ICP-MS User's Booklet

1) Stretch and hook the tubing onto the peristaltic pump, and click on the tubing clamp locks.

Stretch tubing down and hook it on

↓

↖ Click clamp locks on

2) Check the argon cylinder pressures to estimate how much argon is remaining. A full cylinder will have around 2200 psi. A full cylinder will last approximately 5 hours of use.

3) Double-click the "LSA Chemistry Recharge" icon :
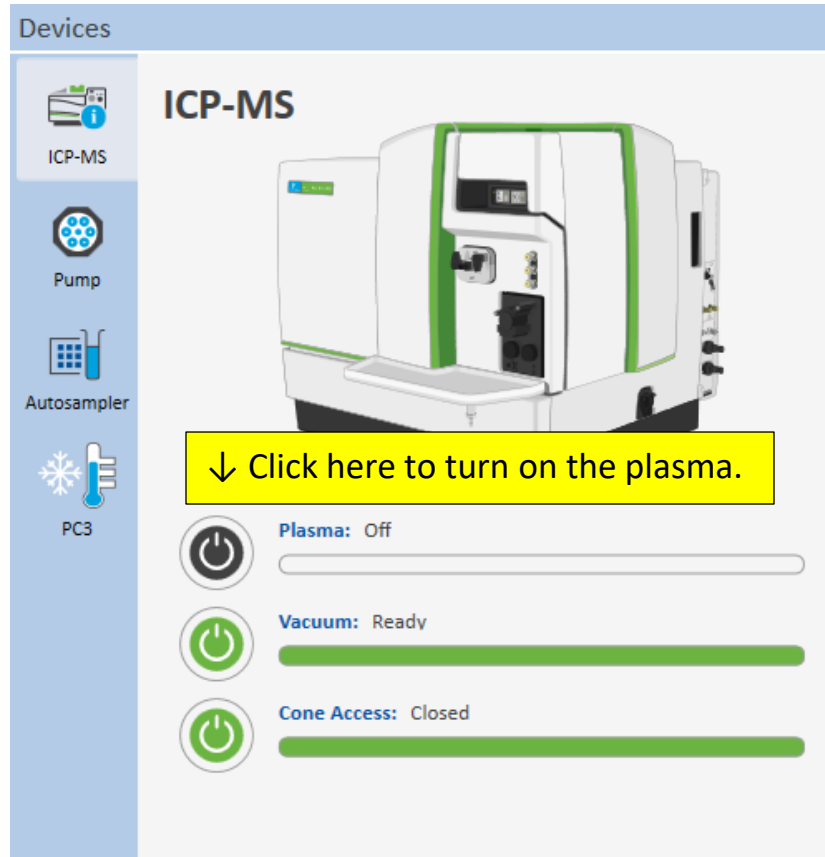
4) Enter your username, your PI's username, and your shortcode and click OK:

5) The Syngistix software will automatically come up

6) After Syngistix loads, you can turn on the plasma:
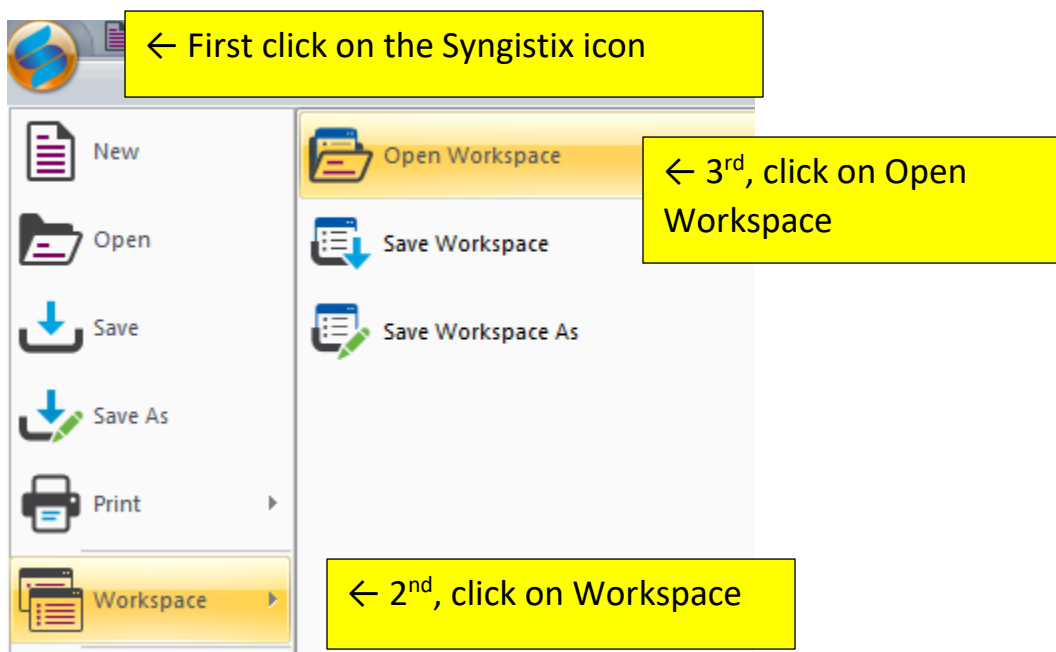

