User Guide

Maurice, Maurice C., Maurice S. and MauriceFlex



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Chapter 1: Let's Get Started

Chapter Overview

- Welcome
- Maurice Systems

Welcome

Congratulations on bringing Maurice into your lab! We welcome you as a new user and are excited to be a part of your work. This user guide will provide you with details on system hardware, operating the system, how to use Compass for iCE software, maintenance procedures and other useful information.

To help you get the most from you new lab addition, we've added some attention phrases to guide you through the user guide:

NOTE	Points out useful information.
IMPORTANT	Indicates information necessary for proper operation of Maurice systems.
CAUTION	Cautions you about potentially hazardous situations that could result in injury to you or damage to the system.
!WARNING!	Warns you that serious physical injury can result if the listed precautions aren't followed.

Maurice Systems

Maurice, Maurice C., Maurice S. and MauriceFlex systems give you identity, purity and heterogeneity data on your biologics, and get you to results faster with short development times and simple workflows!

- They're fluent in cIEF and CE-SDS. They take cIEF up a notch, and CE-SDS is a breeze. You'll get pI and charge heterogeneity data in less than 10 minutes flat with the added bonus of same-time absorbance and native fluorescence for sensitivity down to 0.7 µg/mL. Their size applications have the high res and wide molecular weight range you need and they're done in as little as 5.5 minutes.
- They collect fractions of the charge variants: The feature of icIEF fractionation enables you to isolate the protein charge variants for in-depth characterization by mass spectrometry, and the offline fraction collection gives you the freedom to carry out the intact mass, reduced and subunit mass, and peptide mapping analyses on any vendor's mass spectrometers.
- They make it easy. Just pop in a ready-to-go cartridge, drop in your sample vials or a 96-well plate in the appropriate adaptor, and hit start they'll do the rest!
- **They're time-savers**. Develop methods fast so you get to results even faster. Your cIEF and CE-SDS methods are done in a day. The icing? You can develop platform methods and use them for multiple molecules. No maintenance and clean-up needed between the two applications.
- **They're dependable**. Get reproducible results with tight CVs day in and day out. Your data is reliable no matter what across samples, users, instruments or labs.

Chapter 2: Getting Your Lab Ready

Chapter Overview

- Introduction
- Space Requirements
- Physical Specifications
- Electrical Requirements
- Environmental Requirements
- Software and Computer Requirements
- General Guidelines and Information

Introduction

This chapter will help you prepare the lab for Maurice. Please have the space, electrical and environmental requirements ready prior to scheduling your installation.

NOTE: Please wait for an authorized ProteinSimple Field Service Engineer to unpack and install Maurice for you. Don't try doing this yourself. Handling Maurice incorrectly could cause injury to yourself or damage to the system.

Space Requirements

You need a lab bench or table that can support 100 lb (46 kg) and has enough space for both Maurice and his computer. There should be sufficient clearance for both heat ventilation and to provide access if Maurice needs service.

IMPORTANT

Maurice needs a stable surface and must remain level to work properly. The lab bench or table can't shift or wobble under heavy weight. Don't use anti-vibration tables either, since Maurice may not stay level while he's working.

Dimension	Meters	Feet
Width	1.5	5.0
Depth	0.8	2.5
Height	0.5	1.5

Recommended space requirements for Maurice.

Physical Specifications

Description	Specification		
Maurice's Dimensions (Door Closed)	0.44 m x 0.42 m x 0.61 m (H x W x D) 1.46' x 1.38' x 2.0' (H x W x D)		
Maurice's Dimensions (Door Open)	0.44 m x 0.57 m x 0.61 m (H x W x D) 1.46" x 2.43' x 2.0' (H x W x D)		
Maurice's Weight	46 kg (100 lb)		
Computer Workstation Dimensions	Computer Workstation Dimensions		

For indoor use only. Use up to altitudes of 1524 meters (5000 feet).

