

Operation of Perkin Elmer NexION 2000 ICP-MS

072023MB02

For urgent problems please report to Matt Burleson, AP 346, mburleson@wcu.edu, x2239!*

Scope

This procedure details the operation of the ICP-MS including initial tuning and setup.

Responsibility

Due to the inherent sensitivity of a mass spectrometer and the use of caustic solutions, gloves should be worn at all times when working at the front of the instrument.

1 ppm should be the highest concentration.

Definitions

1. **Extended Dynamic Range (EDR)** - Extended Dynamic Range - provides an electronic dilution that enables the analyst to use the quadrupole in the universal cell to detune sensitivity on specific high concentration elements, so that they can be used with the same low concentration elements in the same calibration. This mode can be useful for the detection of magnesium, calcium, iron and sodium.
2. **Dynamic Reaction Cell (DRC)** - A cell placed after the ion optics but before the mass analyzer quadrupole. The DRC is capable of *both* ion-molecule collisions/reactions to cleanse the ion beam of interferences. When used in collision mode, *Kinetic Energy Discrimination* is used to reject any undesired products. When used in reaction mode, a reaction gas (ammonia, oxygen, etc.) is introduced into the cell to stimulate ion-molecule reactions. The choice of gas is determined by thermodynamics to favor exothermic (spontaneous) reactions, due to the ionization potential of the interferent ion being much larger than the reaction gas.
3. **Kinetic Energy Discrimination (KED)** - One way to remove interferent ions. A low reactive gas (typically He) is used to induce collisions with the polyatomic interferent. Because the interferent has a larger collision cross-section (due to its larger size than that of the analyte ion), it will collide more frequently with the gas, and thus lose more kinetic energy. By placing an energy barrier at the exit of the cell, the lower energy interferent can be eliminated.
4. **Axial Field Technology (AFT)** - The Axial Field technology system improves DRC function performance by applying a linearly accelerating axial field to the DRC system. The net effect of the Axial Field technology system is that matrix effects are decreased, analyte signal is stabilized, and the speed of analysis is significantly improved.
5. **Peak Hopping** - A quantitation approach in which the quadrupole power supply is driven to a discrete position on the analyte mass (normally the maximum point), allowed to settle (settling time), and a measurement is taken for a fixed amount of time (dwell time). The integration time for that peak is the dwell time multiplied by the number of scans (scan time). Multielement peak quantitation involves peak hopping to every mass in the multielement run.
6. **Background Equivalent Concentration (BEC)** - The apparent concentration of the background signal based on the sensitivity of the element at a specified mass. The lower the BEC value, the more easily a signal generated by an element can be discerned from the background. BEC is a believed to be a more accurate indicator of the performance of an ICP-MS system than detection limit, especially when making comparisons of background reduction techniques, such as cool-plasma or collision/reaction cell and interface technology. BEC is the background signal represented as an equivalent concentration and provides an excellent means of gauging the true magnitude of noise. The BEC can be calculated using the formula below:

$$\text{BEC} = (I_{\text{blank}} / (I_{\text{standard}} - I_{\text{blank}})) * C_{\text{standard}}$$

where I_{blank} is the intensity of the blank, I_{standard} is the intensity of the standard and C_{standard} is the concentration of the standard.

7. **Scan Time** - The mass analyzer scan time is the time it takes to scan from one isotope to the next.

8. Quadrupole Ion Deflector (QID) - An ion optics design that bends ion beam at right angles. A software-controlled scanning voltage is applied to the QID to maximize the transmission of ions within a specific mass range into the DRC, thereby improving sensitivity, reducing interferences on the mass range of interest, and eliminating the transmission of photons and neutral species to the mass spectrometer.

9. Isotope Ratio Measurements - A specialized technique that enables measurement of the exact ratio of two isotopes of an element in a sample. This technique is a sensitive indicator of age, reaction or metabolism in nuclear, geochemical or biomedical applications. When you use the isotope ratio technique, you compare the isotope of interest to a reference isotope of the same element.

10. Ion Getter Modes (IGM) - The instrument has three IGMs:

- i. **STD/DRC QID mode**: (Pre-defined IGM; cannot be renamed or deleted) This default QID mode is optimized for Standard and DRC mode analyses.
- ii. **KED mode**: (Pre-defined IGM; cannot be renamed or deleted) This default QID mode is optimized for KED mode analyses.
- iii. **Cold Plasma mode**: (Pre-defined IGM; but CAN be renamed and modified as desired) This mode is still able to obtain extremely low DLs and BECs in both Standard and DRC mode (using NH₃), but performs well on elements with Ar-based interferences or whose sensitivity is enhanced by the reduction of Ar ions in the plasma stream.

Required Reagents

1. NexION Setup Solution.
2. NexION Rinse solution.
3. NexION KED Setup solution (if doing KED).
4. NexION Detection Limit STD/DRC Mode Blank Solution.
5. 5% Nitric Acid Solution (Made from Trace Metals Grade Nitric Acid).

