
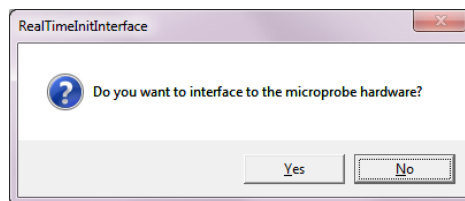


Probe for EPMA Quick Start Instructions

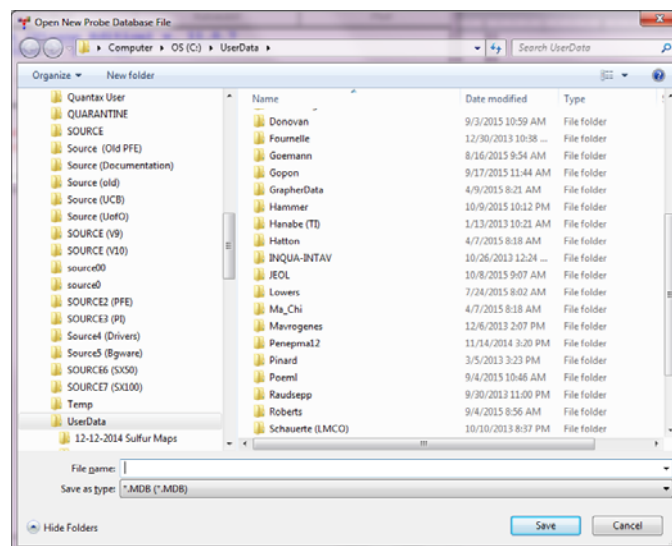
Setting up a New Run for Quantitative Acquisition

This guide is intended as a quick start and just covers the basic steps for creating a new Probe for EPMA run. Please see the Getting Started and Advanced Topics manuals for more details and step by step instructions. On-line context sensitive help is available by simply hitting the F1 key. For menu help, select the menu and then hit the F1 key.

1. Open Probewin.exe (Probe for EPMA) by double-clicking on the Probewin.exe icon shortcut. 
2. When prompted “Do you want to interface to the microprobe” click “Yes”. For off-line data processing click “No”.

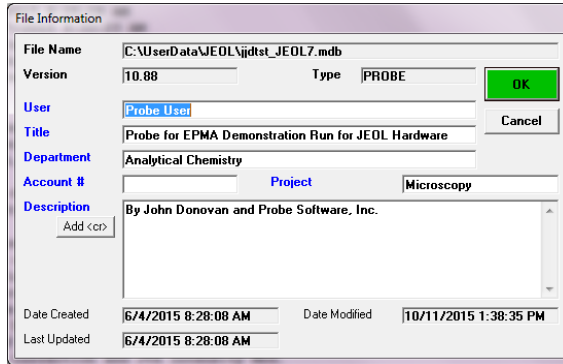


3. Create a new probe run by selecting the File | New menu.
4. In the C:\UserData folder enter a filename that describes your EPMA activity for this session and browse/create a folder that will allow you to locate your data subsequently.



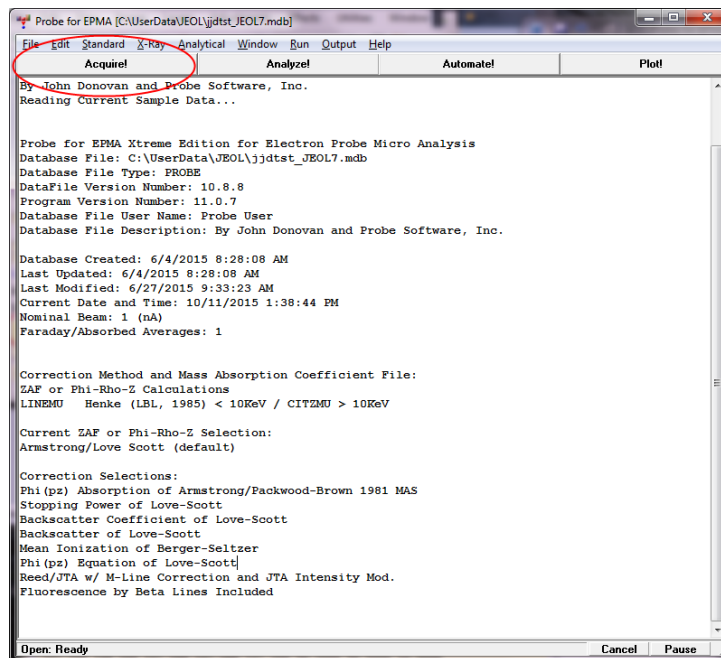
For example if your name is Joe Smith and you are characterizing Al-Ti alloys and the date is 12-08-2009 you might create a probe run file with the following path:
C:\UserData\Smith\12-2009\Al-Ti_12-08-2009.MDB.

Once you enter a filename the program will prompt you with a user information dialog. You should edit the user name and sample identification and if necessary the account number and other information fields which are automatically saved to the USER.MDB user database.

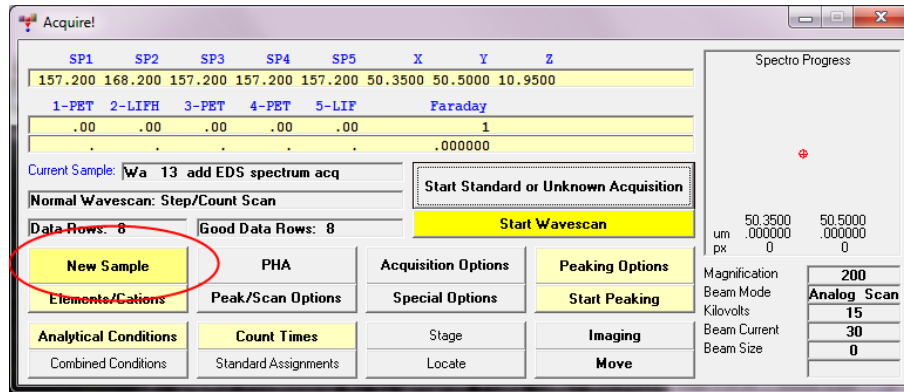


Note: the User database can be subsequently browsed using the Userwin.exe application for reporting, re-charge and/or accounting purposes.

5. Next, open the 'Acquire!' window by clicking the 'Acquire!' button in the Probewin Log window.

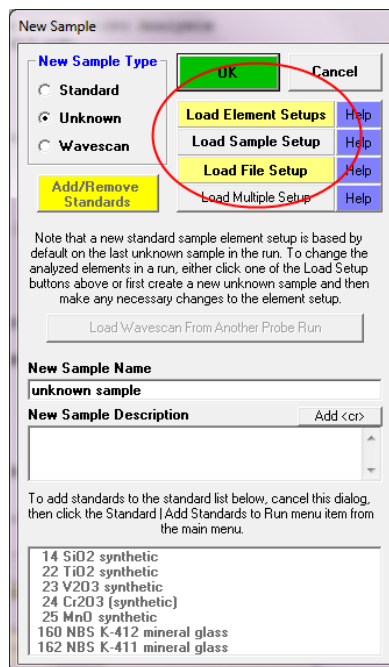


6. In the 'Acquire!' window click the 'New Sample' button to create a new sample template for your analyses. See "Creating a New Run" in the Getting Started Manual for more details.



7. From this 'New Sample' dialog you can:

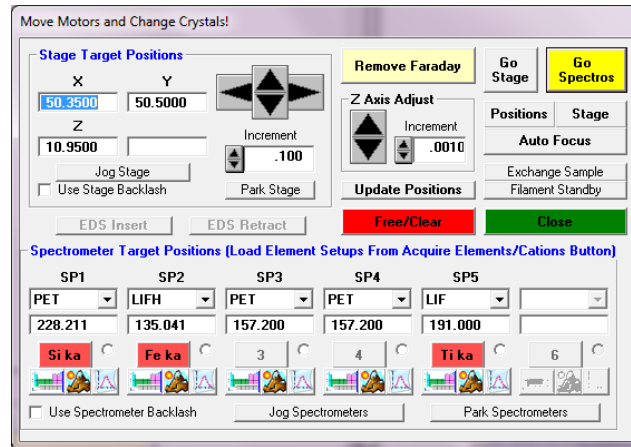
- Create a blank sample (just click OK).
- Or select previously saved individual element setups from the SETUP.MDB element setup database (previously saved from the 'Analyze!' window, 'Add To Setups' button) using the 'Load Element Setups' button.
- Or select a previously saved sample setup from within the current probe run (not available until a sample setup has been saved from the 'Analyze!' window, 'Save Setups' button) using the 'Load Sample Setup' button.
- Or load a sample setup from a previous probe run using the 'Load File Setup' button.



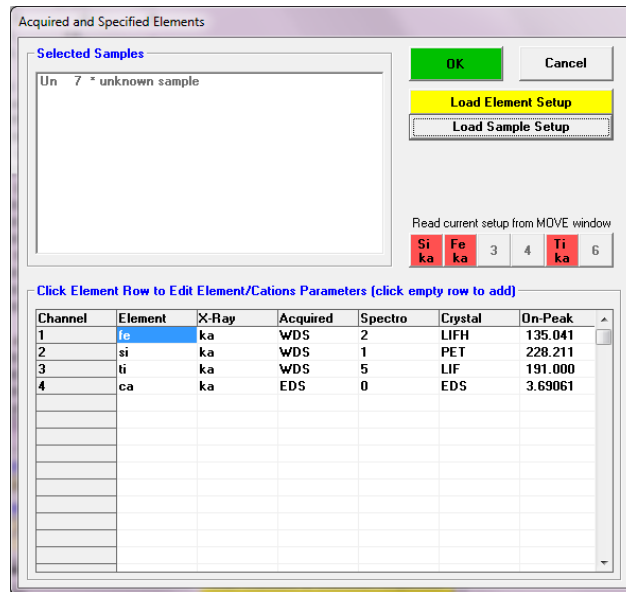
8. If creating a blank sample, one may then use the 'Move' window to select appropriate spectrometers, crystals, and also elements and x-ray lines to move to

using the drop down crystal lists and also the colored periodic table buttons. This would be the case when creating a new run “from scratch”.

Once the first N elements are selected, click the ‘Go Spectros’ button to move the spectrometers to the nominal peak positions for the selected elements. The program will move spectrometers, flipping any crystals that are necessary.