↓ Click here to turn on the plasma.

If the plasma successfully ignites, the indicator will turn green:

Also, the plasma itself may be viewed at the front of the instrument:

7) If you have previously created a workspace, you can open this workspace by clicking on the main Syngistix icon:

← First click on the Syngistix icon

New

Open

Save

Save As

Print

Workspace

Open Workspace

Save Workspace

Save Workspace As

← 3rd, click on Open Workspace

← 2nd, click on Workspace

Opening your workspace will give you easy access to all of your methods, sample lists, and data sets.

8) If you need to create a method, or to edit an existing method, click on the "method" icon on the toolbar:
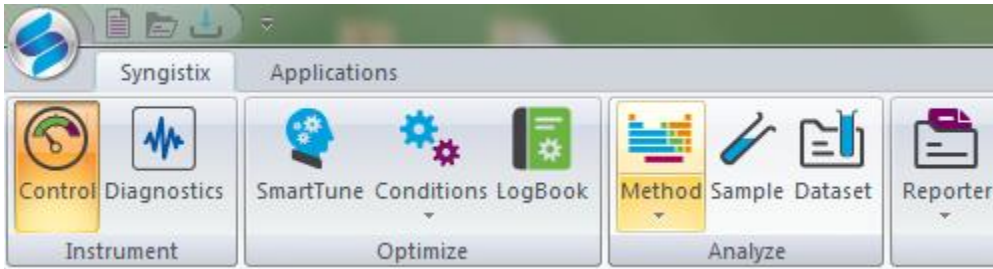
This will bring up the method screen. There are 9 sub-tabs in the method screen. The important ones are "Timing", "Calibration", and "Sampling". First, click on the "Timing" tab, in order to enter the elements and internal standards you wish to use.

Please note:

For internal standards, we have an internal standard mixture that is automatically teed into the sample solution flow. The internal standards which are present are Bismuth, Holmium, Indium, Li^6, Scandium, Terbium, and Yttrium.

↓ Timing Tab   - C:\Users\Public\Documents\PerkinElmer Syngistix\ICPMS\Method\example.mth[Modified]

| Timing | Processing | Equation | Calibration | Sampling | Devices.... | QC.... | Report | Notes |

Sweeps / Reading: 20   Est. Reading Time: 0:00:03.012   MassCal File: default.tun   Browse...