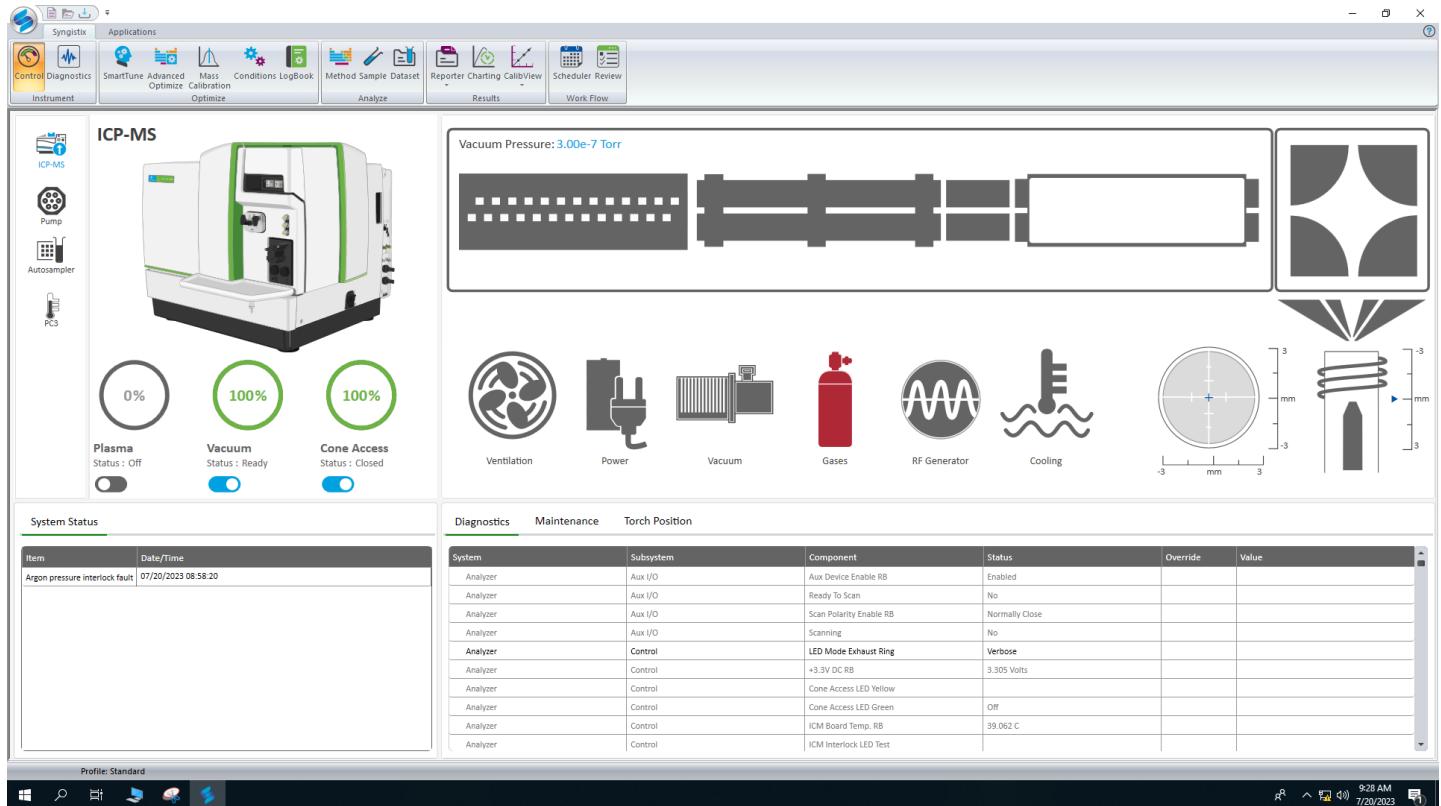
Gases and Startup

1. Turn the chiller on by pressing its power button. Allow the chiller sufficient time to reach 15 C.
2. The ICP-MS uses argon gas for the plasma. The argon can be turned on using the main valves of the four cylinders.

85 - 95 PSI of argon is required!

3. Wearing gloves, visually inspect the tubing of both peristaltic pumps for the autosampler and instrument. Replace the tubing if there is any obvious holes or flat spots.
4. Wearing gloves, affix the tubing to the peristaltic pumps making sure not to cross over each line with another. The pump on the ICP-MS rotates counterclockwise to introduce the sample into the spray chamber.
5. Clamp the tubing to the pumps. The ICP-MS pump has a "Tube saver" feature, so you may observe it rotating clockwise and then counterclockwise

6. Open the Syngistix software by clicking the icon on the desktop. The launch window of the software is shown below.



A red icon indicates a system fault. The image shows an argon gas fault due to the cylinders being off as an example.

7. The instrument's cones, including the sample cone, skimmer cone and hyper skimmer cone, should all be inspected prior to use. Replace any worn cone to ensure optimum beam transmission.

This requires training by Matt Burleson!

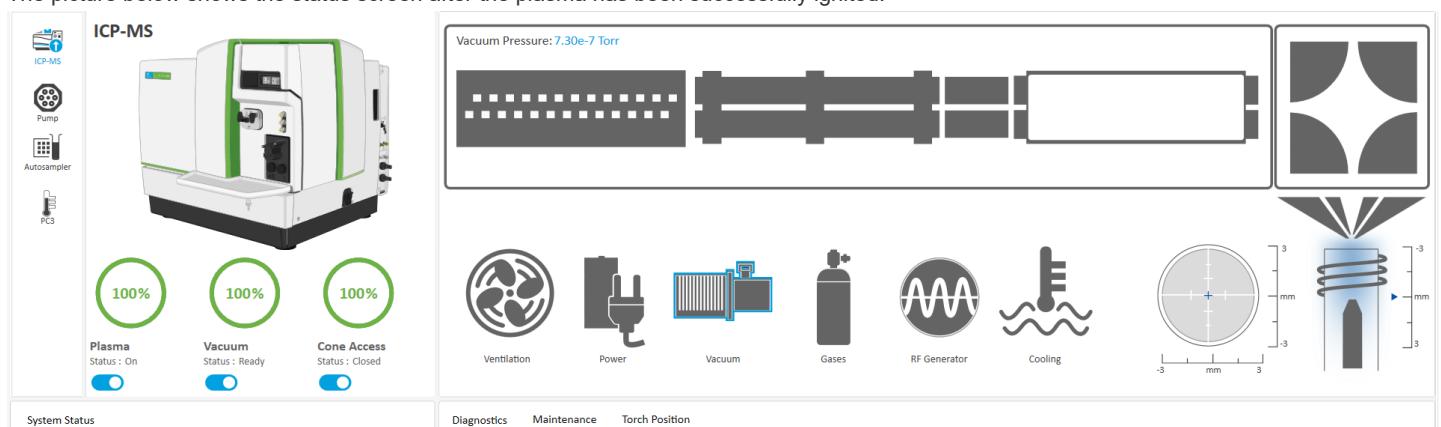
8. With the cones inspected and satisfactory, the plasma can be ignited.

9. Click the toggle switch located under **Plasma** in the main Syngistix window. The plasma ignition process will initiate.

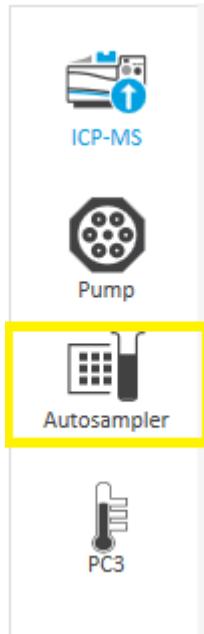
Contact Matt Burleson if the plasma fails to ignite after two attempts.

10. Allow the plasma to stabilize for 20 mins prior to any analysis, including the next steps.

11. The picture below shows the status screen after the plasma has been successfully ignited.



12. Initialize the autosampler by clicking the **Autosampler** icon in the left-hand toolbar shown below in yellow.



13. Click the **Initialize** button to establish connection to the autosampler. The screen should look like the image below if the communication is successful.

Autosampler

Autosampler Type: S10 Port: COM3 Send probe to standby after batch completion

Tray File: s10\s10trayf-157position.try

XYZ locations:

X	Y	Z
0	0	0

Probe positions (Circular buttons numbered 1-160):

5	4	3	2	1	5						
13	12	11	10	9	8	7	6				
25	24	23	22	21	20	19	18	17	16	15	14
37	36	35	34	33	32	31	30	29	28	27	26
49	48	47	46	45	44	43	42	41	40	39	38
61	60	59	58	57	56	55	54	53	52	51	50
73	72	71	70	69	68	67	66	65	64	63	62
85	84	83	82	81	80	79	78	77	76	75	74
97	96	95	94	93	92	91	90	89	88	87	86
109	108	107	106	105	104	103	102	101	100	99	98
121	120	119	118	117	116	115	114	113	112	111	110
133	132	131	130	129	128	127	126	125	124	123	122
145	144	143	142	141	140	139	138	137	136	135	134
157	156	155	154	153	152	151	150	149	148	147	146

Buttons at the bottom:

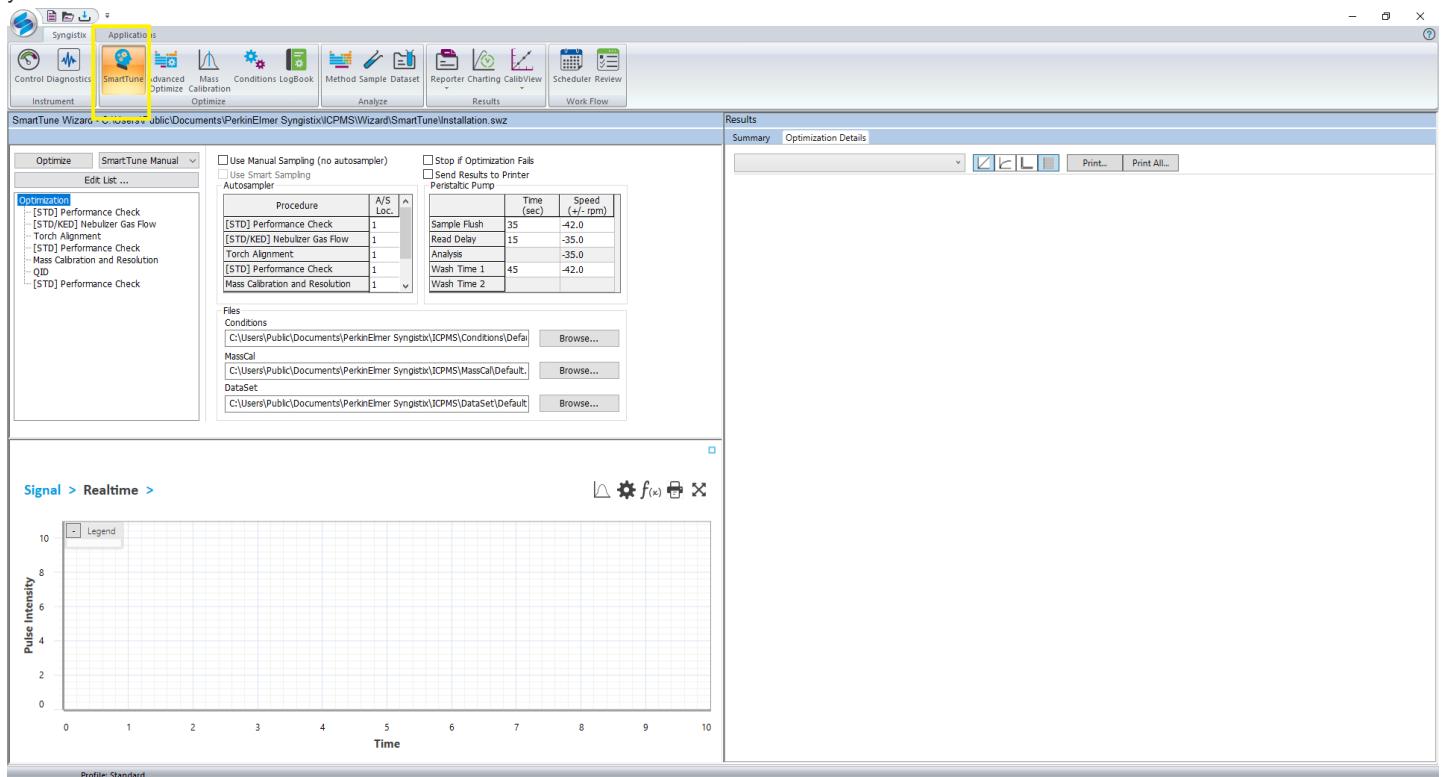
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-
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Ensure that the probe is **NOT** sent to standby after batch completion.

14. Proceed to the Smarttune procedure after the plasma has had 20 minutes to stabilize.

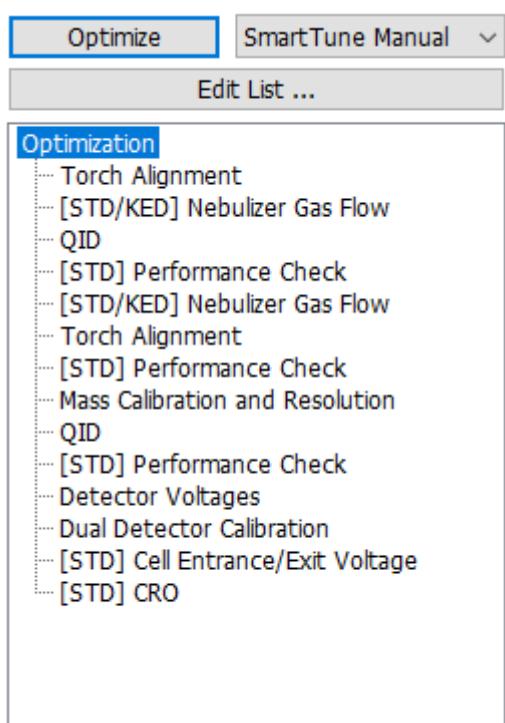
SmartTune Procedure

1. Navigate to the Smarttune window by clicking the Smarttune icon located in the top toolbar of Syngistix. The Smarttune icon is shown below in yellow.



2. Click the **Syngistix Ball** followed by **Open** and select the Smarttune Wizard File labelled as **Installation**.

The optimization list should resemble that shown below.



The optimizations are performed in order. If one fails, the instrument moves onto the next item in the list in an attempt to correct the previous failure.

3. Ensure that the location of the NexION Setup Solution vial matches that shown in the Autosampler dialog box below within the Smarttune window.

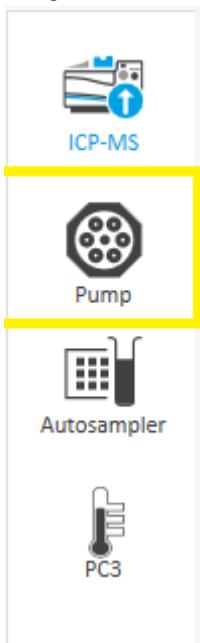
Use Manual Sampling (no autosampler)

Use Smart Sampling

Autosampler

Procedure	A/S Loc.
Torch Alignment	1
[STD/KED] Nebulizer Gas Flow	1
QID	1
[STD] Performance Check	1
[STD/KED] Nebulizer Gas Flow	1

4. Navigate to the **Pump** tab in the left-hand toolbar shown in yellow below.



5. The Setup Solution needs to be in aspirated into the system before the Smarttune procedure is initiated. Change the "Pump Speed" to "-100" and press enter.

Peristaltic Pump

Status
Internal Pump is selected.

Pump Speed (rpm)
0.0 + - ++ ↻ ↻ ▶

Use internal pump Connect

Stop pump on software shutdown

Start pump on plasma ignition at (rpm): -35.0

Enable tubing saver after a delay of (min): 1.0

6. Allow the pump to operate at this speed for about 20 seconds to allow the Setup Solution to enter the nebulizer.

7. After the Setup Solution has had sufficient time to enter the nebulizer, change the pump speed back to "-35" and press enter.

8. Navigate back to the Smarttune window.

9. Click the **Optimize** button shown below to begin the optimization process.

The screenshot shows the Syngistix Applications window with the SmartTune module selected. The 'Optimize' tab is highlighted with a yellow box. The main area displays optimization parameters and a procedure list. On the right, there are tables for 'Peristaltic Pump' settings and file paths for 'Files', 'Conditions', 'MassCal', and 'DataSet'.

Optimization

- [STD] Performance Check
- [STD/KED] Nebulizer Gas Flow
- Torch Alignment
- [STD] Performance Check
- Mass Calibration and Resolution
- QID
- [STD] Performance Check

Procedure

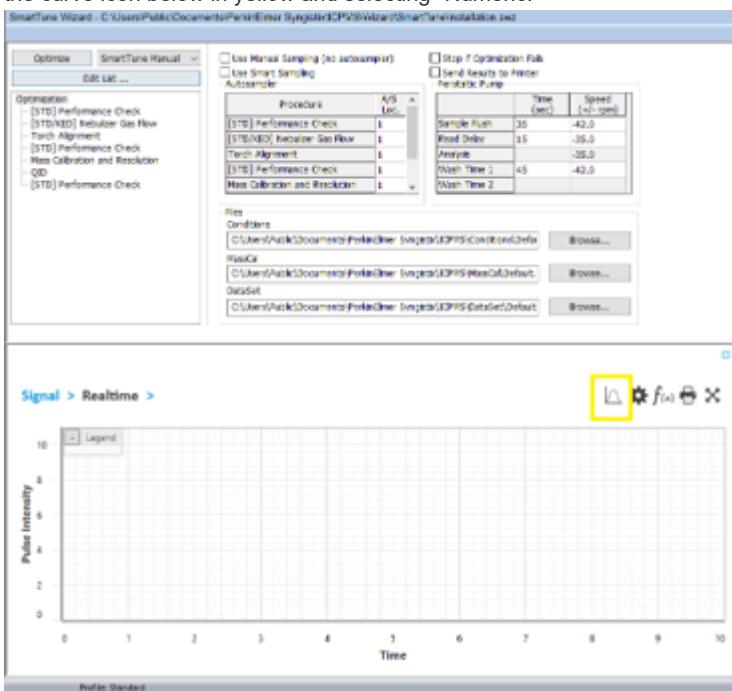
Procedure	A/S Loc.
[STD] Performance Check	1
[STD/KED] Nebulizer Gas Flow	1
Torch Alignment	1
[STD] Performance Check	1
Mass Calibration and Resolution	1