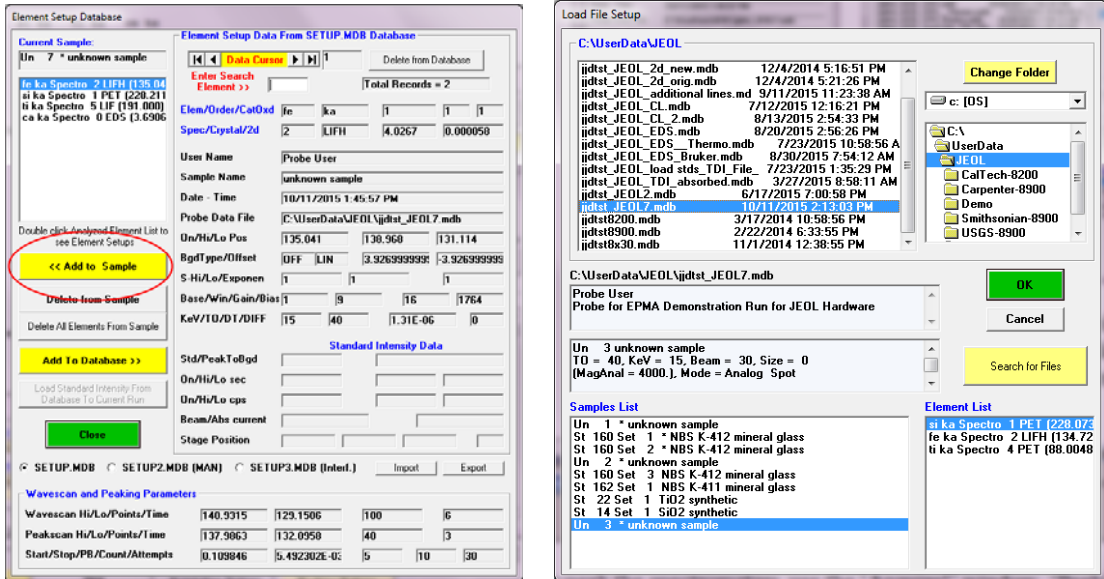


At this point one could use the ‘Peaking’ and ‘PHA’ buttons (see graphic buttons next to the tiny periodic table buttons) in the ‘Move’ window to manually peak the spectrometers (on appropriate standards), but it is probably better to immediately click the ‘Acquire!’ window, ‘Elements/Cations’ button and read in the nominal spectrometer element setups from the Move window using the colored element/x-ray line buttons as shown below.

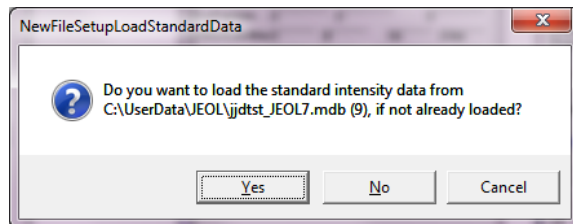


Repeat step 8 for additional elements on the various spectrometers. Later one can use the manual or automated peaking and PHA acquisition from the ‘Acquire!’ or ‘Automate!’ windows to optimize the spectrometer Bragg angle and PHA settings.

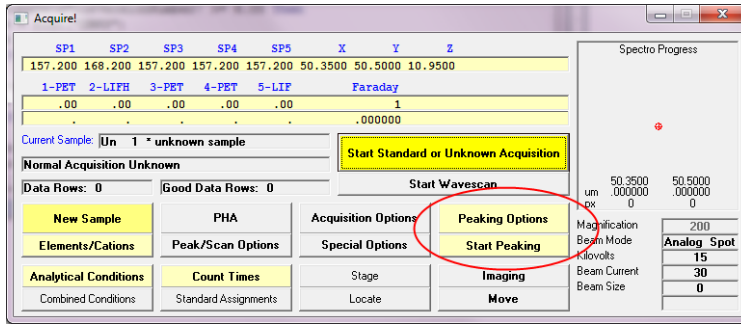
9. However, if the ‘Acquire!’ window, ‘New Sample’ button, ‘Load Element Setups’ or ‘Load File Setup’ buttons were utilized in step 7 above, then the user has already loaded previously saved element or sample setups to obtain optimized spectrometer settings (though it might still be a good idea to re-peak the spectrometers and check the PHA settings as described in the following steps).



Note that if you load a file setup from a previous probe run, the program will ask you if you want to load the standard intensities from the previous run. If the standardization was recently acquired it might be ok to use, though usually one should re-acquire the standards to ensure maximum accuracy.

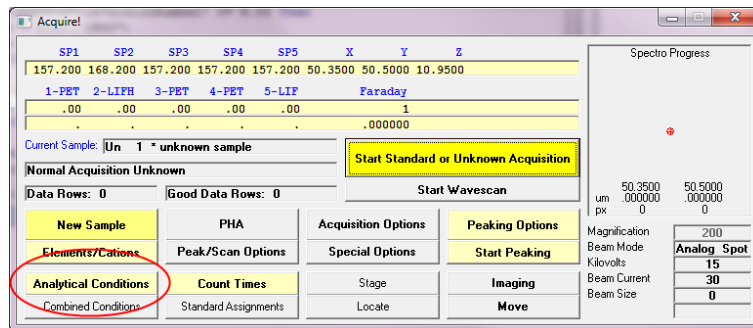


10. To manually peak the spectrometers, use the ‘Acquire!’ window, ‘Peaking Options’ and ‘Start Peaking’ buttons (after manually locating an appropriate standard for peaking for each element or set of elements). See “Manually Peaking Using the Acquire! Window” in the Getting Started manual for more details.

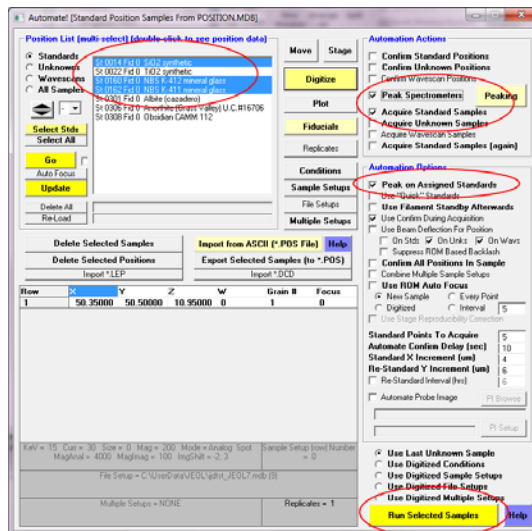


For automated peaking use the ‘Automate!’ window, ‘Peaking’ button to select the elements for peaking (be sure the check the ‘Peak Spectrometers’ checkbox), and then select the standards to peak in the ‘Automate!’ window, ‘Position List’ and click the ‘Run Selected Samples’ button to start the automated peaking.

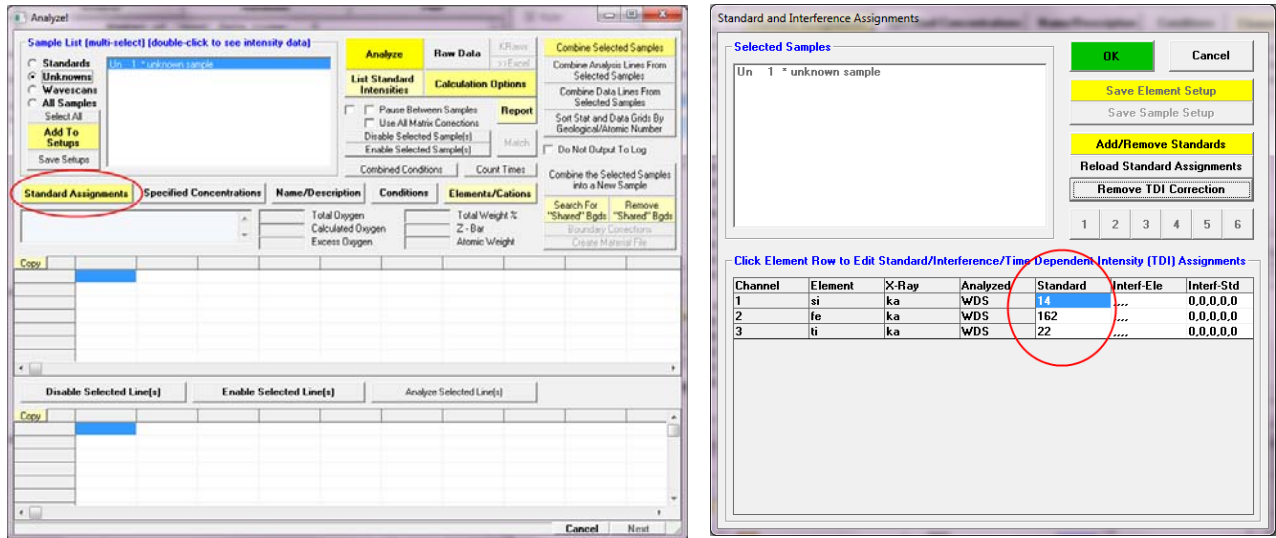
But before starting the automated peaking, this might be a good time to check that the instrument conditions and beam are properly set. You can use the ‘Acquire!’ window, ‘Analytical Conditions’ button to set those parameters.



11. It might be also be a good idea to check the ‘Automate!’ window, ‘Confirm Standard Positions’ checkbox.



12. If the 'Peak On Assigned Standards' checkbox is checked, be sure to assign the elements to specific standards using the 'Analyze!' window, 'Standard Assignments' button so that the program only attempts a peak center on the specified primary standard.

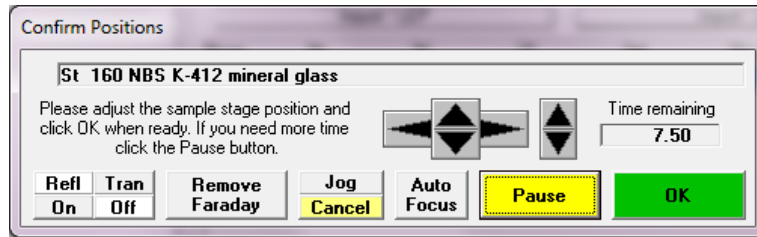


13. Note that a PHA acquisition can be manually or automatically acquired before or after the peaking procedure (normally the PHA acquisition is performed after the peak center).



14. When the 'Automate!' window, 'Run Selected Samples' button is clicked, the program will move automatically to each selected standard and perform the specified

peaking and PHA acquisitions. During this time the program will allow you to pause to confirm (and refocus) the location of each standard on the standard block (the position adjustments will be automatically remembered for next time).