Electrical Requirements

Maurice requires a dedicated, grounded circuit capable of delivering the appropriate current and voltage for your country. The power requirements for all three Maurice systems are 100 V–240 V (AC), 50/60 Hz, 500 W.

In addition to these requirements, Maurice needs the grounded circuits terminate at the receptacles, and receptacles must be located within 10 ft (3 m) of the instrument.

Environmental Requirements

Maurice likes a consistent temperature in the lab (not too hot – not too cold). He works best when conditions stay within these ranges:

Requirement	Specification
Operating temperature range	8–25 °C (64–77 °F)
Operating humidity range	20–80% relative, non-condensing

Software and Computer Requirements

Maurice brings his own computer to the lab with Compass for iCE software pre-installed.

Using Maurice with Compass for iCE

Provided with all Maurice systems, Compass for iCE is used to run cIEF and CE-SDS applications on Maurice, cIEF applications on Maurice C., CE-SDS applications on Maurice S. and cIEF, CE-SDS, MauriceFlex cIEF and MauriceFlex Fractionation applications on MauriceFlex, and analyze resulting data. Just in case you need it, a CD containing Compass for iCE software also comes in the box. If you don't want to analyze your data at Maurice's workstation in the lab, Compass for iCE software can also be installed on a separate workstation, such as your desktop computer. Your computer must meet the recommended requirements listed below to run Compass for iCE software and process data.

Component	Minimum Requirements
Operating System	Windows 10
Processor	Core i5
Memory	8 GB
Free Disk Space	250 GB
Ethernet Ports	2 - One is required to connect to Maurice or MauriceFlex, the other is used for network access
USB Ports	2 - To connect the keyboard and mouse

Using Maurice with Empower®

The optional Maurice Empower[®] Control Kit lets you collect, manage and report Maurice results with the Waters[™] Empower[®] 3 Chromatography Data Software. You can use Empower to control a Maurice, Maurice C. or Maurice S. when performing a Maurice cIEF or CE-SDS PLUS batch. To use Empower[®], contact ProteinSimple to install the instrument software if not previously done. Then install the Maurice ICS driver software following the instructions in the Maurice with Empower[®] Installation Guide on the CD that came in your Maurice Empower[®] Control kit.

To learn how to create Maurice method and sample sets, run samples and view data in Empower[®], open the Run Samples window and click **Help** in the top right corner of the Maurice Control Panel.

Maurice Statu	S			199 - C-21725	E	lelp 🔶
Instrument Status: Serial Number: Tray: Sample Chiller:	IDLE kf1147 VIALS 9.3 °C	Coloriat	Reset	Cartridge Type Serial Number: Injections per batch: Injections remaining:	CE-SDS PLUS 6190617497 48 487 (87 guaranteed)	
Sample Chiller.	5.3 C	Setpoint	10 • Set	Batches remaining: Expires:	22 Jun 2020	

General Guidelines and Information

Intended Use

NOTE: Maurice is for research use only. Not for use in diagnostic procedures.

Lifting and Moving the System: Lift Maurice Correctly

IMPORTANT

Take all the standard precautions when lifting or moving Maurice. Since Maurice systems weigh 46 kg (100 lb), you should not lift him by yourself. Two people should lift him onto the lab bench.

Chapter 3: Maurice

Chapter Overview

- Maurice Systems
- External Components
- Internal Components
- Computer Workstation

Maurice Systems

Maurice, Maurice C., Maurice S. and MauriceFlex systems include the instrument, computer workstation, Compass for iCE software and cIEF, CE-SDS PLUS, Turbo CE-SDS or cIEF Fractionation Cartridges.



Maurice with Computer Workstation



CE-SDS, cIEF and cIEF Fractionation Cartridges

All systems have the same hardware components, computer and software, the only difference between them are the applications you can run:

Application	Cartridge	Maurice	Maurice C.	Maurice S.	MauriceFlex
cIEF	cIEF	•	•		•
cIEF with on- board mixing	cIEF	•	•		
CE-SDS	CE-SDS PLUS or Turbo CE-SDS	•		•	•
MauriceFlex cIEF	cIEF Fractionation				•
MauriceFlex Fractionation	cIEF Fractionation				•

You can run samples for a standard cIEF or CE-SDS batch in 96-well plates or in up to 48 sample vials with an integrated 0.2 mL insert. You can run your sample(s) for a MauriceFlex cIEF or MauriceFlex Fractionation batch in a 96-well plate on a MauriceFlex system. Fractions for a MauriceFlex Fractionation batch are collected in the 96-well plates.