Peristaltic Pump

	Time (sec)	Speed (+/- rpm)
Sample Flush	35	-42.0
Read Delay	15	-35.0
Analysis		-35.0
Wash Time 1	45	-42.0
Wash Time 2		

Files
Conditions: C:\Users\Public\Documents\PerkinElmer Syngistix\ICPMS\Conditions\Default
MassCal: C:\Users\Public\Documents\PerkinElmer Syngistix\ICPMS\MassCal\Default
DataSet: C:\Users\Public\Documents\PerkinElmer Syngistix\ICPMS\DataSet\Default

10. As the optimization process proceeds, it's better to change the Signal window to numeric for a more usable reading. This can be done by clicking the curve icon below in yellow and selecting "Numeric."



11. The software will prompt you to save the results of the optimization. These should be saved as the date they are performed.

12. Navigate to Mass Calibration.

The screenshot shows the Syngistix software interface with the following details:

- Top Bar:** Syngistix Applications menu bar with various icons for Control, Smarture, Advanced Optimize, Mass Calibration, Conditions LogBook, Method Sample Dataset, Analyze, Reporter Charting CalibView, Scheduler Review, and Results.
- Left Panel:** "Mass Calibration & Resolution" section with "Method Tuning.mth". It includes a search bar and two buttons: "Start Mass Cal" and "Peak Width only". A table displays calibration data for elements Li, Mg, In, Pb, and U.
- Table Data:**

Analyte	Mass (amu)	Measured Mass (amu)	Mass Calibration DAC Value	Resolution DAC Value	Measured Peak Width (amu)	Custom Resolution
Li	7.016	7.025	1250	2054	0.704193	■
Mg	23.985	24.025	4639	2056	0.710384	■
In	114.904	114.925	22813	2058	0.694028	■
Pb	207.977	207.975	41432	2056	0.710935	■
U	238.05	238.075	47459	2061	0.677994	■
- Right Panel:** "Numeric > Realtime >" section with "Results Summary" tab selected. It shows rolling averages and replicates.

13. Save the Mass Calibration following the optimization by clicking the top-left icon followed by **Save As**.

Save as "Default."

14. Navigate to Conditions shown below in yellow.

The screenshot shows the Syngistix software interface with the following details:

- Top Bar:** Syngistix Applications menu bar with various icons. The "Conditions LogBook" icon is highlighted with a yellow box.
- Left Panel:** "Conditions" section with "C:\Users\Public\Documents\PerkinElmer Syngistix\ICPMS\Conditions\Default.dac". It includes a search bar and two buttons: "Clear Calibration" and "Calibrate from Dataset".
- Table Data:**

Analyte	Mass	# Points	Coefficient	Gain	N (Max)	Conversion Factor
Li	7.016	108	0.989612	19513.2	6.4159...	0.1999502
Mg	23.985	120	0.994722	13619.1	9.1927...	0.139241
Al	26.981	111	0.995342	13185.2	9.4951...	0.134805
Mn	54.938	66	0.995684	11050.4	1.1329...	0.112979
Co	58.933	68	0.995711	10557.3	1.1858...	0.107937
Ni	59.933	116	0.996037	9746.52	1.2845...	0.0996481
Cu	62.929	101	0.991375	9560.55	1.3095...	0.0977467
Zn	65.926	100	0.998304	9367.01	1.3365...	0.095768
- Bottom Panel:** "Dual Detector Charts" section showing detector response functions for Li, Mg, Al, AI 27, and Mn 55.

15. Save the Conditions following the optimization by clicking the top-left icon followed by **Save As**.

Save as "Default."

16. This concludes the standard optimization of the instrument. The method can now be built following the appropriate procedure.

DRC Optimization (ADVANCED)

Check with Matt Burleson prior to any KED/DRC use. The use of the cell requires an overnight purge performed by Matt Burleson!

This next part seems to be for actual samples, so try it!

Recording the blank optimization profile

1. Click **Method** in the top toolbar followed by the **Syngistix Ball** and lastly **Open**.
2. Locate the **Cell Gas Optimization.mth** file. This pre-defined method uses iron, but you can add more analytes to the method if required by clicking their atomic symbol in the periodic table.
3. Within this same window, define the acquisition profile by clicking under **Profile** and selecting the appropriate profile (std, KED, oxygen DRC or ammonia DRC).
4. Aspirate an ultra-pure blank solution.
5. Click on the **Sample** panel followed by the **Manual** tab and label your sample with an easily identifiable **Sample ID** as you will later use the file for the calculation of the optimum gas flow.
6. Move the sampler probe to the blank solution.
7. Click the **Advanced Optimize** tab in the top toolbar.
8. In the Parameter Description list, select **Gas Flow**.
9. Click **Get Defaults** to retrieve the default parameter range. Alternatively, you can enter your own values as the start, end and step.
10. In the **Optimization Criteria** section, select **Ramp**.
11. To start ramping the gas flow for the Blank, click **Optimize**. In the charting panel to the bottom right of the screen, you can change the data type from linear to logarithmic if desired by clicking on the *Chart Data Type* icon (represented by a Gaussian curve).

Recording the sample optimization profile

1. Move to aspirate the sample solution.
2. In the **Sample** panel, type an easily identifiable **Sample ID** as you will later use the file for the calculation of the optimum gas flow.
3. Click **Optimize** to start escalating the cell gas flow for the sample.

Reprocessing the data to determine optimum flow

1. Open the **Charting** panel.
2. In the Charting toolbar, click the Chart Data Type icon and select **Signal**.
3. In the Charting toolbar, click the *Signal and Spectral Display Options* icon (represented as F(x)) and select **Composite Samples**. The Composite Signal dialog box appears.
4. In the **Calculation** section, select LOD or BEC, as desired, to calculate a plot based on the appropriate formula.
5. In the **Spike Concentration** field, type the concentration of the sample in ppb.
6. Use the browse buttons to select the appropriate datasets for Sample 1 (blank) and Sample 2 (spiked sample).
7. Click **Calculate** to initiate reprocessing.
8. In the chart, click the optimum value for gas flow as determined by the calculation. This updates the value for the analyte on the Advanced Optimized Cell Parameters tab.
9. When satisfied with the optimized gas flows, go back to the **Method** tab and open the method to which you would like to transfer the optimized values.
10. Open the Advanced Optimize panel and select the **Cell Parameters** tab. Click **Send Parameters to Method** to transfer the values to the method.
11. Place the autosampler probe into the flushing solution to flush the sample introduction system.

Optimizing Rejection Parameters

Optimizing RPq

For this process, a matrix blank and then a spiked matrix blank are analyzed (1 - 5 ppb recommended).

