MICROMERITICS-CIRRUS

INTERFACE



micromeritics®

USER GUIDE

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ABOUT THIS MANUAL

The following icons may be found in this document:

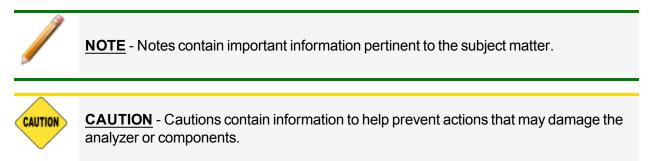


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ABOUT THE SOFTWARE

The *Micromeritics-Cirrus Interface Software* is used with select Micromeritics analyzers integrated with an MKS Cirrus Mass Spectrometer. This software runs within the *MKS Process Eye Professional* application. The Micromeritics-Cirrus Interface Software will perform the following tasks:

- Automatically collect data with the Cirrus Mass Spectrometer via trigger signal from the Micromeritics analyzer
- Customize Peak Jump recipes
- Access standard operations such as Analog scan, Barchart scan, Peak Jump scan, Leak Check, and data storage
- Calibrate detectors
- Scale the Micromeritics analyzer sample thermocouple signal



The MKS Process Eye Professional software must be installed prior to using the Micromeritics-Cirrus Interface Software and the MKS Cirrus Mass Spectrometer. Refer to the Micromeritics-Cirrus Interface Installation Instructions for more information (P/N 292-42805-00).

RECIPES

The interface software controls the analyzer via recipes. A recipe is a list of mass fragments, or mass-to-change ratios (m/z), to be analyzed, along with detector selection and resolution setting. Micromeritics has included preset parameters in the software, enabling users to create *Peak Jump* recipes quickly. Recipes can be saved for future use.

DOCUMENTATION

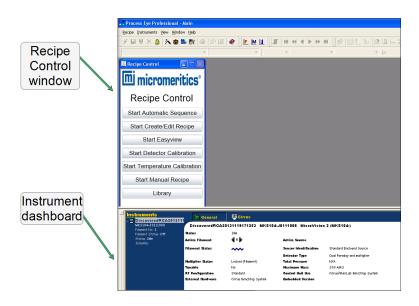
This user guide provides a description of the commands included in the *Micromeritics-Cirrus Interface Software* and instructions on how to use them. It does not include descriptions for all commands related to the Cirrus software. To access the documentation for Cirrus specific software:

- 1. Navigate to the *C:/Micromeritics/MKS* directory where the Micromeritics-MKS application was installed.
- 2. Open the Manual sub-directory, then double click the applicable manual.

START THE INTERFACE SOFTWARE

Double click the *Process Eye Professional* desktop shortcut, or go to *Windows > Start* command to open the *Process Eye Professional* software to display:

- Recipe Control
- Recipe Information



SET UP AND PREPARE FOR OPERATION

The MKS Cirrus Mass Spectrometer pumps are powered on using the *MKS Process Eye Professional Software*. Powering on the pumps (to allow them to get to full performance) and powering on the heaters should be done before using the MKS Cirrus Mass Spectrometer.

1. Click the Cirrus tab on the Status window to access and begin component operation.

Instruments - =: Cirrus	General	Cirrus	
	Cirrus LM92-90 Chamber Pressur Pump Heater Selected Valve		ion IP <u>Click for homepage</u> illary Heater (

- 2. Use the instrument schematic to begin the flow of an inert gas (such as helium, argon, and nitrogen) to remove residual gases from the analyzer and for the next steps.
- 3. Click **Pump** to start the pump. The button changes to yellow to indicate that the internal molecular drag pump is accelerating. After the turbo is up to speed, the button will change to green and the chamber pressure will display.



To avoid damaging the pump, do not move the unit after the turbo pump has begun operating.

The pressure should be less than 2E-5 Torr before switching on a filament or the quadrupole. The trip contact on the cold cathode gauge is connected to the external trip on the RGA control unit to prevent filament operation until the pressure falls below this level. This level should be attained within 20 minutes after starting the vacuum system.

4. Use the *Warm/Bake* options in the *Heater* drop-down list. Do not operate the secondary electron multiplier (SEM) detector with the *Bake* option.

Before the system can be started properly, it will need to run a sufficient amount of time to allow the partial pressure peaks of moisture and other airborne gasses to drop to an acceptable level. This time can be significantly reduced by baking the system. This should be done after the system has run for at least an hour to allow the pressure in the system to drop below 2E-5 Torr. The gas flow rate should be at least 20 sccm.

A dry, inert gas should be flushed continuously through the capillary inlet during bake out. The quadrupole should be running with the filament on but only using the Faraday detector. The multiplier detector will be unavailable during baking.

The total pressure may gradually start to rise during the *Bake* cycle as the system outgases; bake the system until the pressure starts to fall. In normal operation, an initial bake of at least 24 hours is recommended, although, in general, the longer the system is baked the better. If the Cirrus is powered off, it will vent to atmosphere introducing water vapor and should be baked again.

The *Warm/Bake* option should be set to *Bake* for the initial bake-out to reduce the water background. After this period, running at the lower temperature of *Warm* is adequate in preventing the condensation of vapors in the vacuum chamber which could lead to memory effects.

Often it is not necessary to have the system heater on at all, but this will depend on the application. The Cirrus is designed to allow continuous operation with the system heater set to *Warm*.

Refer to the Cirrus 2 Hardware manual for additional information on the *Warm/Bake* option.

5. Use the *Capillary Heater* to lessen the chance of vapor condensing in the capillary leading to memory effects or blockage. Whether or not the capillary needs to be heated depends on the application and the nature of the gases being sampled. The Cirrus is designed to allow the capillary heater to be run continuously.

EXIT THE INTERFACE SOFTWARE

Go to **Recipe > Exit** on the Process Eye Professional main menu.

RECIPE CONTROL

All functions for the *Micromeritics-Cirrus Interface Software* are accessed via the *Recipe Control* window.

	nicromeritics [®]
Re	ecipe Control
Star	t Automatic Sequence
Sta	rt Create/Edit Recipe
	Start Easyview
Star	t Detector Calibration
Start 7	Temperature Calibration
S	tart Manual Recipe
	Library

Recipe Control Window Options Table

Option	Description
Start Automatic Sequence	Collect data automatically via the Micromeritics analyzer digital trigger.
Start Create/Edit Recipe	Create Peak Jump recipes for the Automatic Sequence mode.
Start Easyview	Access a number of operations, including different scan modes and diagnostics.
Start Detector Calibration	Calibrate the Faraday and SEM detectors.
Start Temperature Cal- ibration	Calculate the scaling equation for the Micromeritics analyzer sample thermocouple signal.
Start Manual Recipe	Start and stop recipes created using a recipe wizard.
Library	View mass spectral data for a variety of compounds.