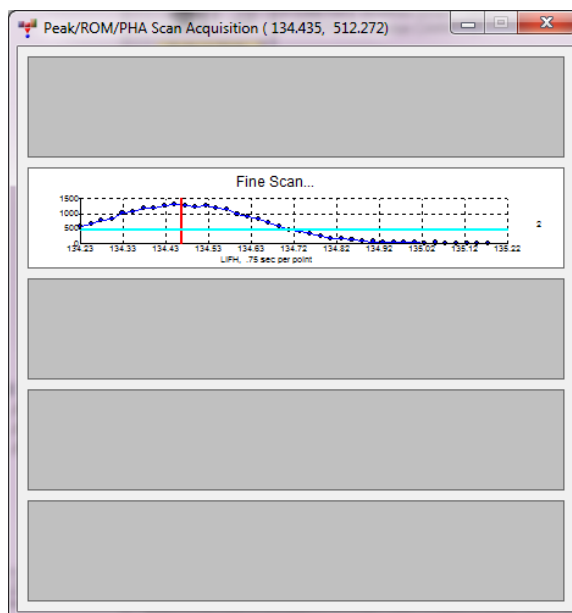
Information about the spectrometer peak intensities will be located in the Probewin Log window. If the peak operation is successful the program will indicate “Yes” under the “peaked” column. A “No” without an asterisk means the spectrometer was not specified or did not peak properly (the asterisk means no peak attempt data yet).

ROM Parabolic Peak Center Results:

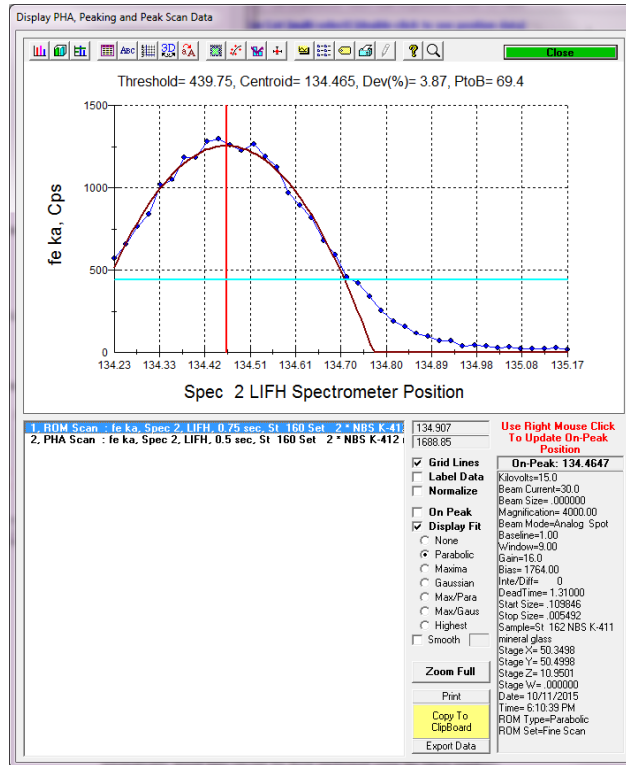
Element	Spectr	Peaked	StartPk	StopPk	Std	Offset	StartI	StopI
ti	ka 1	PET Yes	88.4240	88.4940	522	-.49	1605.5	1572.4
v	ka 2	PETH Yes	79.6966	79.6581	523	.508	2766.4	2737.4
cr	ka 3	LIFH *No	.000000	.000000	524	.071	.0	.0
al	ka 4	TAP Yes	90.9685	91.3303	513	-.43	1717.0	1712.3
fe	ka 5	LiF *No	.000000	.000000	526	.445	.0	.0

The “Offset” is the offset from the theoretical peak position in spectrometer units. Generally the found peak should be within a few % of the calculated peak position or something may be wrong.

Once the spectrometers are all peaked properly and the PHA scans look good as shown here, one may proceed to specify the acquisition times and acquisition order for each element.



15. Note that once the peaking and PHA acquisitions are completed the results can be reviewed from the 'Run' | 'Display, Fit and Export Spectrometer Peaking and PHA Scans' menu.



Note that all spectrometer peaking and PHA acquisitions (PHA, Bias and Gain scans) are automatically stored here (except for those performed using the Move window).

You are now ready to acquire wavescan and/or standard intensities.

Wavescan Acquisition To Check For Off-Peak Interferences

1. At this time it might be appropriate to acquire a wavescan sample to determine if there are any off-peak interferences that need to be dealt with. Usually it is sufficient to acquire a manual wavescan on a sample or standard with a composition similar to your unknown although that is not strictly necessary, since any composition will serve to simply display the KLM markers.
2. First go to an appropriate sample for the wavescan acquisition, then click the 'Acquire!' window, 'New Sample' button and select the 'Wavescan' option. Enter a name such as "check bgds" and click OK.

New Sample

New Sample Type

Standard

Unknown

Wavescan

Add/Remove Standards

OK **Cancel**

Load Element Setup **Help**

Load Sample Setup **Help**

Load File Setup **Help**

Load Multiple Setup **Help**

Note that a new standard sample element setup is based by default on the last unknown sample in the run. To change the analyzed elements in a run, either click one of the Load Setup buttons above or first create a new unknown sample and then make any necessary changes to the element setup.

Load Wavescan From Another Probe Run

New Sample Name

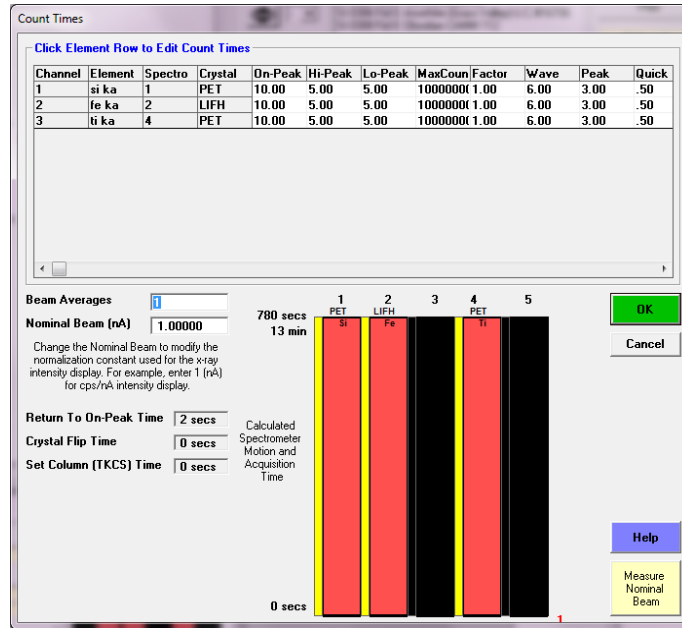
wavescan sample

New Sample Description Add <cr>

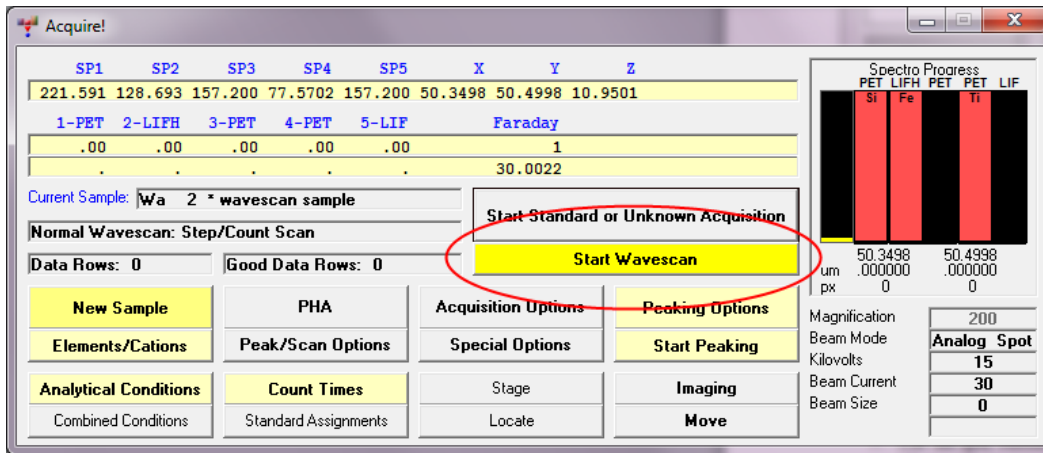
To add standards to the standard list below, cancel this dialog, then click the Standard | Add Standards to Run menu item from the main menu.

14 SiO2 synthetic
22 TiO2 synthetic
160 NBS K-412 mineral glass
162 NBS K-411 mineral glass
301 Albite (cazadero)
306 Anorthite (Grass Valley) U.C. #16706
308 Obsidian CMM 112

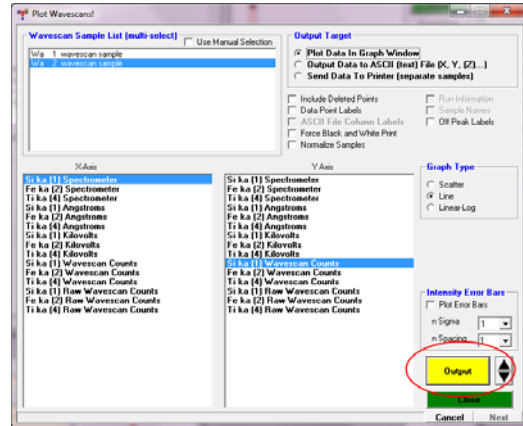
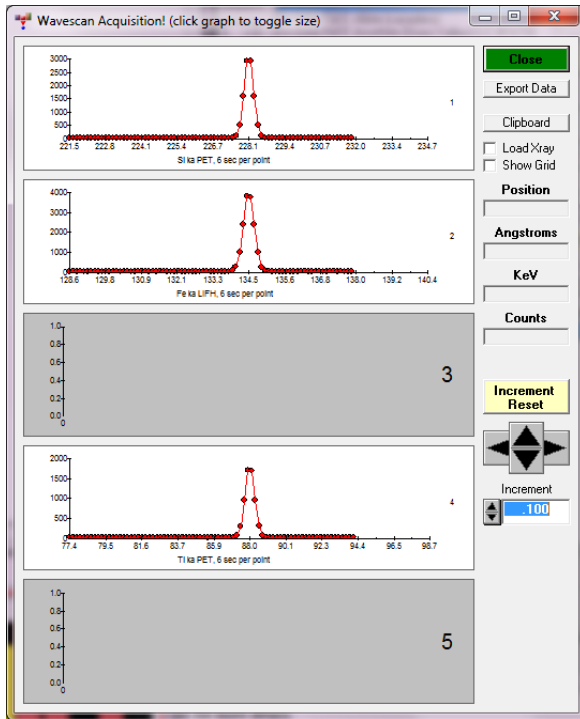
3. Then check the 'Acquire!' window, 'Count Times' dialog to make sure that the count times for the wavescan elements are reasonable, then click OK.