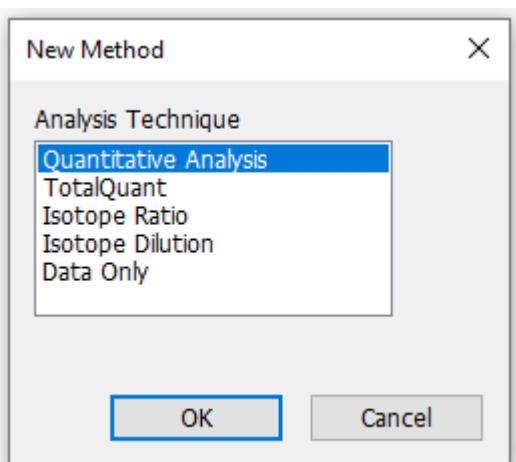
1. Click **Method** in the top toolbar followed by the **Syngistix Ball** and lastly **Open**.
2. Locate the **RPq optimization.mth** file. This pre-defined method uses iron, but you can add more analytes to the method if required by clicking their atomic symbol in the periodic table.
3. Within this same window, define the acquisition profile by clicking under **Profile** and selecting the appropriate profile (std, KED, oxygen DRC or ammonia DRC).
4. Click the **Advanced Optimize** tab in the top toolbar.

5. In the Parameter Description list, select **RPq**.
6. In the Analyte tab, select an analyte (all analytes defined in Step 2 above appear in this list). When an analyte is selected, the cell gas flow and RPa settings for that analyte from the Cell Parameters tab are applied to all analytes during the RPq optimization.
7. Click **Get Defaults** to retrieve the default parameter range. Alternatively, you can enter your own values as the start, end and step.
8. In the **Optimization Criteria** section, select **LOD** or **BEC**.
9. Click **Optimize**. The software acquires data for two solutions, the matrix blank and the spiked matrix blank. Before each analysis, the RPq Optimization dialog box appears, prompting you to aspirate the proper solution.
10. Aspirate the required solution, and then click **OK**. The software automatically records the optimized values on the Cell Parameters tab.
11. When satisfied with the optimized gas flows, go back to the **Method** tab and open the method to which you would like to transfer the optimized values.
12. Open the Advanced Optimize panel and select the **Cell Parameters** tab. Click **Send Parameters to Method** to transfer the values to the method.
13. Save the method.
14. Place the autosampler probe into the flushing solution to flush the sample introduction system.
15. View the results in the Charting panel as described in the previous section.

Method Creation and Analysis

1. Navigate to the "Methods" tab shown below in yellow.

2. Click the top-left icon followed by "New."
3. A popup (shown below) will ask for the desired analysis type. Select the appropriate method type. The instructions below are for a quantitative method.



4. Add your desired analytes using the periodic table to the right-hand side of the software and selecting the most abundant isotope. Be sure to change the Sweeps/reading (the number of sweeps through the mass spectrum that is averaged) to 40 and the number of replicates to at least 3.

Int Std	Scan Mode	Analyte	Mass	MCA Channels	IGM	Dwell Time Per AMU	Integration Time	Corrections	Profile	Ammonia	Helium	Oxygen	RPa	RF
1	Peak Hopping	Mg	23.985	1	STD/DRC...	50	2000		Standard	0	0	0	0	0
2	Peak Hopping	S	31.9721	1	STD/DRC...	50	2000		Standard	0	0	0	0	0
3	Peak Hopping	Ag	106.905	1	STD/DRC...	50	2000		Standard	0	0	0	0	0
4	Peak Hopping	Zn	65.926	1	STD/DRC...	50	2000		Standard	0	0	0	0	0
5														
6														
7														
8														
9														
10														
11														
12														
13														
14														

5. Click the "Calibration" tab within the Method window as shown below in yellow.

Standard	Blank	Standard 1	Standard 2	Standard 3	Standard 4	Standard 5	Standard 6	Standard
Nitric soln		STD1	STD2	STD3	STD4	STD5	STD6	
A/S Location	1	2	3	4	5	6		
Wash Override								

6. Complete the Calibration table so that your samples are in the correct autosampler location and properly labelled such as shown above. You have the option to select the curve type the software will use to generate the calibration curve. Simple linear is a typical selection.

7. Click "Sampling Devices" located beside "Periodic Table."

8. Ensure that the read delay is set to 45 - 60 seconds as shown below.

	Time(seconds)	Speed (+/- rpm)
Sample Flush	35	-42
Read Delay	45	-35
Analysis	35	-35
Wash 1	45	-42
Wash 2	0	0

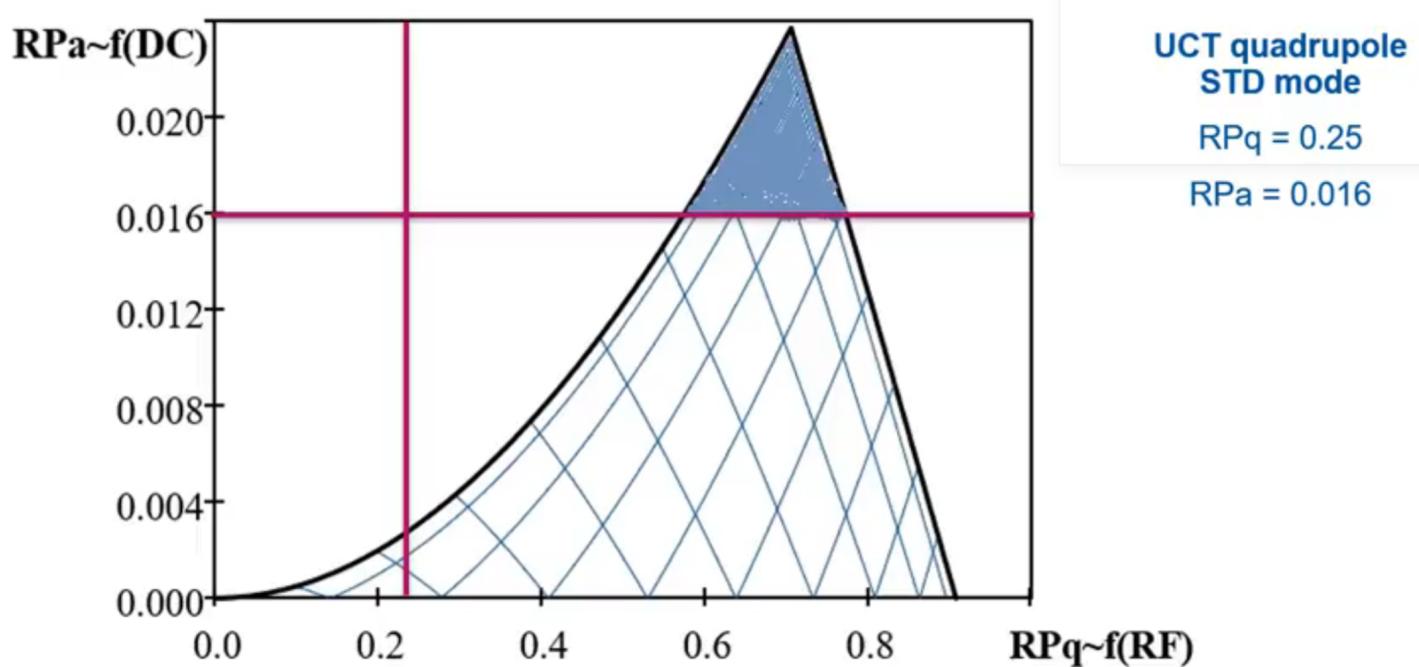
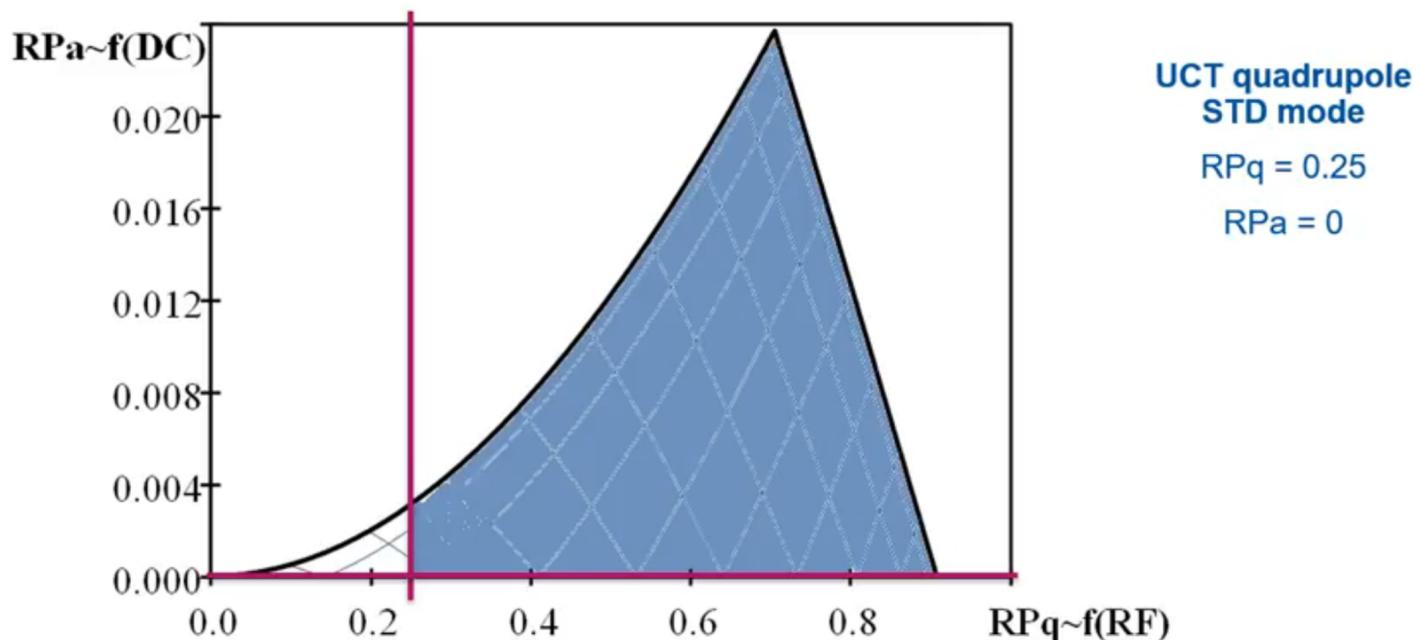
9. Save your method before proceeding to the Sample Analysis section.