Readings / Replicate: 1   Est. Replicate Time: 0:00:03.012   Conditions File: default.dac   Browse...
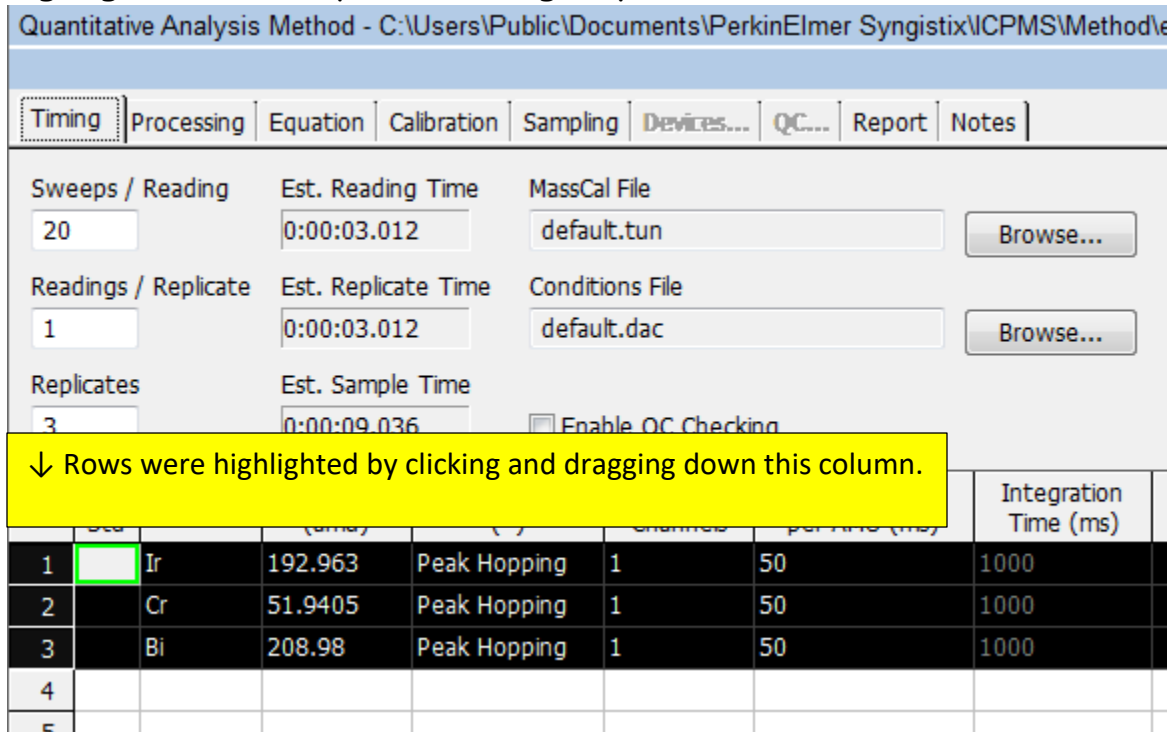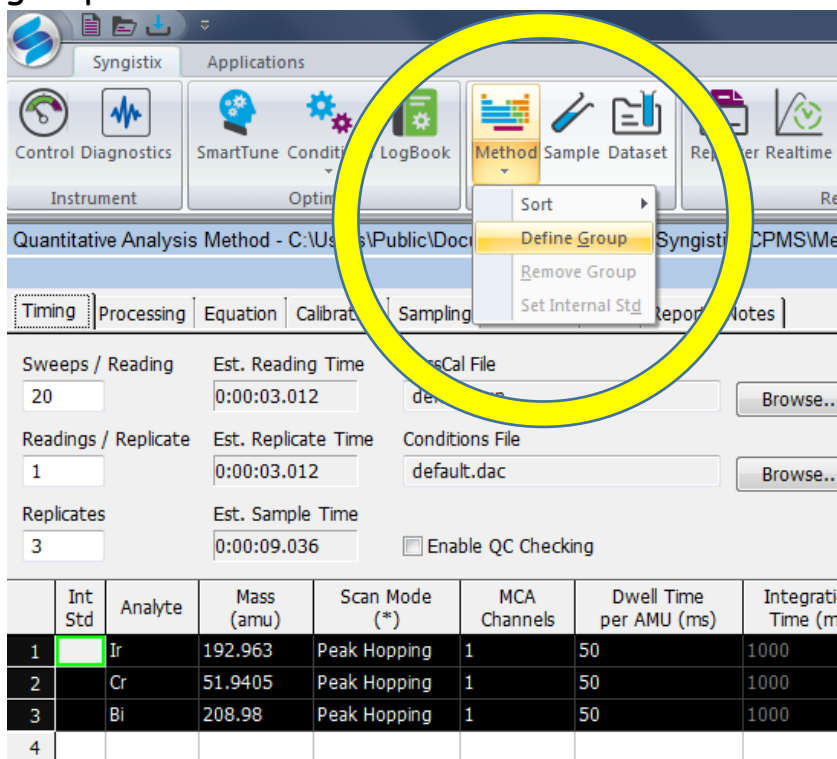
Replicates: 3   Est. Sample Time: 0:00:09.036   ☐ Enable QC Checking