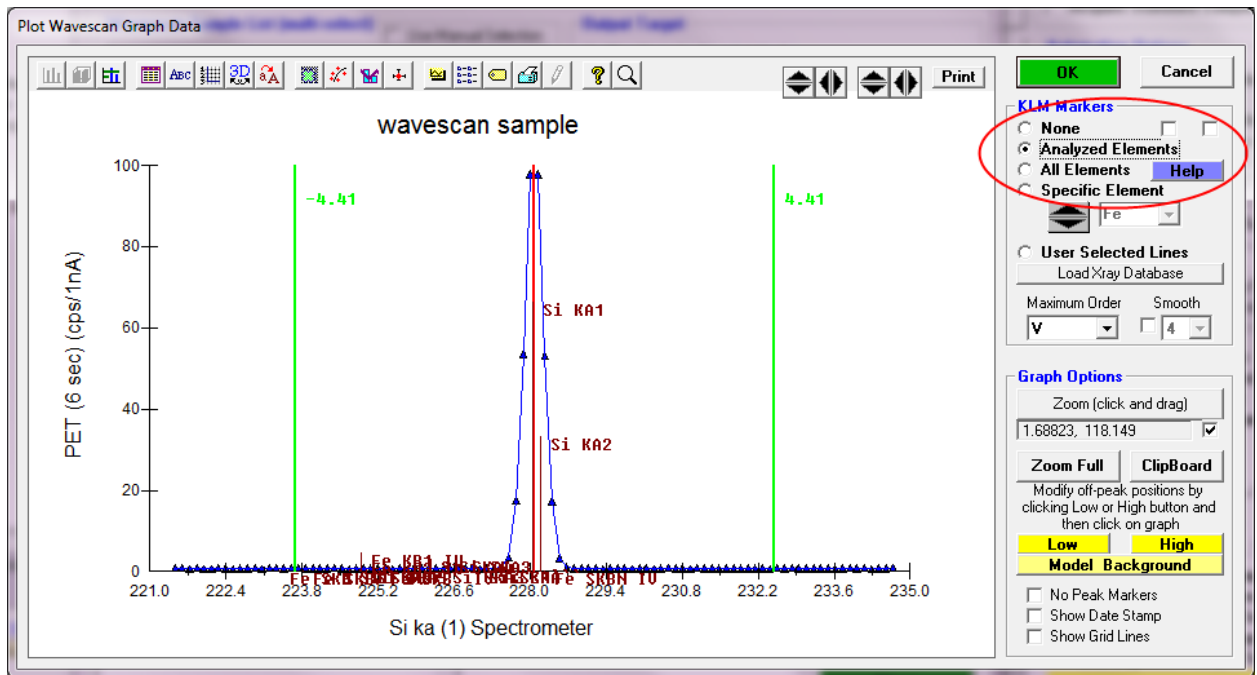
- When you are ready to acquire the wavescan sample, simply click the 'Acquire!' window, 'Start Wavescan' button and the program will automatically acquire an intensity scan for each element automatically.



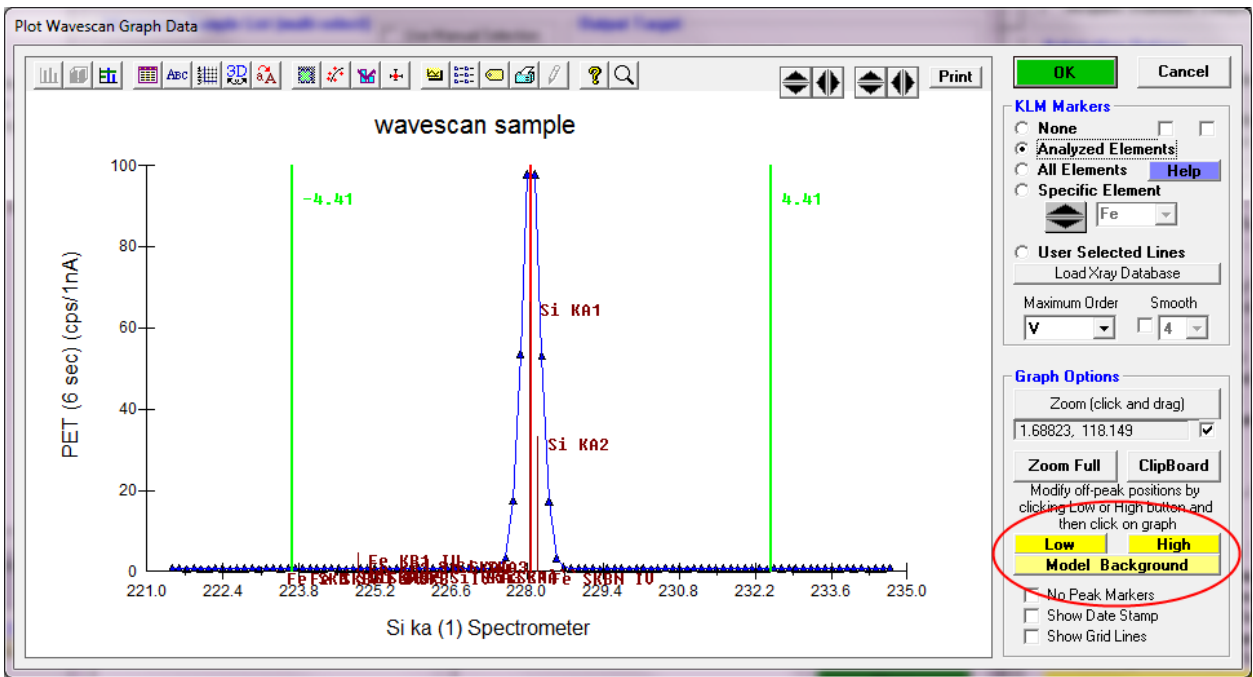
- Once the wavescan acquisition has been completed, use the 'Plot!' window to display the wavescan intensities. See "Off-Peak Adjustments From the Plot! Window" in the Getting Started manual for more details.



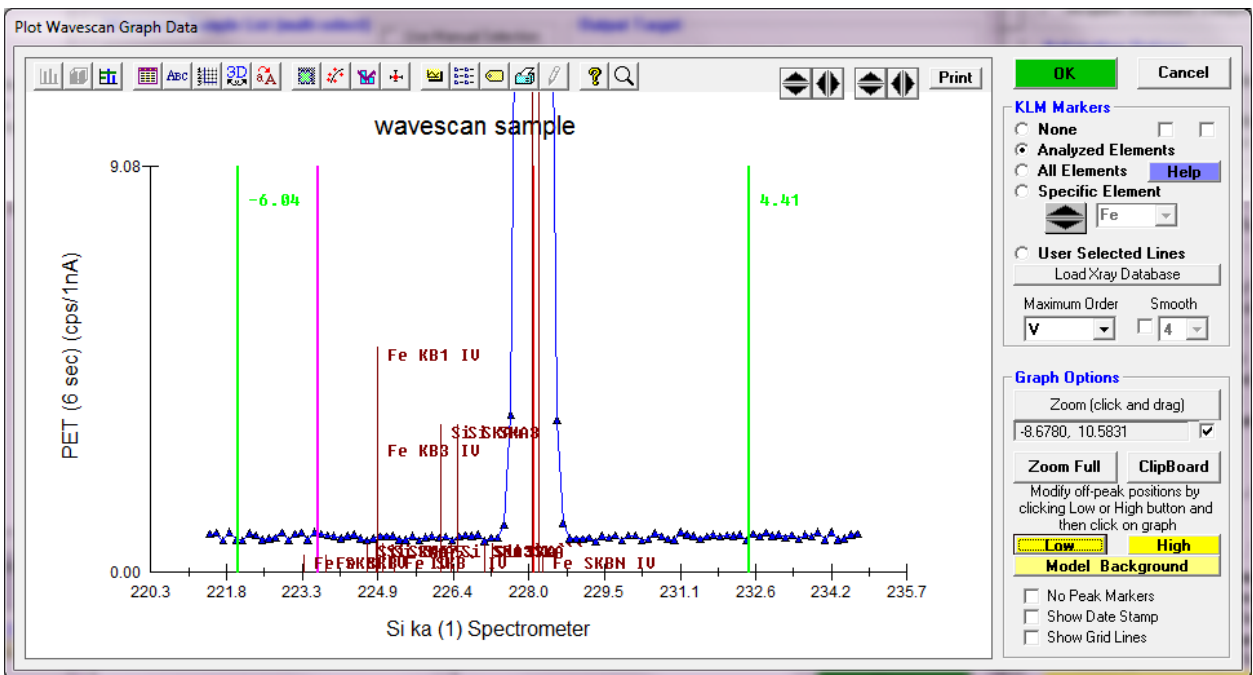
- Use the spin button to select the next spectrometer and element pair and click the 'Output' button to display the wavescan and the current off-peak positions (in green). The x-ray KLM markers can be displayed by selecting the 'Analyzed Elements' option.



Then use the mouse to click and drag the preferred zoom area to see the background better.



- Then simply adjust the off-peak positions by clicking the 'Low' and/or 'High' buttons and clicking on the graph where they should be re-located.



- When you click OK, the new off-peak positions will be utilized automatically in the next unknown or standard acquisition. Repeat steps 7 to 9 for each element in the wavescan.

Acquisition of Standard Intensities

1. In the 'Automate!' window, click on the 'Standards' option and click the 'Select Stds' button to select the current standards in the run. You have previously confirmed standard positions during peaking, but you can check that option again if you would like.
2. Check the 'Acquire Standard Samples' checkbox and then click on the 'Run Selected Samples' button. See "Loading Standard Position Files" in the Getting Started manual for more details.