Setting up EDR Mode (ADVANCED)

1. EDR Mode can be setup within your method by adding an RPa value within the Analysis tab of the Method Editor. You can test several RPA settings at once and then figure out which ones work best for your method. Then, delete the rest.
2. Having added your desired analytes from above, navigate back to the "Analysis" tab within the "Method" window.
3. In the table of analytes, a column labelled as "RPa" can be located. Enter a value between 0.001 to 0.020.

NOTE: A value of 0 in the RPa column deactivates EDR mode. A value between 0.008 and 0.016 is typical. **NEVER** enter a value greater than 0.020.

1. The image below highlights the effect of RPa values on the stability diagram of a quadrupole.



2. The image below shows EDR mode activated for magnesium at three different values with the three different RP_a values highlighted in red.

The screenshot shows the Syngistix software interface for method creation. The 'Method' tab is selected under 'Quantitative Analysis'. The 'Method Parameters' section includes fields for MassCal File (default.tun), Conditions File (default.dac), and Replicates (3). The 'Method Timing' section shows total estimated sample time as 0hrs 0min 6sec. The 'Notes' section is empty. The 'Analytes' section contains a table with the following data:

#	Int Std	Scan Mode	Analyte	Mass	MCA Channels	IGM	Dwell Time Per AMU	Integration Time	Corrections	Profile	RP _a	RP _q
1		Peak Hopping	Mg	23.985	1	STD/DRC...	50	2000		Standard	0	0.25
2		Peak Hopping	Mg (EDR1)	23.985	1	STD/DRC...	50	2000		Standard	0.014	0.25
3		Peak Hopping	Mg (EDR2)	23.985	1	STD/DRC...	50	2000		Standard	0.015	0.25
4		Peak Hopping	Mg (EDR3)	23.985	1	STD/DRC...	50	2000		Standard	0.016	0.25
5												
6												
7												
8												
9												
10												
11												
12												

A red box highlights the RP_a column in the table. To the right of the table is a Periodic Table and a detailed view of the Mg²⁺ mass spectrum.

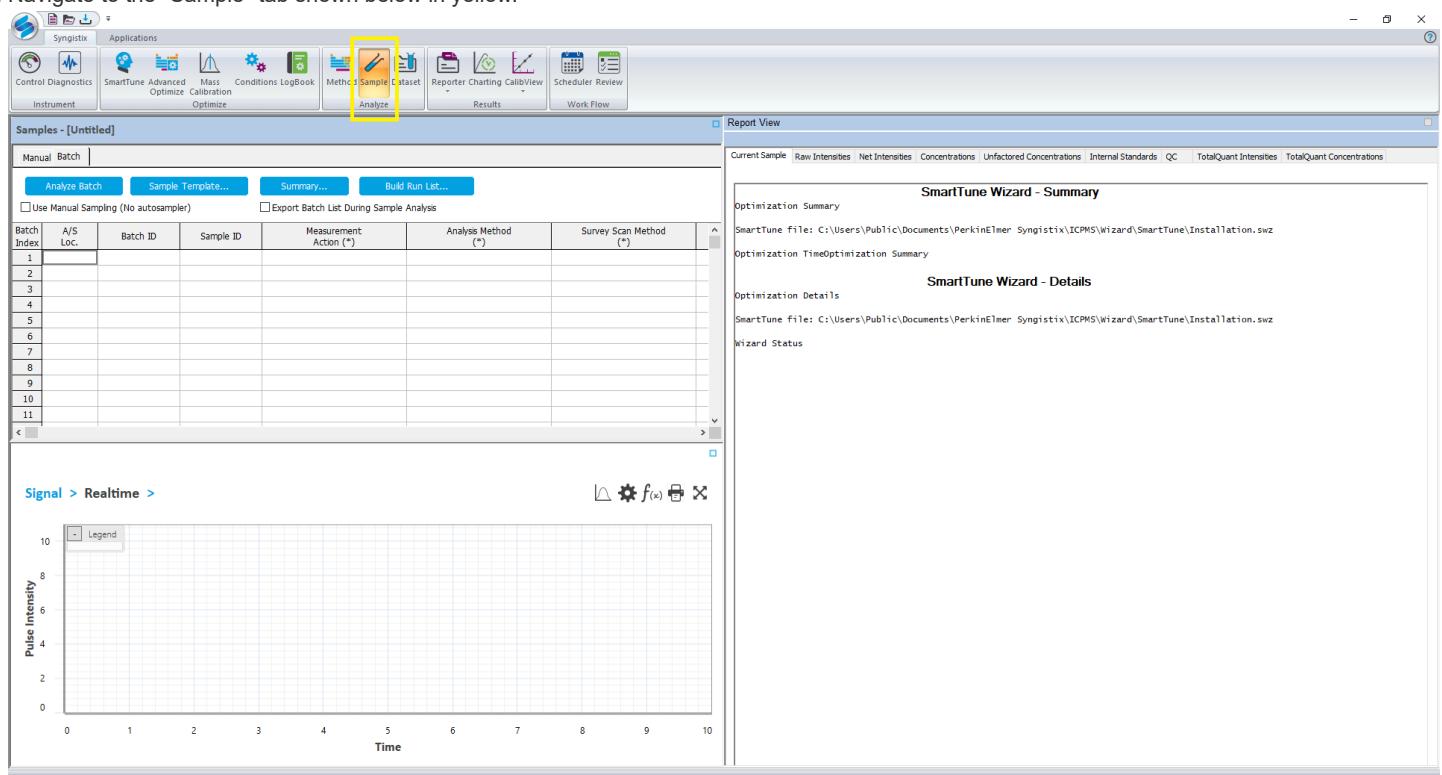
3. Save your method and proceed to the Sample Analysis section.