Maurice C.



Maurice

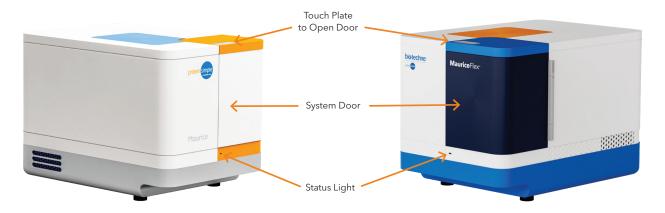




MauriceFlex

Maurice S.

External Components



!WARNING!

You can't replace or service any parts on Maurice systems except for the power entry fuse.

System Door

Maurice's door gives you access to the inside of the instrument to load cartridges, reagents and samples. To open the door, first make sure the status light is a steady blue. Then just touch the metal touch plate on the top. The blue status light will flash and the door will automatically open. Close it by pushing the door from the front until you hear the latch engage and see the status light turn solid.

NOTE: Maurice's door must be closed before starting a batch.

Status Light

The LED on Maurice's front panel tells you what he's doing. Here's what his different status lights mean:

- Start-up (magenta): You've just turned on the power and Maurice is warming up.
- Ready (steady blue): Maurice is powered on and ready to go.

NOTE: If after you power Maurice on the LED doesn't change from magenta to blue, the system didn't initialize. Please call ProteinSimple Technical Support.

- Opening Door (long blue flash followed by blue pulses): Maurice's door is opening.
- Running (pulsing blue): Maurice is running a batch.

- **Paused (blue pulse with magenta flashes):** The batch is paused. You can edit the batch and open Maurice's door to add new samples or reagents.
- Trying to Open Door While Running (red flash): Maurice's door can't be opened when he's running.
- Error (steady red): Maurice has detected an error. To get more information on the error, check the Status pane in the Run Summary Screen in Compass for iCE.



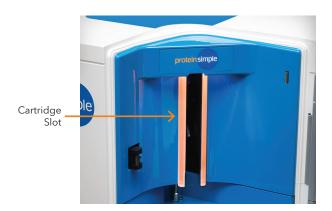
Internal Components

Cartridge Slot

The cartridge slot holds Maurice's ready-to-go application cartridges. The cartridge it holds depends on the system:

- Maurice: cIEF, CE-SDS PLUS and Turbo CE-SDS Cartridges only
- Maurice C.: cIEF Cartridges only
- Maurice S.: CE-SDS PLUS and Turbo CE-SDS Cartridges only
- MauriceFlex: cIEF, CE-SDS PLUS, Turbo CE-SDS and cIEF Fractionation Cartridges

The lights on either side of the cartridge slot will be **orange** after Maurice disengages the cartridge when the door is opened at the end of a batch, and whenever the slot is empty.





The lights change to **blue** once a cartridge is installed correctly.

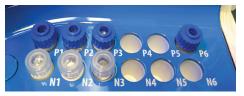


NOTE: You can find cartridge prep, installation and post-run procedures in Chapter 6: "Running cIEF Applications", Chapter 8: "Running MauriceFlex cIEF Applications", Chapter 10: "Running MauriceFlex Fractionation Applications", Chapter 12: "Running CE-SDS PLUS Applications" and Chapter 14: "Running Turbo CE-SDS Applications"

Sample and Reagent Platform

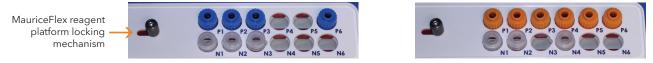
Maurice's sample and reagent platform for performing standard cIEF applications using a cIEF cartridge and CE-SDS applications using a CE-SDS PLUS or Turbo CE-SDS cartridge has two rows for batch reagents. These reagents are kept at room temperature.

