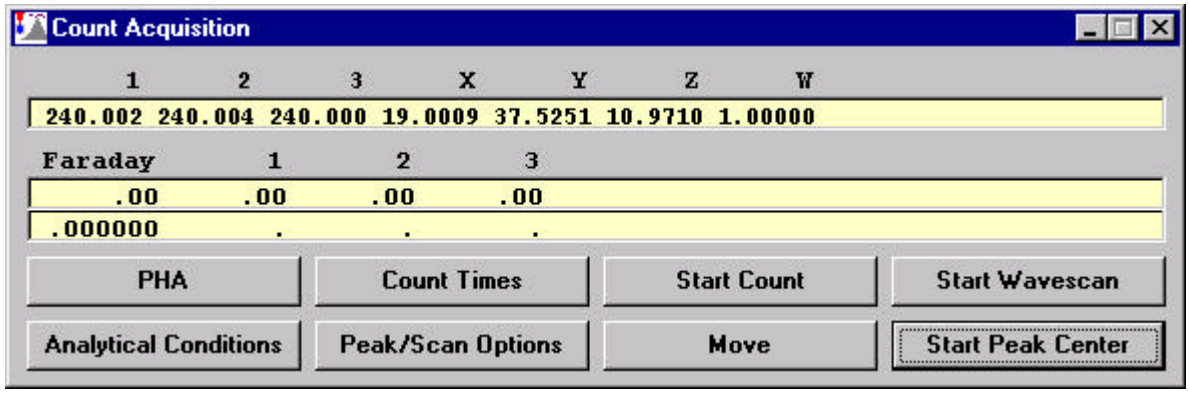


This action launches the STARTWIN (Motion and Counter Control) program and brings up the **Confirm Motor and Crystal Positions** dialog box. Confirm that all of the motors (stage and spectrometer positions) and crystal designations are correctly calibrated. If there is disagreement between the mechanical positions (actual) and the software values, adjust the software values. Use the <tab> key to move between the various *Target Positions* boxes.

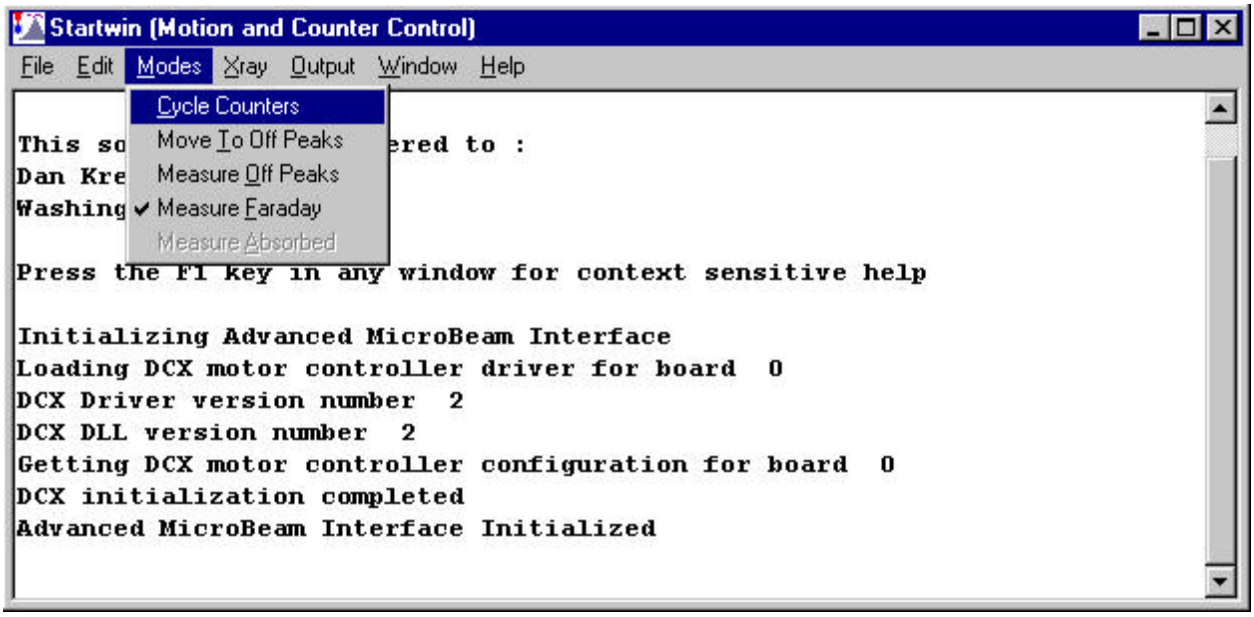


Click the **OK** button to close the **Confirm Motor and Crystal Positions** dialog box when done.

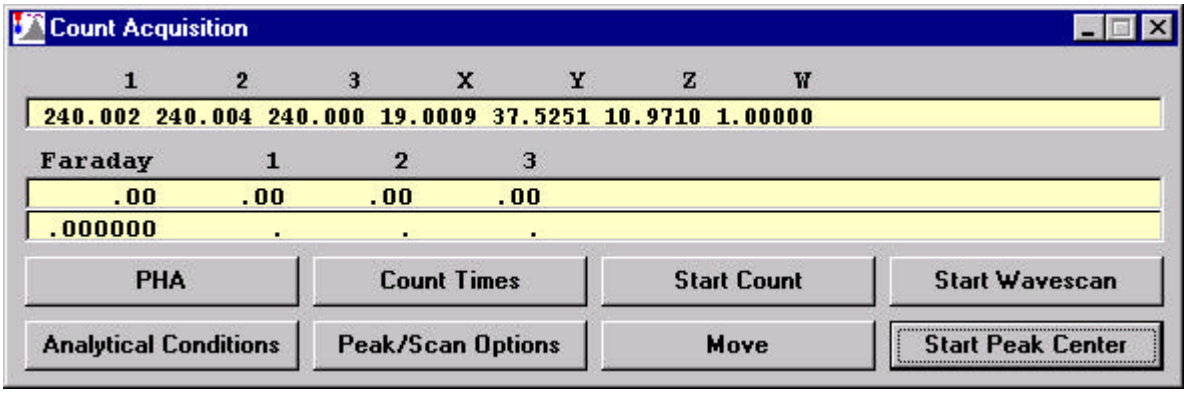
The **Count Acquisition** window opens.



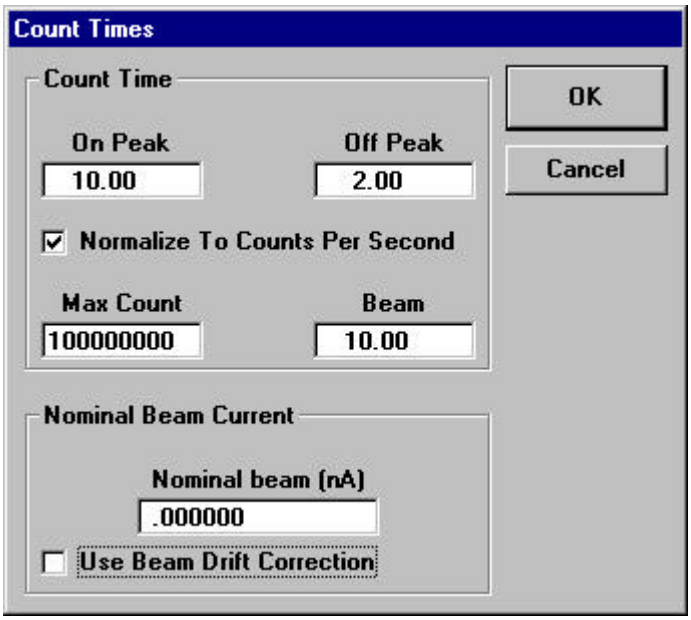
From the STARTWIN log window, select **Modes** from the menu bar and click on **Cycle Counters** from the menu choices. The **Measure Faraday** menu should also be selected.



Next, click the **Count Times** button in the **Count Acquisition** window.

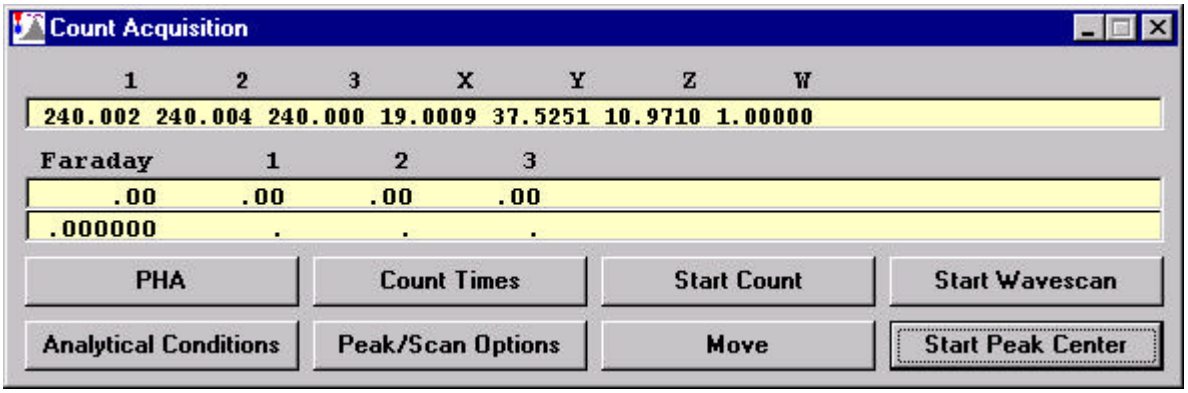


This opens the **Count Times** dialog box. Choose an *On Peak* count time, this will be the interval of time between successive beam measurements. Finally, disable the beam drift correction, confirm that the *Use Beam Drift Correction* box is unchecked.



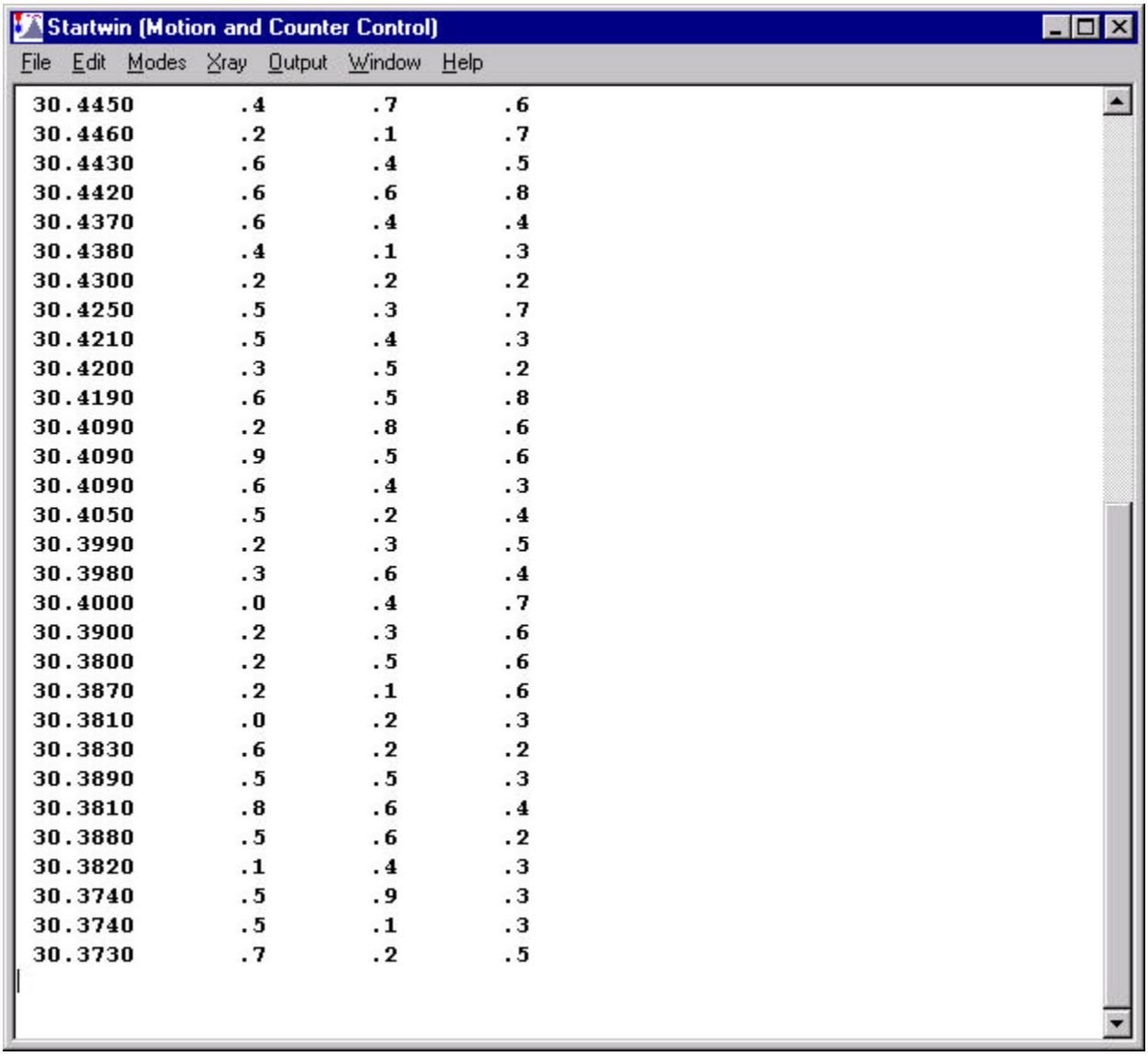
Click the **OK** button returning to the **Count Acquisition** window.

Click the **Start Count** button to initiate a continuous cycle of beam current measurements. In this example, a ten second scalar count will be done followed by a Faraday current measurement. This process repeats until the user cancels the loop.

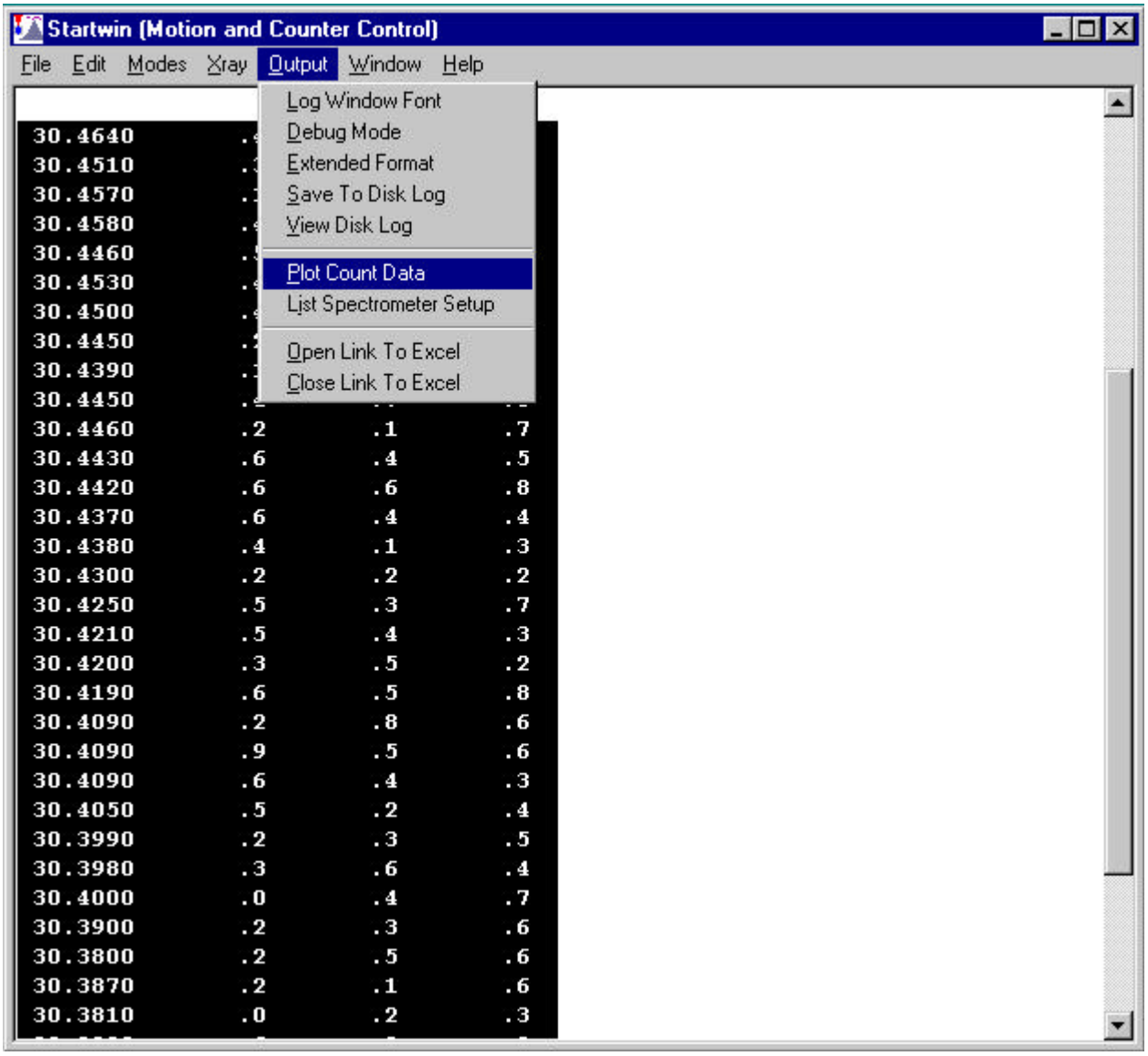


When the user has acquired a suitable number of beam current measurements, click the **Cancel** button in the **Automation Status** window to stop the acquisition cycle.

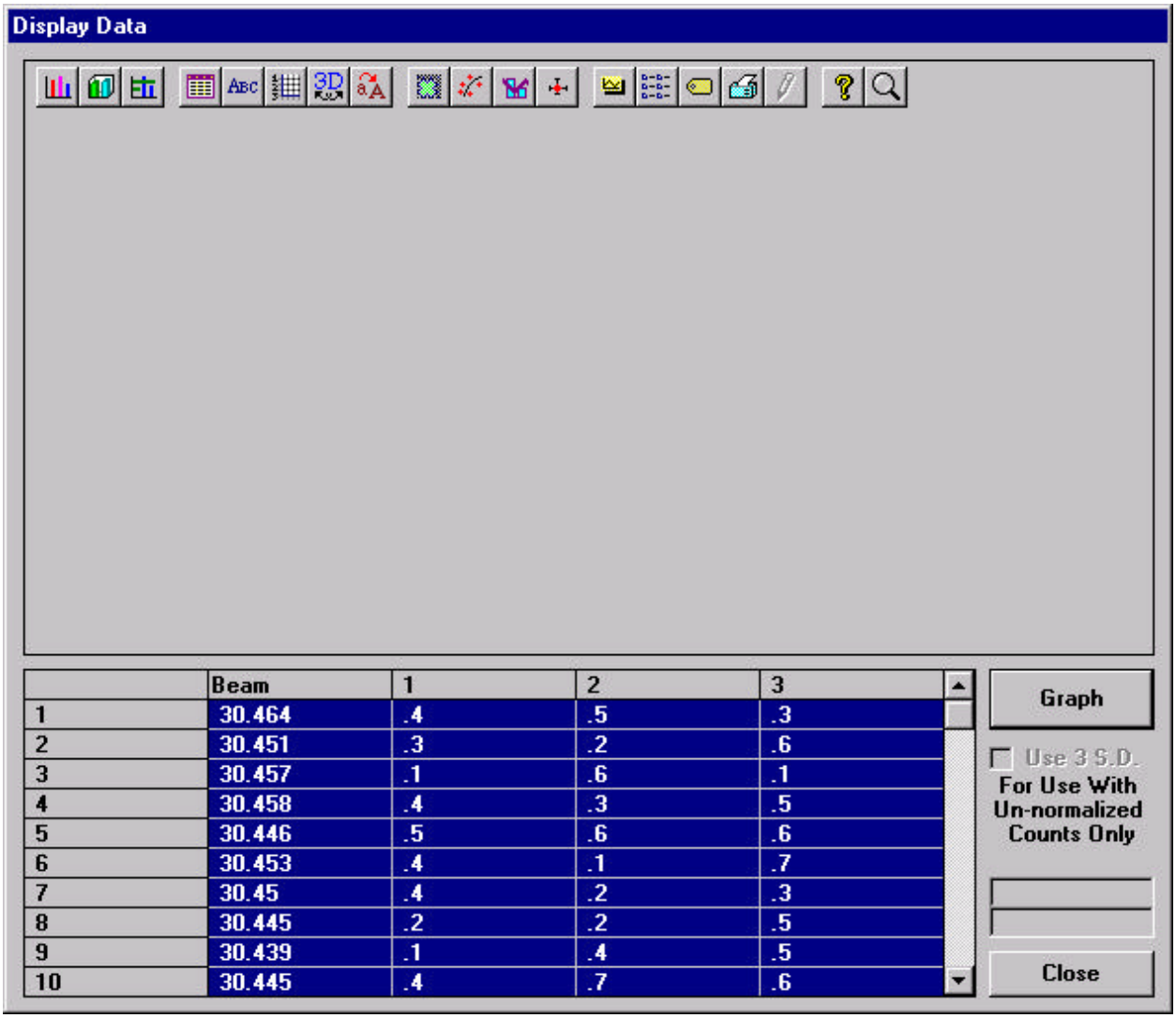
The STARTWIN log window will contain the beam current data acquired so far (in this example, reported in nanoamps). The other three columns represent counts in counts per second acquired by each spectrometer with the beam blanked (essentially detector/electronics noise).



Evaluating the trend between beam current and time may best be viewed in graphical format rather than in looking at a long series of numbers. Use the mouse to select the data set to graph. Then, select **Output** from the menu bar and click **Plot Count Data** from the drop-down menu choices.



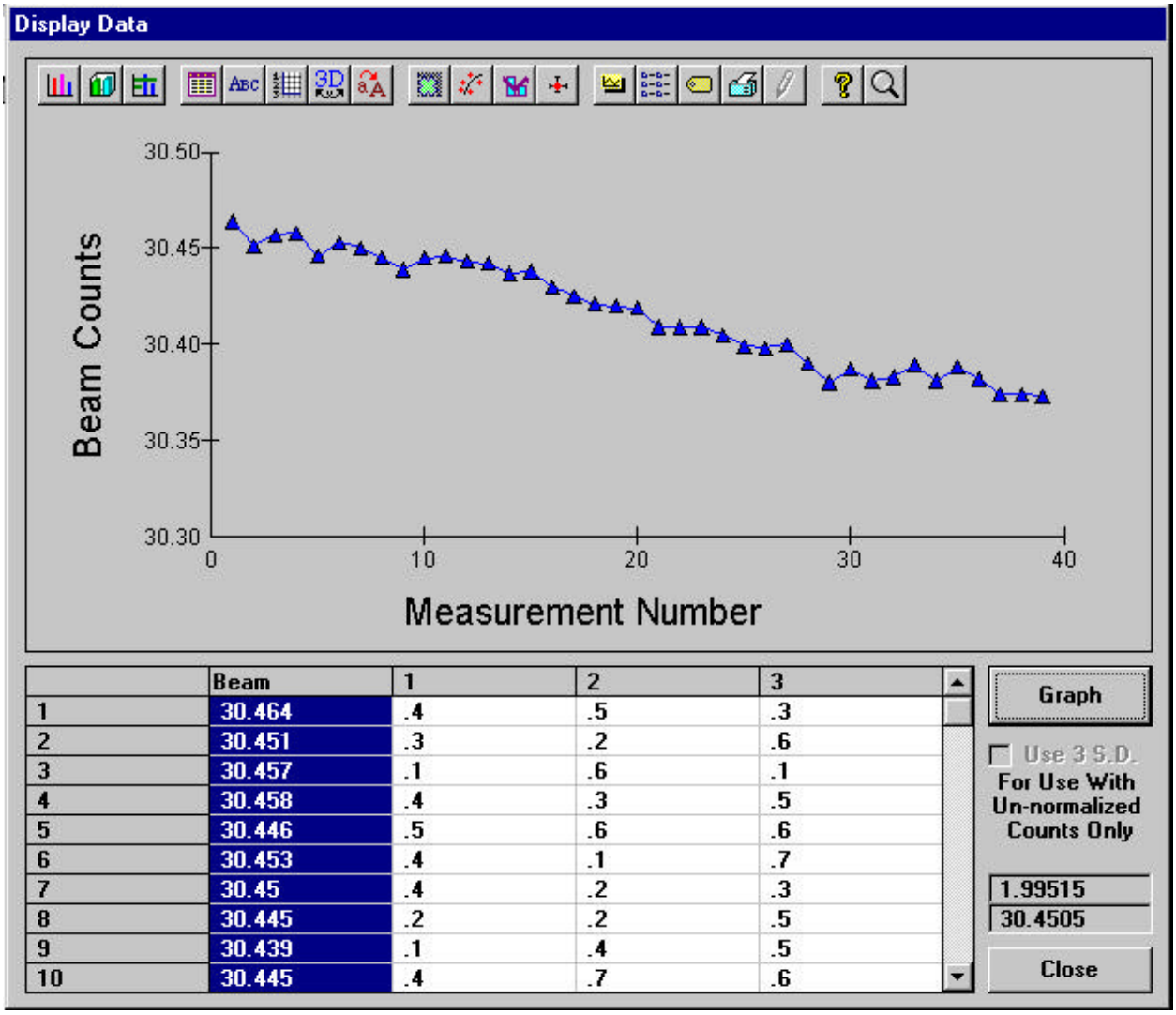
This opens the **Display Data** window.



	Beam	1	2	3
1	30.464	.4	.5	.3
2	30.451	.3	.2	.6
3	30.457	.1	.6	.1
4	30.458	.4	.3	.5
5	30.446	.5	.6	.6
6	30.453	.4	.1	.7
7	30.45	.4	.2	.3
8	30.445	.2	.2	.5
9	30.439	.1	.4	.5
10	30.445	.4	.7	.6

While all data columns were selected by the mouse operation previously, the user may plot a single column of data by clicking the column label of the desired data and then clicking the **Graph** button.

Below, Beam Counts versus Measurement Number (time) are graphed and the overall beam stability with time may be judged.



	Beam	1	2	3
1	30.464	.4	.5	.3
2	30.451	.3	.2	.6
3	30.457	.1	.6	.1
4	30.458	.4	.3	.5
5	30.446	.5	.6	.6
6	30.453	.4	.1	.7
7	30.45	.4	.2	.3
8	30.445	.2	.2	.5
9	30.439	.1	.4	.5
10	30.445	.4	.7	.6

Click the **Close** button to return to the STARTWIN log window.

Brass Alloy Run

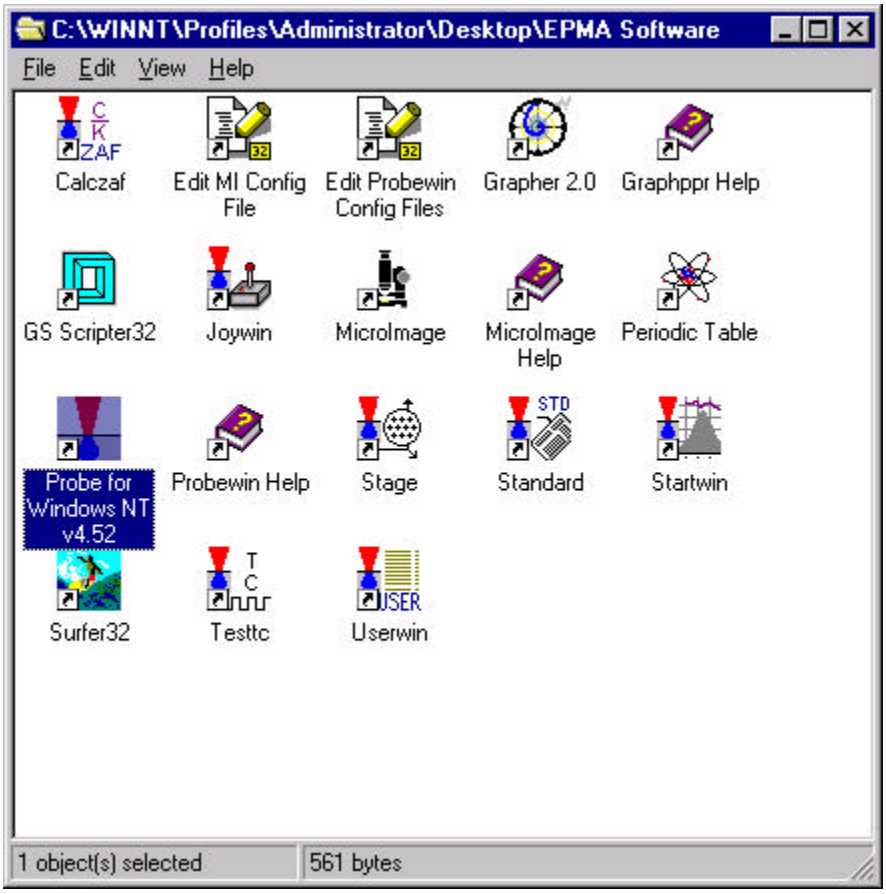
Introduction

This document illustrates step by step how to set up a new PROBE FOR WINDOWS quantitative run and how to analyze an unknown two element alloy sample. This documentation was produced on a three spectrometer JEOL 733 electron microprobe. Your particular run may look very different depending on the specific configuration of your microprobe. This document should be used in conjunction with the User's Guide and Reference documentation and on-line help.

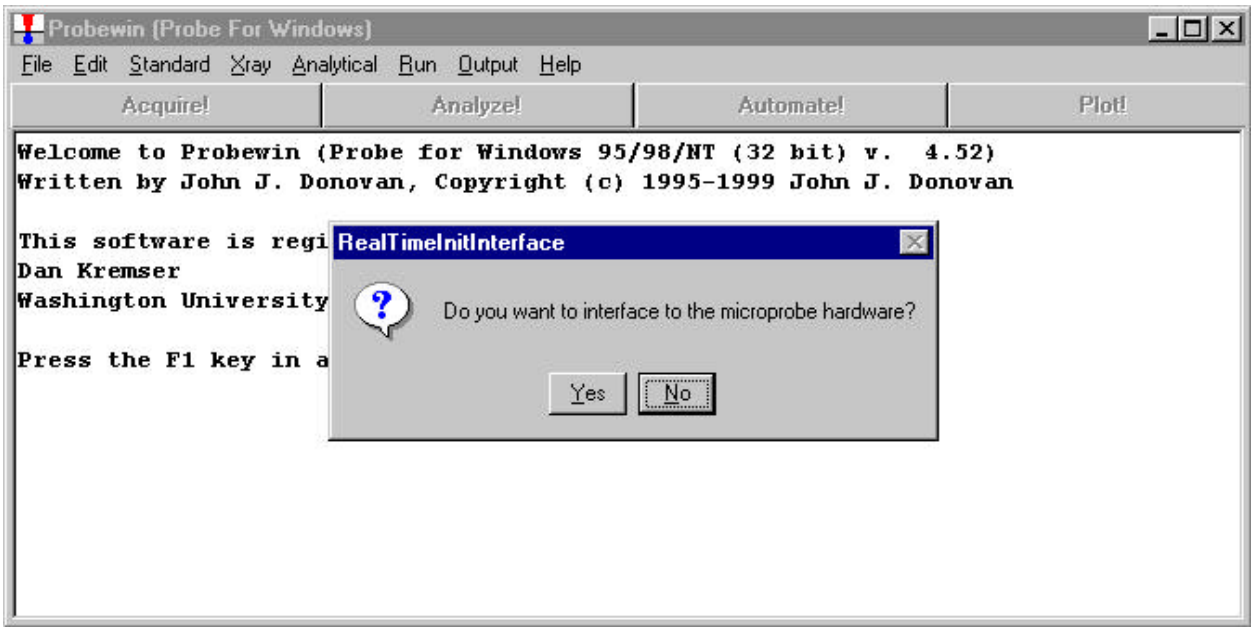
This run will demonstrate some of the basic features of the PROBE FOR WINDOWS program. These include the use of manual and automated spectrometer peaking, manual and automated standard count acquisition and manual unknown sample acquisition. The use of pre-digitized standard positions, the unique wavescan option, off-peak adjustment capabilities and data output methods will be illustrated.

Opening Probe for Windows

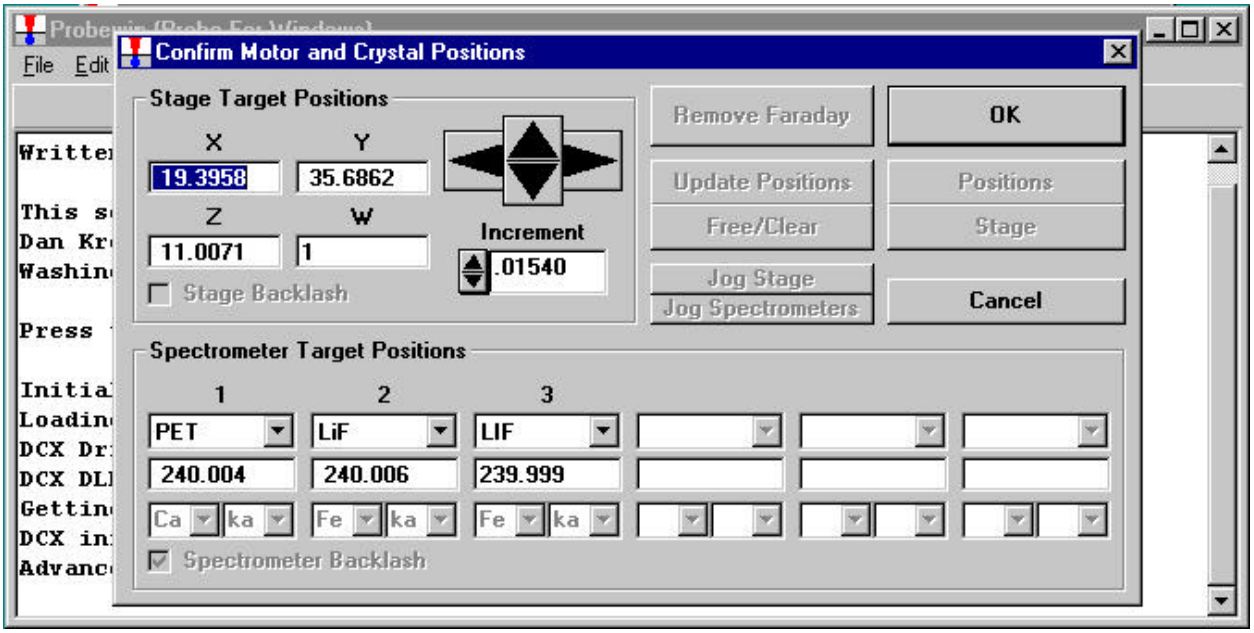
From the Desktop, double-click on the yellow EPMA Software folder opening the EPMA Software group. Double click on the **Probe for Windows …** icon.



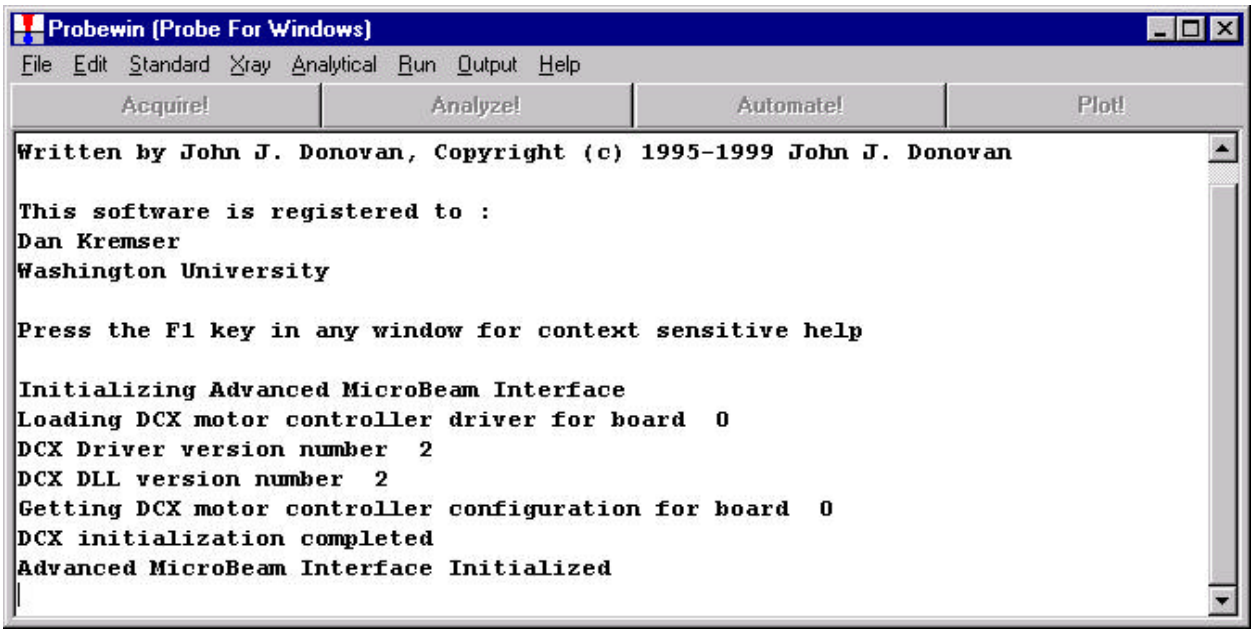
Upon launching PROBEWIN (PROBE FOR WINDOWS), the main log window appears along with the **RealTimeInitInterface** window as illustrated below. To collect real time data click the **Yes** button. The program can also be run off-line without the microprobe interface to re-process previously acquired data or on another computer.



This action causes the **Confirm Motor and Crystal Positions** dialog box to open. Confirm that all of the motors (stage and spectrometer positions) and crystal designations are correctly calibrated. If there is disagreement between the mechanical positions (actual) and the software values, adjust the software values. Use the <tab> key to move between the *Target Positions* text boxes. Click the **OK** button after you have finished to close the **Confirm Motor and Crystal Positions** dialog box.

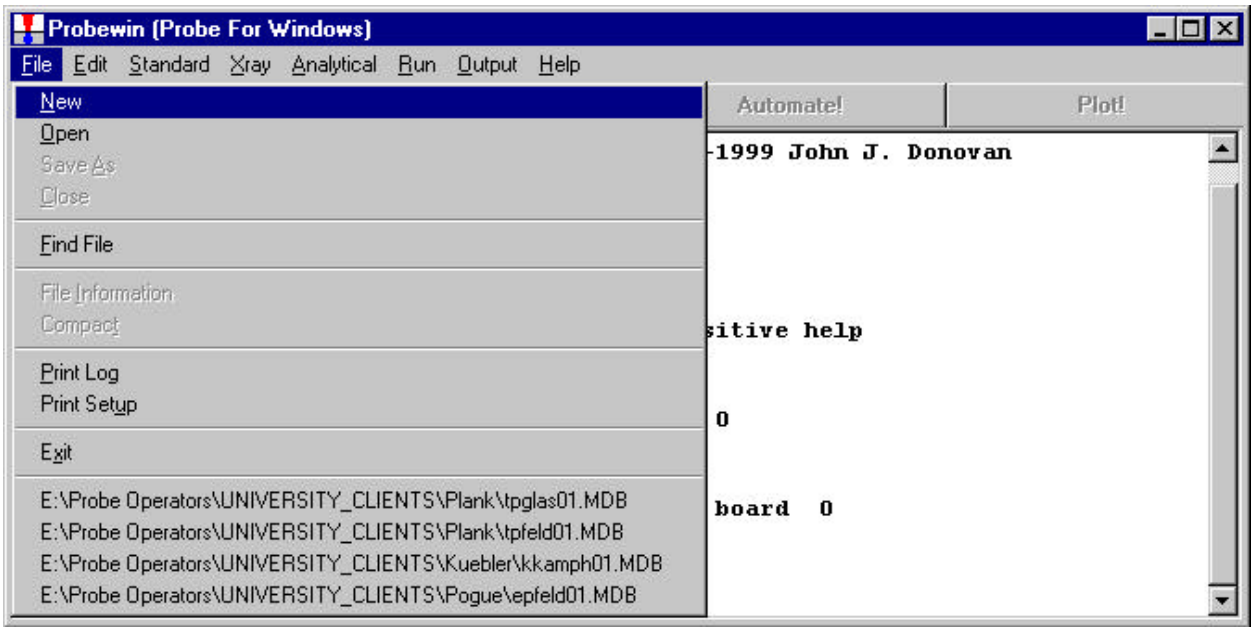


The main PROBE FOR WINDOWS log window is now visible as seen below.

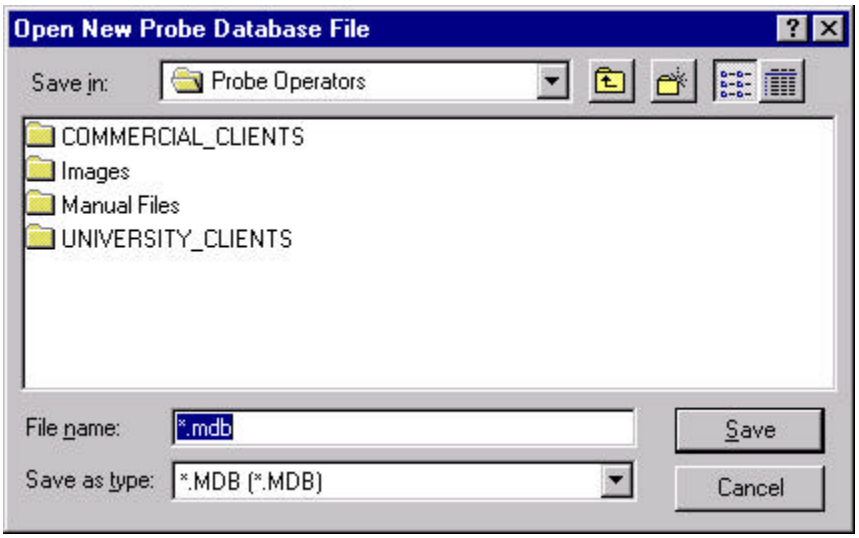


Creating a New Run

To create a new sample run, select **File** from the menu bar and click **New** from the menu.



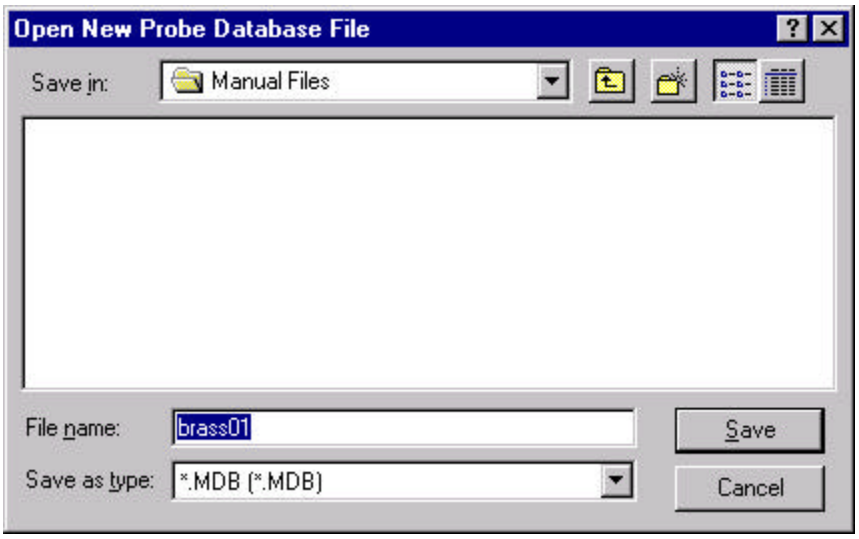
The **Open New Probe Database File** dialog box opens.



Change the *Save in:* location (directory) if desired and type an appropriate run name into the *File name* text box.

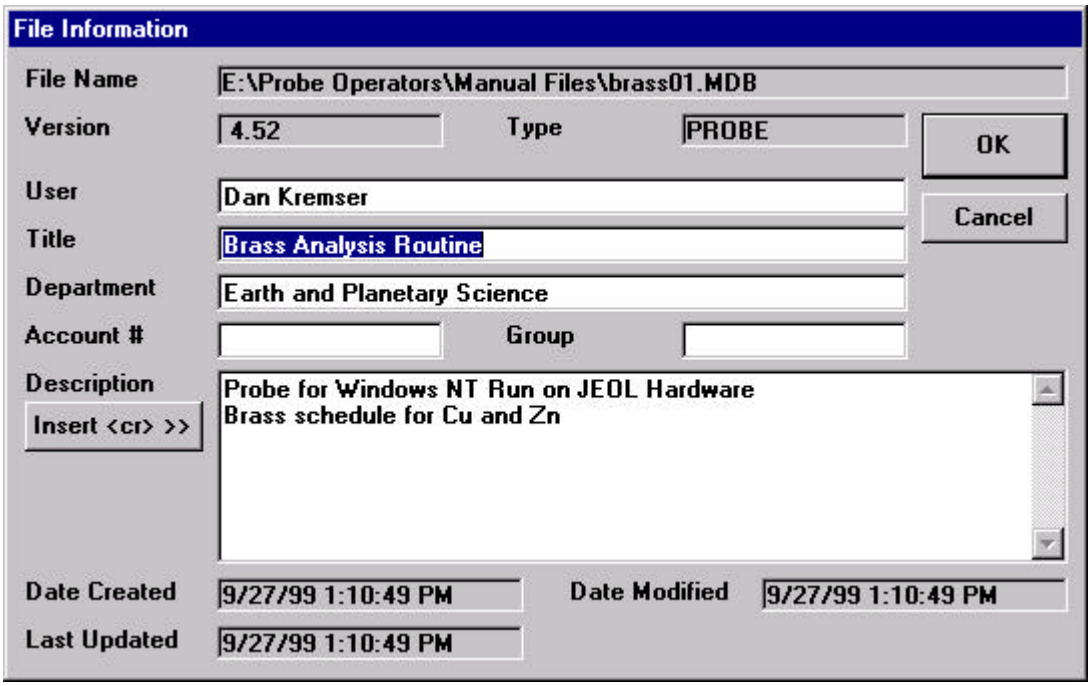
The initial *Save in:* location is specified by the UserDataDirectory keyword in the PROBEWIN.INI file. File names longer than 8 characters are now supported.

The screen capture of the first window in this section indicates that other probe runs (previous four listed) are already established. Any of the existing old runs maybe re-opened to acquire additional data or used as a "setup" file for starting a new run. In this example, a new file designated BRASS01.MDB will be created in the Manual Files directory.

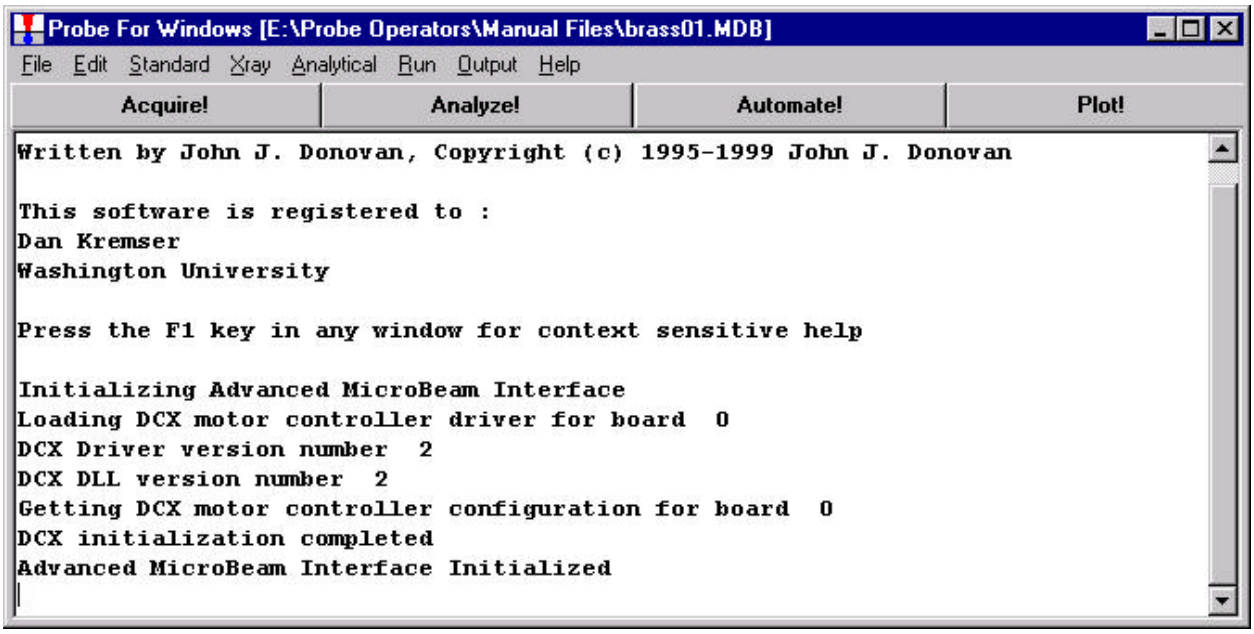


Close the **Open New Probe Database File** window by clicking the **Save** button. This action opens the **File Information** dialog box.

Enter the relevant information for the new run into the *User*, *Title*, and other *Description* text boxes. Use the <tab> key to move between text boxes. When finished, click the **OK** button.



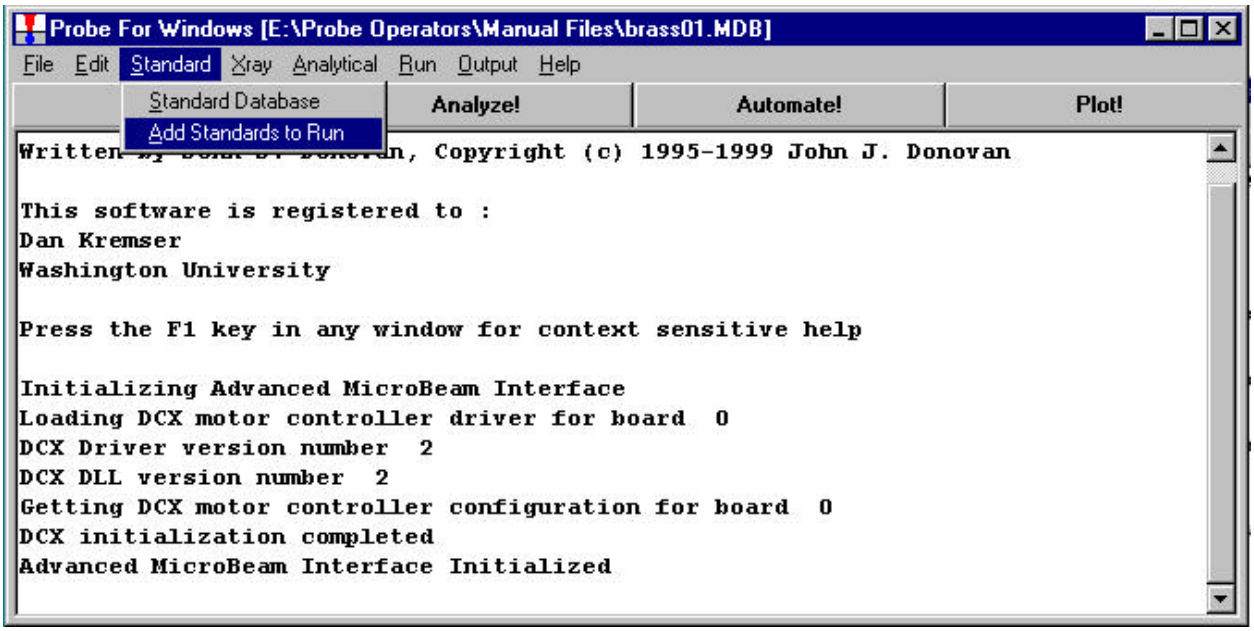
This returns the program to the main PROBE FOR WINDOWS log window. Now the four main Probe buttons: **Acquire!**, **Analyze!**, **Automate!**, and **Plot!** become active.



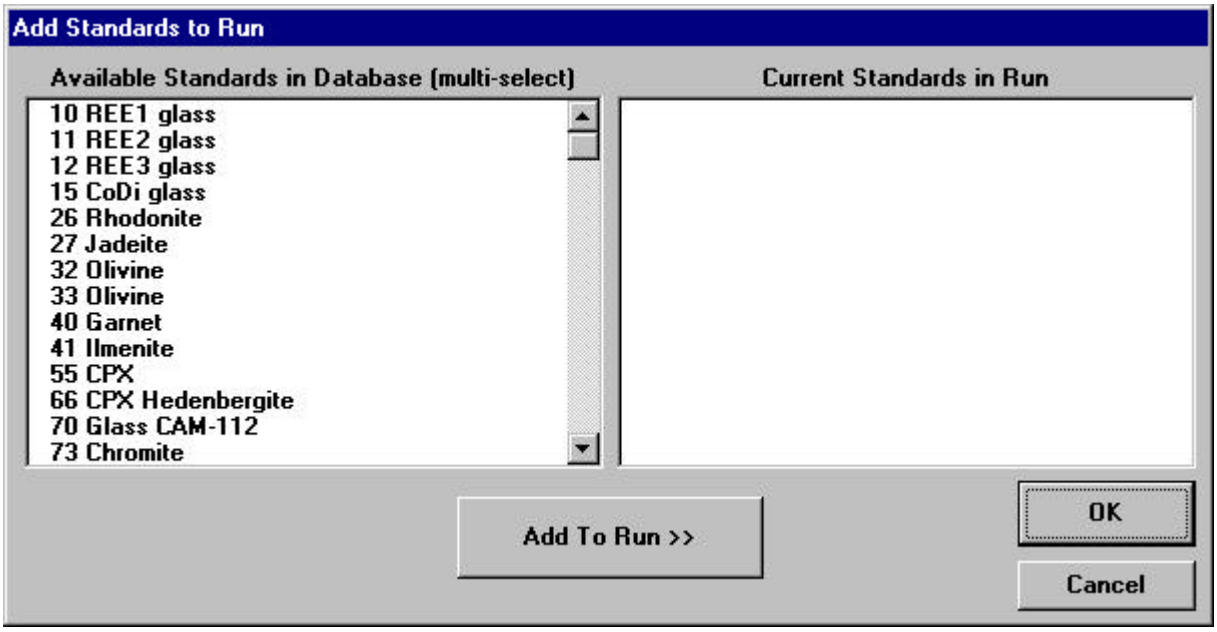
Parameter Initialization

Analytical Standard Selection

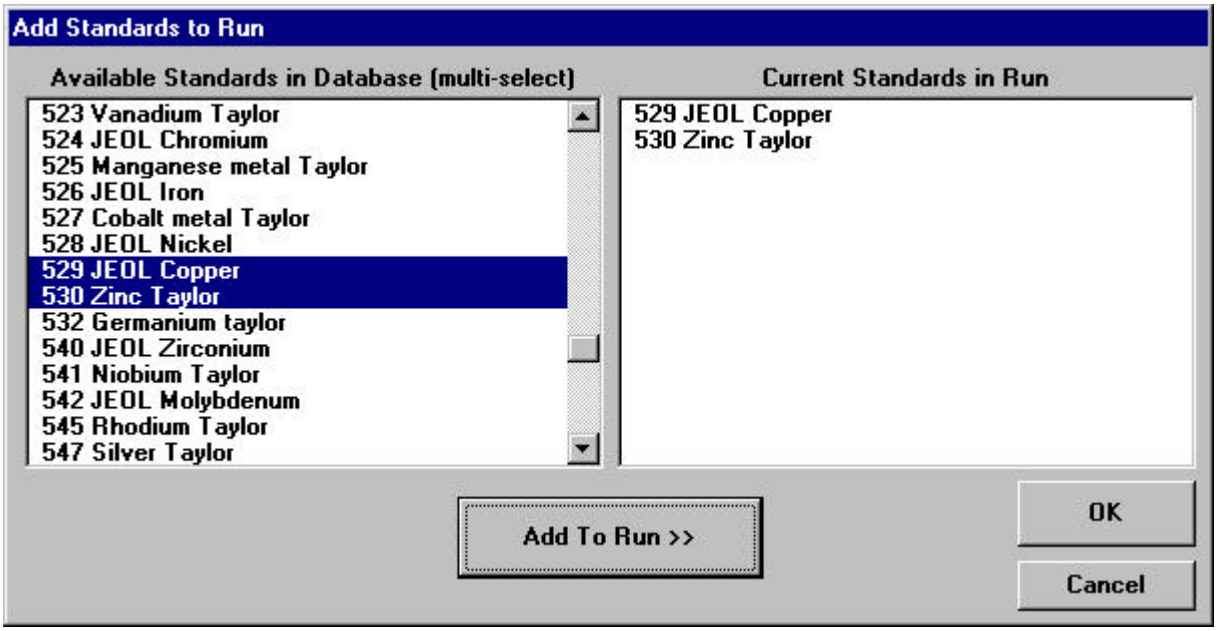
Select the analytical standards to be used in the new probe run. From the main PROBE FOR WINDOWS log window, click **Standard** from the menu bar and select **Add Standards to Run** from the menu.



This opens the **Add Standards to Run** dialog box.



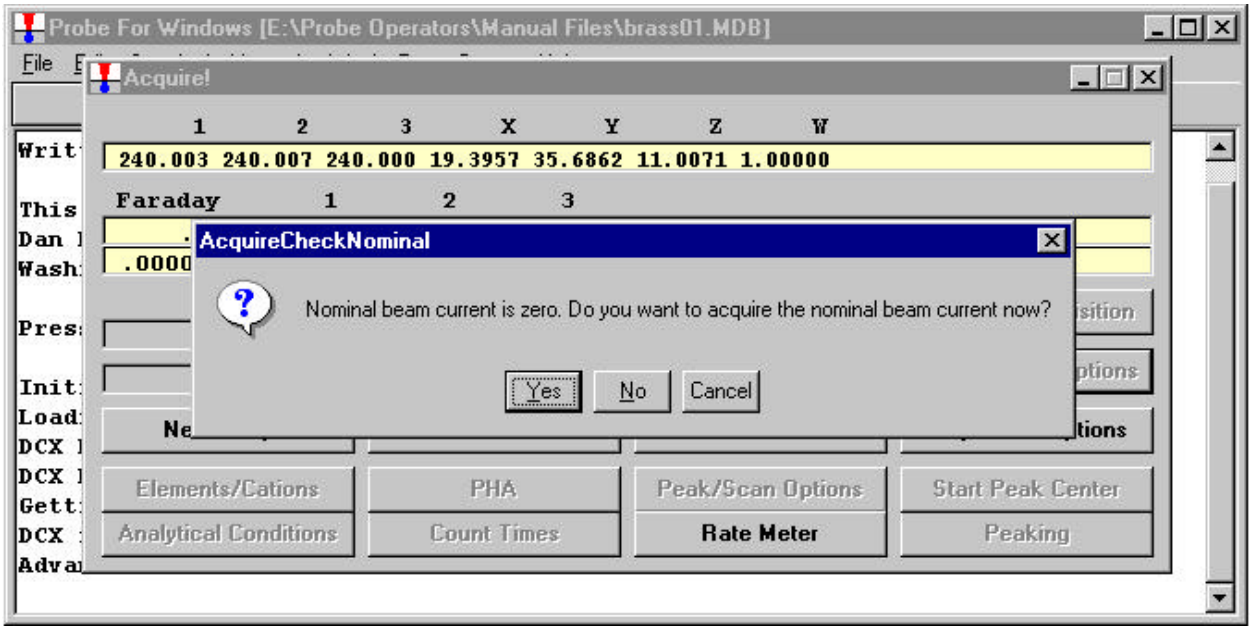
All previously entered standards in the default standard database are accessible. Scroll through the *Available Standards in Database* list box to find the copper and zinc metal standards to be used in this run. Select each and click the **Add To Run** >> button to add each to the *Current Standards in Run* list box.



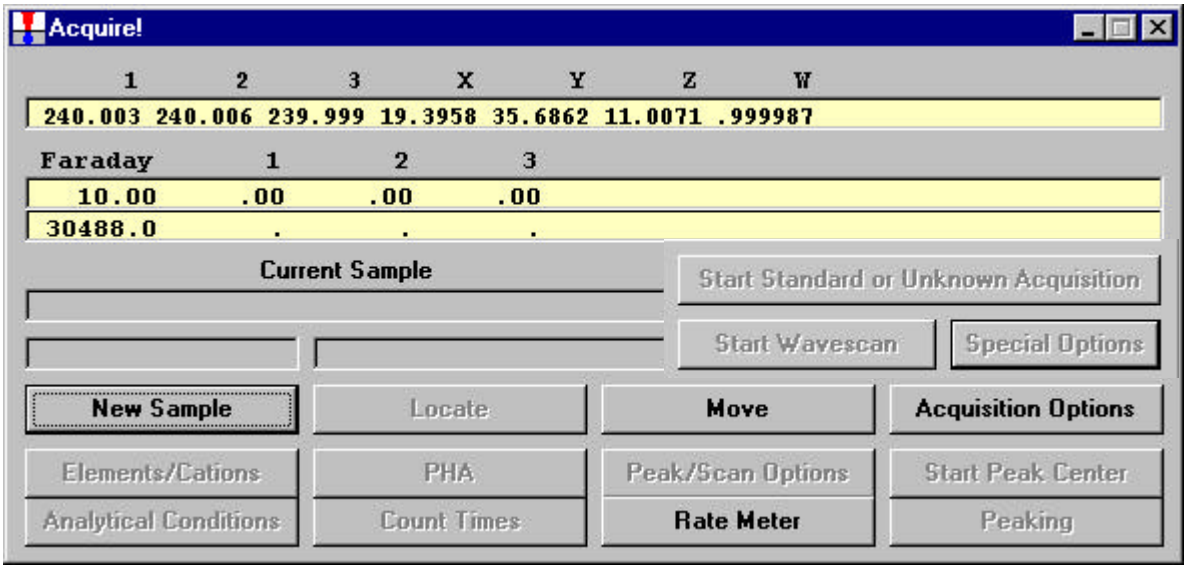
Click the **OK** button of the **Add Standards to Run** window when finished selecting standards. This returns the program to the main log window.

Nominal Beam Current Measurement

Click the **Acquire!** button. This action opens both the **Acquire!** dialog box and the **AcquireCheckNominal** window for the determination of the nominal beam current.

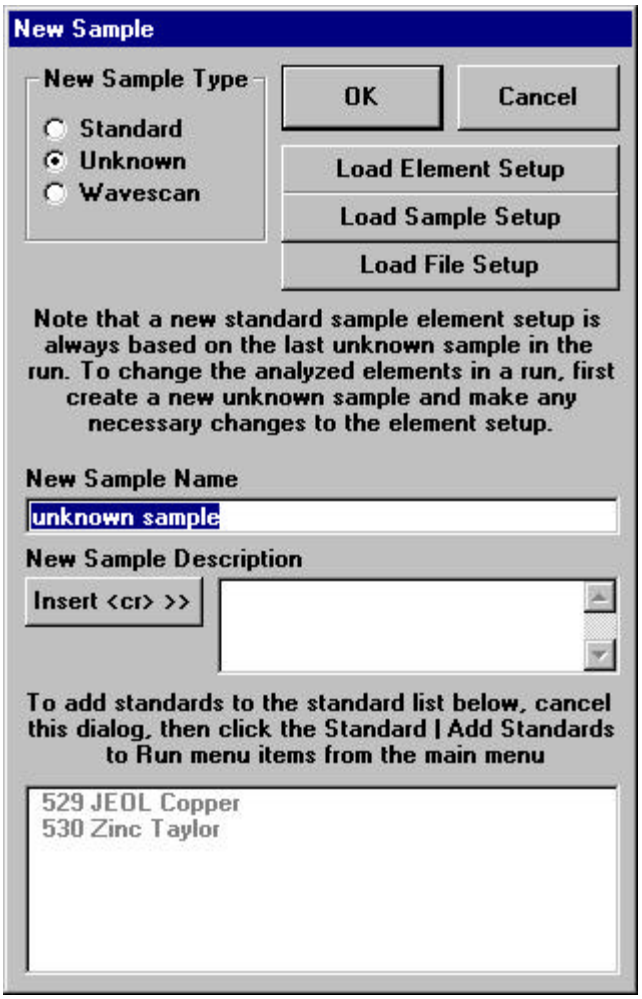


Click the **Yes** button of the **AcquireCheckNominal** window to establish a reference beam current reading. The beam (Faraday Cup counts on a JEOL 733 microprobe) is then measured. In this example the Faraday reading was taken for 10 seconds and recorded 30488 counts or 30.488 nA of beam current.

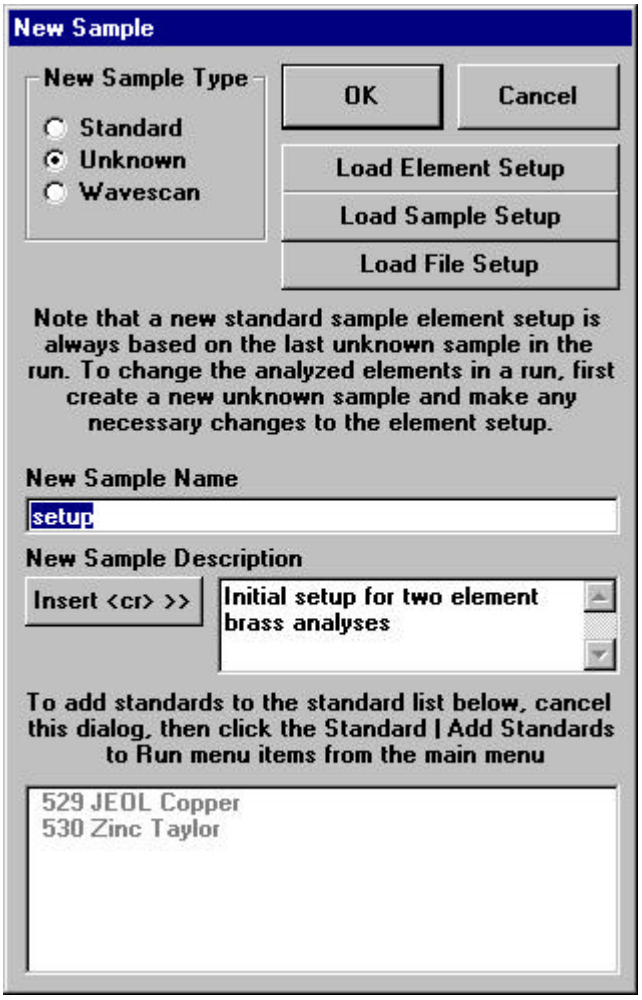


Creating a New Sample

Click the **New Sample** button of the **Acquire!** dialog box. This opens the **New Sample** dialog box.

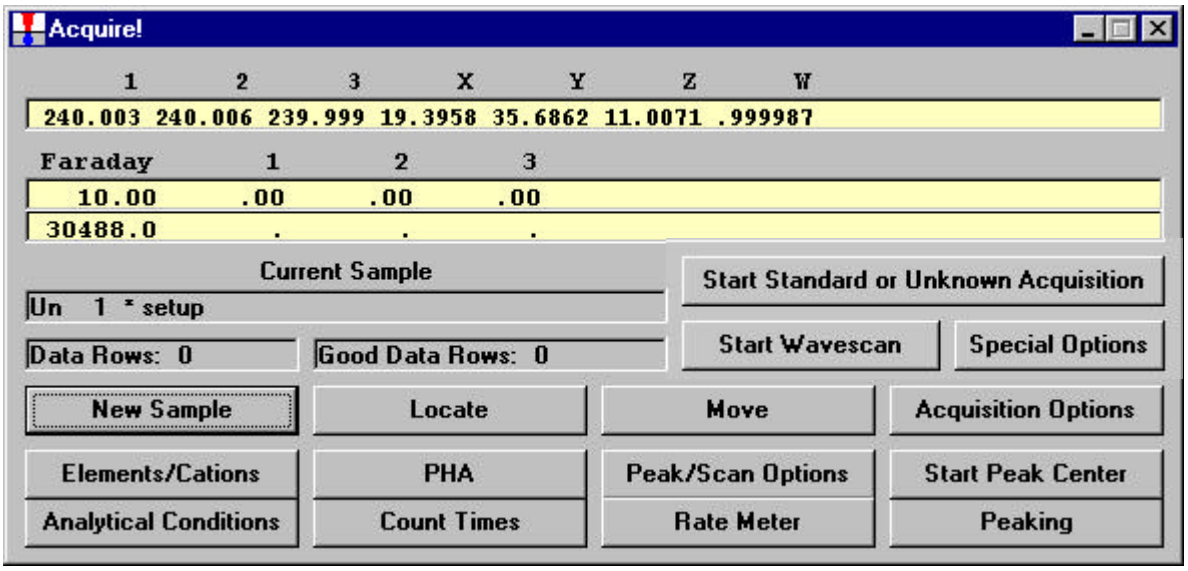


Select *Unknown* from the *New Sample Type* buttons. Type an appropriate sample name and description into the *New Sample Name* and *New Sample Description* text boxes. This first sample will be used as a "template", only to establish the analysis parameters.



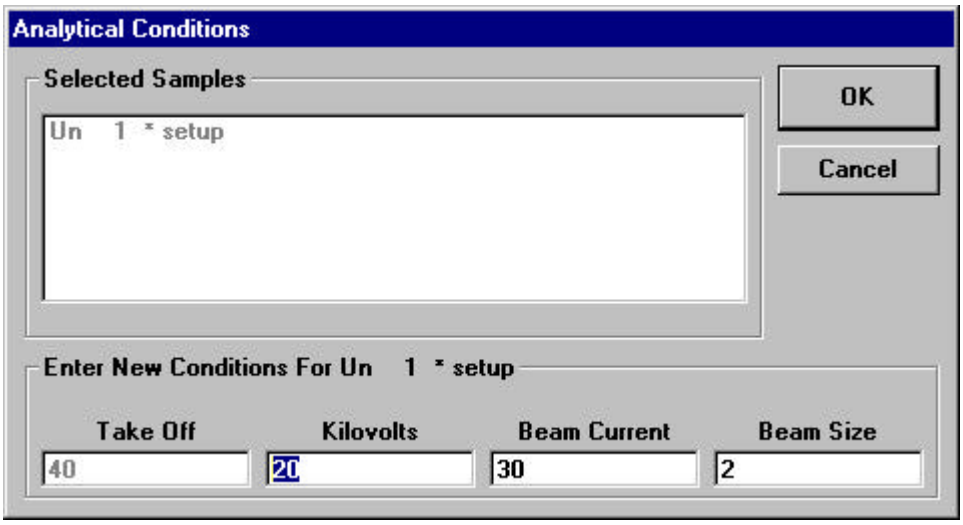
Click the **OK** button of the **New Sample** dialog box.

The program returns to the **Acquire!** window. Notice that the first sample designated *Un 1 * setup* is now listed in the *Current Sample* text box. The * symbol indicating that no data has been collected for this sample yet.



Setting Analytical Conditions

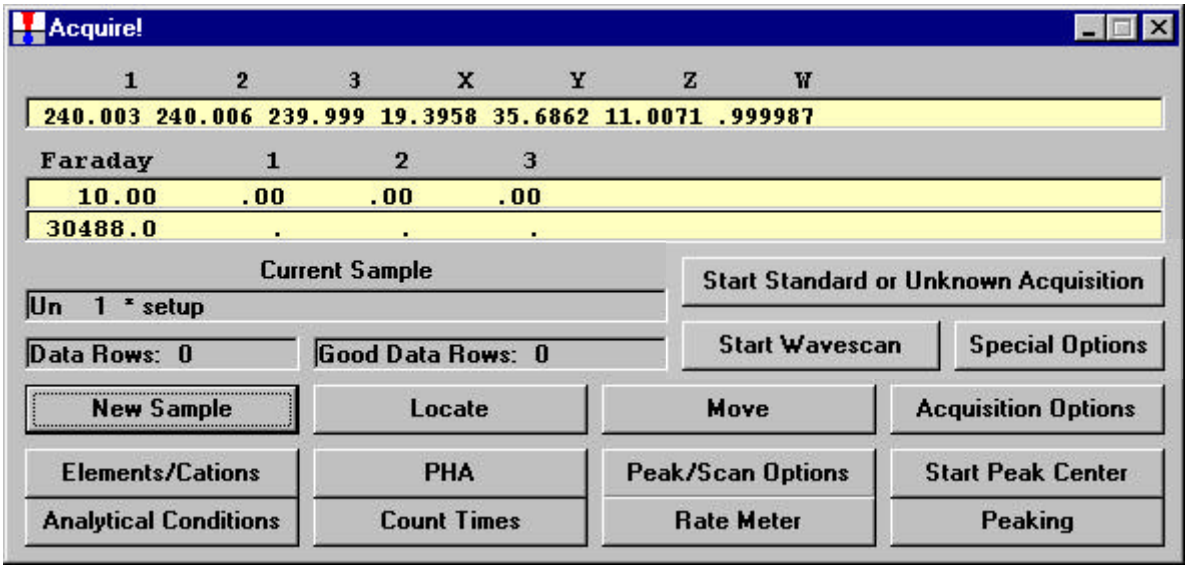
Click the **Analytical Conditions** button to open the **Analytical Conditions** dialog box. Enter the appropriate numbers into the *Kilovolts*, *Beam Current*, and *Beam Size* text boxes for the currently *Selected Sample*. The *Kilovolts*, *Beam Current*, and *Beam Size* will need to be manually adjusted if a column digital interface is not present.



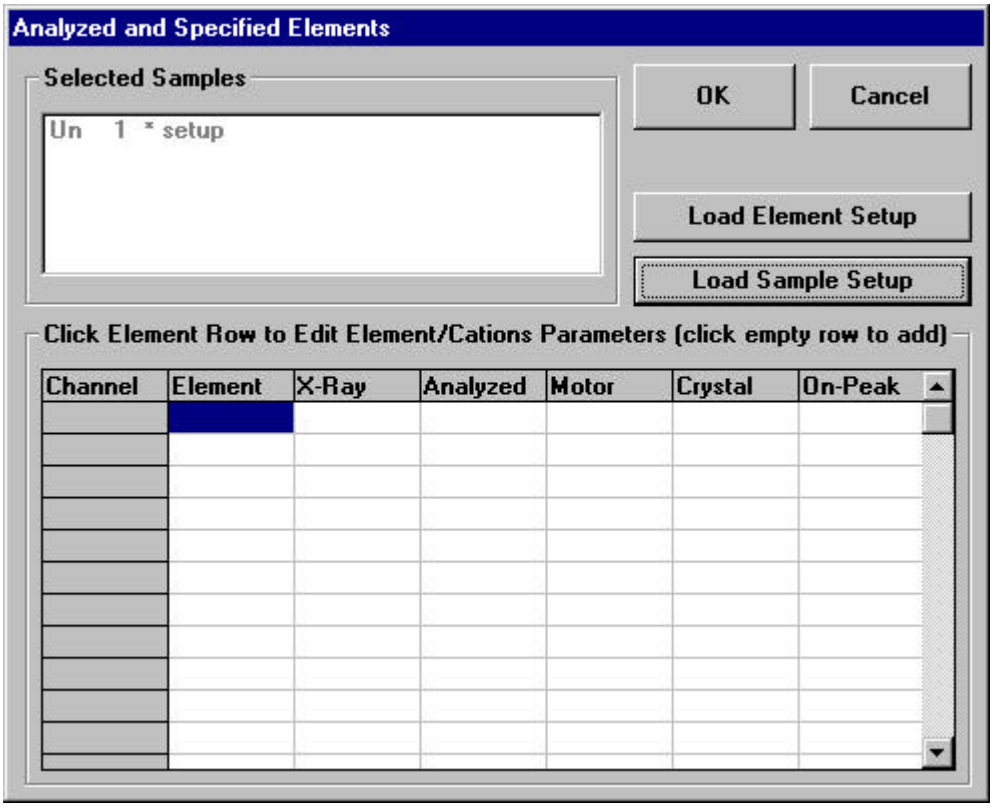
Click the **OK** button when done, returning to the **Acquire!** window.

Element, X-Ray Line and Spectrometer Parameters Selection

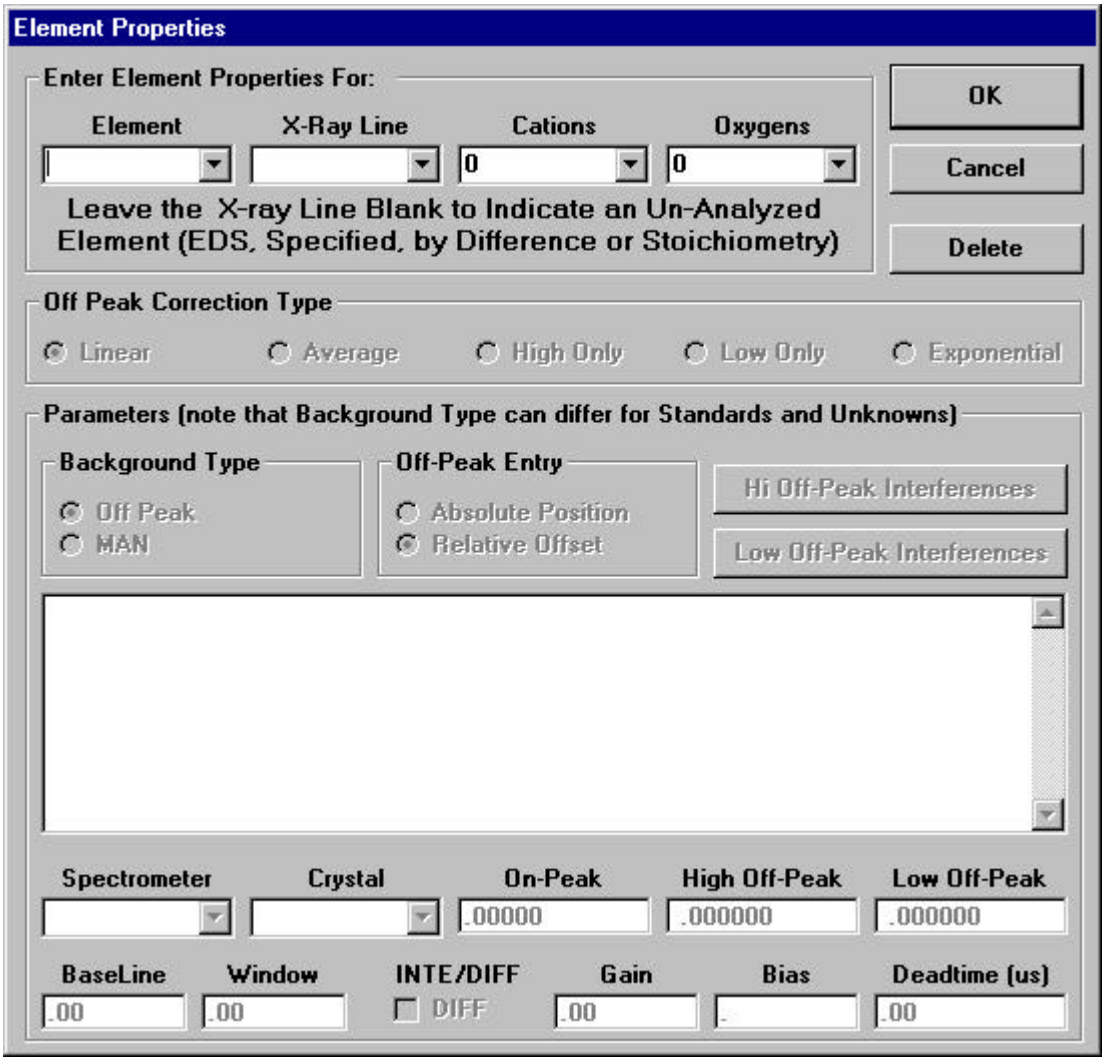
Next, the user specifies the elements to be analyzed. Click the **Elements/Cations** button.



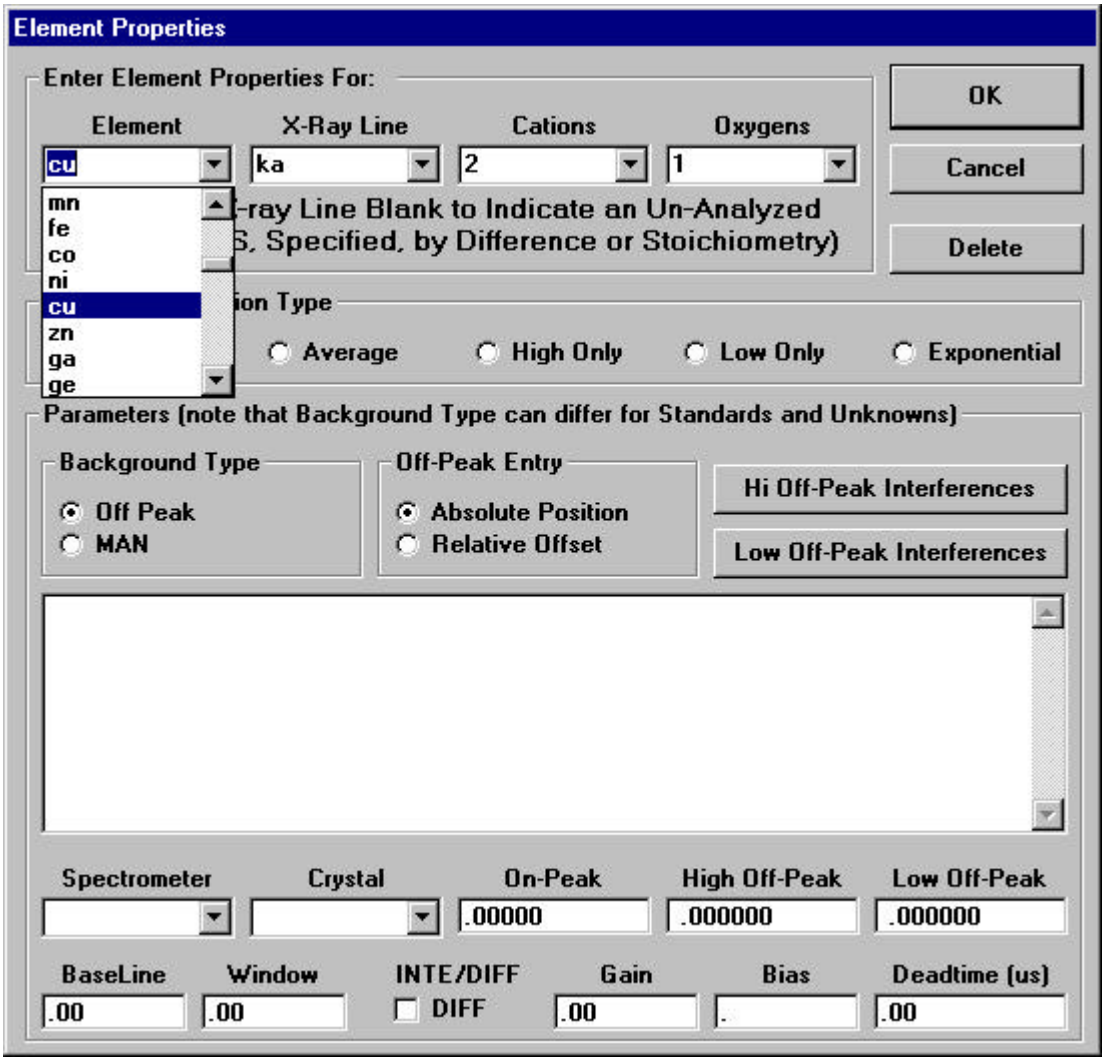
This action opens the **Analyzed and Specified Elements** dialog box. Click on any empty row in the spreadsheet to enter the first element to analyze. The user may enter the analyzed elements in any order however, the analysis output will follow this order.