AUTOMATIC SEQUENCE

Click **Start Automatic Sequence** in the *Recipe Control* window to display the *Automatic Sequence*.

🗮 Micro	nerities Sequence					
		Automatic Seque	ence			
ID	Recipe Name	Save As	Export As Text ?	Filament Enabled ?	Status	
▶ 1	leb2 ·	leb2	\checkmark	\checkmark		
						Υ.
F	Restart After Sequence Completion ?	כ				
В	egin Automatic Sequence Abort Au	tomatic Sequence Save Automa	tic Sequence Loa	d Automatic Sequence		

Use the Automatic Sequence window to:

- Automatically collect data via the Micromeritics analyzer digital trigger.
- Automatically save data files, which can be imported into the Micromeritics analyzer application.
- Enable the filament for each recipe.

This window displays the current sequence configuration, which includes a list of recipes and associated run conditions.

Automatic Sequence Options Table

Options	Description			
(–) Sign	Click to remove recipes.			
(+) Sign	Click to add recipes below the current recipe.			
Abort Automatic Sequence [button]	Stops the sequence run. Enabled when the Automatic Sequence has started.			
Begin Automatic Sequence [button]	Starts the recipe.			
Export As Text [check box]	Select for each recipe to be exported to a text file. Text files are saved to the default <i>Process Eye</i> data directory with a .TXT file extension.			
Filament Enabled [check box]	Select to have the filament turned on during recipe initialization.			
	The filament must be turned on for data collection.			

Options	Description		
ID	Unique number given for each recipe selected.		
Load Automatic Sequence [button]	Enabled when a sequence is not running. Click to display the Load Sequence window to load another sequence. Click OK to save the options.		
Recipe Name [selection]	Select from the list of recipes.		
Restart After Sequence Completion [check box]	Select to have the sequence restart upon completion of the last recipe in the list. Use this option when collecting data in more than one experiment.		
Save As [button]	Unique file name for each analysis. Enter a name for each <i>Process Eye</i> data file in this column. If a name is not specified, the data file will default to the option selected in the <i>Recipe Name</i> column. A sequential 6-digit tag is appended to each file name. For example, <i>Air</i> will be saved as <i>Air_000001.SI-d</i> if no previous versions exist. The file is saved to the default <i>Process Eye</i> Data directory.		
Save Automatic Sequence [button]	Enabled when a sequence is not running. Displays the Save Sequence window to save the current sequence. Select a file from the drop-down list (the file will be overwritten with the current data) or enter a new file name. Click OK to save the options.		
Status	Displays recipe run statuses during an automatic sequence.		

Automatic Sequence Options Table (continued)

To begin an automatic sequence after recipes have been selected and configured:

- 1. Select *Restart After Sequence Completion* to have the sequence restart upon completion of the last recipe in the list (if applicable).
- 2. Click Begin Automatic Sequence.



If prompted to select an instrument, select one from the list, then click Connect.

Recipe Status Instruments	Recipe Information				
- HDiscoveredRGA2013111	Category Ack	EventText	UserText		
MKS104-J0111008 Filoment No: 1	()	Wizard Message	Connected to DiscoveredRGA20131119171253 (MKS104-J0111008)		
Filament Status: Off		Message	Waiting for trigger		
Stotus: Idle	-	l Alarm(s) 🗐 Acksewiedge All			
<u> </u>	eritics Sequence Aleb2				

- The first recipe is initialized and a tab with the recipe name is added to the *Recipe Information* pane.
- A status of *Waiting* displays in the *Status* column until the Micromeritics analyzer *Digital Trigger 1* is set to the high (1) state.

🔀 Micros	eritics Sequence					
		Autor	matic Sequ	ience		
ID	Recipe Name	Save As		Export As Text ?	Filament Enabled ?	Status
▶ 1	leb2	- leb2		\checkmark		Waiting
						Status
						Waiting
R	estart After Sequence Co	mpletion ?				
Be	gin Automatic Sequence	Abort Automatic Sequence	Save Autom	atic Sequence	_oad Automatic Sequenc	e

ENABLE THE TRIGGER FOR AUTOCHEM

The trigger can be enabled using one of two methods:

- Preset in the analysis conditions parameter file, or
- Set manually using the analyzer schematic

PRESET IN THE ANALYSIS CONDITIONS PARAMETER FILE

- 1. Before the Start Recording step, insert a Set Outputs step.
- 2. Enable digital output *D01* to be used as the trigger.
- 3. After the Stop Recording step, insert a Set Outputs step.
- 4. Disable digital output D01.

SET MANUALLY USING THE ANALYZER SCHEMATIC

- 1. Enable manual control, then right click in the Auxiliary I/O display window.
- 2. Select Digital Output 1.

Manual Control: Enabled				
DO: 100				
RO: 000	✓ Digital Output 1			
DI: 00	Digital Output 2			
Aux 1: 1.2	Digital Output 5			
Aux 2: 4.5	Digital Output 4			
	Relay Output 1			
	Relay Output 2			
Auxiliary I/	Relay Output 3			
	Relay Output 4			

ENABLE THE TRIGGER FOR 3FLEX 3500

The trigger can be enabled using one of two methods:

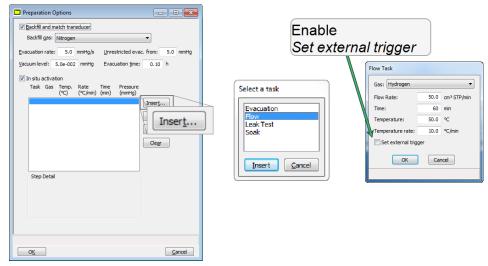
- · Preset in the analysis conditions parameter file, or
- · Set manually using the analyzer schematic

PRESET IN THE ANALYSIS CONDITIONS PARAMETER FILE

- 1. Go to *File > New Sample*.
- 2. On the New Sample Type window, select Chemical Adsorption.
- 3. On the Analysis Conditions tab, click Preparation.