Isotope Ratio Methods

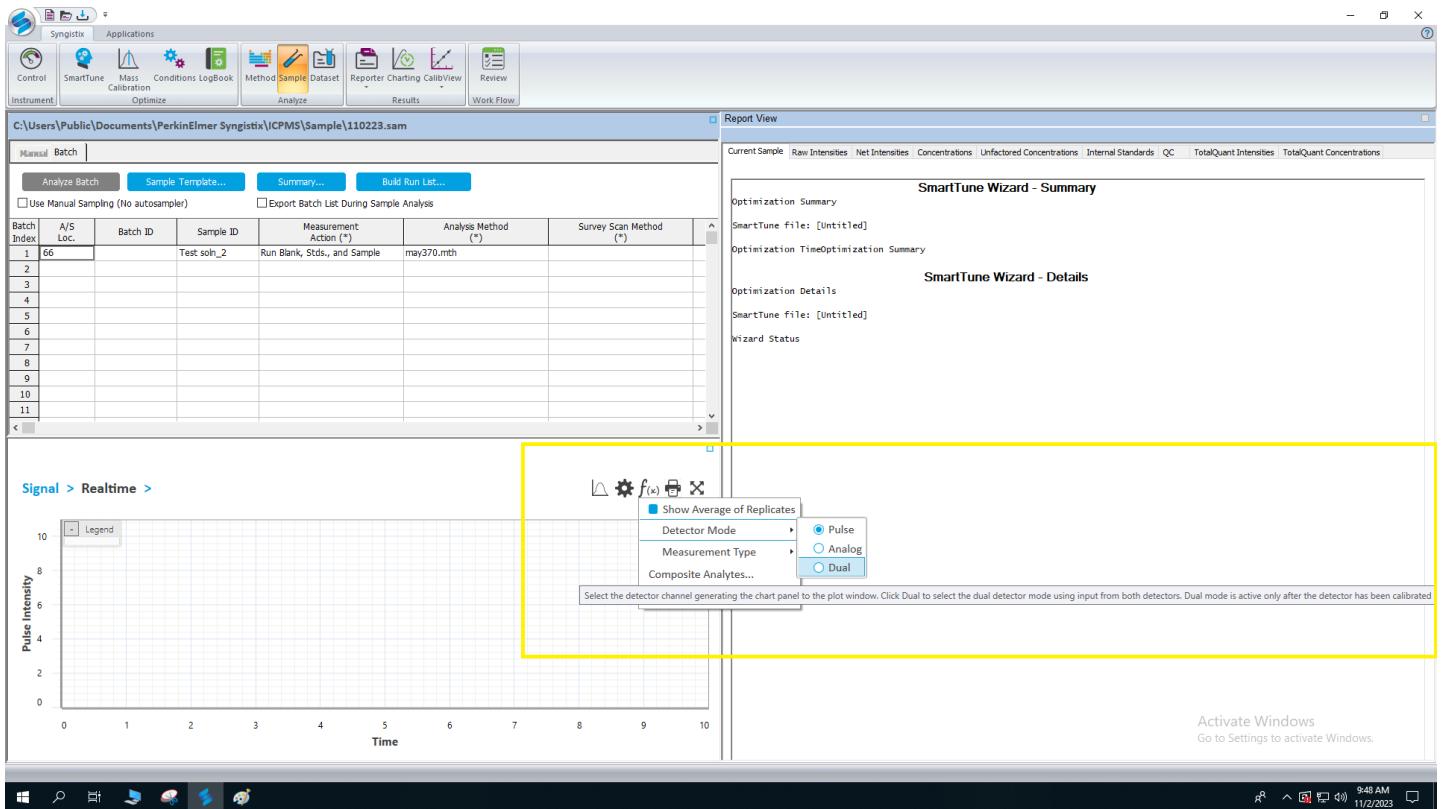
1. Click **Method** in the top toolbar followed by the **Syngistix Ball** and lastly **Open**.
2. Locate the method labelled as **Isotope Ratio.mth**.
3. In the **Method Parameters** settings you can accept the default settings or select your own. To begin, set the **Sweeps/Reading** value to 40 for an integration time of one second for each isotope. If more dwell time is needed, change the value to 60 for an integration time of three seconds.
4. In the **Replicates** field, type a value of at least 3.
5. Add the first analyte to be measured on the first line of the table. Add the isotope of interest of the analyte in the second line. Repeat for each analyte and isotope desired.
6. Select a reference isotope, typically the most abundant isotope.
7. In the **Dwell Time per AMU** column for the first isotope entered, type 25 and press **Enter**. The longer the replicate time, the more precise the ratio measurement will be.
8. For each analyte, select the operating **Profile** desired. Profiles of a single mode should be chosen for isotope ratio methods.
9. For initial method development work, use the default settings for all remaining **Method** panel **Analysis** tab parameters.
10. Click the **Calibration** tab.
11. Define the standards. The **Reference Mass** reverts to the most abundant isotope of the element. To change the value of the reference mass, type the new value and press **Enter**.
12. Type the standard ratios for each mass. To calculate the standard ratio, use the following equation...