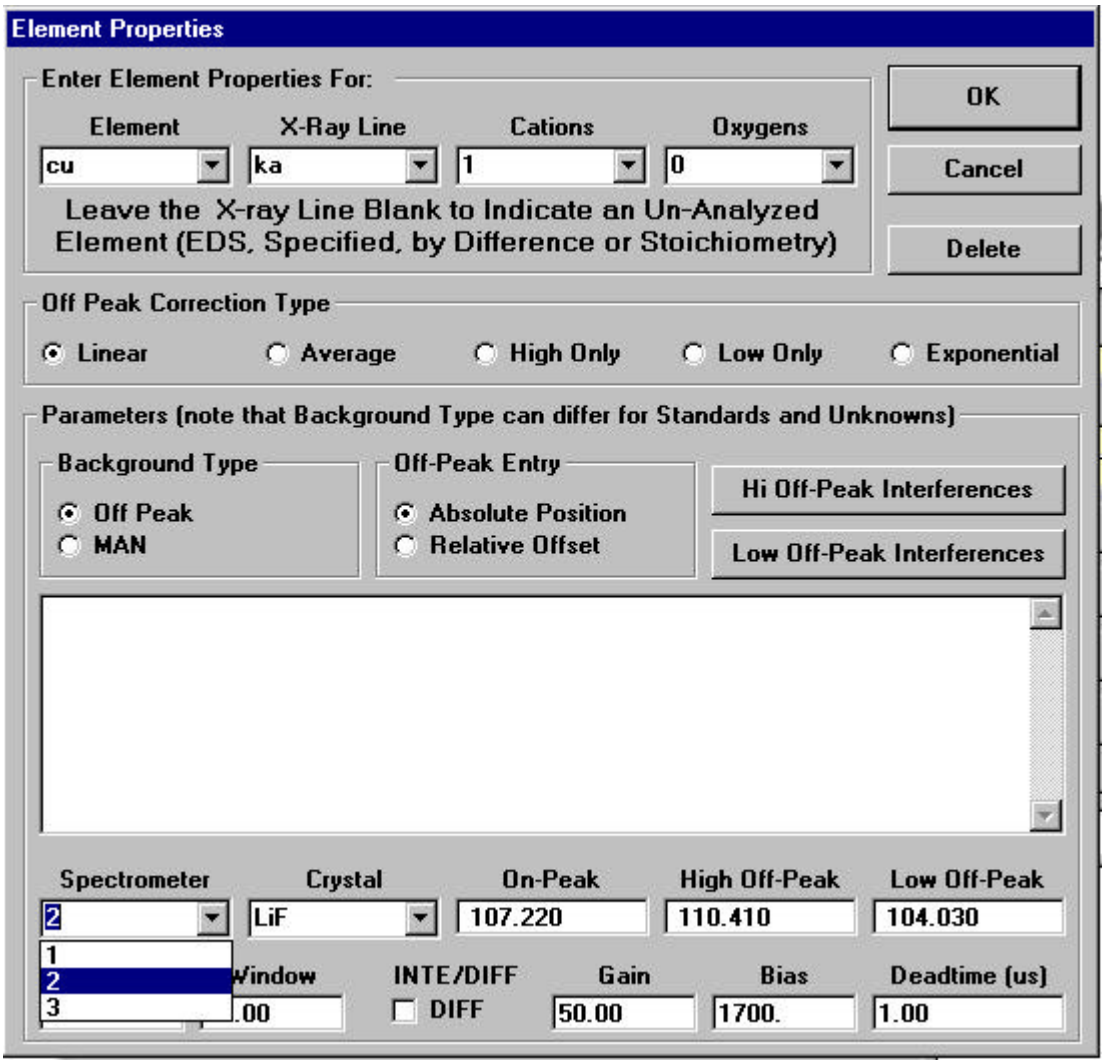
This opens the **Element Properties** dialog box.



In the *Element* field either type in the first element to analyze or use the drop-down menu to select the element symbol. Certain default values listed in this window are based on parameters entered into the previously established configuration files.

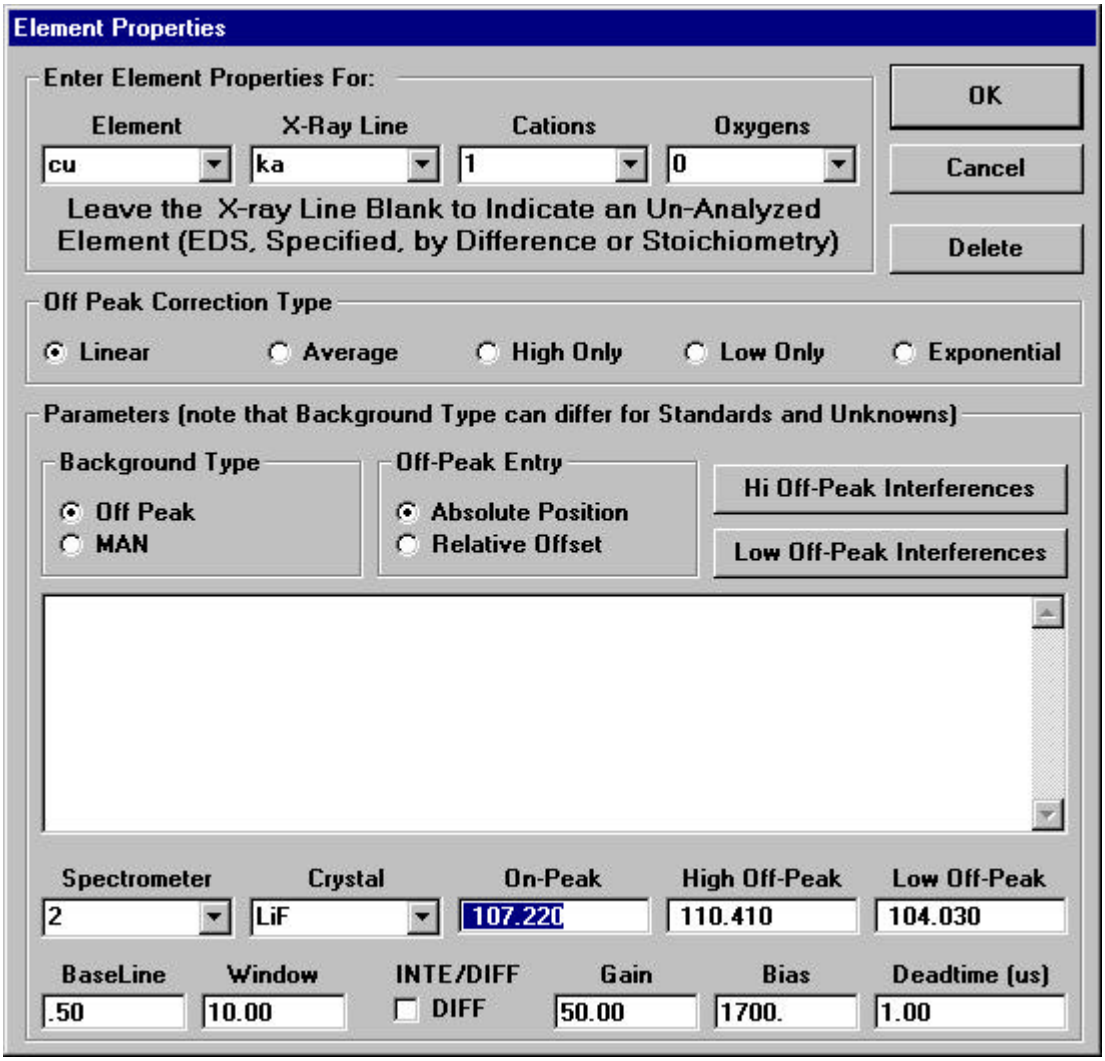


Under the *Enter Element Properties For* section (top of the **Element Properties** dialog box) choose the correct *X-Ray Line*, *Cations*, and *Oxygens* for the first element.



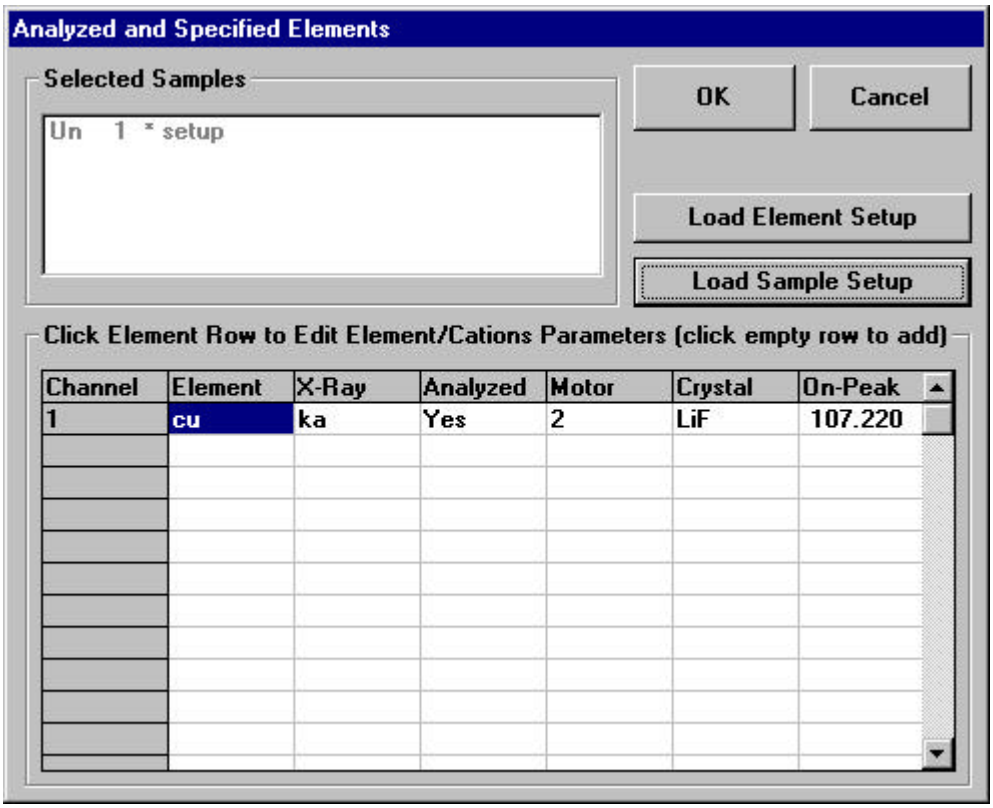
Continue by selecting the *Off Peak Correction Type* and *Background Type*. Two background correction methods are available to the user; off-peak and the MAN (mean atomic number) method (see the User's Guide and Reference documentation for a complete discussion of both types). Next, click the text box under *Spectrometer* and enter the appropriate spectrometer number that will be used to analyze the first element. The drop-down menu may also be used to select the spectrometer number. Choosing a spectrometer number loads various parameters from the configuration files. Each of these parameters in this window should be inspected and edited as needed (use the <tab> key to move between boxes). Accept the nominal *On-* and *Off-Peak* positions listed here. They can be changed later, if necessary.

The next screen shows the edited **Element Properties** dialog box for copper metal.



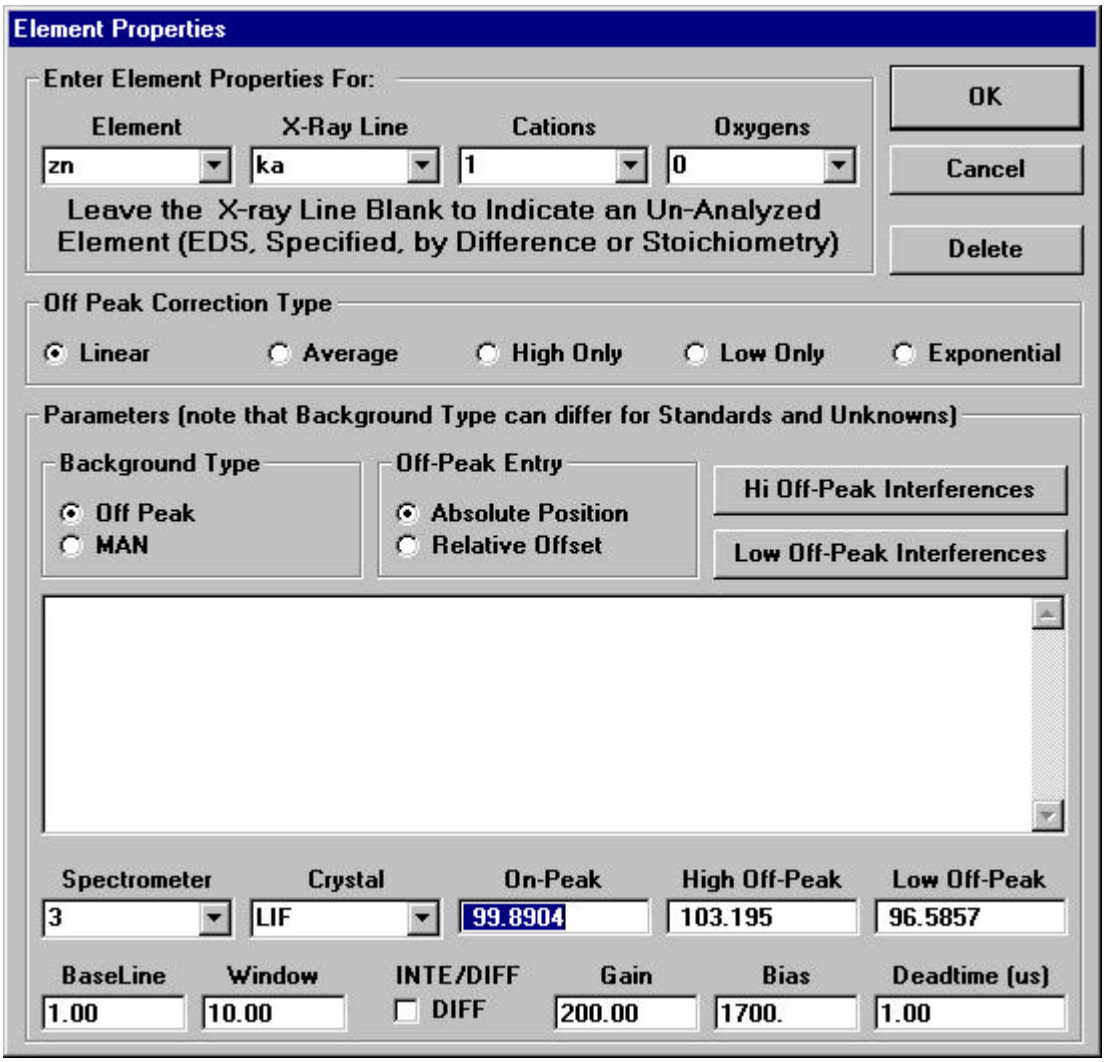
Click the **OK** button of the **Element Properties** dialog box to accept these element parameters for copper.

The program returns to the **Analyzed and Specified Elements** window with copper now entered into the *Element/Cations Parameters* table.



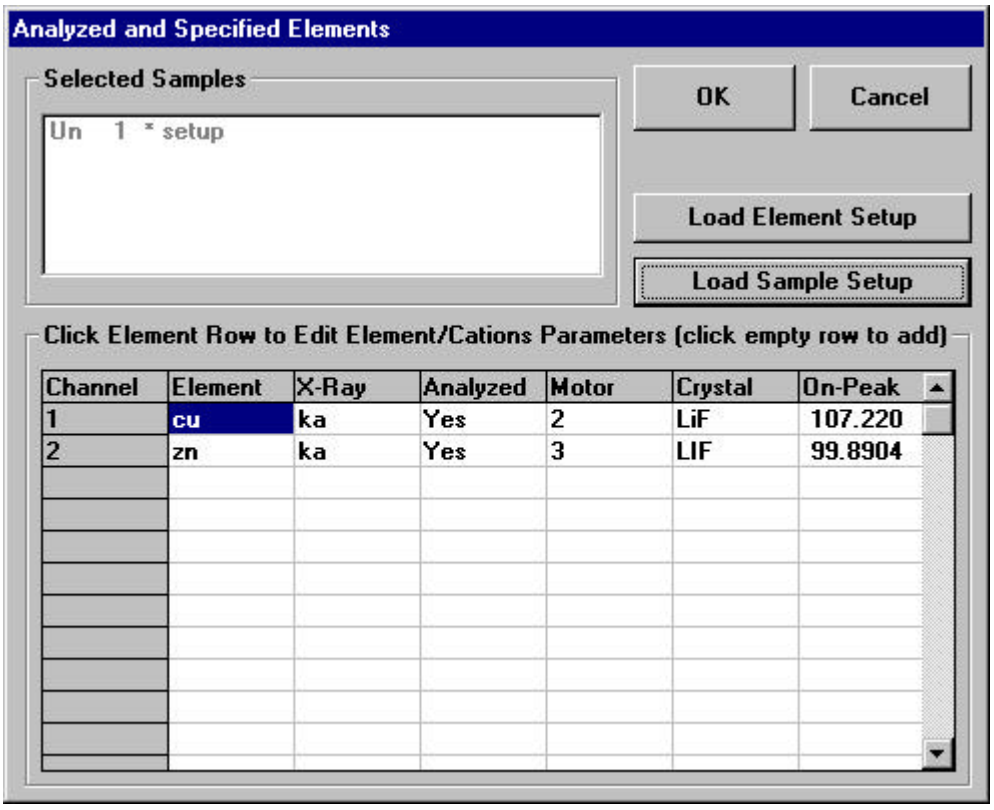
Enter the next element in the run by clicking on any empty row of the **Analyzed and Specified Elements** window. This opens the **Element Properties** dialog box again. Enter the appropriate *Element*, *Spectrometer* and adjust all other text boxes and buttons.

The completed **Element Properties** window for zinc is shown below.

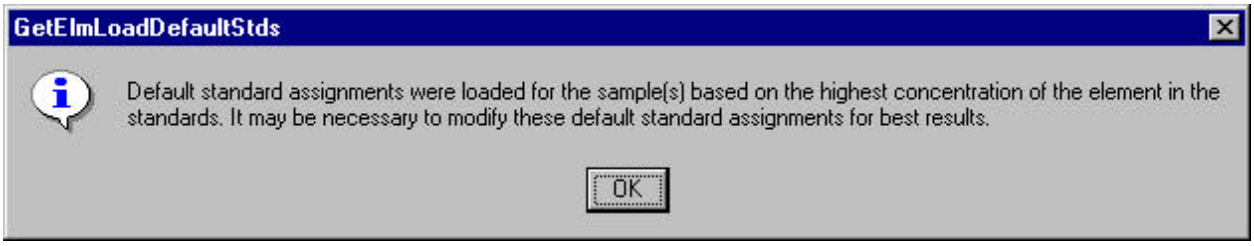


Click the **OK** button of the **Element Properties** to enter zinc into the *Element/Cations Parameters* table of the **Analyzed and Specified Elements** window.

Click the **OK** button of the **Analyzed and Specified Elements** window when done entering elements in the run.



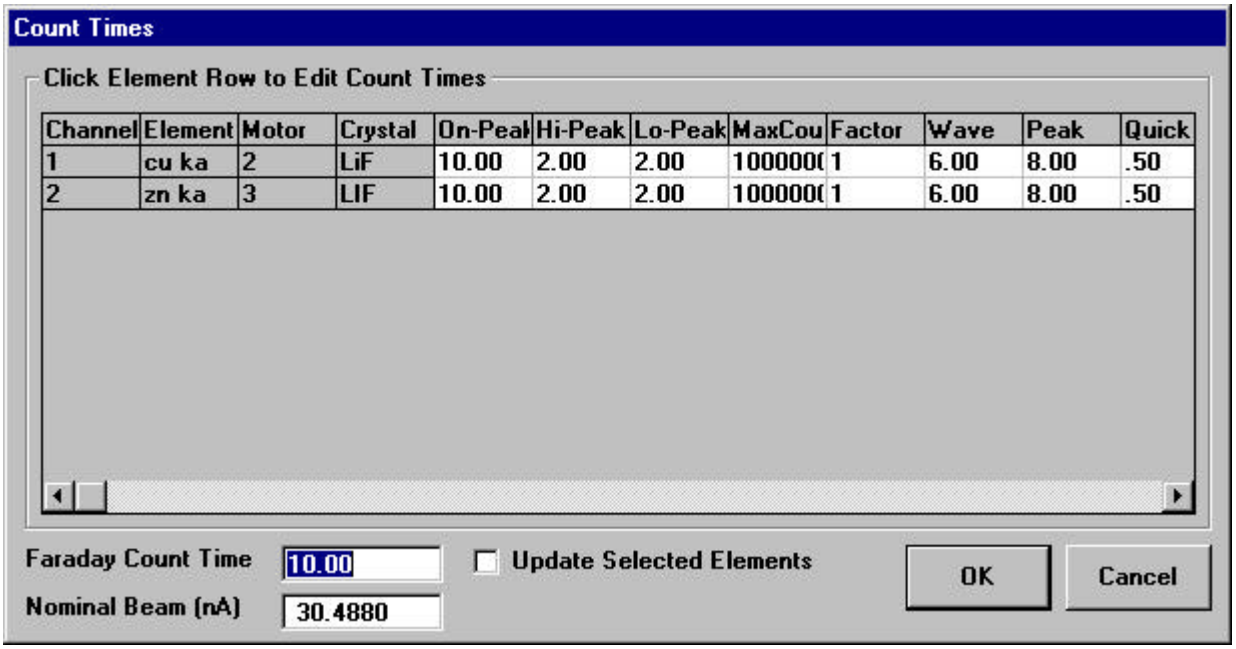
The **GetElmLoadDefaultStds** window opens to inform the user that standard assignments have been made based on elemental concentrations. Standard assignments may be edited via the **Analyze!** window (see User's Guide and Reference documentation).



Click **OK** to return to the main **Acquire!** window.

Setting Count Times

Click the **Count Times** button of the **Acquire!** window. This opens the **Count Times** dialog box. Here various parameters relating to counting times can be adjusted. Initially *On-Peak* count time is set for 10 seconds and both *Hi-Peak* and *Lo-Peak* times are set for 2 seconds based on the configuration file defaults.



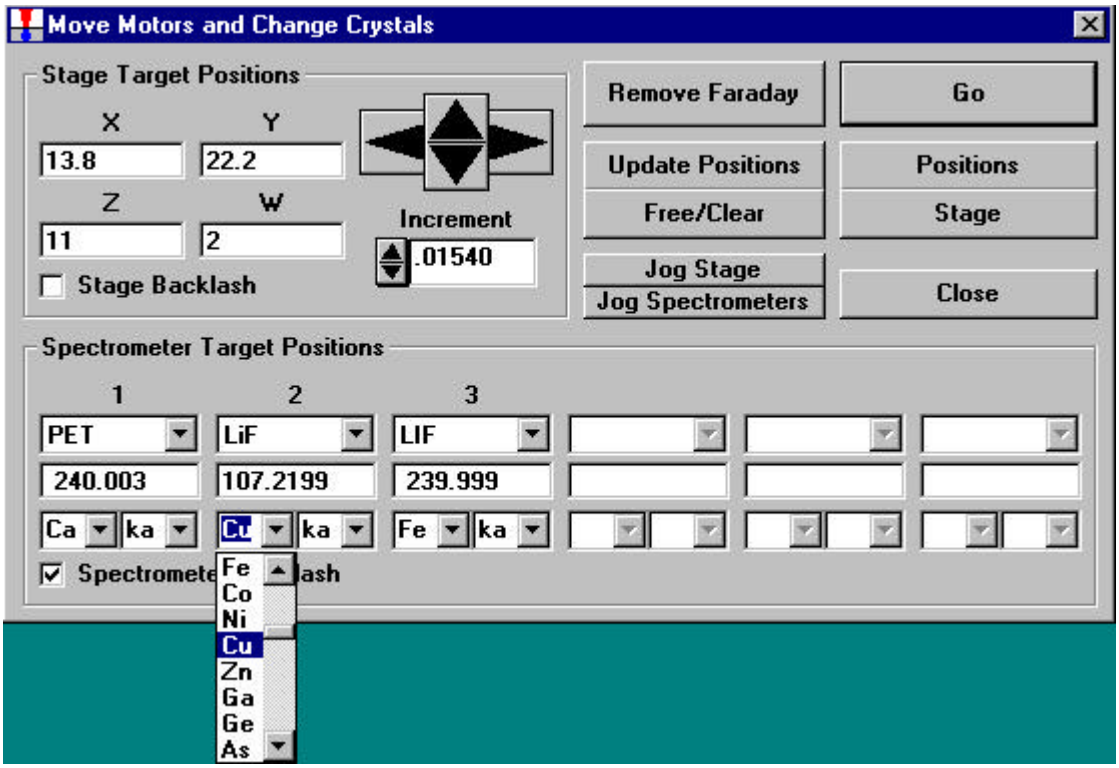
Click the **OK** button of the **Count Times** dialog box to accept these count times and return to the **Acquire!** window.

This completes the initial parameter setup phase for this new run.

Manual Peaking using the Acquire! Window

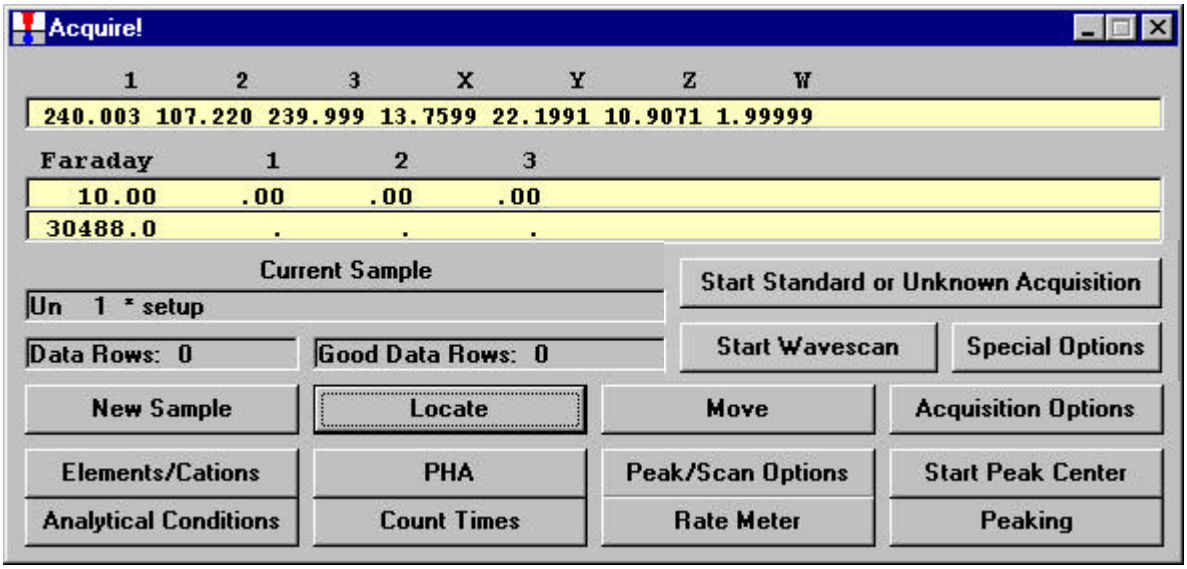
The user may now manually peak center the copper and zinc peak positions from the **Acquire!** window.

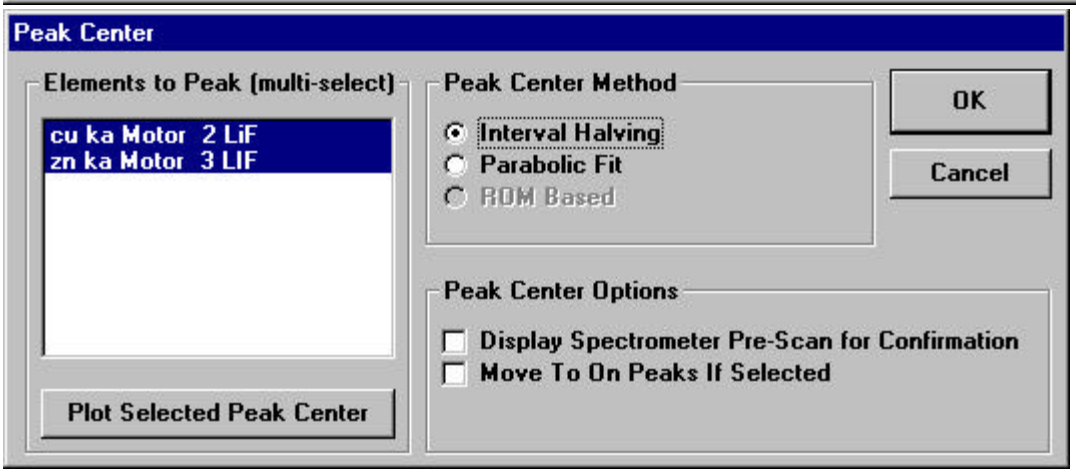
Move to the copper standard by clicking the **Move** button. This opens the **Move Motors and Change Crystals** dialog box. Enter the coordinates of copper metal standard into the *Stage Target Positions* text boxes. Inspect the spectrometer crystal type and position text boxes, edit if required. Alternatively, the user may select the element and x-ray line from the drop-down lists and send the spectrometer directly to the theoretical position. Finally, click the **Go** button.



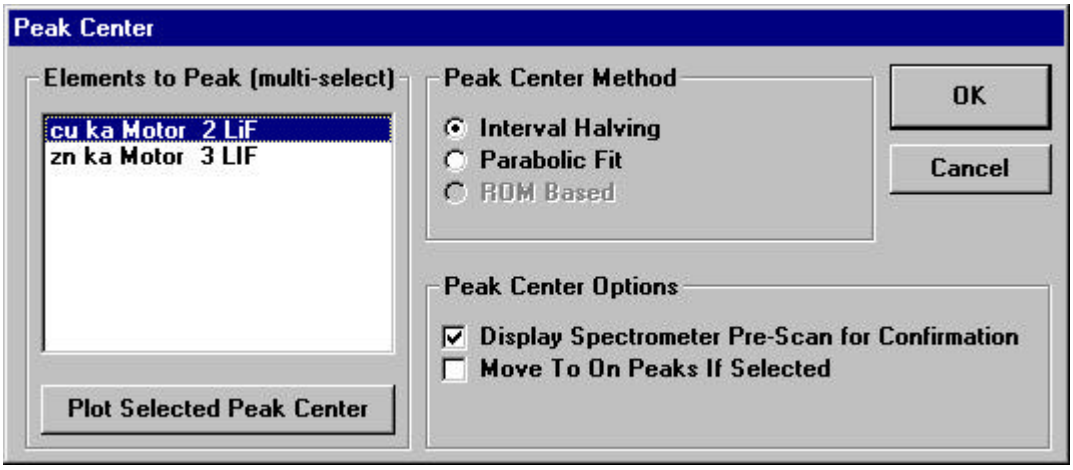
The stage motors will move the stage to the expected position of the copper metal standard. Inspect the final X, Y location of the standard, adjust if necessary and check the focus.

Click the **Peaking** button of the **Acquire!** window.



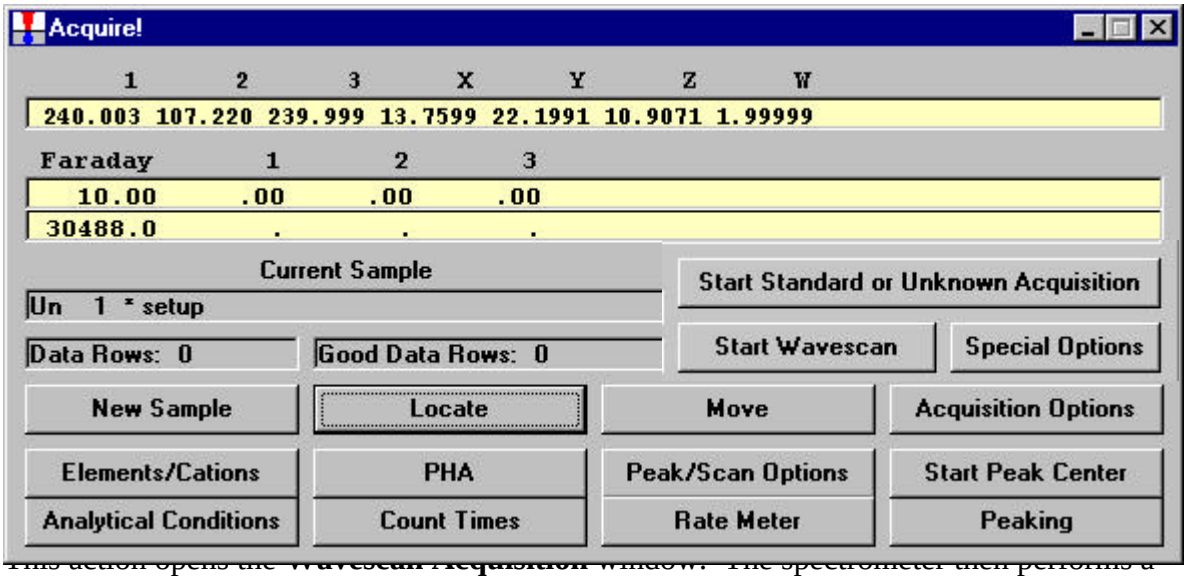


From the *Peak Center Method* group, choose *Interval Halving* (see User's Guide and Reference documentation for discussion of various Peak Center methods) and click *Display Spectrometer Pre-Scan for Confirmation* from the *Peak Center Options* choices. Finally, select the *cu ka Motor 2 LiF* selection under the *Elements to Peak* list box. The **Peak Center** window should appear as follows.



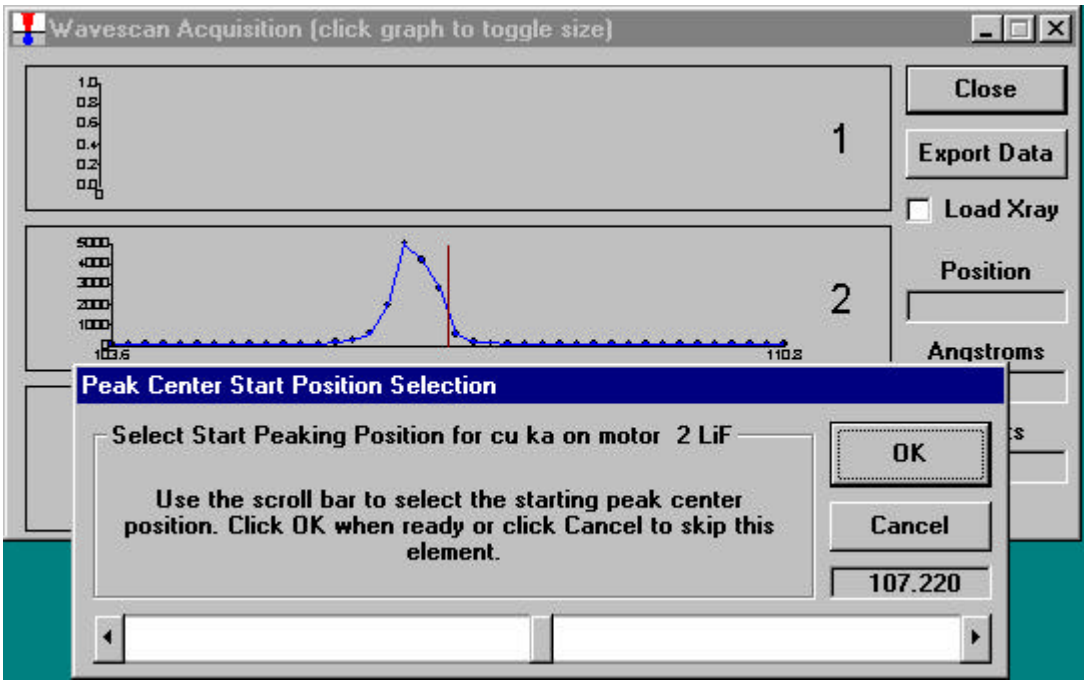
Click the **OK** button to close the **Peak Center** dialog box.

Click the **Start Peak Center** button in the **Acquire!** window.

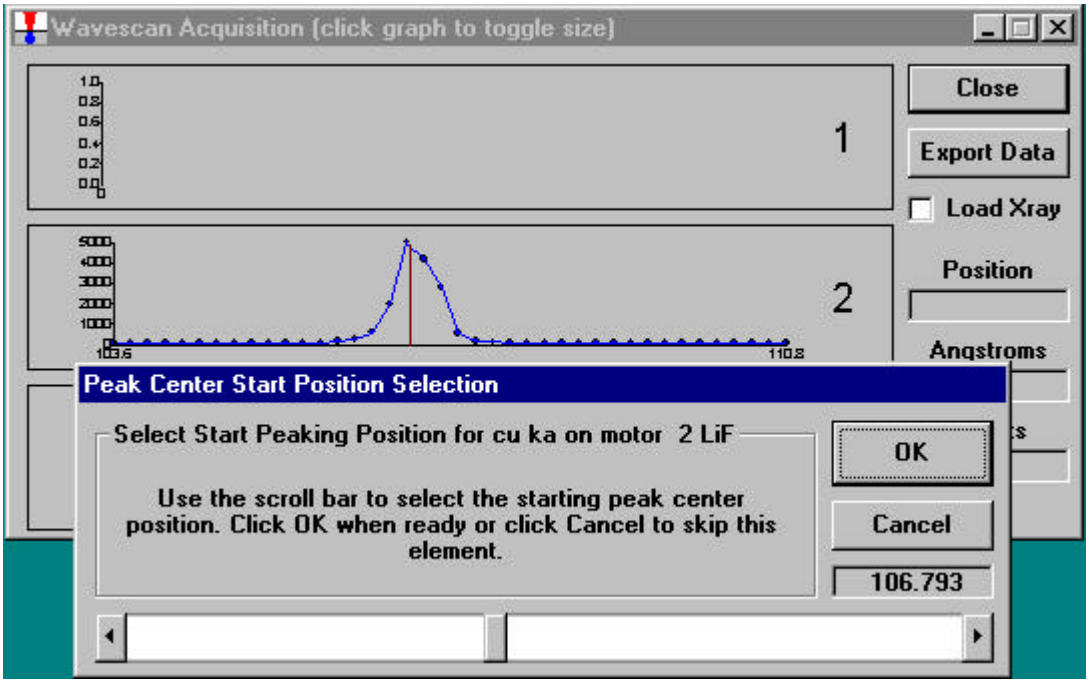


This action opens the **Wavescan Acquisition** window. The spectrometer then performs a spectrometer peak pre-scan (40 step, user defined parameter) on spectrometer 2 in the copper Kα region.

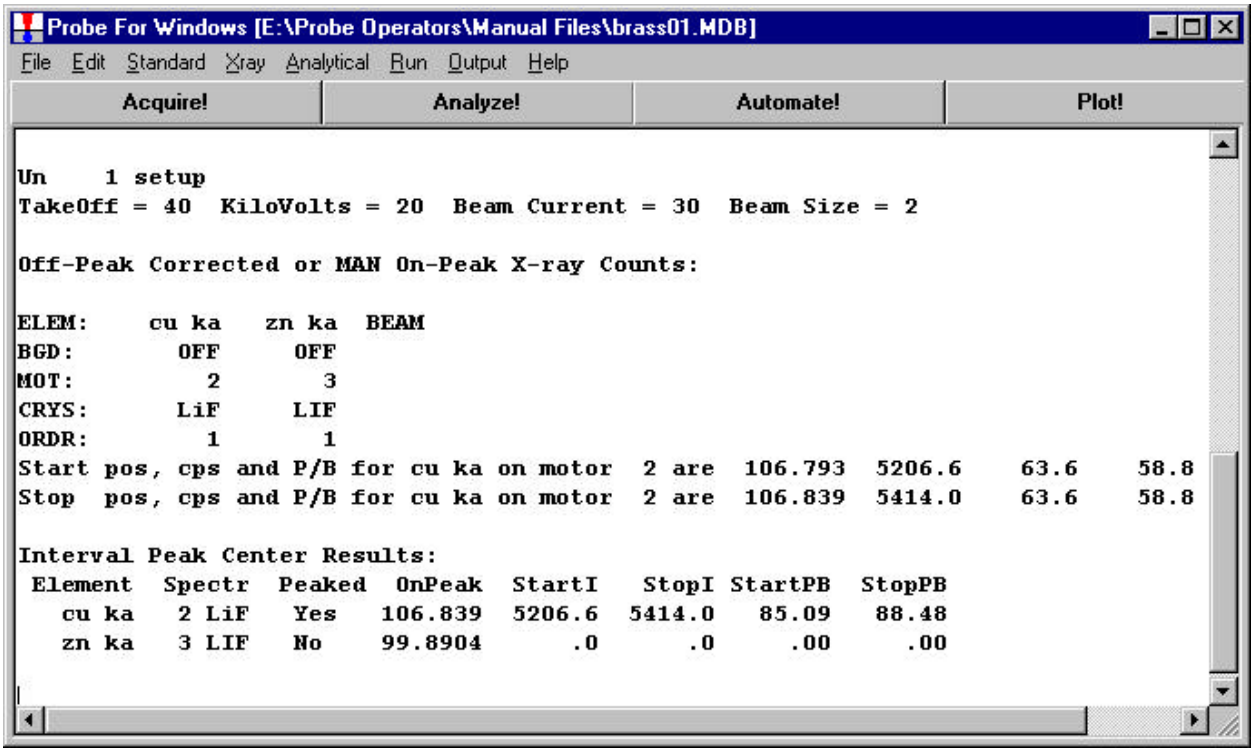
Upon completion of the spectrometer pre-scan the **Peak Center Start Position Selection** window opens.



Slide the scroll bar to move the vertical (red) peak line to match the actual x-ray maximum position. This selects a starting peak center position for the peaking routine.

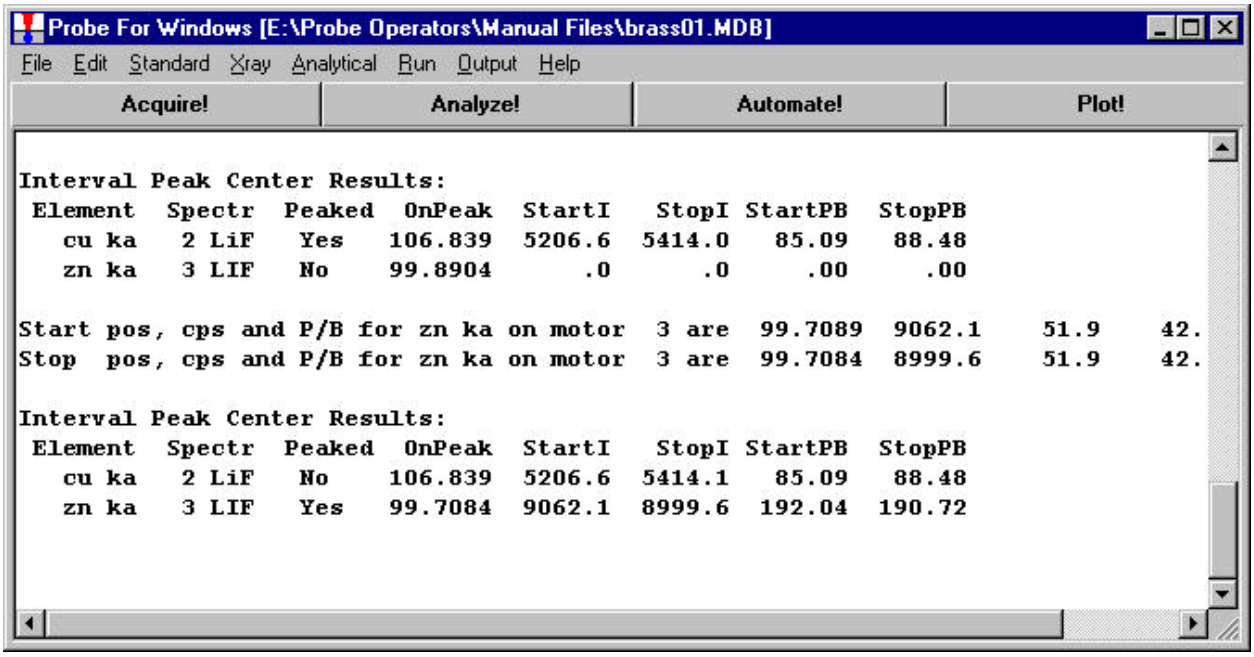


Click the **OK** button when manually centered. This initiates a peak center routine to locate the precise peak center for copper Kα x-rays. The results for copper appear in the main log window, displayed below.



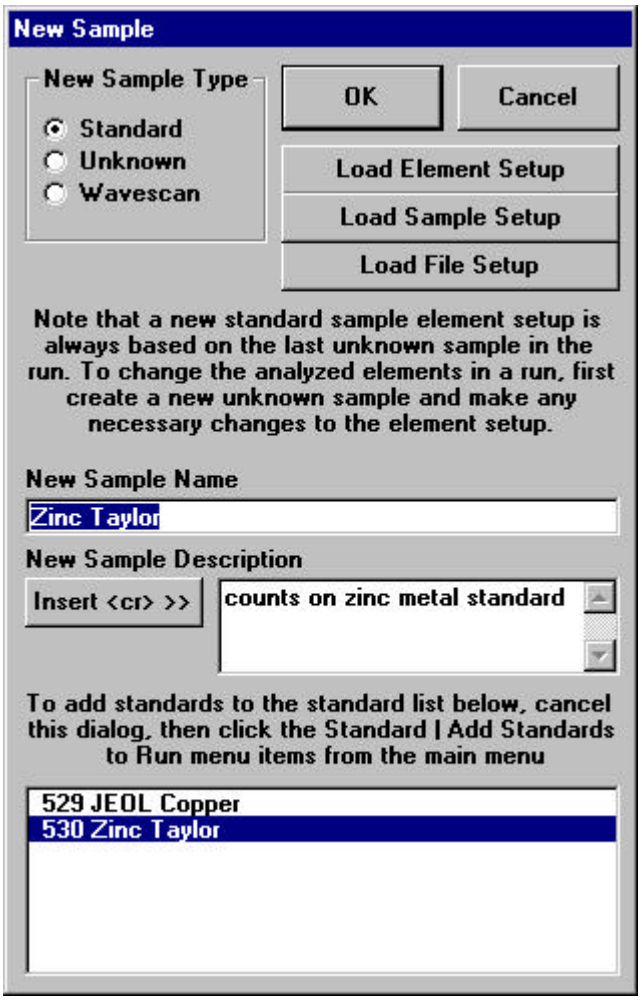
Zinc Kα may also be peaked in this manner. First click the **Move** button of the **Acquire!** window to access the **Move Motors and Change Crystals** dialog box. Enter the appropriate stage target positions for the zinc metal standard and click the **Go** button. When the stage motors stop moving, inspect the location, and adjust the optical focus if necessary. Close the **Move Motors and Change Crystals** window. Then click the **Peaking** button as in the copper example. **Remember** to highlight only *zn ka Motor 3 LIF* this time. Close the **Peak Center** window and finally click the **Start Peak Center** button of the **Acquire!** window.

The results for zinc Kα appear below.



Manual Count Acquisition using the Acquire! Window

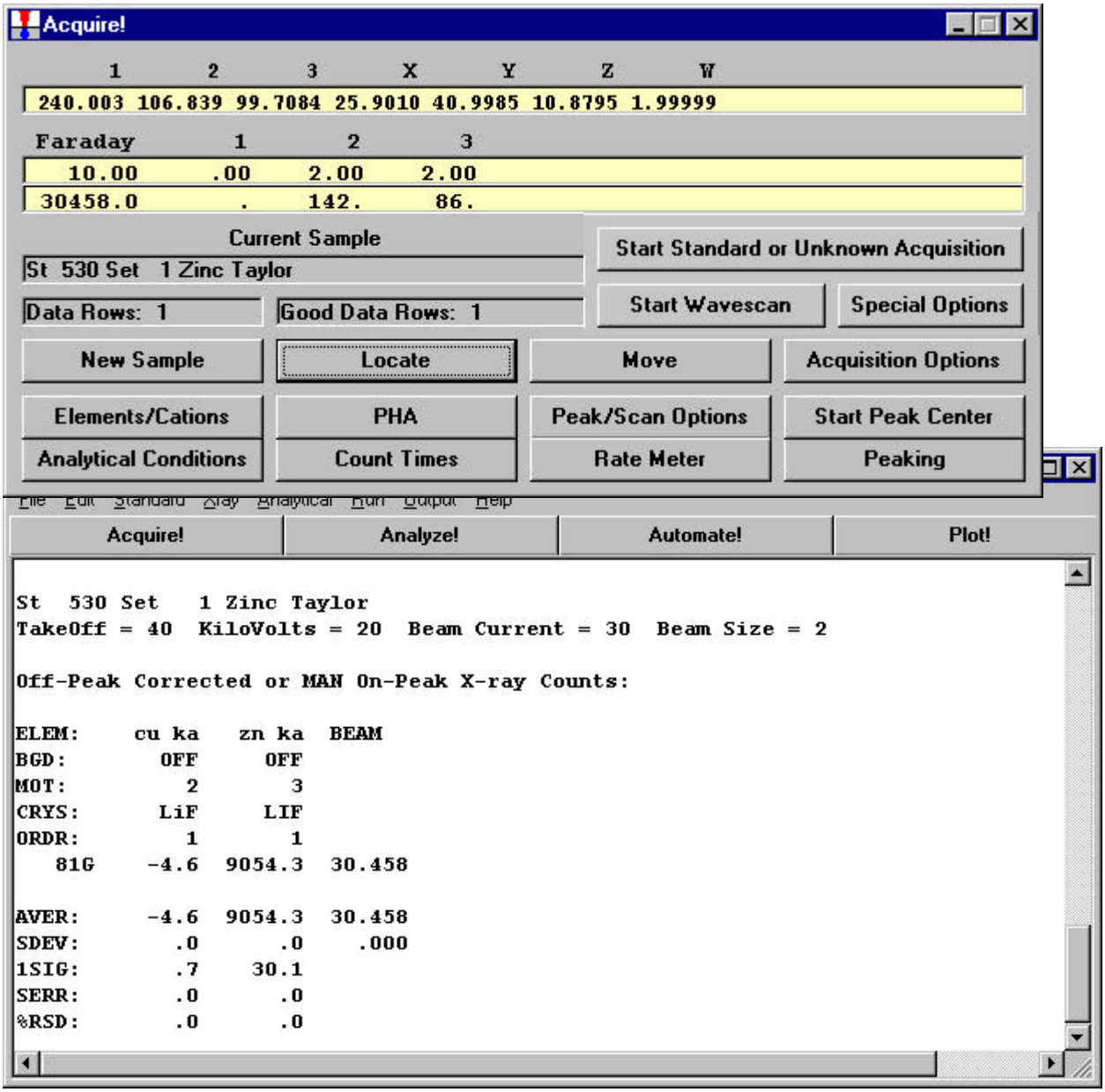
To acquire a single point of x-ray count data for a standard proceed as follows. From the **Acquire!** dialog box click the **New Sample** button. This opens the familiar **New Sample** window. Click on *Standard* from the *New Sample Type* buttons. This allows the user to specify a standard from the list now active at the bottom of the *New Sample* dialog box. Click *530 Zinc Taylor*, its name now appears under *New Sample Name*. Enter any relevant text under *New Sample Description*. Click the **OK** button when done.



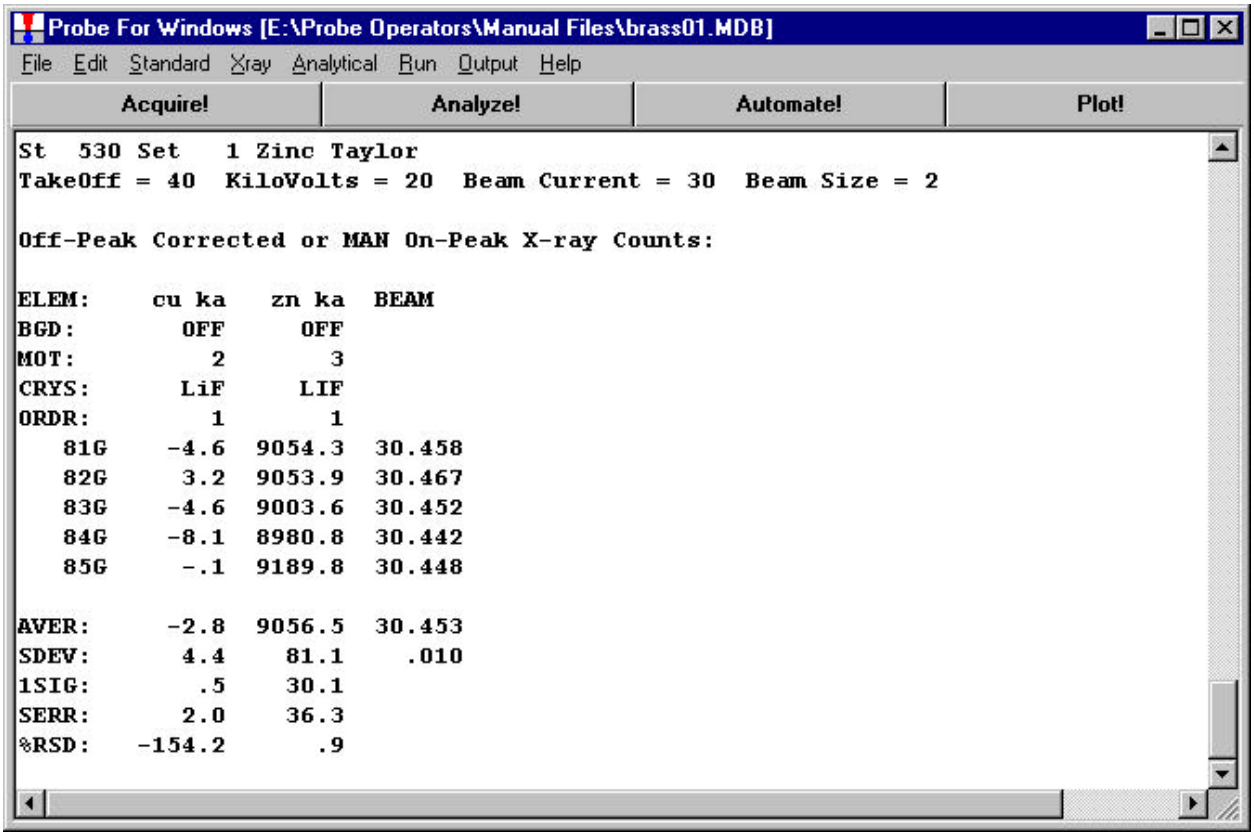
Check the optical focus on the zinc standard and click the **Start Standard or Unknown Acquisition** button of the **Acquire!** window. Notice that the current sample is displayed in the **Acquire!** window. The progress of all data acquisition may be viewed in the **Acquire!** window.

Clicking the **Start Standard or Unknown Acquisition** button initiates the data acquisition. The spectrometers for copper and zinc move to their respective peak positions and count on peak and off peak (both sides in this example) for times specified earlier in the **Count Times** window. The Faraday cup is also measured.

The **Acquire!** window and the main PROBE FOR WINDOWS log window appear as follows upon completion. Faraday cup counts (BEAM) are reported in total counts in the **Acquire!** window and in nanoamps in the main log window.

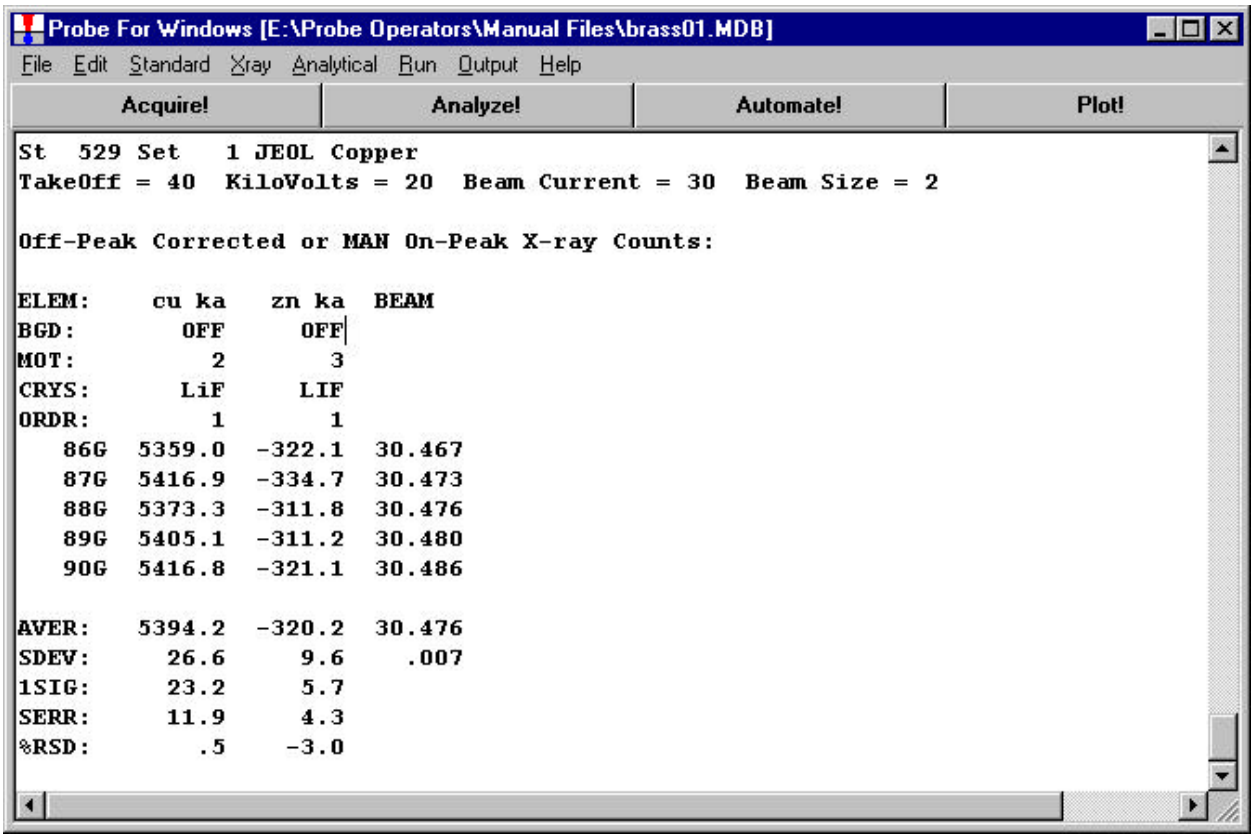


Repeated clicking of the **Start Standard or Unknown Acquisition** button acquires additional intensity data. The following log window illustrates the acquisition of five data points on the zinc metal standard.



Similarly, x-ray counts can be acquired on the copper metal standard. Move back to the copper standard position via the **Move** button and inspect the location and focus. Click the **New Sample** button, select the copper standard from the standard list, click the **OK** button when done.

Start collecting counts by clicking the **Start Standard or Unknown Acquisition** button. Repeating five times as with the zinc standard gives the following main log window output.

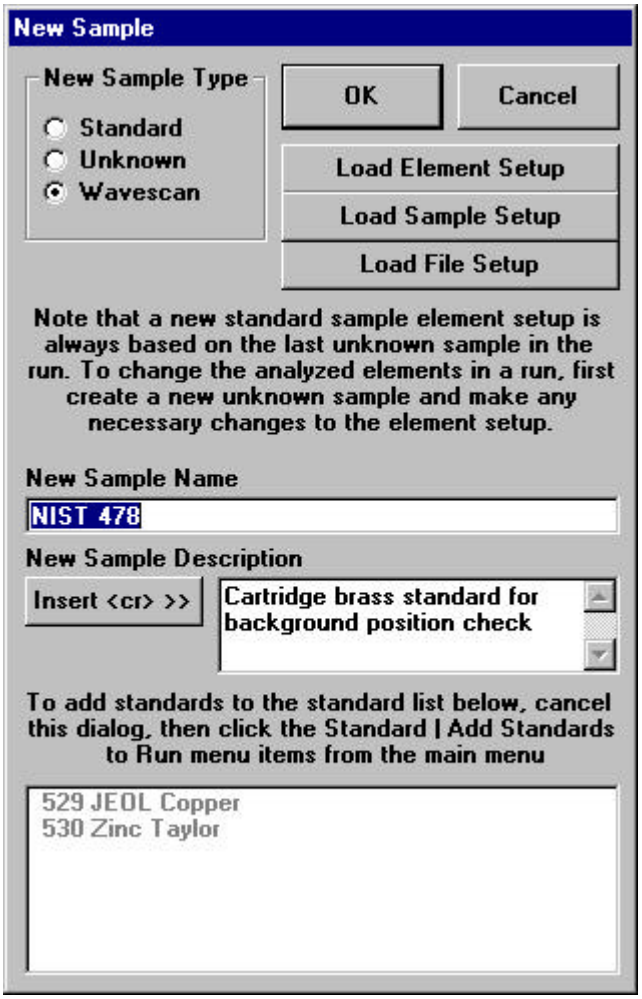


Inspection of the copper data reveals an interesting feature. All of the zinc off-peak corrected counts on the pure copper standard are very negative suggesting that a background position may be incorrectly set. This can be easily checked by moving to an alloy sample containing both elements of interest and performing a wavescan. A Cartridge Brass standard (NIST SRM 478) containing both elements may be used.

Wavescan Acquisitions

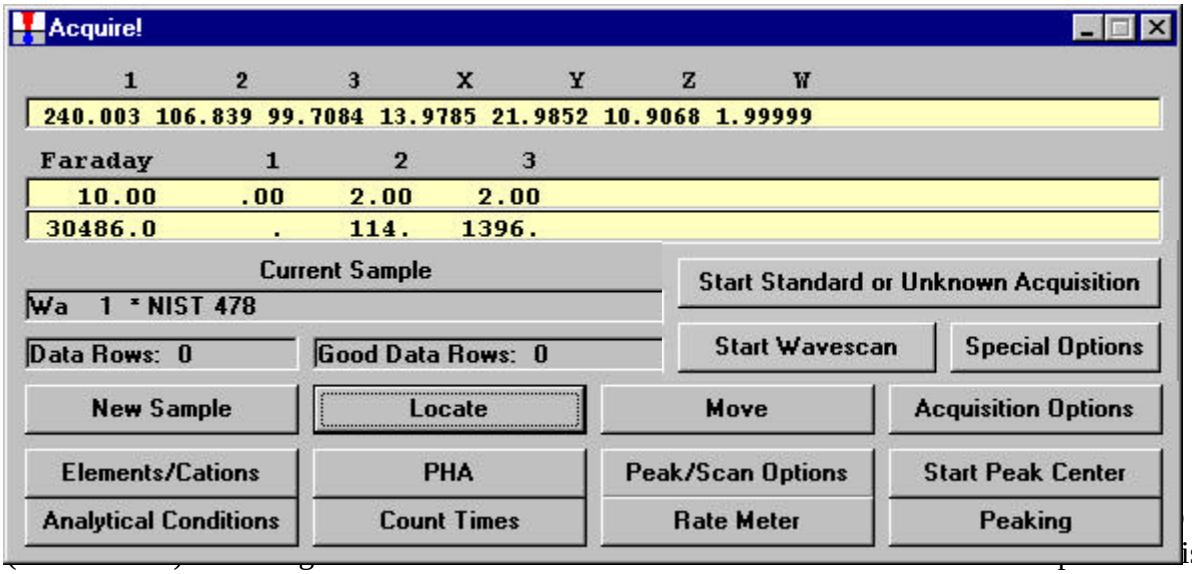
To perform a wavescan acquisition on the Cartridge Brass standard click the **Move** button in the **Acquire!** window to move to this standard.

Click the **New Sample** button. Select *Wavescan* under *New Sample Type*, edit the *New Sample Name* and *New Sample Description* text boxes.

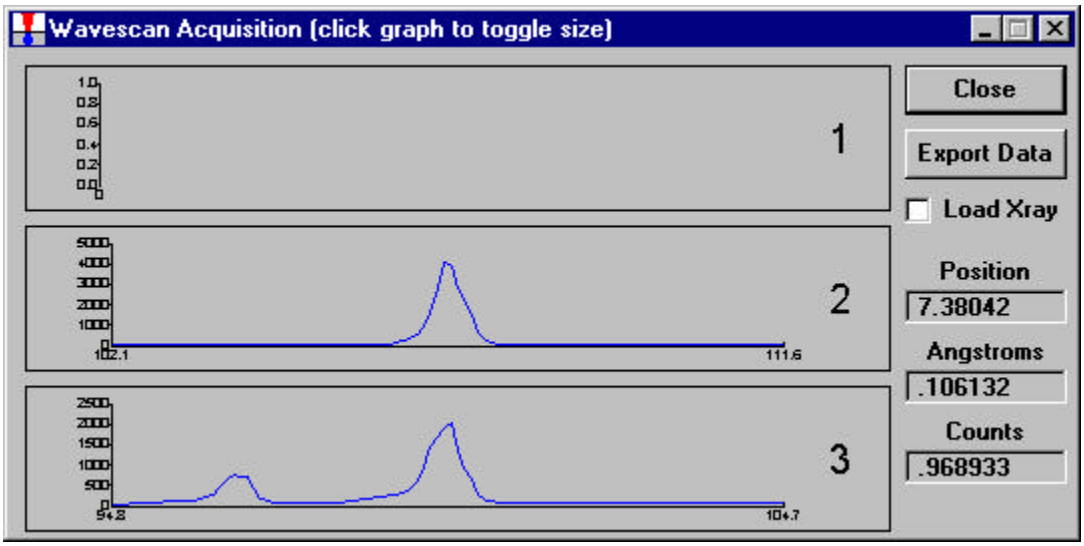


Click **OK** when done.

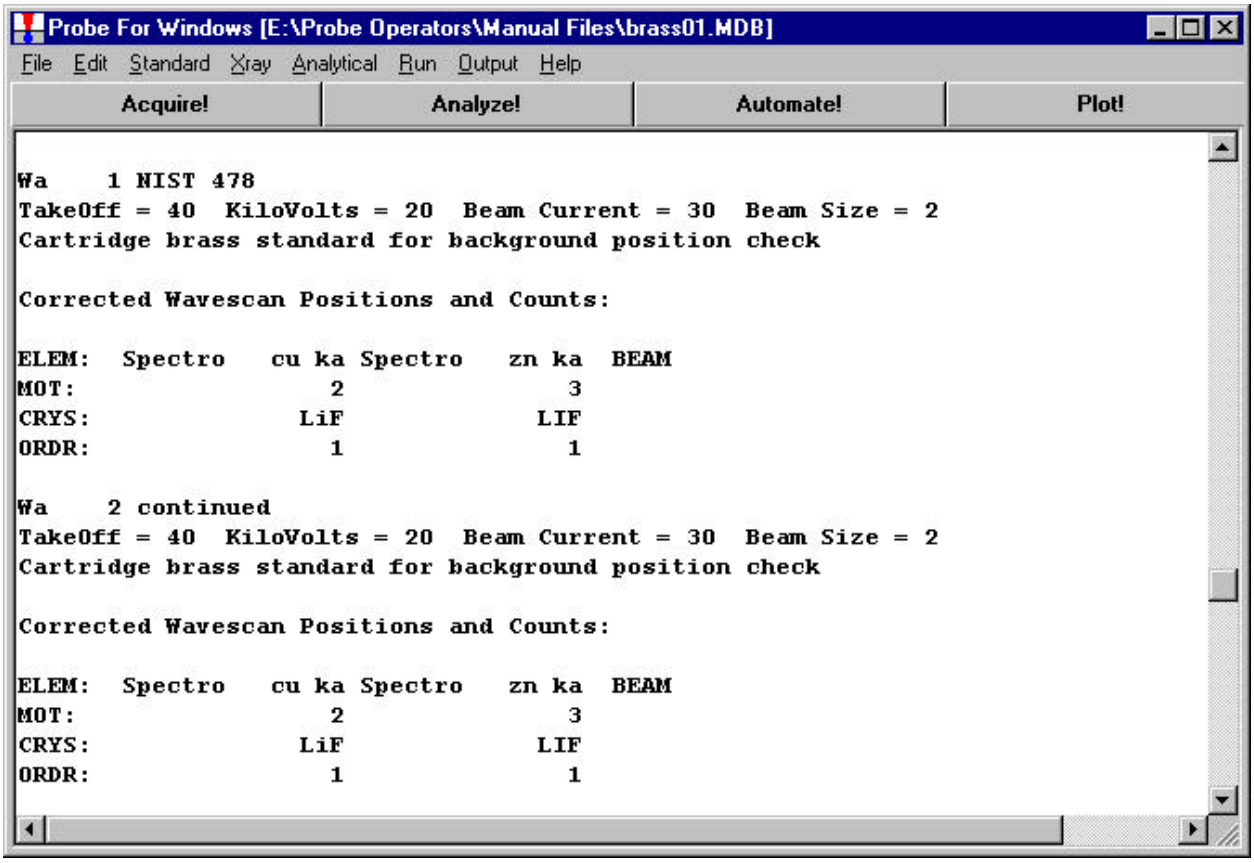
Click the **Start Wavescan** button of the **Acquire!** window.



is example, simply copper and zinc. Graphical output of the completed scan via the **Wavescan Acquisition** window can be seen below.

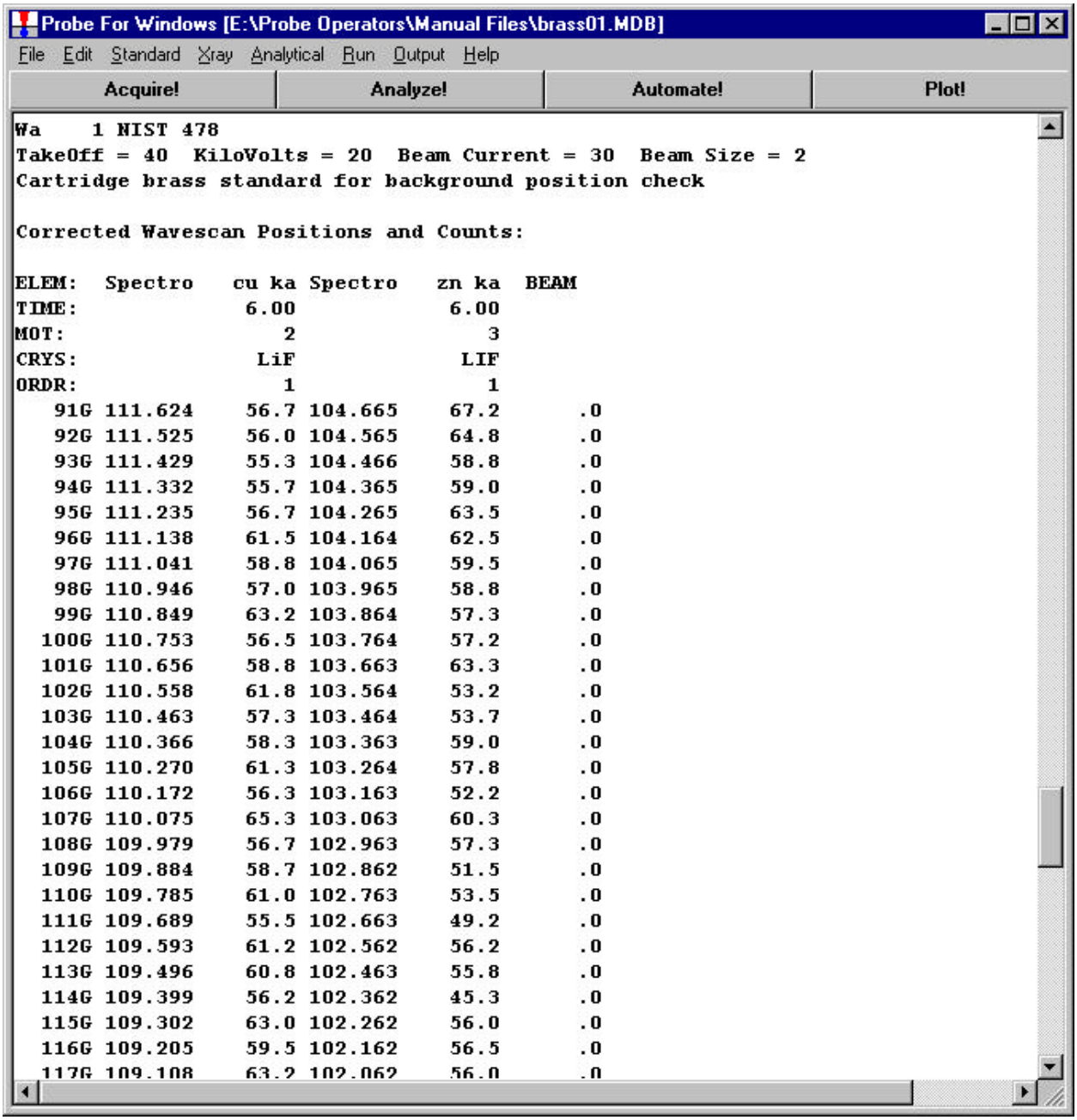


The wavescan labels appear in the main PROBE FOR WINDOWS log window.



The wavescan positions and counts may be displayed in the main log window by clicking the **Analyze!** button opening the **Analyze!** window. Select the *Wavescans* button, then click the **Select All** button and finally clicking the **Data** button.

A portion of a very long list of data is illustrated below.

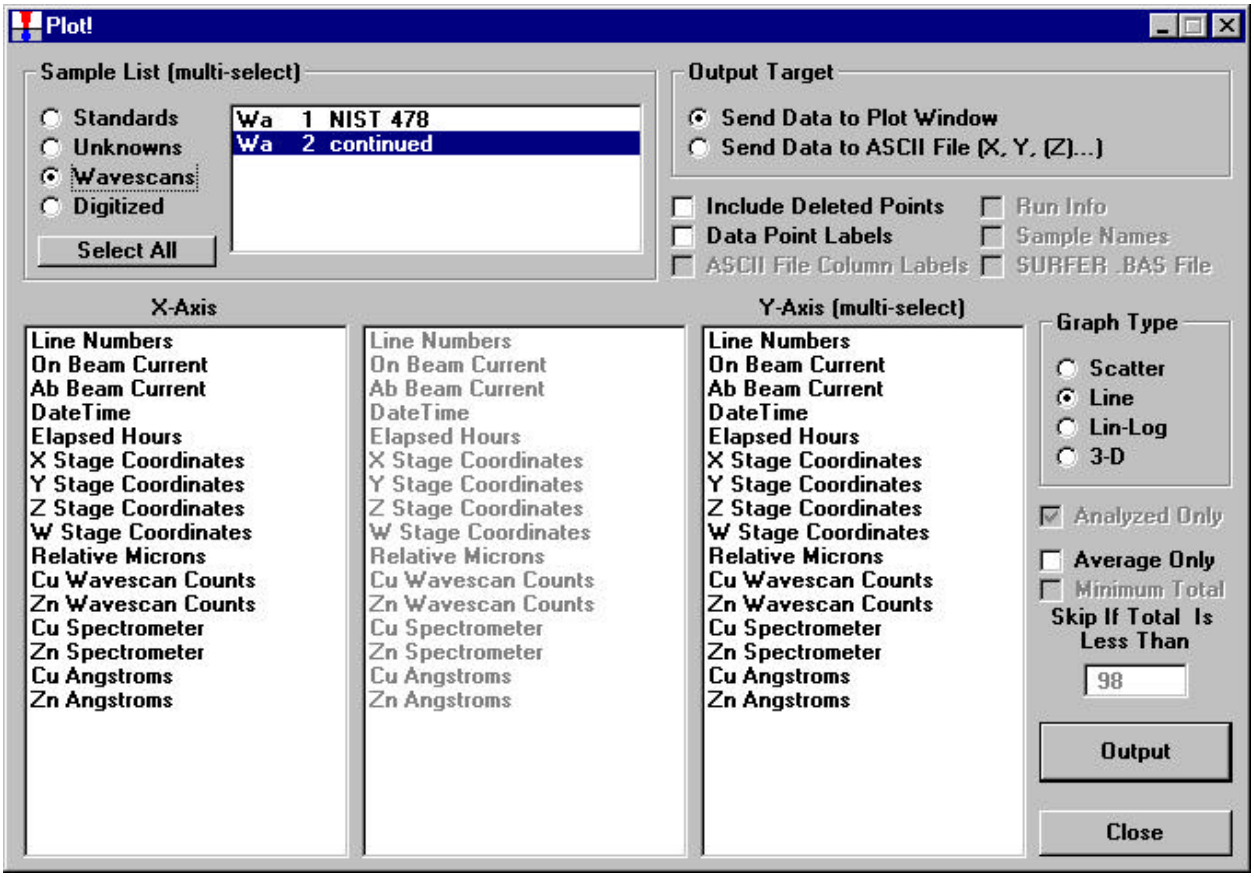



```
Wa    1 NIST 478
TakeOff = 40  KiloVolts = 20  Beam Current = 30  Beam Size = 2
Cartridge brass standard for background position check

Corrected Wavescan Positions and Counts:

ELEM:  Spectro   cu ka Spectro   zn ka  BEAM
TIME:             6.00             6.00
MOT:                 2                3
CRYS:              LiF              LIF
ORDR:                1                1
   91G 111.624    56.7 104.665    67.2       .0
   92G 111.525    56.0 104.565    64.8       .0
   93G 111.429    55.3 104.466    58.8       .0
   94G 111.332    55.7 104.365    59.0       .0
   95G 111.235    56.7 104.265    63.5       .0
   96G 111.138    61.5 104.164    62.5       .0
   97G 111.041    58.8 104.065    59.5       .0
   98G 110.946    57.0 103.965    58.8       .0
   99G 110.849    63.2 103.864    57.3       .0
  100G 110.753    56.5 103.764    57.2       .0
  101G 110.656    58.8 103.663    63.3       .0
  102G 110.558    61.8 103.564    53.2       .0
  103G 110.463    57.3 103.464    53.7       .0
  104G 110.366    58.3 103.363    59.0       .0
  105G 110.270    61.3 103.264    57.8       .0
  106G 110.172    56.3 103.163    52.2       .0
  107G 110.075    65.3 103.063    60.3       .0
  108G 109.979    56.7 102.963    57.3       .0
  109G 109.884    58.7 102.862    51.5       .0
  110G 109.785    61.0 102.763    53.5       .0
  111G 109.689    55.5 102.663    49.2       .0
  112G 109.593    61.2 102.562    56.2       .0
  113G 109.496    60.8 102.463    55.8       .0
  114G 109.399    56.2 102.362    45.3       .0
  115G 109.302    63.0 102.262    56.0       .0
  116G 109.205    59.5 102.162    56.5       .0
  117G 109.108    63.2 102.062    56.0       .0
```

A more complete graphical display of these wavescans may be accomplished using the **Plot!** window.

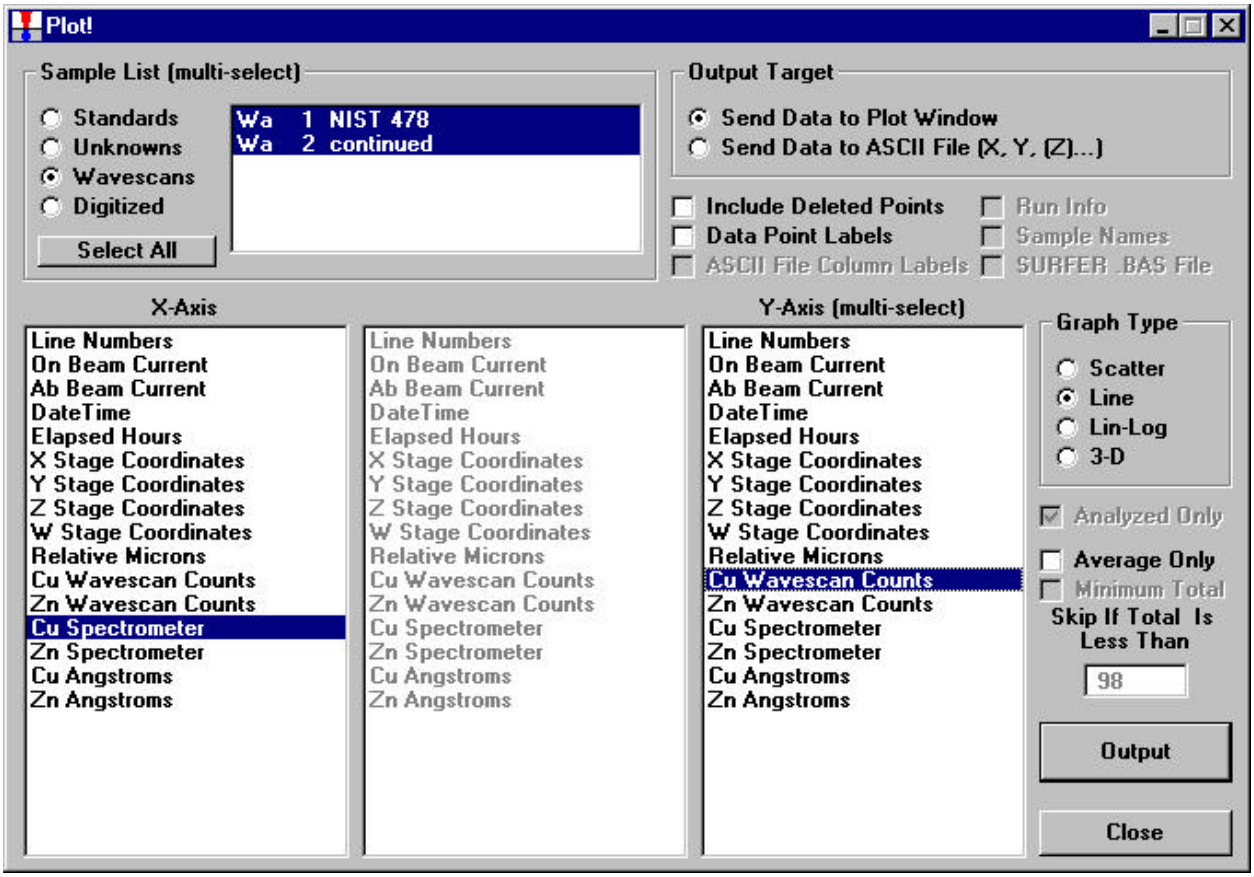
Off-Peak Adjustments from the Plot! Window

Click on the **Plot!** button under the main PROBE FOR WINDOWS log window. The **Plot!** dialog box opens.