	Int Std	Analyte	Mass (amu)	Scan Mode (*)	MCA Channels	Dwell Time per AMU (ms)	Integration Time (ms)	Corrections	Profile (*)
1		Ir	192.963	Peak Hopping	1	50	1000		Standard
2		Cr	51.9405	Peak Hopping	1	50	1000		Standard
3		Bi	208.98	Peak Hopping	1	50	1000		Standard
4									
5									

↑ Insert Elements Here

You can enter elements in the "Analyte" column by either tying in the symbol for the element, or by clicking on the element in the periodic table.

To group elements together to use with an internal standard, first highlight the rows you wish to group:

Then click on the arrow below the Method icon, and click on "define group"

Next, highlight only the row for the internal standard row. Then click on the method icon arrow, and click on "Set Internal Std"

	Int Std	Analyte	Mass (amu)	Scan Mode (*)	MCA Channels	Dwell Time per AMU (ms)	Integration Time (ms)
1		Ir	192.963	Peak Hopping	1	50	1000
2		Cr	51.9405	Peak Hopping	1	50	1000
3		Bi	208.98	Peak Hopping	1	50	1000

↑ Highlight only the internal standard row.

After this has been done, the elements should appear grouped together with an arrow pointing at the internal standard element

	Int Std	Analyte	Mass (amu)	Scan Mode (*)	MCA Channels	Dwell Time per AMU (ms)	Integration Time (ms)
1		Ir	192.963	Peak Hopping	1	50	1000
2		Cr	51.9405	Peak Hopping	1	50	1000
3		Bi	208.98	Peak Hopping	1	50	1000

↑ Elements are grouped together with an arrow pointing at the internal standard.

Next, click on the "Calibration" tab. The important items to set are what type of curve to use (simple linear usually works best), what type of units (usually ug/L) and the concentrations of your calibration standards (I recommend 1, 5, & 10 ug/L)

Quantitative Analysis Method - C:\Users\Public\Documents\PerkinElmer Syngistix\ICPMS\Method\example.mth[Modif

↓ Calibration tab

| Timing | Processing | Equation | Calibration | Sampling | Devices... | QC... | Report | Notes |

◉ External Std.
○ Std. Addition

↓ Curve type

↓ Set concentrations

	Int Std	Analyte	Mass (amu)	Curve Type (*)	Sample Units (*)	Standard Units (*)	Std 1	Std 2	Std 3
1		Ir	192.963	Simple Linear	ug/L	ug/L	1	5	10
2		Cr	51.9405	Simple Linear	ug/L	ug/L	1	5	10
3		Bi	208.98	Simple Linear	ug/L	ug/L			
4									
5									

Set units ↑

Finally, click on the "Sampling" tab. In this tab you define where your blank and calibration standards will be located in the autosampler tray.

Quantitative Analysis Method - C:\Users\Publ   Syngistix\ICPM

↓ Sampling tab

| Timing | Processing | Equation | Calibration | Sampling | Devices... | QC... | Report | Notes |

Peristaltic Pump

	Time (sec)	Speed (+/- rpm)
Sample Flush	30	-100.0
Read Delay	15	-35.0
Analysis		-35.0
Wash	20	-35.0