A			- • •
Sample Description	Degas Conditions	Analysis Conditions	Report Options
Description Analysis Conditions: Analysis Conditions: Adsorptive: Nitrog Pre-analysis evacuation time: Up to Add a Absolute Abs Pre-sure Pre-	Conditions en 0.50 h Pont Every Using conte Doc Equility for any Strapping (m ³ /g STP) (c) (c) (c) (c) (c) (c) (c) (c)	Edt	
Save As	Qlose	Advanced 👻	Preview

4. On the Preparation Options window, click Insert.



mi micromeritics°

- 5. On the Select a task window, select Flow, then click Insert.
- 6. On the Flow Task window, ensure Set external trigger is selected, then click OK.

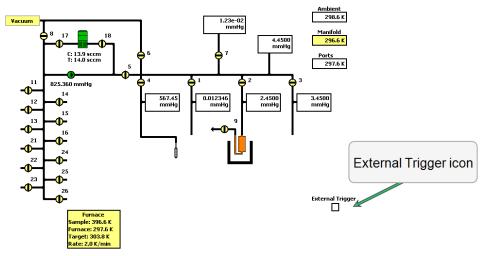


Minimum recommended flow rate is 50 sccm.

- 7. On the *Preparation Options* window, click OK.
- 8. On the *Analysis Conditions* window, click **Save As** to save the sample file parameter changes.

SET MANUALLY USING THE ANALYZER SCHEMATIC

- 1. Go to *Unit [n] > Chemical Adsorption* (if not already selected).
- Go to Unit [n] > Enable Manual Control. Ensure a checkmark displays to the left of the menu item. If the instrument schematic does not display, go to Unit [n] > Show Instrument Schematic.
- 3. Right click the *External Trigger* icon, then select *On*. Alternately, double click the *External Trigger* icon.





The *External Trigger* icon changes to a solid black box to indicate the external trigger is enabled.

ENABLE THE TRIGGER FOR ASAP 2020 PLUS

The trigger can be enabled using one of two methods:

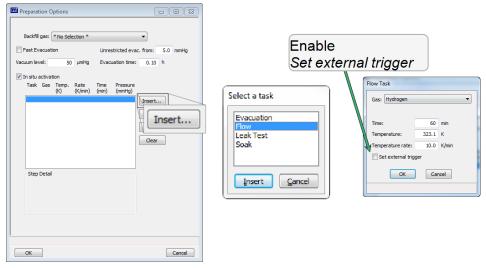
- · Preset in the analysis conditions parameter file, or
- · Set manually using the analyzer schematic

PRESET IN THE ANALYSIS CONDITIONS PARAMETER FILE

- 1. Go to *File > New Sample*.
- 2. On the Analysis Conditions tab, click Preparation.

					_ 0 ×
	Sample scription	Dega Conditi		Analysis Conditions	Report Options
	Conditions: Ru Adsorptive: * N sis evacuation tir	lo Selection *	1	•	Edt
	Starting Pressure (mmHg)	Pressure Increment (mmHg)	Ending Pressure (mmHg)	•	
1	0.000000		0.000	001 Insert	
				Delete	
				Clear	
				Equilibration Inte	rval: 5 s
Prepara	tion Free	Space Te	mperature.	. Dosing	Termination
F	Preparati	on			
Save A	s	Close		Advanced 🔻	Preview

3. On the Preparation Options window, click Insert.



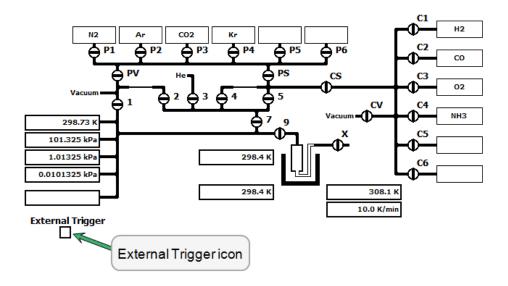
- 4. On the Select a task window, select Flow, then click Insert.
- 5. On the Flow Task window, ensure Set external trigger is selected, then click OK.



Minimum recommended flow rate is 50 sccm.

- 6. On the *Preparation Options* window, click OK.
- 7. On the *Analysis Conditions* window, click **Save As** to save the sample file parameter changes.
- 1. Go to *Unit [n] > Enable Manual Control*. Ensure a checkmark displays to the left of the menu item. If the instrument schematic does not display, go to *Unit [n] > Show Instrument Schematic.*
- 2. Right click the *External Trigger* icon, then select *On*. Alternately, double click the *External Trigger* icon.

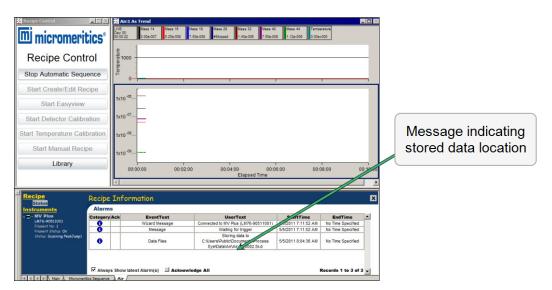
SET MANUALLY USING THE ANALYZER SCHEMATIC



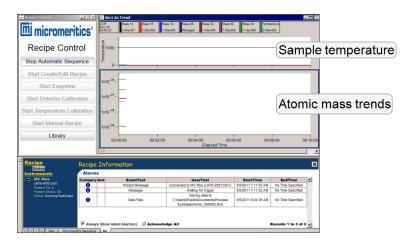
The *External Trigger* icon changes to a solid black box to indicate the external trigger is enabled.

DATA COLLECTION

After the trigger is enabled, the recipe is launched and data collection begins. A message on the *Recipe Information* window states that data collection has started and displays the directory where the data file is saved.



Two windows are opened, one with atomic mass trends and one with the scaled analyzer sample temperature, where mass spectra parameters and temperature axes can be edited. See <u>Recipe</u> Control on page 5.



CLOSE THE DATA FILE

When the Micromeritics analyzer *Digital Output 1* is set to low (0), the recipe stops running and closes the data file. The *Trend View* windows are closed.

Automatic Sequ	uence		
	Export As Text ?	Filament Enabled ?	Status
			Completed 🔂 🖨 🕯 Waiting
3 Monand Steel Segmente	Automatic Sec	-	Enabled ? Status
1 leb2	• leb2		
			Status Waiting
Restart After Sequence Completion 7	-	matic Sequence Load Automa	tic Sequence

On the *Automatic Sequence* window, the *Status* column shows *Completed* for the completed recipe. If there is more than one recipe in the sequence list, the next recipe in the sequence initializes and *Waiting* displays. Once the digital trigger is enabled for the recipe with a *Waiting* status, the recipe launches and data collection begins.