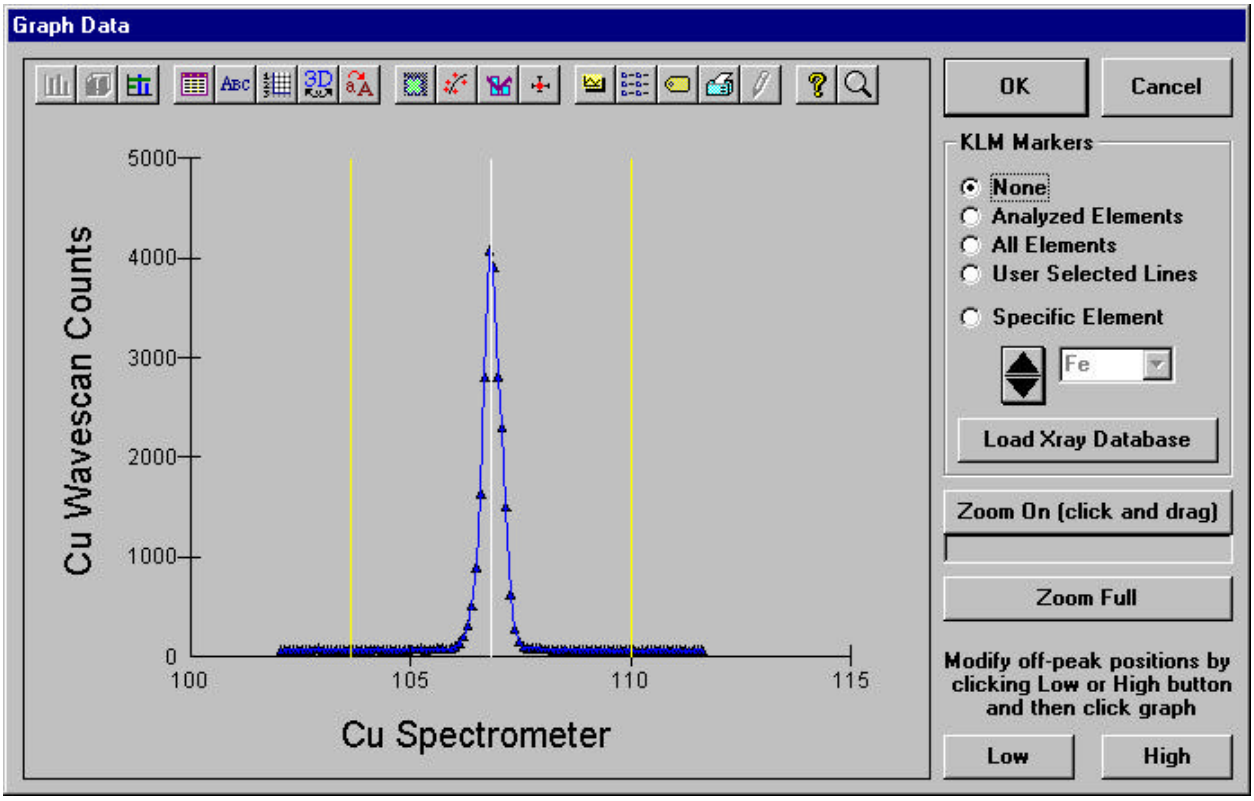


Under *Sample List* the *Wavescans* button should be clicked. Use the mouse to select both wavescan data samples. Since each sample can only accommodate 50 data points, a complete wavescan of 100 points is continued in two sample numbers.

Click on *Cu Spectrometer* from the *X-Axis* list and *Cu Wavescan Counts* from the *Y-Axis* list selections. Choose a *Graph Type*, click the *Line* button and an *Output Target* of *Send Data to Plot Window.* Finally, click the **Output** button to view the graph.

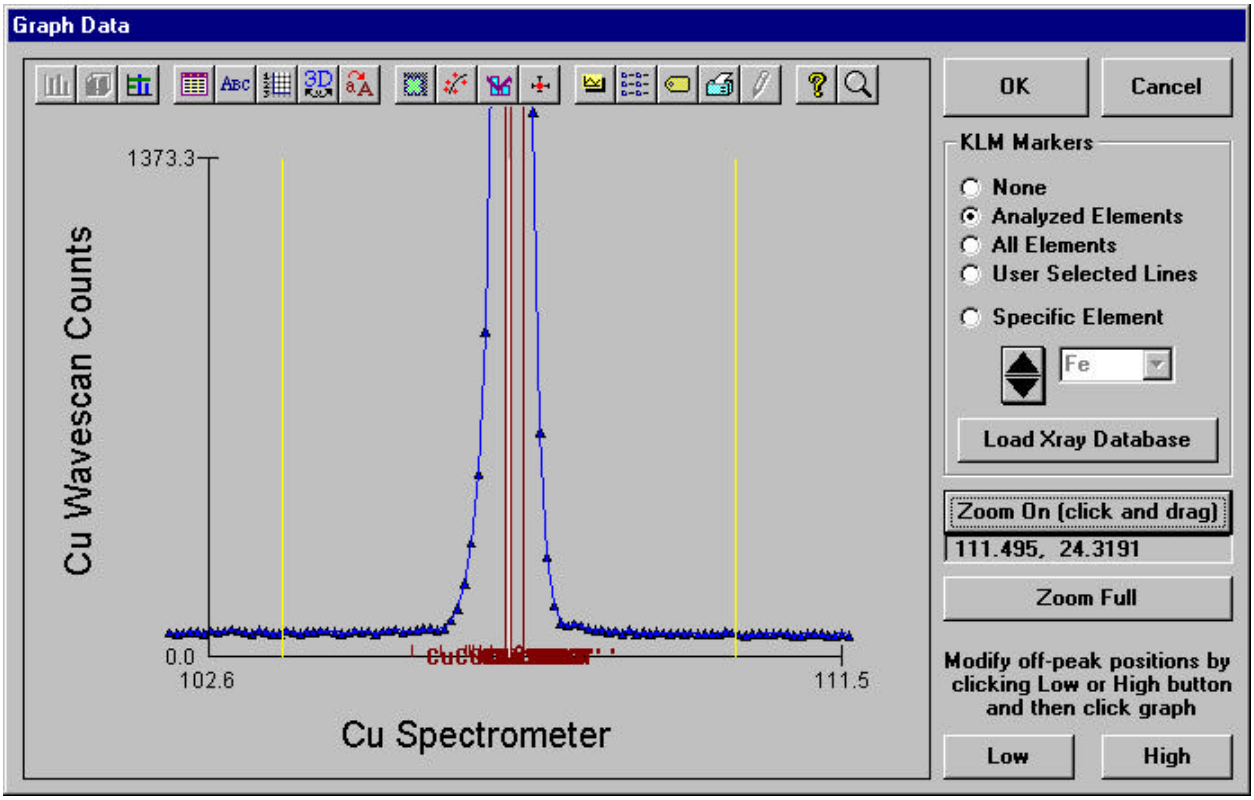


The program then loads the selected data into the **Graph Data** window.



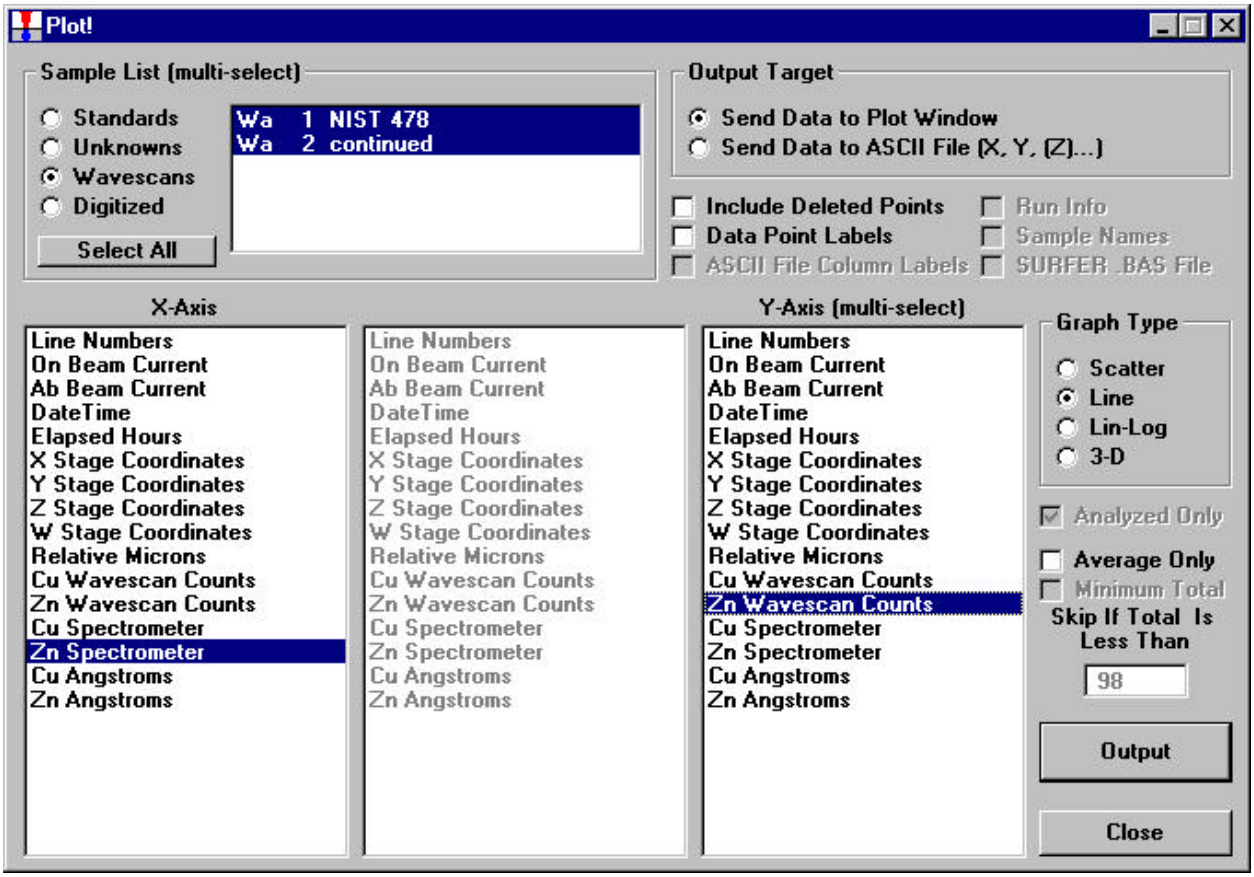
The **Graph Data** module allows a more robust treatment of the wavescan data. The plot of Cu Spectrometer position versus Cu Wavescan Counts is graphed as well as the locations of the on-peak and both off-peaks (vertical lines). Various options are available for evaluation of the data. Besides click and drag *Zoom* capabilities, a large selection of *KLM Markers* options may be enabled.

With the **Zoom On** button active, simply click and drag the mouse over the region the user wishes to magnify. The *Analyzed Elements* button of the *KLM Markers* may be selected, painting the various x-ray line positions for all analyzed elements into this plot.

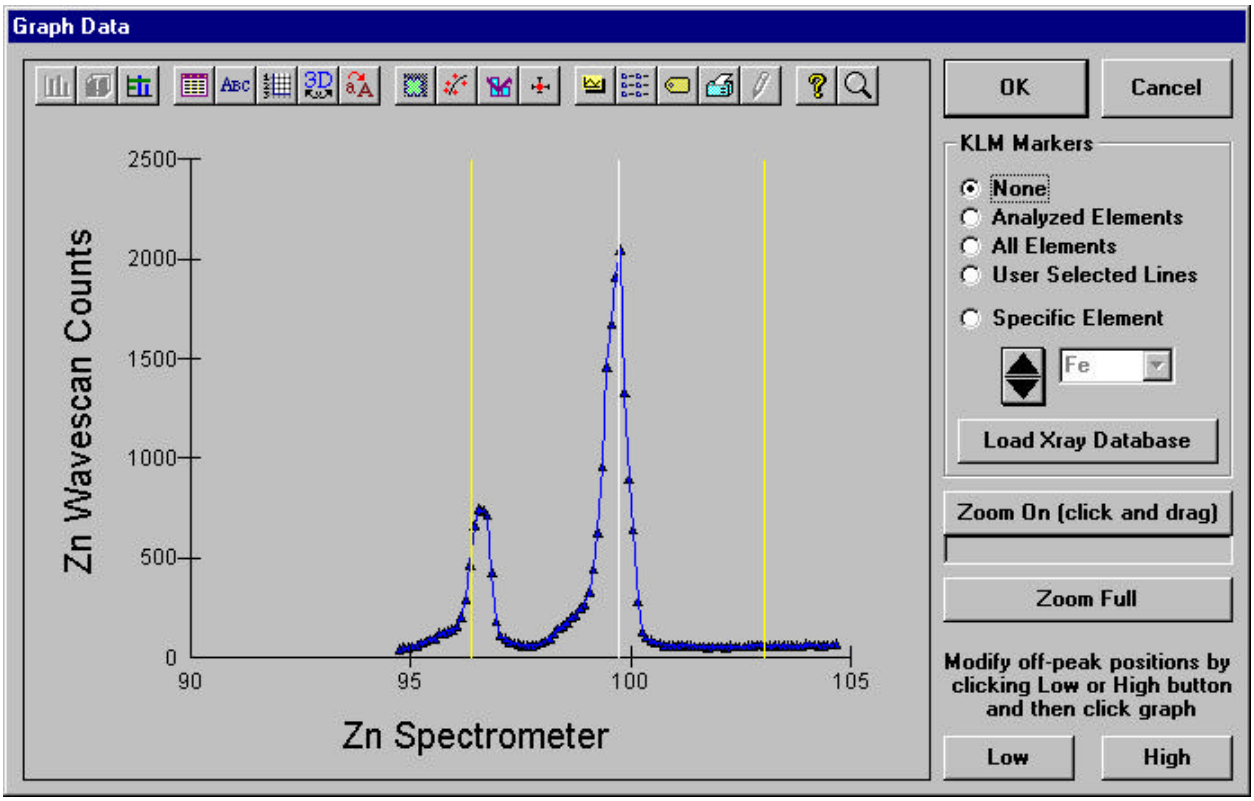


The default choices for both copper background positions (yellow vertical lines) appear sound as no analyzed element lies nearby and the background counts near these peaks are low. Click the **OK** button of the **Graph Data** window to return to the **Plot!** dialog box.

Next, the user evaluates the same data set for zinc. From the **Plot!** dialog box, select *Zn Spectrometer* from the *X-Axis* list and *Zn Wavescan Counts* from the *Y-Axis* list selections. Click the **Output** button.

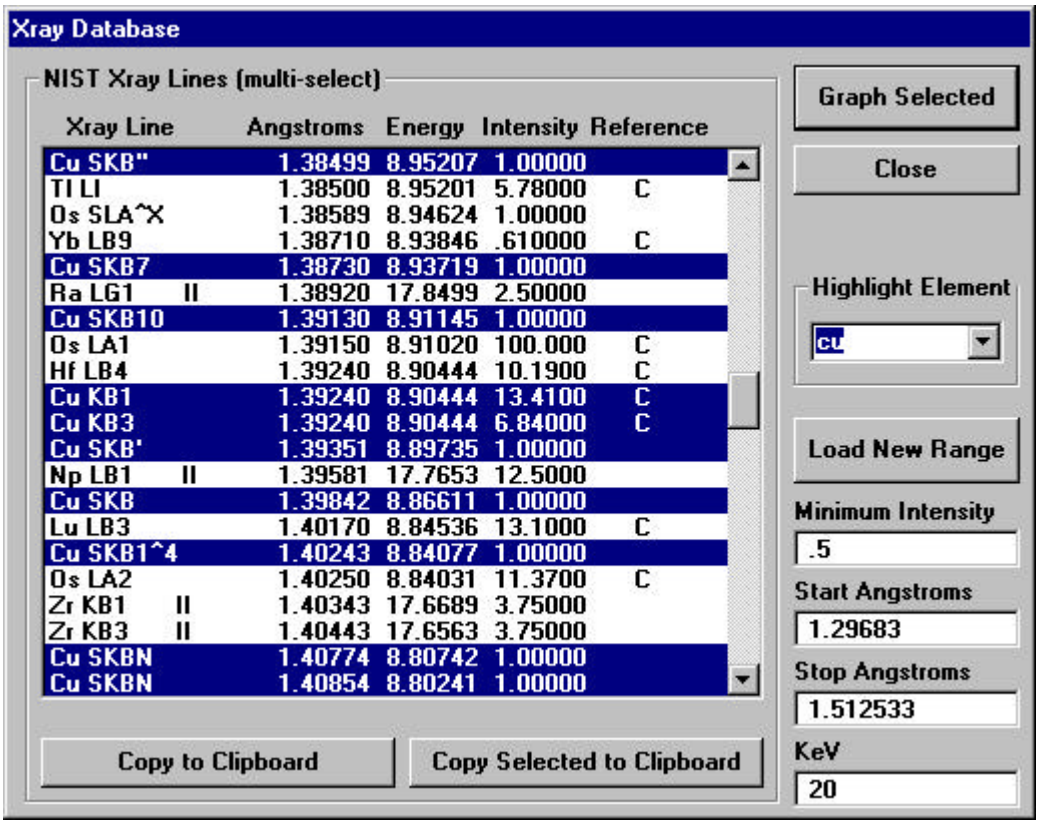


The **Graph Data** window for the zinc data set is shown below. Two peaks are visible and the user observes that the low background position lies on top of the smaller unknown peak.

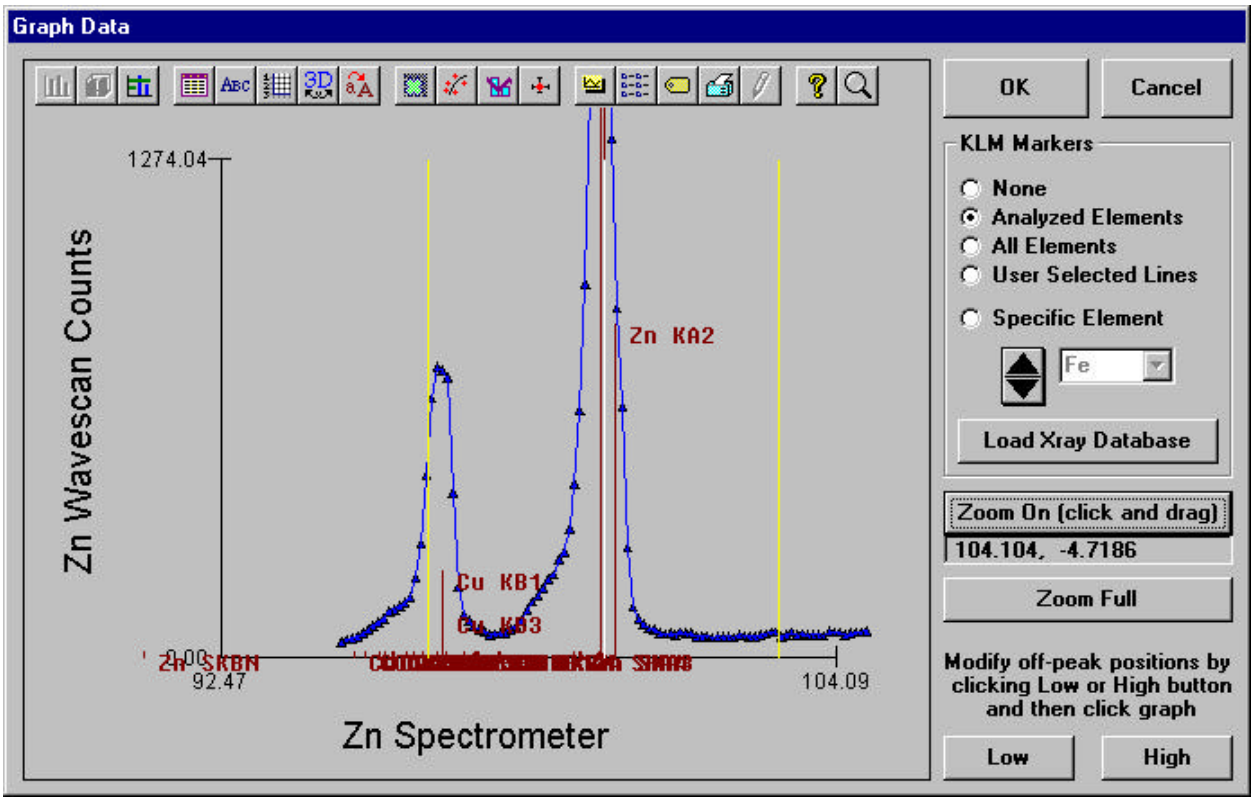


Use either the *KLM Markers* or the NIST x-ray database via the **Load Xray Database** button to evaluate the unknown peak. To open the NIST x-ray database, first click the *User Selected Lines* button, then click the **Load Xray Database** button opening the NIST x-ray line catalog.

The **Xray Database** window opens and the user may select or multi-select any x-ray line to plot on the **Graph Data** window, simply highlight a line(s) and click the **Graph Selected** button.

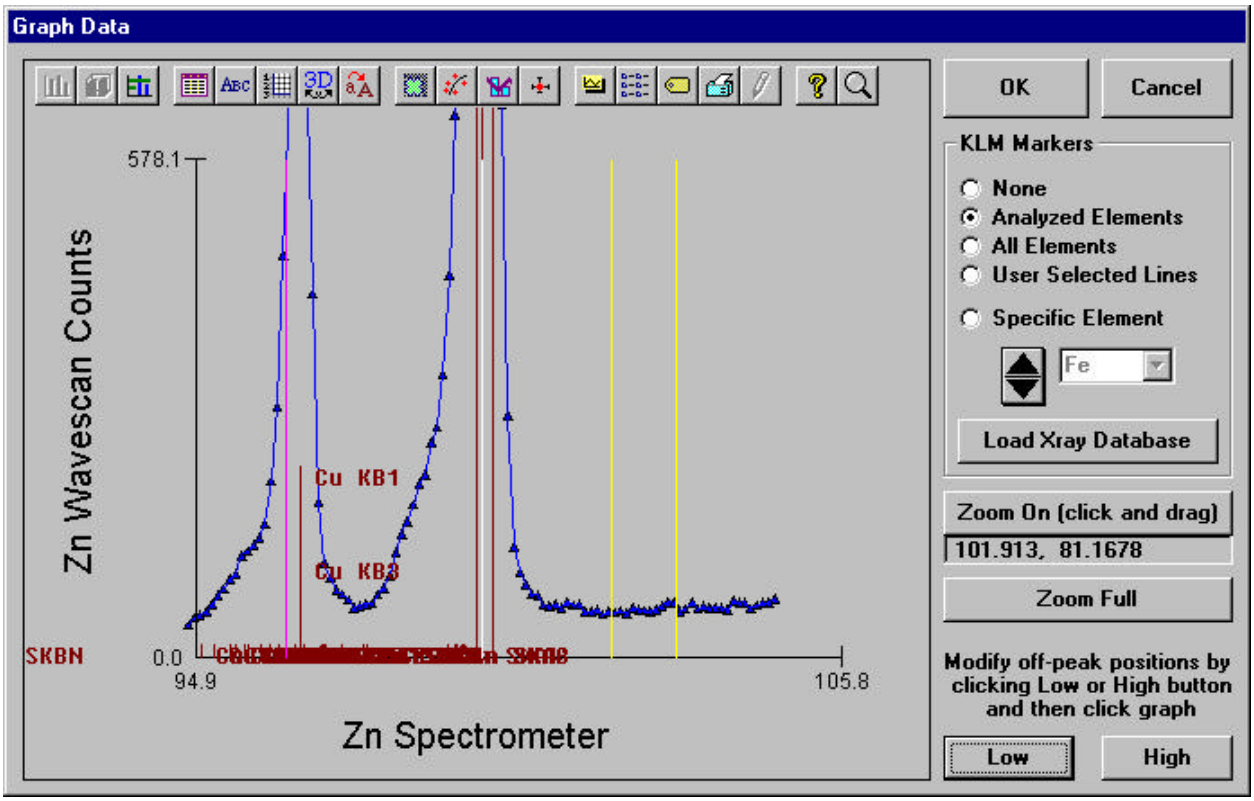


Examination of the data suggests that the second peak is due to the copper Kβ line. It is apparent that the low background position for zinc needs to be adjusted away from the copper Kβ line.

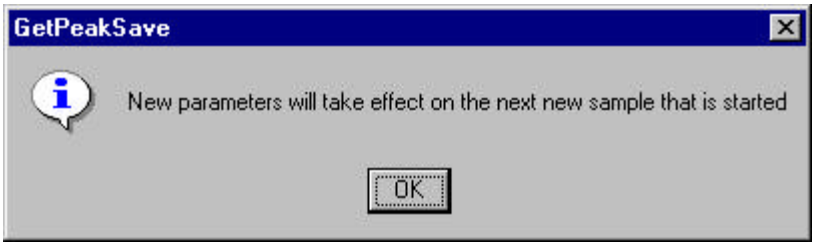


The user adjusts the low off-peak position by clicking the **Low** button, creating a crosshair on the **Graph Data** window. At any place on the plot the Zn Spectrometer position and Zn Wavescan Counts may be read, the values appear in the box below the two-way **Zoom On/ Hot Hit On** button. Move the crosshair to a new low background position and click the mouse. A new vertical line appears.

In the screen capture below both background positions are now on the same side (high side) of the peak avoiding all of the complicated x-ray structure around the low side of the zinc Kα line. Alternatively, if the user scanned further out on the low side (to lower L number) of the copper Kβ line, a suitable position for the low background may also be found.



Click the **OK** button to update this background position in the run and close the **Graph Data** window. The **GetPeakSave** window appears and the user is notified that new parameters (off-peak position) will take effect on the next new sample.

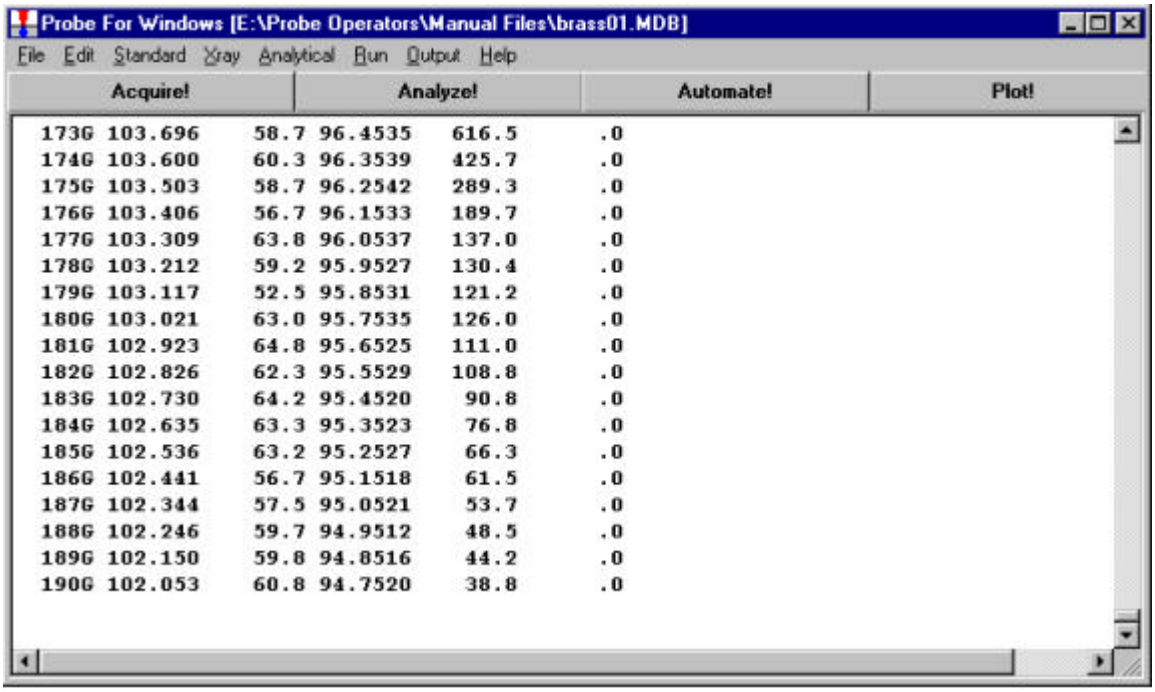


Click this **OK** button, returning to the **Plot!** window.

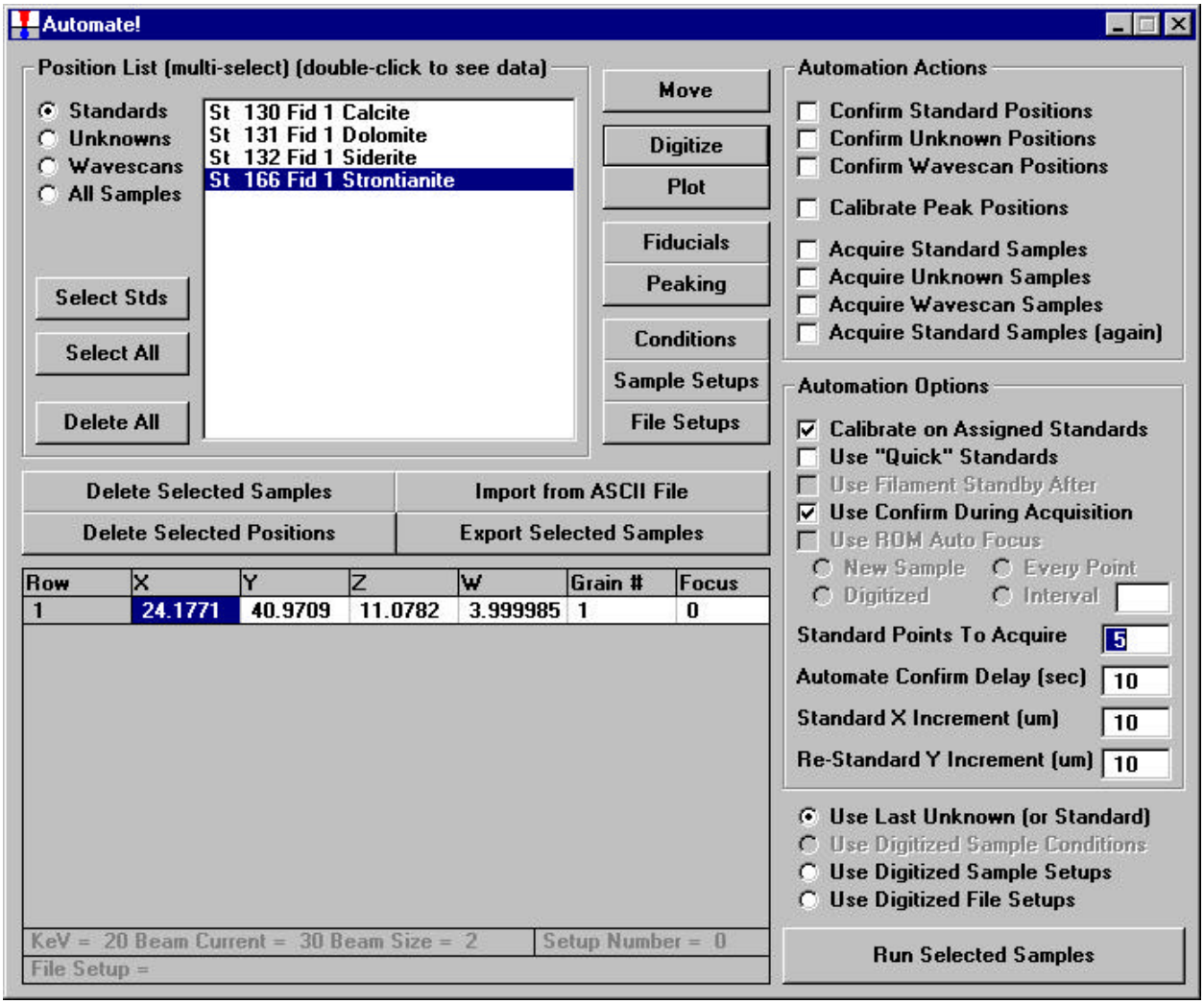
Finally, click the **Close** button to exit the **Plot!** window returning to the main PROBE FOR WINDOW log window.

Loading Standard Position Files

To run analytical standards using automation, requires that the computer know the physical location of all the standards for this run. Click the **Automate!** button from the main PROBE FOR WINDOWS log window.

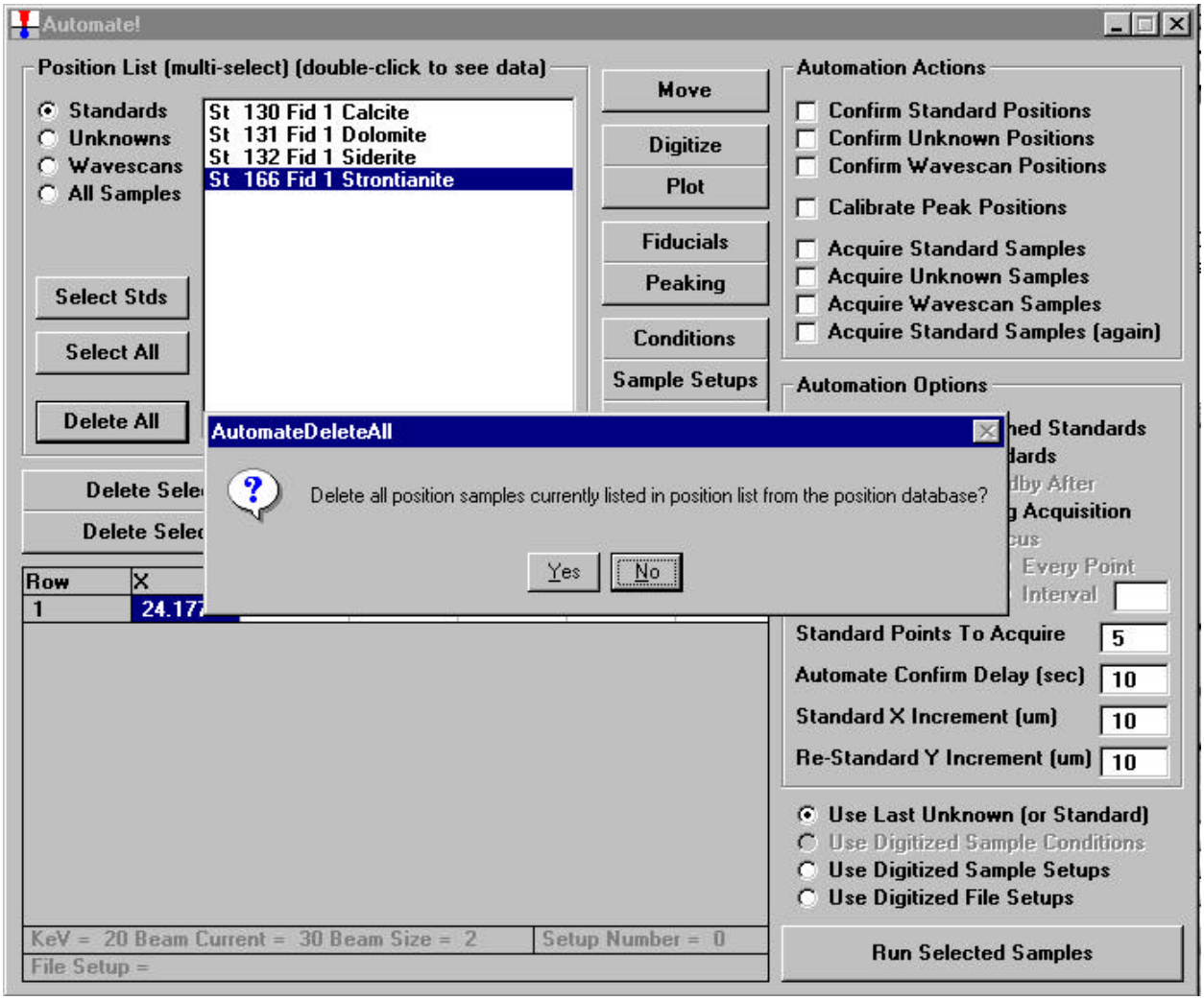


This opens the **Automate!** dialog box shown below.

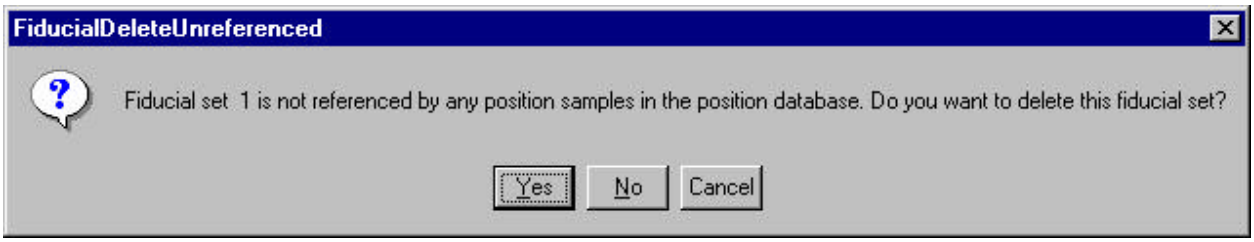


The last set of digitized standards used is visible in the *Position List* list box of the **Automate!** window. Currently, the four carbonate standards digitized for an earlier section of this manual are listed. These will be deleted and replaced by the appropriate standard position file(s). Normally, after initial setup, several sets of digitized standard positions would be visible in this list. Typically, the user would not delete these but rather append other position files to the list.

Click the **Delete All** button. This opens the **AutomateDeleteAll** window, seen below. Click the **Yes** button of the **AutomateDeleteAll** window to clear the *Position List* list box of all displayed position samples.

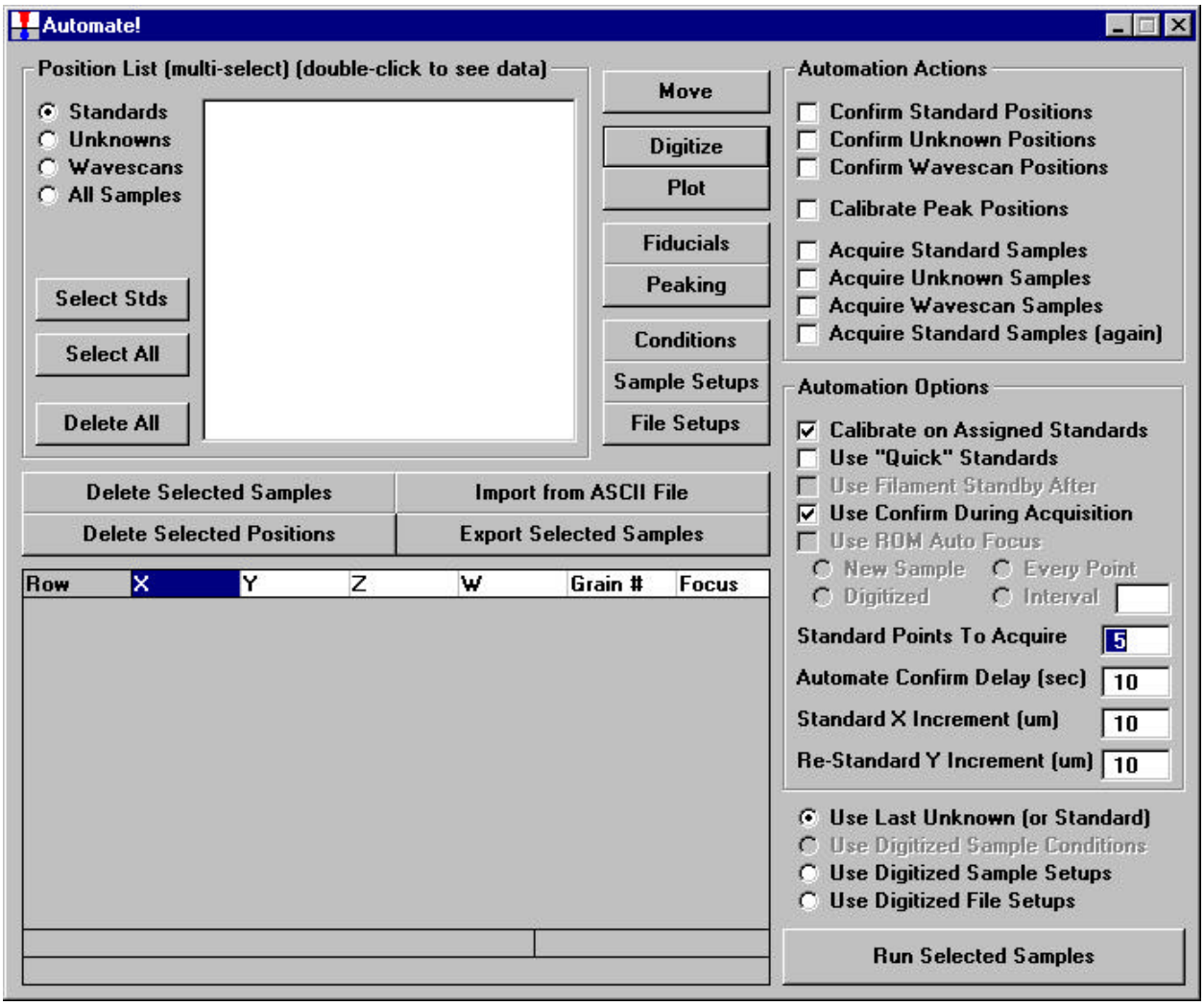


The **FiducialDeleteUnreferenced** window opens.

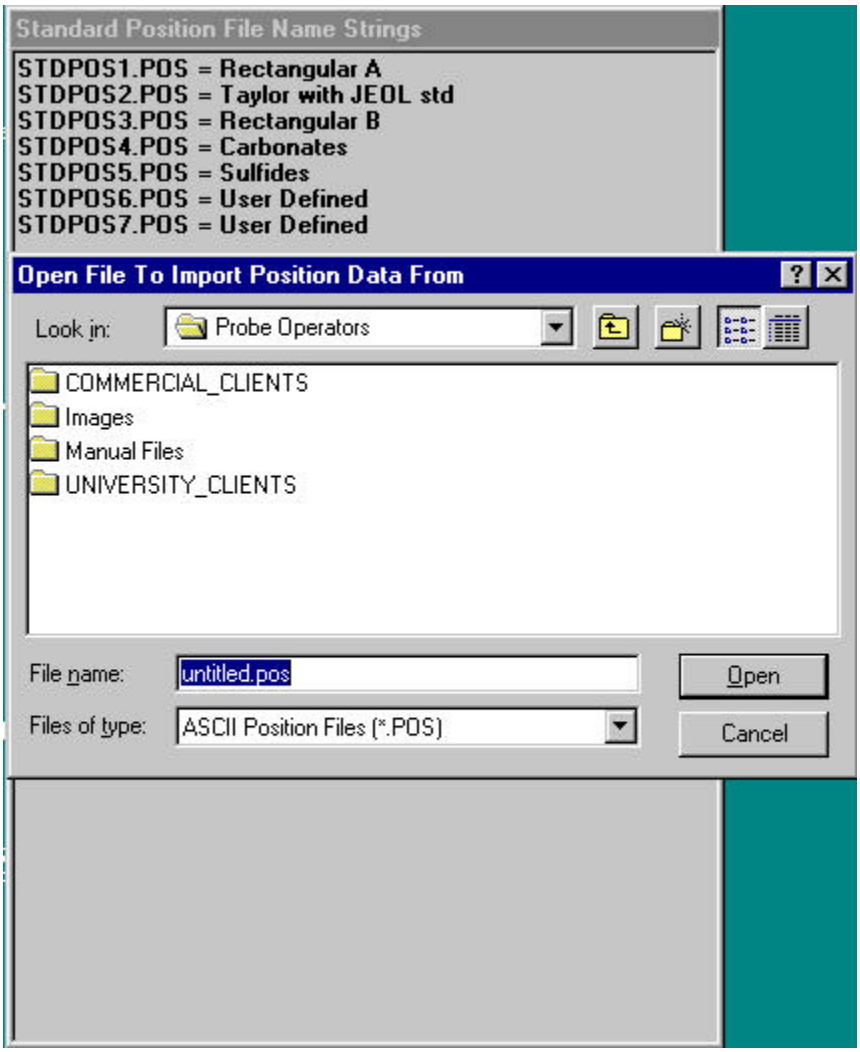


Click the **Yes** button to clear the fiducial coordinate set from the position database.

Click the **Import from ASCII File** button of the **Automate!** dialog box to import position samples from a previously saved ASCII file.

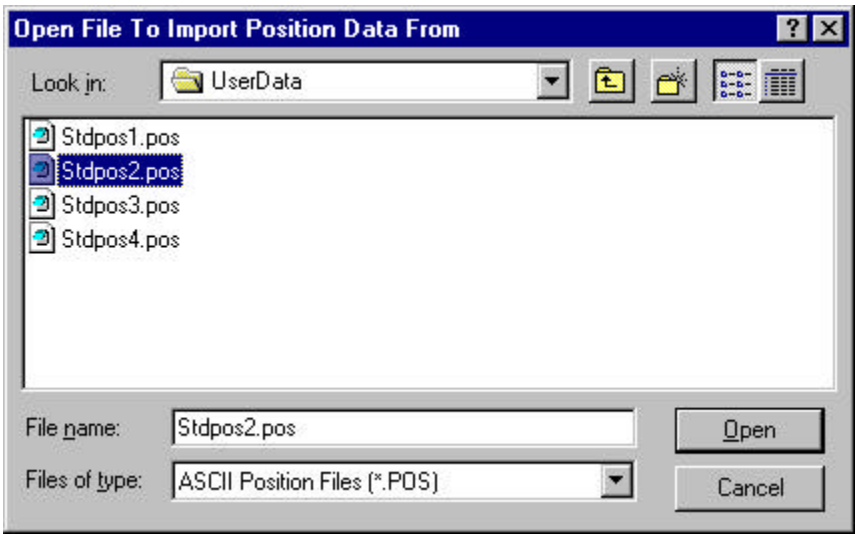


This action opens both the **Standard Position File Name Strings** and the **Open File To Import Position Data From** windows. The former window is based on the name strings in the PROBEWIN.INI file. It is assumed that the user has previously digitized all standard blocks and created STDPOSx.POS files. The metal standards to be used in the brass analysis are digitized in STDPOS2.POS.

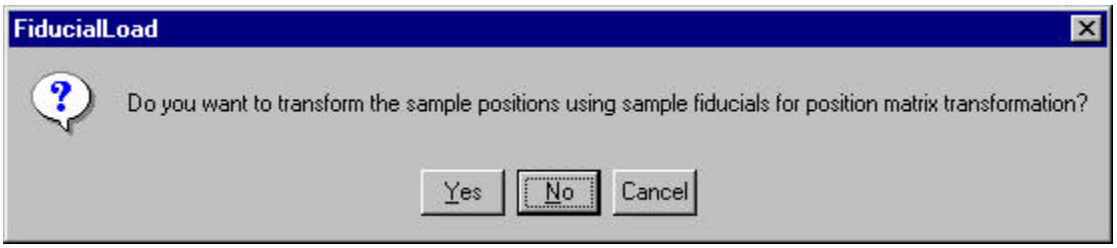


The *.POS files are located in C:\Program Files\Probe for Windows\UserData directory. Edit the *Look in:* location.

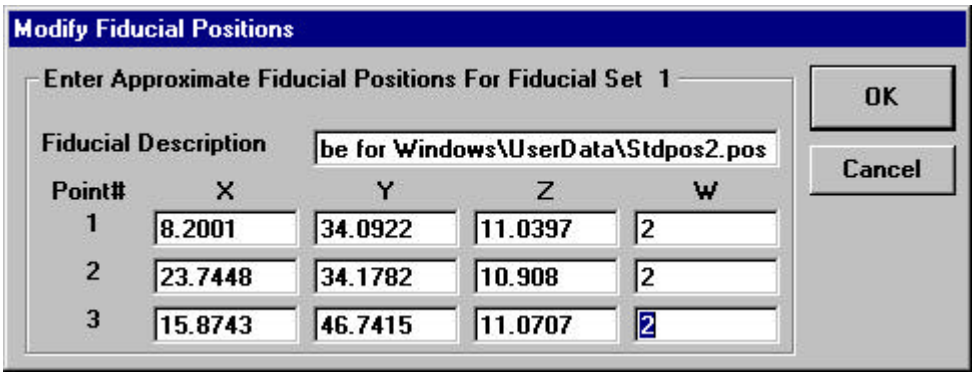
Type in the appropriate file name in the *File name* text box or simply highlight the file in the list and click the **Open** button.



This action opens the **FiducialLoad** window. Click the **Yes** button to do a fiducial transformation on this pre-digitized standard block to obtain an accurate set of standard positions.

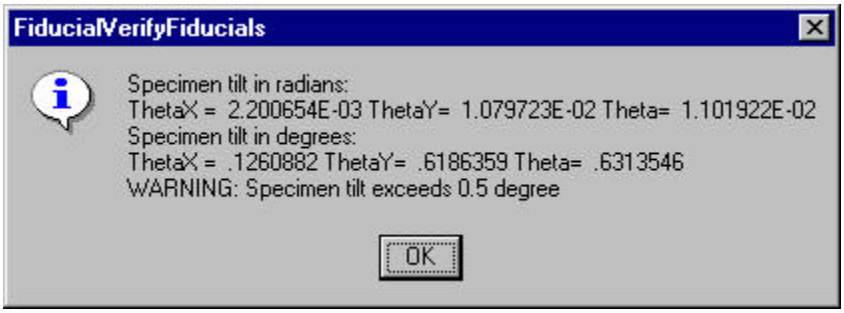


The **Modify Fiducial Positions** window opens. Normally the user would simply accept the defaults or edit the position text boxes for each point, including the appropriate stage location number (JEOL 733 use appropriate W stage position). When done, click the **OK** button.

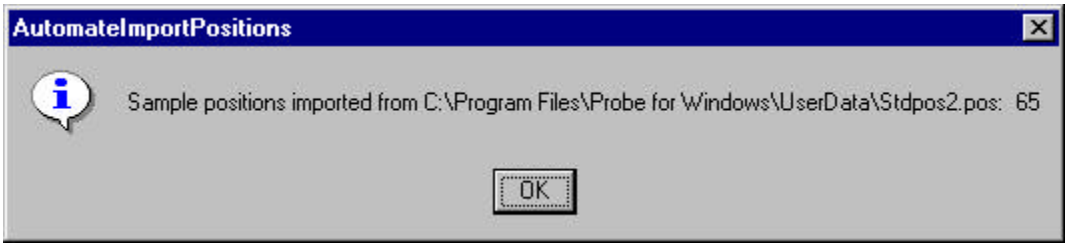


This action causes the stage motors to drive to the first fiducial coordinate in its lookup table. The **FiducialVerifyFiducial** window appears. Adjust the stage motors to center the first fiducial mark, click the **OK** button.

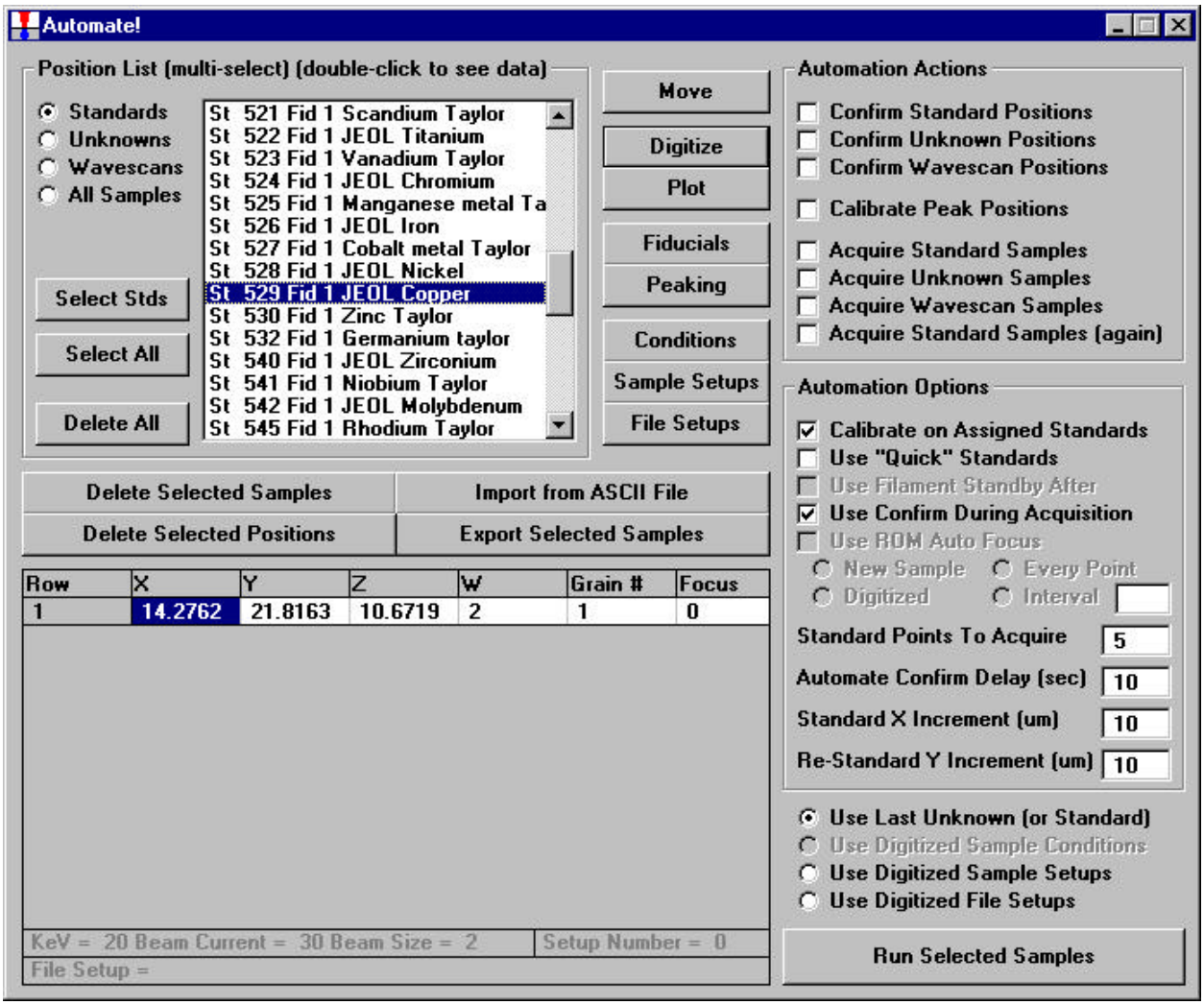
The computer will drive to each of the three fiducial marks for centering. Clicking the **OK** button after the third fiducial mark opens the **FiducialsVerifyFiducials** window. Click this **OK** button.



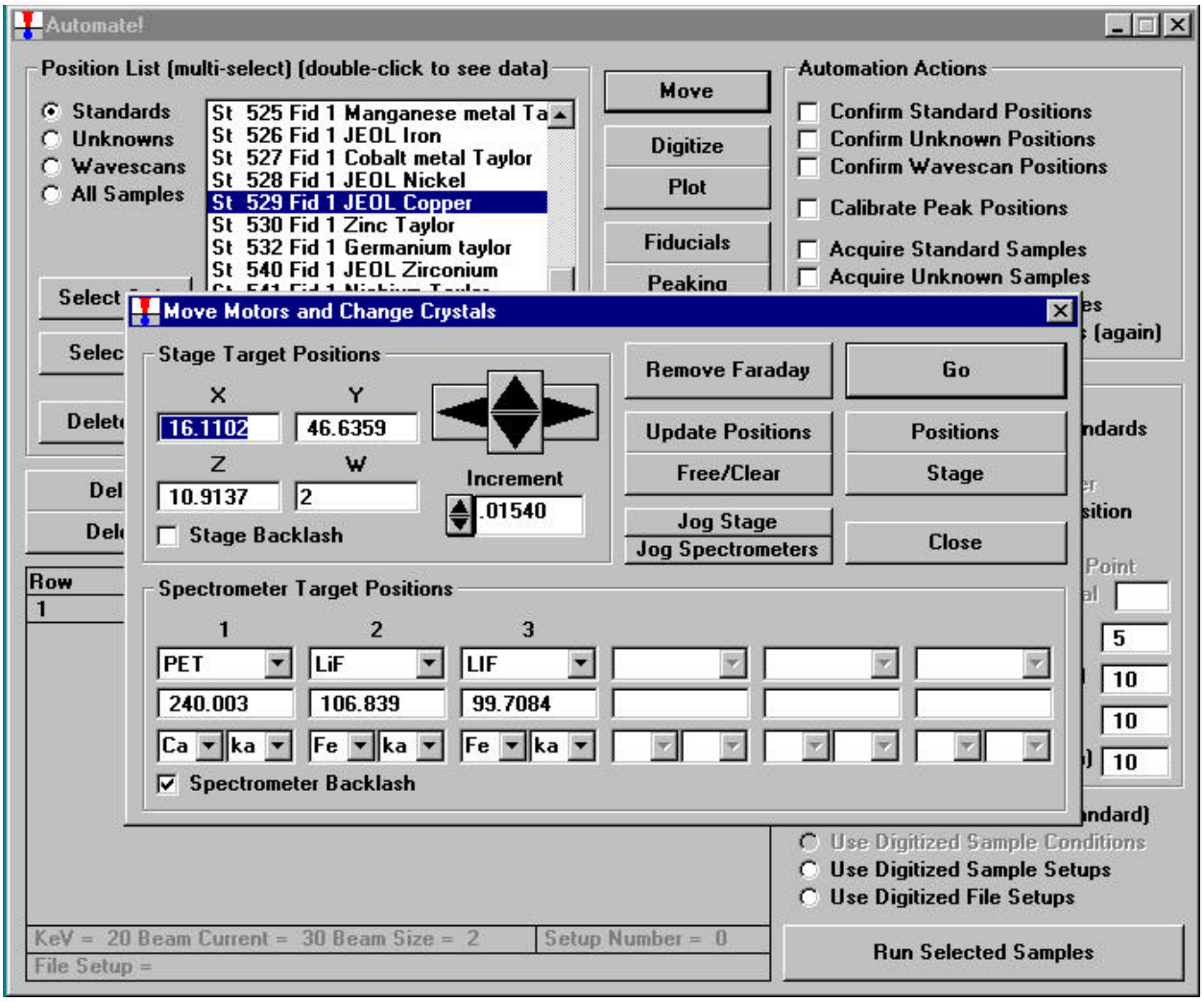
The program then imports and updates the position coordinates of all of the standards in the pre-digitized standard position file. The **AutomateImportPositions** window opens. Click the **OK** button returning to the **Automate!** window.



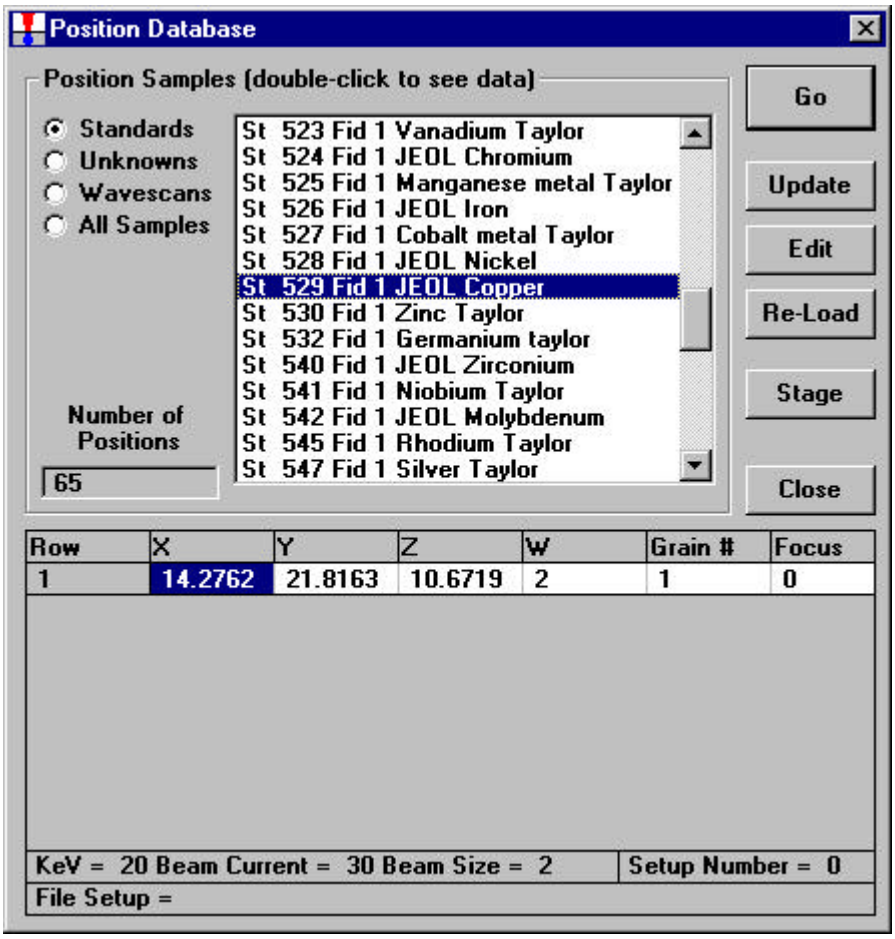
The **Automate!** window would appear as below. The currently transformed standard position file is listed in the *Position List* list box. In this example, the copper standard, number 529, has been highlighted and its coordinates are visible. If an additional standard position file (standard block) is required for use in the automation, the same procedure would be followed.



All of the standards listed in the *Position List* list box may now be accessed by the program during any automation action. For instance, it is now possible to have the computer drive to any standard on this block. The user may click the **Move** button of the **Automate!** window opening the **Move Motors and Change Crystals** dialog box. Then, click the **Positions** button.



This opens the **Position Database** dialog box. From here any sample that has been digitized can be located by simply selecting it and clicking the **Go** button.



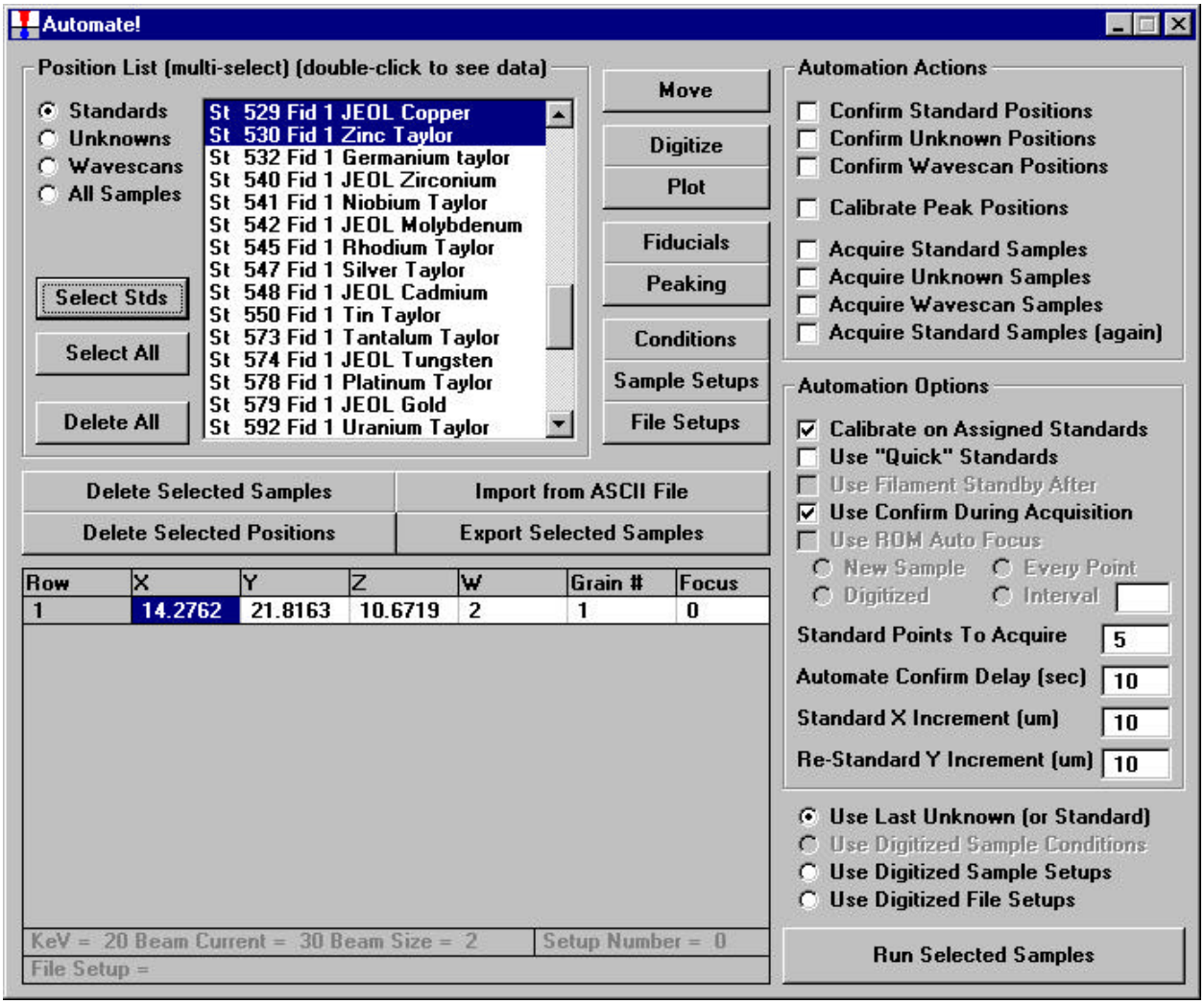
Once the stage motors drive the stage to the chosen standard, exit the **Position Database** by clicking the **Close** button. Likewise, the user may close the **Move Motors and Change Crystals** window by clicking its **Close** button, returning to the **Automate!** window.

Automation Actions

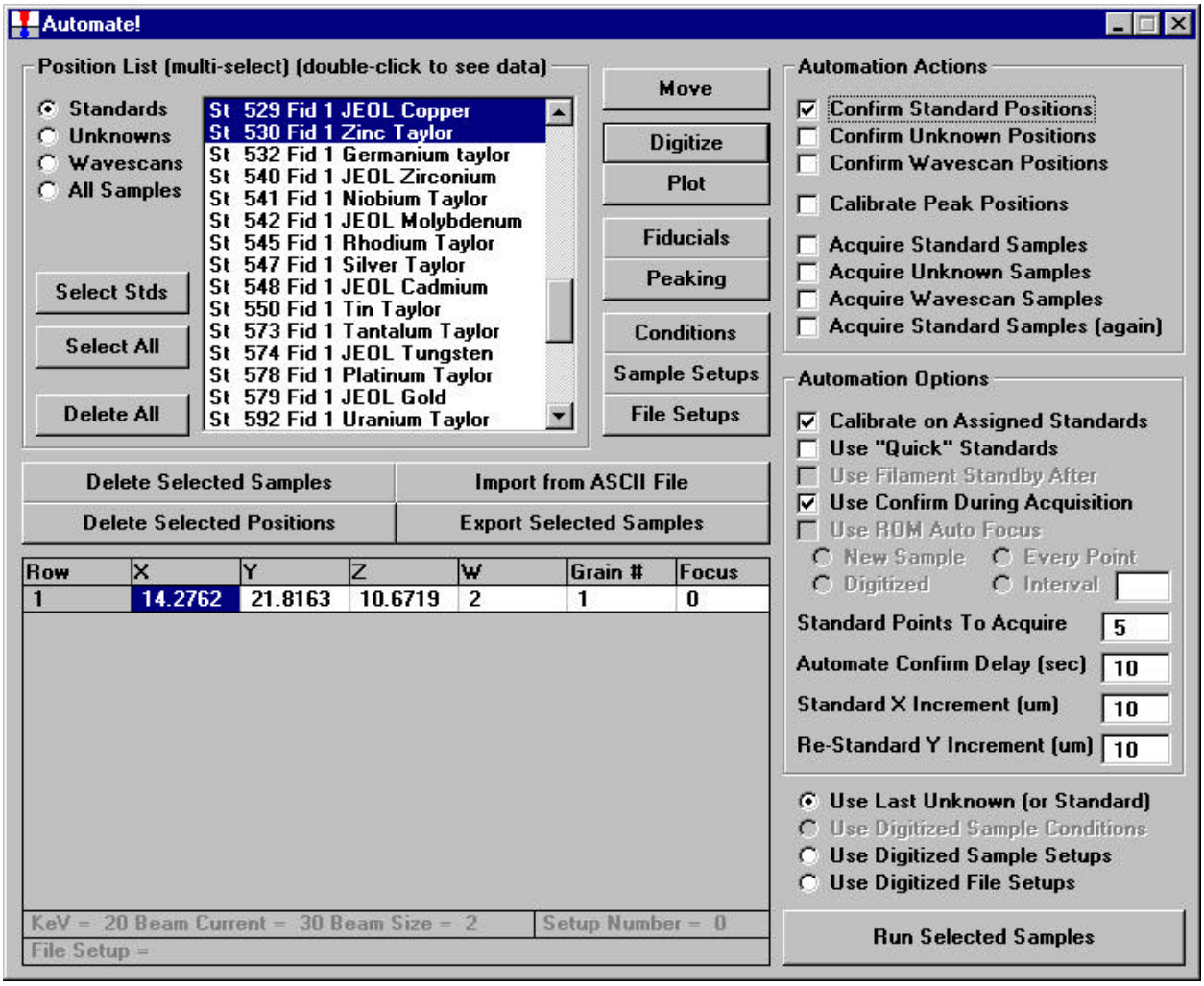
Confirm Standard Positions

All of the basic peak centering and x-ray count acquisition procedures may be automated. This is accomplished via the **Automate!** window.

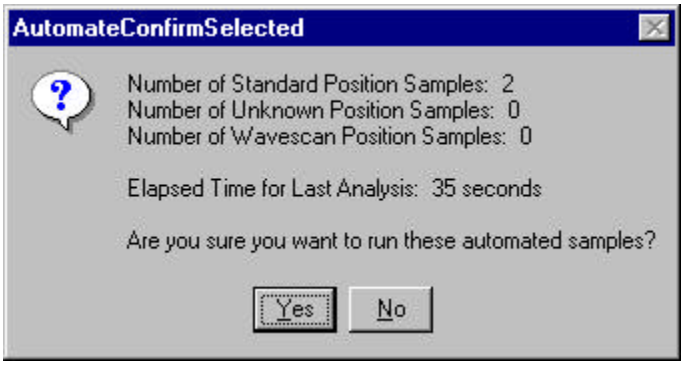
Click the **Select Stds** button of the **Automate!** dialog box. All standards that have been added to the current run will be highlighted in the *Position List* list box. In this example, the two standards copper (529) and zinc (530) metal are highlighted.



The user might start by checking the location and focus of each standard selected for the automated analysis. Click the box for *Confirm Standard Positions* under *Automation Actions*. Click the **Run Selected Samples** button.

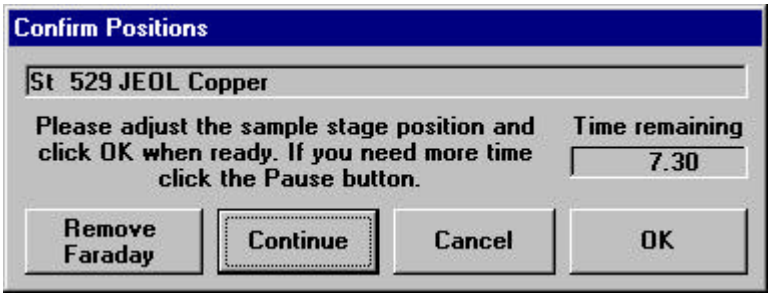


The **AutomateConfirmSelected** window opens informing the user that two standards were chosen and asks if the user wants to run these automated samples, click **Yes**.



The program then sends the stage motors to the fiducial transformed coordinates for the first selected standard and opens the **Confirm Positions** window. Clicking the two-way **Pause/Continue** button suspends the 10 second countdown (user defined in the PROBEWIN.INI file). Adjust the stage motors (X , Y, and Z) to a new, clean analysis position. Click the **OK** button of the **Confirm Positions** window when done, sending the stage to the next standard to confirm its position. Again, the **Confirm Positions** window opens, allowing the user to pause the countdown and adjust the sample position.

If more than one position is digitized, the software moves to the first position and updates all positions for that sample by the same X, Y, and Z offset.

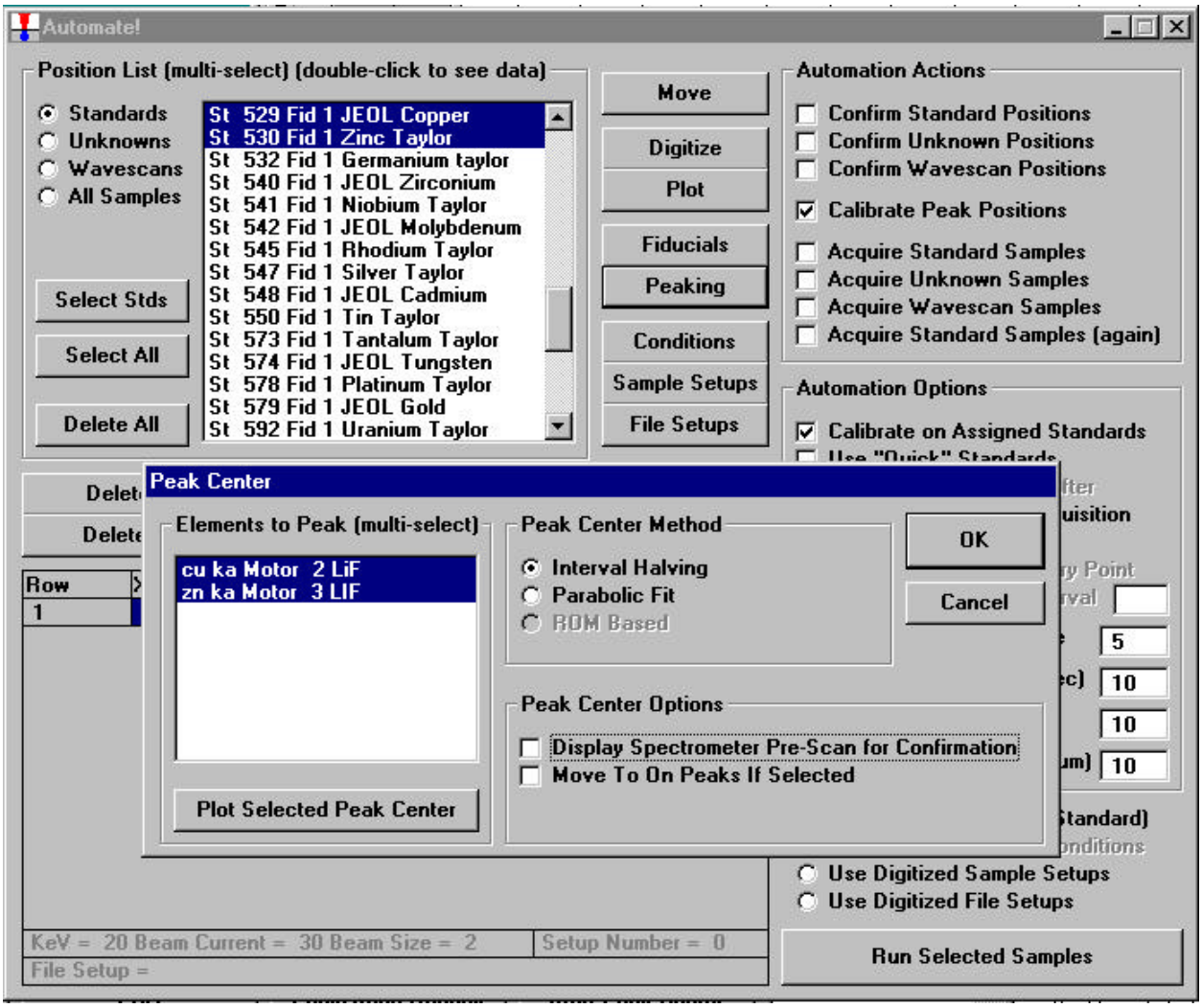


After the final standard is confirmed, the **AcquireStop** window appears. Click this **OK** button returns to the **Automate!** dialog box.

Calibrate Peak Positions

X-ray peaking may be automated from the **Automate!** window as follows. Under *Automation Actions* click only the *Calibrate Peak Positions* box. Under *Automation Options* click the *Calibrate on Assigned Standards* box. This option causes the program to attempt a peak center on a standard position sample if the standard is assigned as the primary standard for that element. If the element has no assigned standard, then the program will attempt to assign one automatically based on the highest concentration of the elements present among the standards in the run.

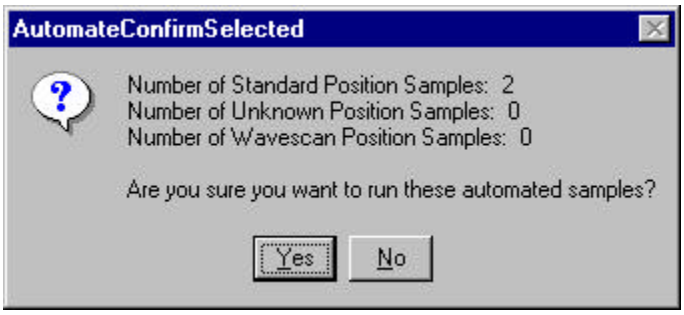
Next, click the **Peaking** button to open the **Peak Center** dialog box.



In the **Peak Center** dialog box, highlight (select) all of the elements in the *Elements to Peak* list box, and click on a *Peak Center Method*. A spectrometer pre-scan is useful if that element has not been run recently or if maintenance has occurred on the spectrometer. Click the **OK** button of the **Peak Center** window.

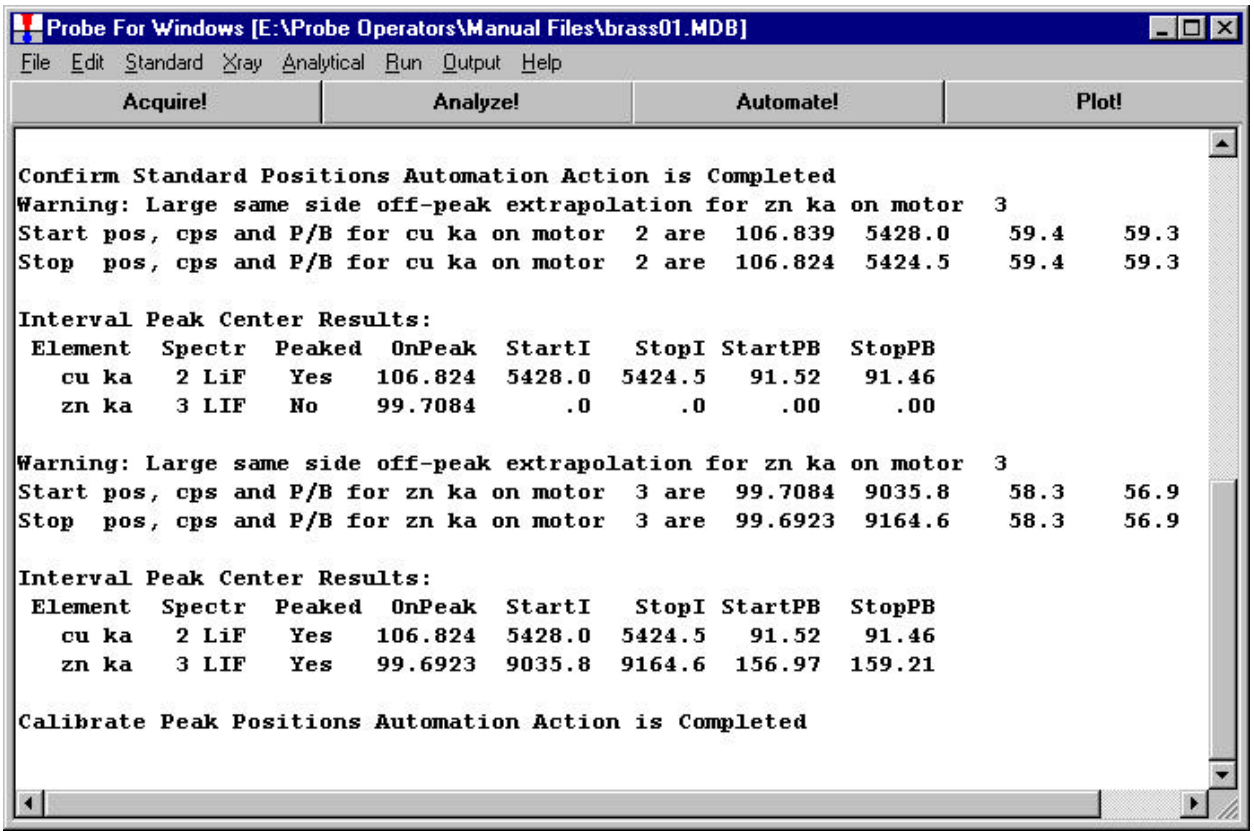
Click the **Run Selected Samples** button from the **Automate!** window.

This opens the **AutomateConfirmSelected** window. To run these automated samples, click **Yes**.



The stage motors move to the position coordinates of the first standard in the *Position List* list box. If the *Use Confirm During Acquisition* box under *Automation Options* is checked then the computer automation will pause at each standard (**Confirm Positions** window will open) for some user defined amount of time to allow the operator to adjust the stage position and focus. The spectrometers go through the peaking routine to peak center the spectrometer position to the intensity maximum for all the elements assigned to that standard. After finding a new peak position and reporting the results to the main log window, the stage motors move on to the coordinates of the next standard highlighted in the *Position List* list box. Once situated on this standard, the spectrometers peak center those elements assigned to it. This procedure continues until all standards are done. When all automation action is complete, the **AcquireStop** window appears and requests the user to click the **OK** button.