- **Row P (top):** These reagents are loaded under pressure during the batch. Only use glass reagent vials with pressure caps in this row. Use **blue** pressure caps with cIEF reagents and **orange** pressure caps with CE-SDS reagents.
- Row N (bottom): Only use reagent vials with clear screw caps in this row.





Reagent platform for cIEF applications (left) and CE-SDS applications (right) on Maurice, Maurice C. and Maurice S.



Reagent platform for cIEF applications (left) and CE-SDS applications (right) on MauriceFlex.

IMPORTANT:

Reagent vials on MauriceFlex must be locked in place by sliding the locking mechanism from the left to the right before starting a batch.

Use glass reagent vials, 2 mL (PN 046-017) for standard cIEF and CE-SDS applications on Maurice, Maurice C., Maurice S. and MauriceFlex.

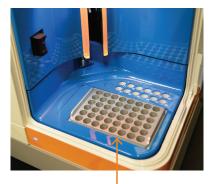
The sample block holds either a 96-well plate or 48-vial metal insert and is temperature-controlled. You can set it to 4 °C, 10 °C, 15 °C or turn the temperature control off in Compass for iCE software.

Sample cooling turns on when the run starts, and takes a few minutes to reach the temperature setting. After a run, the sample block stays at the set temperature until you open Maurice's door, then it shuts off until you start the next run. This prevents excess condensation.

NOTE: Because Maurice holds the sample block temperature after a run until you open the door, samples are still viable for your next run and after overnight runs.



96-well Plate Insert for Maurice, Maurice C. and Maurice S.



48-vial Insert for Maurice, Maurice C. and Maurice S.



96-well Plate Insert for MauriceFlex

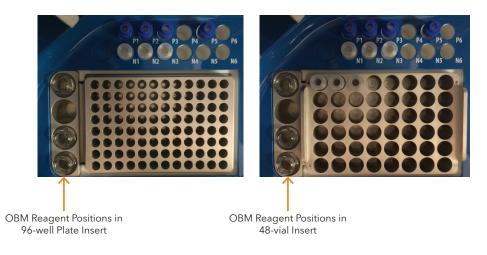


48-vial Insert for MauriceFlex

Chapter 3: Maurice | Internal Components

Maurice-OBM and Maurice C.-OBM instruments will also have four additional reagent locations in the 96-well plate and 48-vial metal inserts. These reagents are also temperature controlled at the same setting used for the samples.

• Column M (left): These reagents are used for on-board mixing. Only use 6 mL reagent vials in this row.



NOTES:

On-board mixing is only availabe on Maurice and Maurice C. systems.

When you're using a 96-well plate, well A1 should be in the top left corner of the insert.

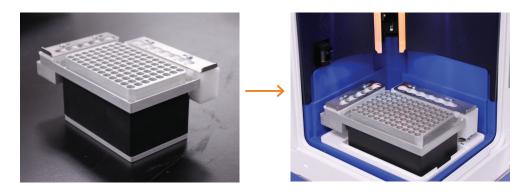
You can only use V-bottom plates with the 96-well plate insert. To ensure performance, we recommend only using 96-well plates from ProteinSimple (PN 046-021).

Remove plate lids before inserting a 96-well plate into Maurice.

You can find info on where to load reagents and samples for cIEF applications in "Step 4: Load Samples and Reagents" on page 99, for CE-SDS PLUS applications in "Step 4: Load Samples and Reagents" on page 299 and for Turbo CE-SDS application in "Step 4: Load Samples and Reagents" on page 368.

Fractionation Adapter

MauriceFlex uses a fractionation adapter for use with MauriceFlex cIEF or MauriceFlex Fractionation Applications.



The fractionation adapter has one row and one column for batch reagents.