The screenshot shows the 'Automate!' software window with the following components:

- Position List (multi-select):** A list of standards including 'St 0014 Fid 0 SiO2 synthetic', 'St 0022 Fid 0 TiO2 synthetic', 'St 0160 Fid 0 NBS K-412 mineral glass', 'St 0162 Fid 0 NBS K-411 mineral glass', 'St 0301 Fid 0 Albite (cazadero)', 'St 0306 Fid 0 Anorthite (Grass Valley) U.C.#16706', and 'St 0308 Fid 0 Obsidian CAMM 112'. The 'Standards' radio button is selected.
- Automation Actions:** A panel with checkboxes for 'Confirm Standard Positions', 'Confirm Unknown Positions', 'Confirm Wavescan Positions', 'Peak Spectrometers', 'Acquire Standard Samples' (checked), 'Acquire Unknown Samples', 'Acquire Wavescan Samples', and 'Acquire Standard Samples (again)'. A 'Peaking' button is also present.
- Automation Options:** A panel with checkboxes for 'Peak on Assigned Standards', 'Use "Quick" Standards', 'Use Filament Standby Afterwards', 'Use Confirm During Acquisition', 'Use Beam Deflection For Position', 'Confirm All Positions In Sample', 'Combine Multiple Sample Setups', 'Use ROM Auto Focus', 'Use Stage Reproducibility Correction', 'Standard Points To Acquire' (5), 'Automate Confirm Delay (sec)' (10), 'Standard X Increment (um)' (4), 'Re-Standard Y Increment (um)' (6), 'Re-Standard Interval (hrs)' (6), and 'Automate Probe Image'.
- Run Selected Samples:** A yellow button at the bottom right of the interface.

Row	X	Y	Z	W	Grain #	Focus
1	50.34978	50.49976	10.95009	0	1	0

KeV = 15 Curr = 30 Size = 0 Mag = 400 Mode = Analog Spot
MagAnal = 4000 MagImag = 400 ImgShift = -2.3

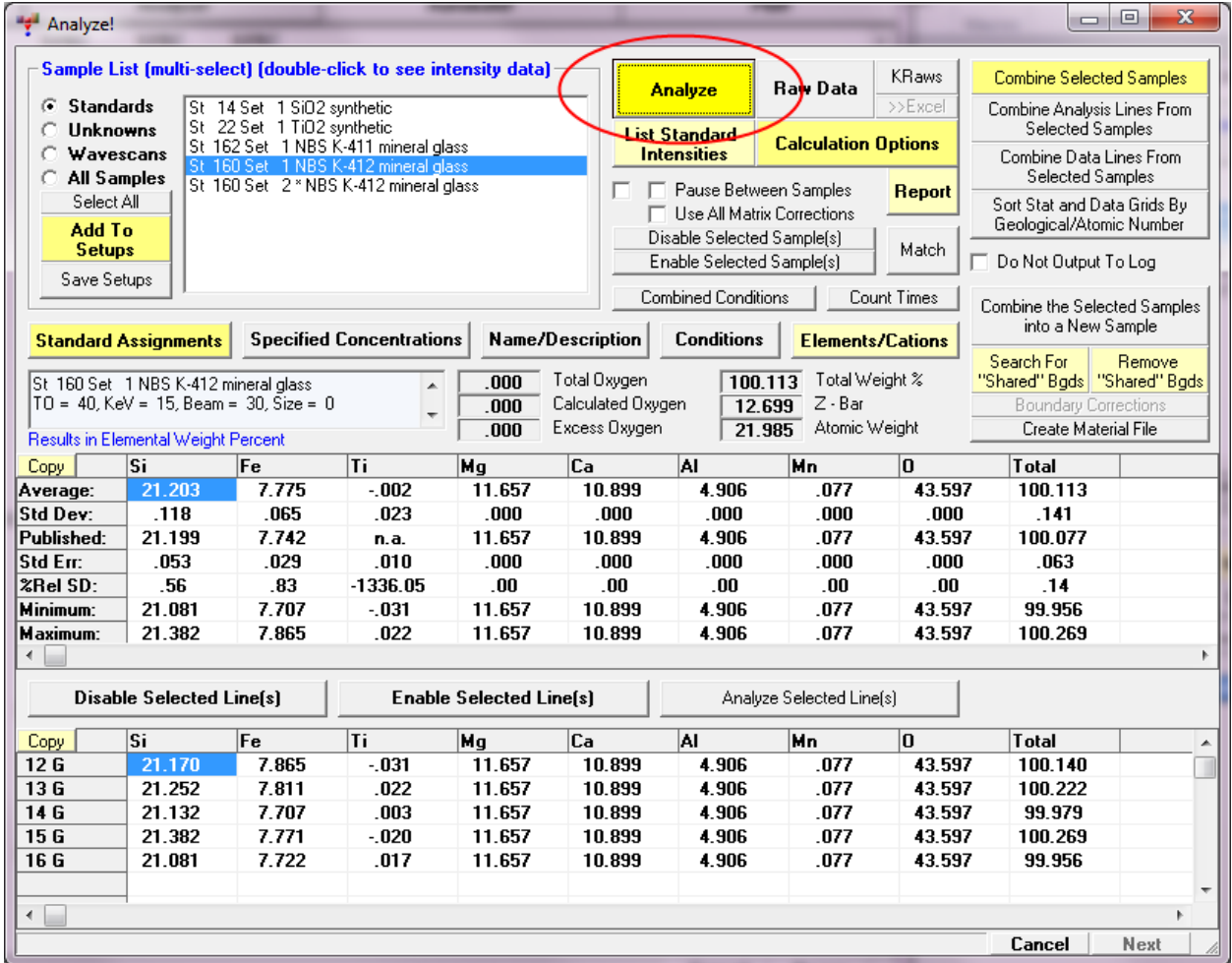
Sample Setup (row) Number = 0

File Setup = NONE

Multiple Setups = NONE

Replicates = 1

- Once primary standards have been run, you can check that they agree with each other by running secondary standard and checking that it analyzes correctly from the ‘Analyze!’ window by selecting the secondary standard and clicking the ‘Analyze’ button.

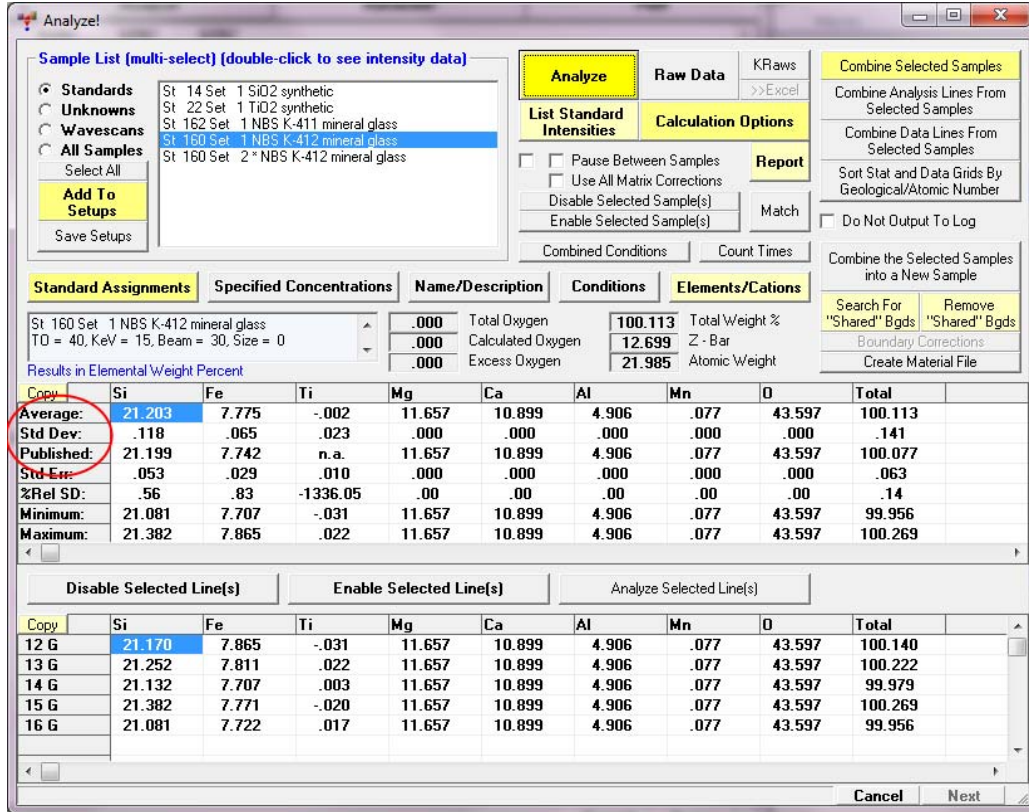


See “Analyze Standard Data” in the Getting Started manual for more details.

In this case a good secondary standard for an Al-Ti alloy might be a NIST standard in which the user can compare the measured ‘Average’ results with the ‘Published’ results from the Standard.MDB standard database.

In the Log window the analysis is printed out with the Published values and the relative percent error (“% VAR”) so the user can quickly compare the expected value with the actual measured value. Note that if the standard being analyzed is the assigned primary standard for that element, then the “% VAR” will be close to zero (but not exactly due to the presence of other elements not assigned as the primary standard for that element).

However elements that are not using the standard as the assigned primary standard (that is a secondary standard) will provide a measurement of the relative accuracy of the instrument assuming that the secondary is close to the composition of the unknown samples to be analyzed.



In the log window the output is similar but more detailed. Here is a NIST Al alloy analyzed using pure metals as elements as primary standards for all elements:

ELEM:	Ti	V	Cr	Al	Fe	SUM
29	.055	.021	.171	89.932	.182	100.061
30	.043	-.030	.206	89.425	.235	99.579
31	.025	-.002	.246	89.452	.190	99.611
32	.058	.004	.198	89.445	.233	99.638
AVER:	.045	-.002	.205	89.563	.210	99.722
SDEV:	.015	.021	.031	.246	.028	.227
SERR:	.007	.011	.015	.123	.014	
%RSD:	33.0	-1153.6	15.0	.3	13.4	
PUBL:	.040	n.a.	.173	89.716	.205	.000
%VAR:	13.09	.00	18.64	-.17	2.41	
DIFF:	.005	.000	.032	-.153	.005	
STDS:	522	523	524	513	526	

Note the “% VAR” and “DIFF” lines which show the relative % error from the published composition and the algebraic difference in absolute weight %.

Using the 'Analyze!' window, 'Data' button it is also useful to check that the "SDEV" or measured standard deviation of the intensities are within 3 sigma of the predicted variance as shown in the line labeled "1SIG".