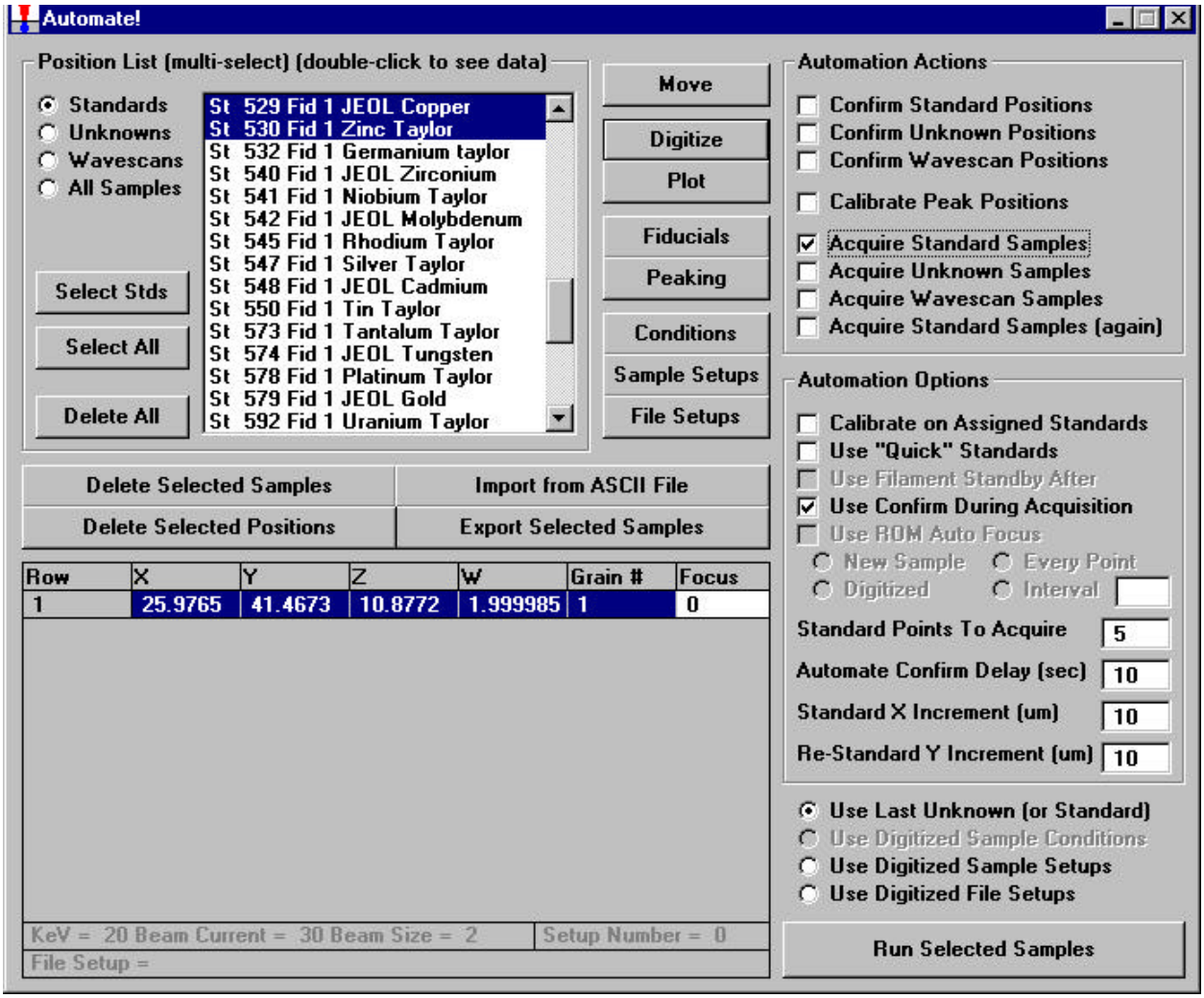
The following summary of the peak automation for the two standards is found in the main log window.



Acquire Standard Samples

The next step is to calibrate the analytical standards in preparation for unknown samples. The user may automate the entire acquisition of x-ray counts on all standards as follows.

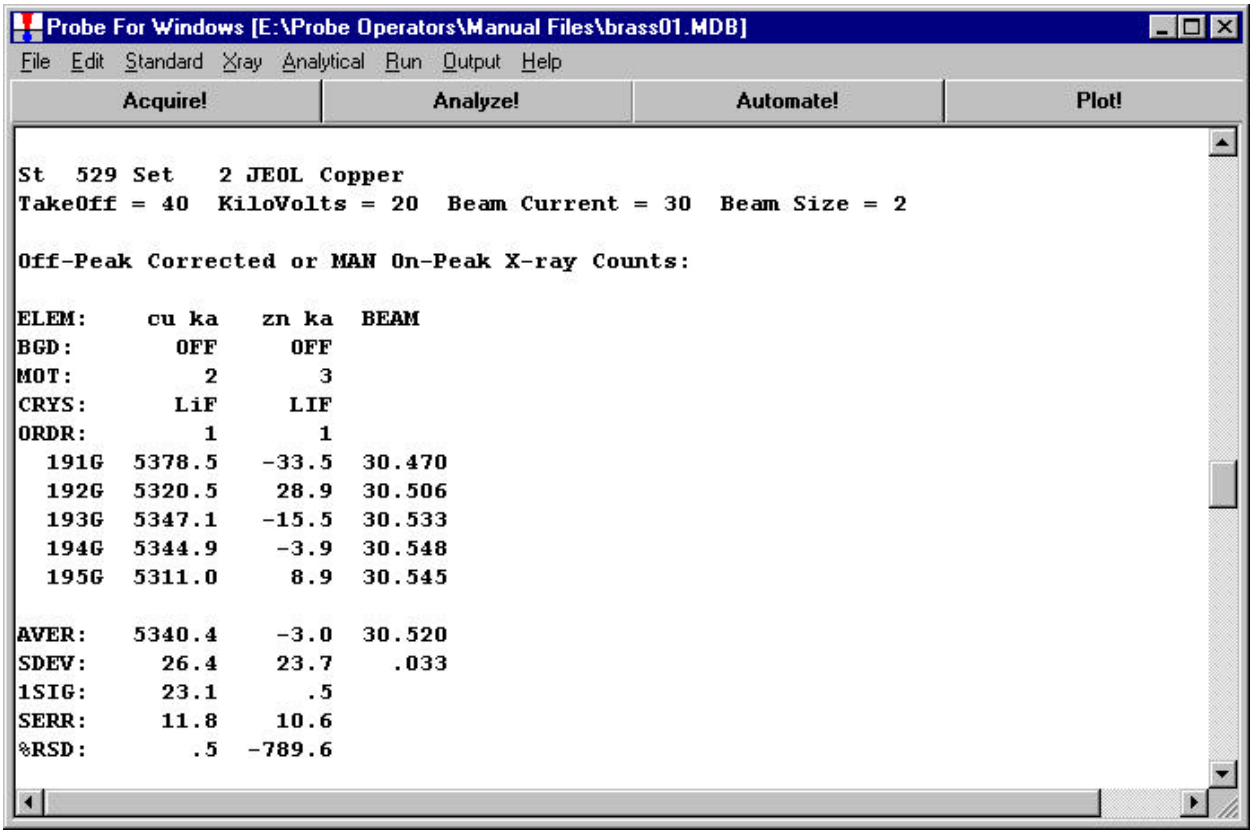
From the **Automate!** dialog box and under *Automation Actions*, click only on the *Acquire Standard Samples* box. Under *Automation Options*, select the number of *Standard Points To Acquire* and whether to use the *Confirm During Acquisition* feature. In this example, five standard points are entered along with a *Standard X Increment* of 10 um. as well as the *Confirm During Acquisition* option. Click the **Run Selected Samples** button.



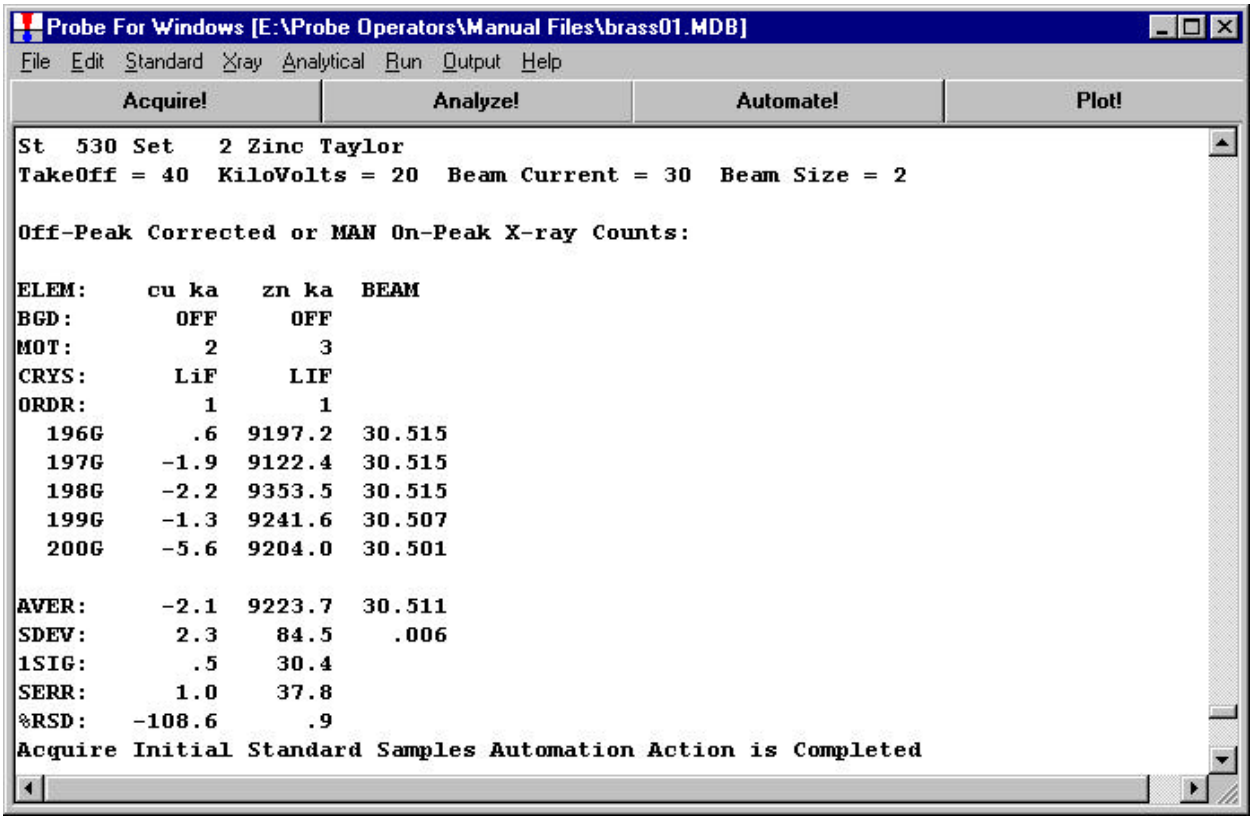
The **AutomateConfirmSelected** window opens again, informing the user that two standards are chosen and asks if you want to run these automated samples, click **Yes**.

The stage moves to the coordinates of the first standard in the *Position List* list box, the **Confirm Positions** window opens, allowing a readjustment of the stage position and optical focus. A complete analysis (all elements in the current sample) are measured, x-rays are counted on peak and at both background positions for times specified in the **Count Times** window. Finally, the Faraday cup is measured. The stage jogs 10 um in the X direction and this procedure is repeated for the number of points specified in the *Automation Options* section of the **Automate!** dialog box. After completing data collection on the first standard, the stage travels to the next standard in the list and acquires five complete analyses on that standard. After finishing the automation schedule the familiar **AcquireStop** window opens and requires the user to click the **OK** button thereby returning to the **Automate!** window.

The log window results for the copper standard x-ray count acquisition is seen below.

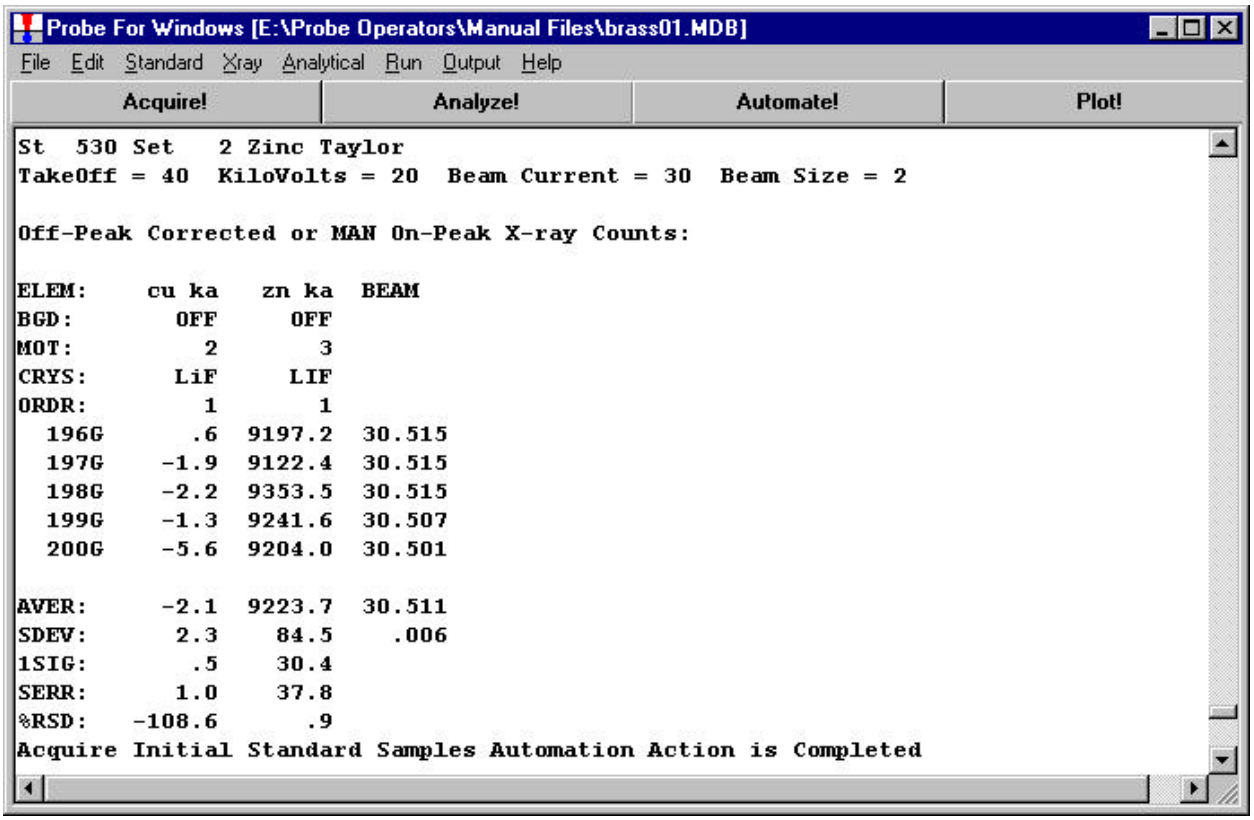


The log window results for the zinc standard x-ray count acquisition is displayed below.

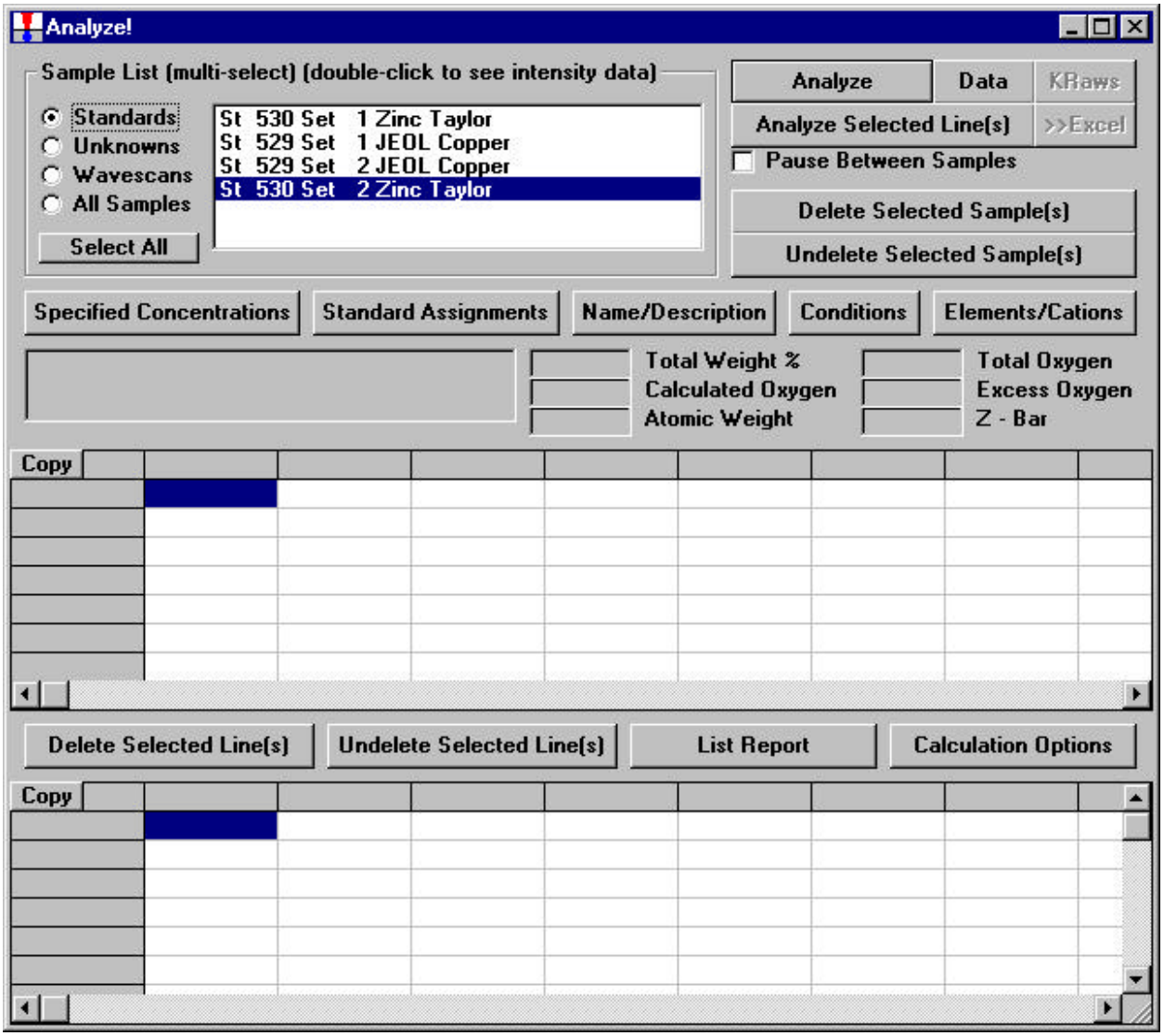


Analyze Standard Data

After standard data is acquired it is useful to analyze the data to check for agreement among standards and for possible interferences. Click the **Analyze!** button in the main PROBE FOR WINDOWS log window.

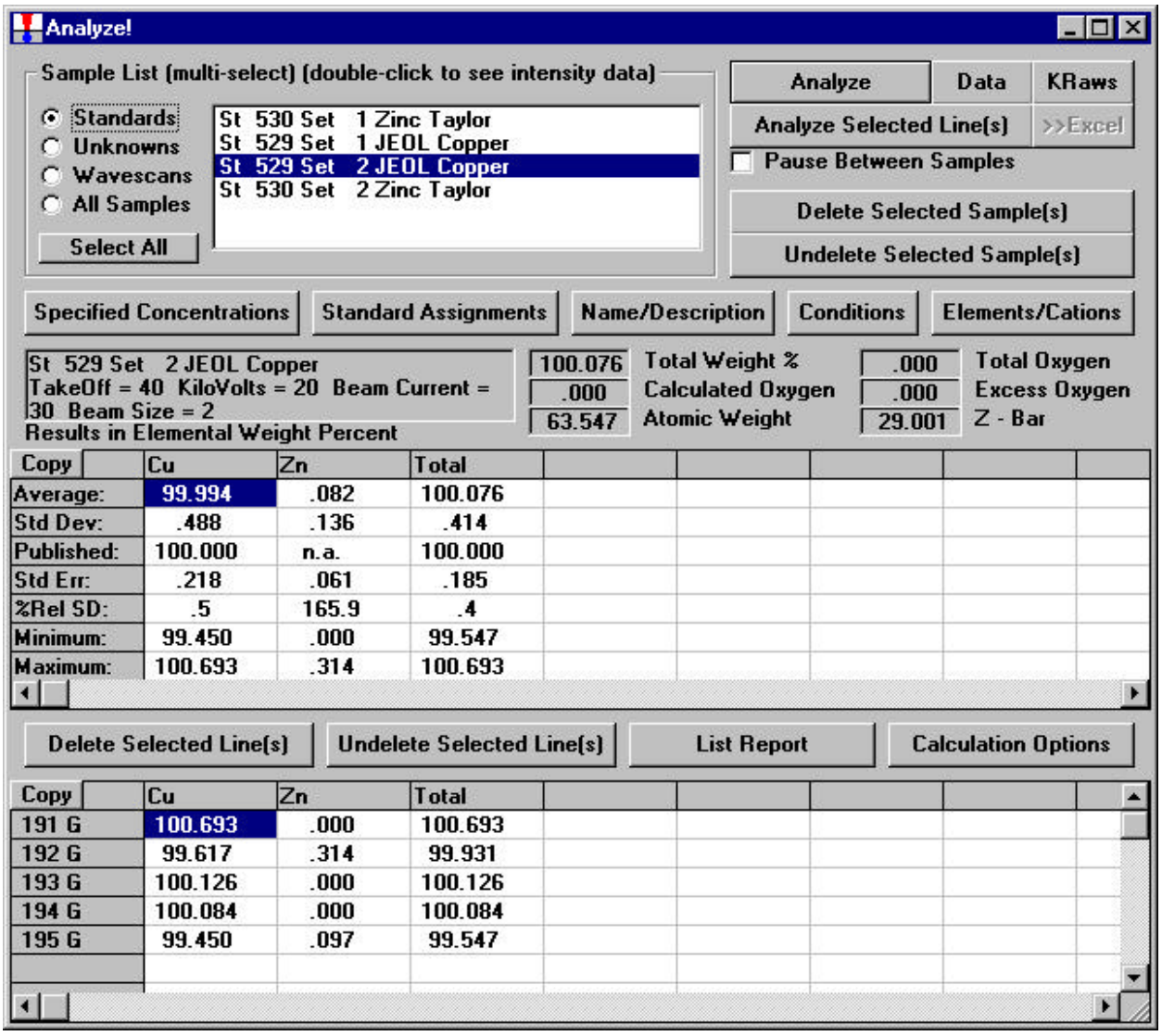


This opens the **Analyze!** dialog box.



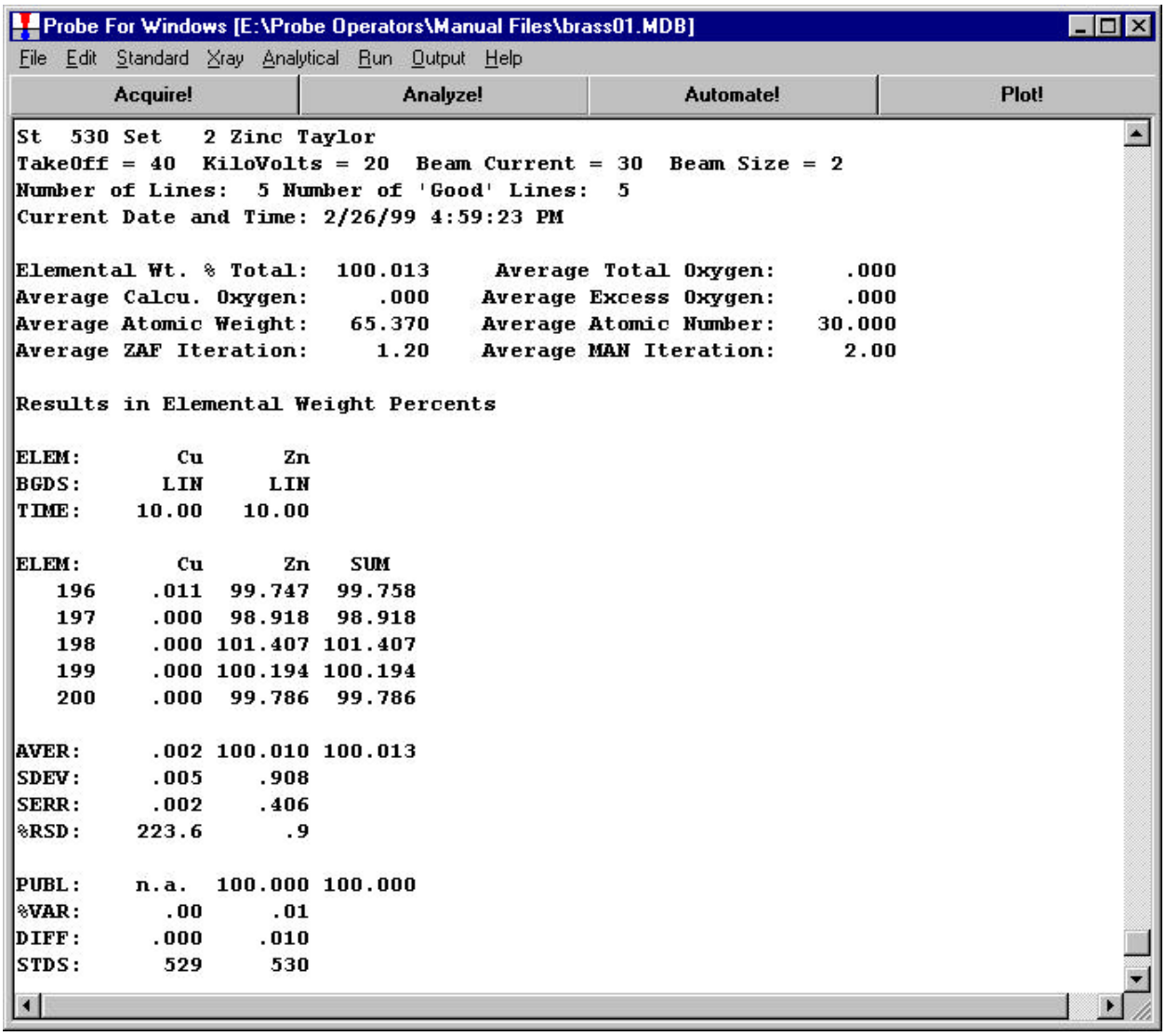
The *Sample List* list box contains the standards acquired so far. To examine the data acquired on the two standards run under automation, first choose the copper metal, selecting *St 529 Set 2 JEOL Copper* and click the **Analyze!** button.

The results for the five automated standard analyses of the copper metal are shown below. Each individual line (191G to 195G) is illustrated along with the *Average*, *Std Dev* and a variety of other statistical parameters for the acquired points (see User's Guide and Reference documentation for additional details).



If the sample that has been run is a standard, the program will show a *Published* line as well in the analysis output. This is the weight percent value for the element as entered in the standard database. If an element is not found in the standard database it is shown as n.a. or not analyzed.

Selecting *St 530 Set 2 Zinc Taylor* and clicking the **Analyze** button exports the following data (zinc metal standard numbers) to the main PROBE FOR WINDOWS log window.



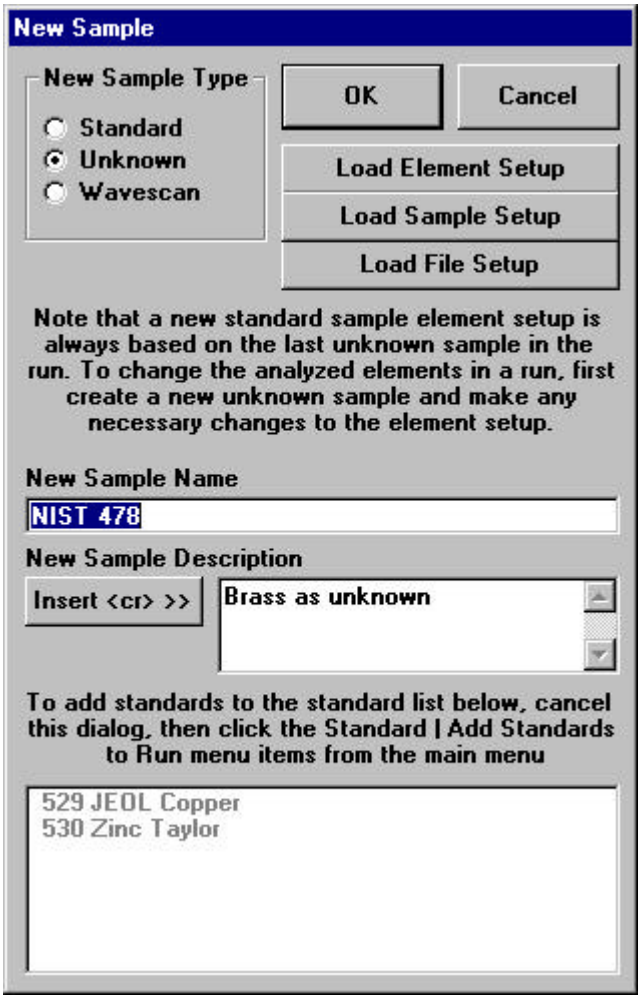
Both standards look ok, the user may move on to analyze unknowns.

Unknown Sample Data Collection and Analysis

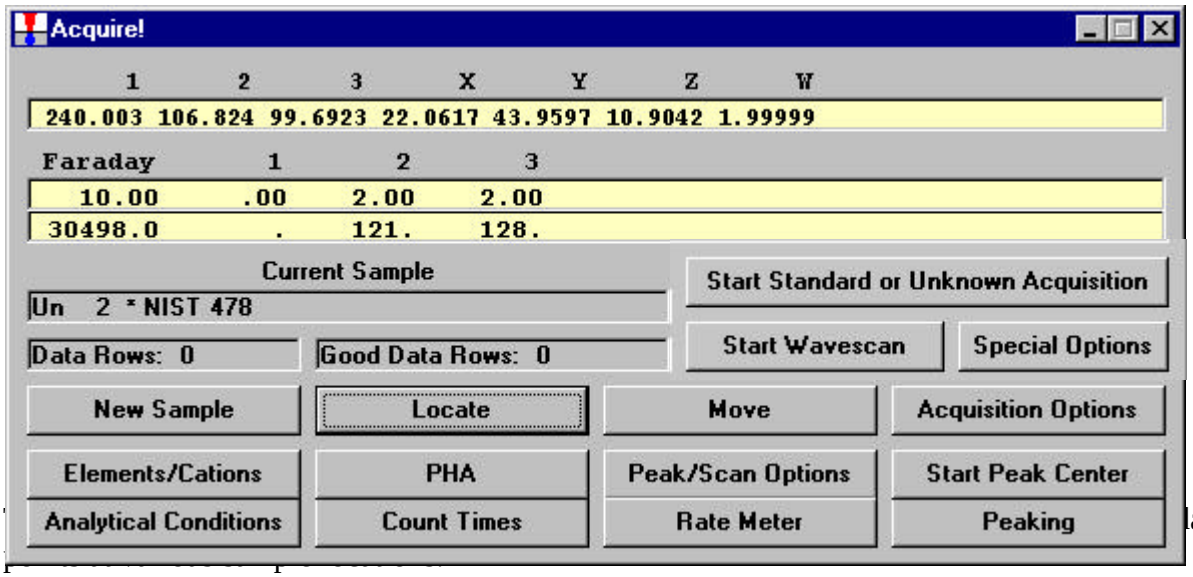
To collect x-ray data on an unknown sample, minimize the **Analyze!** window and/or bring forward the **Acquire!** dialog box to start a new sample.

Click the **Move** button on the **Acquire!** window to drive the stage to the coordinates of the first unknown sample.

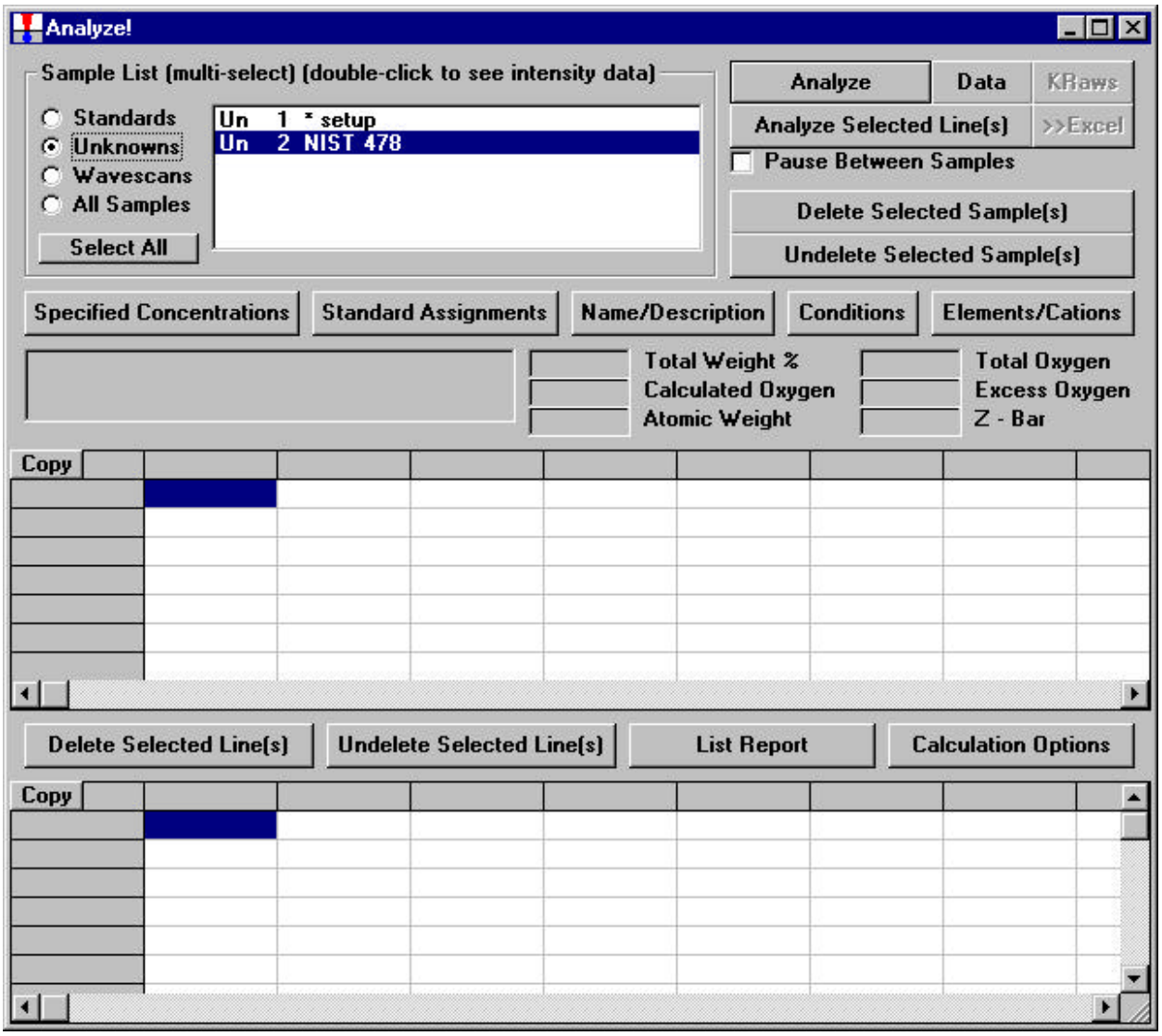
Click the **New Sample** button to activate the **New Sample** dialog box. Enter an appropriate sample name and description into the *New Sample Name* and *New Sample Description* text boxes. Check that the *Unknown* button under *New Sample Type* is checked and then click the **OK** button.



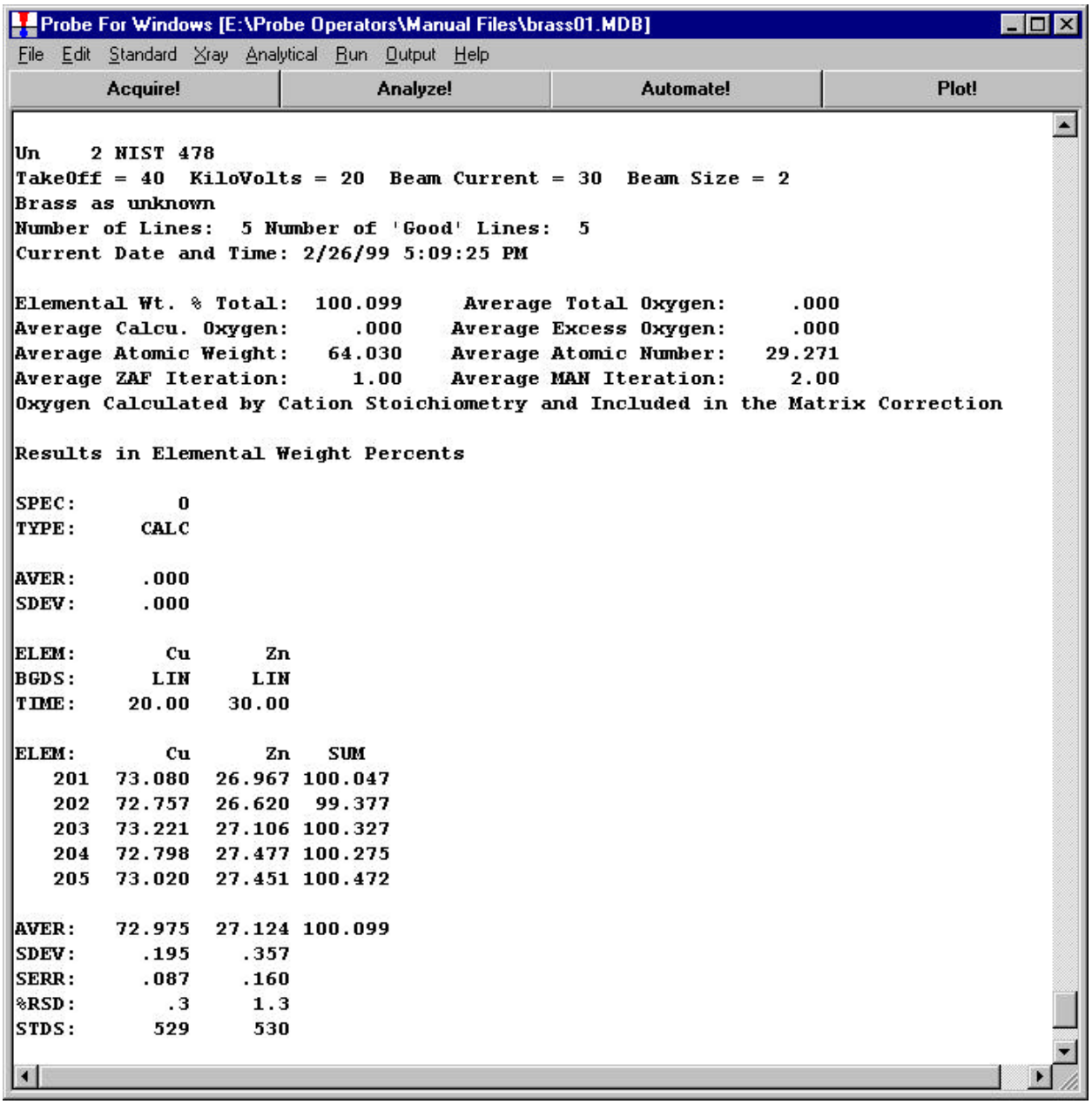
To start acquiring x-ray counts on the first unknown sample (NIST 478), simply click the **Start Standard or Unknown Acquisition** button of the **Acquire!** window.



Next, the **Analyze!** dialog box is reopened or simply brought forward. Click the *Unknowns* button under the *Sample List* buttons and highlight (select) *Un 2 NIST 478*.



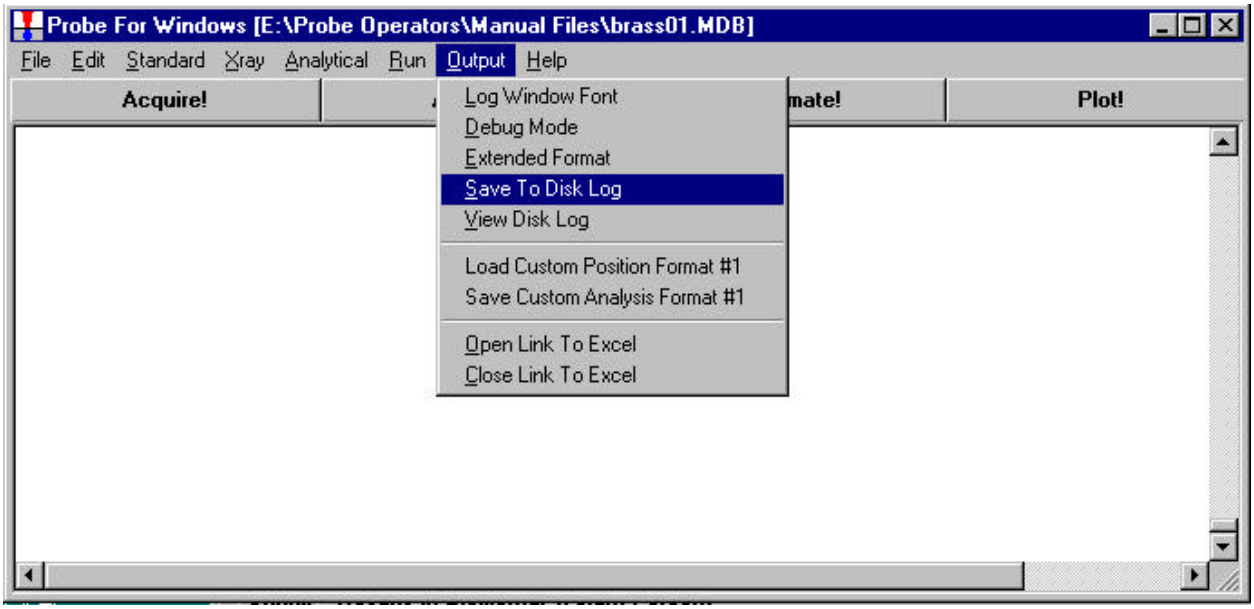
Clicking the **Analyze** button calculated the results for these five points and those values are viewed below, as displayed in the main log window.



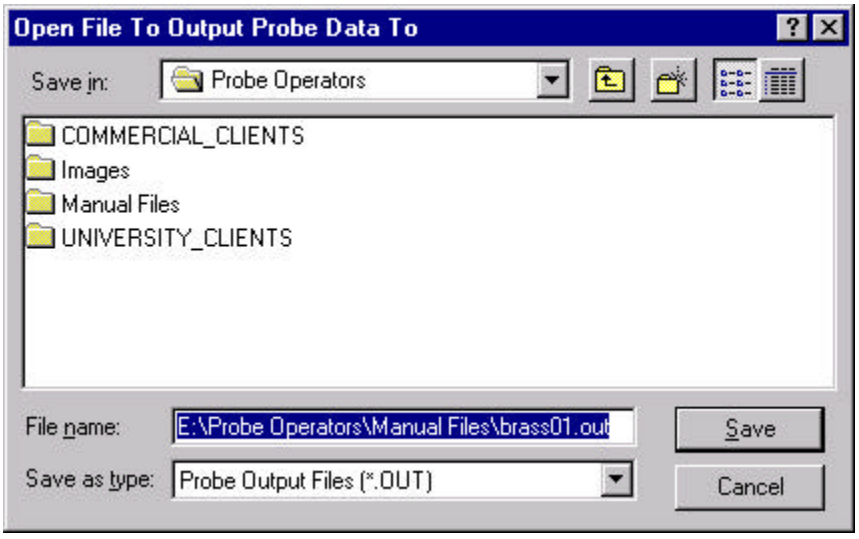
The certified values for NIST 478 are 72.85 wt% copper and 27.10 wt% zinc. This sample can also be used as a secondary standard to check the quality of the standardization. If the sample is a standard sample, the analysis printout will list several other output lines (see page 120, zinc metal). The published, "PUBL" weight percent value for the element as entered in the default standard database and the percent variance, "%VAR" from the published value for each element compared to the actual measured average for the standard are listed. After this is a line labeled "DIFF" which is the difference between the "AVER" and "PUBL" values. These parameters give the user an easy way to evaluate the quality of the standardization.

Output of Analyzed Data

Before closing the run, the user decides to output the data to an ASCII file for importing to another application such as Excel and to the laser printer for a hardcopy. From the main PROBE FOR WINDOWS log window, select **Output** from the menu bar and click **Save to Disk Log** from the menu.

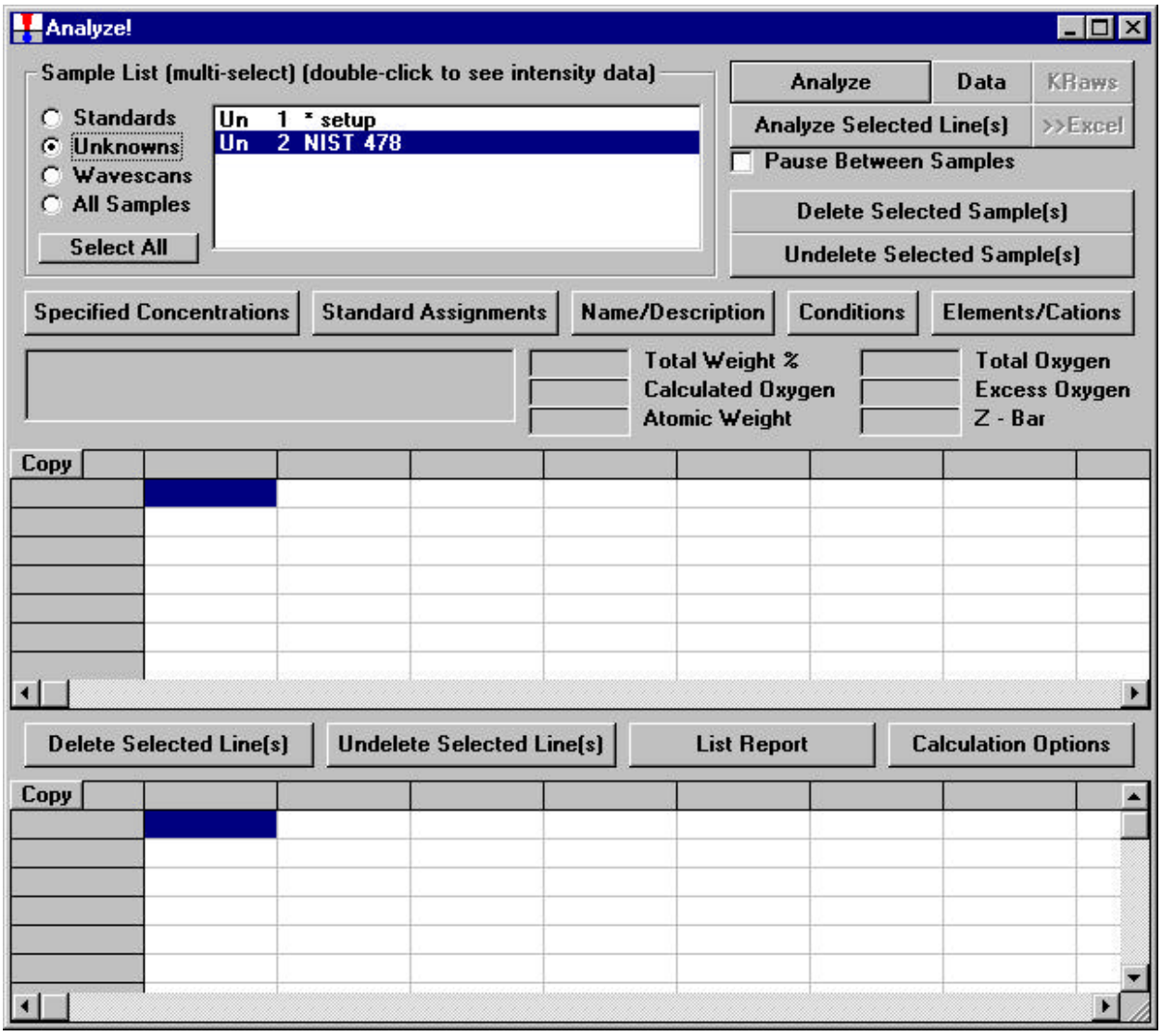


This opens the **Open File To Output Probe Data To** dialog box. Type in a *File name*. This output file has the extension .OUT. Note that all raw data is always automatically saved in the .MDB run file for future re-calculation and /or output. Click **OK** when finished.



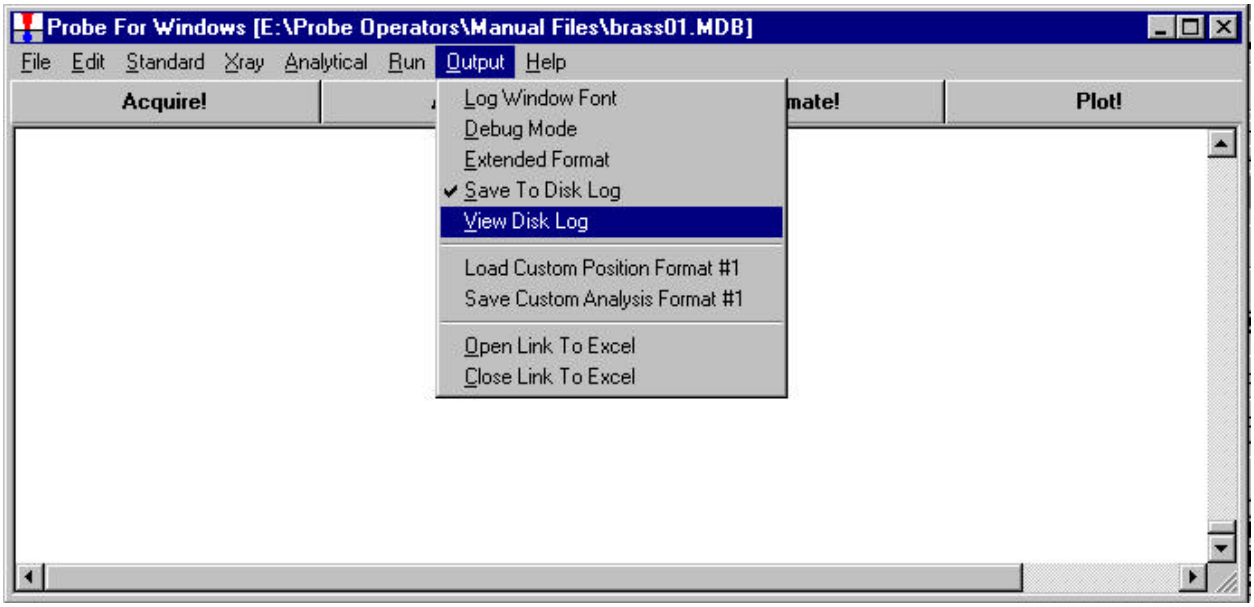
Select the **Analyze!** button in the main PROBE FOR WINDOWS log window, to bring forward the **Analyze!** dialog box.

Select from the *Sample List* of the **Analyze!** window the samples to be output to this file.

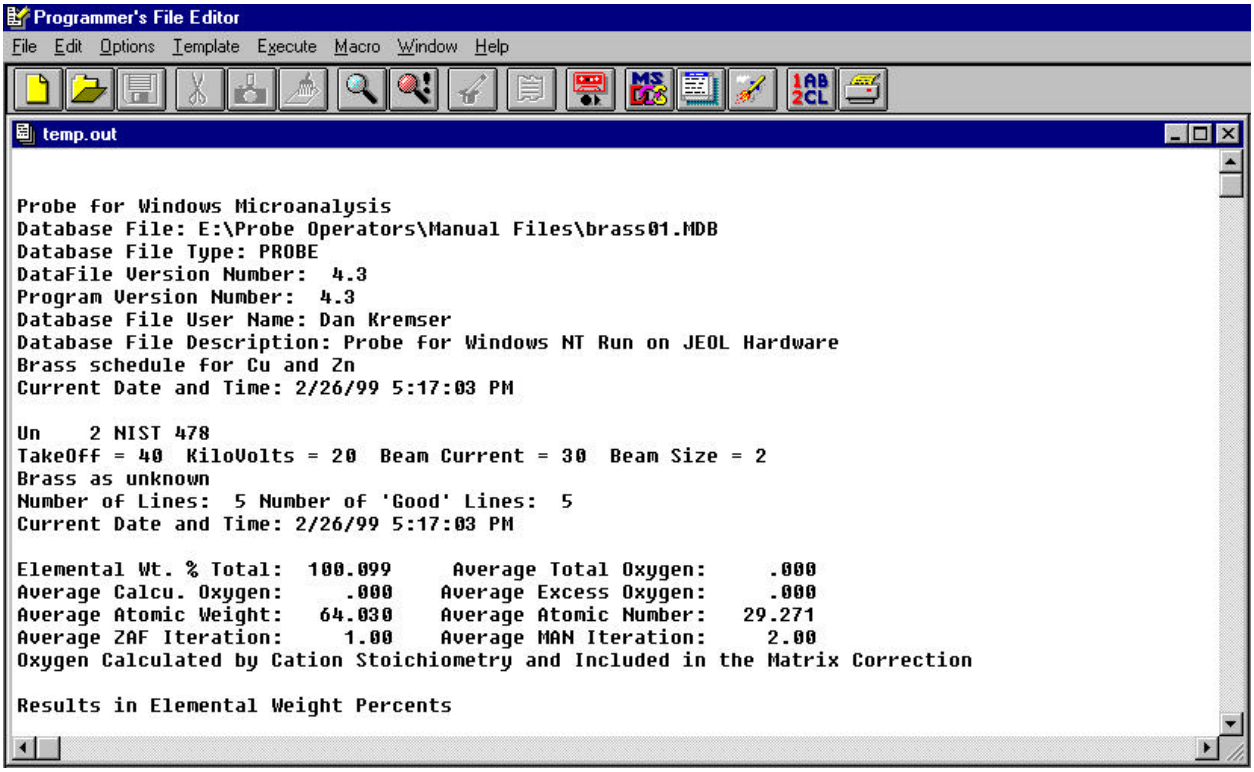


Click the **Analyze** button to reanalyze the samples.

When the program finishes recalculating data to the file, return to the main PROBE FOR WINDOWS log window. Select **Output** from the menu bar again and click **View Disk Log** from the menu.



This opens the file editor. This example utilizes the **Programmer's File Editor**, seen below. A number of text file editors may be used. To utilize a specific editor such as Notepad or Textpad, edit the FileViewer keyword in the PROBEWIN.INI file.



The user might note that the output file is designated TEMP.OUT rather than the BRASS01.OUT specified earlier in the **Open File To Output Probe Data To** window. When the user wishes to view the disk log, the program closes the active log, creates a copy called TEMP.OUT, reopening the original (BRASS01.OUT) for further log writing, and allows the user to view the copy. Each time the user reopens the disk log and assuming new information has been appended, the editor will prompt that the TEMP.OUT file has been altered on disk by another application. Do you want to load this new version? Select the **Yes** button to view the additional material.

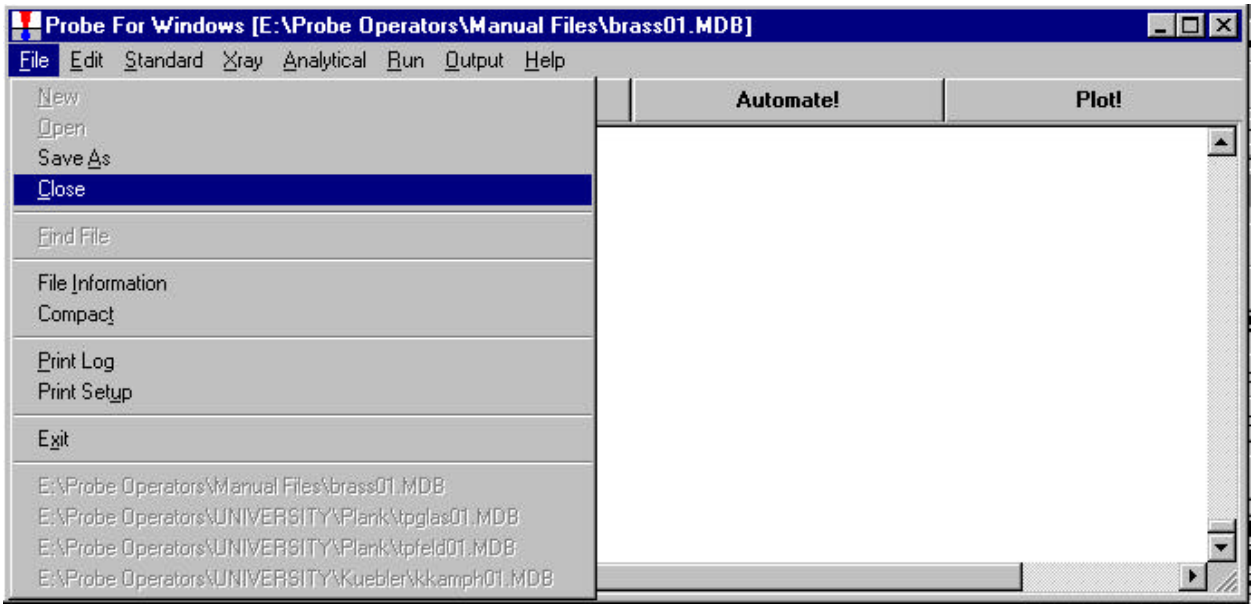
Also, if the user types a comment (to annotate output) into the main PROBE FOR WINDOWS log window, this comment string is echoed into the active disk log. Be aware that the comments entered will be placed at the current end position of the active log window.

The user may now direct the log data to a laser printer for hard copy viewing by selecting **File** from the **Programmer's File Editor** menu bar and clicking on **Print** in the drop-down menu.

Exit the file editor and return to the main PROBE FOR WINDOWS log window.

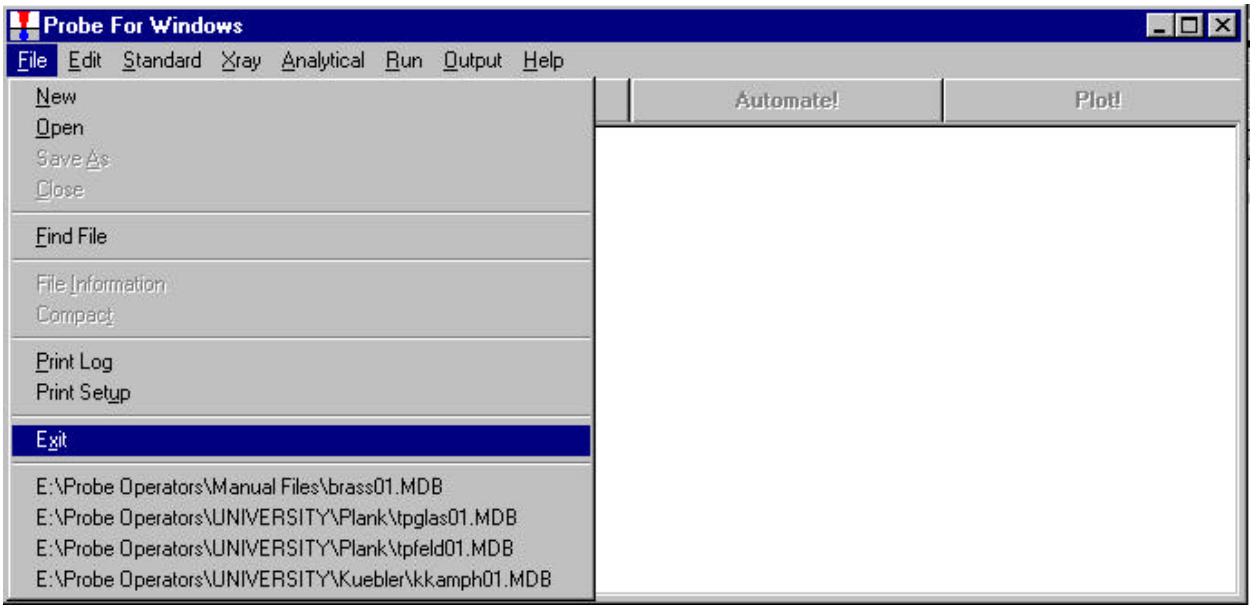
Closing the Current Run and Probe for Windows

The user ends the analysis session from the main PROBE FOR WINDOWS log window. Select **File** from the menu bar and click **Close** from the menu selections.



This opens the **ProbFormCloseFile** window, click **Yes** to close this file.

Close PROBE FOR WINDOWS by selecting **File** from the menu bar and clicking **Exit**.



Silicate Sample Run

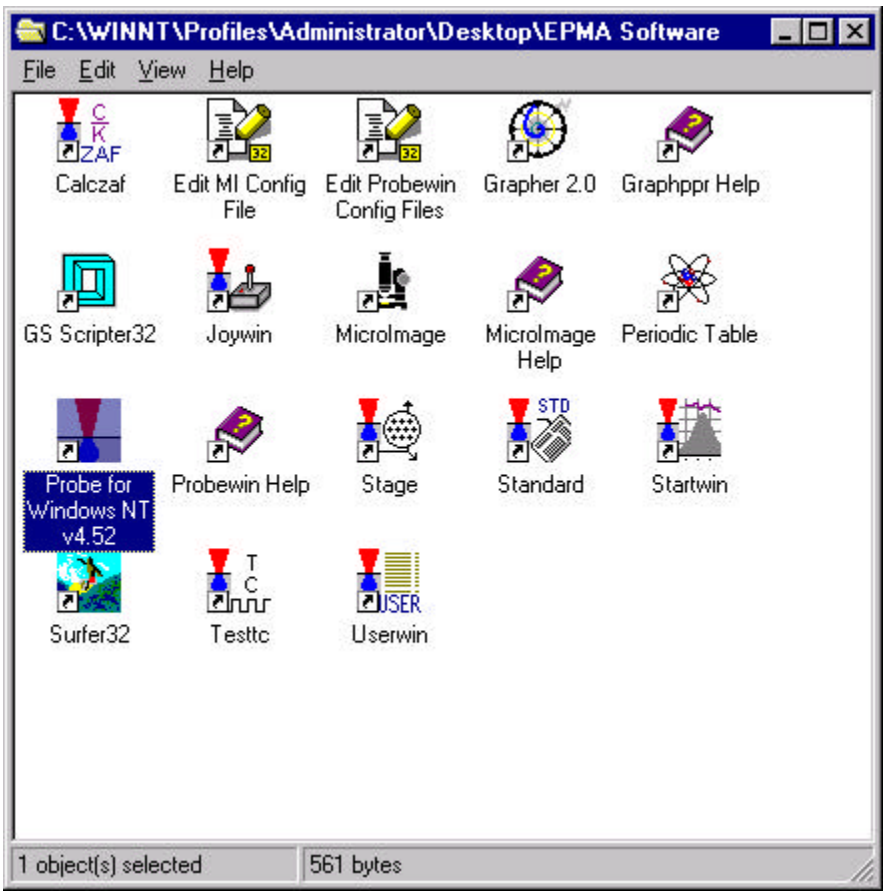
Introduction

This document illustrates step by step how to set up a new PROBE FOR WINDOWS quantitative run and how to analyze an unknown ten element silicate sample. This documentation was produced on a three spectrometer JEOL 733 electron microprobe. Your particular run may look very different depending on the specific configuration of your microprobe. This document should be used in conjunction with the User's Guide and Reference documentation and on-line help.

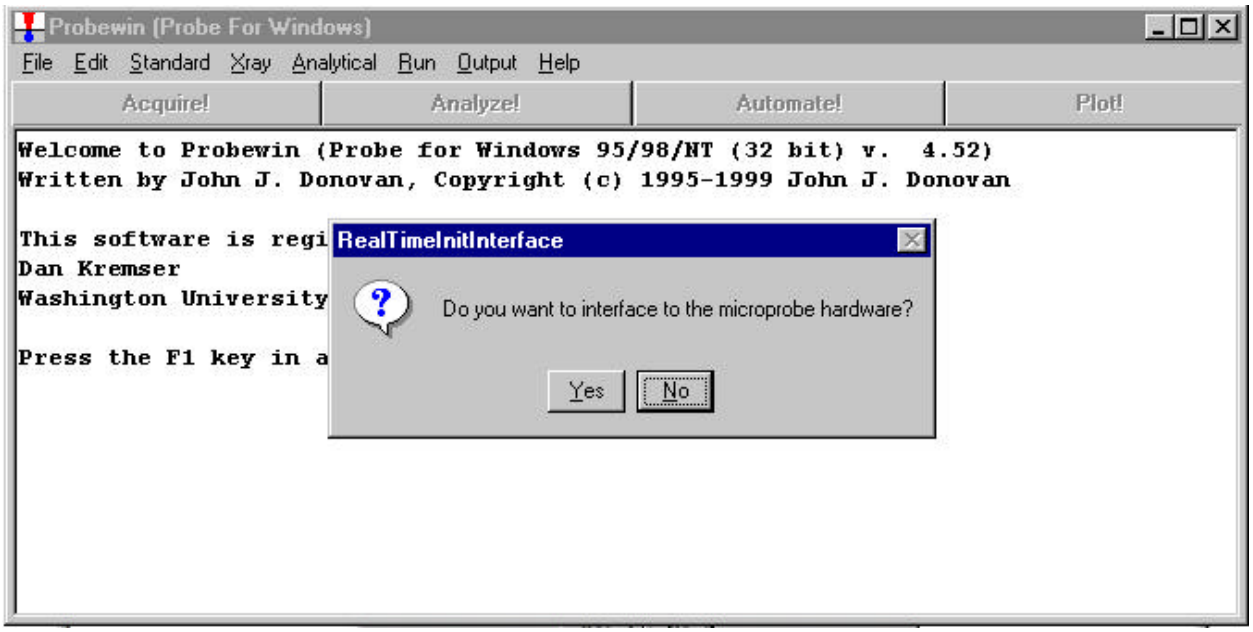
This run will demonstrate some of the powerful features of the PROBE FOR WINDOWS program. These include the use of pre-digitized standard mounts, automated spectrometer peaking, non-linear MAN (mean atomic number) background corrections, automated spectral interference corrections, automated standard acquisitions and digitizing unknown sample acquisitions.

Opening Probe For Windows

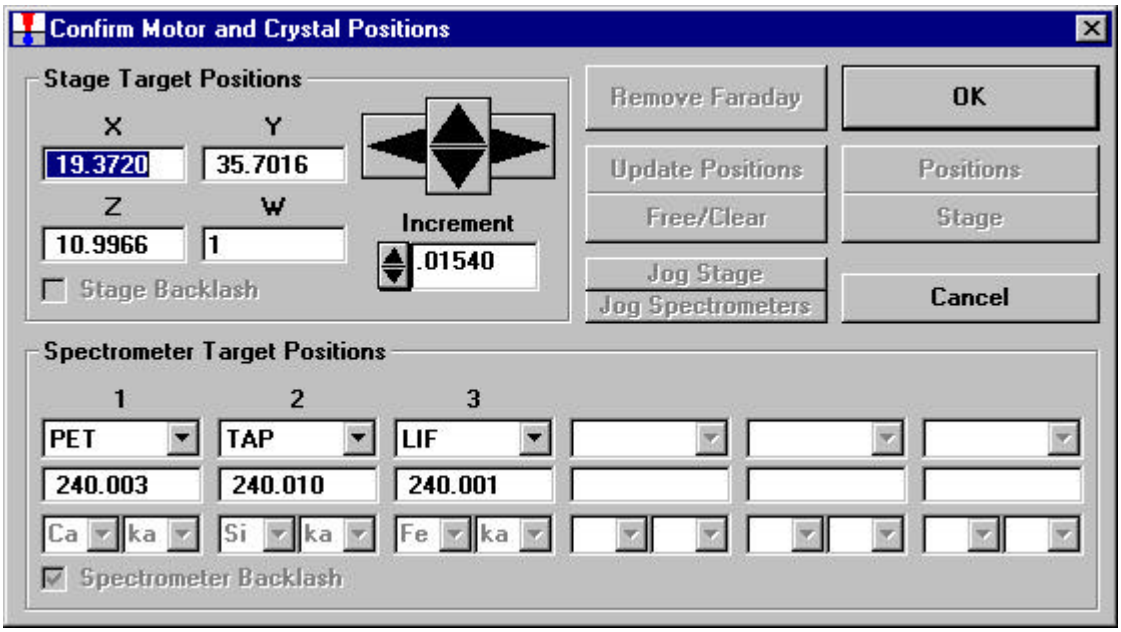
From the Desktop, double-click on the yellow EPMA Software folder opening the EPMA Software group. Double click on the **Probe for Windows …** icon.



Upon launching PROBEWIN (PROBE FOR WINDOWS), the main log window appears along with the **RealTimeInitInterface** window as illustrated below. To collect real time data click the **Yes** button. The program can also be run off-line without the microprobe interface to re-process previously acquired data or on another computer.

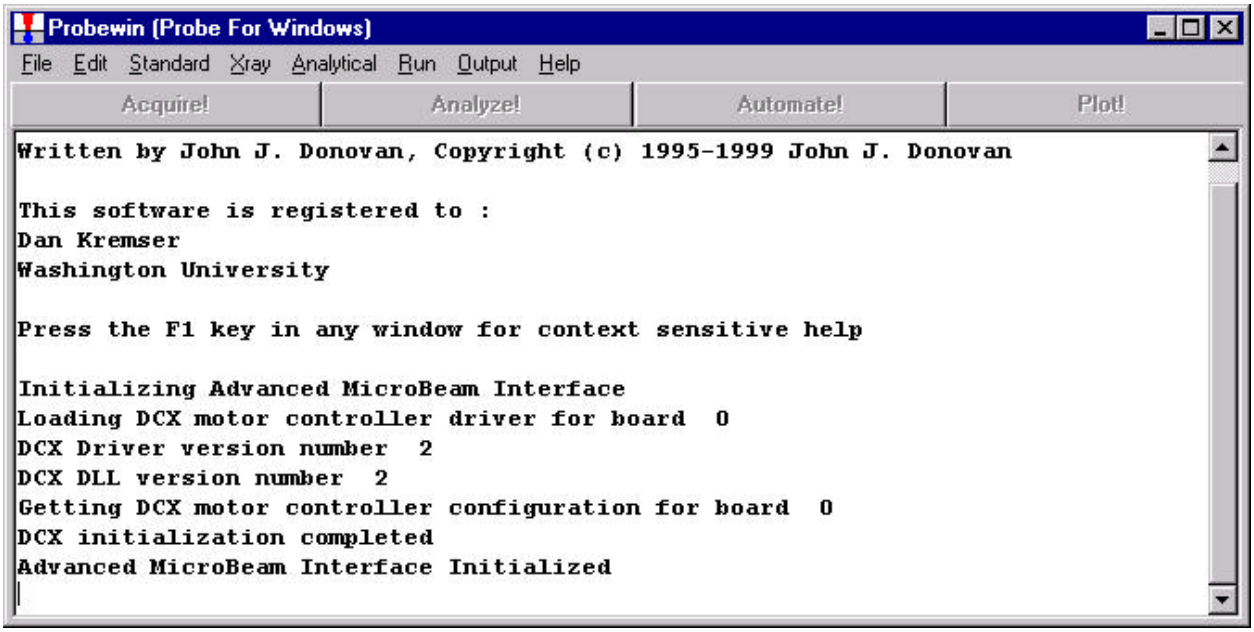


This action causes the **Confirm Motor and Crystal Positions** dialog box to open. Confirm that all of the motors (stage and spectrometer positions) and crystal designations are correctly calibrated. If there is disagreement between the mechanical positions (actual) and the software values, adjust the software values. Use the <tab> key to move between the *Target Positions* text boxes.



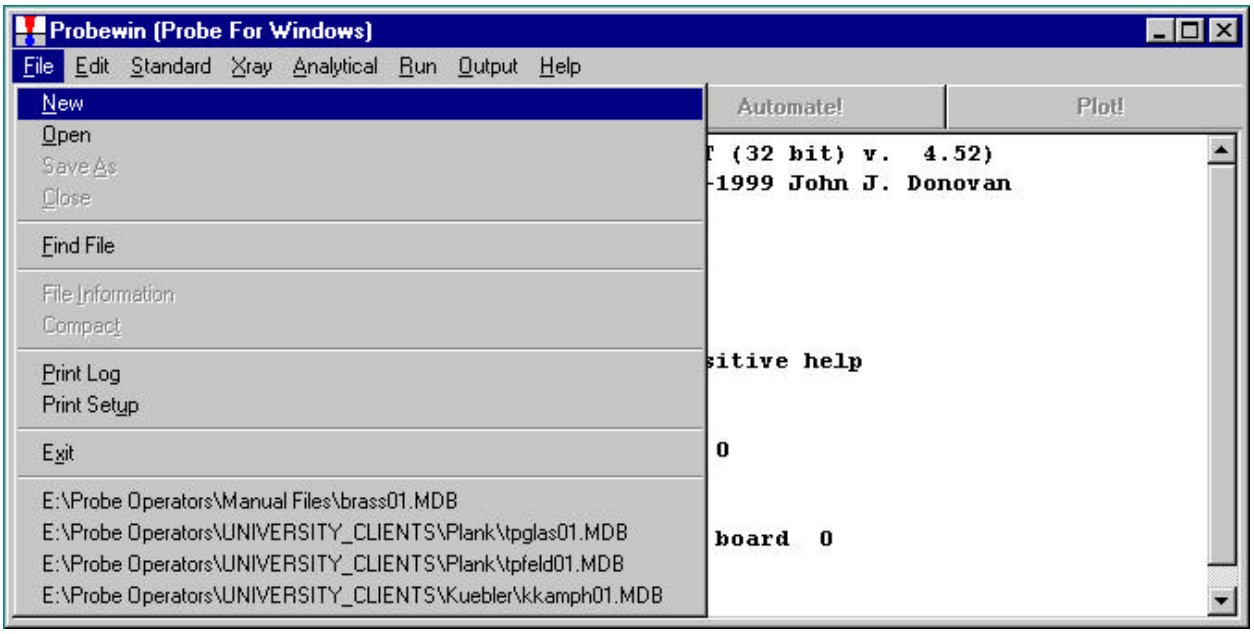
Click the **OK** button after you have finished to close the **Confirm Motor and Crystal Positions** dialog box.

The main PROBE FOR WINDOWS log window is now visible as seen below.

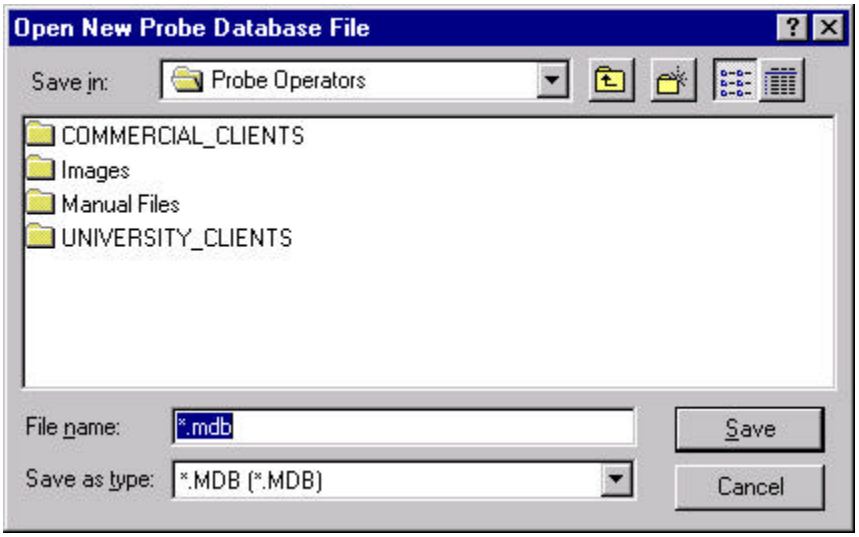


Creating a New Run

To create a new sample run, select **File** from the menu bar and click **New** from the menu.



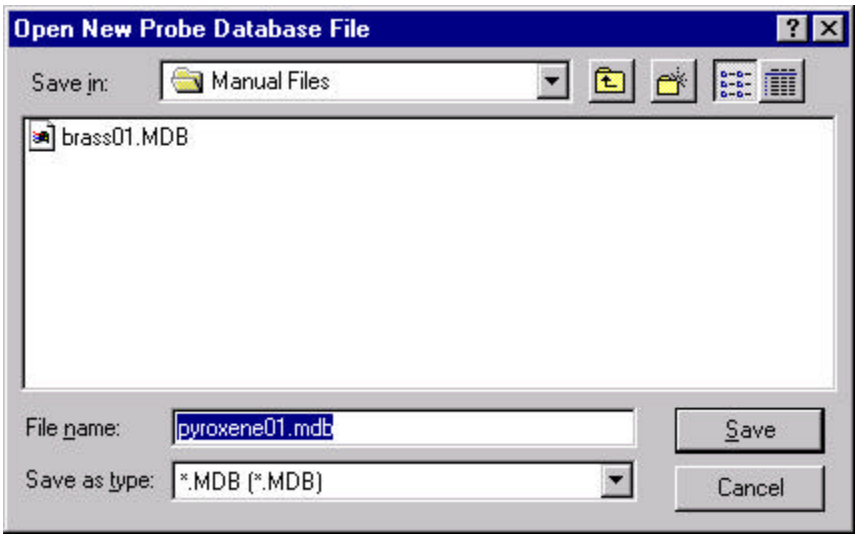
The **Open New Probe Database File** dialog box opens.



Change the *Save in:* location (directory) and type in an appropriate run name into the *File name* text box.

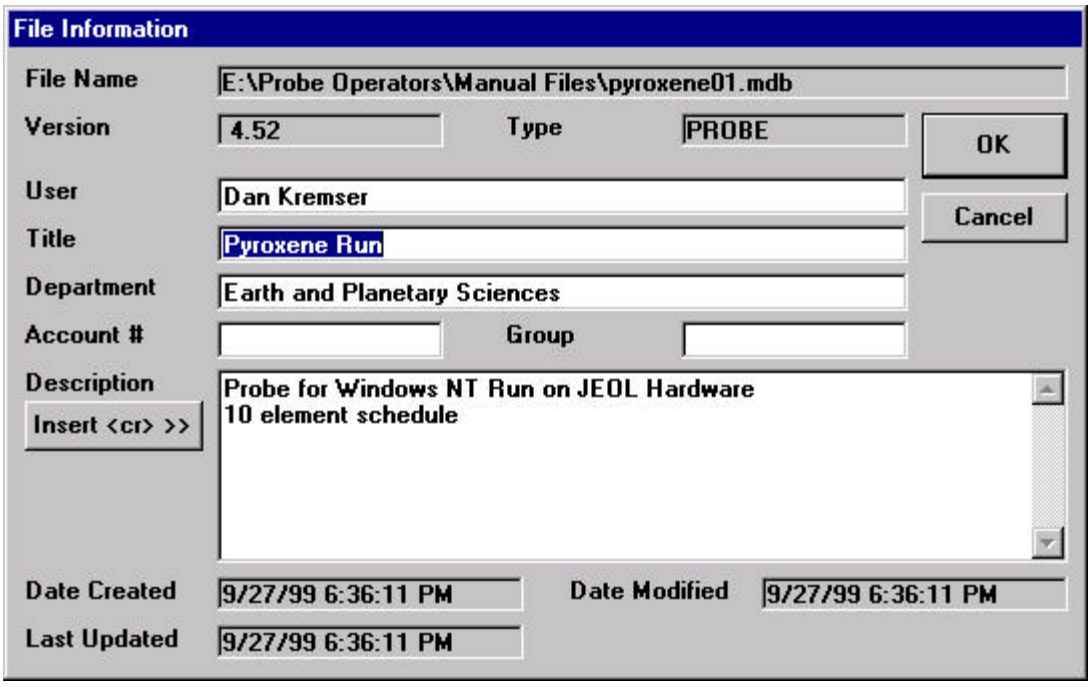
The initial *Save in:* location is specified by the UserDataDirectory keyword in the PROBEWIN.INI file. File names longer than 8 characters are now supported.

The screen capture of the first window in this section indicates that other probe runs (previous four listed) are already established. Any of the existing old runs maybe re-opened to acquire additional data or used as a "setup" file for starting a new run. In this example, a new file designated PYROXENE01.MDB will be created in the Manual Files directory.

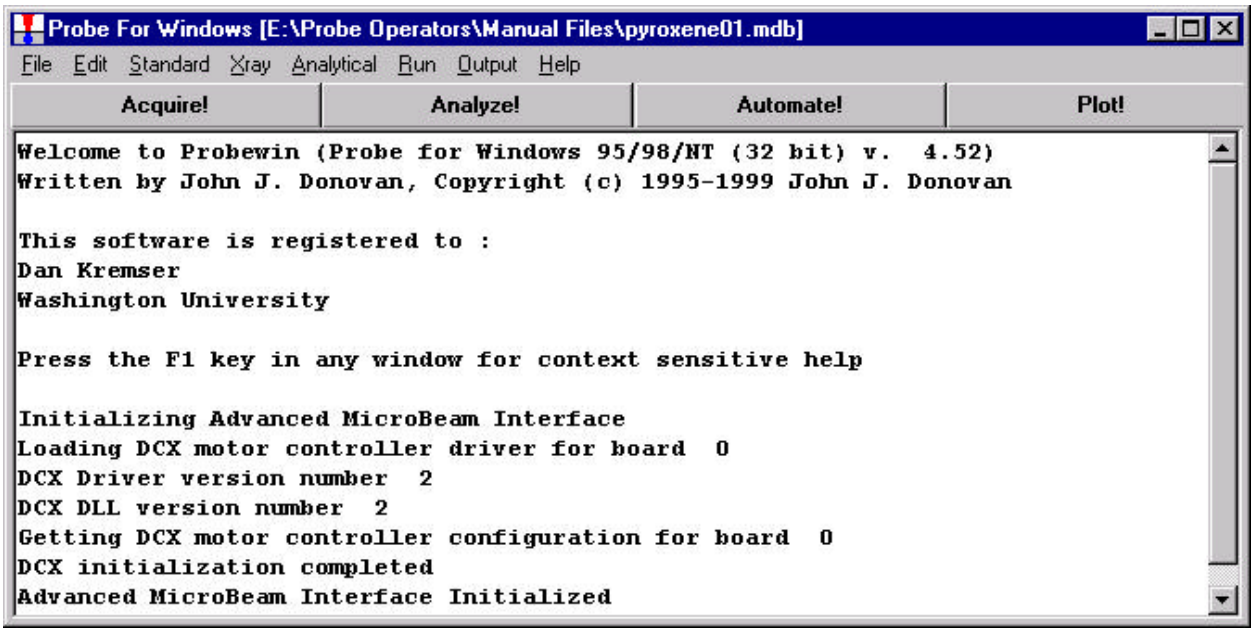


Close the **Open New Probe Database File** window by clicking the **Save** button. This action opens the **File Information** dialog box.

Enter the relevant information for the new run into the *User, Title*, and other *Description* text boxes. Use the <tab> key to move between text boxes. When finished, click the **OK** button.