Axes and Legend Properties

To change the axes and legend properties:

1. Right click on the graph where changes are to be made.

		Trend Pane 1	•	
Channel	Display	Name	Measurement	Add Pane
User defined	~	Mass 14	PeakJump1	-
User defined	~	Mass 16	PeakJump1	Remove Pane
User defined	~	Mass 18	PeakJump1	
User defined	~	Mass 28	PeakJump1	Edit Channel >>
User defined	~	Mass 32	PeakJump1	-
User defined	~	Mass 40	PeakJump1	
User defined	~	Mass 44	PeakJump1	
User defined	~	Temperature	UserMeasure.	Use Standard
Mass 28	~	Nitrogen	< <auto>></auto>	View >>
Mass 32	~	Oxygen	< <auto>></auto>	
Mass 36	~	Argon 36	< <<<<<<<<<<<<<<>>><<<>>> a href="https://www.exaction.com"> a href="https://www.exaction.com">https://www.exaction.comhttps://www.exaction.comhttps://www.exaction.comhttps://www.exaction.com"/> a href="https://www.exaction.com"/>https://www.exaction.com"/>https://www.exaction.com"/>https://www.exaction.com"/>https://www.exaction.comhttps://wwww.exaction.com"/>https://www.exaction.com"/>https://www.ex	
Mass 40	~	Argon	< <auto>></auto>	
Mass 44	~	Carbon dioxide	< <<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<o< td=""><td></td></o<>	
Mass 64		Photoresist 64	< <auto>></auto>	
Mass 69	~	Ruorocarbon	< <auto>></auto>	Check All
u l				Un-check All
Mass 40 Mass 44 Mass 64 Mass 69	that are not	Argon Carbon dioxide Photoresist 64	< <auto>> <<auto>> <<auto>> <<auto>> <<auto>></auto></auto></auto></auto></auto>	Un-check A

- 2. On the *Trend Display Pane and Channel Properties* windows, select the check-boxes in the *Channel* column to display or hide a mass.
- 3. From the Trend Pane, select:
 - Trend Pane 1. Select for the atomic mass spectra.
 - Trend Pane 2. Select for the Micromeritics analyzer sample temperature.
- 4. Click Next.

Show Properties for Trend Pane 1 Colleptoperties for the selected pane Use the individual measurement properties to set the Y-axis scale Max value Associate (proge defermined by the measurement's / accuracy) Use the following explicit settings Current maximum value is 3.3e-006 Max value Associate (proge defermined by the measurement's / accuracy) Use the following explicit settings Current maximum value is 3.3e-006 Max value Associate Associate Current maximum value is 3.3e-006 Max value Min value Current maximum value is 3.3e-006 Max value Associate Current maximum value is 3.3e-006 Min value Current maximum value is 3.3e-006 Max value Current these values to the maximum bounds of the acquired data Stack channels of digtal data Seneral properties for the selected pane Current of the selected pane Current of the selected pane Current these values to the maximum bounds of the acquired data Subsequent Y-Axis autoranging strategy for the selected pane The bounds of the data subsequently change during the lifetime of this view Current of the V-axis based on the current and recommended bounds Current the Y-axis to include the new recommended bounds Current of the the new recommended bounds Current of the the new recommended bounds Current of the data for the selected bounds Current of the form Current of the data buesed Current of the data buesed		properties that define its Y-axis scale and its appearance
Use the individual measurement properties to set the Y-axis scale	Show P	roperties for Trend Pane 1
Log scale (range determined by the measurements / accuracy) Log scale (range determined by the measurements / accuracy) Max value Min value Ja30-006 Ja30-010 Log scale Ja30-006 Ja30-010 Log scale Jost of pressure Int of pressure Retrict these values to the maximum bounds of the acquired date Stack channels of digtal data Grad Y-axis Title Y-axis Minor ticks Percentage of total window J66.7 Subsequent Y-Axis autoranging strategy for the selected pane The bounds of the data subsequently change during the lifetime of this view C Leave the Y-axis to include the new recommended bounds C Bayand the Y-axis to include the new recommended bounds Data to the Y-axis to include the new recommended bounds Data to the Y-axis to include the new recommended bounds Data to the Y-axis to include the new recommended bounds	Scale properties for the s	elected pane
Max value Min value Log scale 33e-006 [3.3e-010] □ Units of pressure Restrict these values to the maximum bounds of the acquired data Stack channels of digital data Grad Y-axis Title Grad Y-axis Title Y-axis Minor ticks Percentage of total window height for this pane Subsequent Y-Axis autoranging strategy for the selected pane If the bounds of the data subsequently change during the Metime of this view C Leave the Y-axis unchanged Autorange the Y-axis based on the current and recommended bounds C Exand the Y-axis include the new recommended bounds		
3 330-006 3 330-010 Construct of pressure Restrict these values to the maximum bounds of the acquired data Stack channels of digital data Sack channels of digital data Sack channels of digital data Area of the selected pane Grid Y-axis Minor ticks Percentage of total window Mode and the data subsequently change during the lifetime of this view C Leave the Y-axis unchanged Autorange the Y-axis sub of the Commended bounds Compared the Y-axis to include the new recommended bounds	Use the following et al.	xplicit settings (Current maximum value is 3.3e-006)
Restrict these values to the maximum bounds of the acquired data Stack channels of digital data Grad Y-axis Title Y-axis Minor ticks Percentage of total window More ticks Percentage of total window More ticks Percentage of total window C Leave the Y-axis unchanged C Autorange the Y-axis based on the current and recommended bounds C Expand the Y-axis based on the current and recommended bounds		Log scale
Stack channels of digital data Grid Y-axis Title Y-axis Minor ticks Percentage of total window Height for this pane Kithe bounds of the data subsequently change during the lifetime of this view C Leave the Y-axis unchanged Autorange the Y-axis to include the new recommended bounds Description C Expand the Y-axis to include the new recommended bounds	3.33e-006	3.33e-010 Units of pressure
Y-axis Minor ticks Percentage of total window height for this pane 66.7 bibsequent Y-Axis autoranging strategy for the selected pane If the bounds of the data subsequently change during the lifetime of this view C Leave the Y-axis unchanged C Autorange the Y-axis based on the current and recommended bounds C Expand the Y-axis to include the new recommended bounds	General properties for the	a selected pane
height for this pane 1 ^{55,7} Subsequent Y-Axis autoranging strategy for the selected pane If the bounds of the data subsequently change during the lifetime of this view C Leave the Y-axis sunchanged C Autorange the Y-axis based on the current and recommended bounds C Expand the Y-axis to include the new recommended bounds	Grid	Y-axis Title
If the bounds of the data subsequently change during the lifetime of this view C Leave the Yaxis unchanged C Autorange the Y-axis based on the current and recommended bounds C Expand the Y-axis to include the new recommended bounds	Y-axis Minor ticks	Percentage of total window height for this pane 66.7
Leave the Y-axis unchanged Autorange the Y-axis based on the current and recommended bounds Bipand the Y-axis to include the new recommended bounds	Subsequent Y-Axis autor	anging strategy for the selected pane
C Autorange the Y-axis based on the current and recommended bounds C Expand the Y-axis to include the new recommended bounds	If the bounds of the d	ata subsequently change during the lifetime of this view
C Expand the Y-axis to include the new recommended bounds	C Leave the Y-ax	is unchanged
 Use the new recommended bounds 		
		commended bounds