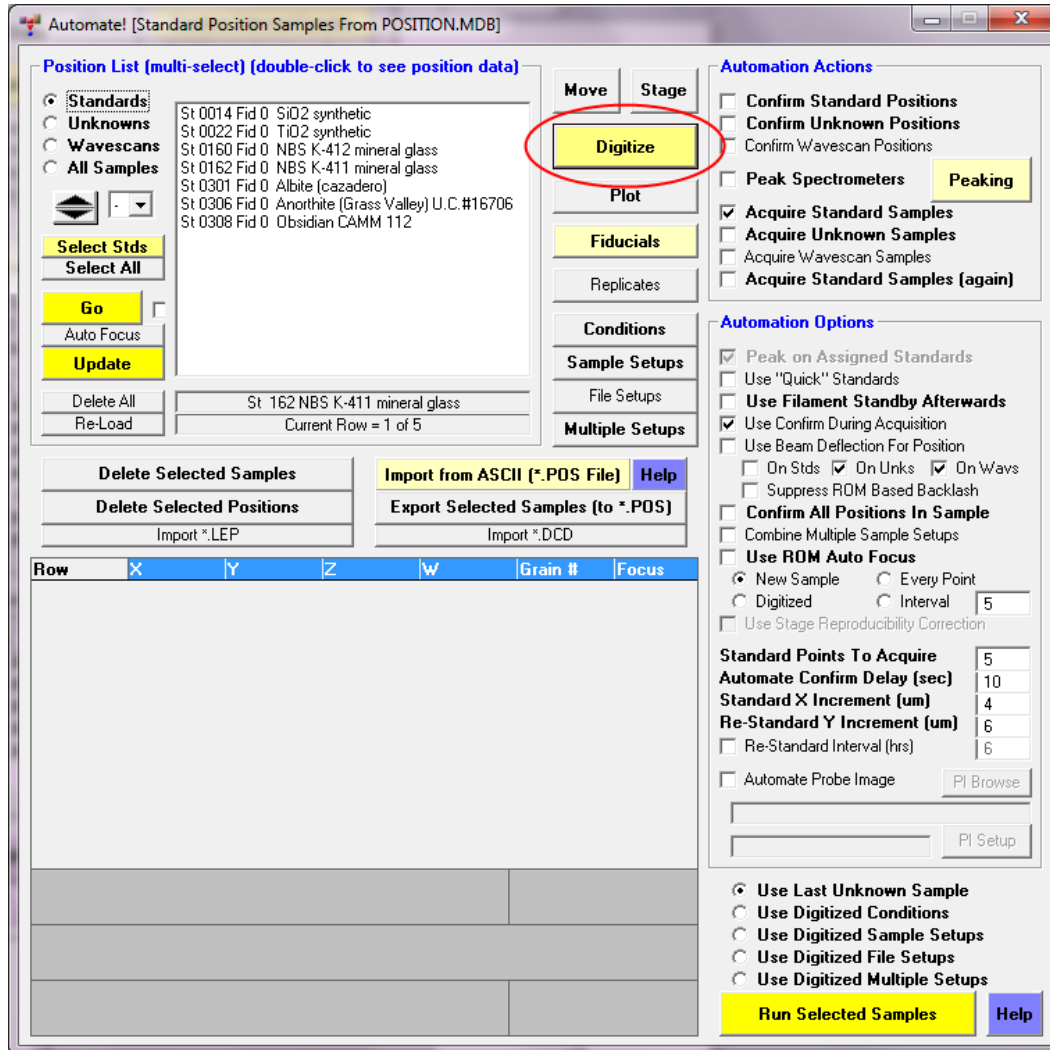
On-Peak (off-peak corrected) or MAN On-Peak X-ray Counts (cps/lnA) (and Faraday Current):

ELEM:	ti ka	v ka	cr ka	al ka	fe ka	BEAM
BGD:	OFF	OFF	OFF	OFF	OFF	
SPEC:	1	2	3	4	5	
CRYST:	PET	PETH	LIFH	TAP	LiF	
ORDER:	1	1	1	1	1	
29G	.16	.06	.51	267.70	.54	29.982
30G	.13	-.09	.61	265.97	.70	29.991
31G	.07	-.01	.73	266.07	.57	30.015
32G	.17	.01	.59	266.01	.70	30.016
AVER:	.13	-.01	.61	266.44	.63	30.001
SDEV:	.04	.06	.09	.84	.08	.017
1SIG:	.06	.06	.08	.94	.07	
SIGR:	.78	.98	1.13	.90	1.19	
SERR:	.02	.03	.05	.42	.04	
%RSD:	33.0	-1153.5	15.0	.3	13.4	

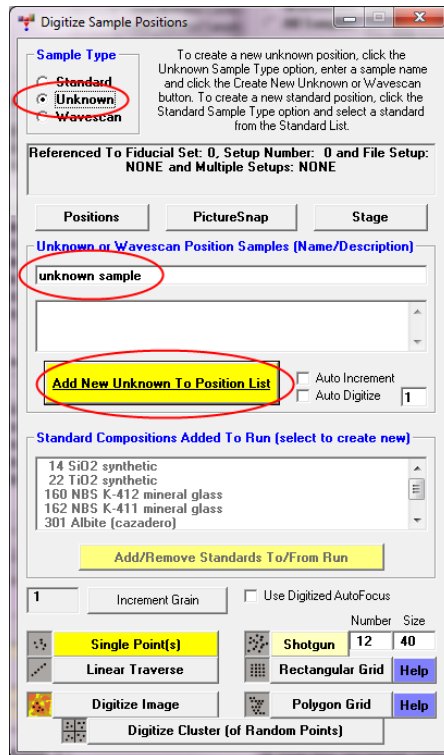
Variances larger than 3 sigma may indicate sample inhomogeneity or instrument instability.

Digitizing Position Samples

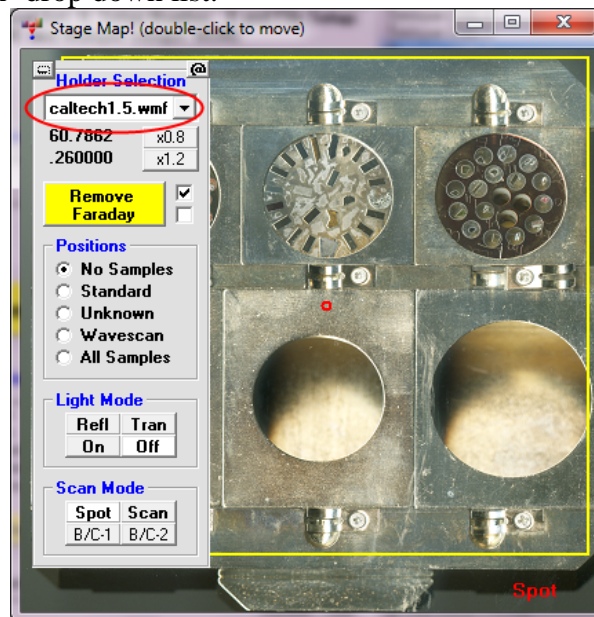
1. From the 'Automate!' window click on the 'Digitize' button. You will now be able to digitize stage positions of samples you wish to acquire intensity data for.



2. In the 'Digitize Sample Positions' window choose the 'Unknown' option and enter a sample name in the text field (a sample description is optional) and click the 'Add New Unknown or Wavescan To Position List' to add an empty position sample to the 'Automate!' window position sample list.

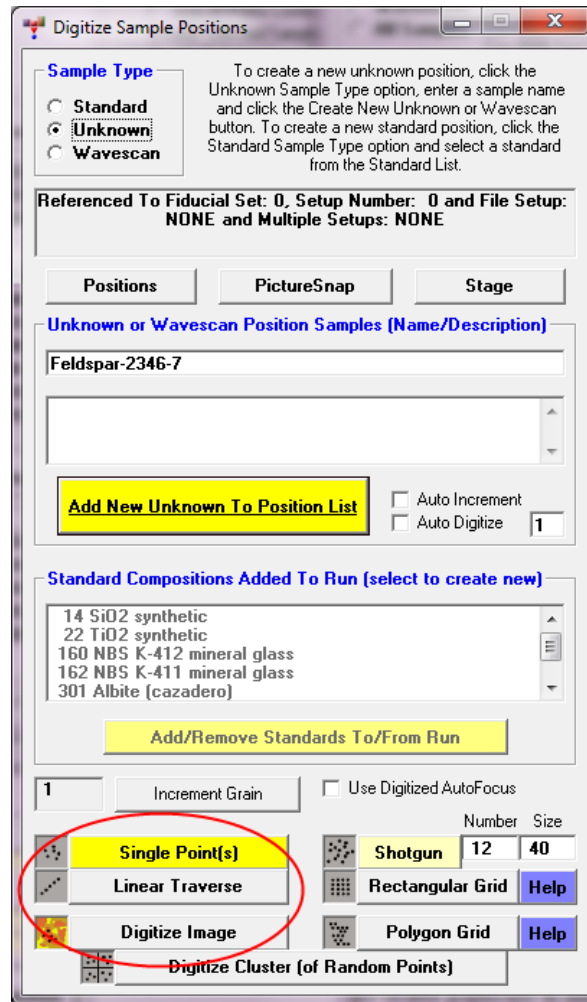


- Then click on the 'Stage' button to bring up the 'Stage Map' window to navigate to the sample coordinates. Select the appropriate stage map image or drawing from the 'Holder Selection' drop down list.



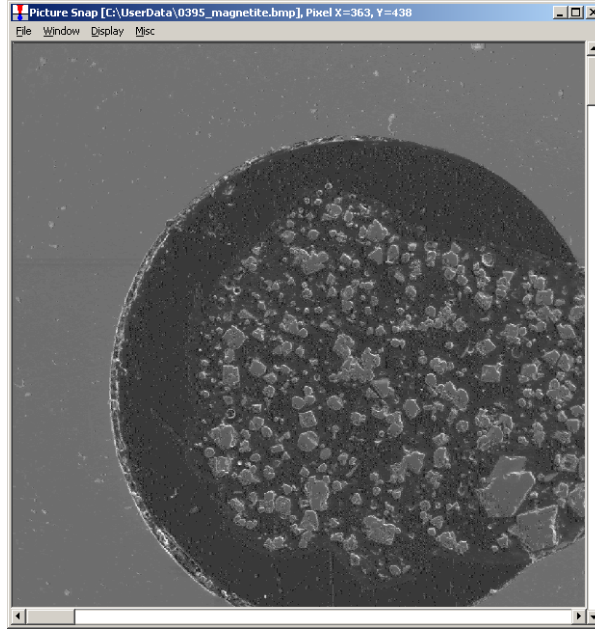
- In the 'Stage Map' window, double-click on where you think your sample is. Use the instrument joystick or stage fine adjustment controls and locate your first acquisition position. Once you find a good spot, focus on the sample surface using reflected light, using the instrument Z stage position adjustment.