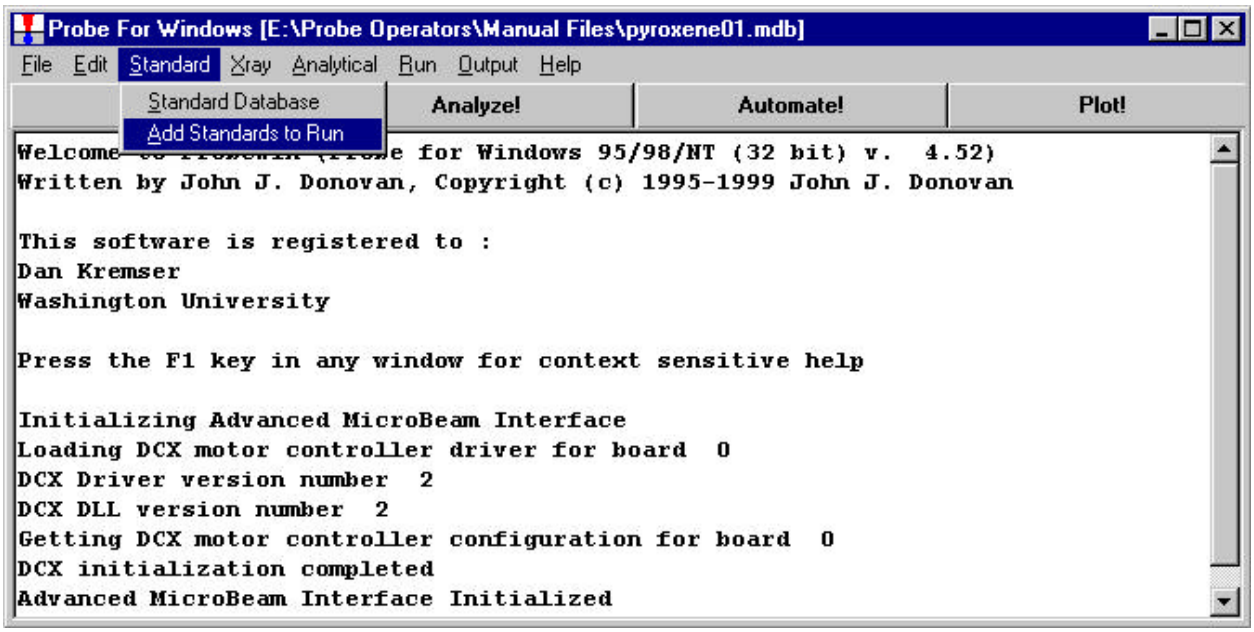
This returns the program to the main PROBE FOR WINDOWS log window. Now the four main Probe buttons: **Acquire!**, **Analyze!**, **Automate!**, and **Plot!** become active.


Probe For Windows [E:\Probe Operators\Manual Files\pyroxene01.mdb]
File Edit Standard Xray Analytical Run Output Help
Acquire!
Analyze!
Automate!
Plot!
Welcome to Probewin (Probe for Windows 95/98/NT (32 bit) v. 4.52)
Written by John J. Donovan, Copyright (c) 1995-1999 John J. Donovan
This software is registered to :
Dan Kremser
Washington University
Press the F1 key in any window for context sensitive help
Initializing Advanced MicroBeam Interface
Loading DCX motor controller driver for board 0
DCX Driver version number 2
DCX DLL version number 2
Getting DCX motor controller configuration for board 0
DCX initialization completed
Advanced MicroBeam Interface Initialized

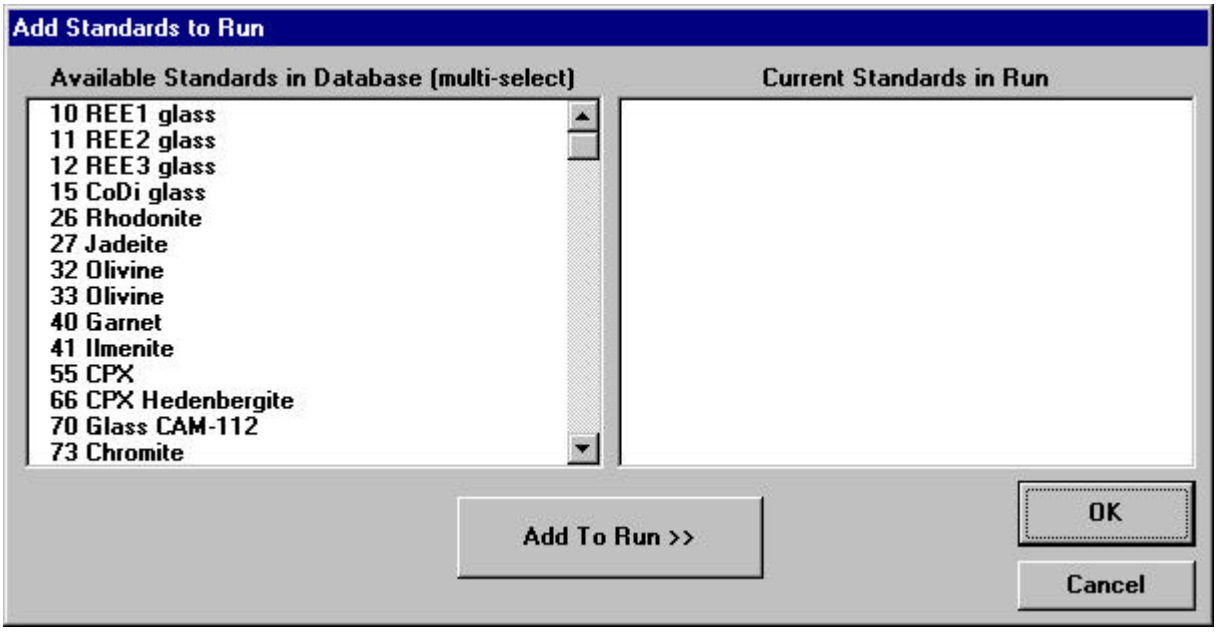
Parameter Initialization

Analytical Standard Selection

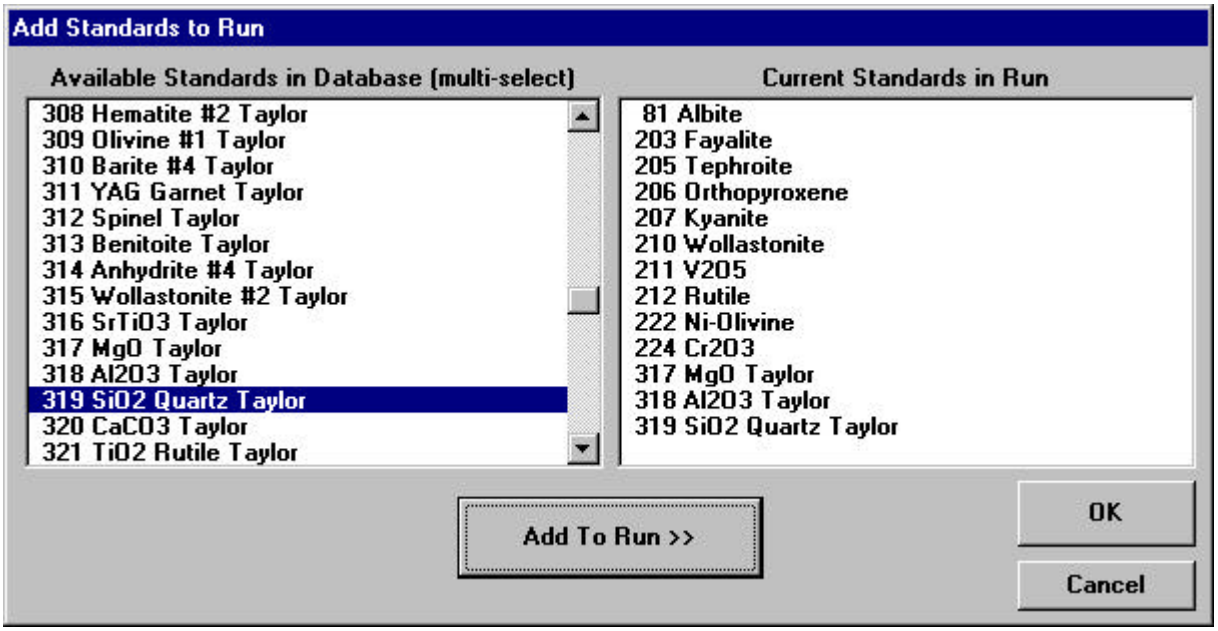
Select the analytical standards to be used in the new probe run. From the main PROBE FOR WINDOWS log window click **Standard** from the menu bar and select **Add Standards to Run** from the menu.



This opens the **Add Standards to Run** dialog box.



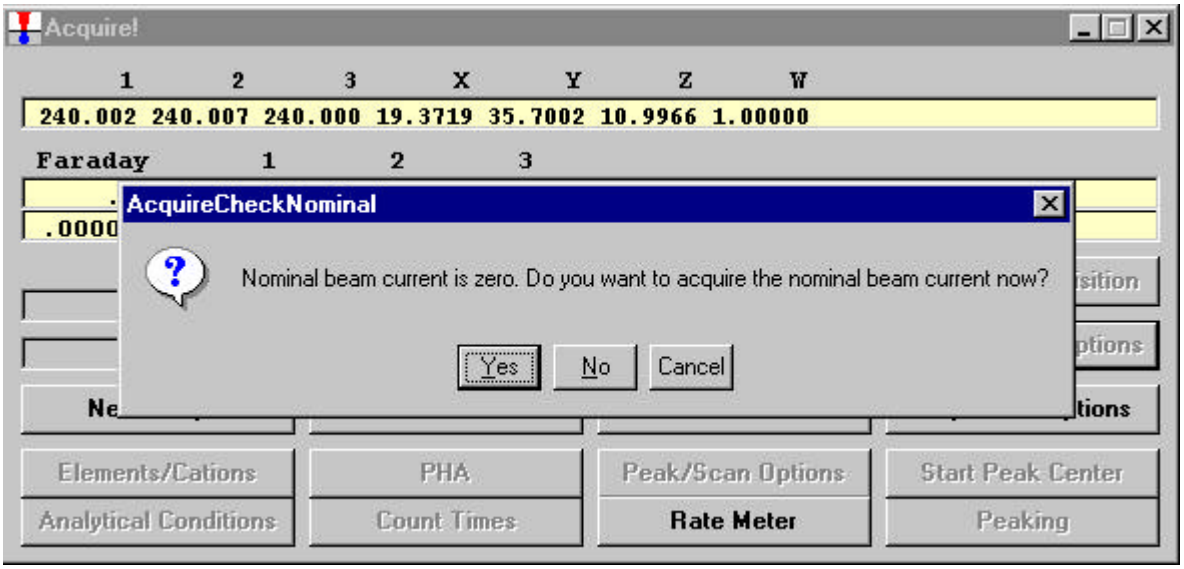
All previously entered standards in the default standard database are accessible. Scroll through the *Available Standards in Database* list box to find the standards to be used in this run. Select both primary analytical standards and the MAN background standards. Some standards may be run as both. Select each and click the **Add To Run** >> button to add each to the *Current Standards in Run* list box.



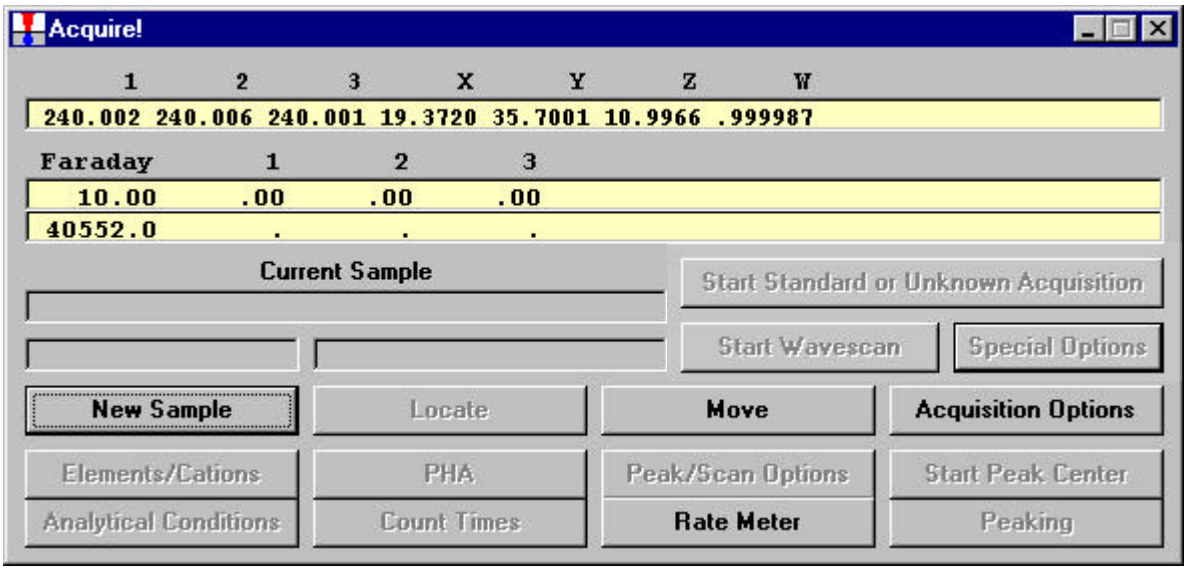
Click the **OK** button of the **Add Standards to Run** window when finished selecting standards. This returns the program to the main log window.

Nominal Beam Current Measurement

Click the **Acquire!** button. This action opens both the **Acquire!** dialog box and the **AcquireCheckNominal** window for the determination of the nominal beam count.

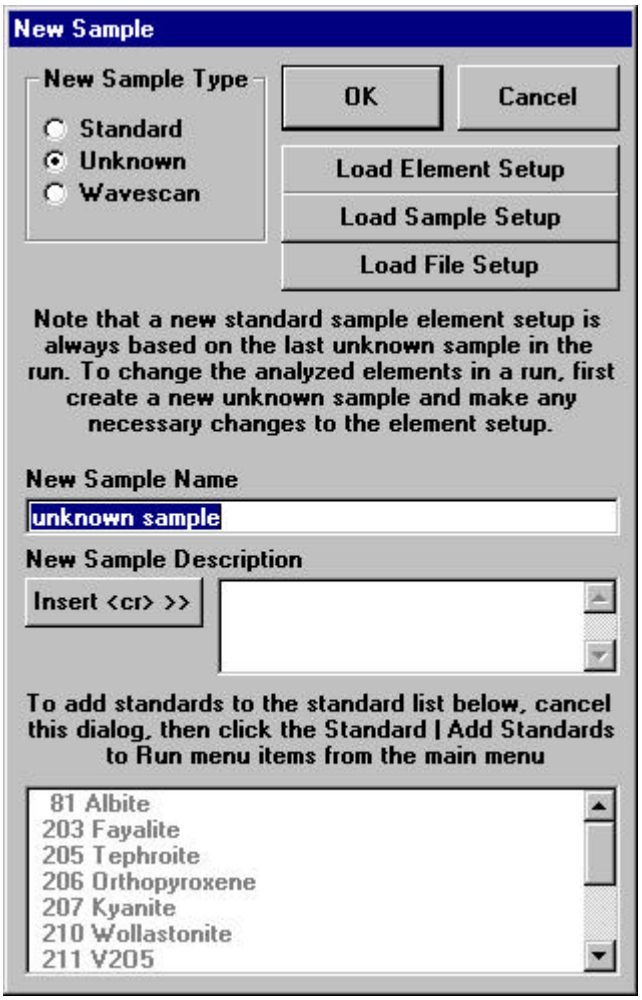


Click the **Yes** button on the **AcquireCheckNominal** window to establish a reference beam current reading. The beam (Faraday Cup counts on a JEOL 733 microprobe) is then measured. In this example the Faraday reading was taken for 10 seconds and recorded 40552 counts or 40.552 nA of beam current.

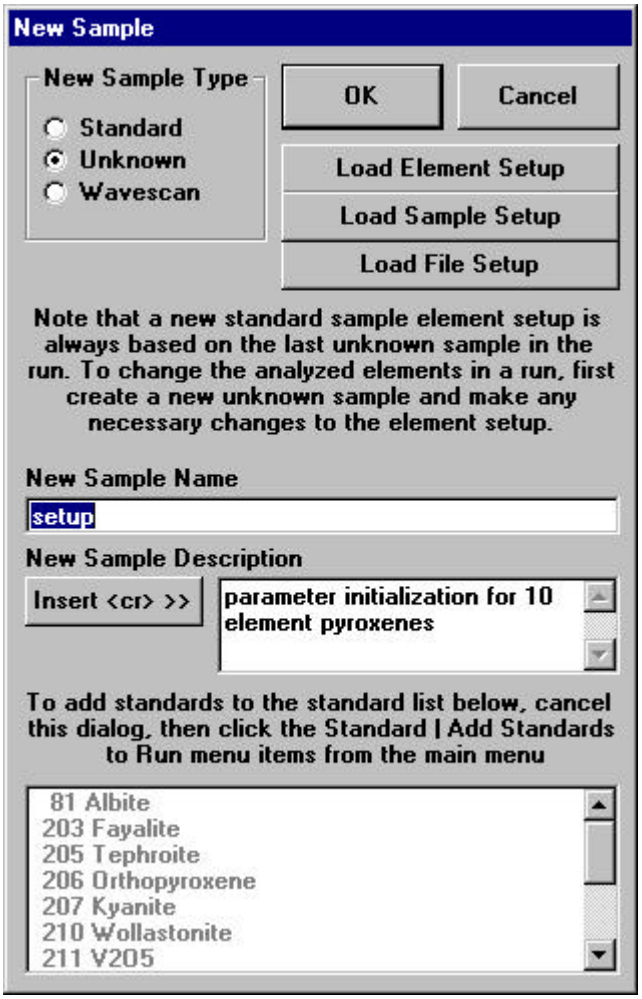


Creating a New Sample

Click the **New Sample** button of the **Acquire!** dialog box. This opens the **New Sample** dialog box.

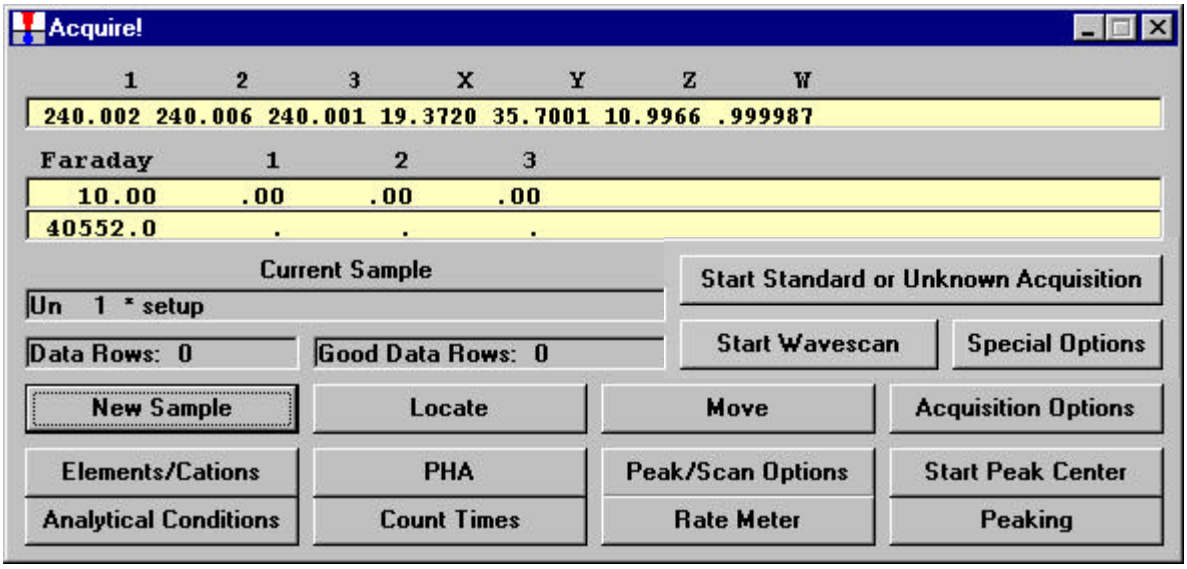


Select *Unknown* from the *New Sample Type* buttons. Type an appropriate sample name and description into the *New Sample Name* and *New Sample Description* text boxes. This first sample will be used only to establish the analysis parameters.



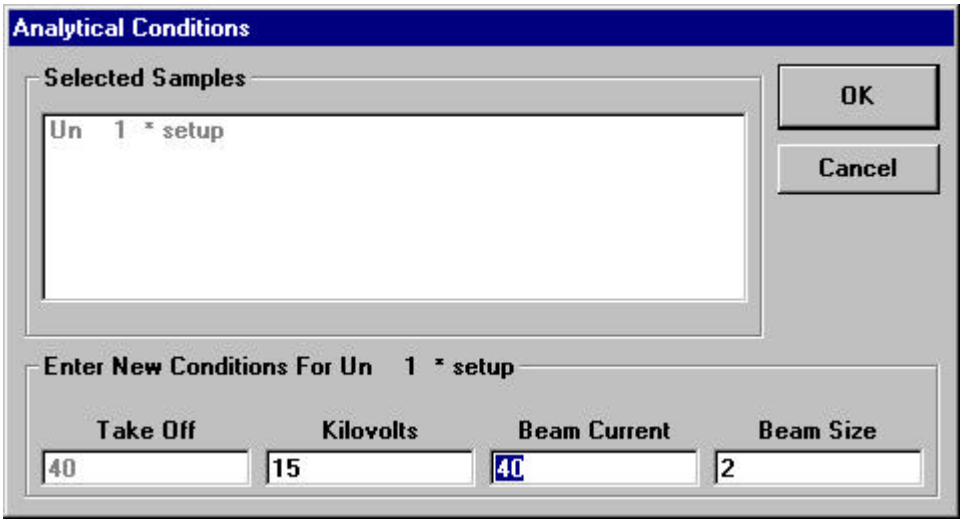
Click the **OK** button of the **New Sample** dialog box.

The program returns to the **Acquire!** window. Notice that the first sample designated *Un 1 * setup* is now listed in the *Current Sample* text box. The * symbol indicating that no data has been collected for this sample yet.



Setting Analytical Conditions

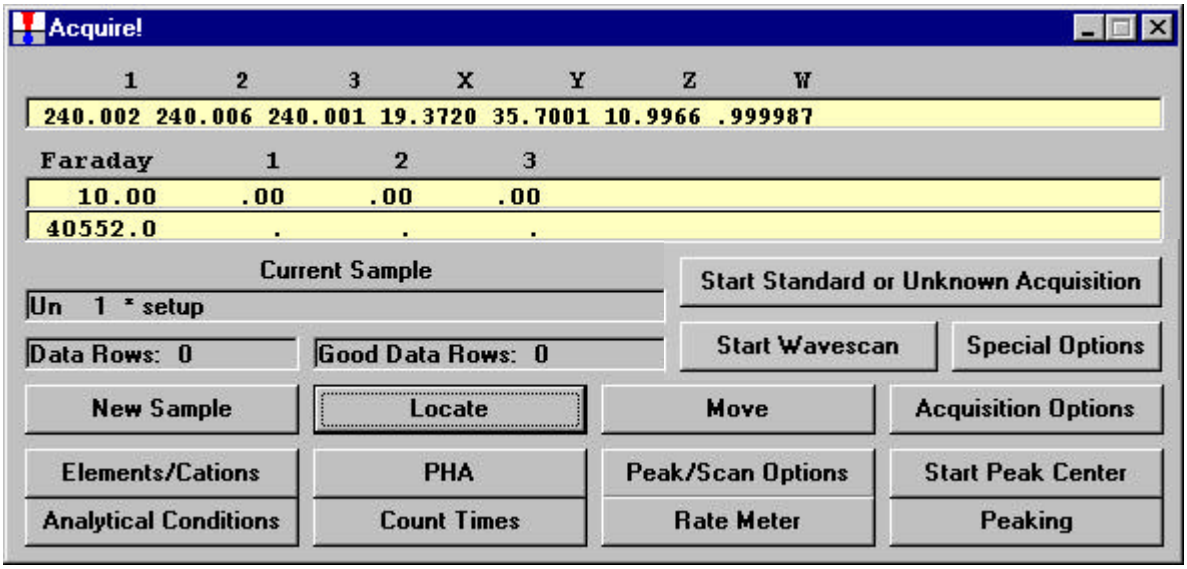
Click the **Analytical Conditions** button to open the **Analytical Conditions** dialog box. Enter the appropriate numbers into the *Kilovolts*, *Beam Current*, and *Beam Size* text boxes for the currently *Selected Sample*. The *Kilovolts*, *Beam Current*, and *Beam Size* will need to be manually adjusted if a column digital interface is not present.



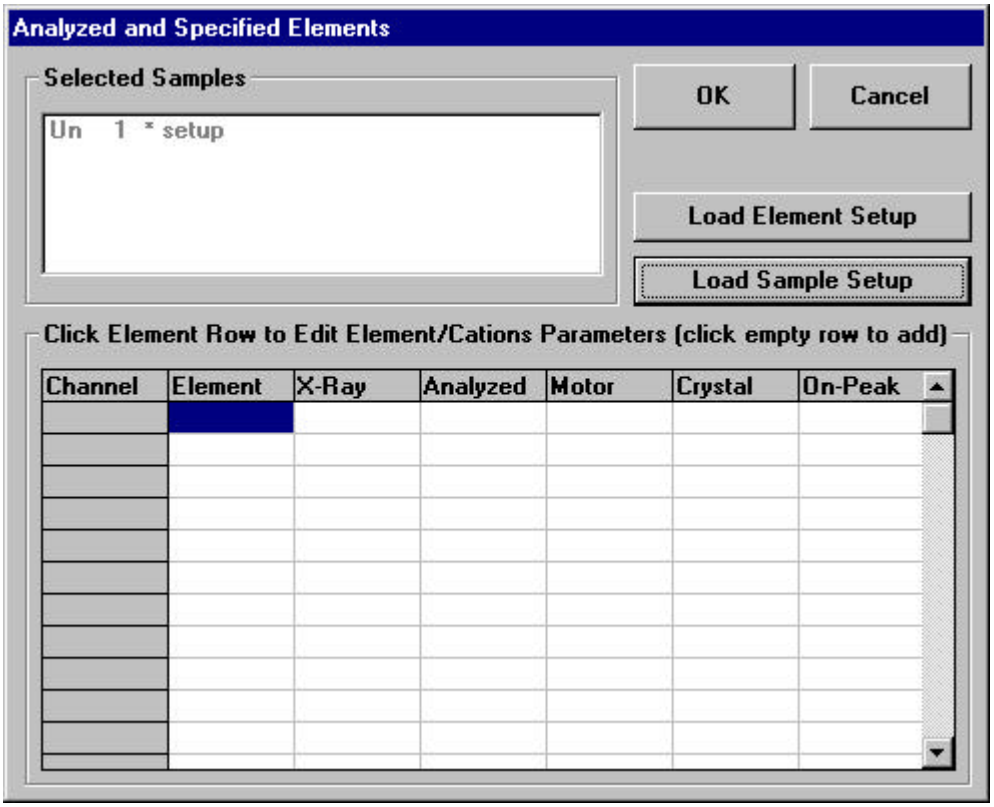
Click the **OK** button when done, returning to the **Acquire!** window.

Element, X-Ray Line, and Spectrometer Parameters Selection

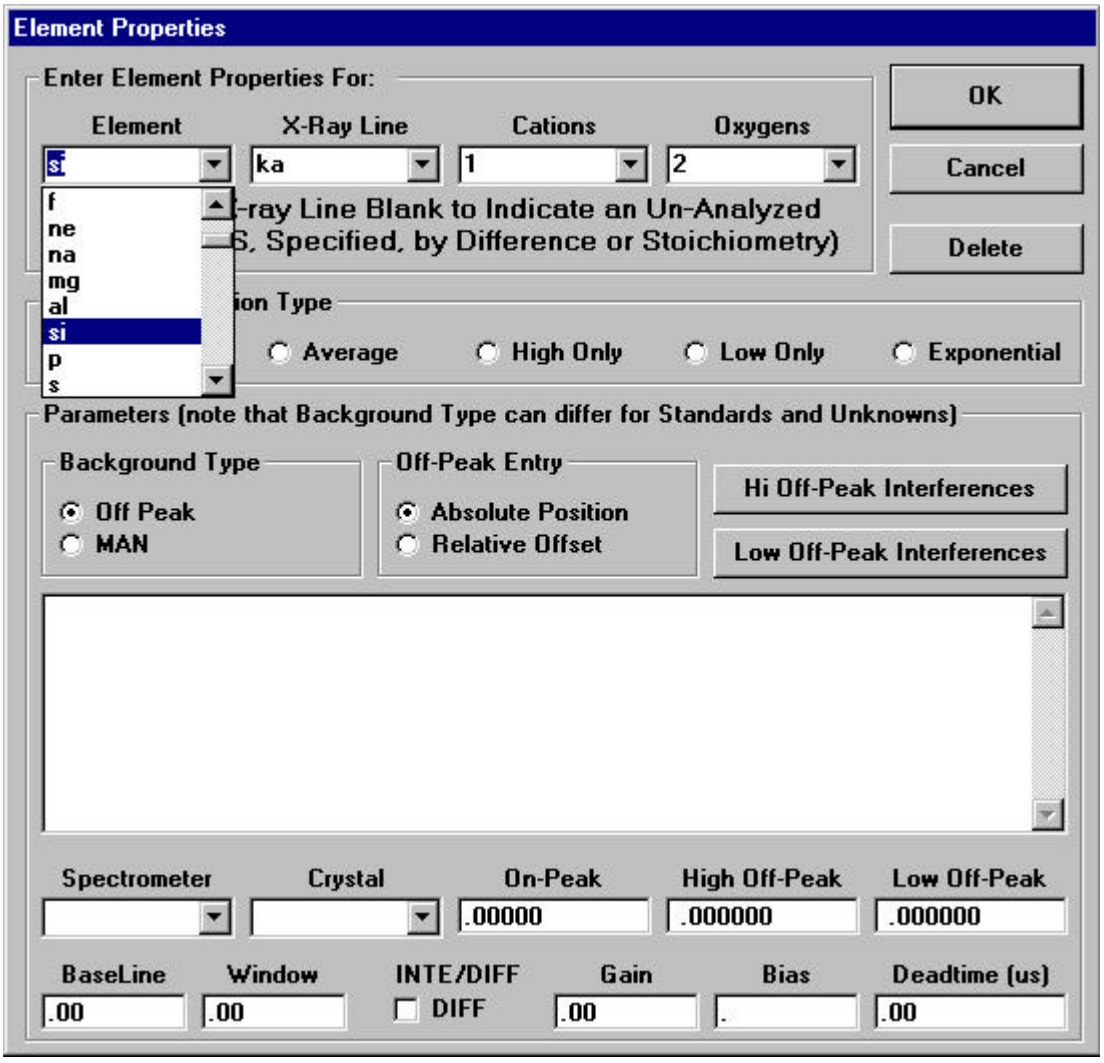
Next, the user specifies the elements to be analyzed. Click the **Elements/Cations** button.



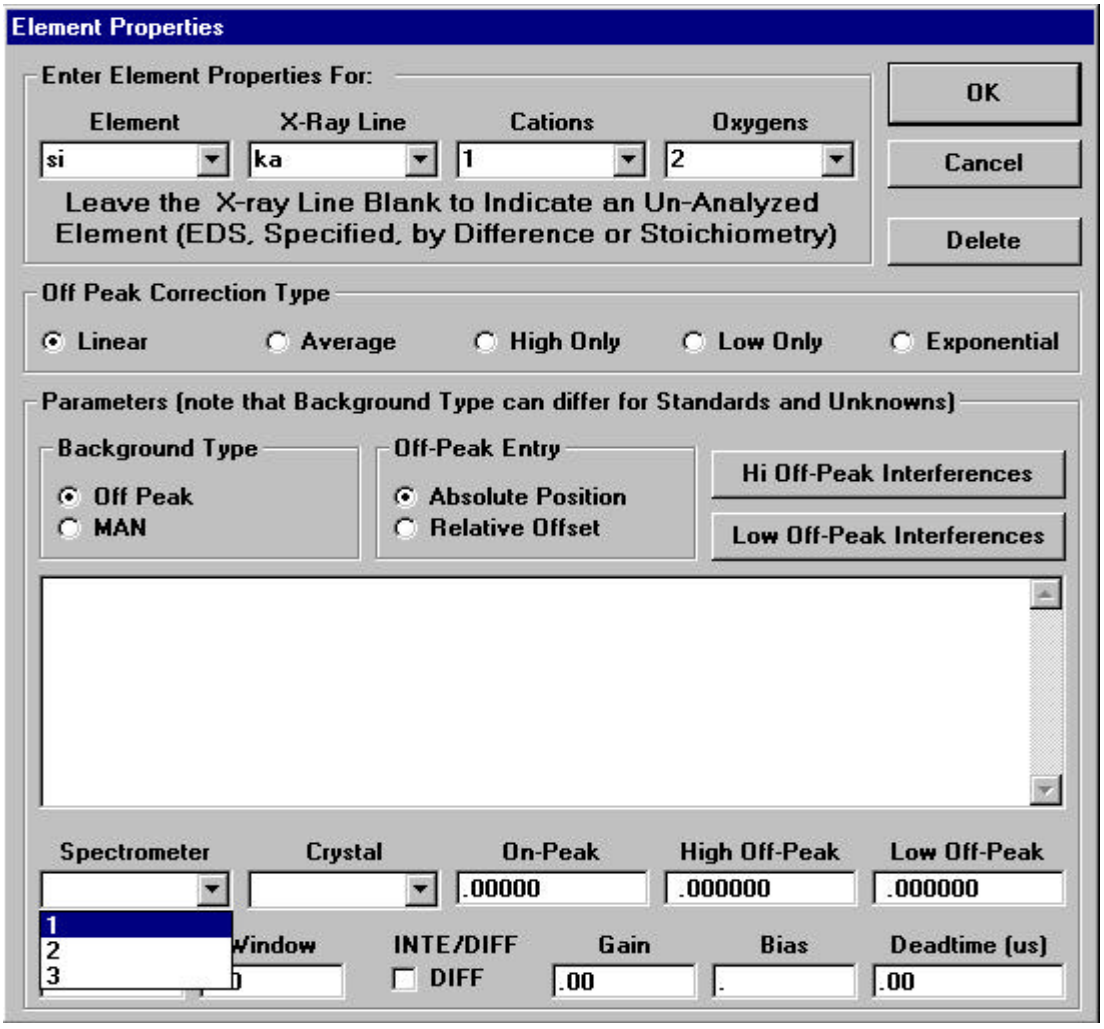
This action opens the **Analyzed and Specified Elements** dialog box. Click on the first empty row under the *Element* column to enter the first element to analyze. The user may enter the analyzed elements in any order however, the analysis output will follow this order.



This opens the **Element Properties** dialog box. In the *Element* field either type in the first element to analyze or use the drop-down menu to select the element symbol. Certain default values listed in this window are based on parameters entered into the previously established configuration files.



Under the *Enter Element Properties For* section (top of the **Element Properties** dialog box) choose the correct *X-Ray Line, Cations,* and *Oxygens* for the first element.

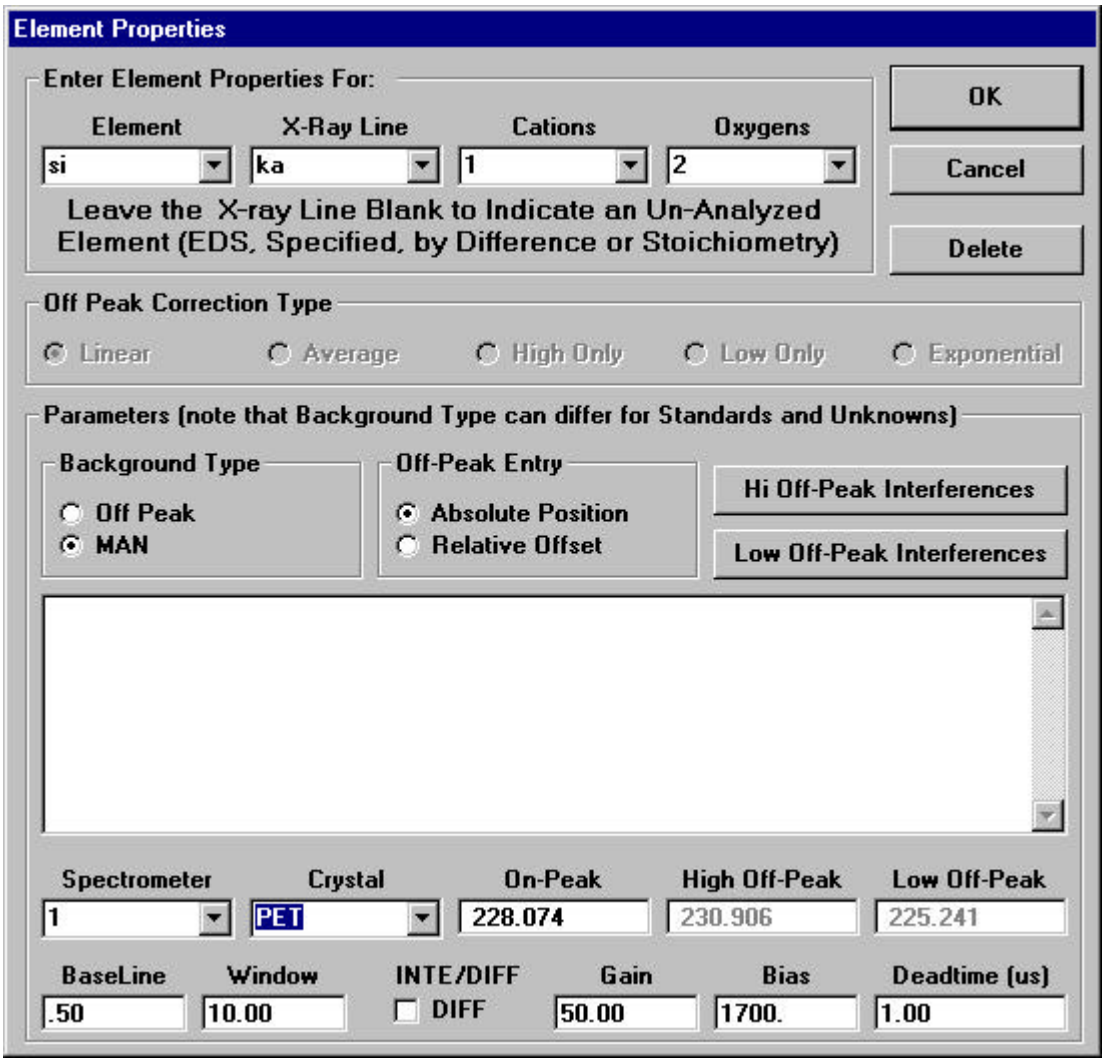


There are two common methods for performing a background correction on wavelength dispersive x-ray data; off-peak backgrounds and MAN (mean atomic number) background corrections. The off-peak method entails measuring the background on each element in the sample of interest with the spectrometer adjusted to a position, typically on each side of the analytical peak. This method while somewhat time-consuming can accurately determine the background contribution for major, minor and trace element concentrations.

The MAN method relies on the fact that most of the background (continuum) production in the sample is directly proportional to the average atomic number of the sample. The MAN correction is an empirical calibration curve method involving the measurement of standards of known composition (hence average atomic number). If many samples are to be analyzed for their major and minor element concentrations then substantial time may be saved using the MAN method. However, if the user is required to measure high atomic number samples and/or trace concentrations, more accurate data may be obtained with off-peak background corrections.

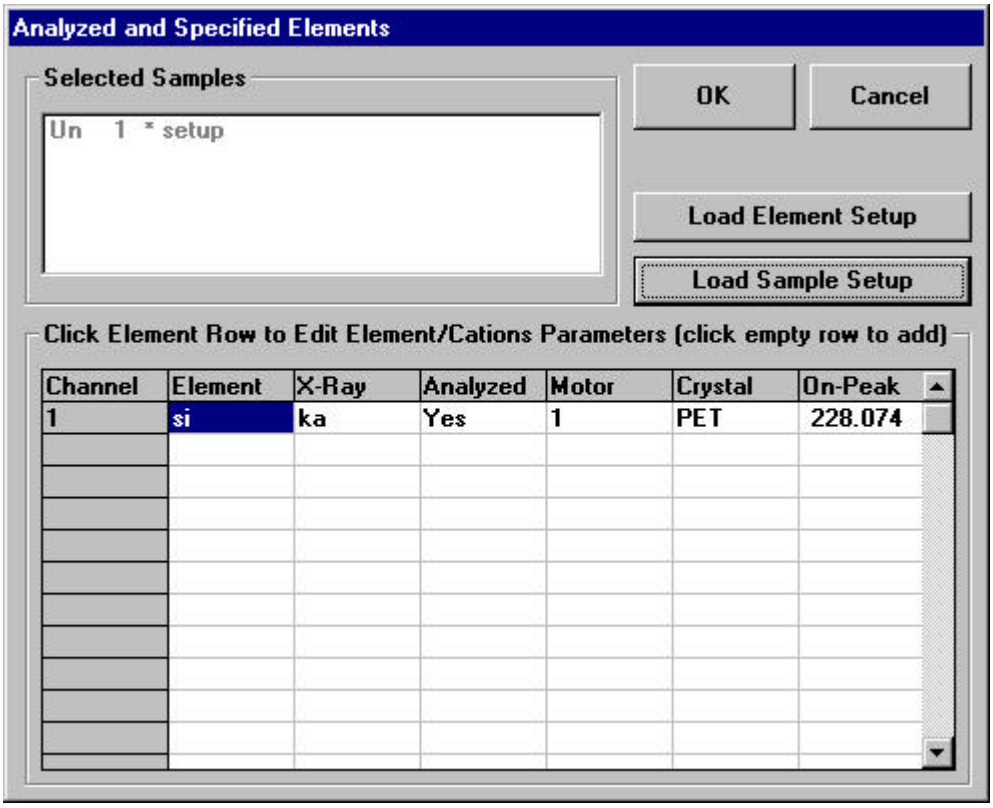
Continue by selecting *MAN* for the *Background Type*. Selecting *MAN* deactivates the *Off Peak Correction Type* buttons as well as the *High* and *Low Off-Peak* boxes. Next, click the text box under *Spectrometer* and enter the appropriate spectrometer number that will be used to analyze the first element. The drop-down menu may also be used to select the spectrometer number. Choosing a *Spectrometer* and *Crystal* loads various parameters from the configuration files. Each of these parameters in this window should be inspected and edited as needed (use the <tab> key to move between boxes).

The next screen shows the edited **Element Properties** dialog box for silicon.

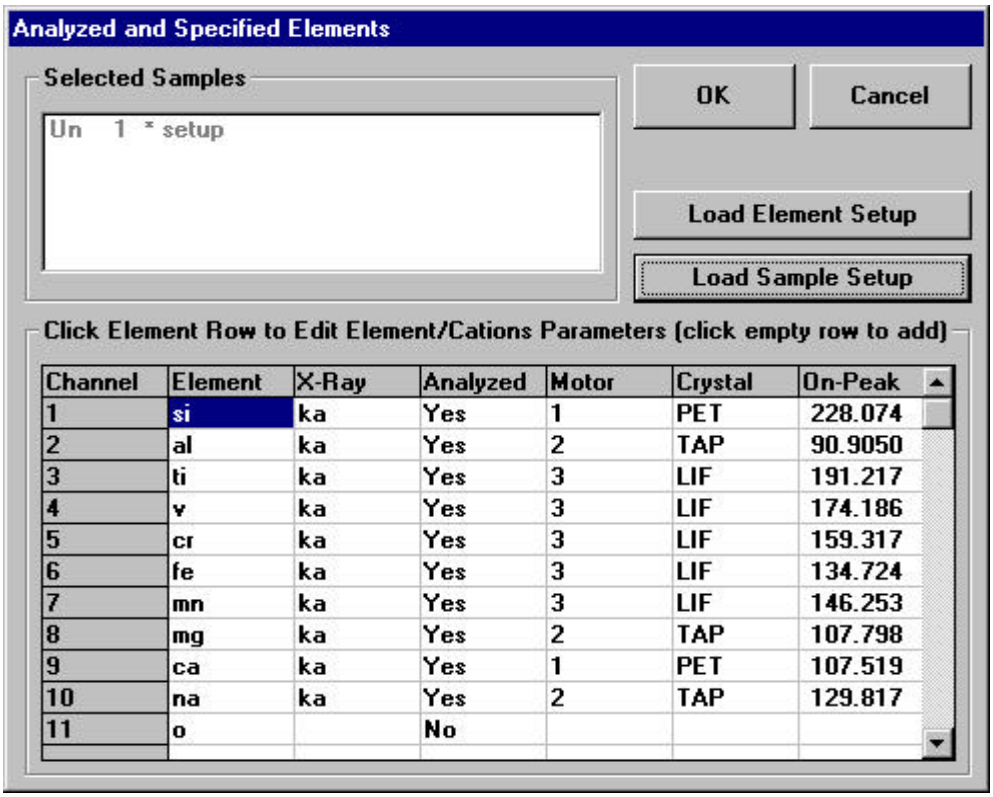


Click the **OK** button of the **Element Properties** dialog box to accept these element parameters for silicon.

The program returns to the **Analyzed and Specified Elements** window with silicon now entered into the *Element/Cations Parameters* table.



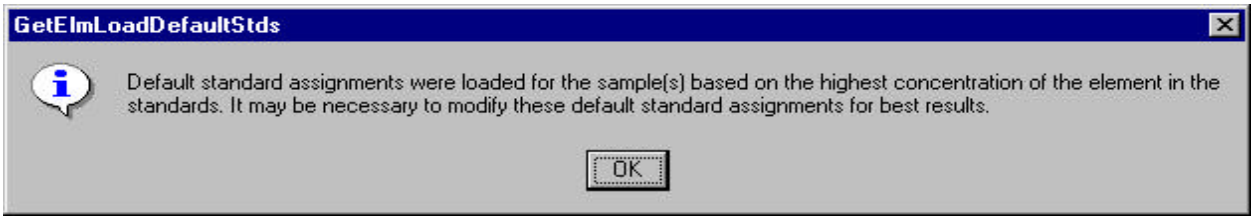
Enter the next element in the run by clicking on the next empty *Element* row of the **Analyzed and Specified Elements** window. This opens the **Element Properties** dialog box again. Enter the appropriate *Element*, *Spectrometer*, *Crystal* and adjust all other text boxes and buttons. Repeat the element entry process until all of the elements are listed in the **Analyzed and Specified Elements** window. The remaining nine element entries are not shown here to save space. Finally, oxygen is added to the element list as a not analyzed element for subsequent formula calculations. This is done by entering o (for oxygen) in the *Element* text box and leaving the *X-Ray Line* text box empty. See User's Guide and Reference documentation for more details.



Channel	Element	X-Ray	Analyzed	Motor	Crystal	On-Peak
1	si	ka	Yes	1	PET	228.074
2	al	ka	Yes	2	TAP	90.9050
3	ti	ka	Yes	3	LIF	191.217
4	v	ka	Yes	3	LIF	174.186
5	cr	ka	Yes	3	LIF	159.317
6	fe	ka	Yes	3	LIF	134.724
7	mn	ka	Yes	3	LIF	146.253
8	mg	ka	Yes	2	TAP	107.798
9	ca	ka	Yes	1	PET	107.519
10	na	ka	Yes	2	TAP	129.817
11	o		No			

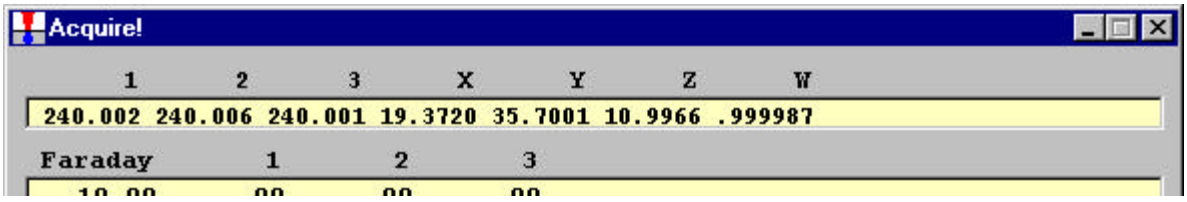
Click the **OK** button of the **Analyzed and Specified Elements** window when done entering elements in the run.

The **GetElmLoadDefaultStds** window opens to inform the user that standard assignments have been made based on the highest concentration of the element in the standard. The user will edit these choices shortly. Click **OK** to return to the main **Acquire!** window.

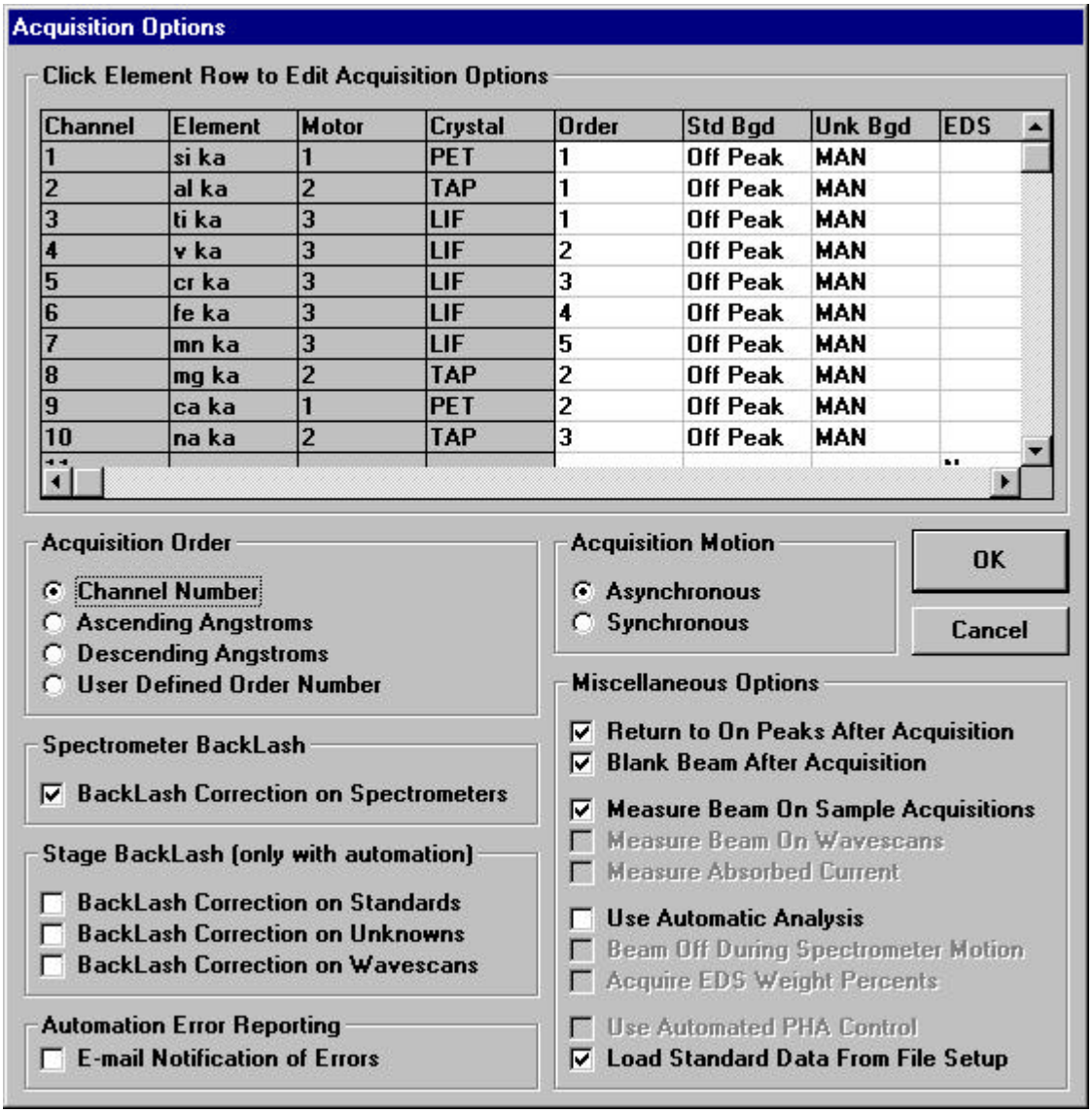


Editing Acquisition Options

The user may change the element acquisition order of the spectrometers by clicking the **Acquisition Options** button in the **Acquire!** dialog box.

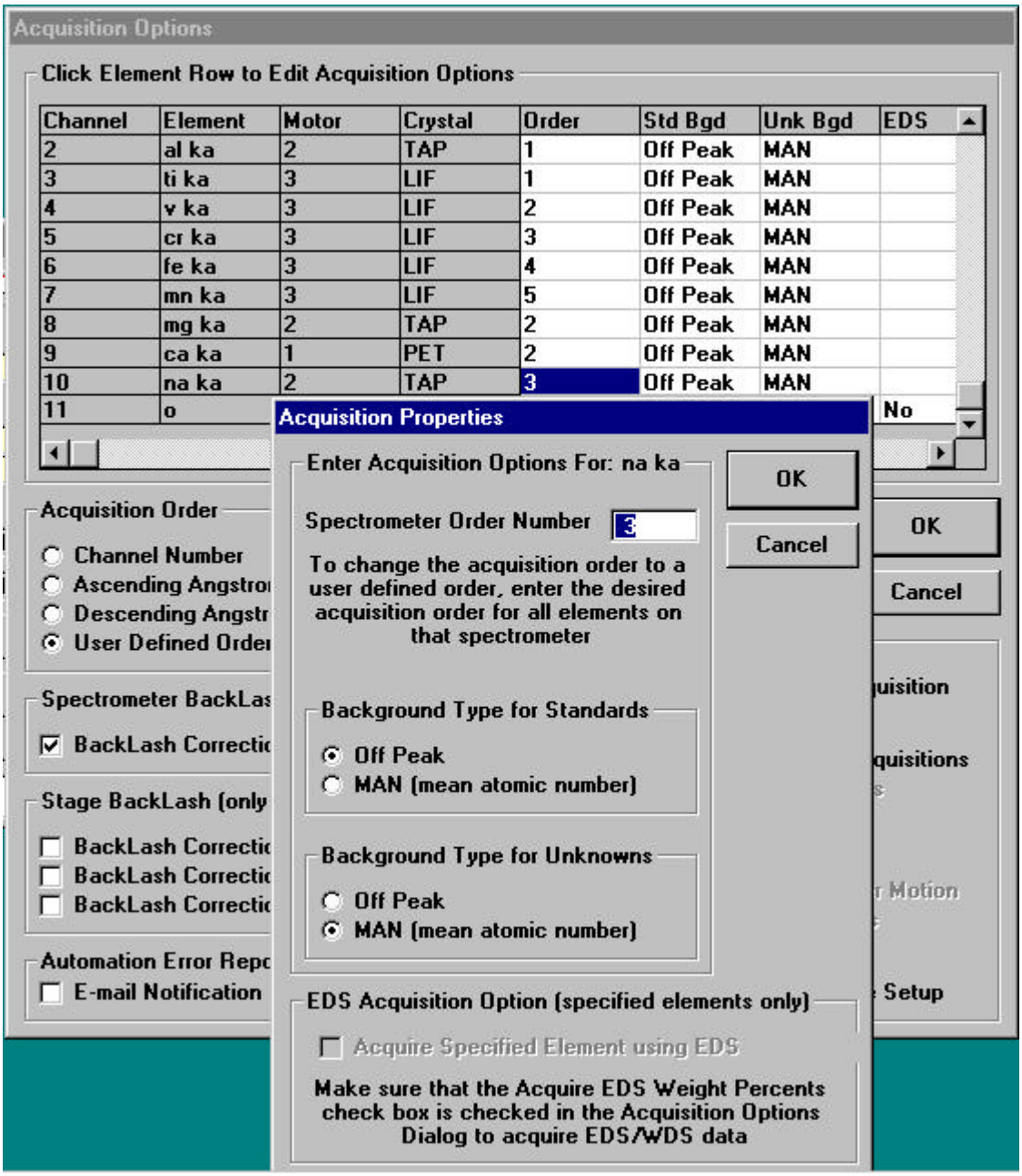


This opens the **Acquisition Options** dialog box.

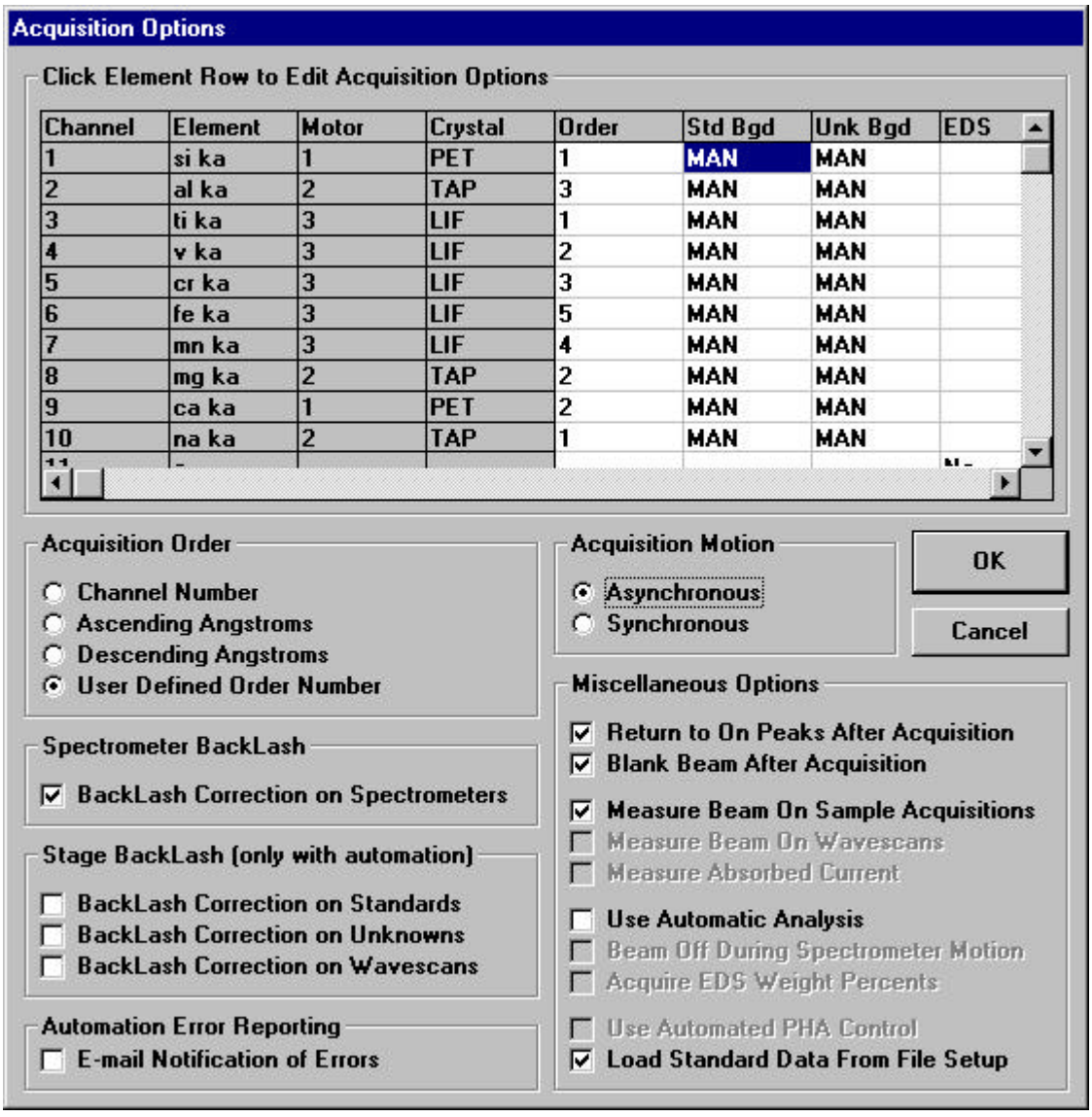


To change the order that the spectrometer measures an element, select the *User Defined Order Number* button under *Acquisition Order* and click the row of the element to edit.

This opens the **Acquisition Properties** dialog box, seen below. Here, the user will re-define na to be counted on the first spectrometer pass due to its susceptibility to being volatilized by long exposure to the electron beam. In samples containing volatile elements the user may wish to consider running the volatile element calibration routine (see User's Guide and Reference documentation and/or Advanced Topics manual).



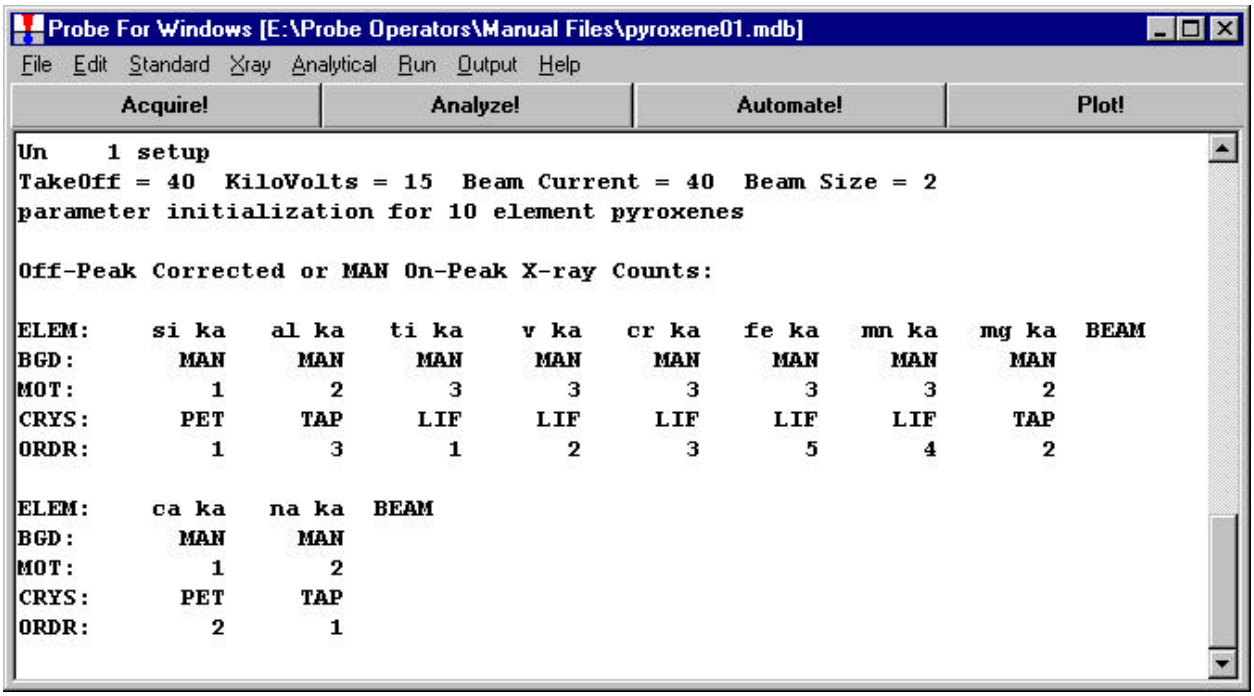
Edit the *Spectrometer Order Number* for all elements to change the acquisition order. Further, the user wishes to use the same background correction method for both standards and unknowns, edit the *Background Type for Standards* to *MAN* for each element. Click the **OK** button returning to the **Acquisition Options** window. For spectrometer efficiency and element volatilization issues the user redefines the acquisition order as seen below.



Click the **OK** button of the **Acquisition Options** window to return to the **Acquire!** dialog box.

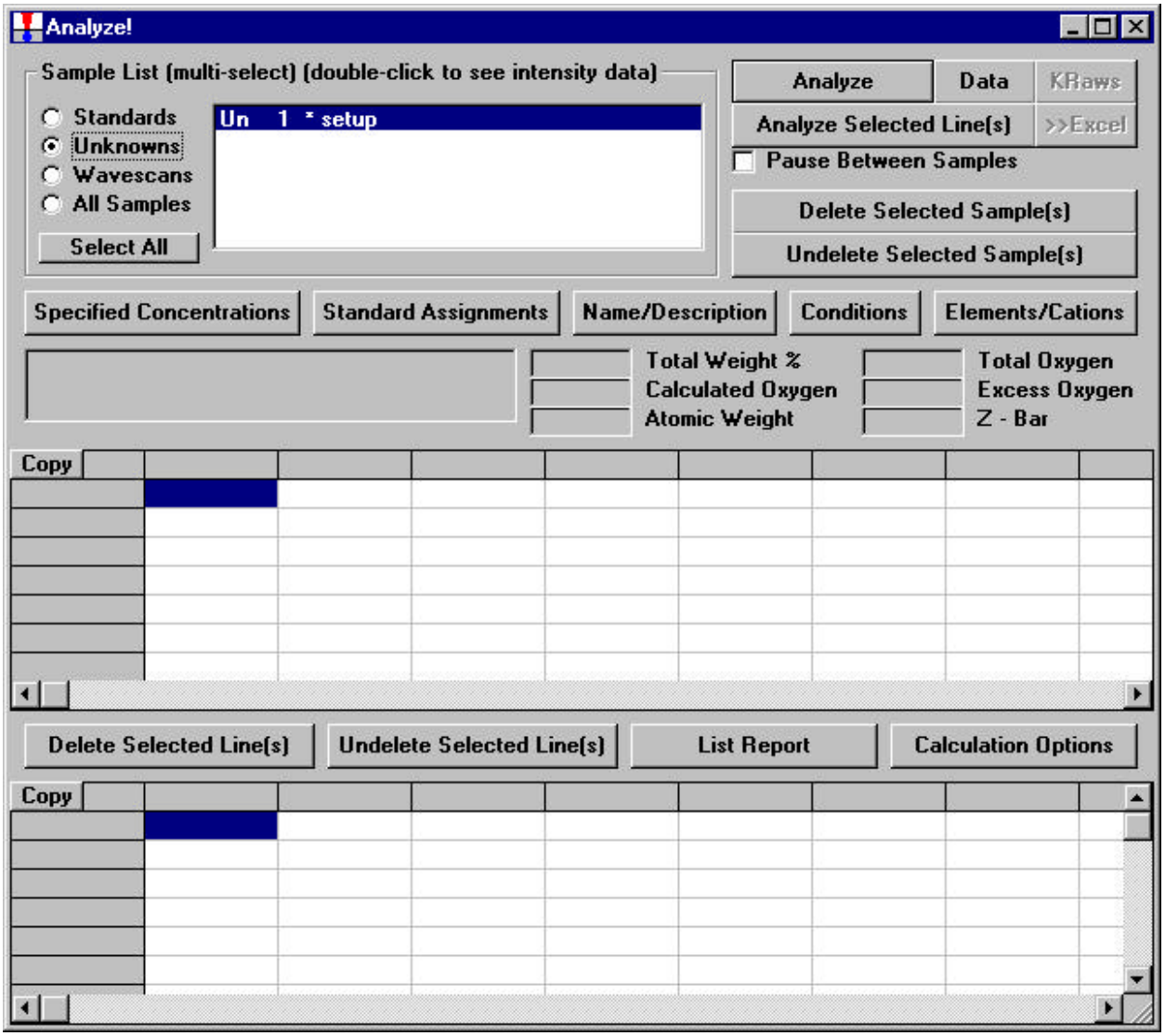
Modifying Standard Assignments

The standard assignments chosen by PROBE FOR WINDOWS may be inspected and edited by clicking the **Analyze!** button from the main log window.



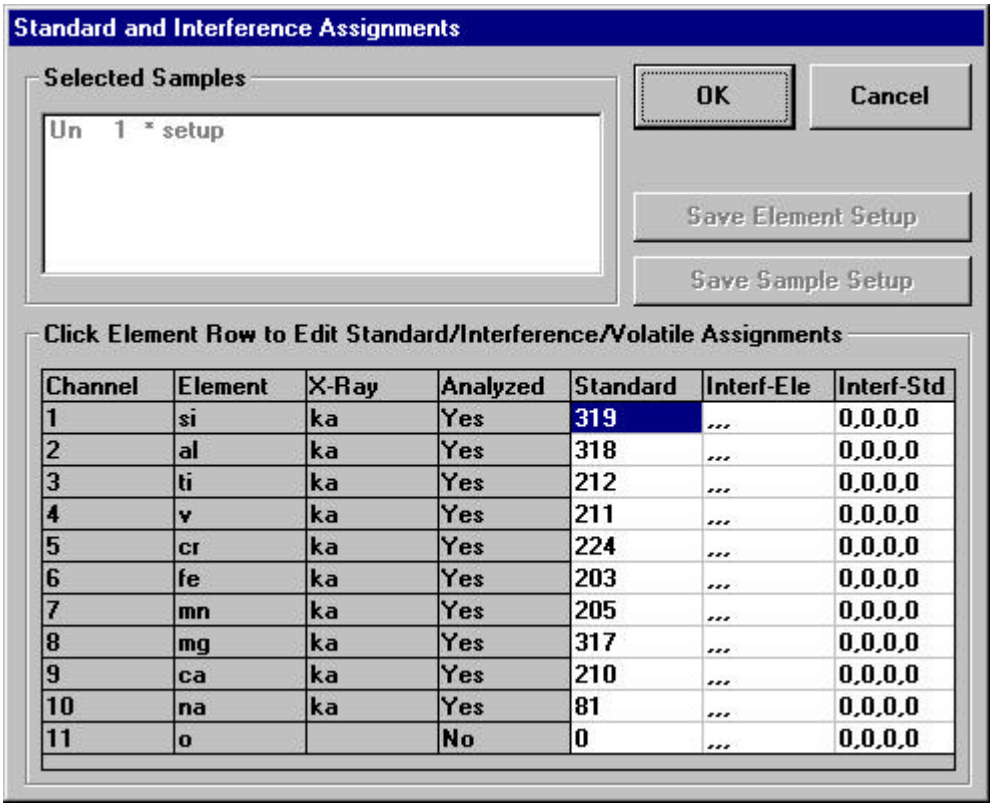
The program automatically wraps element data output to eight elements per line. If the extended format menu is checked (activated from the **Output** menu) then the data is written out (in log window and to disk file, if enabled) as far as necessary to the right.

This opens the **Analyze!** dialog box.



Click the **Standard Assignments** button.

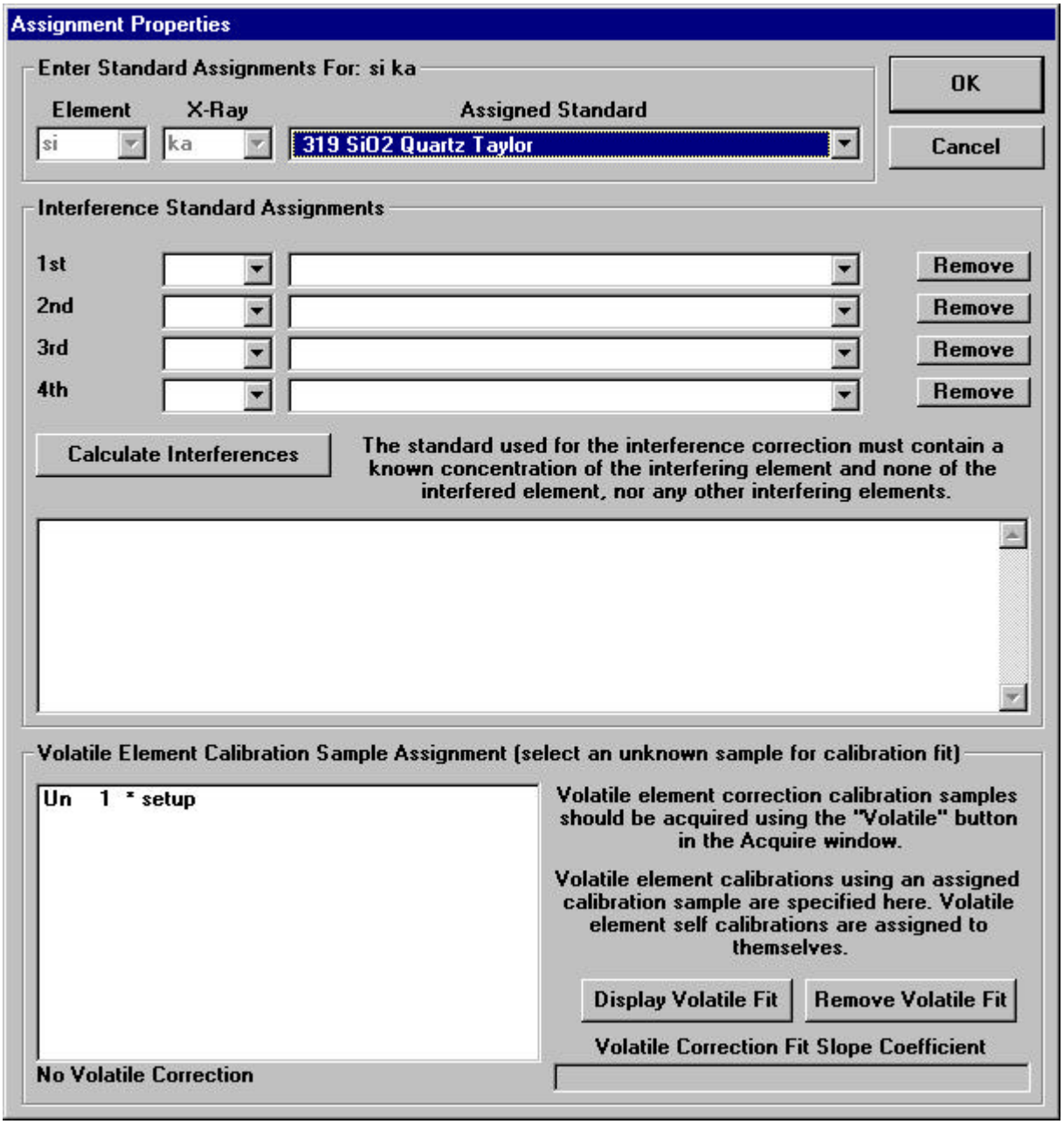
The **Standard and Interference Assignments** dialog box opens.



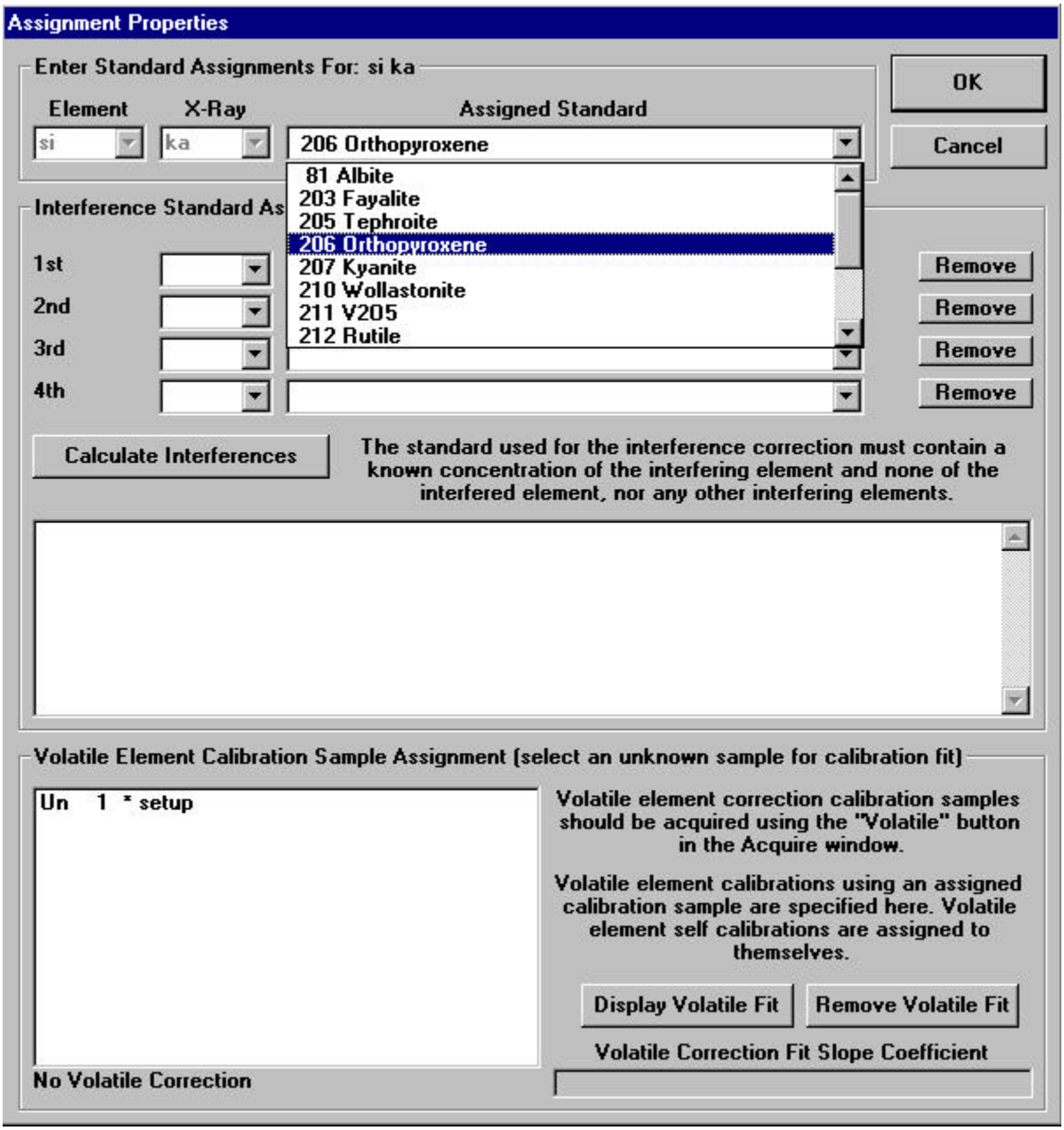
Channel	Element	X-Ray	Analyzed	Standard	Interf-Ele	Interf-Std
1	si	ka	Yes	319	...	0,0,0,0
2	al	ka	Yes	318	...	0,0,0,0
3	ti	ka	Yes	212	...	0,0,0,0
4	v	ka	Yes	211	...	0,0,0,0
5	cr	ka	Yes	224	...	0,0,0,0
6	fe	ka	Yes	203	...	0,0,0,0
7	mn	ka	Yes	205	...	0,0,0,0
8	mg	ka	Yes	317	...	0,0,0,0
9	ca	ka	Yes	210	...	0,0,0,0
10	na	ka	Yes	81	...	0,0,0,0
11	o		No	0	...	0,0,0,0

Click the row of the element that the user wishes to change the standard assignment for.

This opens the **Assignment Properties** dialog box. The default standard assignments are based on the highest concentration of the element in the standards currently in the run. In addition to standard assignments, the user may assign spectral interference corrections and volatile element calibrations from this window.

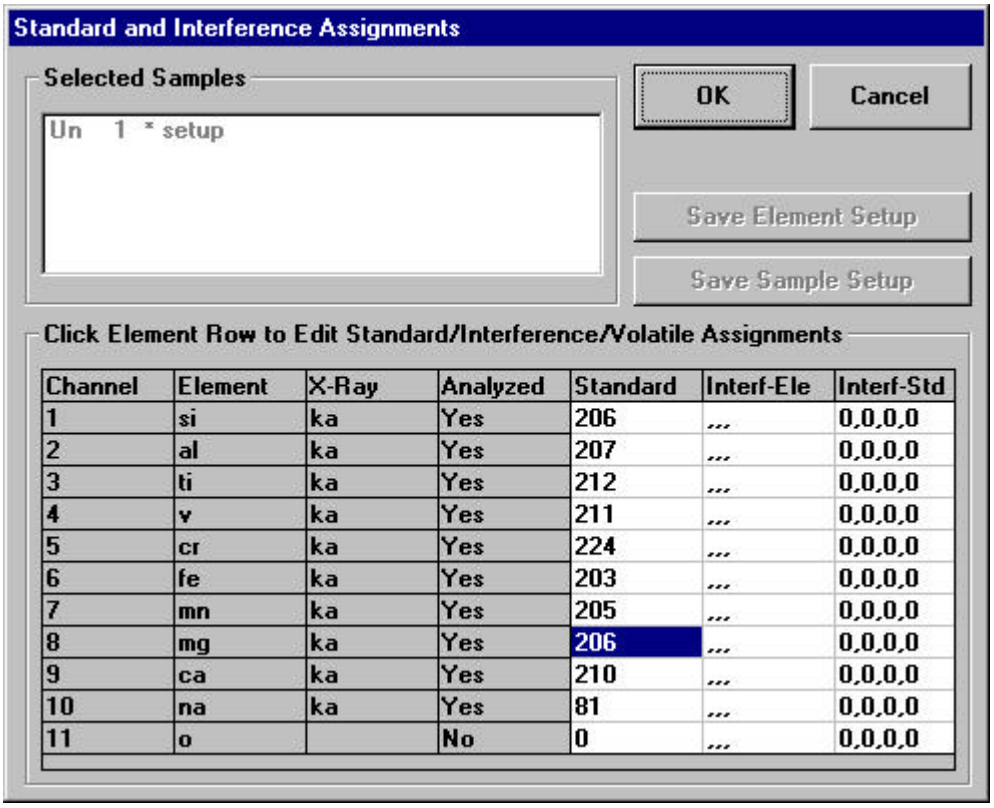


Click the *Assigned Standard* menu box. A scrollable list of all standards added to the current run are displayed. Select a new standard for element si.



Click the **OK** button returning to the **Standard and Interference Assignments** dialog box.

Repeat these editing steps until all necessary element standard assignments have been modified. In this example, the standard assignments for si, al, and mg are edited, resulting in the following window.