5. On the *Properties for Trend View Pane Y-axis* window, edit the values in the *Max value* and *Min value* fields.



These value changes apply limits to the partial pressure for the mass spectra (*Trend Pane 1*) and temperature scale for the Micromeritics analyzer (*Trend Pane 2*).

- 6. Select *Log scale* to display the y-axis in logarithmic form. Leave it unchecked to display the y-axis in linear form.
- 7. Edit other window parameters as needed, then click Next.

Each pane shares a commo	on set of properties for the Time Axis
Display clock time Elap Display elapsed time	stat 5/ 5/2011 x 12.08.30 Phint paed 0 dd 4 hh 3 mm 55 si ipan 0 dd 0 hh 10 mm 0 si
Scroll display	Display days Minor time ticks Annotations
Bapsed Time Origin View creation time Time of my choice: Specific data source start time	5/ 5/2011 Y 8:04:36 Ali PeakJump 1 Y
Key Legend C None C Top legend C Side legend	
Save all the settings as a new or m	odfied view definition

- 8. On the *Time Axis Display and Legend Properties* window, select *Display elapsed time* to change the elapsed time displayed on the time axis (x-axis).
- 9. Edit the *Elapsed start* and *Span* fields, if applicable. The default span time is 10 minutes.
- 10. Select *Save all the settings as a new or modified view definition* to have the modified settings saved as the defaults.
- 11. Click Finish to save changes and return to the graph display.

DATA AND RGA RECALL

Only a limited amount of spectra and temperature data is stored in the data buffer used for the live display; therefore, some data may appear truncated when viewing in *Process Eye*. An auxiliary program called *RGA Recall* has been included so that the entire set of data can be reviewed. To access *RGA Recall*:

- 1. In Windows Explorer, navigate to the applicable data directory, then locate the data file.
- 2. Right click the data file, then select Open with RGA Recall from the menu.

😸 CaOx_000001.SI-d	4/6/2011 5:56 PM				
CaOx_000001.txt	Open with RGA Recall Open with	11 5:56 PM			
CaOx_000002.SI-d	 Always available offline Sync 	11 9:09 PM			
🕞 CaOx_000003.SI-d	Restore previous versions	11 10:28 PM			
CaOx_000003.txt	Send to	11 10:28 PM			
🛃 CaOx_000004.SI-d	Cut	11 1:06 AM			
CaOx_000004.txt	Сору	11 1:06 AM			
🛃 CaOx_000005.SI-d	Create shortcut	11 2:24 AM			
CaOx_000005.txt	Delete	11 2:23 AM			
🕞 CaOx_000006.SI-d	Rename	11 7:59 AM			
CaOx_000006.txt	Properties	11 7:59 AM			

The entire data set displays. Certain parameters of the mass spectra and temperature axes panes can then be edited.

F CaOx_000001 : .	Alarms										
Show Al Alarms and E	vents	• «»									
Date/Time	Severity	Event	Message	Duration	Data Set	Recipe file					
4/6/2011 10:53:17	Blue	Data Files	Storing data to C \Process Eye\Dat	K n∕a	DataSet1	CəDx Sir				ſ	Recipe data
											set
🚰 CaOx_000001 :											
CURSOR											
1x10 ⁴⁰² 1x10 ⁴⁰ 1x10 ⁴⁰ 1x10 ⁴⁰ 1x10 ⁴⁰ 1x10 ⁴⁰ 1x10 ⁴⁰ 1x10 ⁴⁴ 1x10 ⁴⁶ 1x10 ⁴⁶ 1x10 ⁶⁶											
1x10 ⁻⁰¹											Sample
1x10 ⁻⁰³											temperature
1x10 ⁻⁰⁴ 1x10 ⁻⁰⁵											
1x10 ⁻⁰⁵	00:0	1:00	00:02:00 00:03:0	D	00:04:00	00:05:00 Elapsed Time	00:06:00	00:07:00	00:08:00	00:09:00	00:10:00
											<u>></u>
CaOx_000001 : CURSOR Mass 18		55 44									
1x10 ⁴⁰² 1x10 ⁴⁰¹ 1x10 ⁴⁰⁰ 1x10 ⁴⁰¹										,	
1x10*01											Atomic mass
1x10*00											trends
									1		
00:00:00	00:0	1:00	00:02:00 00:03:0		00:04:00	00:05:00 Elapsed Time	00:06:00	00:07:00	00:08:00	00:09:00	00:10:00
LST											2

If the data file being opened is currently running, the file will not open. A prompt displays indicating either to open a copy of the file or wait until the file is inactive before trying *RGA Recall* again.

CREATE / EDIT RECIPE

Use to create, configure, or edit *Peak Jump Recipes* for the *Automatic Sequence* mode. A recipe specifies the actions that the Cirrus software is to take during data acquisition.

Create Edit Recipe	23
Either select an existing recipe from the drop down list for editing:	355
	•
Or enter a name for a new recipe:	
OKCan	cel



The Micromeritics analyzer sample thermocouple signal is included in each *Peak Jump* recipe created.