Sample Analysis

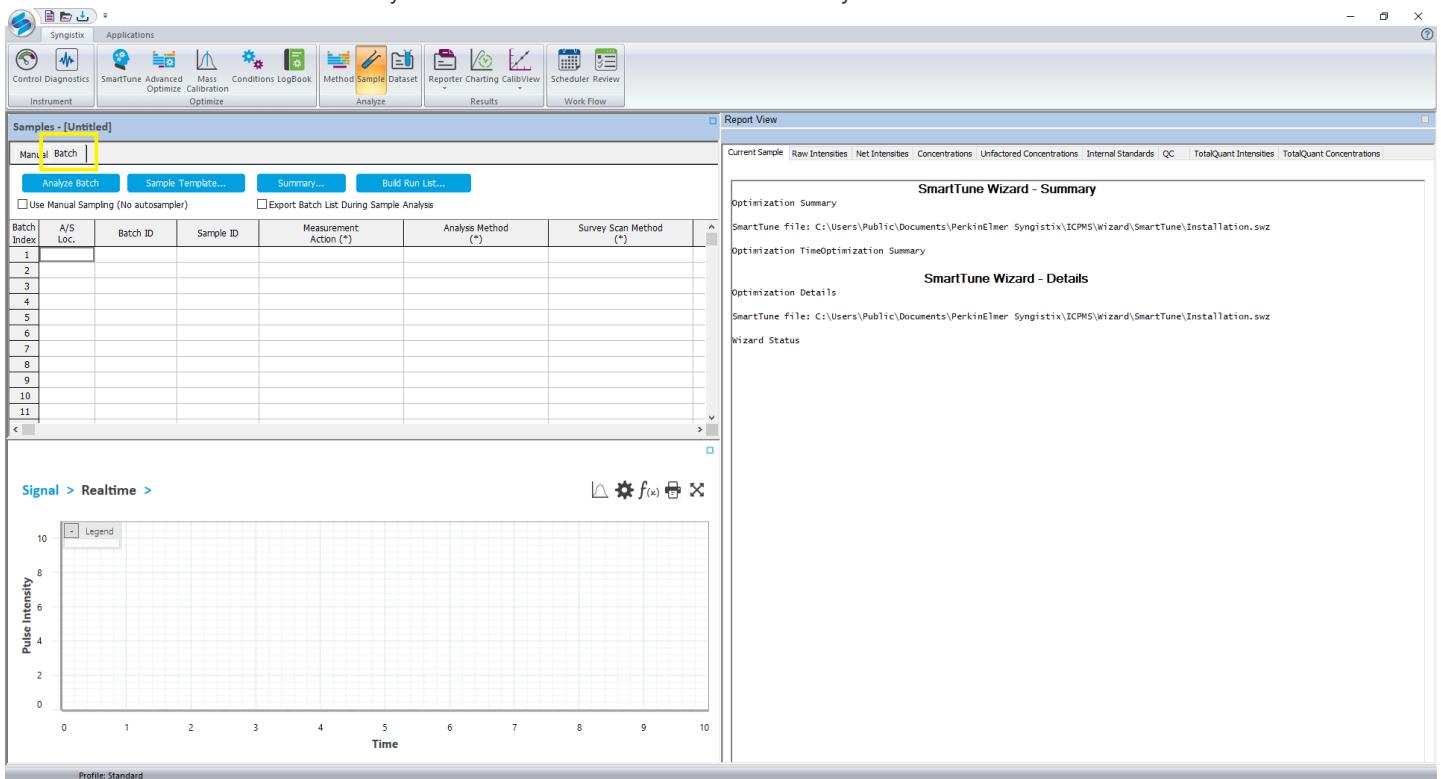
1. Navigate to the "Sample" tab shown below in yellow.



2. It is recommended to set the realtime display to dual detector mode as any intensity greater than 2 million will result in an "S" for shutdown of the pulse detector. To do this, click **f(x)** and select **Dual** under detector mode as shown below.



3. Click the "Batch" button to build an analysis list. The "Batch" button is shown below in yellow.



4. Ensure that the "Use Manual Sampling" box is not checked if using an autosampler.

5. Click "Sample Template..." to open the Sample Template Data window shown below. The image shows an example of entering four samples.

Sample Template Data

X

Sample ID	
Prefix	
Sam	
Number	Increment
1	1
Suffix	
Autosampler Position	
Number	Range
17	Start Row
1	End Row
	1
	4
<input type="button" value="Generate"/> <input type="button" value="Cancel"/>	

6. Click "Generate" to enter the samples into the batch index.

7. Right-click in the "Analysis Method" column. A popup labelled "Select Method File" will show. Select the method you intend to use.

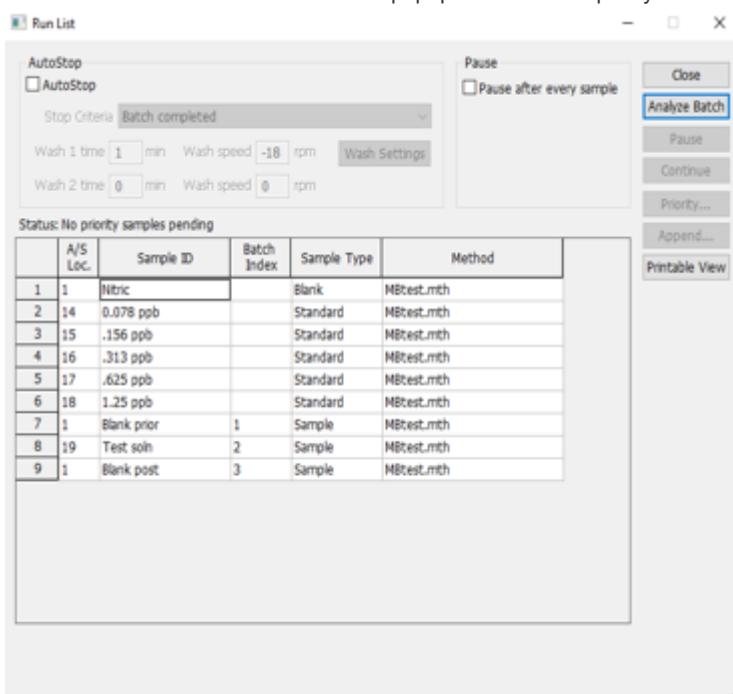
8. Click to highlight the entire "Analysis Method" window. Right-click and select "Fill Down" to have the rest of the rows populated with this same method as shown below.

Samples - C:\Users\Public\Documents\PerkinElmer Syngistix\ICPMS\Sample\MBTest.sam[Modified]							
Manual Batch							
Analyze Batch		Sample Template...		Summary...		Build Run List...	
<input type="checkbox"/> Use Manual Sampling (No autosampler)				<input type="checkbox"/> Export Batch List During Sample Analysis			
Batch Index	A/S Loc.	Batch ID	Sample ID	Measurement Action (*)	Analysis Method (*)	Survey Scan Method (*)	
1	17	1	Sam1	Run Blank, Stds., and Sample	mbtest.mth		
2	18		Sam2	Run Sample	mbtest.mth		
3	19		Sam3	Run Sample	mbtest.mth		
4	20		Sam4	Run Sample	mbtest.mth		
5							
6							
7							
8							
9							
10							
11							

9. In the Measurement Action column, ensure that "Run Blank, Stds., and Sample" is selected in the first row of the batch list. Any entry following the first row can have the measurement action set to "Run Sample."

10. Click the "Batch Index" button at the top-left of the batch table to highlight all samples.

11. Click "Build Run List..." and ensure the popup shows all samples you intend to analyze such as below.



12. Click "Analyze Batch" to begin the analysis.

Data Analysis

- As the analysis proceeds, the "Calib View" window can be used to see the real time results as your standards are analyzed. Standards can be removed from this curve by clicking the blue "X" that represents each data point.
- Click the "Reporter" tab to open the "Report View Screen."
- Clicking the "Net Intensities" tab will allow you to see the measured signal intensity for each element measured by the instrument, with any related blank subtractions applied..
- Clicking the "Concentrations" tab will allow you to see the adjusted sample concentration for each element measured by the instrument.

Exporting Data

1. Both the net intensities and concentrations from above can be exported by selecting their respective tab within the Report View Screen.
2. Click the "Export All..." button towards the bottom middle of the screen.
3. Click "Yes" to the popup warning you that the export may take several minutes.
4. Navigate to your folder and click "Save" to export your data.

System Shutdown

1. At the end of your analysis, flush the system with the NexION Rinse solution for 15 minutes.
2. Pump air for five minutes to allow the spray chamber to drain.
3. Turn the plasma off.

Keep the chiller on for 15 minutes after the plasma has been off to allow internal cooling!*

4. Remove the tubing from the peristaltic pumps of the system and autosampler.
5. Turn the argon gas off using the cylinder valves.

Inform Matt Burleson if any tank's output is below 85 psi.

6. The software can now be closed. Click "No" to each popup before the software closes.
7. After the 15 minutes have passed, the chiller may be turned off.