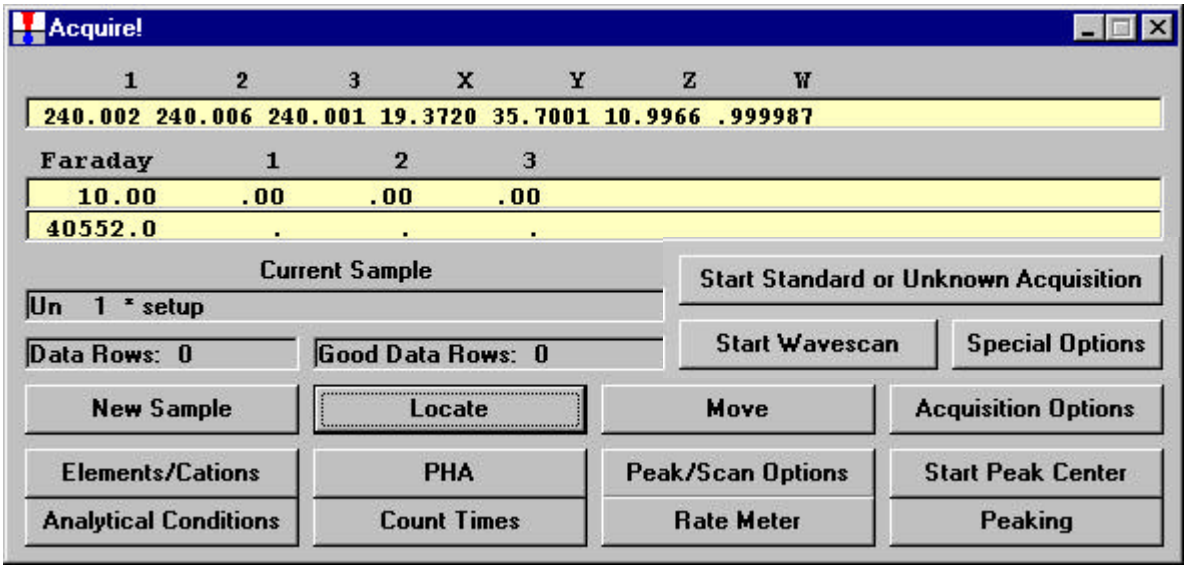


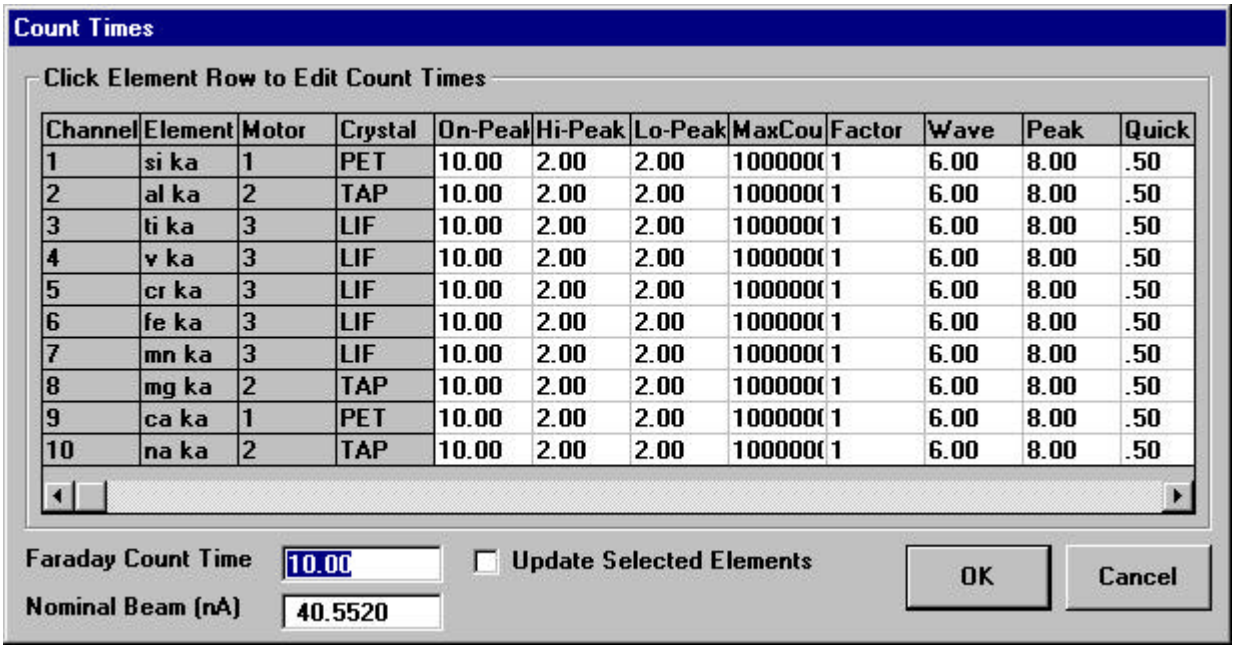
Channel	Element	X-Ray	Analyzed	Standard	Interf-Ele	Interf-Std
1	si	ka	Yes	206	...	0,0,0,0
2	al	ka	Yes	207	...	0,0,0,0
3	ti	ka	Yes	212	...	0,0,0,0
4	v	ka	Yes	211	...	0,0,0,0
5	cr	ka	Yes	224	...	0,0,0,0
6	fe	ka	Yes	203	...	0,0,0,0
7	mn	ka	Yes	205	...	0,0,0,0
8	mg	ka	Yes	206	...	0,0,0,0
9	ca	ka	Yes	210	...	0,0,0,0
10	na	ka	Yes	81	...	0,0,0,0
11	o		No	0	...	0,0,0,0

Click the **OK** button of the **Standard and Interference Assignments** dialog box returning to the **Analyze!** window.

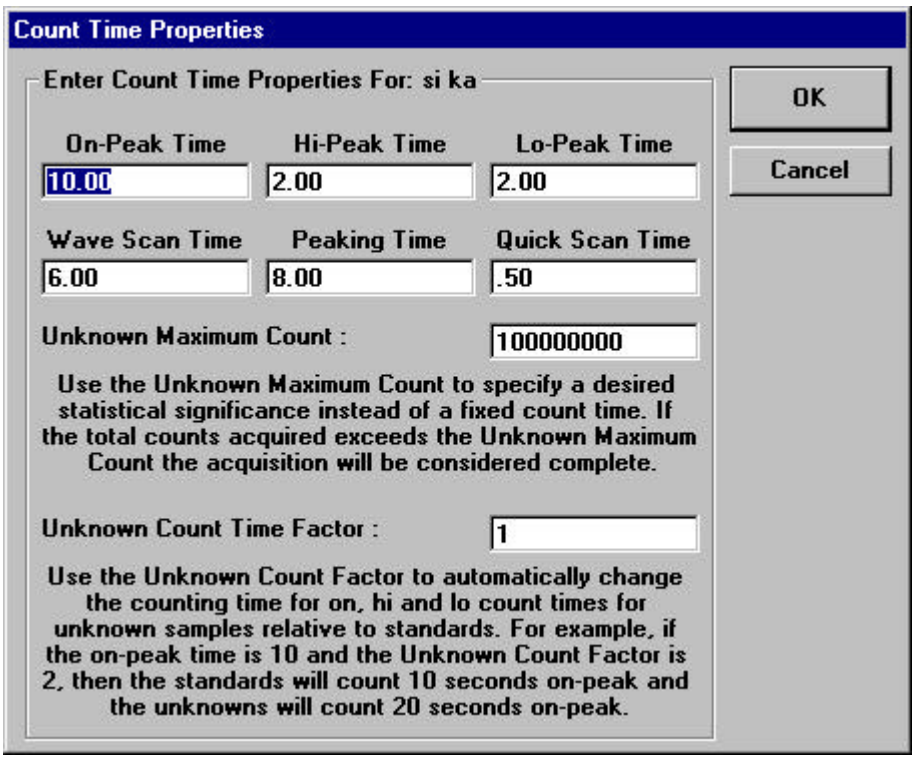
Setting Count Times

Click the **Count Times** button of the **Acquire!** window.





To edit the count times for any element click that row in the spreadsheet. This opens the **Count Time Properties** dialog box.



Edit the *Count Time* text boxes with new times. To adjust the count times on unknowns, change the *Unknown Count Time Factor*. This is the multiplicity factor for acquiring unknown sample elements relative to the count times specified for the standards.

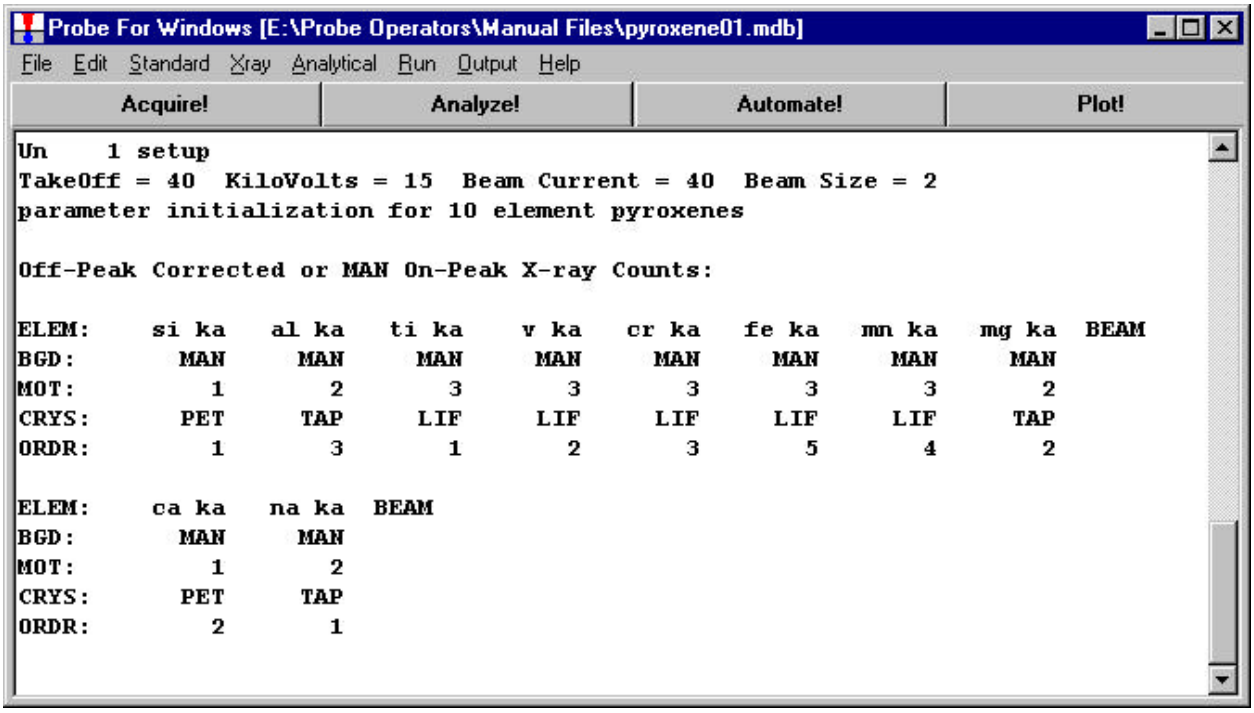
The *Unknown Maximum Count* text box is used to specify a statistics based count time. This feature is most useful if the user wishes to count for 30 seconds or 40000 counts whichever comes first. For samples with high count rate elements, the actual analysis time would be shorter.

Click the **OK** button of the **Count Time Properties** window.

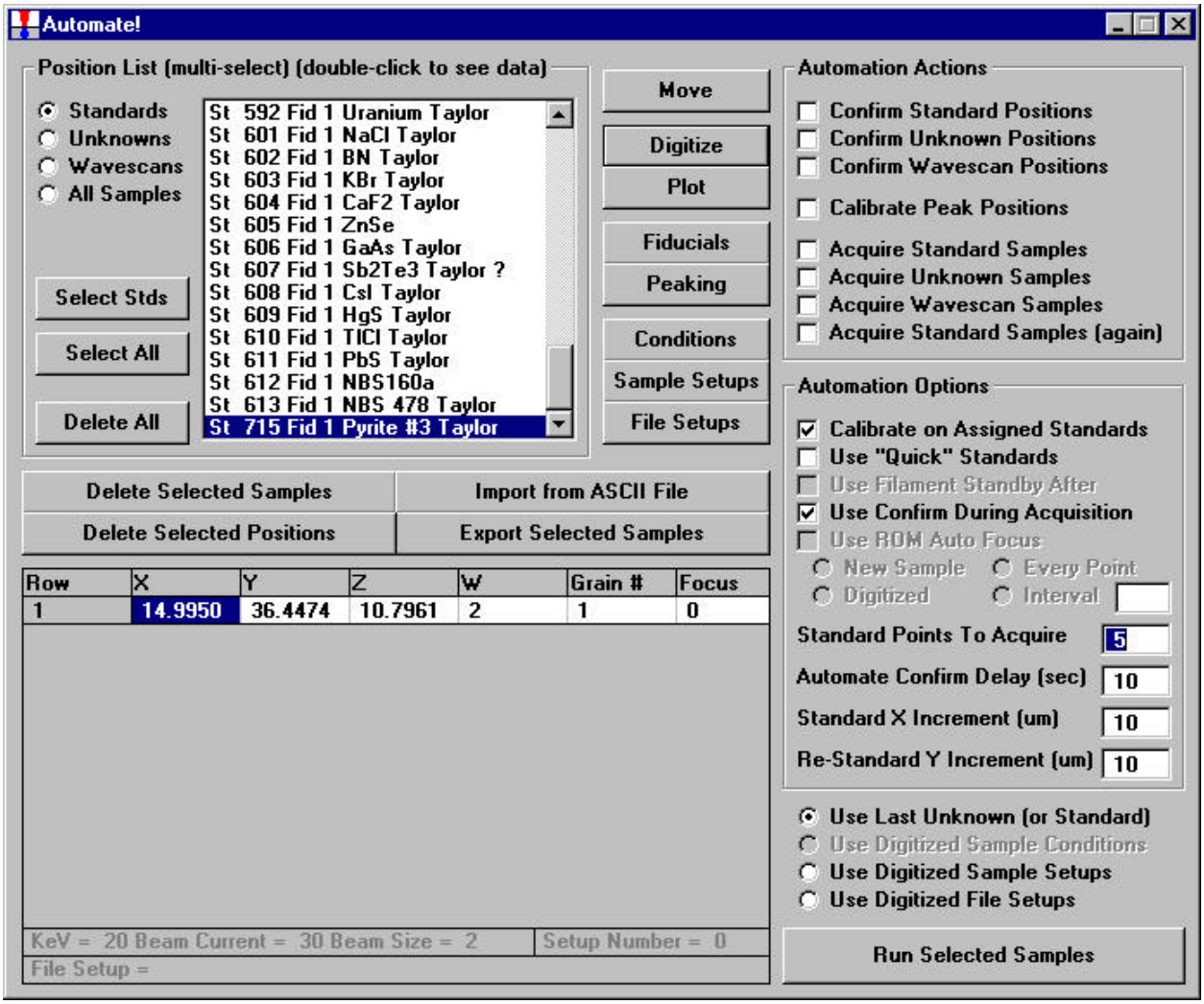
Finally, click the **OK** button of the **Count Times** dialog box to accept any modified count times and return to the **Acquire!** window.

Loading Standard Position Files

To run analytical standards using automation, requires that the computer know the physical location of all the standards for this run. Click the **Automate!** button from the main PROBE FOR WINDOWS log window.

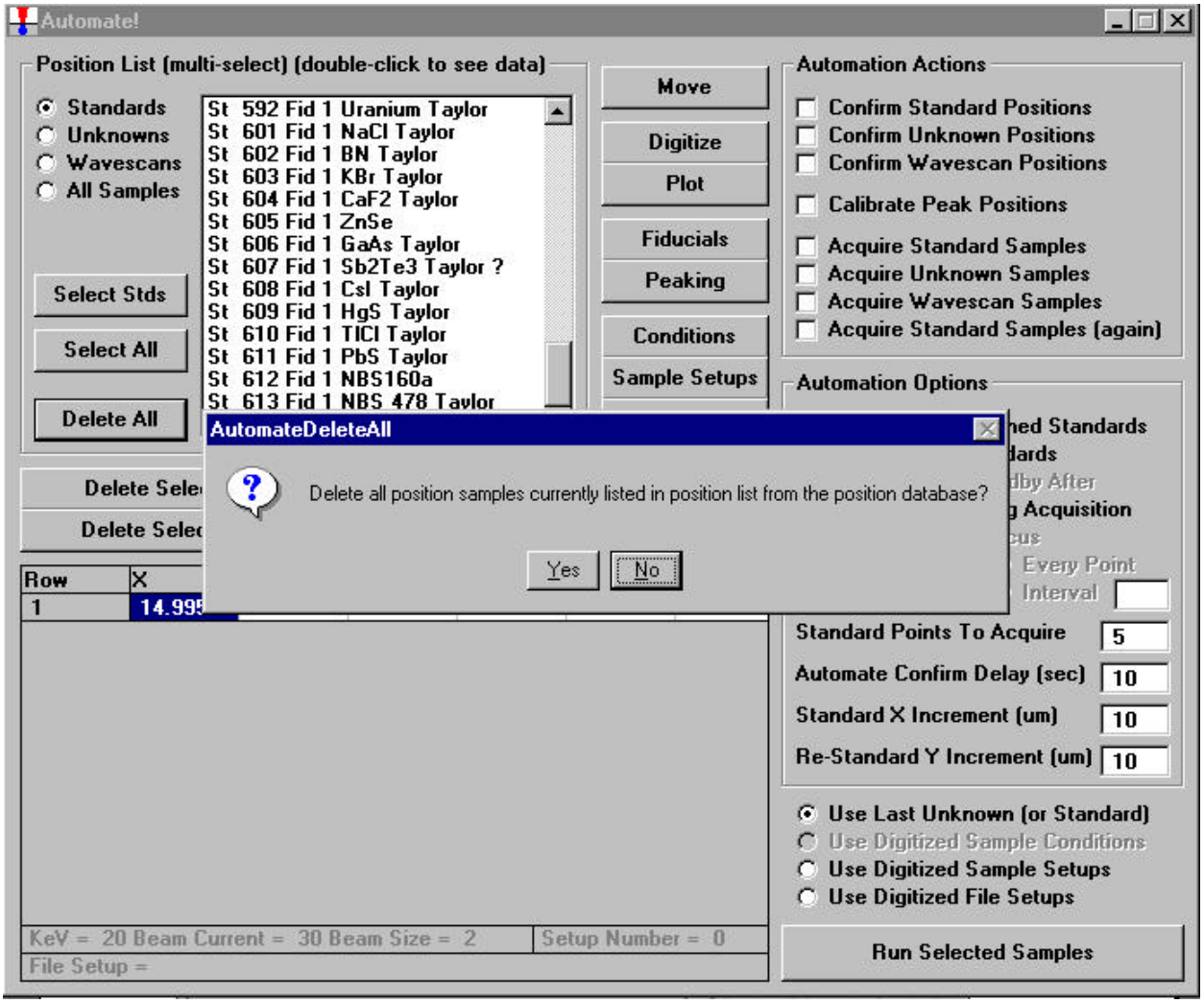


This opens the **Automate!** dialog box shown below.

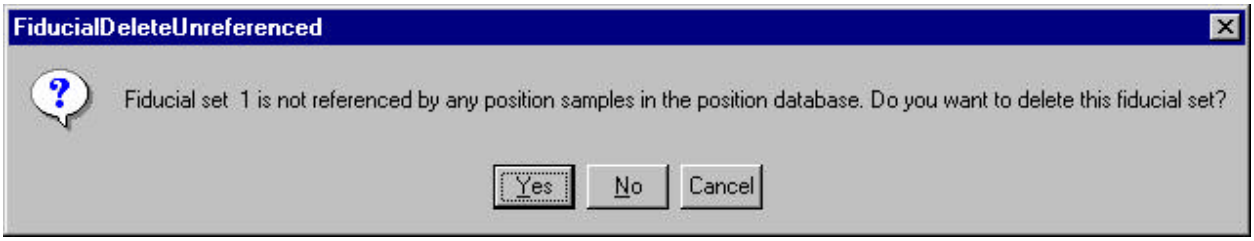


The last set of digitized standards used is visible in the *Position List* list box of the **Automate!** window. Currently, the standard block for the brass alloy run digitized previously are listed. These will be deleted and replaced by the appropriate standard position file(s).

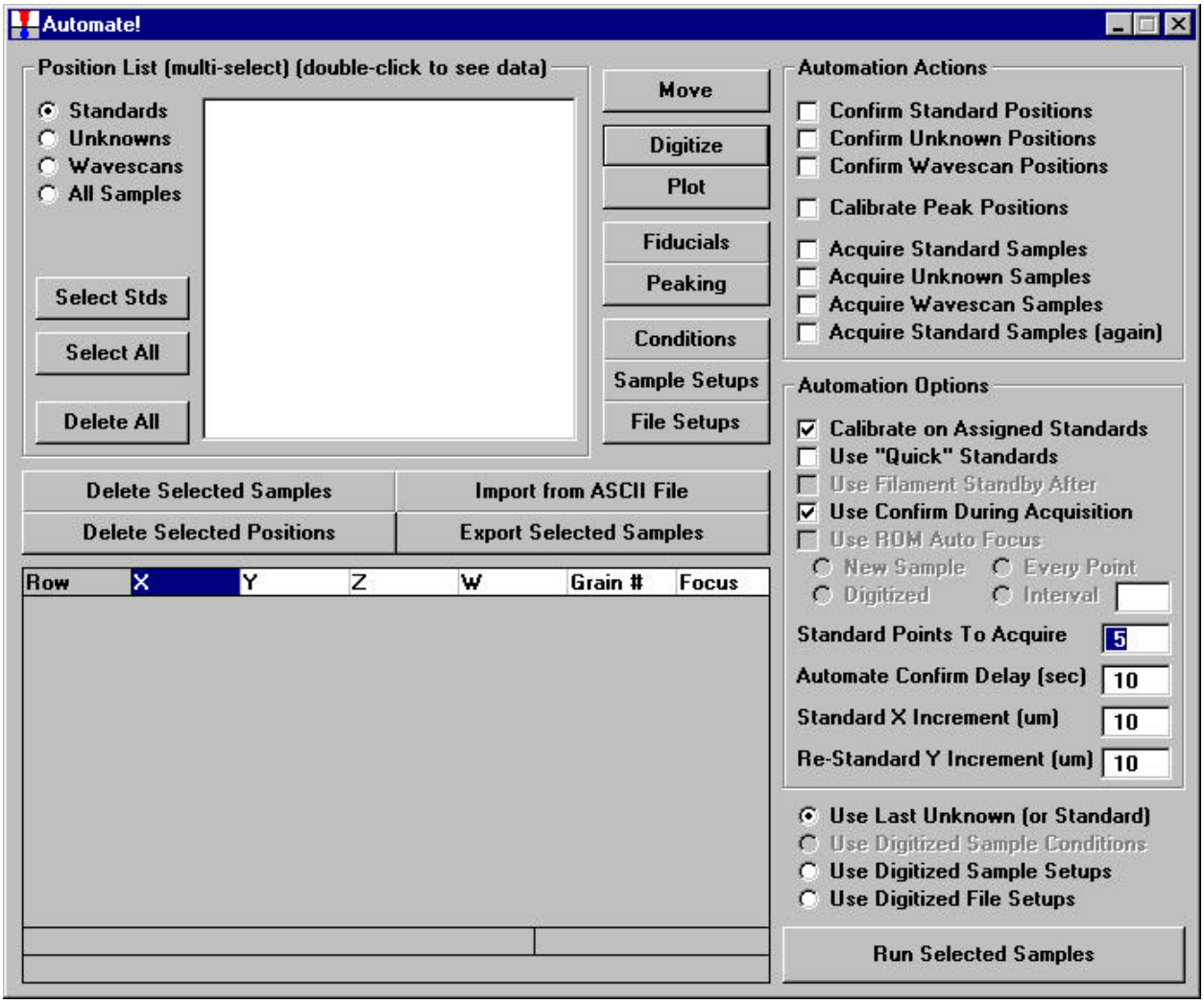
Click the **Delete All** button. This opens the **AutomateDeleteAll** window. Click the **Yes** button of the **AutomateDeleteAll** window to clear the *Position List* list box of all displayed position samples.



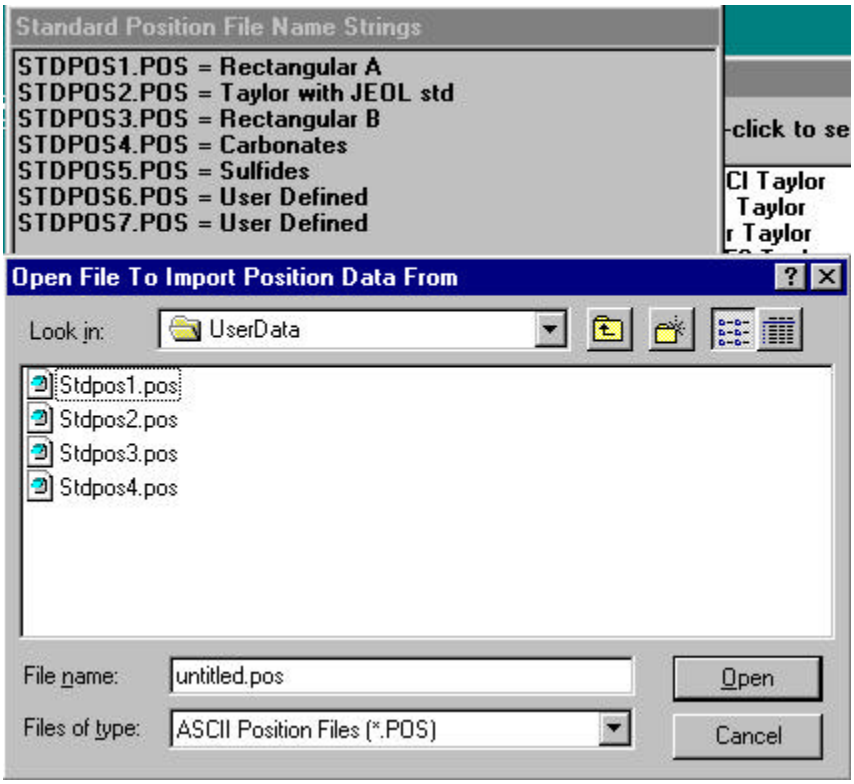
The **FiducialDeleteUnreferenced** window opens. Click the **Yes** button to clear the fiducial coordinate set from the position database.



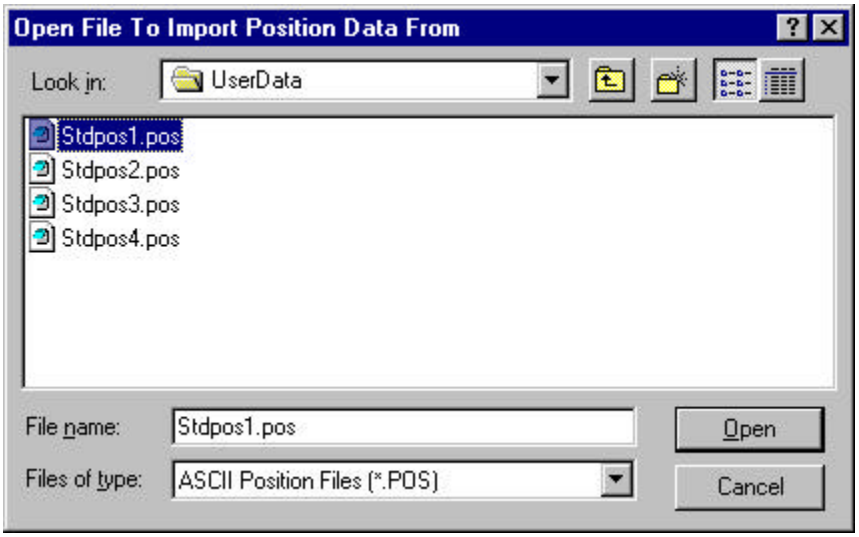
Click the **Import from ASCII File** button of the **Automate!** dialog box to import position samples from a previously saved ASCII file.



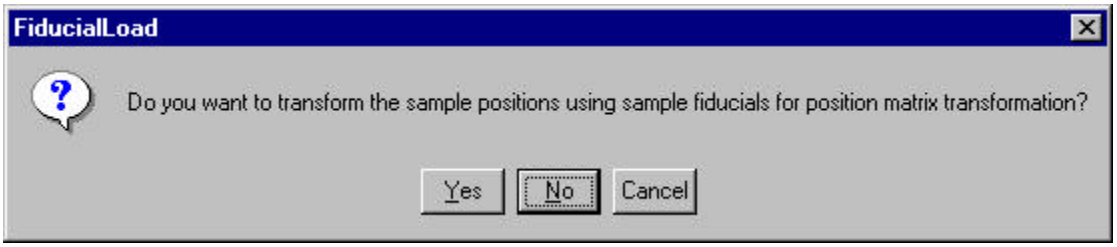
This action opens both the **Standard Position File Name Strings** and the **Open File To Import Position Data From** windows. The former window is based on the name strings in the PROBEWIN.INI file. The user has previously digitized all standard blocks and created STDPOSx.POS files. Three STDPOSx.POS files are typically loaded for silicate runs; STDPOS1.POS, STDPOS2.POS, and STDPOS3.POS. The default location for *.POS files is at C:\Program Files\Probe for Windows\UserData.



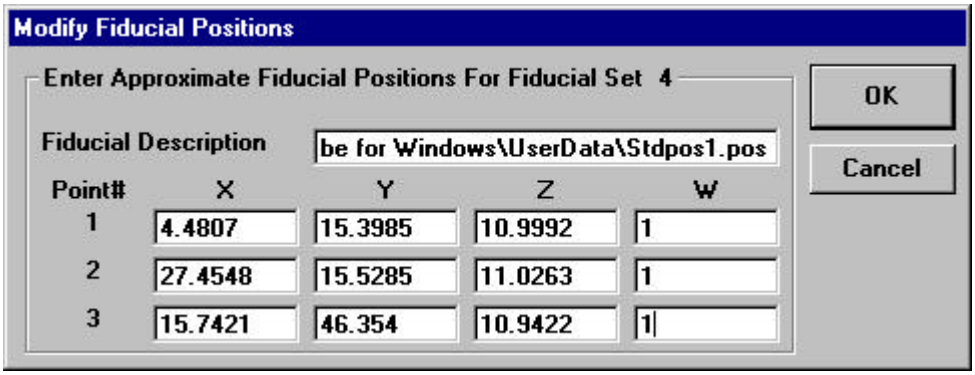
Type in the appropriate file name in the *File name* text box or simply highlight the file in the list and click the **Open** button.



This action opens the **FiducialLoad** window. Click the **Yes** button to do a fiducial transformation on this pre-digitized standard block to obtain an accurate set of standard positions.

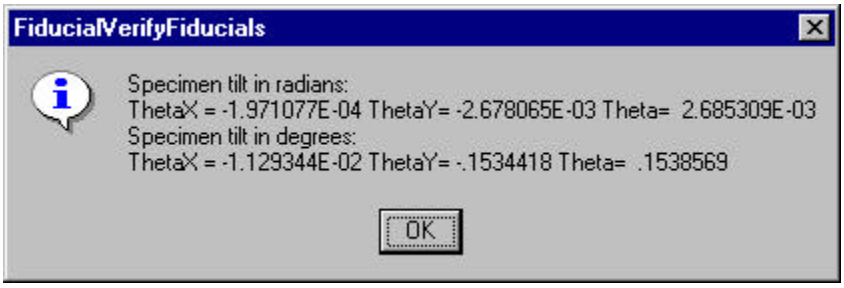


The **Modify Fiducial Positions** window opens. Normally the user would simply accept the defaults or edit the position text boxes for each point, including the appropriate stage location number (JEOL 733 use appropriate W stage position). When done, click the **OK** button.

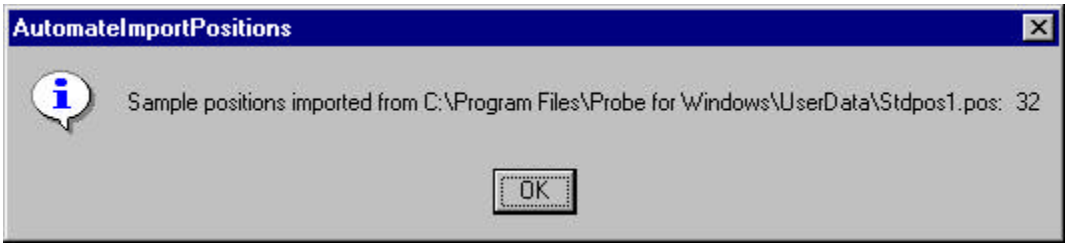


This action causes the stage motors to drive to the first fiducial coordinate in its lookup table. The **FiducialVerifyFiducial** window appears. Adjust the stage motors to center the first fiducial mark, click the **OK** button.

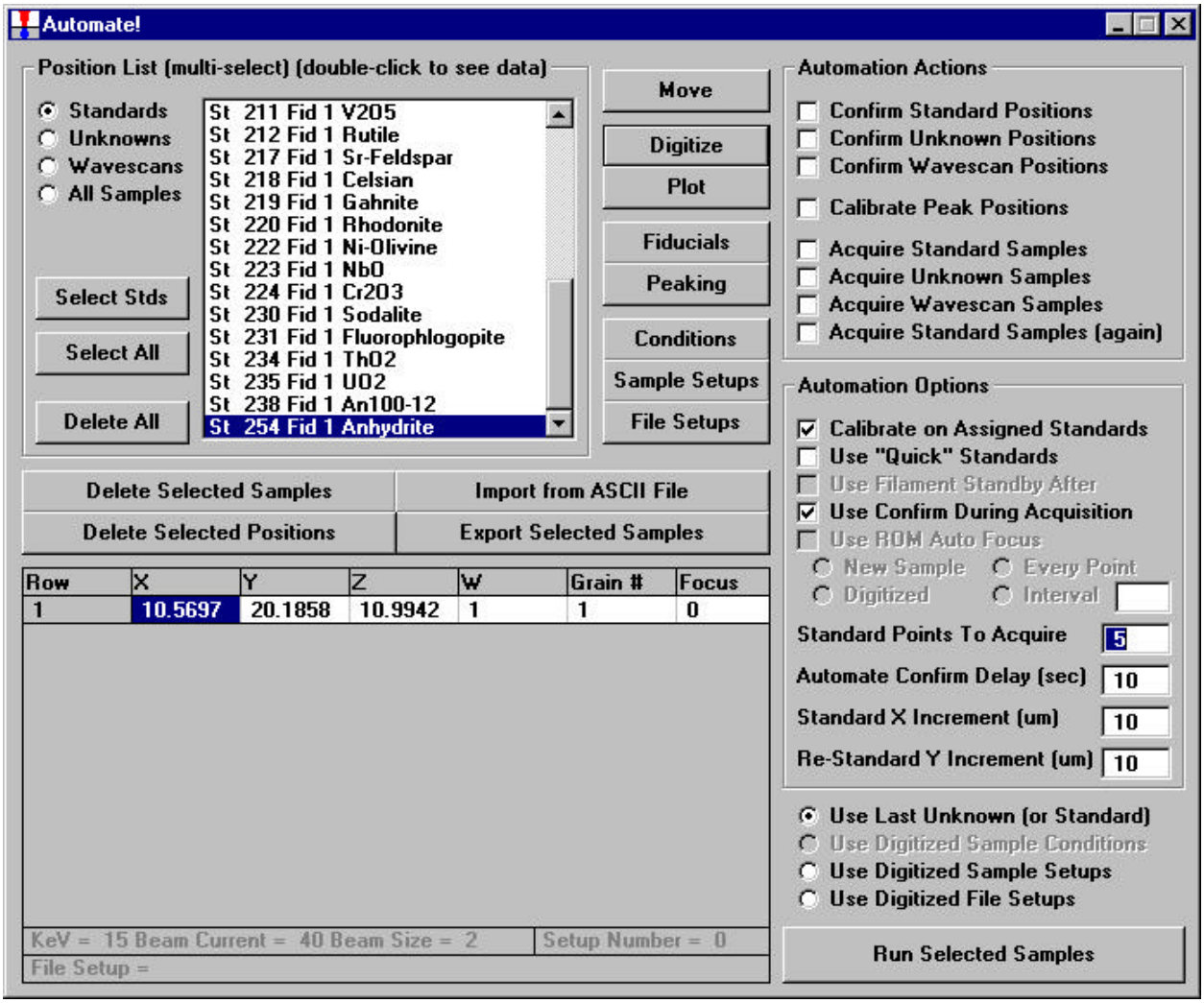
The computer will drive to each of the three fiducial marks for centering. Clicking the **OK** button after the third fiducial mark opens the **FiducialsVerifyFiducials** window. Click this **OK** button.



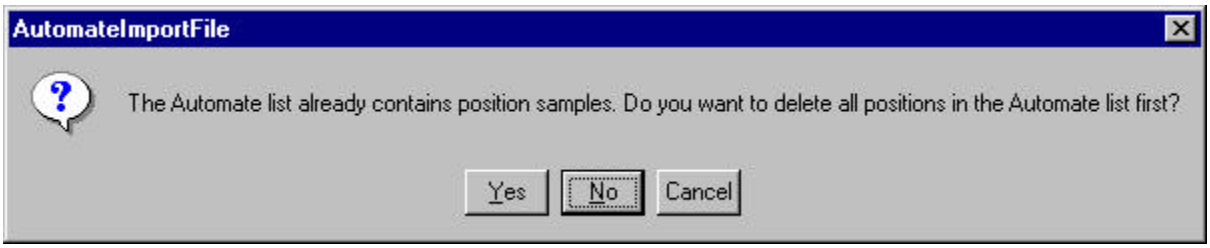
The program then imports and updates the position coordinates of all of the standards in the pre-digitized standard position file. The **AutomateImportPositions** window opens. Click the **OK** button returning to the **Automate!** window.



The **Automate!** window would appear as below. The currently transformed standard position file is listed in the *Position List* list box.

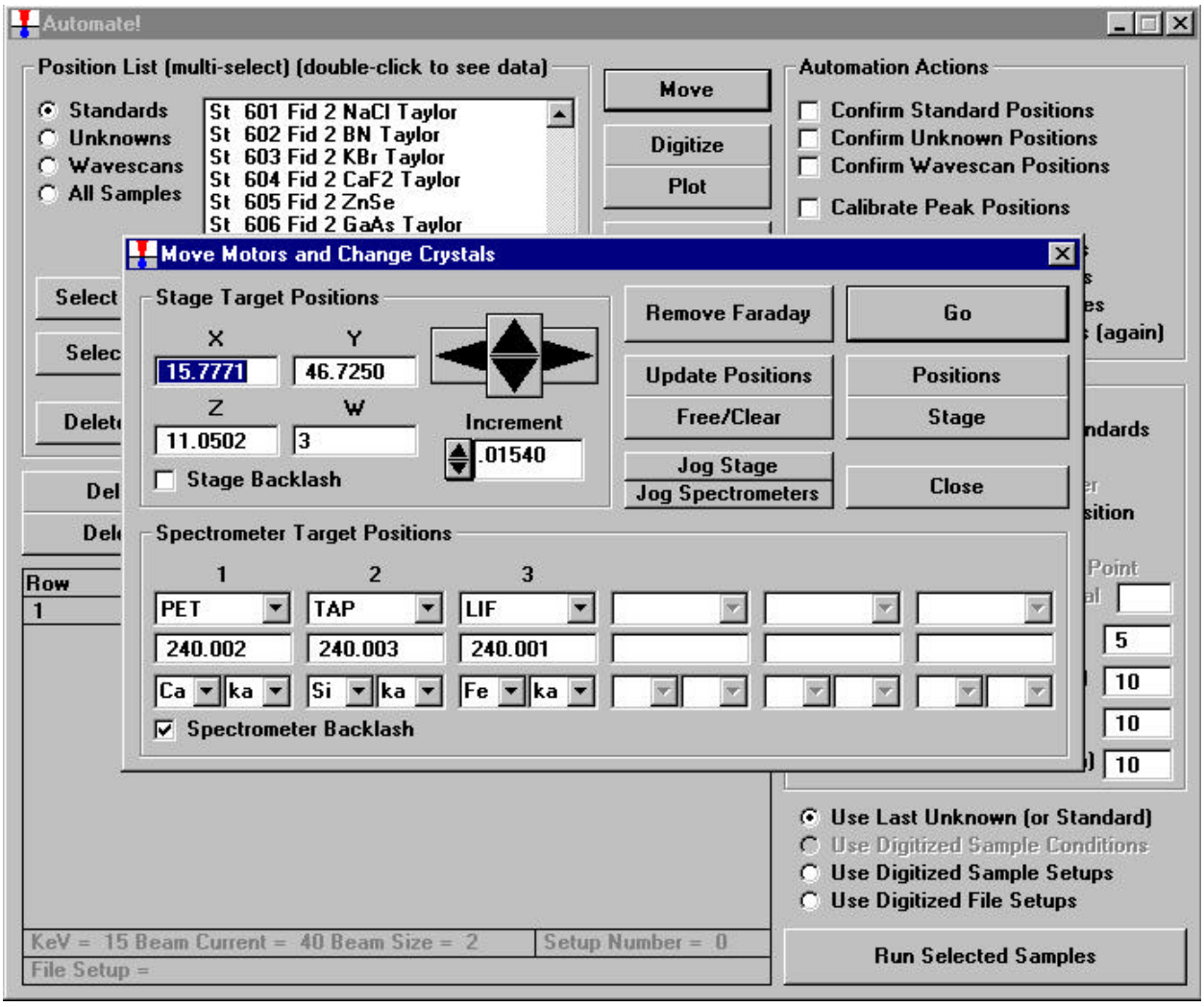


Repeat the same loading procedure for the other two standard position files required for use in the automation. After clicking the **Import from ASCII File** button, the **AutomateImportFile** window opens.

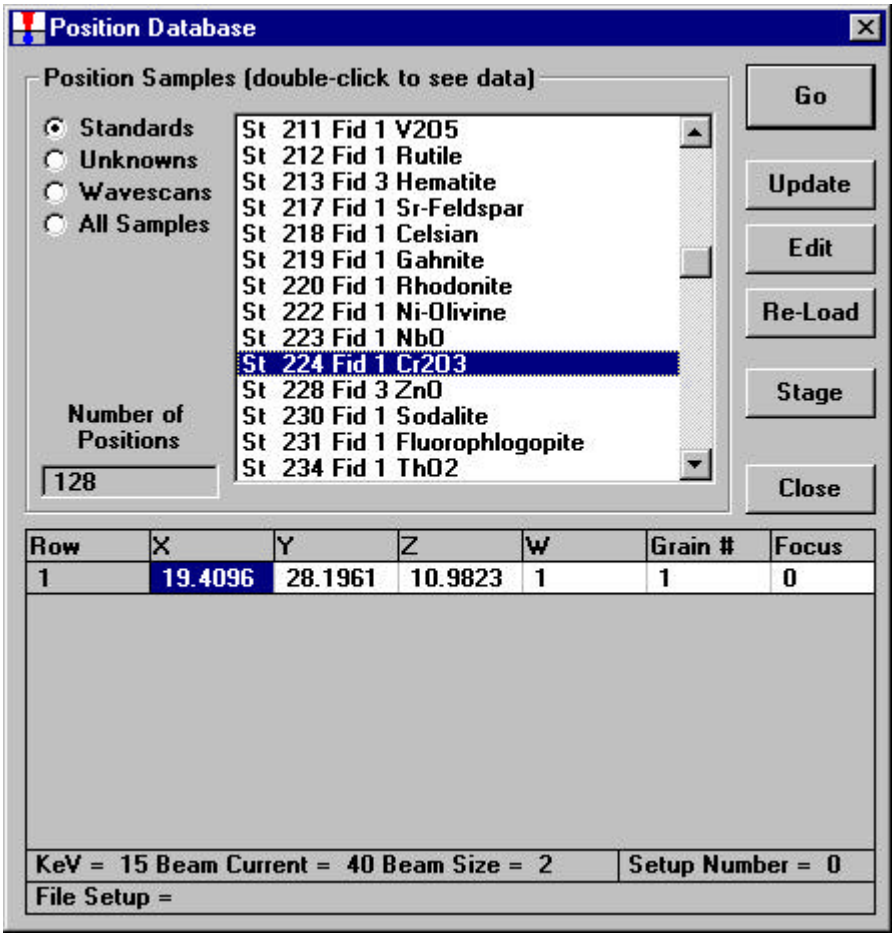


Typically, when using more than one standard mount, the user would not delete all positions in the *Position List*, instead appending the additional position files to the first file.

All of the standards loaded are listed in the *Position List* list box of the **Automate!** window. These may now be accessed by the program during any automation action. For instance, it is now possible to have the computer drive to any standard located on the three blocks. The user may click the **Move** button of the **Automate!** window opening the **Move Motors and Change Crystals** dialog box. Then, click the **Positions** button.



This opens the **Position Database** dialog box. From here any sample that has been digitized can be located by simply selecting it and clicking the **Go** button.



Once the stage motors drive the stage to the chosen standard, exit the **Position Database** by clicking the **Close** button. Likewise, the user may close the **Move Motors and Change Crystals** window by clicking its **Close** button, returning to the **Automate!** window.

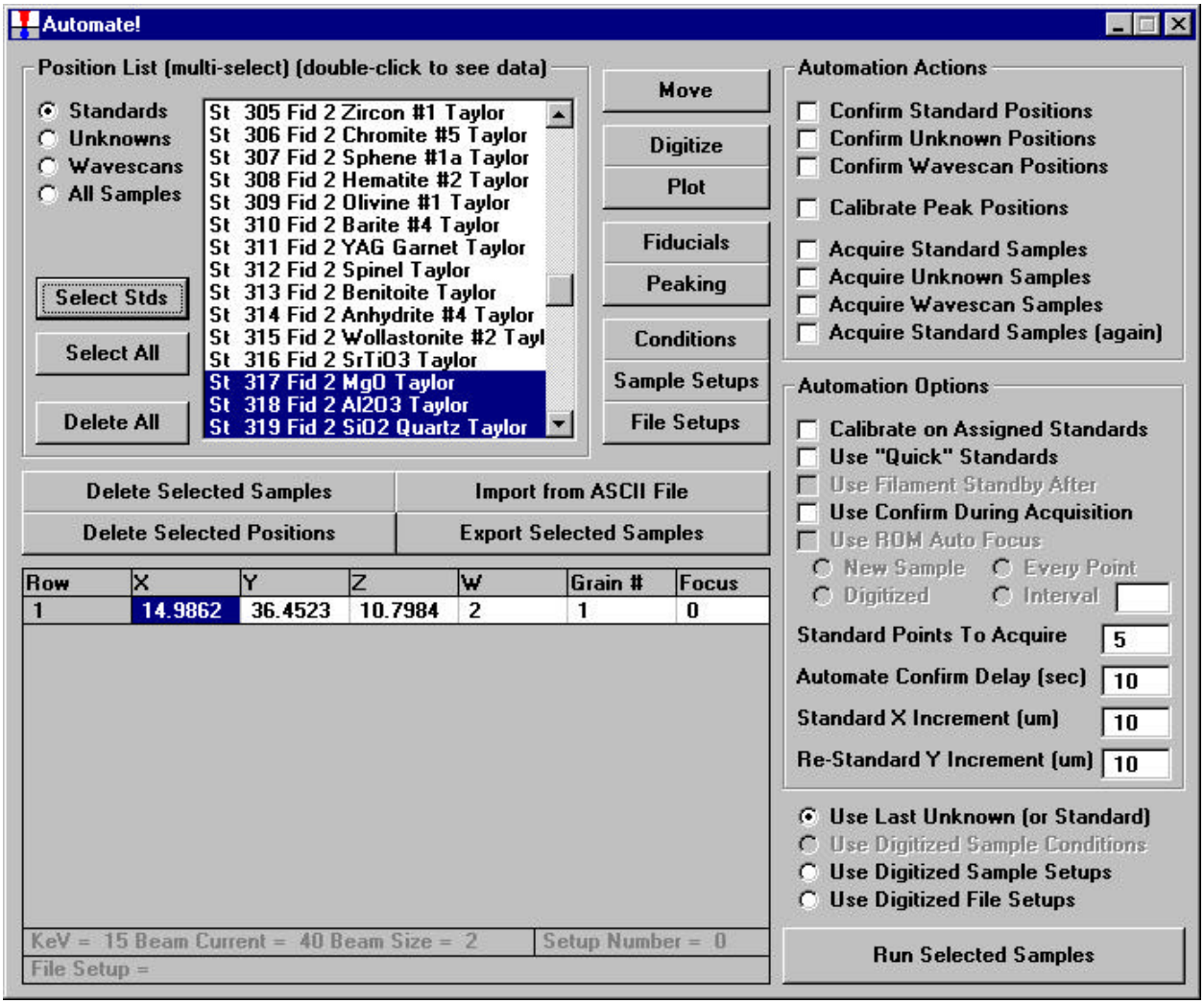
This concludes the initial parameter setup portion of PROBE FOR WINDOWS.

Automation Actions

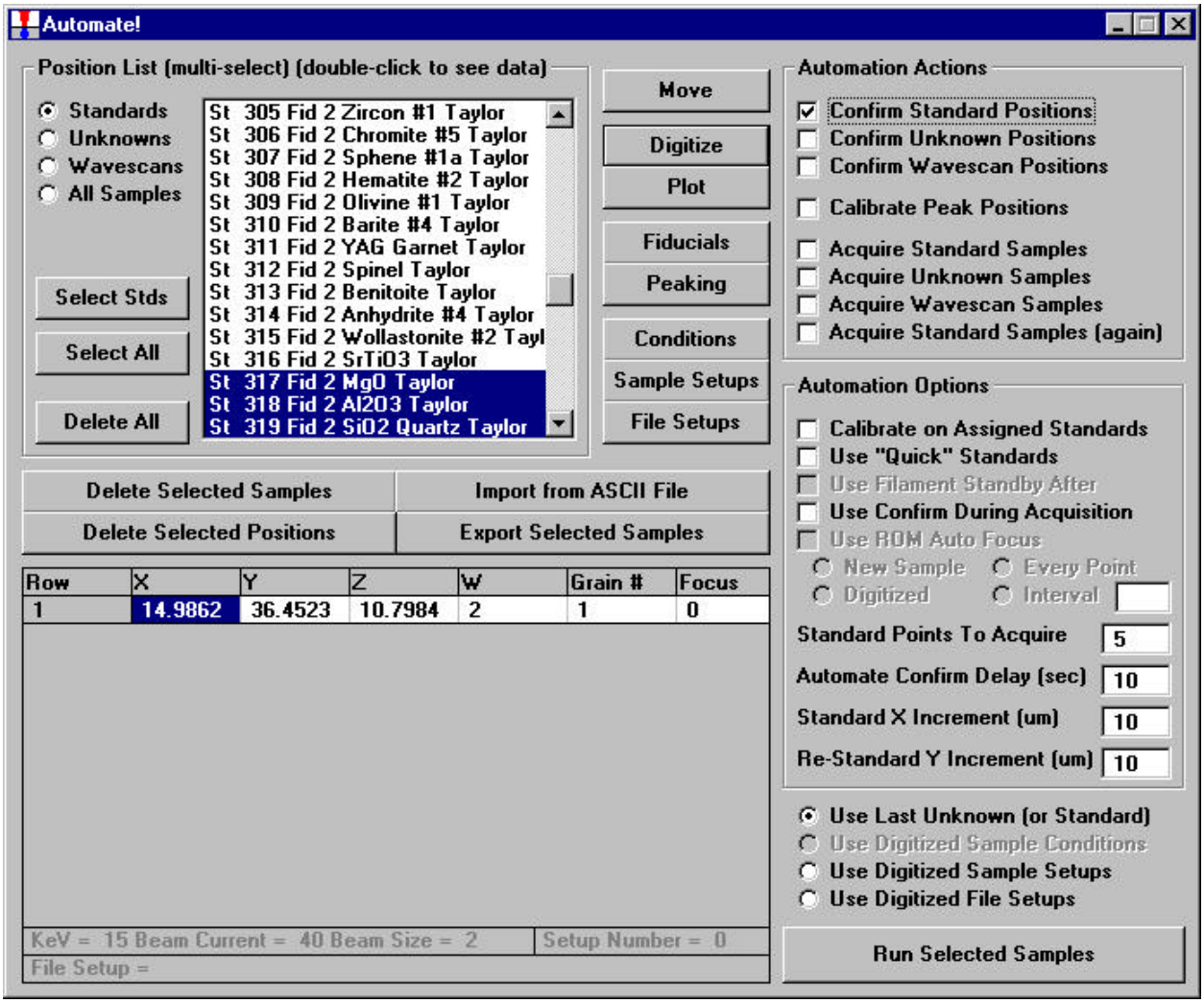
Confirm Standard Positions

All of the basic peak centering and x-ray count acquisition procedures may be automated. This is accomplished via the **Automate!** window.

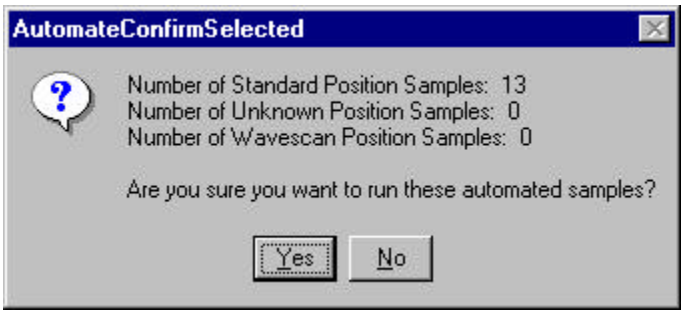
Click the **Select Stds** button of the **Automate!** dialog box. All standards that have been added to the current run will now be highlighted in the *Position List* list box.



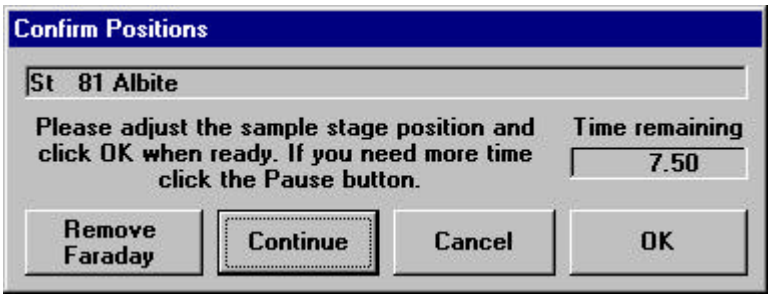
The user might start by checking the location and focus of each standard selected for the automated analysis. Click the box for *Confirm Standard Positions* under *Automation Actions*. Click the **Run Selected Samples** button.



The **AutomateConfirmSelected** window opens informing the user that thirteen standards were chosen and asks if you want to run these automated samples, click **Yes**.



The program then sends the stage motors to the fiducial transformed coordinates for the first selected standard and opens the **Confirm Positions** window. Clicking the two-way **Pause/Continue** button suspends the 10 second countdown (user defined in the PROBEWIN.INI file). Adjust the stage motors (X, Y, and Z) to a new, clean analysis position. Click the **OK** button of the **Confirm Positions** window when done, sending the stage to the next standard to confirm its position. Again, the **Confirm Positions** window opens, allowing the user to pause the countdown and adjust the sample position.

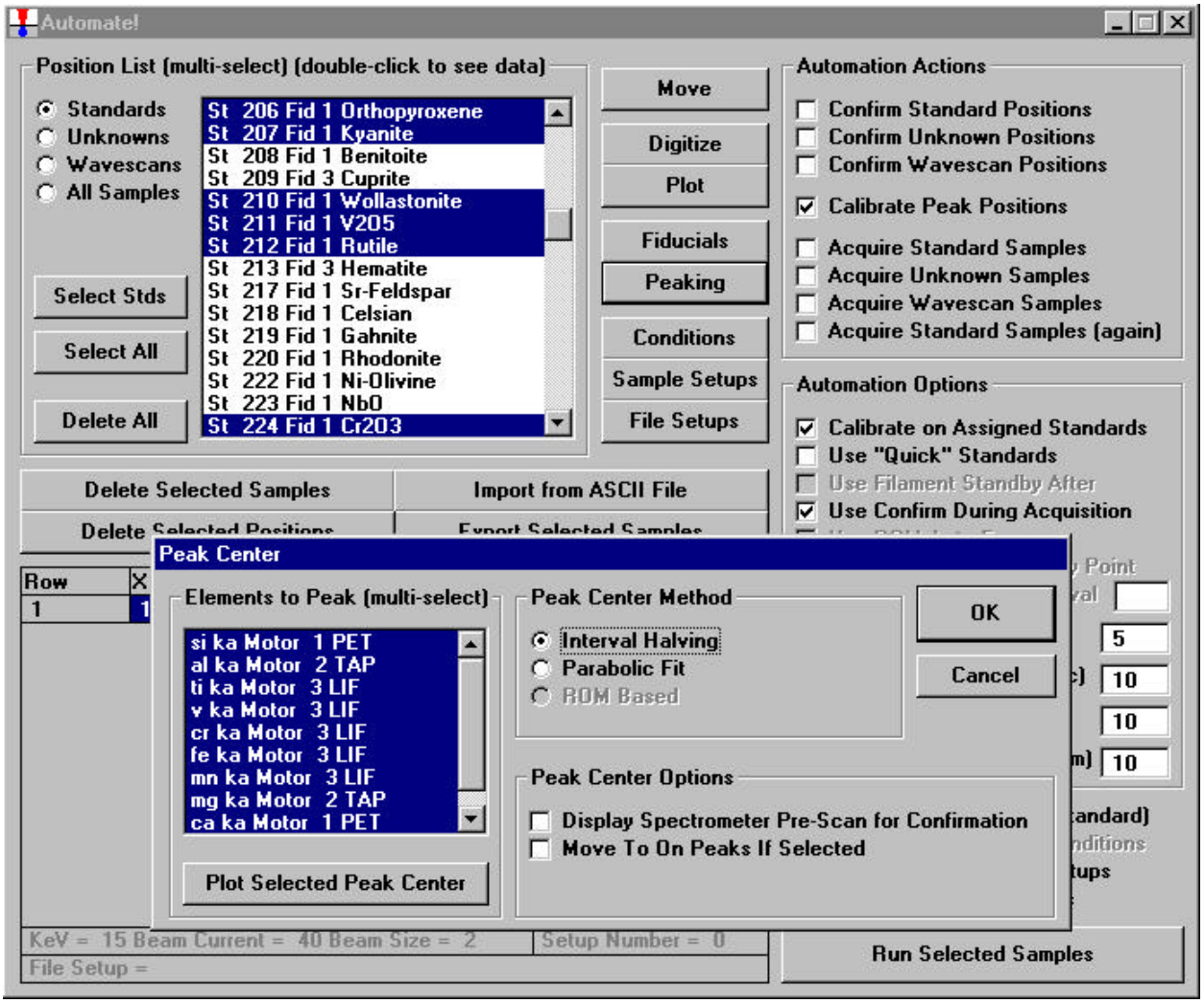


After the final standard is confirmed, the **AcquireStop** window appears. In this example standards on several standard blocks are located and confirmed. Click this **OK** button returning to the **Automate!** dialog box.

Calibrate Peak Positions

X-ray peaking may be automated from the **Automate!** window as follows.

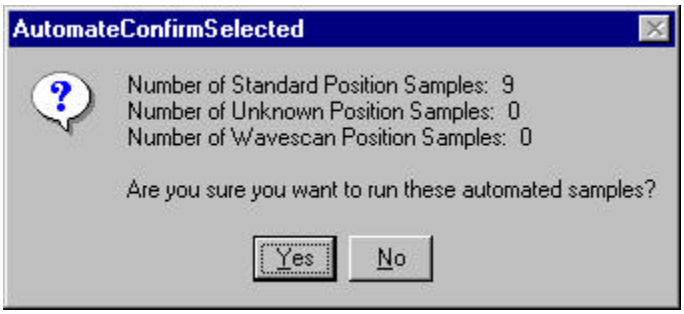
The **Select Stds** button from the previous step highlighted all of the standards added to the current run. Presently the *Position List* list box in the **Automate!** window contains both the analytical and MAN background standards for the current run. Since x-ray peak centering is only done on the primary analytical standards, either re-select the primary analytical standards or de-select the additional MAN background standards from the *Position List* list box. Under *Automation Actions* click only the *Calibrate Peak Positions* box. Under *Automation Options* click the *Calibrate on Assigned Standards* and *Use Confirm During Acquisition* boxes. Finally, click the **Peaking** button to open the **Peak Center** dialog box.



In the **Peak Center** dialog box, select all the elements from the *Elements to Peak* list box, next click on a *Peak Center Method.* A spectrometer pre-scan is useful if that element has not been run recently or if maintenance has occurred on the spectrometer. Click the **OK** button of the **Peak Center** window.

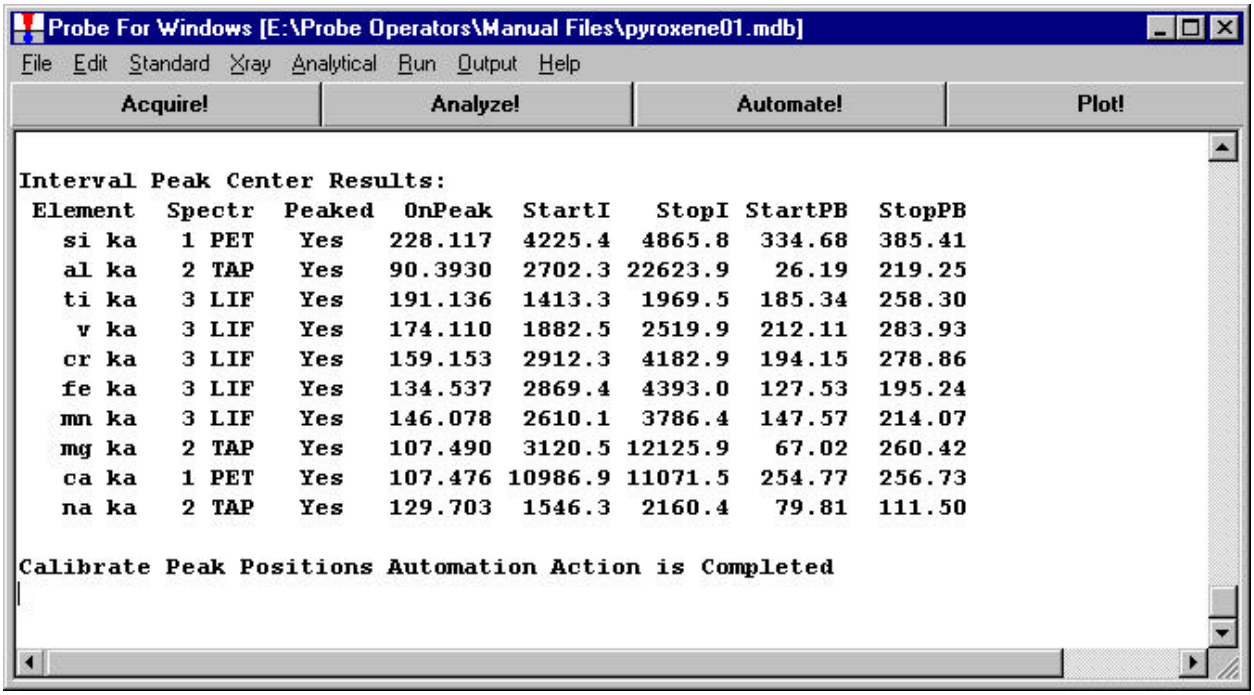
Click the **Run Selected Samples** button from the **Automate!** window.

This opens the **AutomateConfirmSelected** window. To run these automated samples, click **Yes**.



The stage motors move to the position coordinates of the first standard highlighted in the *Position List* list box and the **Confirm Positions** window opens. This window allows the user to readjust if necessary the stage motors (X, Y, and Z) to a new, clean analysis position. Click the **OK** button of the **Confirm Positions** window when done and the spectrometers go through the peaking routine to peak center the spectrometer position to the x-ray maximum for all the elements assigned to that standard. After finding a new peak position and reporting the results to the main log window, the stage motors move on to the coordinates of the next standard highlighted in the *Position List* list box. Once situated on this standard, the spectrometers peak center those elements assigned to it. This procedure continues until all standards are done. When all automation action is complete, the **AcquireStop** window appears and requests the user to click the **OK** button.

The following summary of the peak center automation for the primary standards is found in the main log window.

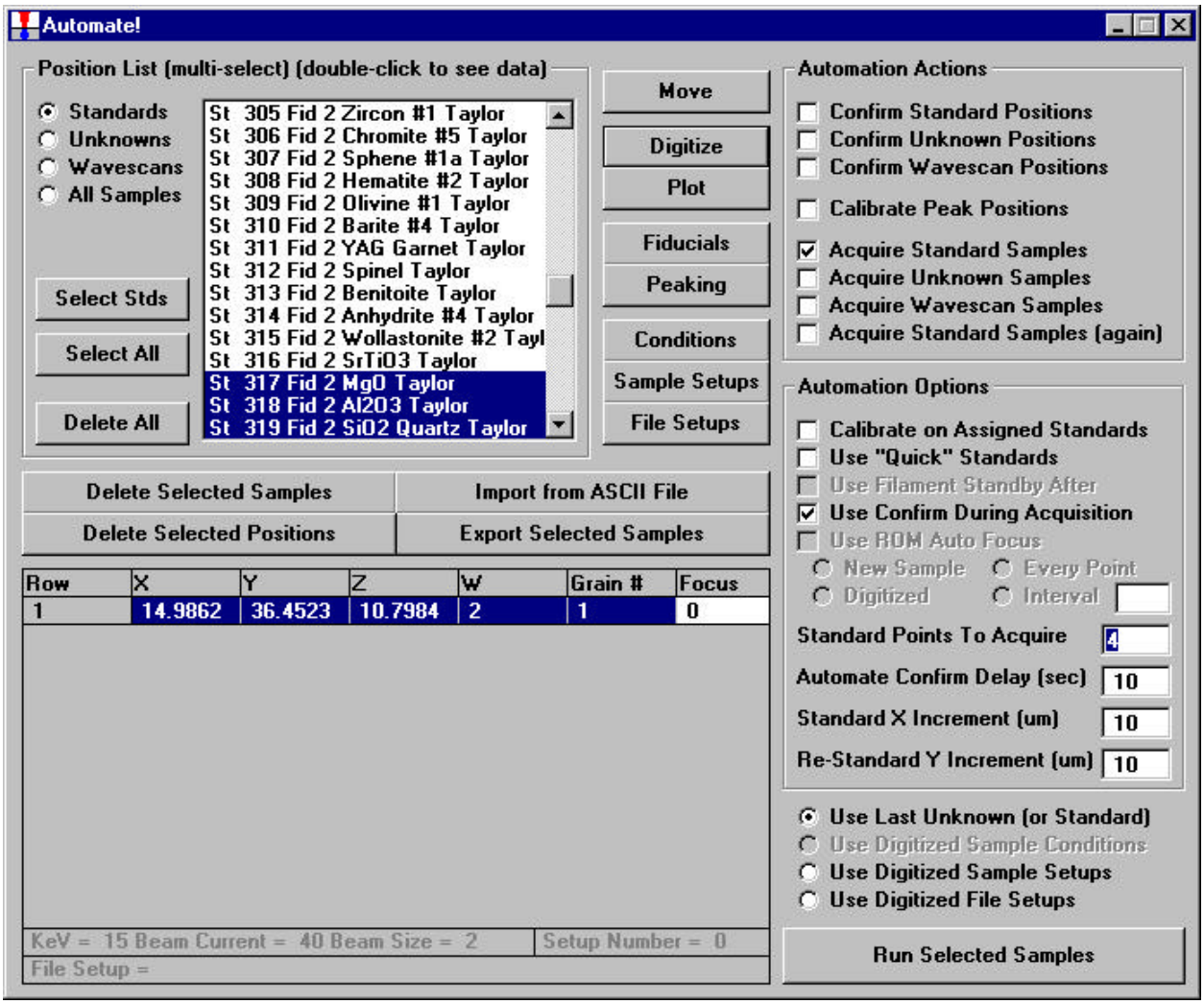


All elements were peak centered using the Interval Halving method. The new peak locations (OnPeak) along with the start and stop intensities in counts per second and
peak-to-backgrounds are listed. The final on-peak intensities (StopI) are valuable for adjusting count time parameters for your standardizations to improve statistics.

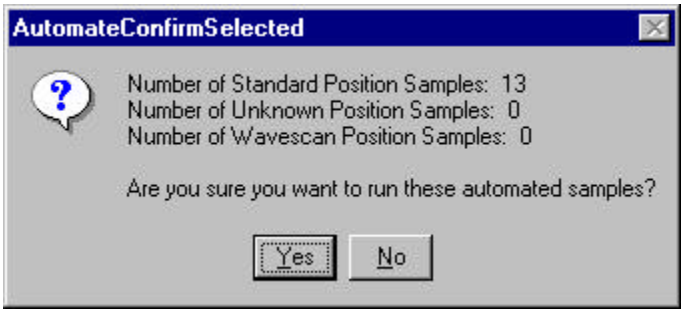
Acquire Standard Samples

The next step is to calibrate the analytical and MAN background standards in preparation for unknown samples. The user may choose to run both types of standards together or separate them. In the latter case, the MAN background standards would normally be acquired first since backgrounds drift less than peak intensities.

Here, the user will automate the entire acquisition of x-ray counts on all standards. Click the **Select Stds** button in the **Automate!** dialog box. This selects all current standards in the run, highlighting them in the *Position List* list box. Next, under *Automation Actions*, click only on the *Acquire Standard Samples* box. From the *Automation Options* choices select the number of *Standard Points To Acquire* and whether to *Use Confirm During Acquisition*. In this example, four standard points are chosen along with a *Standard X Increment* of 10 um. Finally, click the **Run Selected Samples** button.

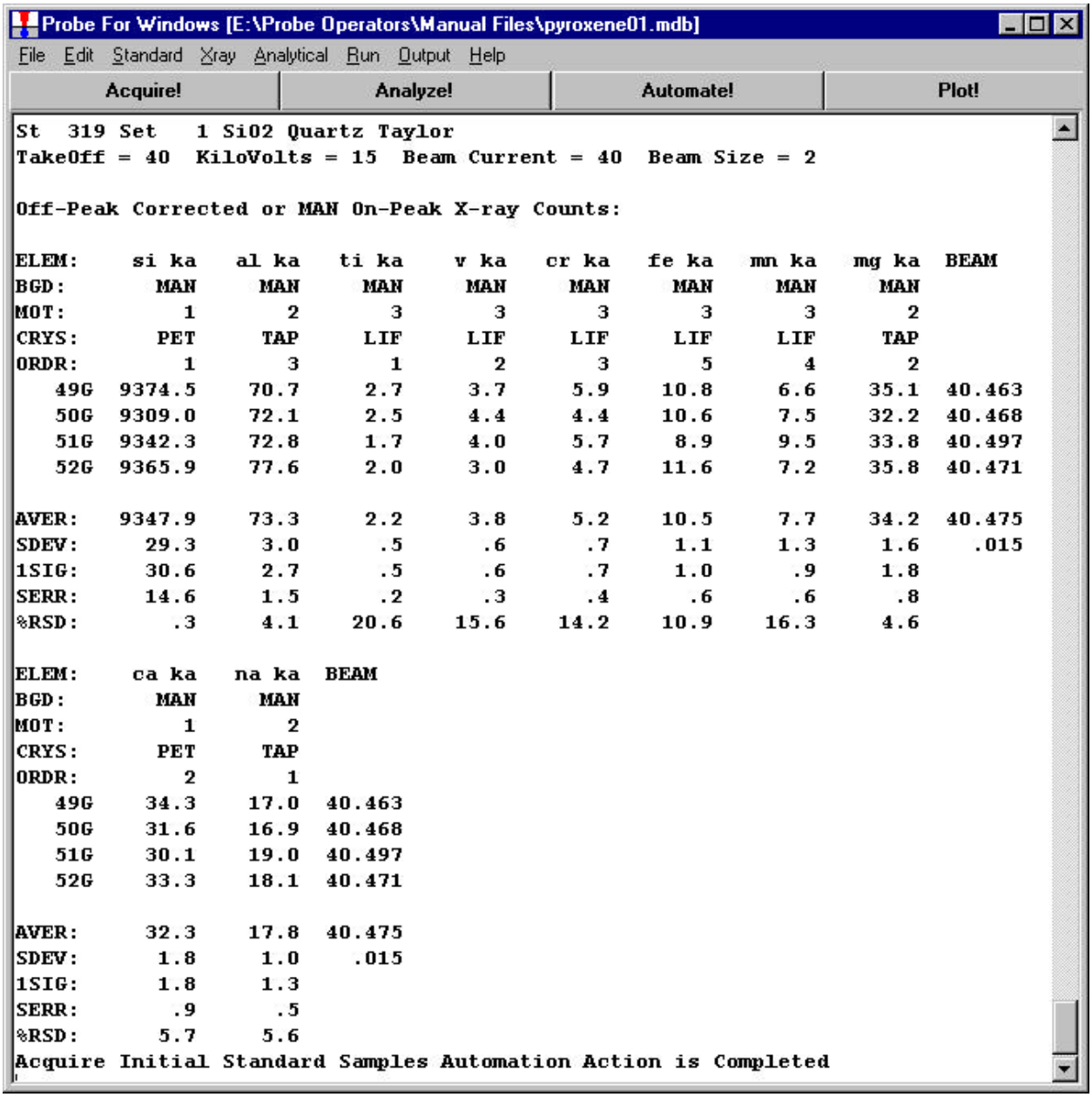


The familiar **AutomateConfirmSelected** window opens again, informing the user that thirteen standards are chosen and asks if you want to run these automated samples, click **Yes**.



The stage moves to the coordinates of the first highlighted standard in the *Position List* list box. If the *Use Confirm During Acquisition* box is checked then the **Confirm Positions** window will open. A complete analysis is acquired on all elements in the current sample, x-rays are counted on peak only for times specified in the **Count Times** window. Finally, the Faraday cup is measured. The stage jogs 10 um in the X direction and this procedure is repeated for the number of points specified in the *Standard Points To Acquire* text box of the **Automate!** dialog box. After completing data collection on the first standard, the stage travels to the next highlighted standard in the list box and acquires four complete analyses on that standard. This procedure is repeated for all selected standards. After finishing the automation schedule the **AcquireStop** window opens and requires the user to click the **OK** button thereby returning to the **Automate!** window.

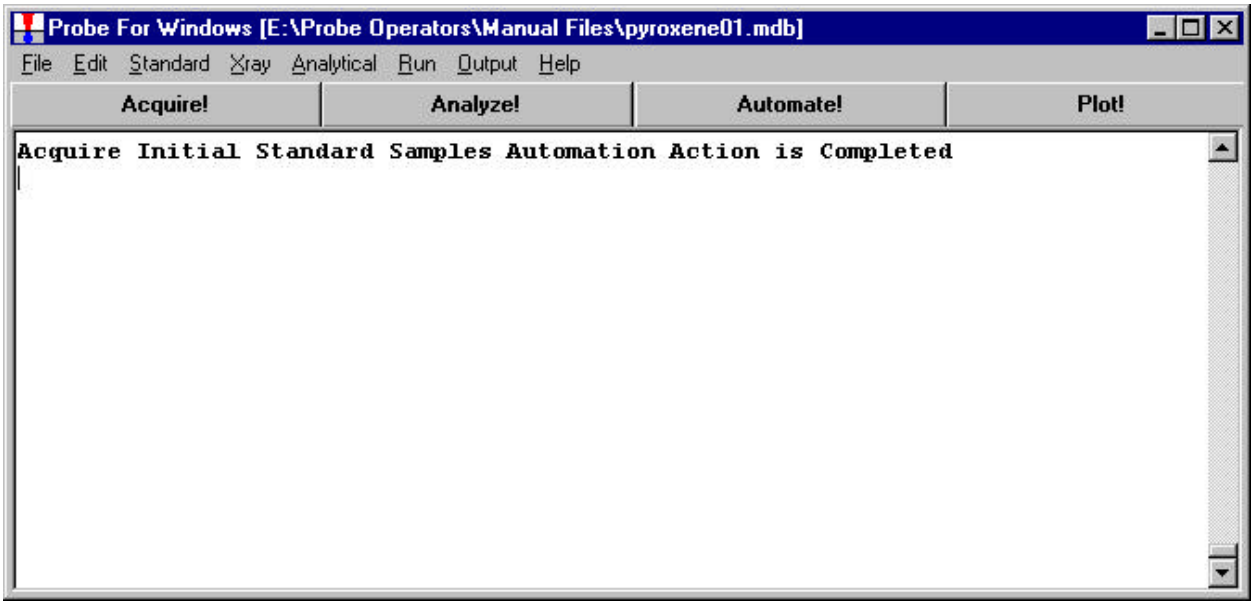
The following log window illustrates typical on-peak x-ray count data (in cps) for the Taylor Quartz standard.



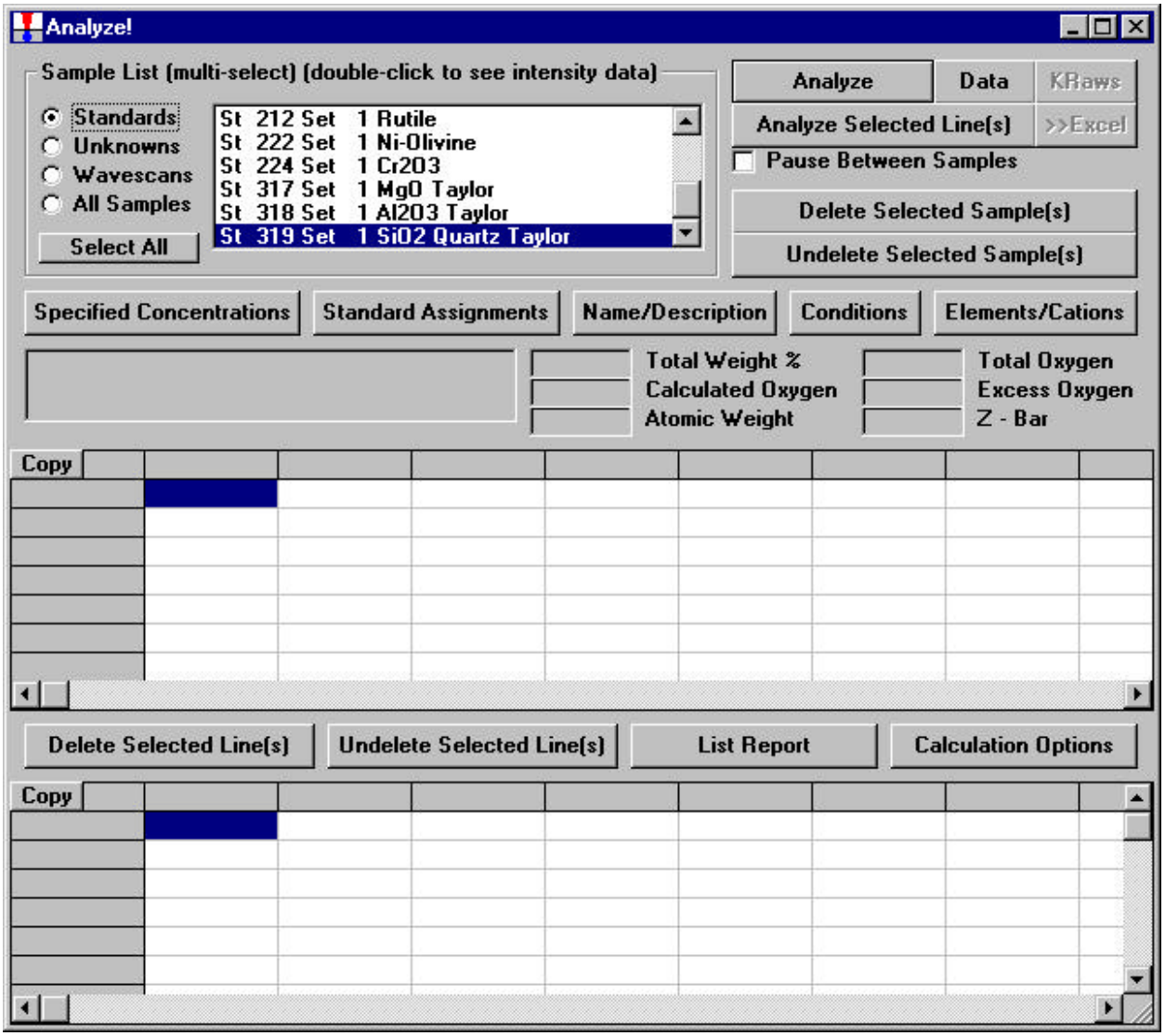
In addition to the four individual lines of count data, the *AVER*, *SDEV*, *1SIG*, *SERR*, and *%RSD* are calculated. The *AVER* (average) is the average intensity reading of each element column. The *SDEV* (standard deviation) is the range of these results, *1SIG* (one sigma) is the predicted standard deviation, and the *SERR* (standard error) is essentially the precision of the average. The *%RSD* number is the *SDEV* divided by the *AVER* times 100. See the User's Guide and Reference documentation for exact equations. The output of the raw data counts for the remaining twelve standards are not shown here to save space.

Evaluate Standard Count Data

After all the standard data is acquired it is useful to examine the raw on-peak counts to check for and delete any obviously bad data points. Click the **Analyze!** button in the main PROBE FOR WINDOWS log window.

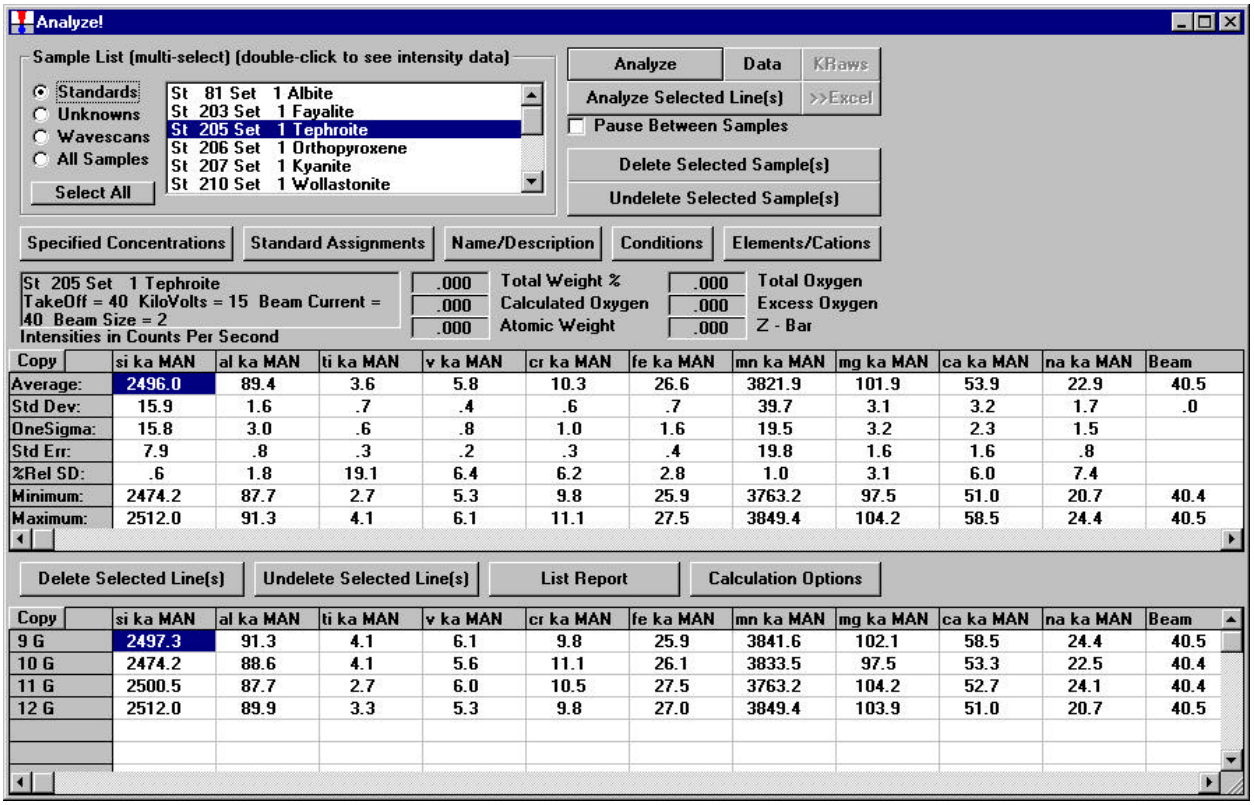


This opens the **Analyze!** dialog box.