Auto Diluter

Dil. Factor   Dil. To Vol.
10   10

1st. Dil. Pos   Probe Purge
1   10

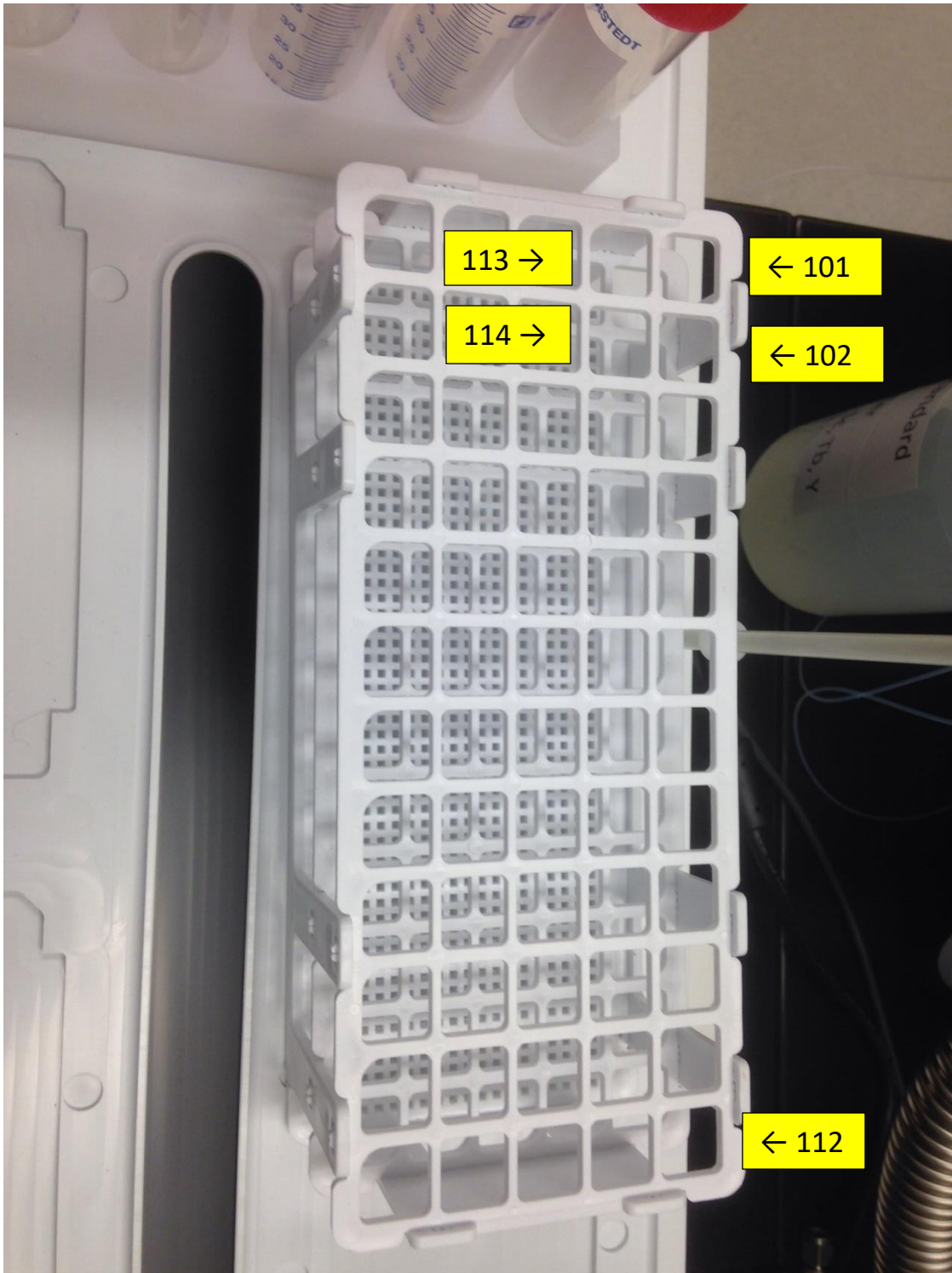☑ Peristaltic Pump Under Computer Control

↓ set Autosampler locations

	Standard	Solution ID	A/S Loc.	Wash Override (sec)
1	Blank	Blank	101	
2	Standard 1	1 ppb Cr & Ir	102	
3	Standard 2	5 ppb Cr & Ir	103	
4	Standard 3	10 ppb Cr & Ir	104	

Type in names describing each solution ↑

After you have finished creating a method, you should save it by clicking on the Syngistix icon and clicking on "Save As". You will then have a method that can be used for analyzing those particular elements.