1. Select a recipe from the drop-down list, or enter the name for a new one. Click OK.

		Detector		Skip On Saturation ?	Accuracy		
1	2	Mult 1	•		5	-	
2	18	Mult 1	•) 🖸	5		
3	1	Faraday	•		7		

- 2. On the *Recipe Settings* window, use (+) and (-) buttons to add or delete a mass to the *Peak Jump* scan.
 - (+) sign. Adds a mass below the selected one. The ID is added automatically. All fields contain program defaults.
 - (-) sign. Deletes the selected mass.
- 3. Select and edit the *Mass* field as needed. **NOTE:** See <u>*Library on page 33*</u> if mass spectra information is needed.
- 4. Click the down arrow in the *Detector* column to choose the detector to be used for the selected mass. Select the *Faraday* detector or any of the three gain configurations from the detector options.

Scanning for concentrated species (> 20% of mixture composition) on the Mult1, Mult2, or Mult3 detector is not recommended. For recipes where a short cycle time is crucial, use only one detector (Faraday, Mult1, Mult2, or Mult3). Switching between detectors involves changing settings for internal electrical components, resulting in a high cycle time.

5. Select the *Skip On Saturation* checkboxes (recommended). When selected, masses that saturate the SEM detector (Mult1, Mult2, or Mult3) will be removed from the recipe after five consecutive saturated measurements.



Saturating the SEM detector with a high concentration of ions may damage the detector.

6. Click the down arrow on options in the *Accuracy* column, then select the accuracy level. This parameter controls the time for converting the signal in the analog to digital electronics. The range is 0 (fastest scan and cycle rate with the lowest noise filtering) to 8 (longest scan with the highest noise filtering).



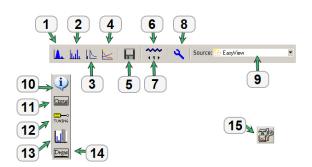
For recipes where a short cycle time is crucial, select the same accuracy level for all masses.

7. Click OK to save changes and close the window. Click Cancel to discard all changes.

EASYVIEW

To launch the *EasyView* software suite, click **Start Easyview** on the *Recipe Control* window to access typical RGA operations. When *EasyView* is activated, the **Start Easyview** button on the *Recipe Control* window changes to **Stop Easyview**. Click **Stop Easyview** to exit the *EasyView* application.

For additional information on the following toolbars, refer to the *EasyView* and *Process Eye User Guides*.



EasyView Functions Table

Legend	Description
1	Starts or stops Analog scan mode.
2	Starts or stops Barchart scan mode.
3	Starts or stops Leak Check scan mode.
4	Starts or stops Peak Jump scan mode. When started, adds the Peak Settings button to the <i>EasyView</i> window. See legend item 15 for Peak Settings button information.
5	Disk store. Allows data to be saved.
6	Filament status. Turns active filament off (blue) and on (red).
7	Filament number. Toggles between filaments.
8	Performs a diagnostic on the Cirrus electronics and associated sensor.
9	Select an option to change the electron energy for ionization (generally, 40eV or 70 eV).
10	Returns the status window to the General Information page.
11	Displays the status of the turbo pump, manifold heater, and capillary heater.
12	Activates <i>Tuning</i> mode. Use to adjust the tuning of the RGA (peak alignment and resolution).

EasyView Functions Table (continued)

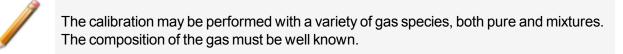
Legend	Description
13	Calibration mode. Provides a calibration factor calculated for converting the measured ion-current to the gas being used. It is recommended to use the Start Detector Calibration on the <i>Recipe Control</i> pane for this calibration.
14	Opens the <i>Degas Settings</i> page for degassing the ion source of selected MKS RGAs.
15	Visible when <i>Peak Jump</i> mode is activated. Use to edit recipe parameters.

DETECTOR CALIBRATION

Use *Start Detector Calibration* to calibrate the Faraday and SEM detectors. Detector calibration is recommended at the beginning of each workday when the Cirrus analyzer is used on a daily basis.

- Faraday calibration. Compares the Faraday detector ion current associated with a particular mass against the known partial pressure of that mass. A Faraday calibration defines the basic ion source sensitivity in amps per pressure unit for a given set of ion source conditions.
- **Multiplier calibration**. Uses the basic ion source sensitivity to find a voltage that amplifies the ion source signal by a given gain setting. The multiplier calibration uses mass fragments with signals less intense than the fragment used for the Faraday calibration.

				(Calibra	ation			
Sele	t Gas	Air	•						
Farac	lay Calil	bration							
Press	ure 760	N	ass 28	Pe	rcentage	8	Status : N/A		
Multip	olier 1 C	alibration							
Mass	29	Gain	50	Status : N	1/A				
Multip	olier 2 C	alibration							
Mass	29	Gain	500	Status : N	I/A				
Multip	olier 3 C	alibration							
Mass	29	Gain	1000	Status : N	I/A				
	20		1000				Save	Run	Stop



CONFIGURATION SETTINGS

Before specifying calibration parameters, review the recommended calibration configuration settings.

Gas	Pressure	Faraday Mass	Percentage	Multiplier Mass
Air	760	28	78	29
Pure nitrogen	760	28	100	29
Pure argon	760	40	100	36
Pure helium	760	4	100	8

Calibration Configuration Settings Table

CALIBRATION PARAMETERS

- 1. Click the *Select Gas* down arrow, then choose the applicable gas.
- 2. Follow the instructions in the next table for each calibration entered:

Calibration Instructions Table

Туре	Instructions
Faraday	 Enter the inlet pressure (in Torr) in the <i>Pressure</i> field. The typical atmospheric pressure entry of <i>760</i> is used. Enter the mass in the <i>Mass</i> field. Typically, this is the mass of dominant species in the calibration gas. If using pure argon as the calibration gas, the entered mass would be <i>40</i>. If using air as the calibration gas, the entered mass would be <i>40</i>. If using air as the calibration gas, the entered mass would be <i>28</i> for nitrogen. In the <i>Percentage</i> field, enter the percentage contribution of the partial pressure of the selected mass to the inlet pressure entered previously. If using pure argon as the calibration gas, enter <i>100</i> for the contribution of mass <i>40</i>. If using air as the calibration gas, enter <i>78</i> for the contribution of mass <i>28</i> (diatomic nitrogen).
Multiplier	 Enter a mass that will not saturate the SEM detector. This is the mass used to perform a calibration against the comparative Faraday detector reading. If using pure argon as the calibration gas, enter mass 36 (has a 0.337% contribution to the partial pressure of pure argon). If using air as the calibration gas, enter mass 29 (has a 0.57% contribution to the partial pressure of air). Use the same mass for all three multiplier detectors. The values in the <i>Gain</i> fields are appropriate in most cases and should remain unchanged.