- In the 'Digitize Sample Positions' window, click on 'Single Point(s)' or 'Linear Traverse' or whatever mode you want to digitize coordinate data and click OK once you have established the coordinates for that acquisition. You may create any number of position samples, with any sample name and digitize any number of points in each position sample.

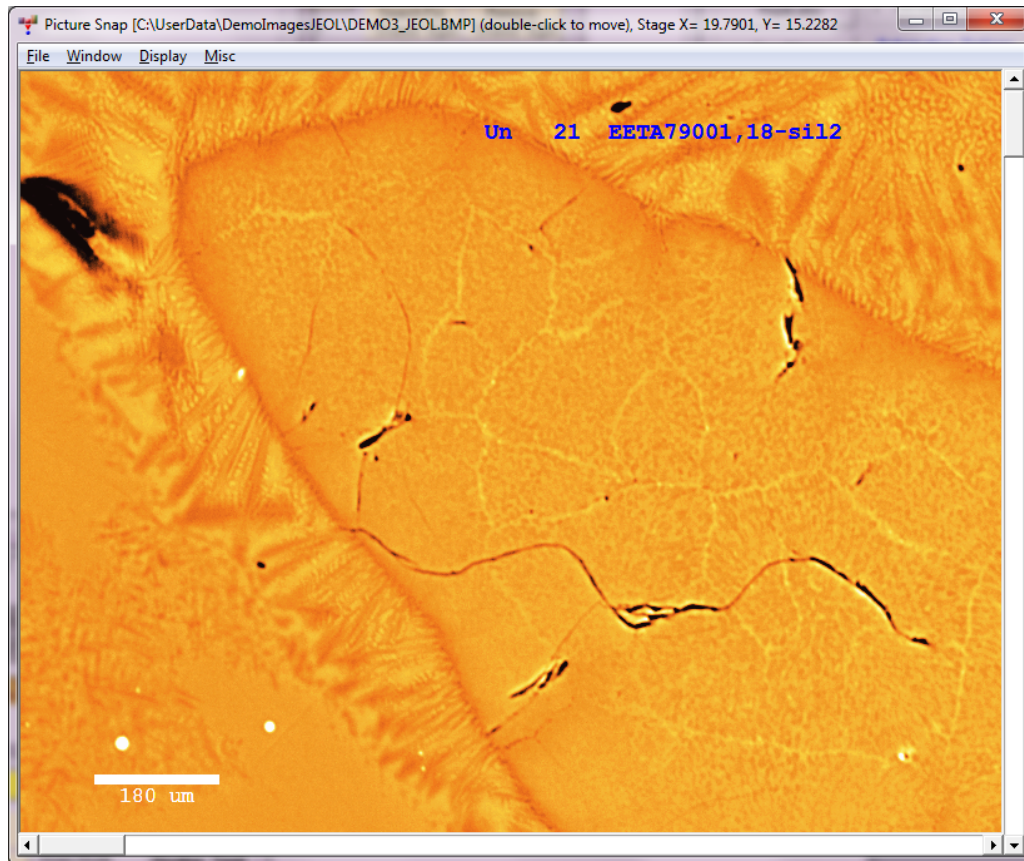


- Repeat steps 4 and 5 until all of your unknown samples have been digitized.
- In the 'Stage Map' window, choose to show locations of the sample by selecting from the 'Positions' options, for example 'Unknowns' to double check where your coordinate positions are located graphically in instrument stage coordinates.

Tip: **Picture Snap!** is a great tool included in Probe for EPMA. It simply requires an image file (jpeg, bmp, or gif) of your sample mount from any source (slide scanner, flat bed scanner or electron image from any instrument). Access Picture Snap! from the Probewin log window, 'Run' menu by selecting the 'Display Picture Snap!' menu.



Load your image file and then choose the 'Window' | 'Calibrate' menu. In the 'Picture Snap Calibration' window, select either the 'Two Points' option (for orthogonal rectangular samples) or the 'Three Points' option (for round samples subject to rotation).

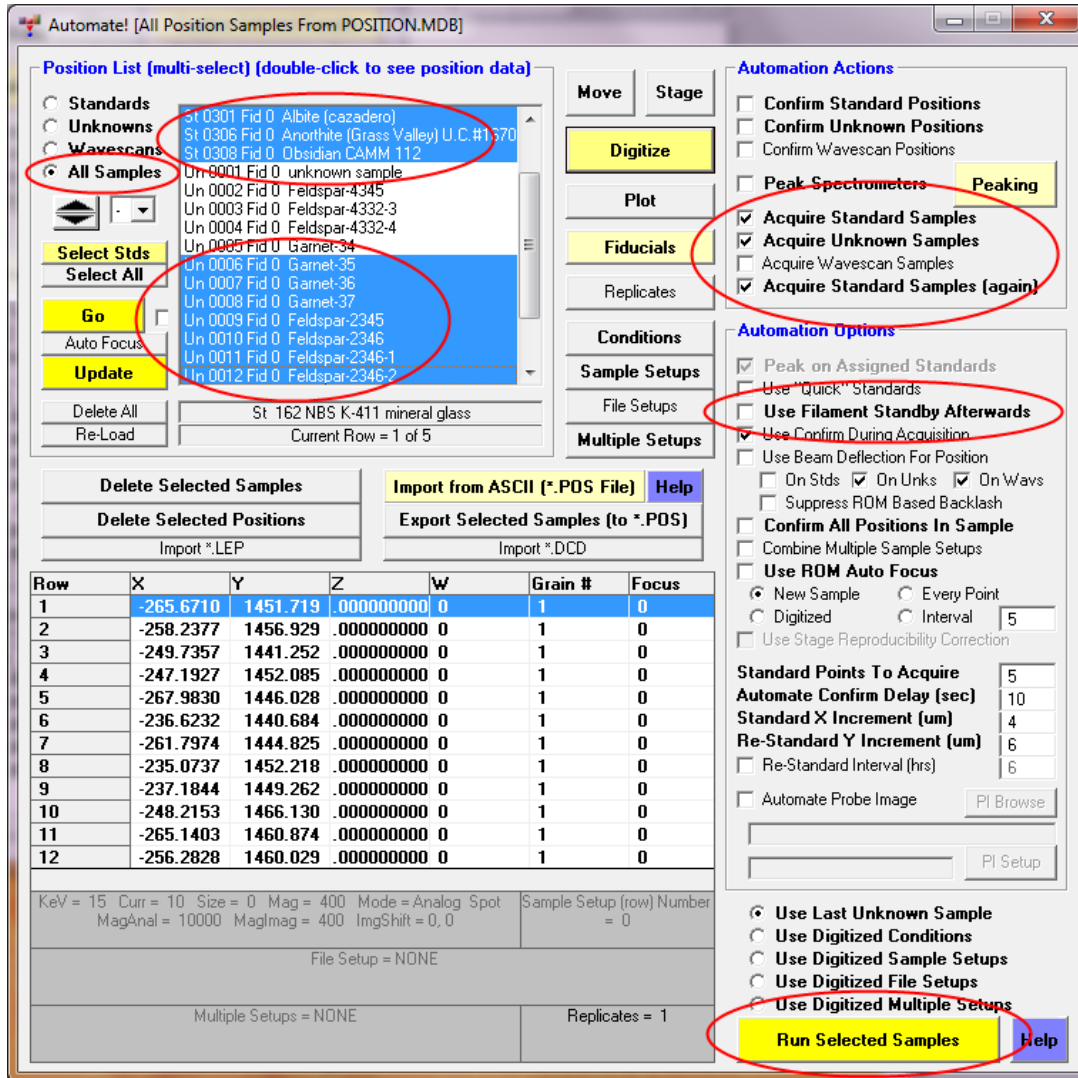


Use the stage controls and navigate to 2 or 3 points that you can easily recognize on the image and also find the stage coordinates of in the instrument imaging system (visible light or electron imaging). Click 'Read Current Stage Coordinate' to read the stage position of the feature. Generally choose 2 points that are diagonally opposed on the sample or if using three points, choose points that describe a triangle over most of the image area for best accuracy. Then also click the 'Pick Pixel Coordinate On Picture' and click the corresponding spot on the picture for the image coordinates for each calibration position.

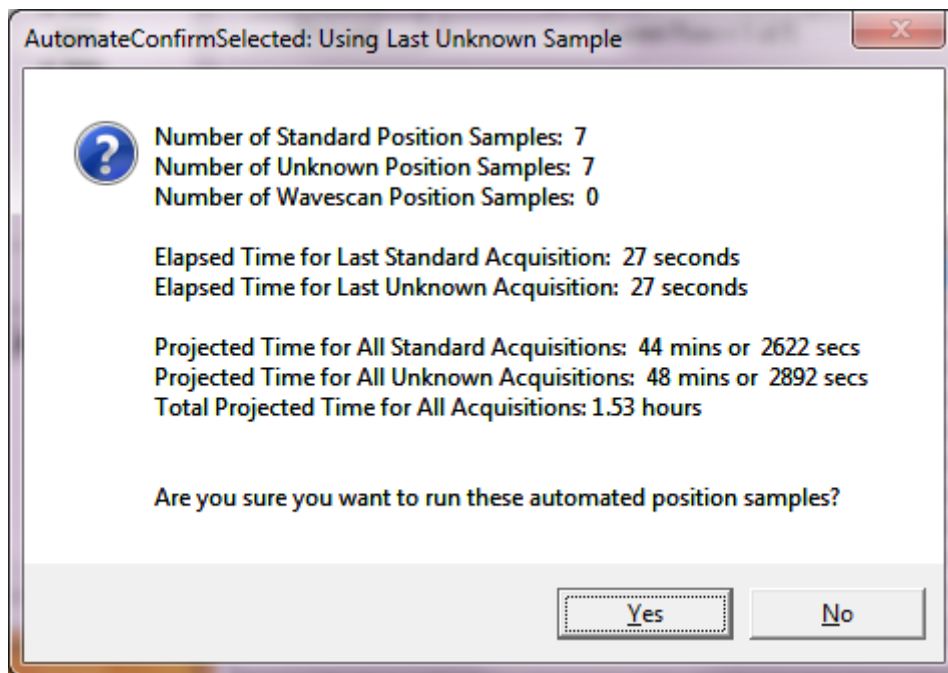
When finished choosing reference points click the 'Calibrate Picture' button. Now you should be able to navigate anywhere on your image by double-clicking the feature in the image. Other menus allow you to display the position sample coordinates as they are digitized.