Here is a picture of the autosampler tray, showing how the locations are numbered:

9) Click on the "Sample" tab to set up your samples to run:

To fill in the Batch table for your samples, first enter where the sample is located in the autosampler tray. Next, give an ID name for the Batch. Then give each sample a name under Sample ID.
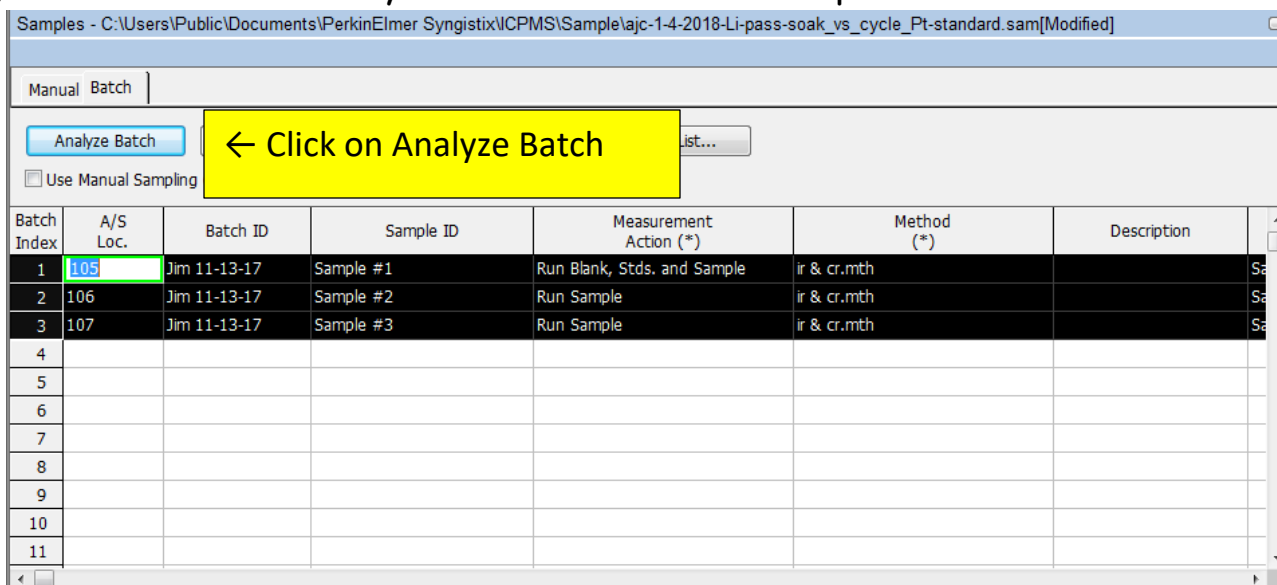
For the first sample in the list, the Measurement Action should be "Run Blank, Stds. And Sample". For every sample after that, the Measurement Action should be only "Run Sample".