The *Sample List* list box contains the list of the standards that data has been acquired on. To examine the raw count data acquired on any standard run under automation, first select the standard of interest and click the **Data** button.

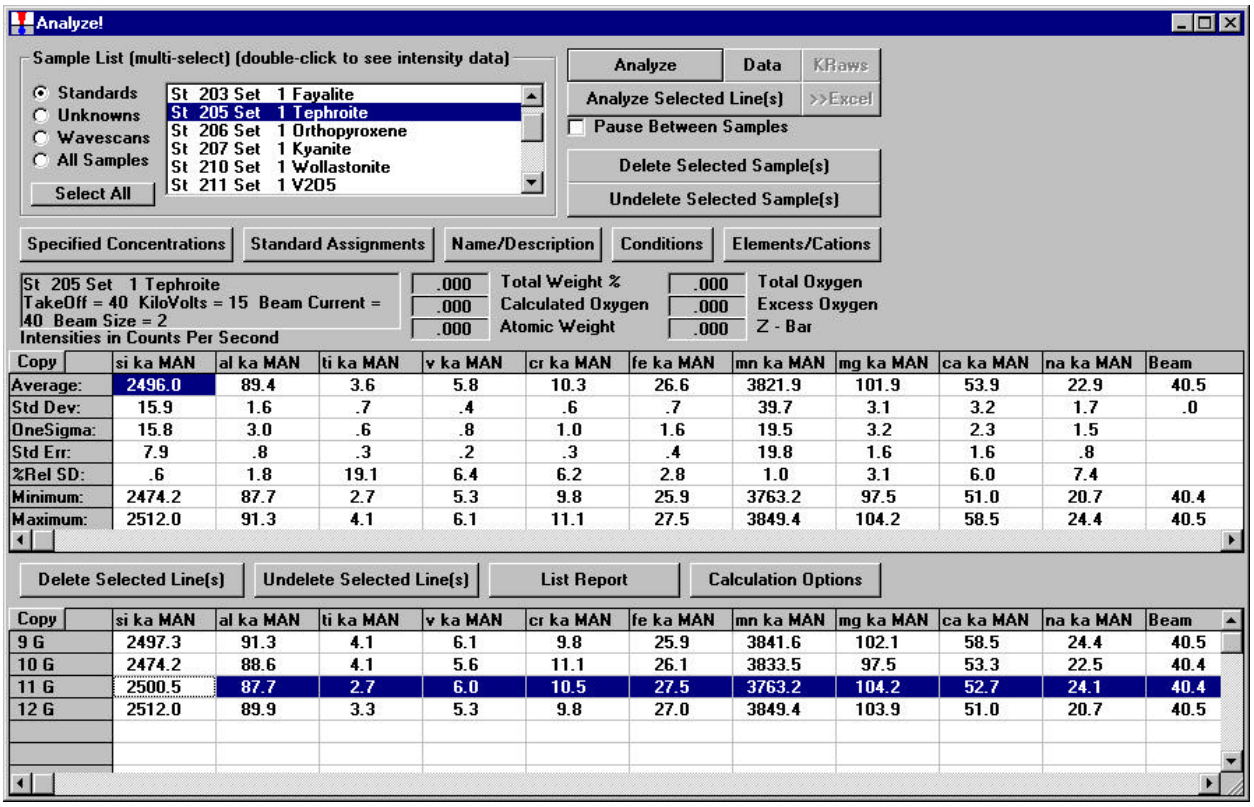
The raw count data for the four automated standard analyses of the Tephroite standard are shown below. Each individual line (9G to 12G) is illustrated along with the *Average*, *Std Dev*, *OneSigma*, *Std Err*, *%Rel SD*, *Minimum* and *Maximum* of the acquired points. This count data is also printed to the log window.



Copy	si ka MAN	al ka MAN	ti ka MAN	v ka MAN	cr ka MAN	fe ka MAN	mn ka MAN	mg ka MAN	ca ka MAN	na ka MAN	Beam
Average:	2496.0	89.4	3.6	5.8	10.3	26.6	3821.9	101.9	53.9	22.9	40.5
Std Dev:	15.9	1.6	.7	.4	.6	.7	39.7	3.1	3.2	1.7	.0
OneSigma:	15.8	3.0	.6	.8	1.0	1.6	19.5	3.2	2.3	1.5	
Std Err:	7.9	.8	.3	.2	.3	.4	19.8	1.6	1.6	.8	
%Rel SD:	.6	1.8	19.1	6.4	6.2	2.8	1.0	3.1	6.0	7.4	
Minimum:	2474.2	87.7	2.7	5.3	9.8	25.9	3763.2	97.5	51.0	20.7	40.4
Maximum:	2512.0	91.3	4.1	6.1	11.1	27.5	3849.4	104.2	58.5	24.4	40.5

Copy	si ka MAN	al ka MAN	ti ka MAN	v ka MAN	cr ka MAN	fe ka MAN	mn ka MAN	mg ka MAN	ca ka MAN	na ka MAN	Beam
9 G	2497.3	91.3	4.1	6.1	9.8	25.9	3841.6	102.1	58.5	24.4	40.5
10 G	2474.2	88.6	4.1	5.6	11.1	26.1	3833.5	97.5	53.3	22.5	40.4
11 G	2500.5	87.7	2.7	6.0	10.5	27.5	3763.2	104.2	52.7	24.1	40.4
12 G	2512.0	89.9	3.3	5.3	9.8	27.0	3849.4	103.9	51.0	20.7	40.5

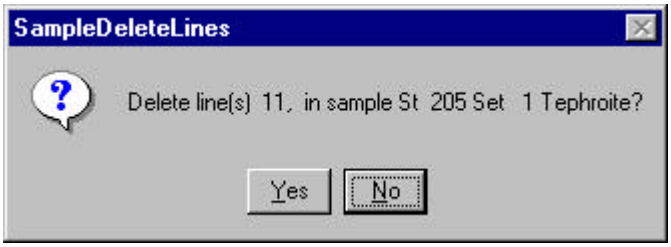
Examine the raw count data for each standard. If more than one sample/standard is selected for analysis, select the *Pause Between Samples* check box. When this box is checked, the program will automatically pause after displaying each analysis until the user clicks the **Cancel** or **Next** buttons on the **Analysis Status** window. If there are any bad data points, use the **Delete Selected Line(s)** button to flag a line of data as bad. In the Tephroite standard, seen below, line 11G (good) is deemed a bad data point since its cps value is very low compared to the other three lines. Click on the line number, highlighting the line. Next click the **Delete Selected Line(s)** button.



Copy	si ka MAN	al ka MAN	ti ka MAN	v ka MAN	cr ka MAN	fe ka MAN	mn ka MAN	mg ka MAN	ca ka MAN	na ka MAN	Beam
Average:	2496.0	89.4	3.6	5.8	10.3	26.6	3821.9	101.9	53.9	22.9	40.5
Std Dev:	15.9	1.6	.7	.4	.6	.7	39.7	3.1	3.2	1.7	.0
OneSigma:	15.8	3.0	.6	.8	1.0	1.6	19.5	3.2	2.3	1.5	
Std Err:	7.9	.8	.3	.2	.3	.4	19.8	1.6	1.6	.8	
%Rel SD:	.6	1.8	19.1	6.4	6.2	2.8	1.0	3.1	6.0	7.4	
Minimum:	2474.2	87.7	2.7	5.3	9.8	25.9	3763.2	97.5	51.0	20.7	40.4
Maximum:	2512.0	91.3	4.1	6.1	11.1	27.5	3849.4	104.2	58.5	24.4	40.5

Copy	si ka MAN	al ka MAN	ti ka MAN	v ka MAN	cr ka MAN	fe ka MAN	mn ka MAN	mg ka MAN	ca ka MAN	na ka MAN	Beam
9 G	2497.3	91.3	4.1	6.1	9.8	25.9	3841.6	102.1	58.5	24.4	40.5
10 G	2474.2	88.6	4.1	5.6	11.1	26.1	3833.5	97.5	53.3	22.5	40.4
11 G	2500.5	87.7	2.7	6.0	10.5	27.5	3763.2	104.2	52.7	24.1	40.4
12 G	2512.0	89.9	3.3	5.3	9.8	27.0	3849.4	103.9	51.0	20.7	40.5

This opens the **SampleDeleteLines** window.



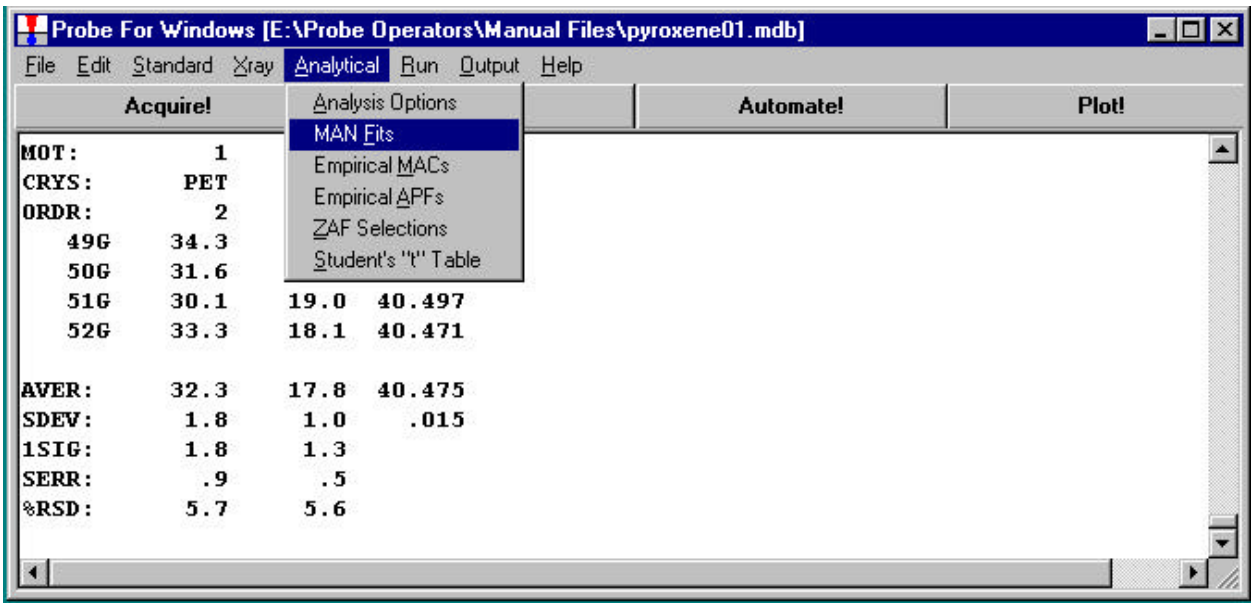
Click the **Yes** button. The computer will flag this line with a B (bad) and ignore this data for any subsequent calculations.

Click the **Data** button again to re-analyze the remaining data lines for statistical parameters. Remember one can always undelete data lines with the **Undelete Selected Line(s)** button.

At this point, the user has collected all standardization data and is ready to make MAN background assignments.

Assign MAN Background Calibrations

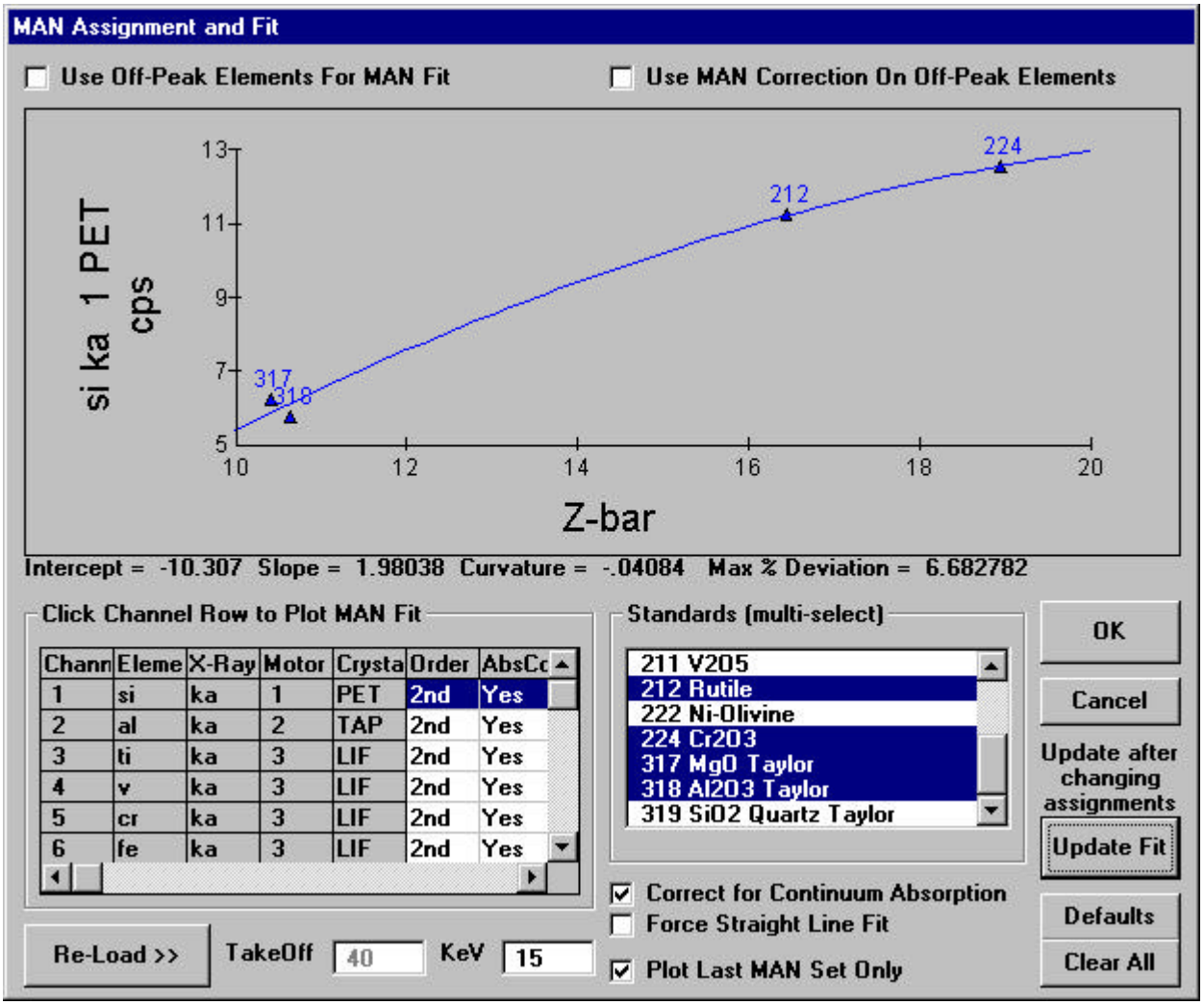
From the main PROBE FOR WINDOWS log window, select **Analytical** from the menu bar and click **MAN Fits** from the menu choices.



This opens the **MANLoadNewElements** window.

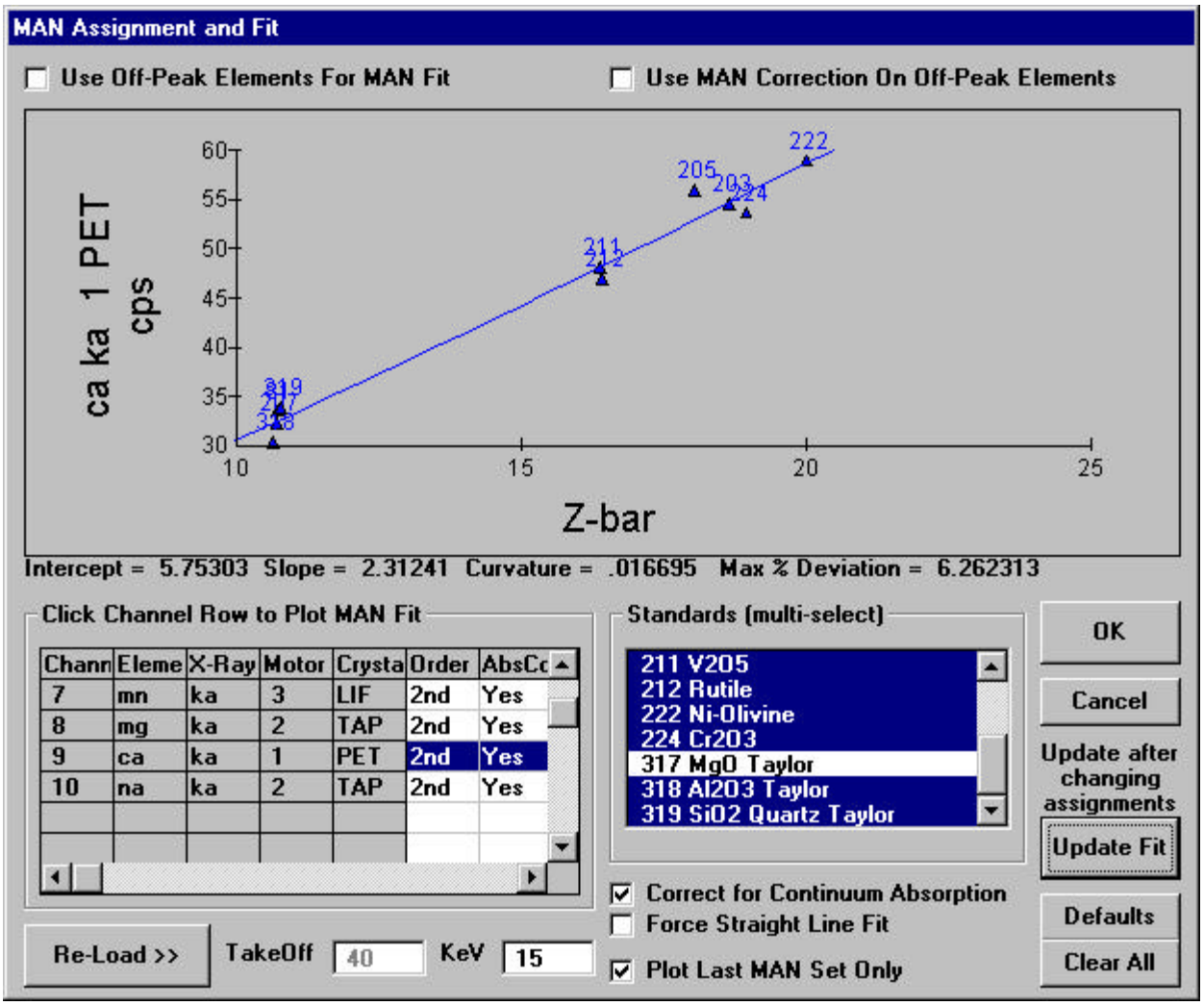
Click the **OK** button.

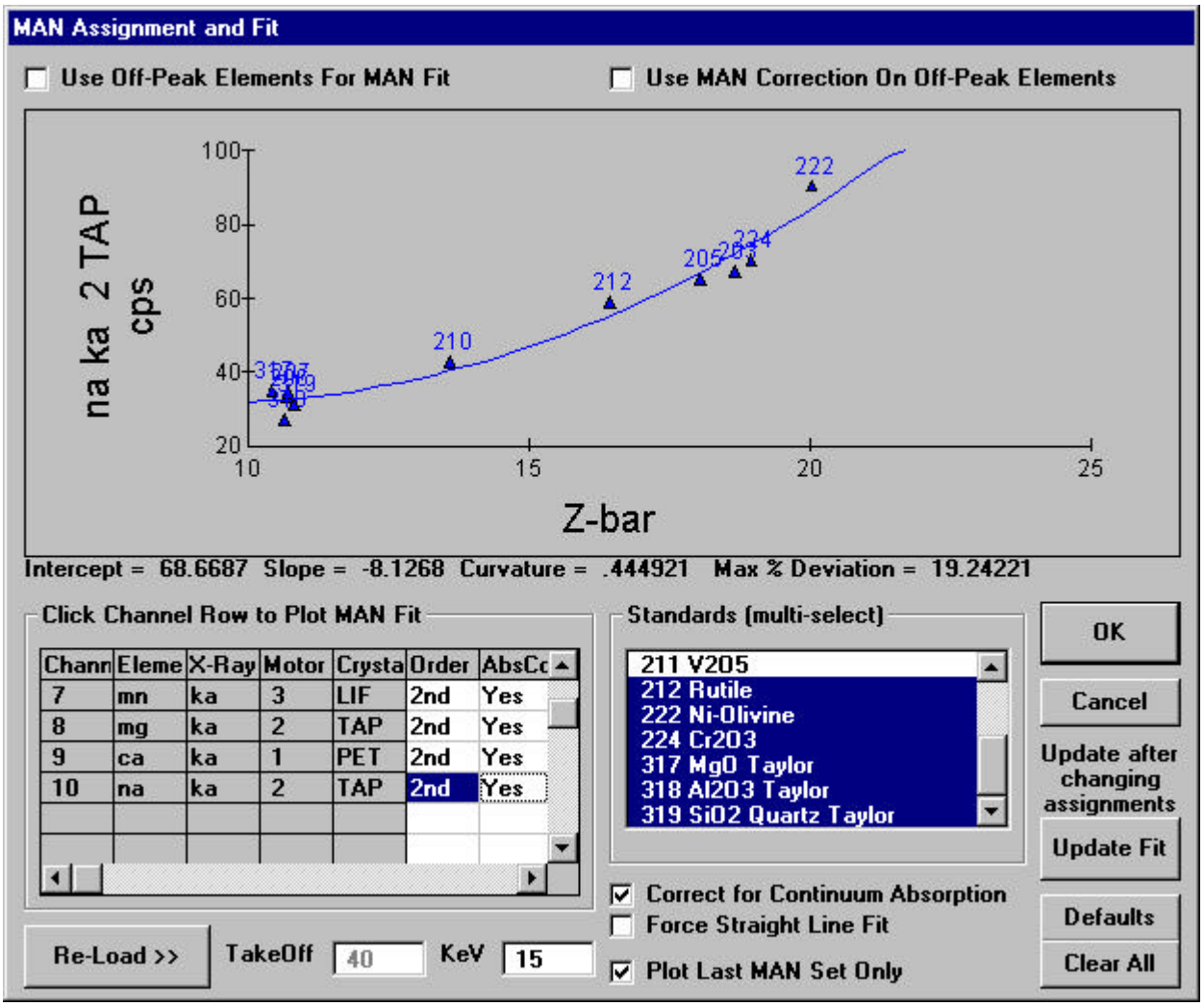
This opens the **MAN Assignment and Fit** dialog box.

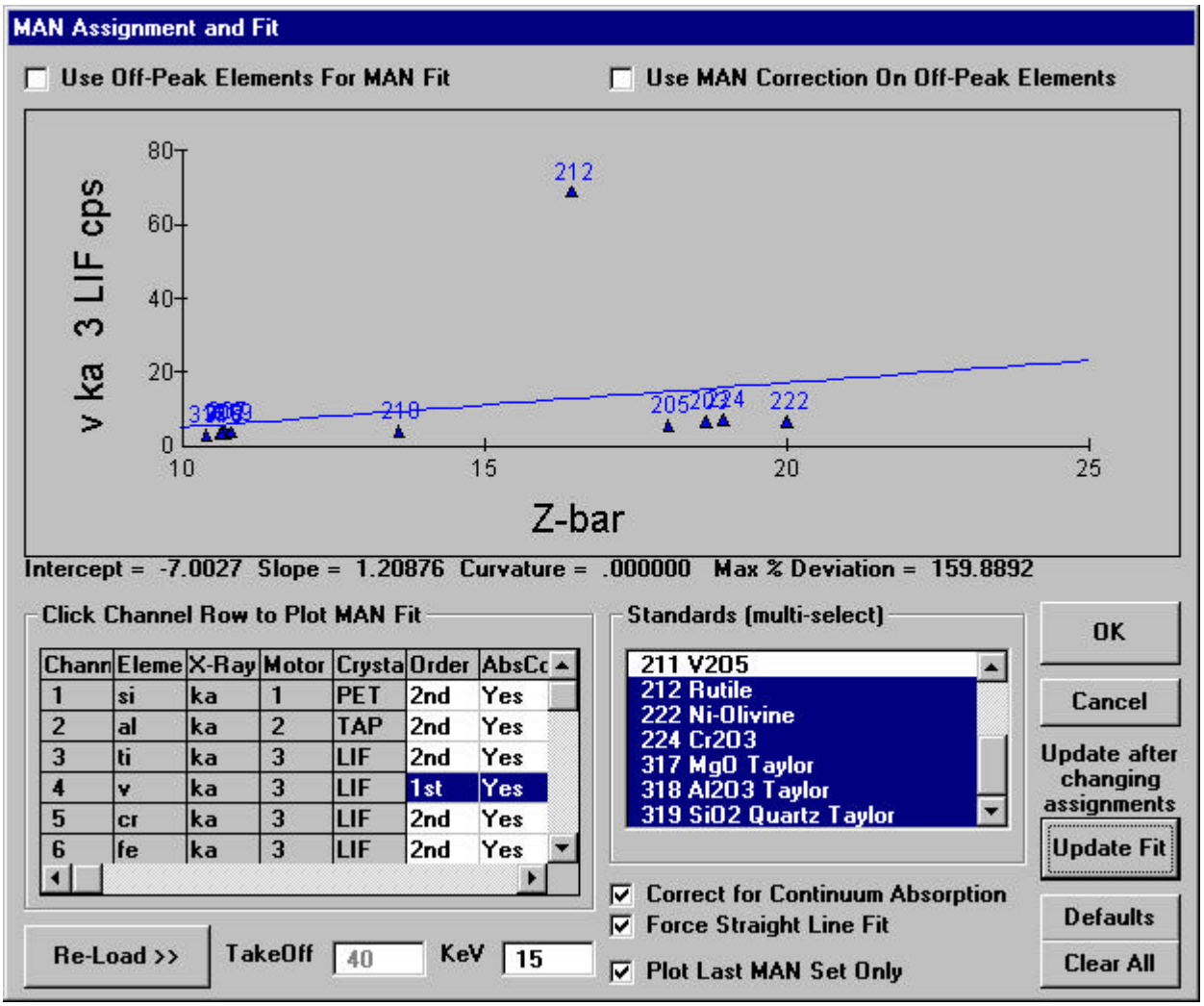


From this dialog box, the user may display and modify the MAN background assignments and fits used for the background correction of all elements in the current run. The advantage of this method is that it requires only a simple calibration of the analyzing channel over a range of atomic number. Substantial time may be saved when many samples are to be analyzed. However, if measuring high atomic number samples and/or trace concentrations, the off-peak background correction technique is usually superior.

For each element, select standards from the *Standards* list box that do not contain the element itself. In this way the measured background counts can be plotted as a function of the average atomic number (Z-bar). Choose at least five standards per element and compute a second-order polynomial or force a straight line fit (if deemed appropriate) between background counts and MAN for each. For further details and suggestions, see the User's Guide and Reference documentation. Several fits (ca, na, and v) are illustrated respectively, below.




MAN Assignment and Fit
Use Off-Peak Elements For MAN Fit
Use MAN Correction On Off-Peak Elements
na ka 2 TAP cps
100
80
60
40
20
10
15
20
25
Z-bar
222
224
205
212
210
Intercept = 68.6687 Slope = -8.1268 Curvature = .444921 Max % Deviation = 19.24221
Click Channel Row to Plot MAN Fit
Chann Eleme X-Ray Motor Crysta Order AbsCc
7 mn ka 3 LIF 2nd Yes
8 mg ka 2 TAP 2nd Yes
9 ca ka 1 PET 2nd Yes
10 na ka 2 TAP 2nd Yes
Standards (multi-select)
211 V205
212 Rutile
222 Ni-Olivine
224 Cr203
317 MgO Taylor
318 Al203 Taylor
319 SiO2 Quartz Taylor
OK
Cancel
Update after changing assignments
Update Fit
Correct for Continuum Absorption
Force Straight Line Fit
Plot Last MAN Set Only
Defaults
Clear All
Re-Load >>
TakeOff 40
KeV 15



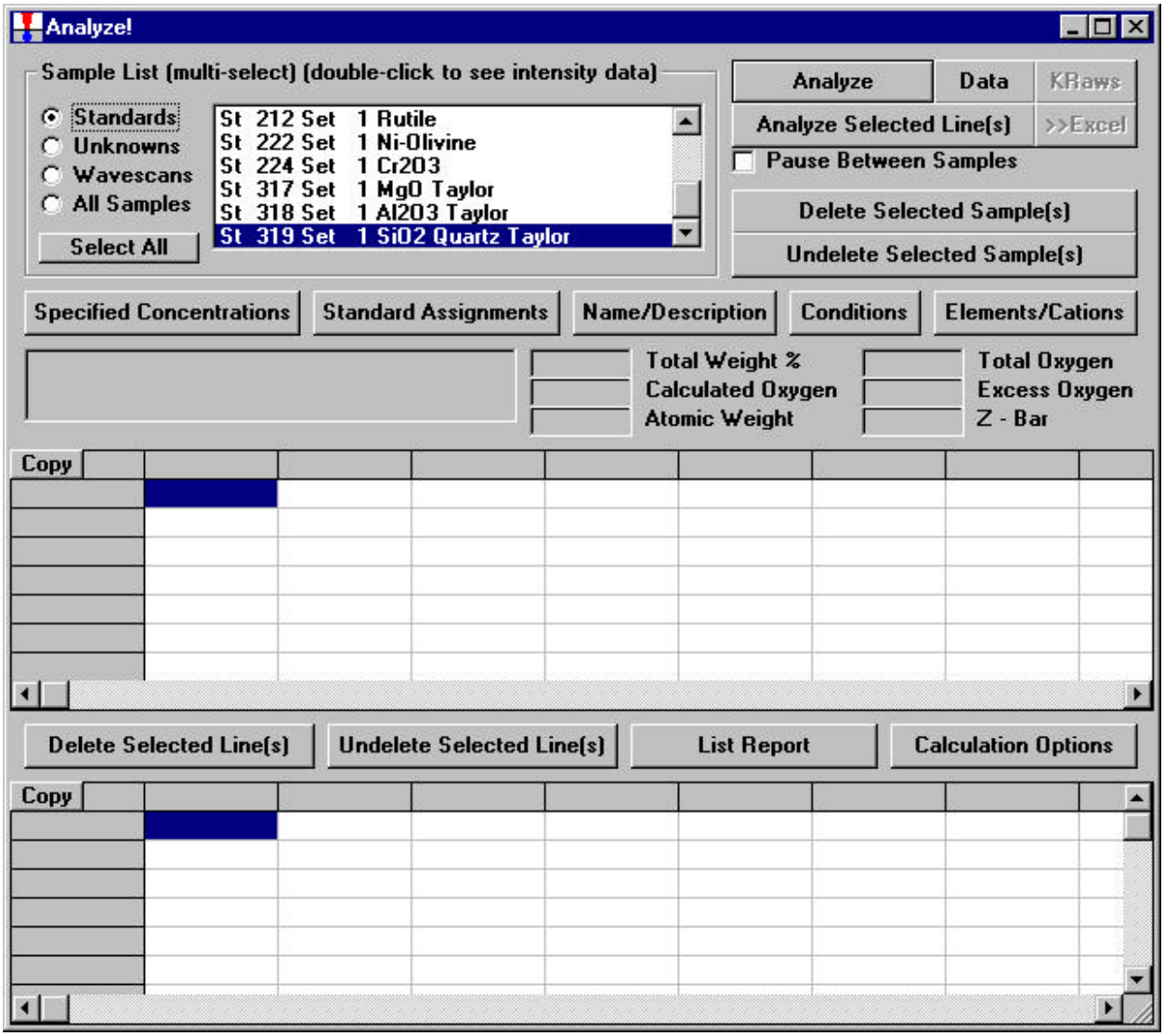
The V plot above illustrates another effect in WDS analysis; spectral interferences. The well-known transition metal interferences are easily visible in these types of plots. The Kβ x-ray line for the element of atomic number x interfers with the Kα x-ray line of element x+1 (Ti with V, V with Cr, Cr with Mn and Mn with Fe). Above, standard 212 is pure TiO_2 with no V_2O_3 but an apparent V x-ray signal is seen. The 212 standard is removed and the MAN background fit updated by clicking the **Update Fit** button. All of these interferences will be examined shortly.

When done adjusting individual elements, click the **OK** button to store the updated MAN background corrections.

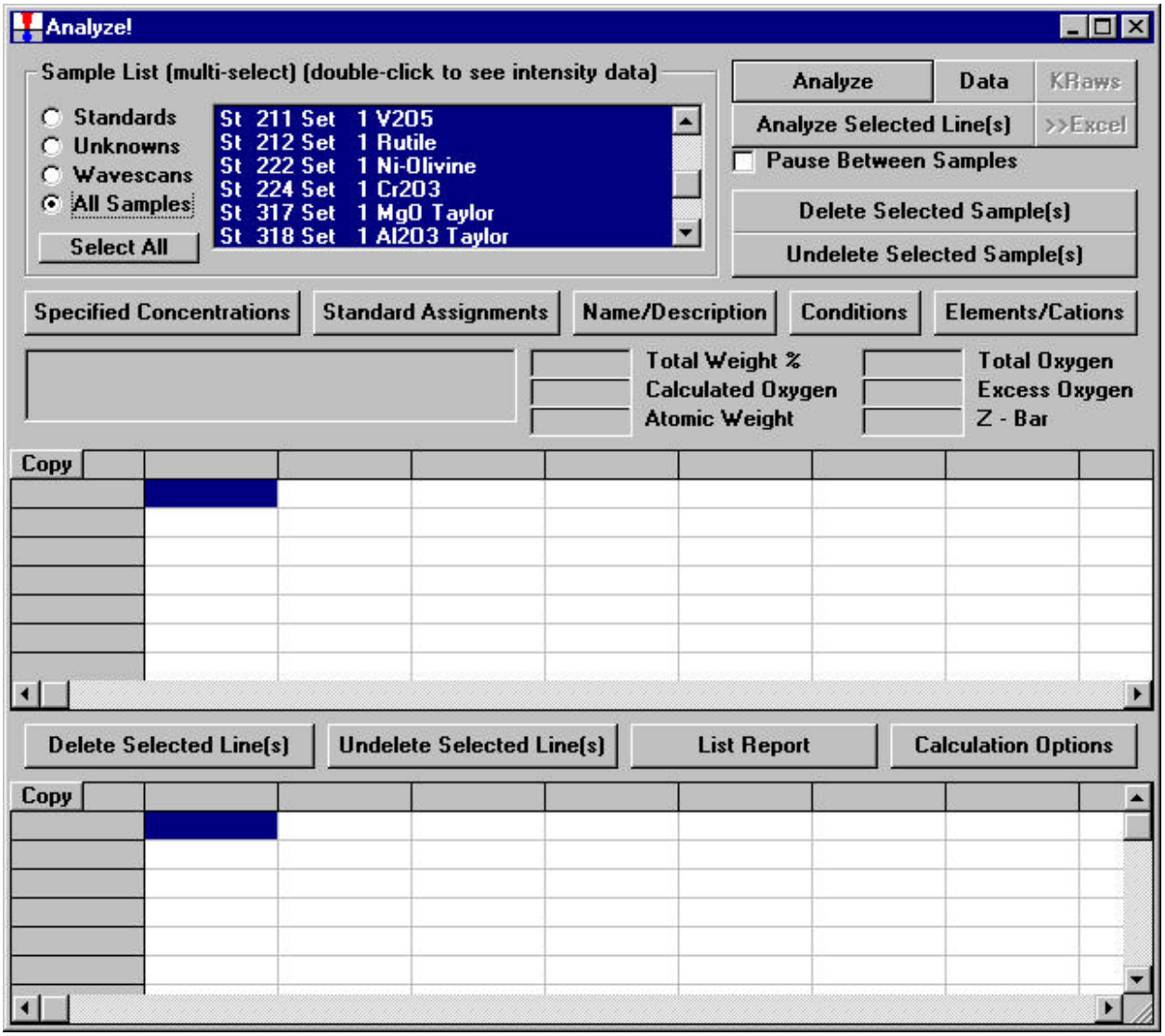
Analyze Standard Samples

The user will now analyze all of the standard data re-calculating the x-ray counts to compositions in oxide weight percent. Since the program treats all samples as unknowns, the results of the standards provides a valuable check on the quality of the analysis.

Click the **Analyze** button in the main PROBE FOR WINDOWS log window. This opens the **Analyze!** dialog box.

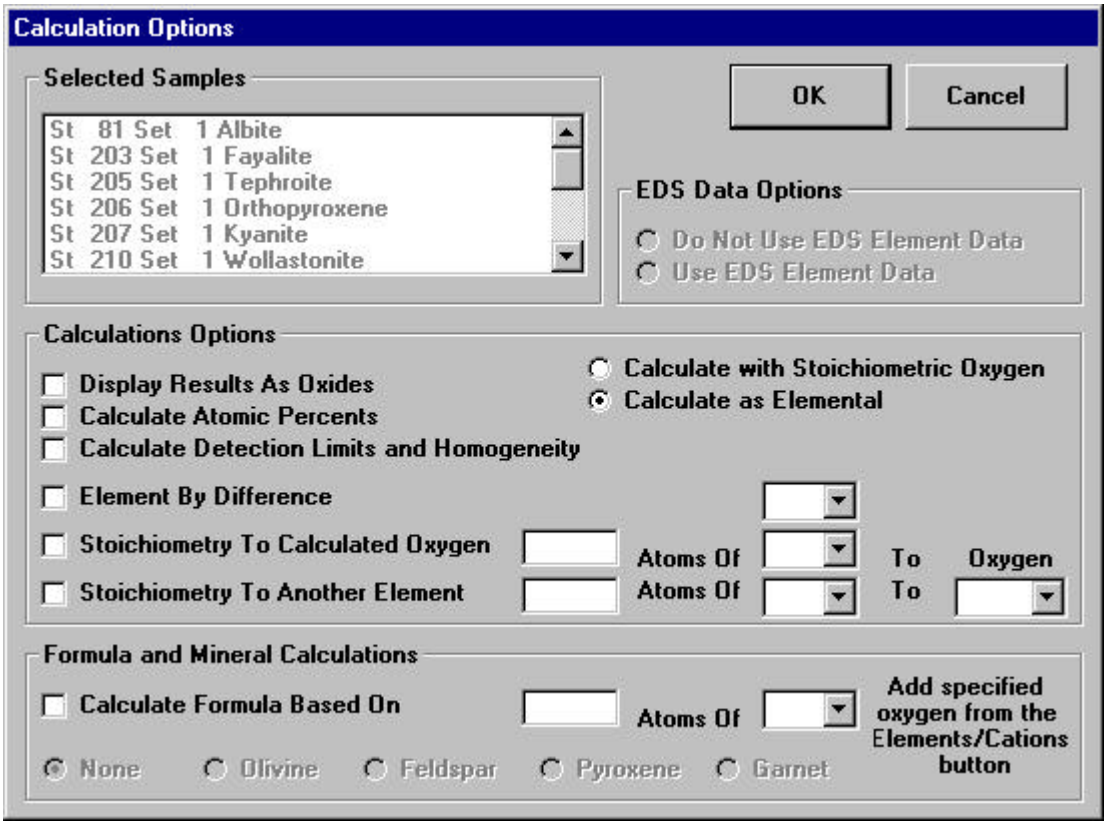


Under *Sample List* select the *All Samples* button. Click the **Select All** button highlighting all standards.



Click the **Calculation Options** button in the **Analyze!** window.

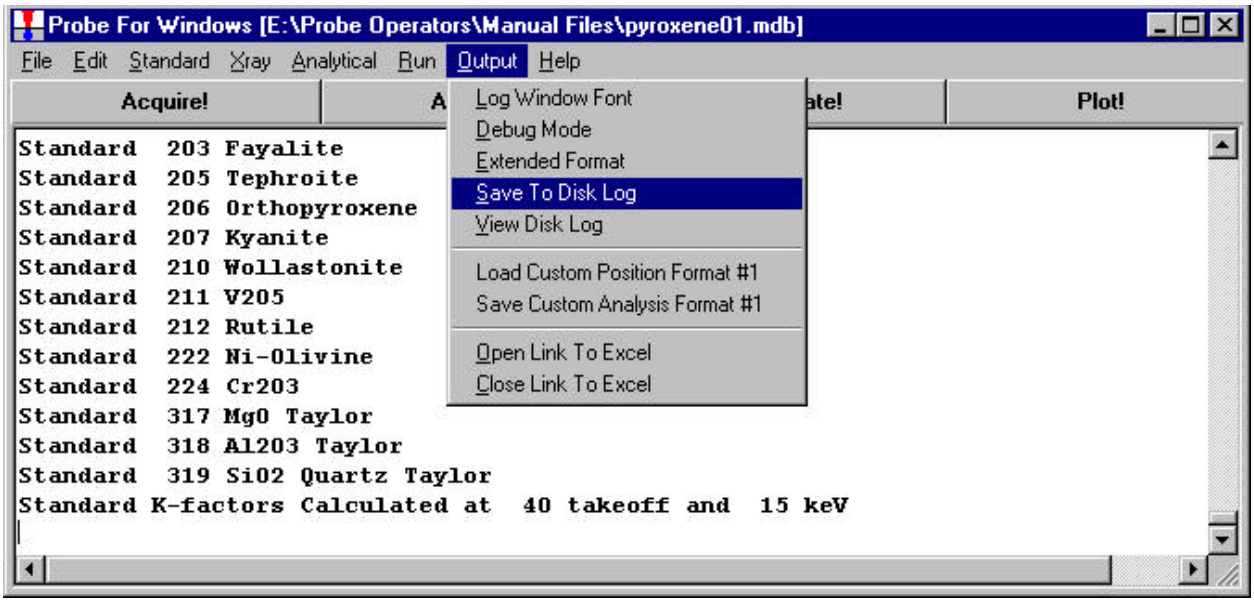
This action opens the **Calculation Options** dialog box.



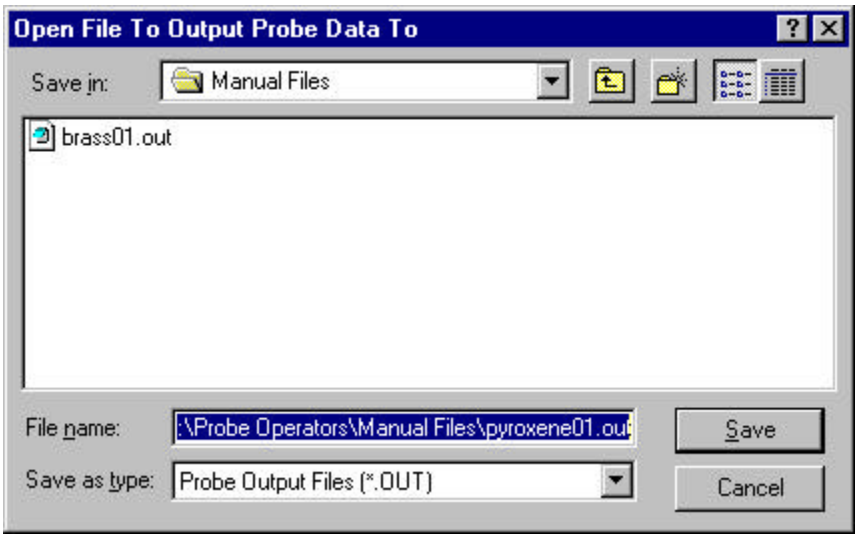
Under *Calculations Options* click the *Display Results As Oxides* box. Elemental results are always calculated and output to the log window. Click the **OK** button to output data in oxide form.

Analyzing all of the data on the standards will create a large amount of output, possibly overflowing the log window buffer, depending on the value specified in the LogWindowBufferSize parameter in the PROBEWIN.INI file. The size of the log window buffer is limited only by the amount of memory available. Setting this parameter to 512000 bytes is roughly equivalent to 300 pages of average density text. In some cases saving all log window output to a user specified text file for viewing with a text editor or printing to a laser printer may be best.

Select **Output** from the menu bar in the main log window and click **Save to Disk Log**.

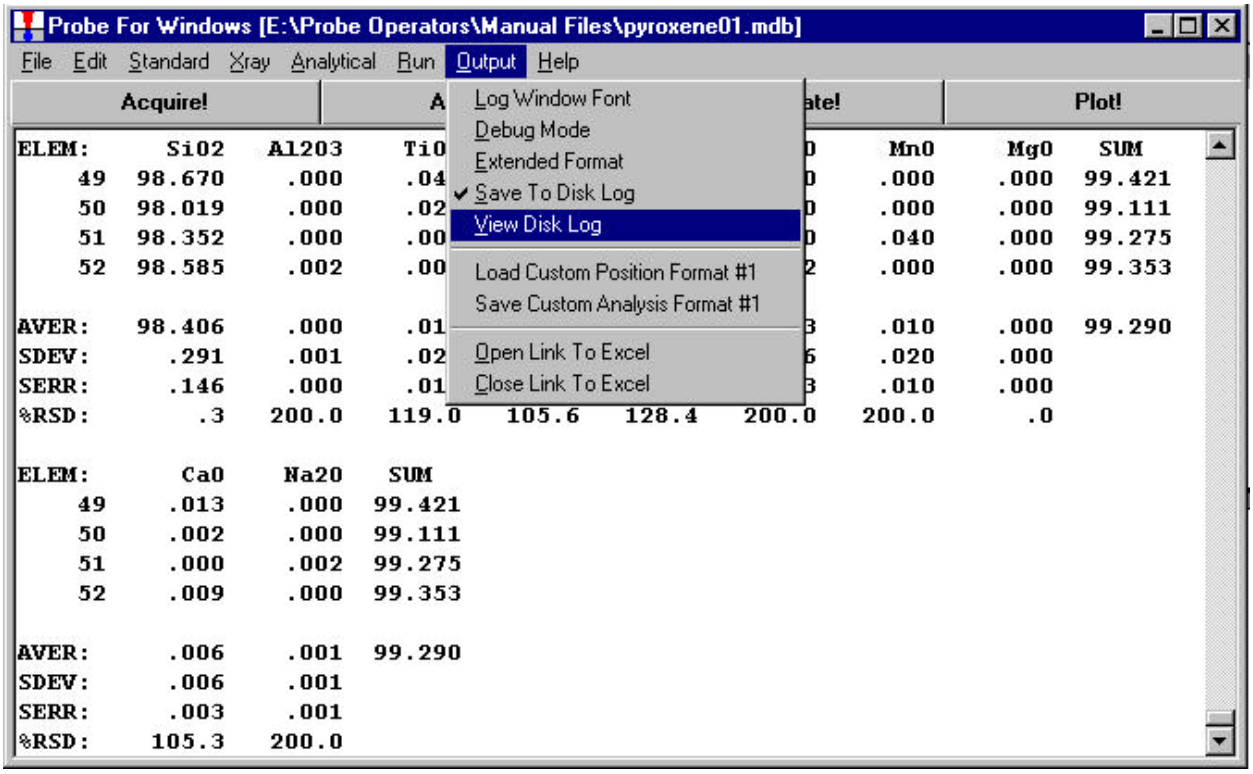


This opens the **Open File To Output Probe Data To** dialog box. The *Save in:* location will be the directory specified for the original file name (PYROXENE01.MDB). All subsequent files created by the user will use this location. Edit the *File name* if desired. The default output file has the extension .OUT. Note that the raw data is always saved in the .MDB run file for future re-calculation and /or output. Click **Save** when finished.

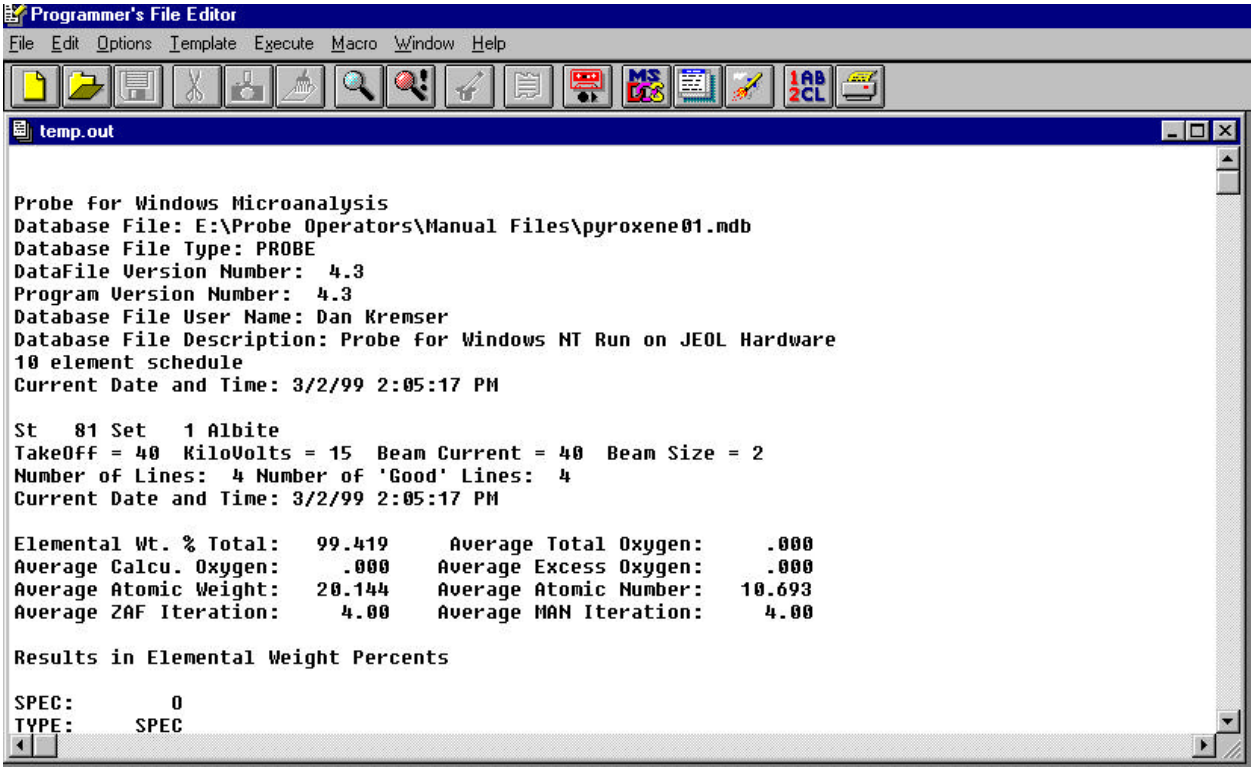


Select the **Analyze!** button in the main PROBE FOR WINDOWS log window, to bring forward the **Analyze!** dialog box. Click the **Select All** button highlighting all standards again. Then click the **Analyze** button. This will analyze all selected standard data into the specified text file.

To view this data return to the main PROBE FOR WINDOWS log window and select **Output** from the menu bar again and click **View Disk Log** from the menu.

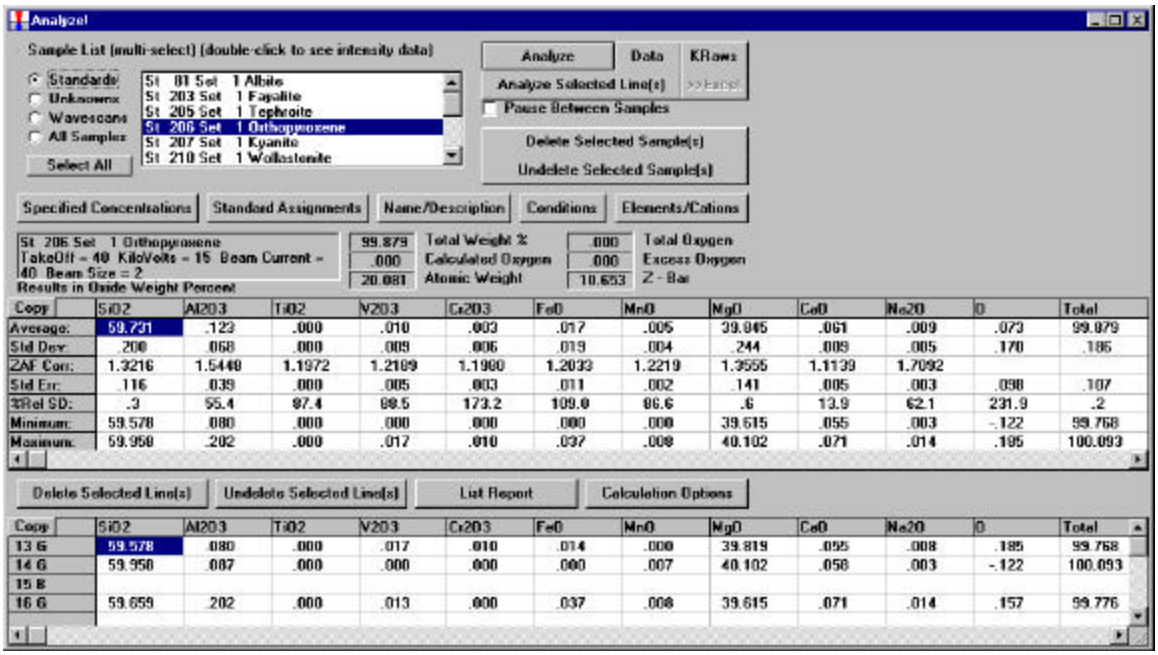


This opens the file editor. This example utilizes the **Programmer's File Editor**, seen below. A number of text file viewers may be used. To utilize a specific editor such as Textpad or Word, edit the FileViewer keyword in the PROBEWIN.INI file.

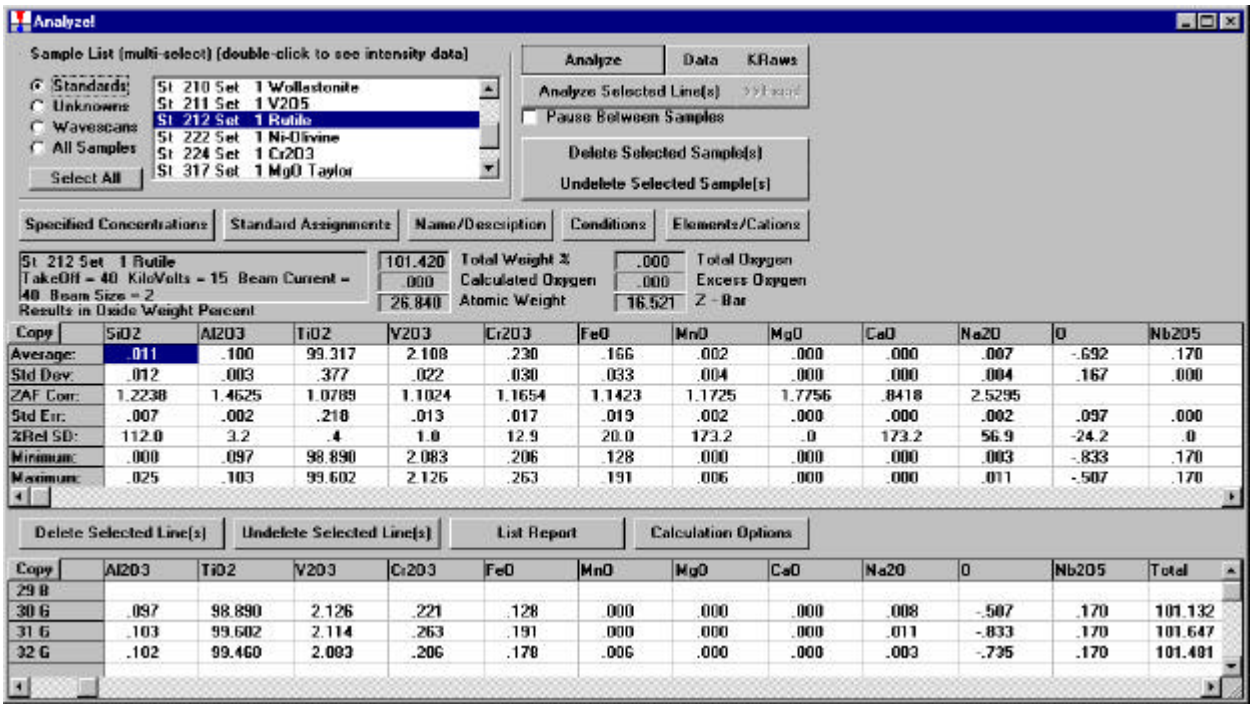


The user may now scroll through the analyzed standards using the text editor or may direct the file data to a laser printer by selecting **File** from the **Programmer's File Editor** menu bar and clicking on **Print** in the drop-down menu.

Since all elements were acquired on all standards, examination of the oxide weight percents will provide a check on the quality of the calibration. Several of the standard compositions will be displayed. The first example is the Orthopyroxene standard displayed in the **Analyze!** window below. This is the primary standard for magnesium and silicon. Both elements show excellent agreement with the published standard database values.



The analysis of the Rutile standard reveals several interesting points; 1) the TiO_2 concentration is very close to the published value of 99.26 and 2) an apparent 2.1 weight percent concentration of V_2O_3 is found! This sample has no vanadium, here the user sees the notorious Ti-V spectral interference. This interference overestimates the amount of V_2O_3 in the sample resulting in the total exceeding 100%. This will be corrected for (shortly) using the automatic interference correction routine.

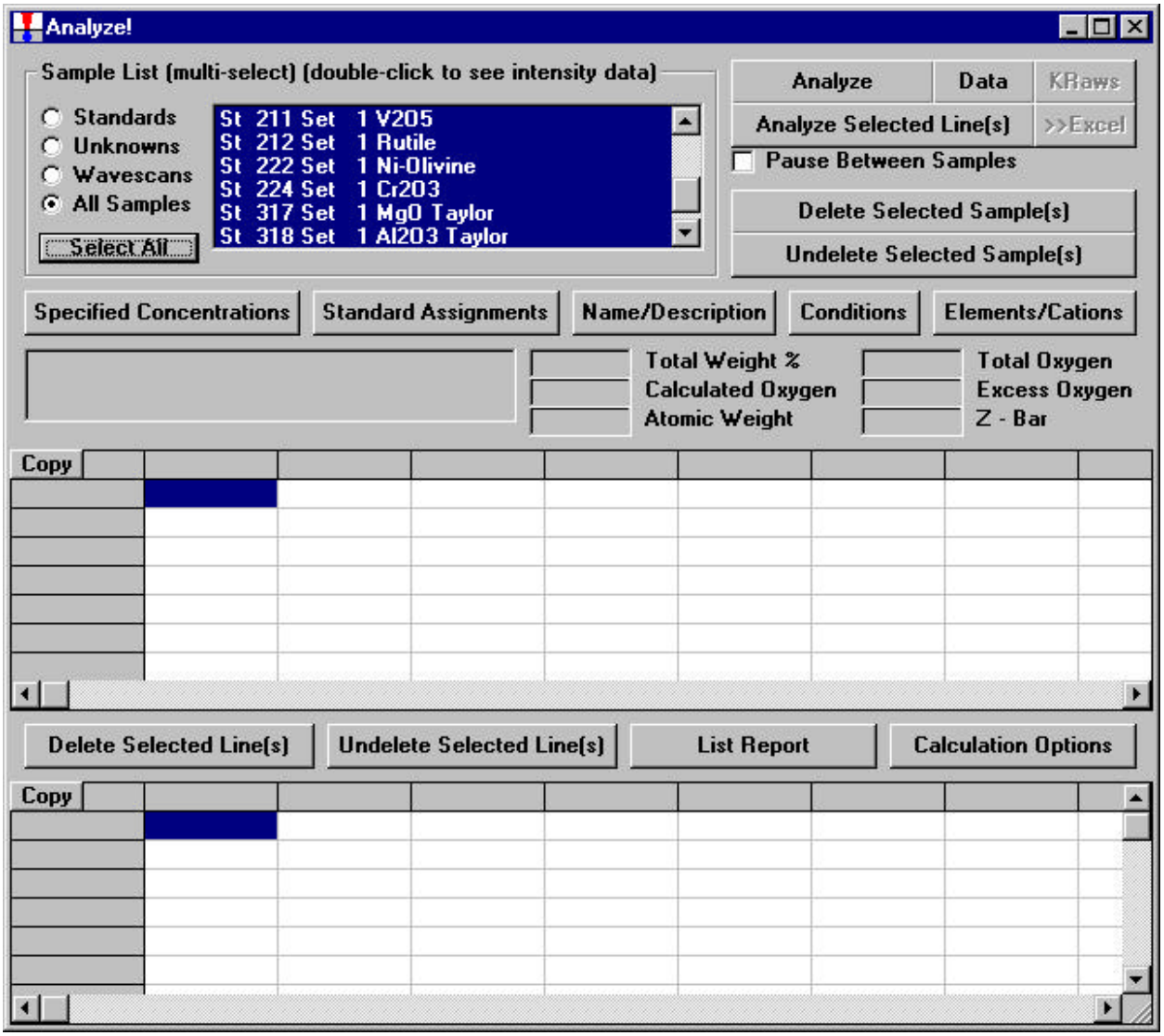


All of the data lines gathered on the standards are examined and appear close to their standard database values. To save space they will not be reproduced here.

Spectral Interference Assignments

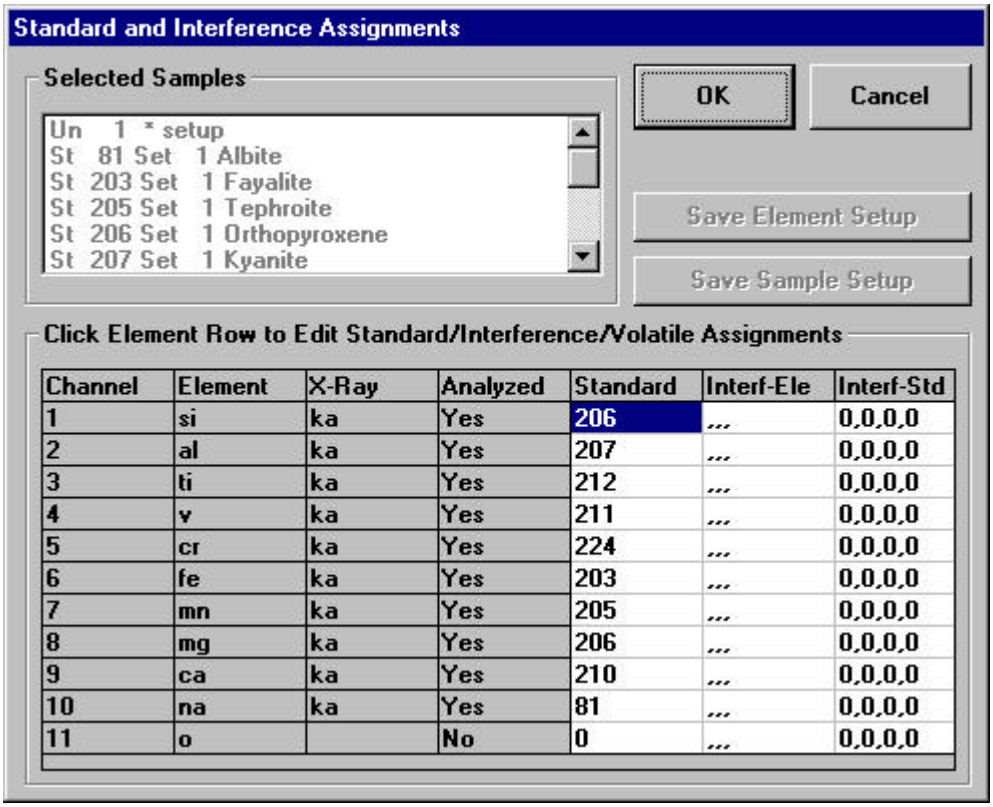
PROBE FOR WINDOWS allows the user to select a fully quantitative correction for spectral interferences. The program can only correct for interferences if both the interfered and interfering elements are analyzed for. Further, data for an interference calibration standard must be acquired that contains a major concentration of the interfering element and none of the interfered element or any other elements that interfere with the interfered element.

Select the *All Samples* button in the *Sample List* and click the **Select All** button in the **Analyze!** window.



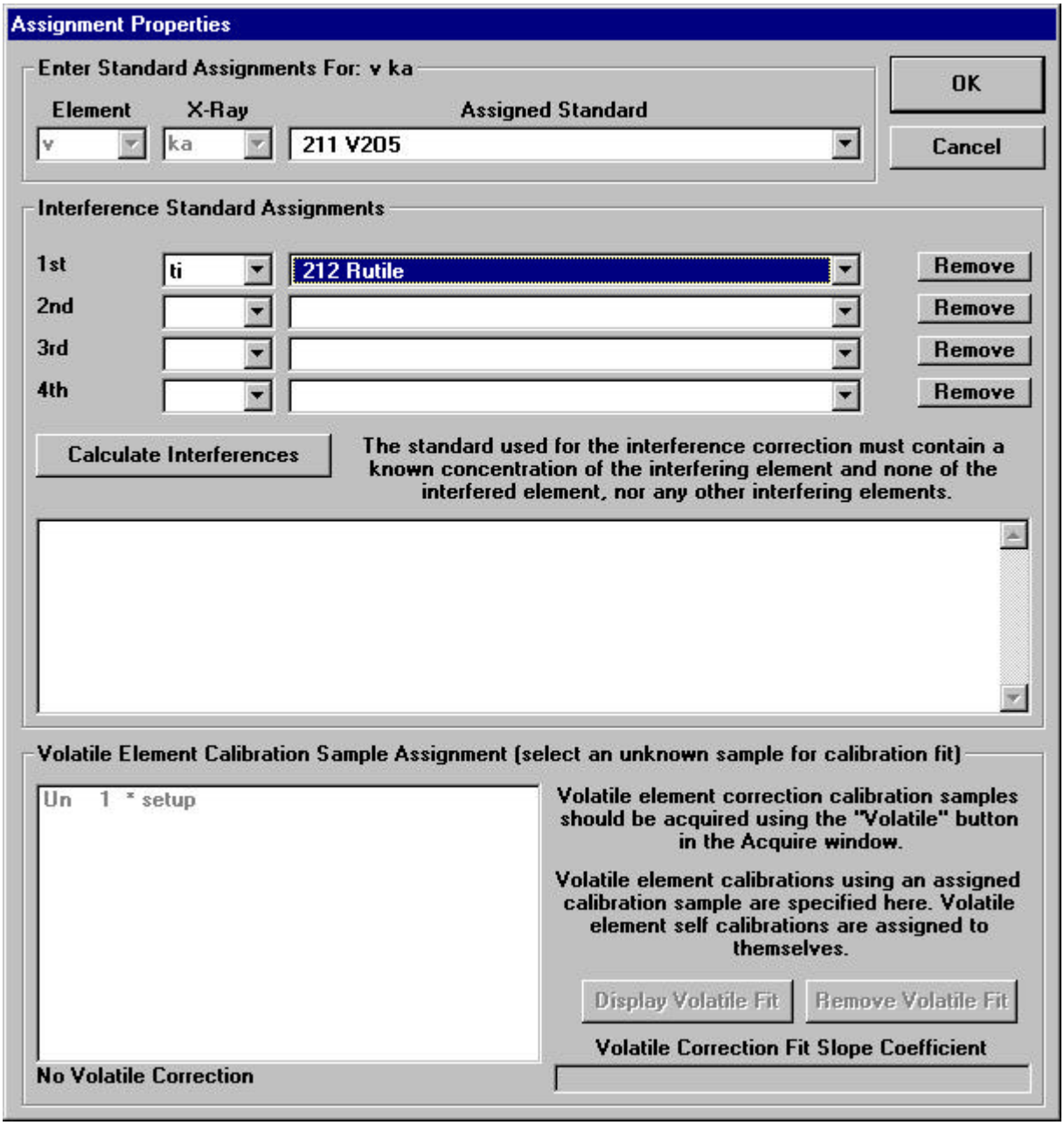
Next, click the **Standard Assignments** button.

Clicking this button opens the **Standard and Interference Assignments** dialog box.



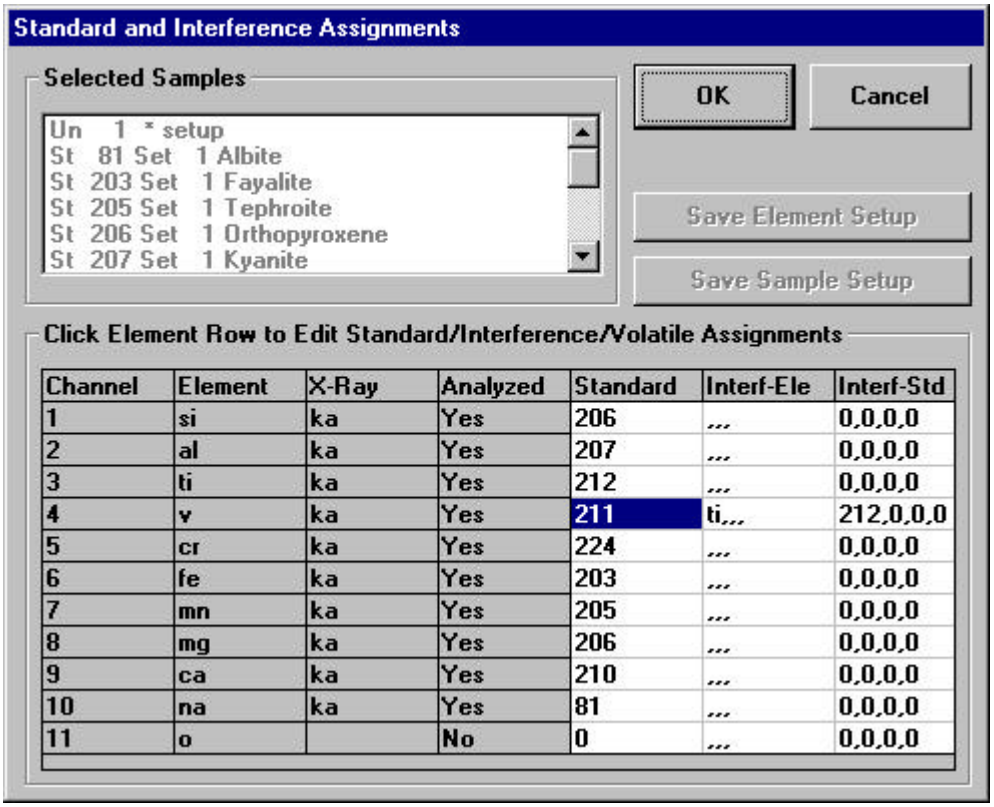
Click on the element row to edit the *Interference Assignments.*

The **Assignment Properties** dialog box opens. Select the first *interference element* for this element and the corresponding *standard* that contains a known amount of the interfering element but none of the interfered element.



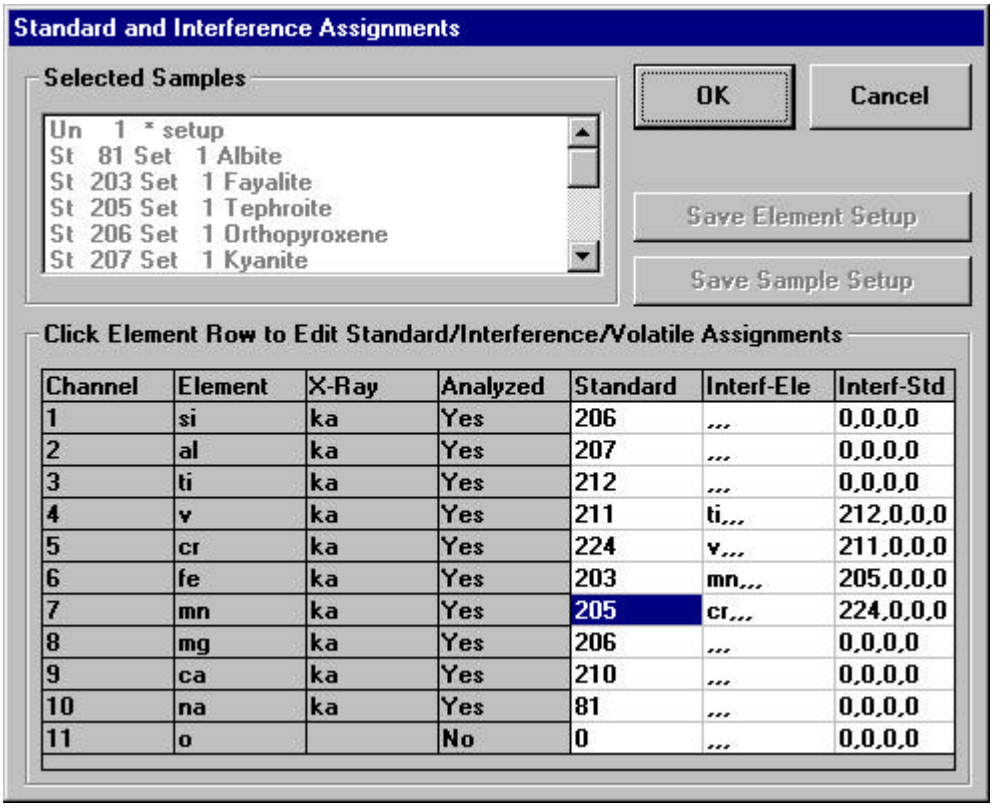
Click the **OK** button when finished.

The **Standard and Interference Assignments** window will appear as below.



Channel	Element	X-Ray	Analyzed	Standard	Interf-Ele	Interf-Std
1	si	ka	Yes	206	,,,	0,0,0,0
2	al	ka	Yes	207	,,,	0,0,0,0
3	ti	ka	Yes	212	,,,	0,0,0,0
4	v	ka	Yes	211	ti,,,	212,0,0,0
5	cr	ka	Yes	224	,,,	0,0,0,0
6	fe	ka	Yes	203	,,,	0,0,0,0
7	mn	ka	Yes	205	,,,	0,0,0,0
8	mg	ka	Yes	206	,,,	0,0,0,0
9	ca	ka	Yes	210	,,,	0,0,0,0
10	na	ka	Yes	81	,,,	0,0,0,0
11	o		No	0	,,,	0,0,0,0

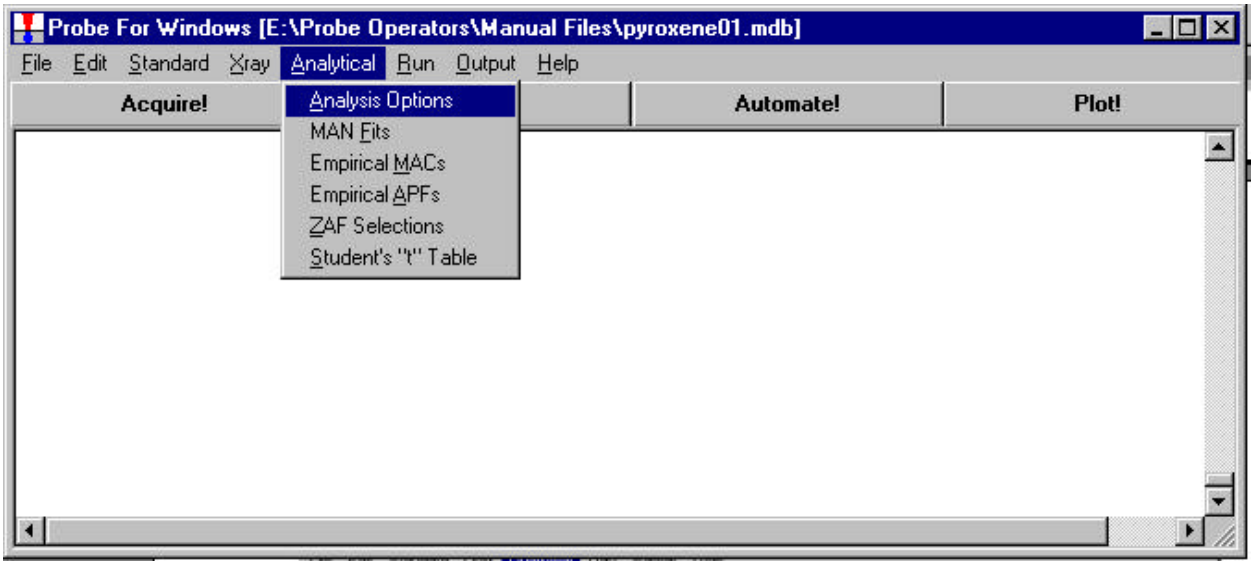
Repeat these editing steps for all of the other element interferences, resulting in the following **Standard and Interference Assignments** window.



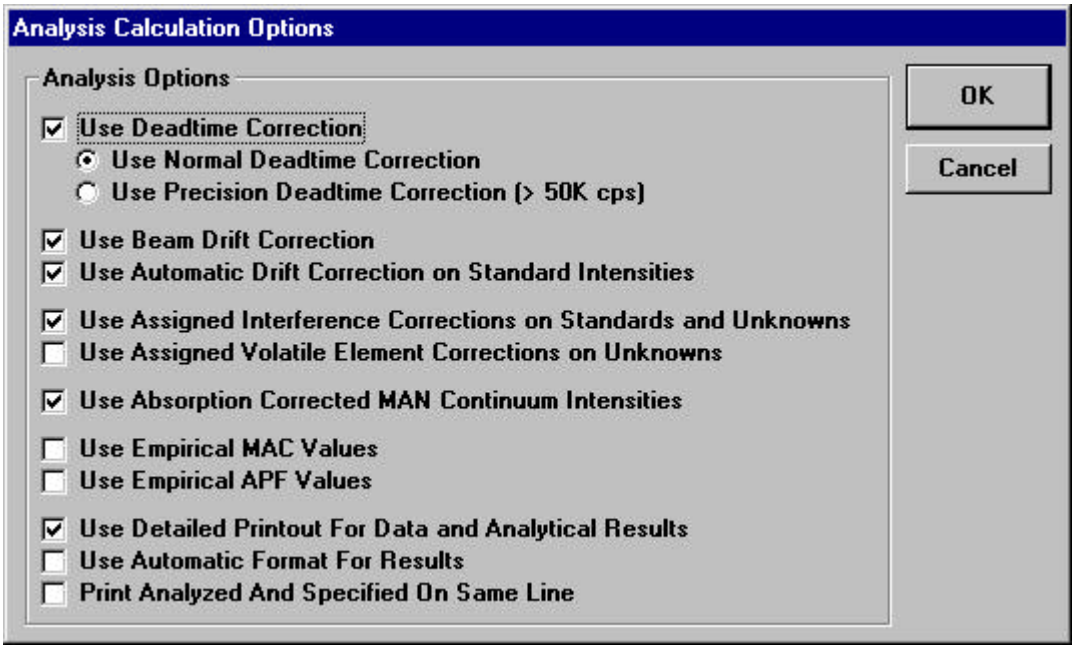
Channel	Element	X-Ray	Analyzed	Standard	Interf-Ele	Interf-Std
1	si	ka	Yes	206	,,,	0,0,0,0
2	al	ka	Yes	207	,,,	0,0,0,0
3	ti	ka	Yes	212	,,,	0,0,0,0
4	v	ka	Yes	211	ti,,,	212,0,0,0
5	cr	ka	Yes	224	v,,,	211,0,0,0
6	fe	ka	Yes	203	mn,,,	205,0,0,0
7	mn	ka	Yes	205	cr,,,	224,0,0,0
8	mg	ka	Yes	206	,,,	0,0,0,0
9	ca	ka	Yes	210	,,,	0,0,0,0
10	na	ka	Yes	81	,,,	0,0,0,0
11	o		No	0	,,,	0,0,0,0

Click the **OK** button when finished returning to the **Analyze!** window.

Next, the user might check the analysis options that are currently assigned. From the main PROBE FOR WINDOWS log window, select **Analytical** from the menu bar and click **Analysis Options** from the menu choices.

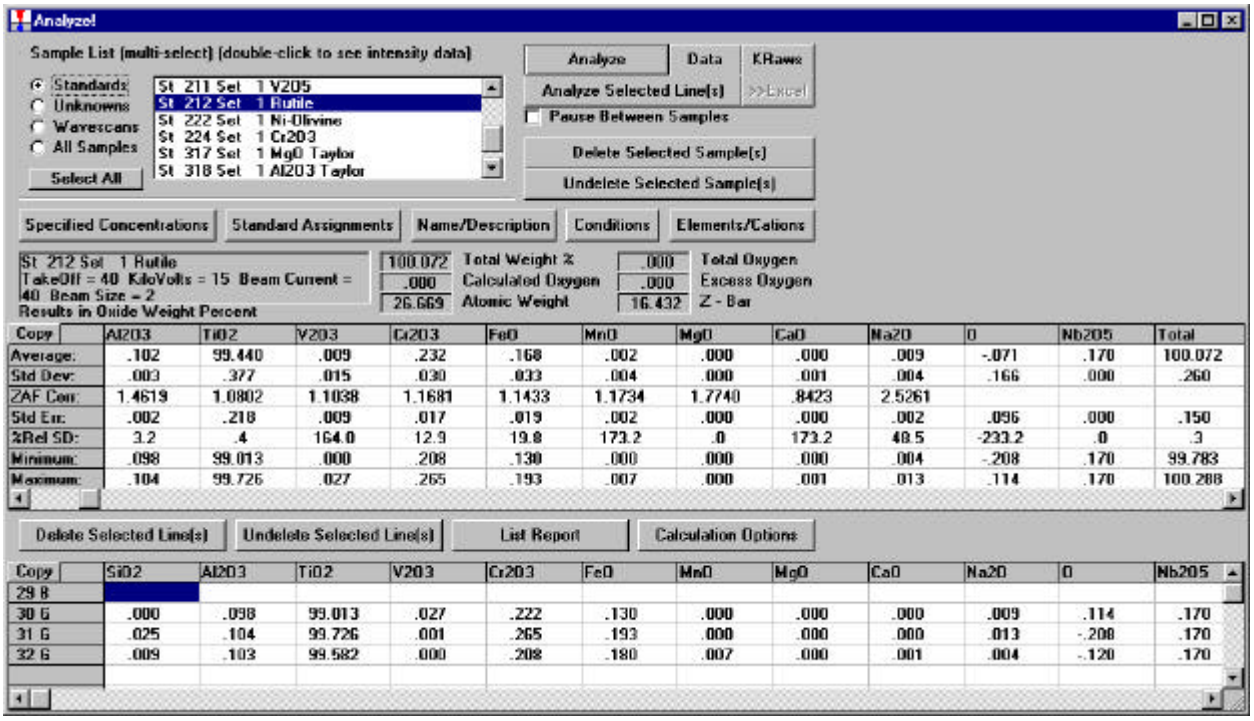


This opens the **Analysis Calculation Options** window. Check that the appropriate boxes are marked.