BEGIN CALIBRATION

1. Click Run to begin calibration. The Faraday calibration and SEM calibrations will run sequentially.

The *Status* field will change from *N/A* to *Passed* if the calibrations completed a successful run.

				Calib	ration			
Sele	ct Gas Nit	rogen	•					
Fara	day Calibrat	ion						
	ure 760		lass 28	Percentage	100	Status : Pa	ssed	
Multi	olier 1 Calib	ration						
Mass	29	Gain	50	Status : Passed				
Multi	olier 2 Calib	ration						
Mass	29	Gain	500	Status : Passed				
Multi	olier 3 Calib	ration						
Mass	29	Gain	1000	Status : Passed				
						Save	Run	Stop

2. Click Save.

Save Confirmati	on		23
		o save the new c urrent calibration	
		OK	Cancel

- 3. On the *Save Confirmation* window, click **OK** to overwrite the current calibration and close the window.
- 4. Click Stop Detector Calibration to close the Calibration window.

TEMPERATURE CALIBRATION

START TEMPERATURE CALIBRATION

Use *Start Temperature Calibration* to calibrate the Micromeritics analyzer sample thermocouple signal.

Micromeritics Temperature Calibration	
Temperatu	ire Calibration
To recalibrate the temperature input please enter 3 different temperature points. Simply enter the temperature and click on the Read Voltage button when the system is at that temperature. Current Voltage = 0.202	Temperature Calibration
Point 1 : Temperature = 25 Measure Voltage Voltage = 0.000	1600-
Point 2 : Temperature = 200 Measure Voltage Voltage = 0.000	1400-
Point 3 : Temperature = 500 Measure Voltage Voltage = 0.000	1200-
When you have 3 valid data points click on Calibrate Calibrate	§ 1000-
Current Values : Point 1 Temperature = 25 Voltage = 0	§ 1000- ■ Current Calbration ■ Messured Points ■ eoo-
Point 2 Temperature = 200 Voltage = 0 Point 3 Temperature = 500 Voltage = 0	600- Measured Points New Calibration
Slope = 164.068 Intercept = -2.489	400-
New Values : Slope = 0.000 Intercept = 0.000 R = 0.000	200-
To manually calibrate, edit slope and offset Re-Plot	
To save new calibration click save.	Voltage
To retain existing calibration simply exit Save	

When using the standard Micromeritics analyzer-MKS Cirrus interface cable, the thermocouple signal is transmitted to the Cirrus on analog input channel 4. To collect temperature data, the analog input signal (in volts) must be scaled to temperature in degrees Celsius (°C).

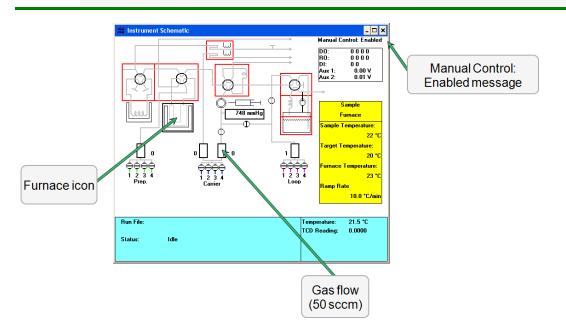
The 3Flex 3500 Chemisorption and ASAP 2020 Plus analyzers only use a single Digital I/O interface cable to connect to the Mass Spectrometer.

AUTOCHEM ANALYZERS

- 1. Ensure that the AutoChem analyzer furnace is closed and a sample tube is installed.
- 2. Start the AutoChem analyzer application.
- 3. Open the instrument schematic, then enable manual control.
- 4. Ensure gas is flowing at a rate similar to experimental conditions.



The instrument schematic illustrated here may differ slightly from yours; however, the process is the same.



POINT 1: TEMPERATURE CALIBRATION

- 1. Right click the furnace icon on the AutoChem instrument schematic, then select *Set Temperature*.
- 2. On the Sample Furnace window, enter 100 in the Set point field, then enter 20 in the Ramp rate field.

🔲 Sample Furnace	. ×
<u>S</u> et point	100 °C
<u>R</u> amp rate	20.0 *C/min
0 <u>K</u>	<u><u>C</u>ancel</u>
Enter a value between 0.	1 and 90.0.

- 3. Click OK.
- 4. Observe the Sample Temperature reading on the AutoChem instrument schematic. When the sample temperature reaches approximately 100 °C and stabilizes, enter the sample temperature in the *Point 1: Temperature* field on the *Process Eye Professional Temperature Calibration* window.
- 5. Click Measure Voltage for Point 1. The analog input voltage will be associated with the AutoChem analyzer sample temperature and the measured voltage displayed at the end of the row.

POINT 2: TEMPERATURE CALIBRATION

- 1. Right click the furnace icon on the AutoChem instrument schematic, then select Set Temperature.
- 2. On the Sample Furnace window, enter 450 in the Set point field, then enter 50 in the Ramp rate field.

Sample Furnace	×
Set point 450 *C	
Ramp rate 50.0 *C/min	
0 <u>K</u> ancel	
Enter a value between -120 and 1100.	

- 3. Click OK.
- 4. Observe the Sample Temperature reading on the AutoChem instrument schematic. When the sample temperature reaches approximately 450 °C and stabilizes, enter the sample temperature in the *Point 2: Temperature* field on the *Process Eye Professional Temperature Calibration* window.
- 5. Click Measure Voltage for Point 2. The analog input voltage will be associated with the AutoChem analyzer sample temperature and the measured voltage displayed at the end of the row.

POINT 3: TEMPERATURE CALIBRATION

- 1. Right click the furnace icon on the AutoChem instrument schematic, then select *Set Temperature*.
- 2. On the *Sample Furnace* window, enter 800 in the *Set point* field, then enter 50 in the *Ramp rate* field.

Sample Furnace	×
Set point 800 *C	
Ramp rate 50.0 *C/m	in
0 <u>K</u> ancel	1
Enter a value between -120 and 1100.	

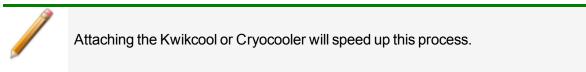
- 3. Click OK.
- 4. Observe the Sample Temperature reading on the AutoChem instrument schematic. When the sample temperature reaches approximately 800 °C and stabilizes, enter the sample temperature in the *Point 3: Temperature* field on the *Process Eye Professional Temperature Calibration* window.
- 5. Click Measure Voltage for Point 3. The analog input voltage will be associated with the AutoChem analyzer sample temperature and the measured voltage displayed at the end of the row.