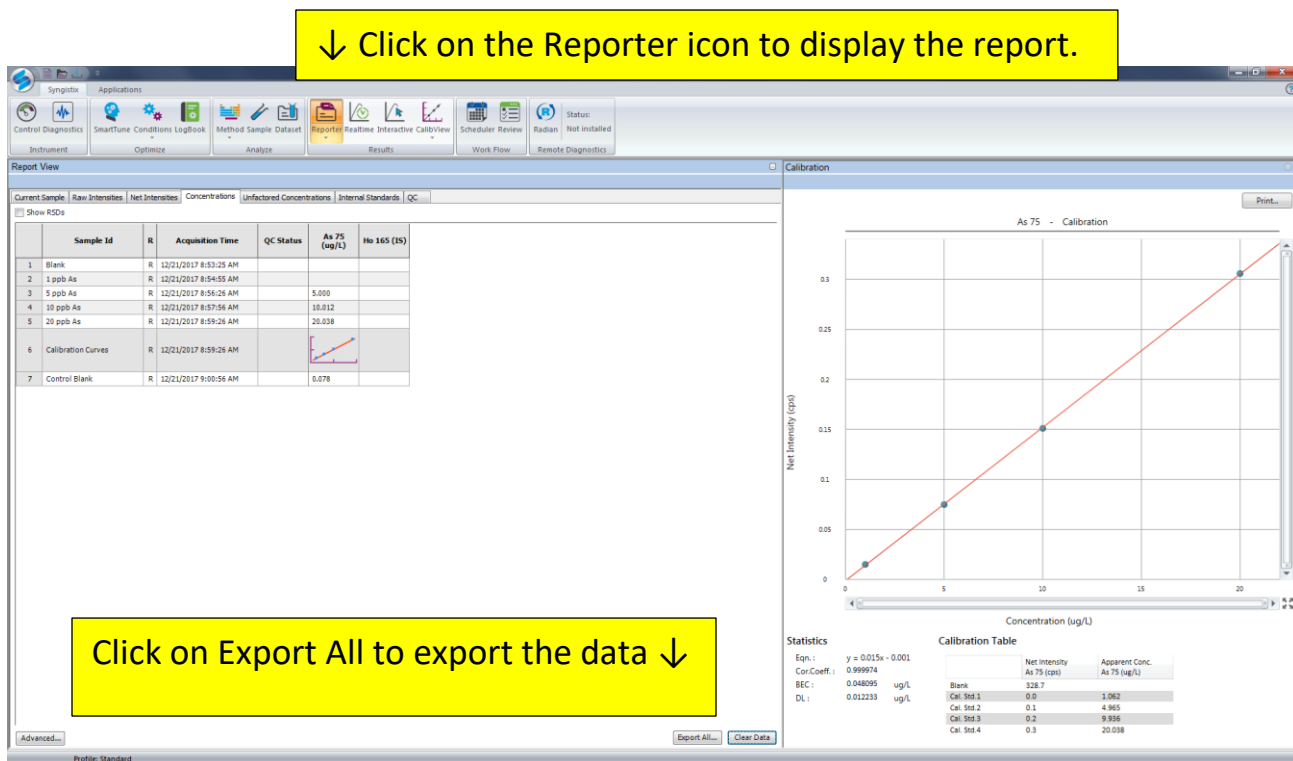Finally, enter the method to be used to analyze the samples.

10) All of the sample rows you wish to run must be high-lighted.

11)   Then click on "Analyze Batch" to run the samples.

12)   When the samples are finished, click on the "Reporter" icon to display the report. Click on the Export All button to export the data.


After you click on Export All, it will ask you where you wish to save the report and to give it a file name. It exports all of the data into an Excel spreadsheet. The picture of the calibration curves, however, does not get exported. The only way to save a picture of the calibration curves is to click

on the Print button near the top of the calibration curve, and then save it as an Adobe pdf.