Automated Sample Acquisition

1. In the 'Automate!' window choose the 'All Samples' option. Then click the 'Select Stds' button and establish that you picked the correct standards for your samples. Then holding down the <ctrl> button select the unknowns you also wish to acquire intensities for.

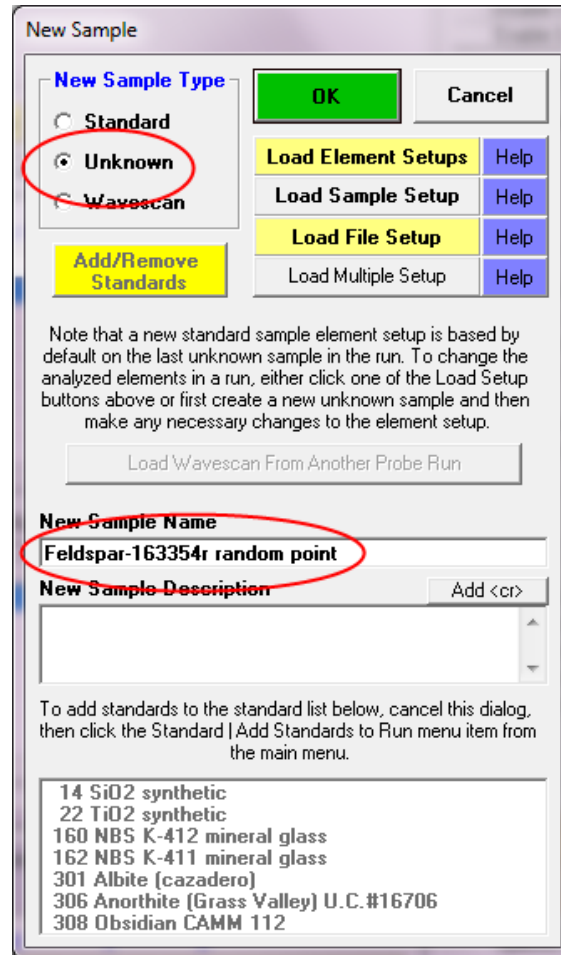


2. Now click the following checkboxes: 'Confirm Standard Positions', 'Acquire Standard Samples' (optional since you may have just done this), 'Acquire Unknown Samples', 'Acquire Standards Again', and optionally the 'Use Filament Standby Mode Afterwards' and 'Use Confirm During Acquisition'.
3. Double-check everything and click the 'Run Selected Samples' button. This will bring up a confirmation dialog with the total time estimate. Check carefully and click "Yes" and the automated run will start. The standard positions will be confirmed again. Make sure they are still in focus.



Manual Acquisition

1. You may also simply acquire sample data manually using the ‘Acquire!’ window. Simply click the ‘Acquire!’ window, ‘New Sample’ button, click the ‘Unknown’ option (or click the ‘Standard’ option and select a standard from the list for running a standard manually) and enter a sample name. Note that wavescan samples can be acquired from this same window and should be used to check for off-peak interferences.



2. Then click the ‘Acquire!’ window, ‘Start Standard Or Unknown Acquisition’ button to start the manual data acquisition. The elapsed time meter will display the acquisition progress. When finished you should acquire additional replicate points until the average and standard deviations look reasonable. See “Manual Count Acquisition Using the Acquire! Window” in the Getting Started manual for more details.

The screenshot shows the 'Acquire!' software interface. At the top, there is a table with columns SP1, SP2, SP3, SP4, SP5, X, Y, and Z. Below this is another table with columns Si-PET, Fe-LIFH, 3-PET, Ti-PET, 5-LIF, and Absorbed. The 'Current Sample' field is set to 'Un 2 * Feldspar-163354r random point'. A yellow button labeled 'Start Standard or Unknown Acquisition' is visible. Below this are buttons for 'New Sample', 'PHA', 'Acquisition Options', 'Peaking Options', 'Elements/Cations', 'Peak/Scan Options', 'Special Options', 'Start Peaking', 'Analytical Conditions', 'Count Times', 'Stage', 'Imaging', 'Combined Conditions', 'Standard Assignments', 'Locate', and 'Move'. On the right side, there is a 'Spectro Progress' window with a bar chart showing peaks for Si, Fe, and Ti. Below the chart are numerical values for 'um' and 'px' for Si and Fe. At the bottom right, there are settings for Magnification (4000), Beam Mode (Analog Spot), Kilovolts (15), Beam Current (30), and Beam Size (0).

SP1	SP2	SP3	SP4	SP5	X	Y	Z
228.074	134.465	157.200	88.0044	157.200	50.3498	50.4998	10.9501

Si-PET	Fe-LIFH	3-PET	Ti-PET	5-LIF	Absorbed
3.83	3.80	.00	3.77	.00	1
1085.	14361.	.	21925.	.	.000000

Current Sample: Un 2 * Feldspar-163354r random point

Normal Acquisition Unknown

Data Rows: 0 Good Data Rows: 0

Magnification: 4000
 Beam Mode: Analog Spot
 Kilovolts: 15
 Beam Current: 30
 Beam Size: 0

- Click the 'New Sample' button again to name a different unknown sample for manual acquisition. Note that your samples may be specified any way (up to 100 points per sample) that you prefer, although usually all data points in a single samples should be related spatially or compositionally since an average and standard deviation will be calculated for each sample.

Analyzing Your Data

To obtain your composition results simply use the ‘Analyze!’ window and select the samples to analyze and click the ‘Analyze’ button.

The screenshot shows the 'Analyze!' software interface. The 'Sample List' on the left contains two entries: 'Un 1 * unknown sample' and 'Un 2 Feldspar-163354r random point'. The 'Analyze' button is highlighted with a red circle. The 'Calculation Options' section is also highlighted with a red circle and contains several checkboxes: 'Pause Between Samples', 'Use All Matrix Corrections', 'Disable Selected Sample(s)', and 'Enable Selected Sample(s)'. The 'Report' button is also visible. Below the sample list, there are tabs for 'Standard Assignments', 'Specified Concentrations', 'Name/Description', 'Conditions', and 'Elements/Cations'. The 'Elements/Cations' tab is active, showing a table of elemental weight percentages for various elements (Si, Fe, Ti, Mg, Ca, Al, Mn, O) and a 'Total' column. The table includes rows for 'Average', 'Std Dev', 'Published', 'Std Err', '%Rel SD', 'Minimum', and 'Maximum'. At the bottom, there are buttons for 'Disable Selected Line(s)', 'Enable Selected Line(s)', and 'Analyze Selected Line(s)'. The 'Cancel' and 'Next' buttons are at the bottom right.

Copy	Si	Fe	Ti	Mg	Ca	Al	Mn	O	Total
Average:	21.203	7.775	-.002	11.657	10.899	4.906	.077	43.597	100.113
Std Dev:	.118	.065	.023	.000	.000	.000	.000	.000	.141
Published:	21.199	7.742	n.a.	11.657	10.899	4.906	.077	43.597	100.077
Std Err:	.053	.029	.010	.000	.000	.000	.000	.000	.063
%Rel SD:	.56	.83	-1336.05	.00	.00	.00	.00	.00	.14
Minimum:	21.081	7.707	-.031	11.657	10.899	4.906	.077	43.597	99.956
Maximum:	21.382	7.865	.022	11.657	10.899	4.906	.077	43.597	100.269

Use the ‘Calculation Options’ to add oxygen by stoichiometry, atomic percents, detection limits, etc. Use the ‘Elements/Cations’ button to add unanalyzed elements for calculation purposes (leave the x-ray line blank).

Calculation Options

Selected Samples

Un 2 Feldspar-163354r random point

OK Cancel

EDS Spectral Data And Calculations

Do Not Use EDS Element Data
 Use EDS Element Data [Help](#)
 EDS Quant Method

Integrated Intensity Data Options

Do Not Use Integrated Intensities
 Use Integrated Intensities

Sample Conductive Coating (need to explicitly turn on in Analytical | Analysis Options)

Element	Density	Thickness (Å)	Use Standard menu to specify standard coatings
c	2.1	200	<input checked="" type="checkbox"/> Use Unknown Conductive Coating Help

Calculations Options

Display Results As Oxides
 Calculate Atomic Percents
 Calculate Detection Limits and Sensitivity
 Calculate Projected Detection Limits
 Calculate Homogeneity Ranges
 Calculate Alternate Homogeneity Ranges
 Calculate Pearson's Linear Correlation Coefficients

Element By Difference (as elemental) : [Help](#)
 Formula By Difference (e.g. Li2B4O7):

Stoichiometry To Calculated Oxygen: Atoms Of To 1 Oxygen [Help](#)
 Stoichiometry To Another Element: Atoms Of To [Help](#)
 Hydrogen Stoichiometry To Excess Oxygen: H:O Ratio .00 (OH = 1, H2O = 2) [Help](#)

Calculate with Stoichiometric Oxygen
 Calculate as Elemental
 Calculate Chemical Age (U, Th, Pb, Y) [Help](#)
 [Help](#)

Formula and Mineral Calculations

Calculate Formula Based On Atoms Of Sum Add specified oxygen, etc. from the Elements/Cations button
 No Mineral End-Member Calculation
 Olivine Feldspar Pyroxene Garnet (Ca,Mg,Fe,Mn) Garnet (Al,Fe,Cr)
 Amphibole (Ague, Auto Normalization) Biotite (Brimhall and Ague, Halog Code)

Many more output options are available from the Probewin Log window, 'Output' menu and the 'Plot!' window. See "Output of Analyzed Data" in the Getting Started manual for more details.

Tips & Common Problems

1. Note that by acquiring intensity data for all the elements in each standard you can examine the complete analysis of each and see that you should be able to get close to zero concentrations on standards that do not contain the element of interest. This is very important for trace elements- that is: can you measure zero? If the concentration is significantly negative then it is likely that one or more off-peak positions is being interfered by a secondary x-ray peak.
2. Establish which spectrometers should be used for which elements. You will want to avoid crystal flipping within a single sample. Put in proper count times for what you are doing. Check that the count times are approximately balanced for all spectrometers to avoid a spectrometer sitting idle (you might as well be counting photons).
3. Use the 'Stage Map' window displaying the unknowns to show where all of your random points or linear traverses are. Figure out which numbers correspond to the unknowns you want.
4. If you made a mistake in the digitizing go to the 'Automate!' window and double click on the sample you need to alter. The sample positions you have digitized will come up in the box below the sample position list. Choose the duplicate or mis-digitized points and click on 'Delete Selected Positions' then OK.
5. Consider acquiring images on all your sample positions. These positions can be plotted on the images once the acquisition has completed.