RETURN THE FURNACE TO ROOM TEMPERATURE

- 1. Right click the furnace icon, then select Set Temperature.
- 2. On the Sample Furnace window, enter 25 in the Set point field, then enter 50 in the Ramp rate field.

🔲 Sample Furnace	×
Set point 25 *C	
<u>Ramp rate</u> 50.0 *C/min	
0 <u>K</u> ancel	
	_
Enter a value between -120 and 1100.	

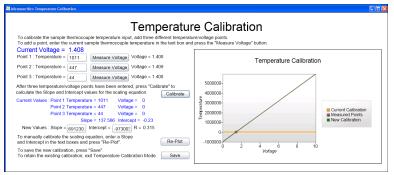
3. Click OK.



ENABLE CALIBRATION

After all three temperatures have been entered and associated with input voltages, the **Calibrate** button on the *Process Eye Professional Temperature Calibration* window is enabled.

 Click Calibrate. A linear fit is applied to the collected points to determine a scaling equation. The temperatures, associated analog voltage values, and the Slope and Intercept results are displayed.



- 2. Click Save.
- 3. On the *Save Confirmation* window, click **OK** to overwrite the current calibration and close the window.
- 4. Click **Stop Temperature Calibration** on the *Recipe Control* pane to close the calibration window.

ENTER A SCALING EQUATION

As an alternative to fitting a line to three temperature and analog signal values, a scaling equation can be manually entered for the thermocouple signal.

1. Where New Values is displayed, enter the applicable values in the Slope and Intercept fields.

New Values : Slope = 327914(Intercept = -461867 R = 0.364

- 2. Click Re-Plot to display the new scaling function on the chart.
- 3. Click Save.
- 4. Click **OK** to overwrite the current calibration and close the window.
- 5. Click **Stop Temperature Calibration** on the *Recipe Control* window to close the calibration window.

3FLEX AND ASAP 2020 PLUS CHEMISORPTION ANALYZERS

The 3Flex 3500 Chemisorption analyzer and the ASAP 2020 Plus Chemisorption analyzer do not provide an analog temperature signal to the Mass Spectrometer, so there is no corresponding temperature calibration necessary. These analyzers transmit elapsed time versus sample temperature data in ASCII format every half second while the Mass Spectrometer signal is active via Ethernet on TCP/IP port 54200. This data can be captured using any TCP/IP capable data capture software or with a Python script. The captured data must then be combined with the Mass Spectrometer data for use.

MANUAL RECIPE

The *Start Manual Recipe* option provides access to recipes created using the *Recipe Wizard*. For detailed instructions on using the *Recipe Wizard*, refer to the *Recipe Wizard User Guide* included with the Cirrus II documentation.

Manual Recipe Select	ion X
press "Run" to	al recipe from the list and start. This will close any
recipe that is c	urrently running.
recipe that is c	urrently running.

- 1. Click the down arrow to select the applicable recipe from the list.
- 2. Click Run.
- 3. Click Stop Manual Recipe on the Recipe Control window to close the window.

LIBRARY

The Library provides access to mass spectra for a variety of compounds.

RGA Information Recall - Ace	taldehyde					
File Edit Scan View Window H						
🖙 🗊 🗈 🔒 🗐 🗗 🗗	9 7 A B 8 B B 5	805• @@	= \$ \$ e = 1_	11 10 13 1		
<u>×</u>	Acetaldehyde : Alarms					_ 🗆 ×
File Name	Show All Alarms and Events	• · · · ·				
Acetaldehyde	Show jointeams and evens	<u> </u>				
Acetic Acid	Date/Time Sevenity	15		10	Data Set	Recipe file
Acetone	Date/Time Severity 11/16/2001 08:26:05 Blue	Event Mess Data Files Storic	age g data to C:\Documents and Se	Duration n/a	Data Set DataSet1	Library Files, SI-r
Acetylene Air (drv)	11/16/2001 08:26:05 Blue		tum: Mass = 29 Intensity = 100	n/a	DataSet1	Library Files, SI-r
Ammonia		Accidicity of Spec	iun. muss - 25 microny - 166	100	Databett	Clordly Files. STT
Argon						
Arsine						
Benzene						
Boron Trifluoride						
Butane Carbon Dioxide						
Carbon Disulphide						
Carbon Monoxide						
Carbon Tetrachloride						
Diborane						
Diphosphine						
Dislane						
DP 0i DC705 DP 0i PPE						>
Ethane	Acetaldehvde : BarChart1					
Ethanol	Acetaldenyde : BarChart1					<u>_0 ×</u>
Ethylene	1 Mass 1					
Ethylene Glycol	2 500 009					
Fomblin	1x10 04 2.508-008					
Formic Acid Freen 11	3					
Freen 12	1 1					
Freen 13	5 1x10 ⁻⁰⁵					
Heium	0					
Hydrogen	L 1x10-05					
Hydrogen Chloride	1x10-08					
Hydrogen Sulphide						
Isopropyl Alcohol Krypton	1 3					
Methane						
Methanol	1x10 ⁻⁰⁷					
Methyl Ethyl Ketone						
MPOI	Δ			1	1	
Neon	5 10	15 20 25 30		50 55 6	i0 65	70 75 80
Nitric Oxide			Scan 1 of 1			
Nitrogen						<u></u>
				ta\Líbrary Files	Pressure in Torr	

- 1. In the *File Name* list, double click the applicable compound to display mass spectral data.
- 2. Click the X in the upper right corner to close the window.

POWER OFF THE MASS SPECTROMETER

The Mass Spectrometer should be allowed to run continuously unless it will not be used for an extended period of time or needs to be powered down for maintenance.

- 1. Power OFF the capillary and system heaters.
- 2. Power OFF the filaments.

Instruments - == Cirrus	General Cirrus
 	Cirrus LM92-90909090 MicroVision IP <u>Click for homepage</u> Chamber Pressure 6.2E-006 Torr Pump Heater <u>Off</u> Capillary Heater Selected Valve Valve 1 <u>Off</u>

- 3. Wait 10 minutes to allow the filaments to cool.
- 4. Click the **Pump** button to stop the turbo. The pumps will stop and the vent valve will open after a few minutes.
- 5. Wait 5 minutes for the system to cool further and come to a full stop.