13) When you are finished using the instrument, click on the Control icon. You can then turn the plasma off.
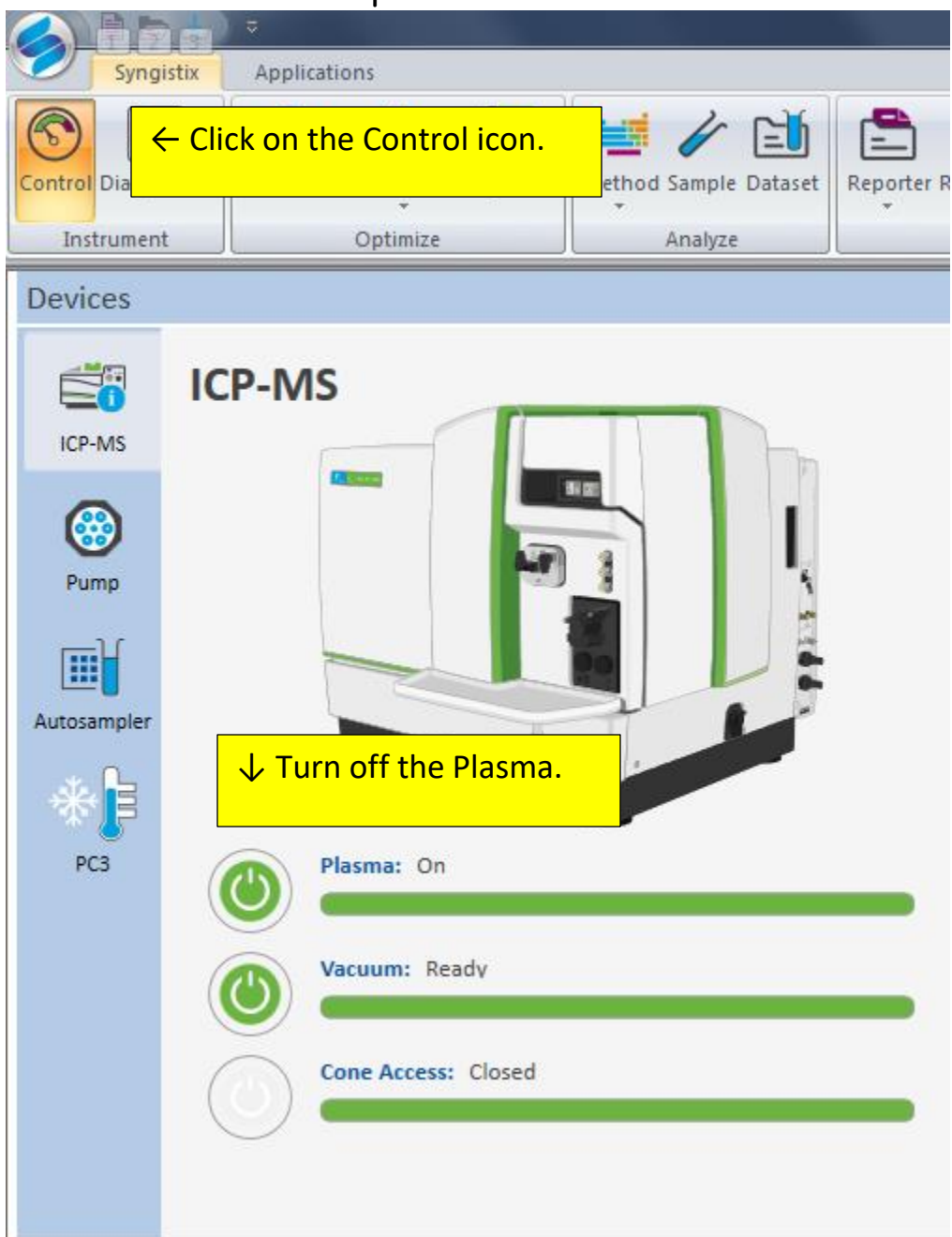
14) Finally, close the Syngistix software. Please note, there is a bug in the software. When you try to close Syngistix, you will see an error message that Syngistix has encountered a problem. Click on "Close the Program"

← Click on Close the Program.
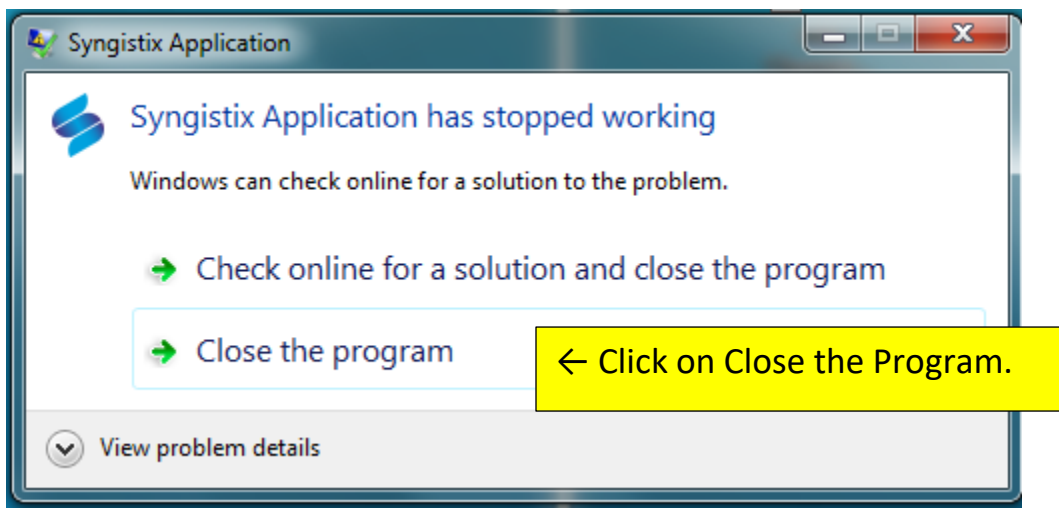
15) Un-do the tubing clamps and un-hook the tubing from the peristaltic pump:

← Un-do the clamps.

← Un-hook the tubing.