Click the **OK** button returning to the main log window.

The user then reanalyzes the standards (**Analyze** button in the **Analyze!** window), utilizing the spectral interference correction routine. The results for the Rutile standard are dramatic; the apparent 2.1 wt% V_2O_3 concentration has been replaced with an average 0.01 wt% content (which is below the detection limit).



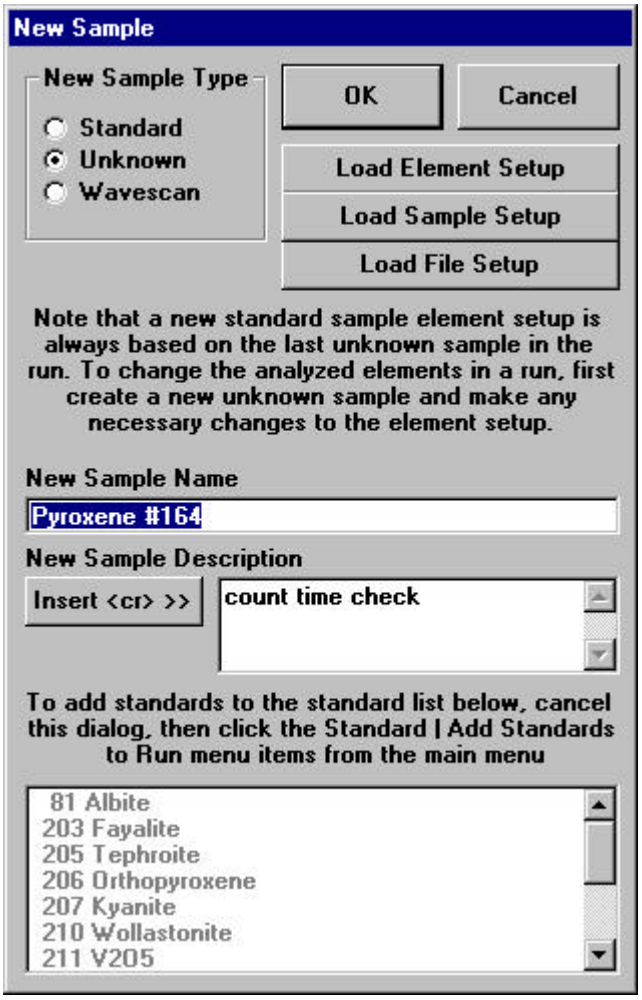
The user is ready to move on to unknown samples.

Unknown Sample Data Collection and Analysis

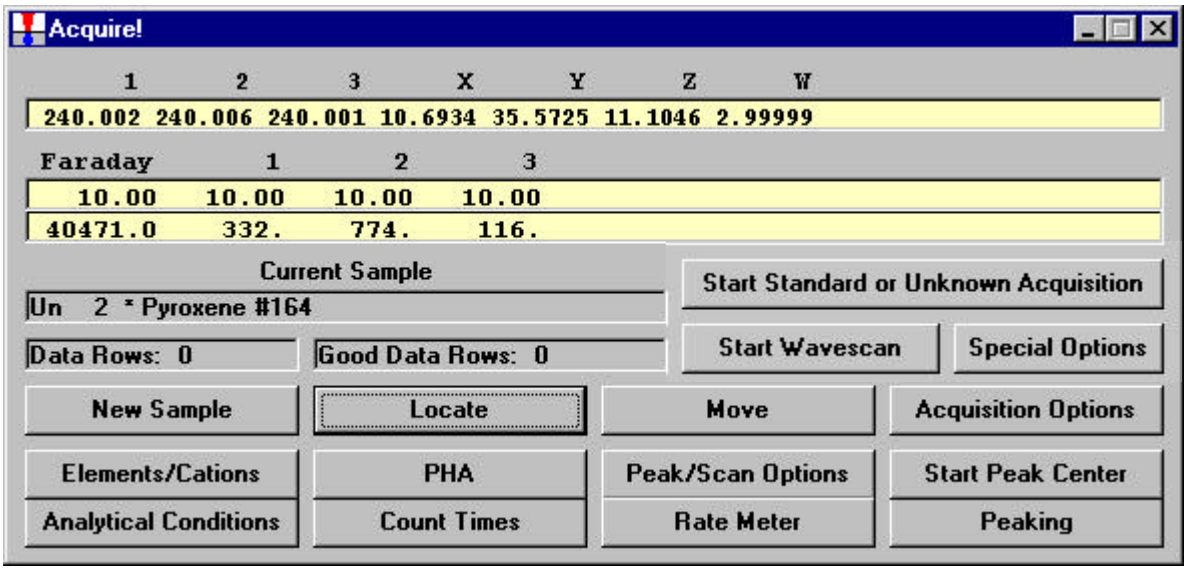
To collect x-ray data on an unknown sample, minimize the **Analyze!** window and/or bring forward the **Acquire!** dialog box to start a new sample.

Click the **Move** button on the **Acquire!** window to drive the stage to the coordinates of the first unknown sample.

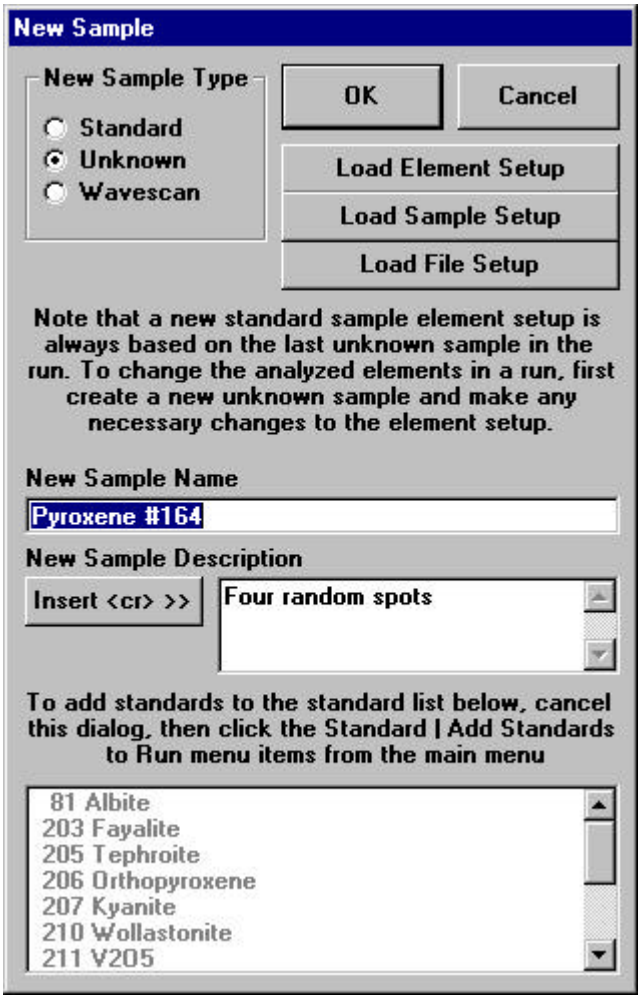
Click the **New Sample** button to activate the **New Sample** dialog box. Check that the *Unknown* button under *New Sample Type* is marked. Enter an appropriate sample name and description into the *New Sample Name* and *New Sample Description* text boxes. Finally, click the **OK** button.



To start acquiring x-ray counts on the first unknown sample, simply click the **Start Standard or Unknown Acquisition** button of the **Acquire!** window.

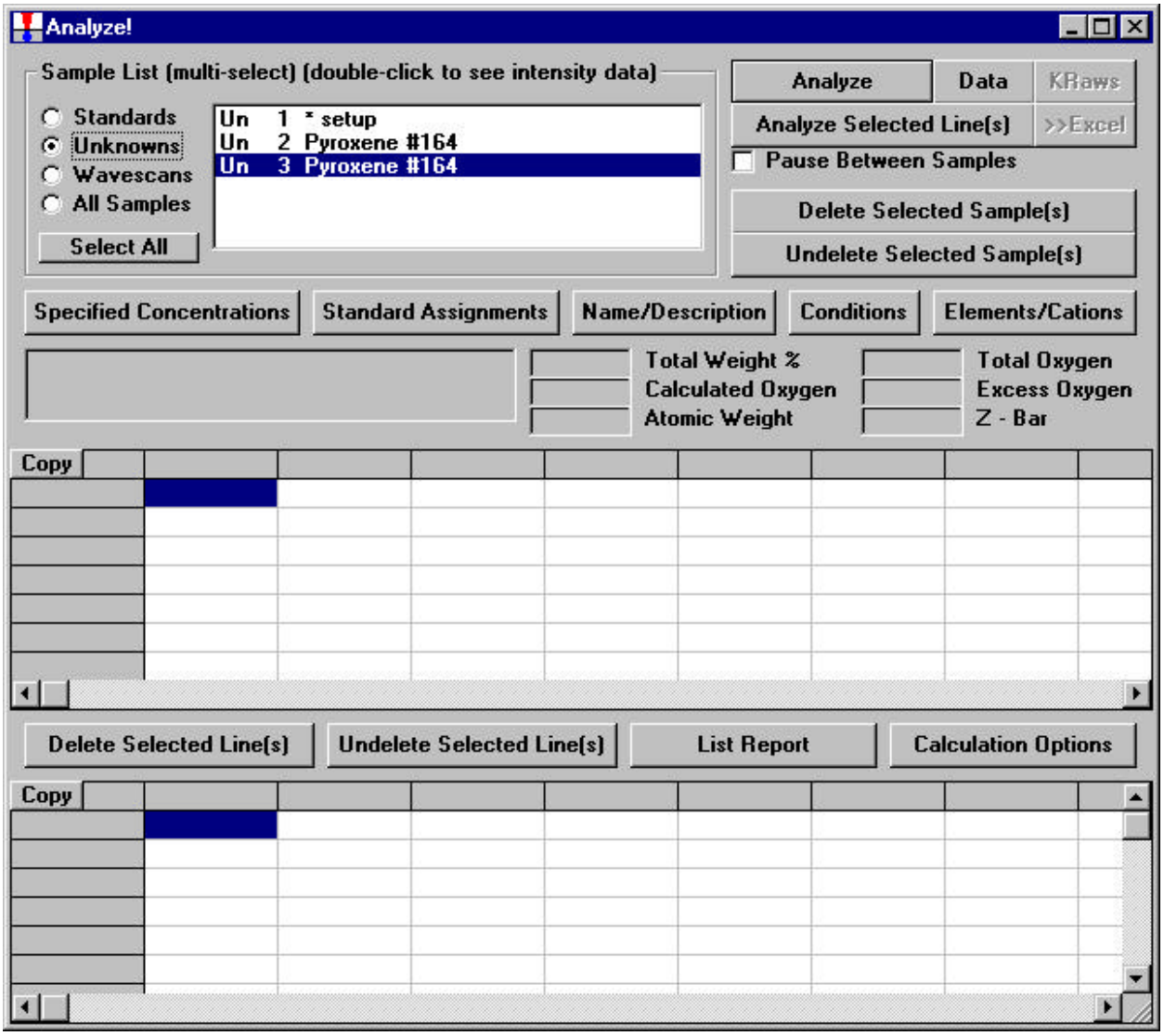


Pyroxene #164, a chromium augite, is run once to obtain representative count rate information for the adjustment of element count times using the **Count Times** button to improve statistics and lower detection limits. Four random spots are then acquired (a **New Sample** is started) on the same pyroxene.



The **Start Standard or Unknown Acquisition** button in the **Acquire!** window is clicked four times, to acquire four data points.

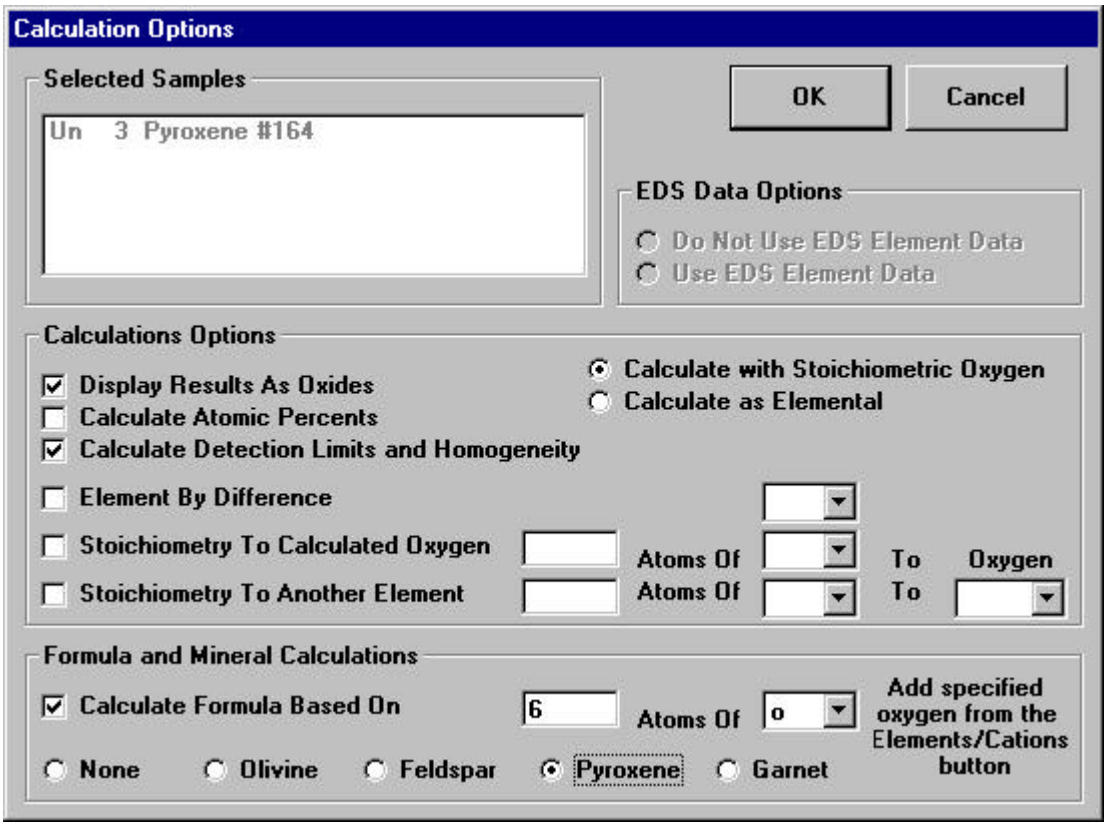
Next, the **Analyze!** dialog box is reopened or simply brought forward. Click the *Unknowns* button and select *Un 3 Pyroxene #164.*



Click the **Calculation Options** button.

This opens the **Calculation Options** dialog box.

Make the following changes; under *Calculations Options* check *Display Results as Oxides, Calculate Detection Limits and Homogeneity,* and *Calculate with Stoichiometric Oxygen*. Under *Formula and Mineral Calculations* check the *Calculate Formula Based On* box. Select *Pyroxene* and enter *6 Atoms of Oxygen* in the other two text boxes.



Click the **OK** button closing the **Calculation Options** window, returning to the **Analyze!** dialog box.

Clicking the **Analyze** button calculated the results for these four points and those values are viewed below, as copied from the text editor.

Un   3 Pyroxene #164
TakeOff = 40 KiloVolts = 15 Beam Current = 40 Beam Size = 2
Four random spots
Number of Lines: 4 Number of 'Good' Lines: 4
Current Date and Time: 3/2/99 5:50:23 PM

Elemental Wt. % Total: 99.452   Average Total Oxygen: 43.832
Average Calcu. Oxygen: 43.832   Average Excess Oxygen: .000
Average Atomic Weight: 21.746   Average Atomic Number: 12.383
Average ZAF Iteration: 3.00   Average MAN Iteration: 4.00
Oxygen Calculated by Cation Stoichiometry and Included in the Matrix Correction

Results in Elemental Weight Percents

SPEC:	O
TYPE:	CALC
AVER:	43.832
SDEV:	.141

ELEM:	Si	Al	Ti	V	Cr	Fe	Mn	Mg
BGDS:	MAN	MAN	MAN	MAN	MAN	MAN	MAN	MAN
ABS%:	-20.93	-28.32	-3.15	-2.06	-1.43	-.53	-.83	-32.30
TIME:	10.00	20.00	30.00	30.00	30.00	30.00	30.00	40.00

ELEM:	Si	Al	Ti	V	Cr	Fe	Mn	Mg	SUM
54	23.345	4.050	.332	.016	.608	3.684	.087	10.364	99.414
55	23.528	4.050	.306	.046	.608	3.626	.084	10.386	99.776
56	23.230	4.026	.276	.033	.627	3.678	.110	10.399	99.185
57	23.352	4.034	.314	.018	.634	3.712	.097	10.356	99.432
AVER:	23.364	4.040	.307	.028	.619	3.675	.094	10.376	99.452
SDEV:	.123	.012	.023	.014	.013	.036	.012	.020	
SERR:	.061	.006	.012	.007	.007	.018	.006	.010	
%RSD:	.5	.3	7.5	49.3	2.1	1.0	12.5	.2	
STDS:	206	207	212	211	224	203	205	206	

STKF:	.2112	.2706	.5519	.5083	.6408	.4982	.4894	.1774
STCT:	4872.5	23252.8	1851.9	2467.5	4164.4	4400.5	3826.7	12205.5

UNKF:	.1823	.0282	.0026	.0002	.0053	.0309	.0008	.0701
UNCT:	4206.0	2420.2	8.6	1.1	34.1	272.6	6.1	4826.2
UNBG:	7.1	69.3	2.2	4.1	6.3	12.8	9.0	41.6

ZCOR:	1.2815	1.4345	1.1938	1.2087	1.1795	1.1908	1.2112	1.4796
KRAW:	.8632	.1041	.0047	.0005	.0082	.0619	.0016	.3954
PKBG:	595.82	35.90	4.85	1.28	6.40	22.30	1.67	117.06
INT%:	.00	.00	.00	-23.19	-.14	.00	-1.30	.00

ELEM:	Ca	Na
BGDS:	MAN	MAN
ABS%:	-3.20	-46.94
TIME:	40.00	30.00

ELEM:	Ca	Na	SUM
54	12.482	.631	99.414
55	12.466	.656	99.776
56	12.503	.625	99.185
57	12.469	.632	99.432
AVER:	12.480	.636	99.452
SDEV:	.017	.013	
SERR:	.008	.007	
%RSD:	.1	2.1	

```
STDS:      210      81

STKF:    .3205   .0500
STCT:  11337.2  2170.0

UNKF:    .1149   .0033
UNCT:   4063.9   143.0
UNBG:     35.6    19.2

ZCOR:   1.0863  1.9327
KRAW:    .3585   .0659
PKBG:   115.28    8.44
INT%:      .00     .00

Results in Oxide Weight Percents

SPEC:        O
TYPE:     CALC

AVER:     .000
SDEV:     .000

ELEM:     SiO2   Al2O3    TiO2    V2O3   Cr2O3     FeO     MnO     MgO   SUM
    54  49.943   7.652    .553    .024    .889   4.739    .112  17.186  99.414
    55  50.334   7.653    .510    .067    .889   4.665    .108  17.223  99.776
    56  49.698   7.607    .461    .049    .916   4.732    .142  17.245  99.185
    57  49.959   7.623    .524    .027    .927   4.775    .125  17.173  99.432

AVER:   49.983   7.634    .512    .042    .905   4.728    .122  17.207  99.452
SDEV:     .263    .023    .039    .021    .019    .046    .015    .033
SERR:     .131    .011    .019    .010    .010    .023    .008    .016
%RSD:       .5      .3     7.5    49.3     2.1     1.0    12.5      .2

ELEM:      CaO    Na2O   SUM
    54  17.465    .851  99.414
    55  17.443    .884  99.776
    56  17.495    .842  99.185
    57  17.446    .852  99.432

AVER:   17.462    .857  99.452
SDEV:     .024    .018
SERR:     .012    .009
%RSD:       .1     2.1

Results Based on 6 Atoms of o

SPEC:        O
TYPE:     CALC

AVER:    6.000
SDEV:     .000

ELEM:       Si      Al      Ti       V      Cr      Fe      Mn      Mg   SUM
    54   1.821    .329    .015    .001    .026    .145    .003    .934  10.016
    55   1.827    .327    .014    .002    .026    .142    .003    .932  10.013
    56   1.818    .328    .013    .001    .026    .145    .004    .940  10.021
    57   1.822    .328    .014    .001    .027    .146    .004    .934  10.016

AVER:    1.822    .328    .014    .001    .026    .144    .004    .935  10.017
SDEV:     .004    .001    .001    .001    .001    .002    .000    .004
SERR:     .002    .000    .001    .000    .000    .001    .000    .002
%RSD:       .2      .2     7.4    49.1     2.3     1.2    12.8      .4
```

ELEM:	Ca	Na	SUM
54	.682	.060	10.016
55	.678	.062	10.013
56	.686	.060	10.021
57	.682	.060	10.016
AVER:	.682	.061	10.017
SDEV:	.003	.001	
SERR:	.002	.001	
%RSD:	.4	1.8	

Pyroxene Mineral End-Member Calculations

	Wo	En	Fs
54	38.7	53.0	8.2
55	38.7	53.2	8.1
56	38.7	53.1	8.2
57	38.7	53.0	8.3
AVER:	38.7	53.1	8.2
SDEV:	.0	.1	.1

Detection limit at 99 % Confidence in Elemental Weight Percent (Single Line):

ELEM:	Si	Al	Ti	V	Cr	Fe	Mn	Mg
54	---	---	.029	.028	.025	---	.026	---
55	---	---	.029	.028	.025	---	.026	---
56	---	---	.029	.028	.025	---	.026	---
57	---	---	.029	.028	.025	---	.026	---
AVER:	---	---	.029	.028	.025	---	.026	---
SDEV:	---	---	.000	.000	.000	---	.000	---
SERR:	---	---	.000	.000	.000	---	.000	---

ELEM:	Ca	Na
54	---	.011
55	---	.011
56	---	.011
57	---	.011
AVER:	---	.011
SDEV:	---	.000
SERR:	---	.000

Percent Analytical Error (Single Line):

ELEM:	Si	Al	Ti	V	Cr	Fe	Mn	Mg
54	.5	.5	7.3	57.4	3.7	1.2	15.7	.2
55	.5	.5	7.7	27.5	3.7	1.2	16.1	.2
56	.5	.5	8.2	35.8	3.6	1.2	12.8	.2
57	.5	.5	7.5	53.7	3.6	1.2	14.3	.2
AVER:	.5	.5	7.7	43.6	3.7	1.2	14.7	.2
SDEV:	.0	.0	.4	14.3	.0	.0	1.5	.0
SERR:	.0	.0	.2	7.2	.0	.0	.8	.0

ELEM:	Ca	Na
54	.3	1.7
55	.3	1.7
56	.2	1.7
57	.3	1.7
AVER:	.3	1.7

SDEV: .0 .0
SERR: .0 .0

Range of Homogeneity in +/- Elemental Weight Percent (Average of Sample):

ELEM:	Si	Al	Ti	V	Cr	Fe	Mn	Mg
60ci	.063	.007	.009	.001	.005	.017	.002	.010
80ci	.106	.011	.015	.002	.009	.028	.004	.017
90ci	.152	.016	.022	.003	.013	.041	.006	.025
95ci	.205	.021	.029	.004	.018	.055	.008	.034
99ci	.377	.039	.054	.008	.032	.101	.014	.062

ELEM:	Ca	Na
60ci	.009	.006
80ci	.015	.010
90ci	.021	.014
95ci	.028	.019
99ci	.052	.036

Test of Homogeneity at 1.0 % Precision (Average of Sample):

ELEM:	Si	Al	Ti	V	Cr	Fe	Mn	Mg
60ci	yes	yes	no	no	yes	yes	no	yes
80ci	yes	yes	no	no	no	yes	no	yes
90ci	yes	yes	no	no	no	no	no	yes
95ci	yes	yes	no	no	no	no	no	yes
99ci	no	yes	no	no	no	no	no	yes

ELEM:	Ca	Na
60ci	yes	yes
80ci	yes	no
90ci	yes	no
95ci	yes	no
99ci	yes	no

Level of Homogeneity in +/- Percent (Average of Sample):

ELEM:	Si	Al	Ti	V	Cr	Fe	Mn	Mg
60ci	.3	.2	2.9	4.8	.9	.5	2.5	.1
80ci	.5	.3	4.9	8.1	1.5	.8	4.2	.2
90ci	.6	.4	7.0	11.6	2.1	1.1	6.0	.2
95ci	.9	.5	9.5	15.7	2.9	1.5	8.1	.3
99ci	1.6	1.0	17.5	28.8	5.2	2.7	14.8	.6

ELEM:	Ca	Na
60ci	.1	.9
80ci	.1	1.6
90ci	.2	2.3
95ci	.2	3.1
99ci	.4	5.6

Detection Limit in Elemental Weight Percent (Average of Sample):

ELEM:	Si	Al	Ti	V	Cr	Fe	Mn	Mg
60ci	---	---	.014	.009	.008	---	.008	---
80ci	---	---	.024	.014	.014	---	.013	---
90ci	---	---	.035	.021	.020	---	.018	---
95ci	---	---	.047	.028	.027	---	.025	---
99ci	---	---	.087	.051	.049	---	.045	---

Projected Detection Limits (99% CI) in Elemental Weight Percent (Average of Sample):

ELEM:	Si	Al	Ti	V	Cr	Fe	Mn	Mg
TIME:	.16	.31	.47	.47	.47	.47	.47	.63
PROJ:	---	---	.692	.410	.395	---	.361	---
TIME:	.31	.63	.94	.94	.94	.94	.94	1.25
PROJ:	---	---	.489	.290	.279	---	.255	---
TIME:	.63	1.25	1.88	1.88	1.88	1.88	1.88	2.50
PROJ:	---	---	.346	.205	.197	---	.180	---
TIME:	1.25	2.50	3.75	3.75	3.75	3.75	3.75	5.00
PROJ:	---	---	.245	.145	.140	---	.128	---
TIME:	2.50	5.00	7.50	7.50	7.50	7.50	7.50	10.00
PROJ:	---	---	.173	.102	.099	---	.090	---
TIME:	5.00	10.00	15.00	15.00	15.00	15.00	15.00	20.00
PROJ:	---	---	.122	.072	.070	---	.064	---
TIME:	10.00	20.00	30.00	30.00	30.00	30.00	30.00	40.00
PROJ:	---	---	.087	.051	.049	---	.045	---
TIME:	20.00	40.00	60.00	60.00	60.00	60.00	60.00	80.00
PROJ:	---	---	.061	.036	.035	---	.032	---
TIME:	40.00	80.00	120.00	120.00	120.00	120.00	120.00	160.00
PROJ:	---	---	.043	.026	.025	---	.023	---
TIME:	80.00	160.00	240.00	240.00	240.00	240.00	240.00	320.00
PROJ:	---	---	.031	.018	.017	---	.016	---
TIME:	160.00	320.00	480.00	480.00	480.00	480.00	480.00	640.00
PROJ:	---	---	.022	.013	.012	---	.011	---
TIME:	320.00	640.00	960.00	960.00	960.00	960.00	960.00	1280.00
PROJ:	---	---	.015	.009	.009	---	.008	---
TIME:	640.00	1280.00	1920.00	1920.00	1920.00	1920.00	1920.00	2560.00
PROJ:	---	---	.011	.006	.006	---	.006	---

ELEM:	Ca	Na
60ci	---	.009
80ci	---	.014
90ci	---	.021
95ci	---	.028
99ci	---	.051

Projected Detection Limits (99% CI) in Elemental Weight Percent (Average of Sample):

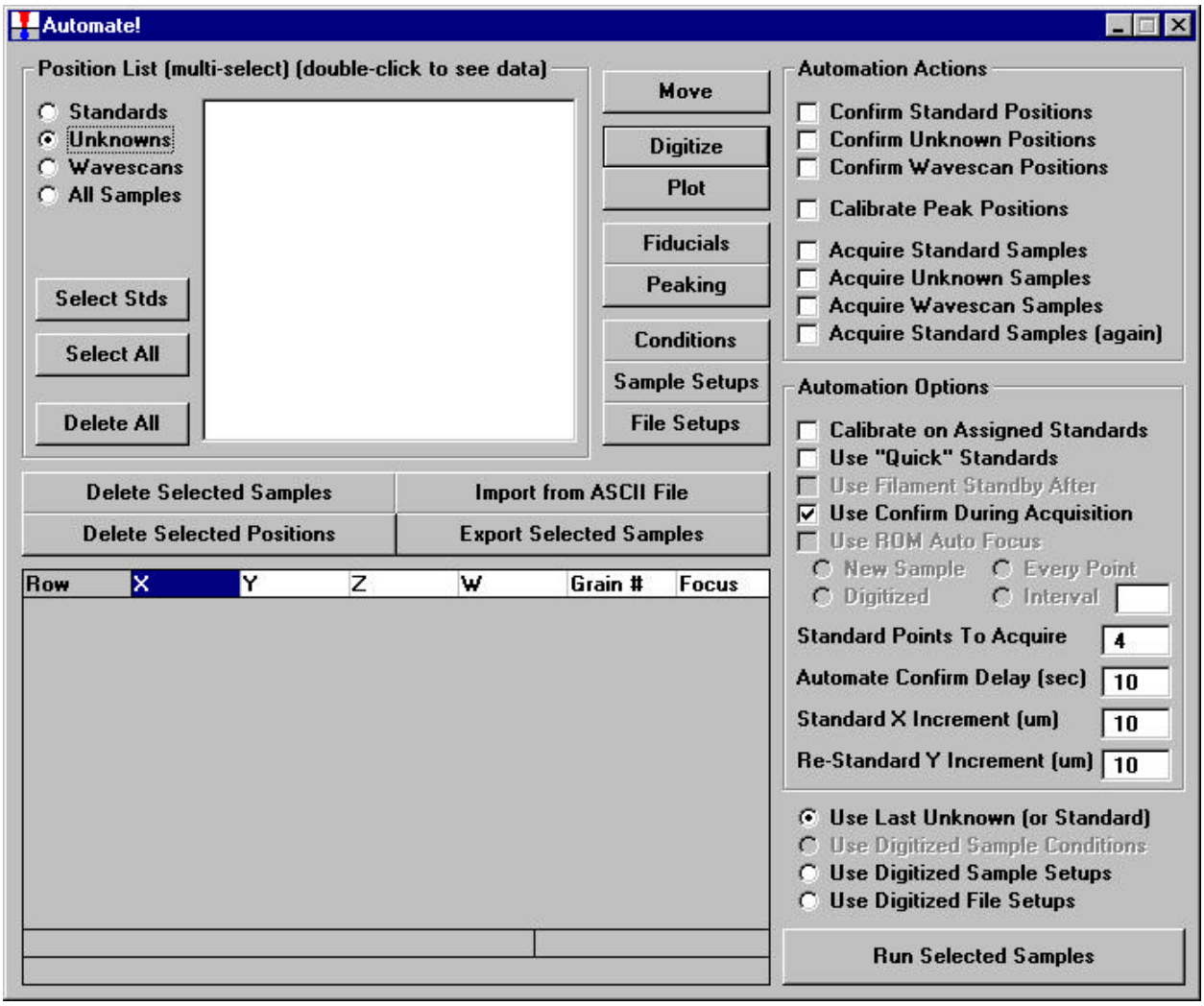
ELEM:	Ca	Na
TIME:	.63	.47
PROJ:	---	.411
TIME:	1.25	.94
PROJ:	---	.291
TIME:	2.50	1.88
PROJ:	---	.206
TIME:	5.00	3.75
PROJ:	---	.145
TIME:	10.00	7.50
PROJ:	---	.103
TIME:	20.00	15.00
PROJ:	---	.073
TIME:	40.00	30.00
PROJ:	---	.051
TIME:	80.00	60.00
PROJ:	---	.036
TIME:	160.00	120.00
PROJ:	---	.026
TIME:	320.00	240.00
PROJ:	---	.018
TIME:	640.00	480.00
PROJ:	---	.013
TIME:	1280.00	960.00

```
PROJ:      ---    .009
TIME:  2560.00 1920.00
PROJ:      ---    .006

Analytical Sensitivity in Elemental Weight Percent (Average of Sample):

ELEM:       Si      Al      Ti       V      Cr      Fe      Mn      Mg
  60ci    .089    .009    .013    .002    .008    .024    .003    .015
  80ci    .149    .015    .021    .003    .013    .040    .006    .025
  90ci    .215    .022    .031    .005    .019    .057    .008    .035
  95ci    .290    .030    .041    .006    .025    .078    .011    .048
  99ci    .532    .055    .076    .012    .046    .143    .020    .088

ELEM:       Ca      Na
  60ci    .012    .008
  80ci    .021    .014
  90ci    .030    .020
  95ci    .040    .027
  99ci    .074    .050
```

The user may obtain a large amount of information besides elemental and oxide weight percent data; these expanded capabilities include formula and mineral end member calculations, an extended set of detection limit and statistics including homogeneity and analytical sensitivity. See the User's Guide and Reference documentation for calculation details.

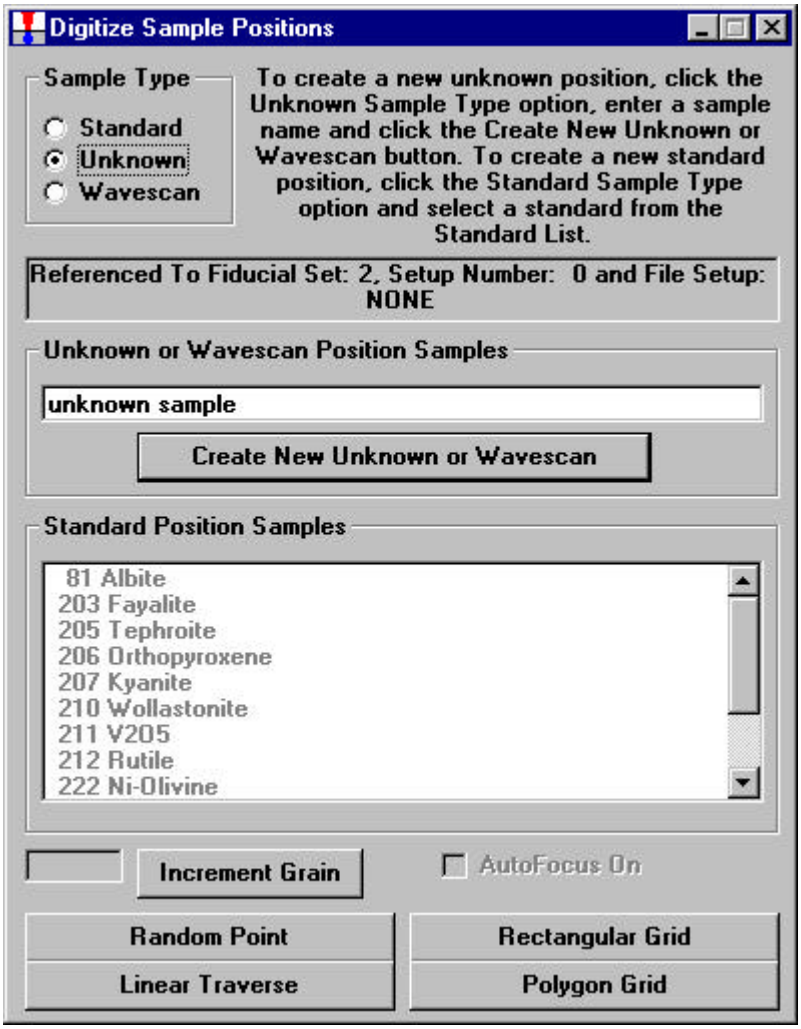
Digitized Sample Data Collection and Analysis

Next the user will perform a digitized traverse across an unknown pyroxene grain. The user can digitize standards, unknowns or wavescan positions based on random points, linear traverse or rectangular or polygon gridded areas. Check that the *Unknowns* button is clicked.

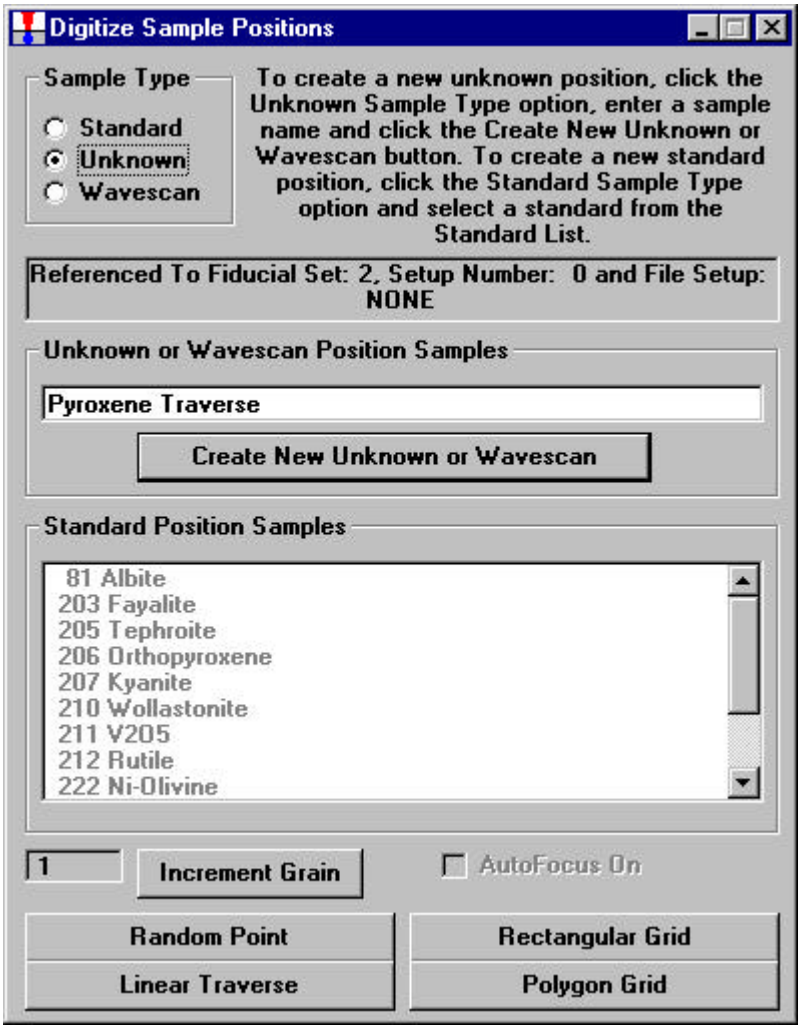


Click the **Digitize** button in the **Automate!** window.

This opens the **Digitize Sample Positions** dialog box.

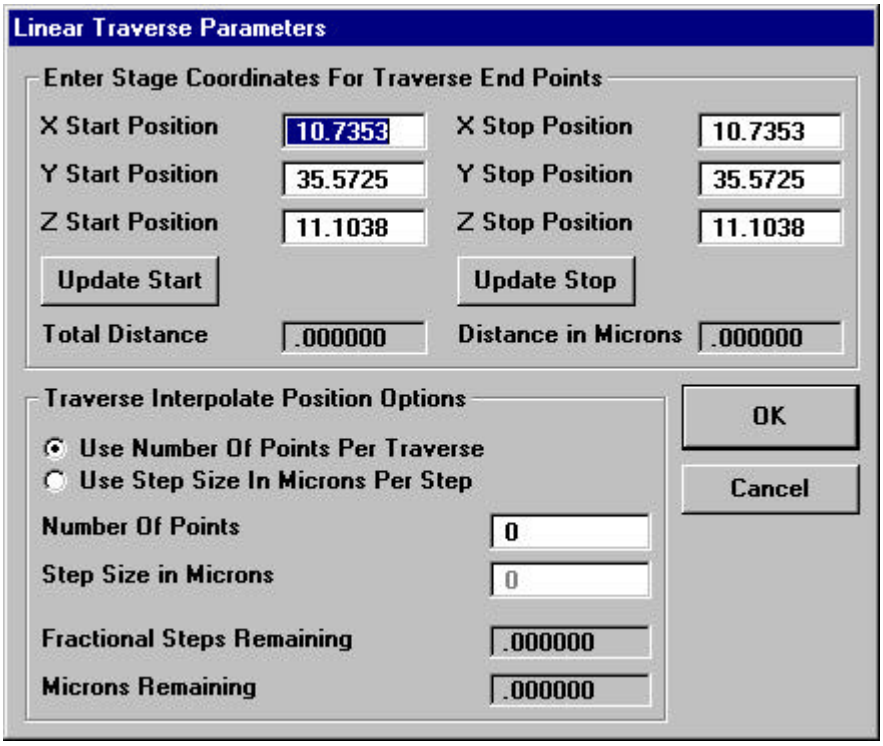


To create an unknown digitized sample click *Unknown* under *Sample Type* and enter a sample name in the *Unknown or Wavescan Position Samples* text box. Next, click the **Create New Unknown or Wavescan** button. The unknown sample will now appear in the *Position List* list box of the **Automate!** window.



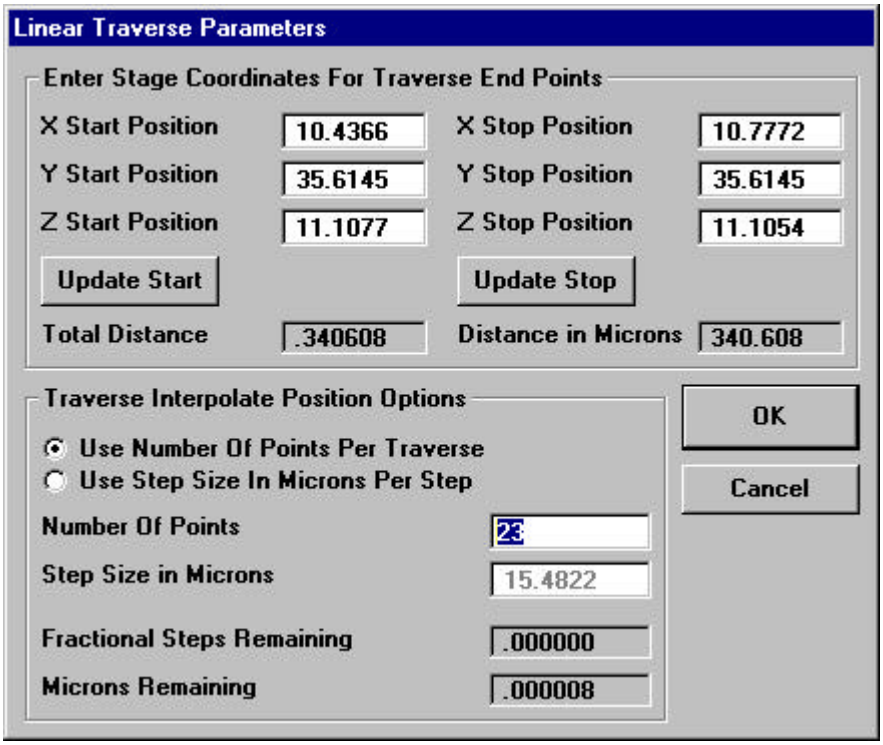
Finally, click the **Linear Traverse** button to create a traverse of digitized points. Other options are rectangular and polygon grids.

The **Linear Traverse Parameters** dialog box opens.



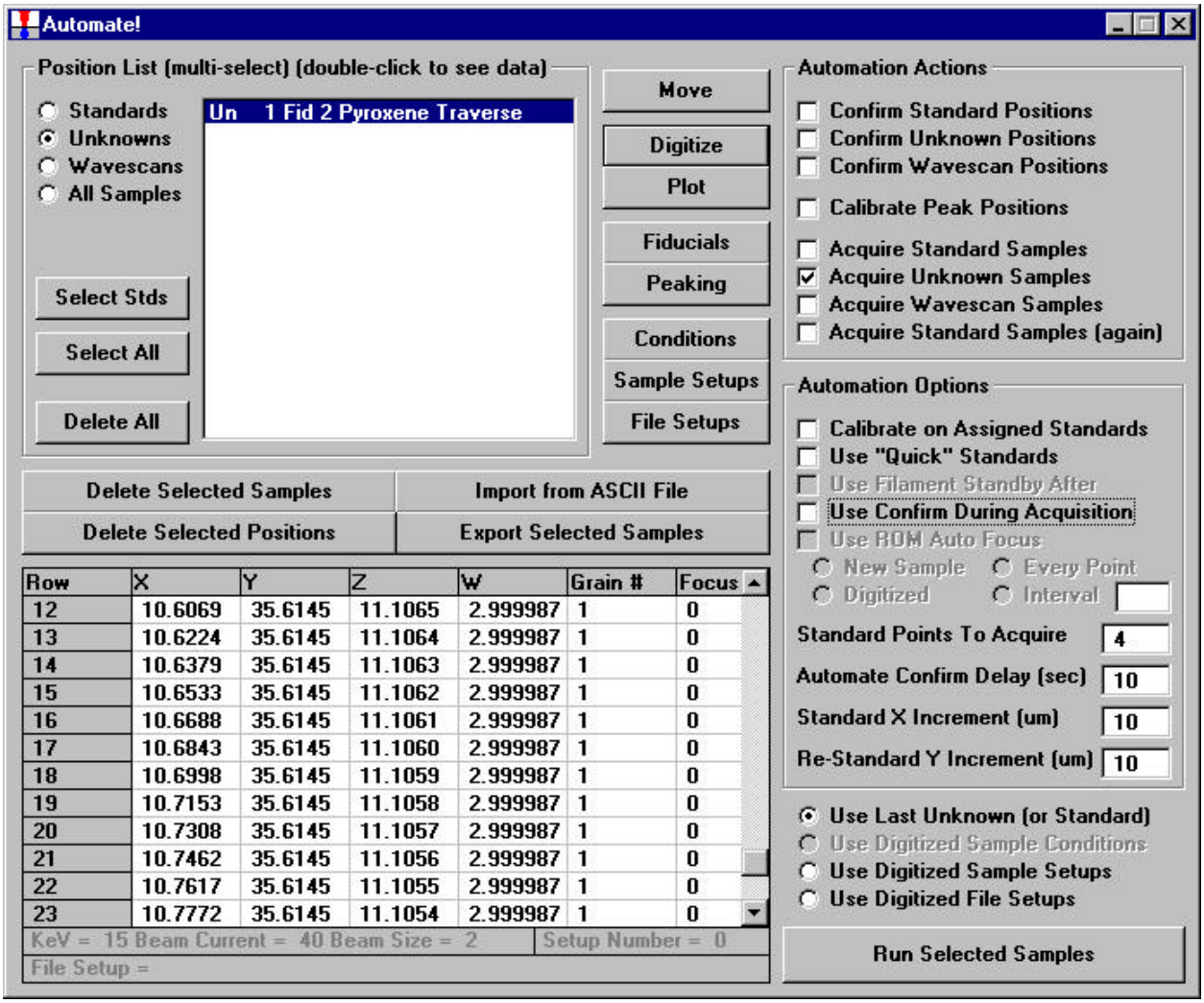
Move to the start position of the linear traverse, click the **Update Start** button. Move to the stop position and click the **Update Stop** button. The total distance is displayed.

Select the *Use Number of Points Per Traverse* or *Use Step Size in Microns Per Step* button and adjust the text boxes appropriately.

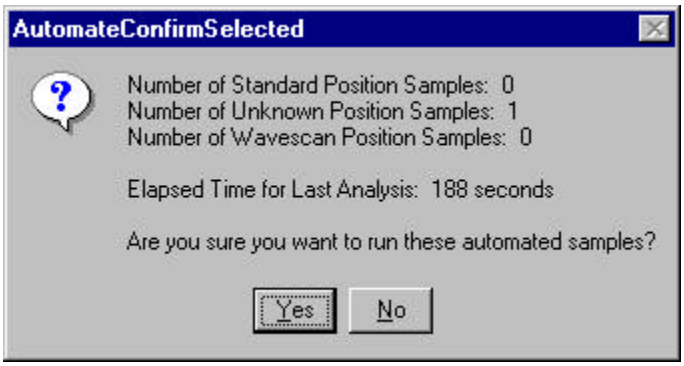


Click the **OK** button returning to the **Automate!** window.

Now all of the calculated analysis positions have been digitized and listed. Under *Automation Actions* click the *Acquire Unknown Samples* button.

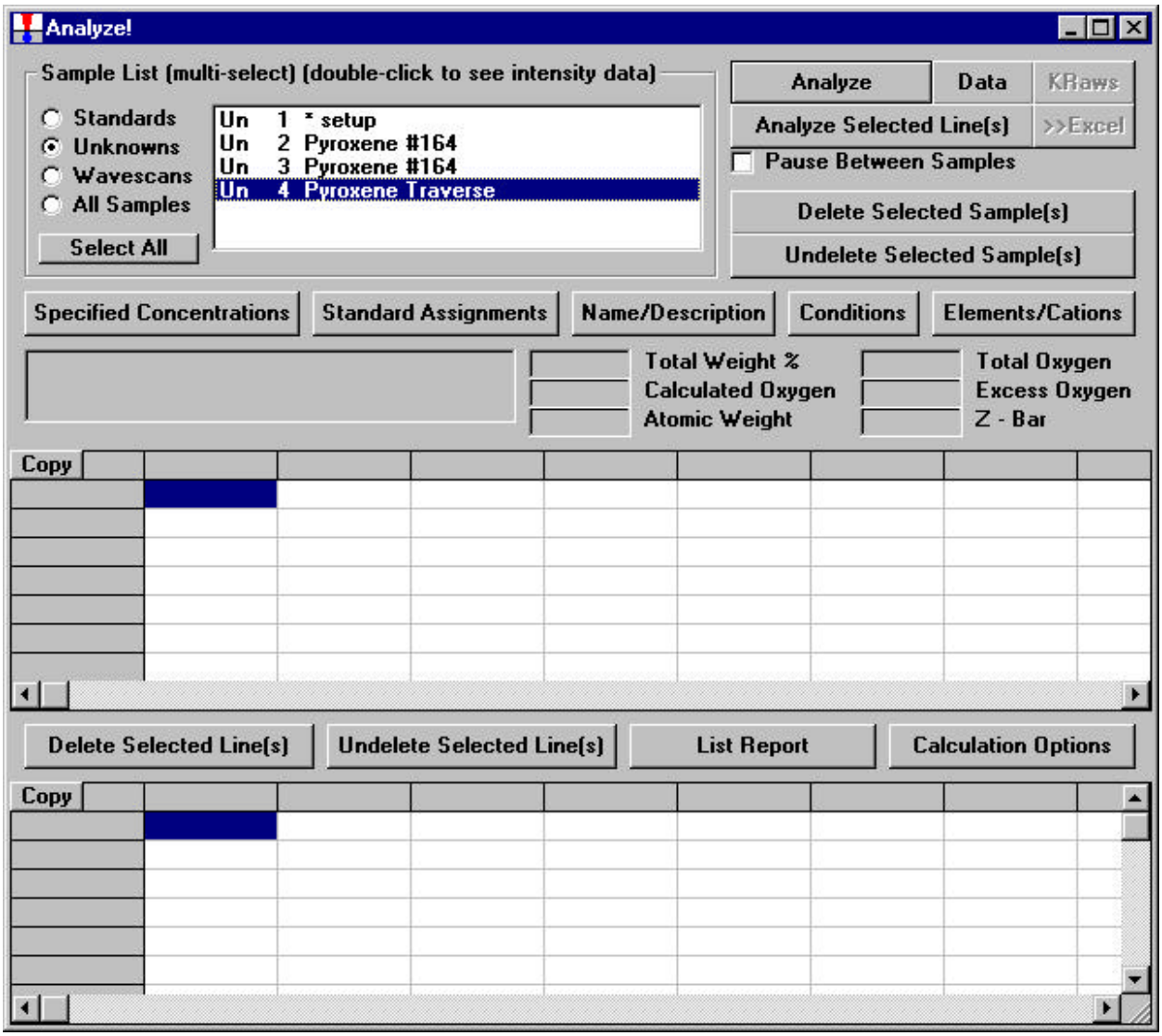


Click **Run Selected Samples** button to initiate the traverse. The **AutomateConfirmSelected** window opens, click **Yes**.



When the traverse is completed the familiar **AcquireStop** window appears. Click the **OK** button returning the user to the **Automate!** dialog box.

To analyze the data obtained from the traverse, the user opens the **Analyze!** window and selects the *Un 4 Pyroxene Traverse* unknown sample in the *Sample List*.



Again, save the log window output to the text editor. Click the **Analyze** button to calculate compositions and finally view the disk log in the text editor. A portion is shown below.

```
Un    4 Pyroxene Traverse
TakeOff = 40  KiloVolts = 15  Beam Current = 40  Beam Size = 2
```

Traverse across grain
Number of Lines: 23 Number of 'Good' Lines: 23
Current Date and Time: 3/2/99 7:49:52 PM

Elemental Wt. % Total: 99.372   Average Total Oxygen: 43.828
Average Calcu. Oxygen: 43.828   Average Excess Oxygen: .000
Average Atomic Weight: 21.738   Average Atomic Number: 12.377
Average ZAF Iteration: 3.00   Average MAN Iteration: 4.00
Oxygen Calculated by Cation Stoichiometry and Included in the Matrix Correction

Results in Elemental Weight Percents

SPEC:	O								
TYPE:	CALC								
AVER:	43.828								
SDEV:	.109								
ELEM:	Si	Al	Ti	V	Cr	Fe	Mn	Mg	
BGDS:	MAN	MAN	MAN	MAN	MAN	MAN	MAN	MAN	
ABS%:	-20.88	-28.28	-3.15	-2.06	-1.43	-.53	-.83	-32.28	
TIME:	10.00	20.00	30.00	30.00	30.00	30.00	30.00	20.00	

ELEM:	Si	Al	Ti	V	Cr	Fe	Mn	Mg	SUM
58	23.353	4.003	.283	.019	.594	3.728	.093	10.347	99.132
59	23.482	4.013	.292	.020	.607	3.668	.102	10.316	99.545
60	23.441	3.999	.345	.010	.614	3.625	.111	10.362	99.385
61	23.407	3.981	.282	.026	.616	3.623	.102	10.315	99.211
62	23.366	3.997	.301	.019	.602	3.598	.069	10.373	99.241
63	23.555	3.961	.300	.009	.626	3.705	.098	10.374	99.613
64	23.473	3.981	.308	.015	.593	3.701	.110	10.398	99.439
65	23.356	4.015	.299	.027	.598	3.707	.099	10.345	99.316
66	23.286	4.021	.316	.021	.586	3.618	.083	10.324	99.059
67	23.446	3.987	.287	.006	.628	3.688	.095	10.299	99.360
68	23.312	4.026	.272	.029	.568	3.644	.088	10.276	98.900
69	23.447	4.012	.337	.026	.583	3.627	.098	10.376	99.576
70	23.456	4.025	.287	.009	.585	3.680	.102	10.308	99.352
71	23.282	4.009	.265	.025	.590	3.643	.094	10.353	98.987
72	23.546	3.992	.282	.021	.602	3.679	.094	10.311	99.598
73	23.564	4.004	.299	.015	.573	3.590	.087	10.297	99.446
74	23.492	3.974	.309	.014	.576	3.624	.084	10.315	99.305
75	23.560	4.016	.295	.015	.612	3.640	.096	10.331	99.637
76	23.624	3.985	.272	.026	.590	3.630	.094	10.337	99.739
77	23.440	4.012	.280	.004	.625	3.692	.100	10.336	99.503
78	23.553	4.021	.284	.015	.613	3.688	.088	10.303	99.597
79	23.410	4.018	.269	.031	.590	3.670	.107	10.290	99.243
80	23.450	3.968	.287	.029	.620	3.644	.101	10.284	99.368
AVER:	23.448	4.001	.293	.019	.600	3.657	.095	10.329	99.372
SDEV:	.093	.019	.020	.008	.017	.038	.010	.033	
SERR:	.019	.004	.004	.002	.004	.008	.002	.007	
%RSD:	.4	.5	6.8	42.0	2.9	1.0	10.0	.3	
STDS:	206	207	212	211	224	203	205	206	
STKF:	.2112	.2706	.5519	.5083	.6408	.4982	.4894	.1774	
STCT:	4872.5	23252.8	1851.9	2467.5	4164.4	4400.5	3826.7	12205.5	
UNKF:	.1831	.0279	.0025	.0002	.0051	.0307	.0008	.0698	
UNCT:	4223.6	2398.0	8.2	.8	33.0	271.3	6.2	4805.4	
UNBG:	7.1	69.4	2.2	4.1	6.3	12.8	9.0	41.6	
ZCOR:	1.2808	1.4337	1.1940	1.2089	1.1797	1.1909	1.2113	1.4793	
KRAW:	.8668	.1031	.0045	.0003	.0079	.0616	.0016	.3937	

PKBG:	598.50	35.57	4.68	1.18	6.23	22.21	1.68	116.59
INT%:	.00	.00	.00	-30.47	-.10	.00	-1.24	.00

ELEM:	Ca	Na
BGDS:	MAN	MAN
ABS%:	-3.21	-46.92
TIME:	20.00	30.00

ELEM:	Ca	Na	SUM
58	12.369	.638	99.132
59	12.512	.636	99.545
60	12.404	.628	99.385
61	12.476	.629	99.211
62	12.504	.649	99.241
63	12.410	.628	99.613
64	12.360	.636	99.439
65	12.453	.650	99.316
66	12.499	.638	99.059
67	12.480	.632	99.360
68	12.420	.646	98.900
69	12.513	.649	99.576
70	12.445	.627	99.352
71	12.445	.647	98.987
72	12.507	.630	99.598
73	12.449	.657	99.446
74	12.469	.621	99.305
75	12.467	.633	99.637
76	12.530	.631	99.739
77	12.535	.618	99.503
78	12.458	.628	99.597
79	12.462	.631	99.243
80	12.532	.644	99.368
AVER:	12.465	.636	99.372
SDEV:	.049	.010	
SERR:	.010	.002	
%RSD:	.4	1.6	
STDS:	210	81	
STKF:	.3205	.0500	
STCT:	11337.2	2170.0	
UNKF:	.1147	.0033	
UNCT:	4058.2	143.0	
UNBG:	35.5	19.2	
ZCOR:	1.0865	1.9321	
KRAW:	.3580	.0659	
PKBG:	115.18	8.44	
INT%:	.00	.00	

Results in Oxide Weight Percents

SPEC: O
TYPE: CALC

AVER: .000
SDEV: .000

ELEM:	SiO2	Al2O3	TiO2	V2O3	Cr2O3	FeO	MnO	MgO	SUM
58	49.960	7.564	.472	.028	.868	4.796	.120	17.158	99.132
59	50.237	7.583	.486	.030	.887	4.719	.132	17.107	99.545
60	50.149	7.556	.575	.015	.898	4.664	.143	17.183	99.385
61	50.076	7.522	.471	.039	.900	4.661	.132	17.106	99.211
62	49.989	7.552	.502	.029	.880	4.629	.089	17.201	99.241
63	50.392	7.484	.500	.014	.915	4.767	.126	17.203	99.613
64	50.217	7.521	.514	.022	.867	4.761	.142	17.242	99.439
65	49.967	7.585	.498	.039	.874	4.768	.128	17.155	99.316
66	49.816	7.597	.528	.030	.856	4.654	.108	17.120	99.059
67	50.160	7.534	.478	.009	.918	4.745	.123	17.078	99.360
68	49.874	7.607	.453	.043	.830	4.688	.113	17.041	98.900
69	50.162	7.580	.562	.038	.851	4.667	.126	17.207	99.576
70	50.180	7.606	.478	.013	.854	4.735	.132	17.095	99.352
71	49.809	7.575	.443	.037	.862	4.686	.121	17.169	98.987
72	50.373	7.542	.470	.030	.879	4.733	.121	17.099	99.598
73	50.412	7.565	.498	.023	.838	4.618	.112	17.076	99.446
74	50.258	7.509	.516	.021	.842	4.663	.108	17.105	99.305
75	50.403	7.589	.492	.022	.895	4.683	.124	17.133	99.637
76	50.539	7.529	.454	.038	.862	4.670	.121	17.142	99.739
77	50.146	7.580	.468	.006	.913	4.749	.129	17.140	99.503
78	50.388	7.598	.474	.021	.896	4.745	.114	17.086	99.597
79	50.082	7.591	.449	.046	.863	4.722	.139	17.064	99.243
80	50.168	7.498	.479	.043	.906	4.688	.131	17.054	99.368
AVER:	50.163	7.560	.490	.028	.876	4.705	.123	17.129	99.372
SDEV:	.200	.036	.033	.012	.026	.049	.012	.054	
SERR:	.042	.007	.007	.002	.005	.010	.003	.011	
%RSD:	.4	.5	6.8	42.0	2.9	1.0	10.0	.3	

ELEM:	CaO	Na2O	SUM
58	17.306	.860	99.132
59	17.506	.857	99.545
60	17.356	.847	99.385
61	17.457	.848	99.211
62	17.495	.875	99.241
63	17.365	.846	99.613
64	17.295	.857	99.439
65	17.425	.876	99.316
66	17.489	.860	99.059
67	17.462	.852	99.360
68	17.379	.871	98.900
69	17.508	.875	99.576
70	17.413	.845	99.352
71	17.413	.872	98.987
72	17.499	.850	99.598
73	17.418	.886	99.446
74	17.447	.837	99.305
75	17.443	.853	99.637
76	17.532	.851	99.739
77	17.539	.833	99.503
78	17.431	.847	99.597
79	17.436	.851	99.243
80	17.535	.867	99.368

AVER:	17.441	.857	99.372
SDEV:	.069	.014	
SERR:	.014	.003	
%RSD:	.4	1.6	

Results Based on 6 Atoms of o

SPEC:	O
TYPE:	CALC

AVER:	6.000
SDEV:	.000

ELEM:	Si	Al	Ti	V	Cr	Fe	Mn	Mg	SUM
58	1.826	.326	.013	.001	.025	.147	.004	.935	10.015
59	1.828	.325	.013	.001	.026	.144	.004	.928	10.013
60	1.827	.325	.016	.000	.026	.142	.004	.933	10.011
61	1.829	.324	.013	.001	.026	.142	.004	.931	10.013
62	1.825	.325	.014	.001	.025	.141	.003	.936	10.017
63	1.832	.321	.014	.000	.026	.145	.004	.932	10.010
64	1.829	.323	.014	.001	.025	.145	.004	.936	10.013
65	1.824	.326	.014	.001	.025	.146	.004	.934	10.017
66	1.823	.328	.015	.001	.025	.142	.003	.934	10.017
67	1.829	.324	.013	.000	.026	.145	.004	.928	10.012
68	1.827	.328	.012	.001	.024	.144	.004	.931	10.015
69	1.825	.325	.015	.001	.024	.142	.004	.933	10.015
70	1.829	.327	.013	.000	.025	.144	.004	.929	10.012
71	1.824	.327	.012	.001	.025	.144	.004	.937	10.018
72	1.832	.323	.013	.001	.025	.144	.004	.927	10.011
73	1.834	.324	.014	.001	.024	.141	.003	.926	10.009
74	1.832	.323	.014	.001	.024	.142	.003	.930	10.010
75	1.831	.325	.013	.001	.026	.142	.004	.928	10.010
76	1.834	.322	.012	.001	.025	.142	.004	.928	10.009
77	1.827	.325	.013	.000	.026	.145	.004	.931	10.014
78	1.832	.326	.013	.001	.026	.144	.004	.926	10.009
79	1.828	.327	.012	.001	.025	.144	.004	.929	10.013
80	1.830	.322	.013	.001	.026	.143	.004	.927	10.013
AVER:	1.829	.325	.013	.001	.025	.143	.004	.931	10.013
SDEV:	.003	.002	.001	.000	.001	.002	.000	.003	
SERR:	.001	.000	.000	.000	.000	.000	.000	.001	
%RSD:	.2	.6	6.7	42.1	2.9	1.0	9.9	.4	

ELEM:	Ca	Na	SUM
58	.678	.061	10.015
59	.683	.060	10.013
60	.678	.060	10.011
61	.683	.060	10.013
62	.684	.062	10.017
63	.676	.060	10.010
64	.675	.061	10.013
65	.681	.062	10.017
66	.686	.061	10.017
67	.682	.060	10.012
68	.682	.062	10.015
69	.683	.062	10.015
70	.680	.060	10.012
71	.683	.062	10.018
72	.682	.060	10.011
73	.679	.062	10.009
74	.681	.059	10.010
75	.679	.060	10.010
76	.682	.060	10.009
77	.684	.059	10.014

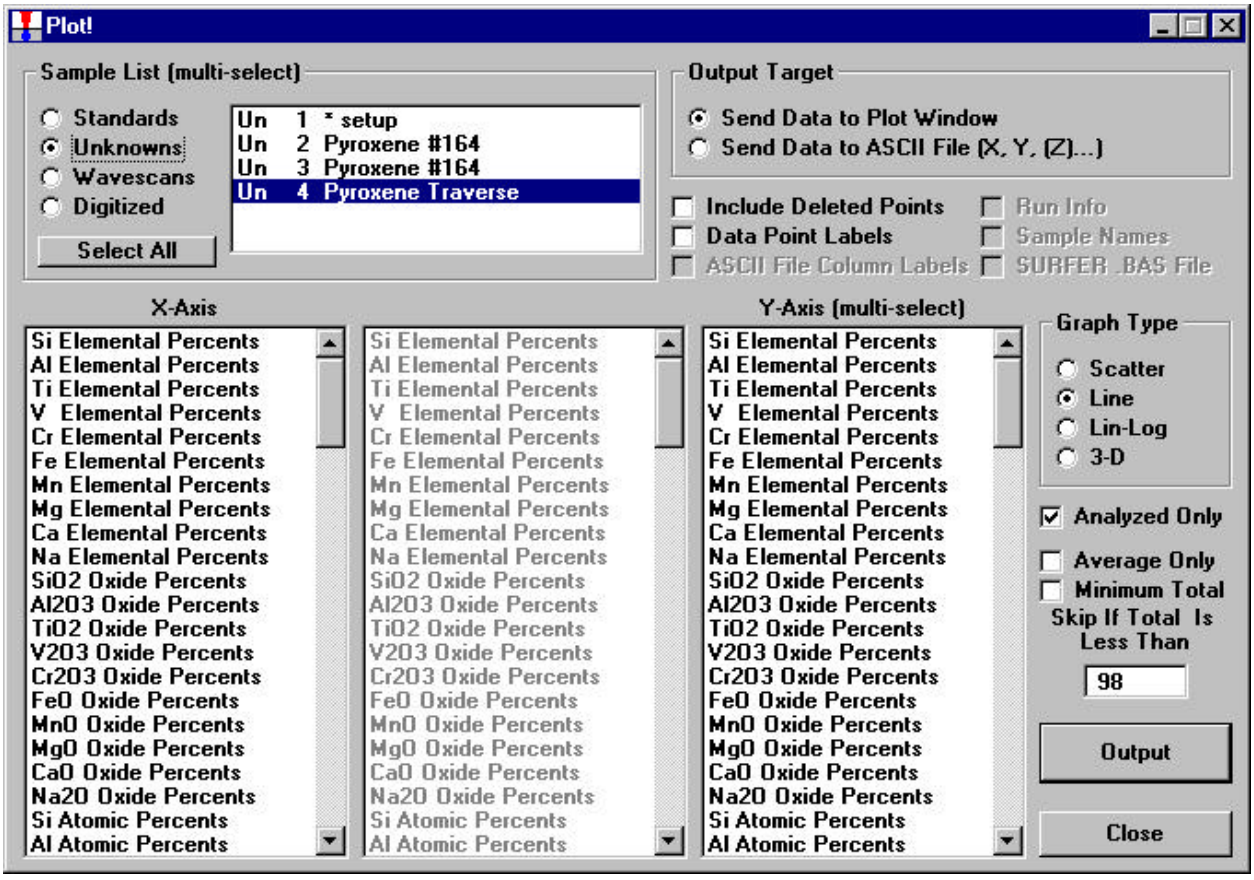
78	.679	.060	10.009
79	.682	.060	10.013
80	.685	.061	10.013
AVER:	.681	.061	10.013
SDEV:	.003	.001	
SERR:	.001	.000	
%RSD:	.4	1.7	

Pyroxene Mineral End-Member Calculations

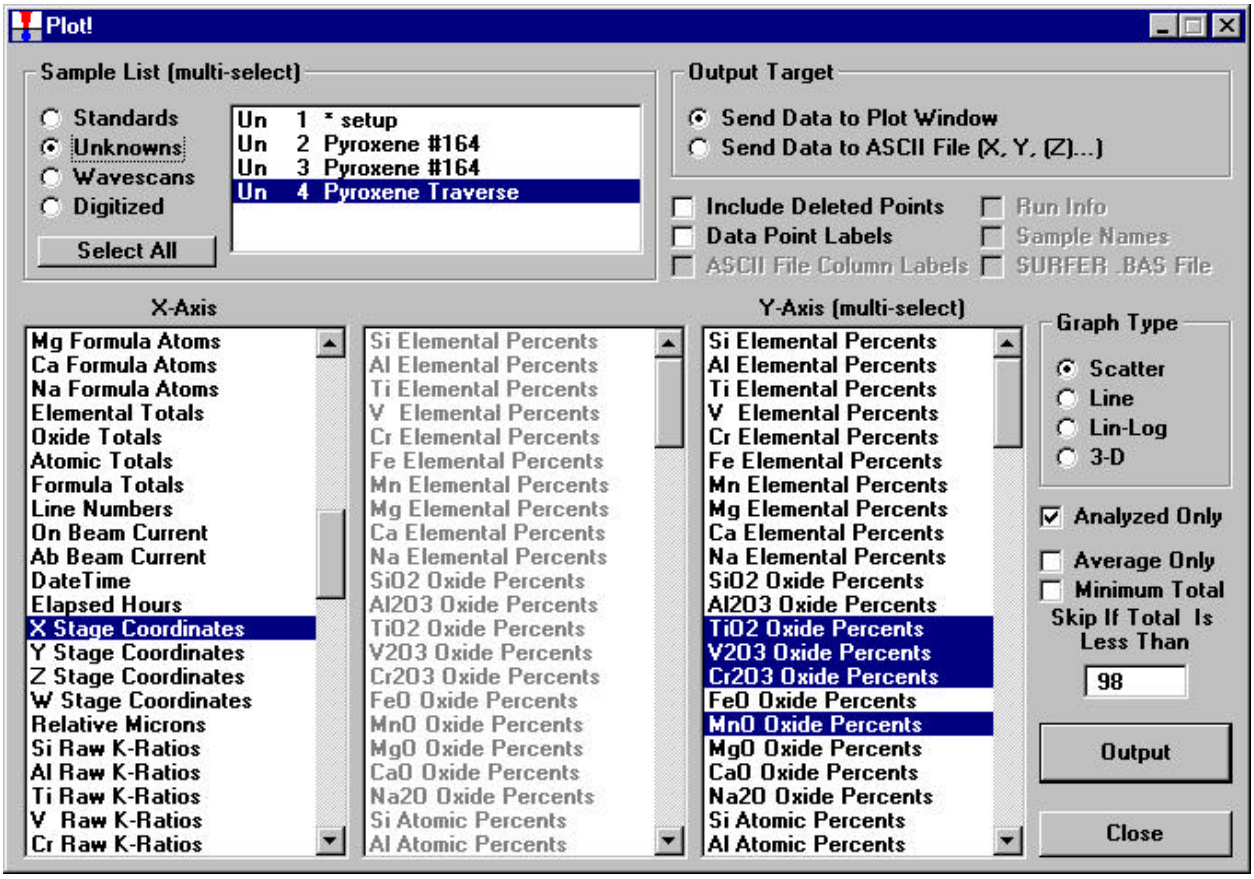
	Wo	En	Fs
58	38.5	53.1	8.3
59	38.9	52.9	8.2
60	38.7	53.2	8.1
61	38.9	53.0	8.1
62	38.8	53.1	8.0
63	38.6	53.2	8.3
64	38.4	53.3	8.3
65	38.7	53.0	8.3
66	38.9	53.0	8.1
67	38.9	52.9	8.2
68	38.8	53.0	8.2
69	38.8	53.1	8.1
70	38.8	53.0	8.2
71	38.7	53.1	8.1
72	38.9	52.9	8.2
73	38.9	53.1	8.0
74	38.9	53.0	8.1
75	38.8	53.0	8.1
76	38.9	53.0	8.1
77	38.9	52.9	8.2
78	38.8	52.9	8.2
79	38.9	52.9	8.2
80	39.0	52.8	8.1
AVER:	38.8	53.0	8.2
SDEV:	.1	.1	.1

Plotting Analysis Data

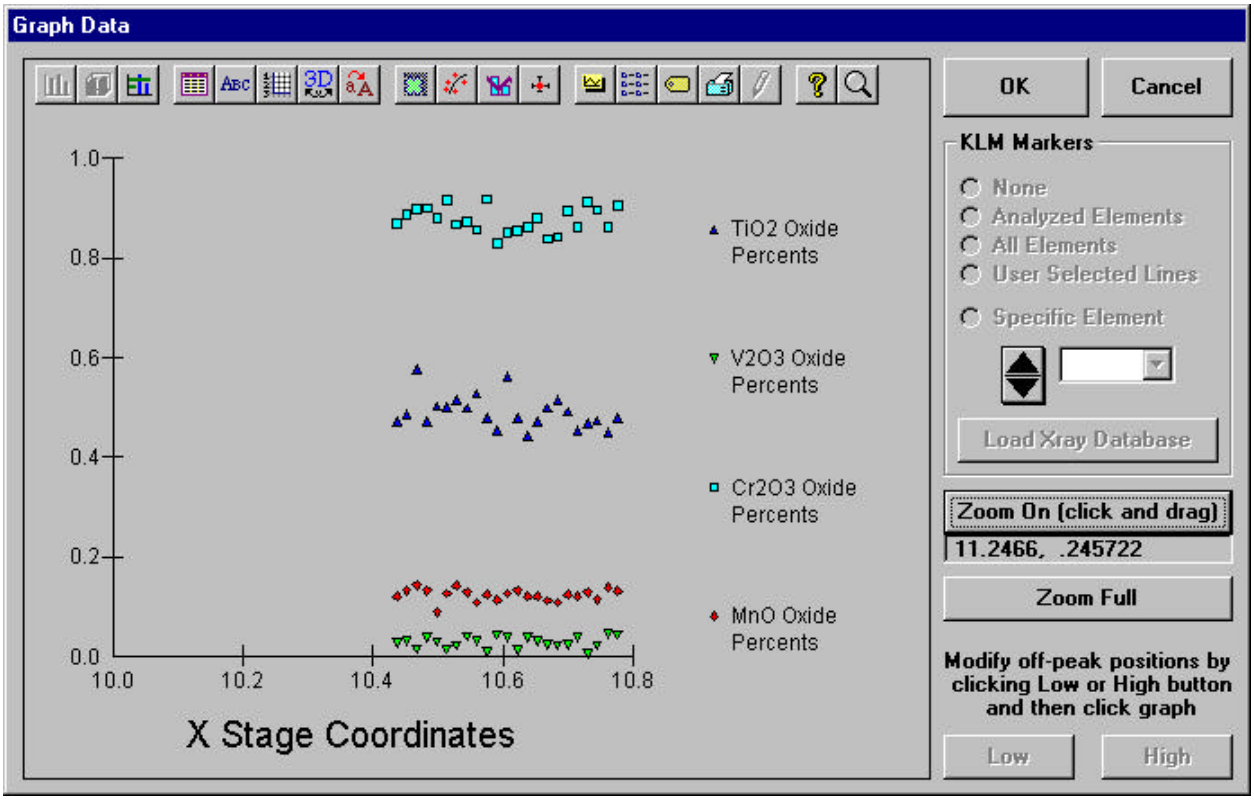
The use may wish to examine the traverse data in a graphical presentation. Click the **Plot!** button in the main PROBE FOR WINDOWS log window. This opens the **Plot!** dialog box.



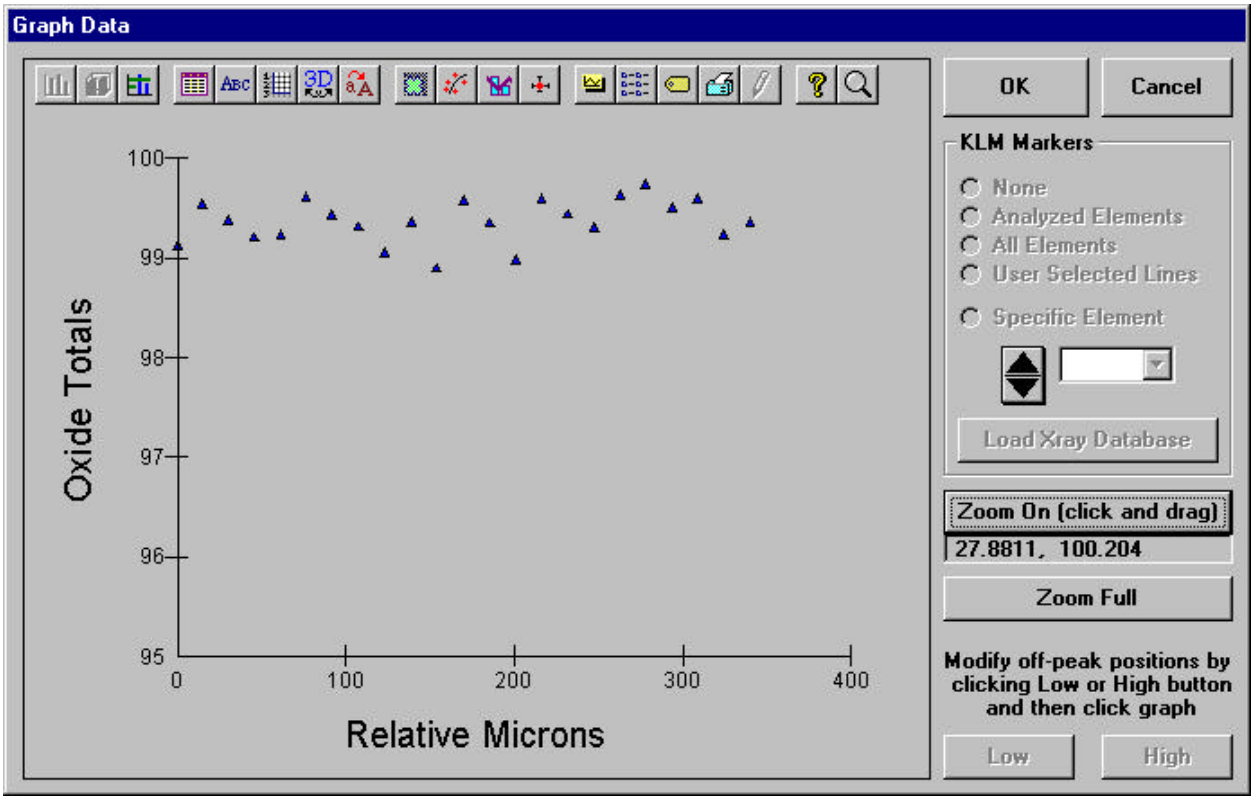
First, choose the pertinent samples from the *Sample List* list box. Select the required *X-Axis*, *Y-Axis* (and *Z-Axis)* items from the axis lists. Choose a *Graph Type* and the button *Send Data to Plot Window.* Finally, click the **Output** button.



Here the user selects the *X-Stage Coordinates* for the *X-Axis* and multi-selects the TiO_2, V_2O_3, Cr_2O_3 and *MnO Oxide Percents* for the *Y-Axis*. This graph is displayed below. Furthermore, the weight percent concentration of any point may be read directly off the plot using the two-way **Hot Hit On/Zoom On** button.

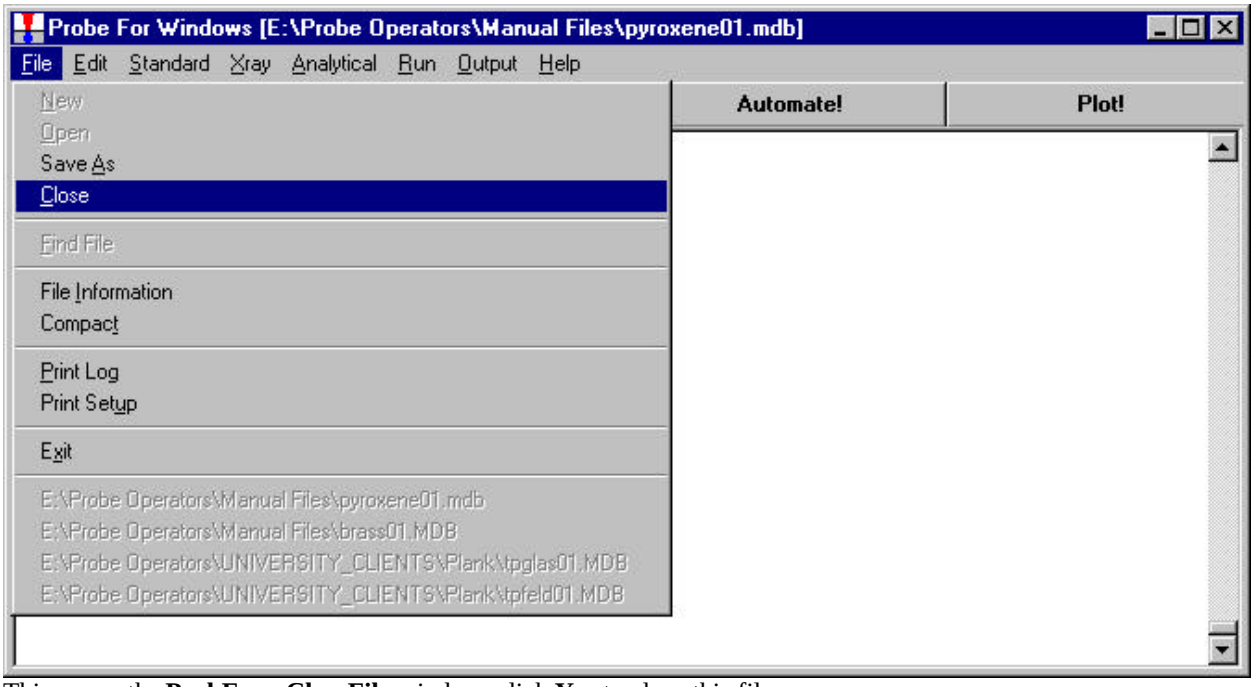


Another graph of interest is *Relative Microns* (traverse steps) versus *Oxide Totals.*



Closing the Current Run and Probe for Windows

The user ends the analysis session from the main PROBE FOR WINDOWS log window. Select **File** from the menu bar and click **Close** from the menu selections.



This opens the **ProbFormCloseFile** window, click **Yes** to close this file.

Close PROBE FOR WINDOWS by selecting **File** from the menu bar and clicking **Exit**.