- Row R (top): These reagents are kept at room temperature. Only use glass vials with insert, 0.3 mL (PN 110-0018) for the Fluorescence Calibration Standard and 2 mL crimp top glass vials (PN 110-0019) for reagents in this row. Caps are not required on the vials.
- Column K (left): These reagents are temperature controlled. Only use 2 mL crimp top glass vials (PN 110-0019) vials for reagents in this row. Caps are not required on the vials.



NOTES:

Remove all the vials in rows P and N of the reagent platform before installing the fractionation adapter if a CE-SDS or standard cIEF application was previously performed.

When installing the fractionation adapter, confirm the adapter is seated and sitting flat in MauriceFlex.

Reagent vials on MauriceFlex must be locked in place before starting a batch. The vial locking mechanism default state is locked. Pull the locking mechanism on Row R to the right and the locking mechanism on Column K down to unlock and place vials in the fractionation adapter. Release the locking mechanism to lock the vials in place.

If the fractionation adapter locking mechanism does not spring back upon release, check that all the vials are seated.



Unlocked Row

Unlocked Column

The fractionation adapter can hold a 96-well plate and is temperature-controlled. You can set it to 10 °C, 15 °C or turn the temperature control off in Compass for iCE software.

Sample cooling turns on when the run starts, and takes a few minutes to reach the temperature setting. After a run, the sample block stays at the set temperature until you open MauriceFlex's door, then it shuts off until you start the next run. This prevents excess condensation.

NOTES:

MauriceFlex holds the sample block temperature after a run until you open the door.

When placing the 96-well plate in MauriceFlex, well A1 should be in the top left corner of the insert.

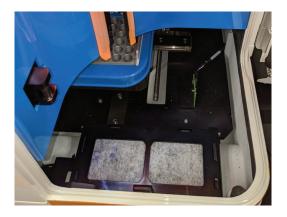
You can only use V-bottom plates with the 96-well plate insert. To ensure performance, we recommend only using 96-well plates from ProteinSimple (PN 046-021).

Remove plate lids before inserting a 96-well plate into MauriceFlex.

You can find info on where to load reagents and samples for MauriceFlex cIEF applications in "Step 2: Load Samples and Reagents" on page 161 and for MauriceFlex Fractionation applications in "Step 2: Load Samples and Reagents" on page 226.

Filter

The optional Maurice System Filter Upgrade adds a fan and filter assembly to the Maurice system to help eliminate odors or vapors that may be present in sample plates from substances such as beta-mercaptoethanol (β ME). The Maurice Filter Kit (PN 046-576) comes with replacement carbon filters and plate lids to cover sample plates when transporting them to and from Maurice.



For more information on filters see "Installing or Replacing the System Filter" on page 795.

Using the Plate Lid

The plate lid is provided for use with Maurice 96-well plates (PN 046-021). We recommend using the lid whenever you run reduced samples on a Maurice CE-SDS PLUS and Turbo CE-SDS batches. For best results, keep the lid on the plate whenever it's not in the Maurice sample block, including after samples are loaded in the wells, when transporting the plate around the lab, and immediately after a batch is completed and the door is opened.

IMPORTANT

Be sure to remove the plate lid before you start a batch! Leaving the lid on the plate will result in damage to the cartridge.

Rear Panel

Located on Maurice's rear panel is the power entry, power switch and network connector.



• System Power - The main system power components consist of the power input, fuse and power switch

!WARNING!

Only use the power supply cord provided with Maurice. If the cord is damaged, please contact ProteinSimple Technical Support.

!WARNING!

You can't replace or service any parts on Maurice except the power entry fuse.

!WARNING! SHOCK HAZARD

Disconnect the power cord from Maurice's power input to disconnect power to the instrument.

• Network connection - A 10/100/1000 Mbps Ethernet (RJ-45 connector) is used to connect Maurice to a computer or local network.

NOTE: Serial numbers are used to identify individual instruments.

System Labels

A full system label is located on the rear panel. It includes the ProteinSimple location, system model, power requirements, serial number and certification markings.



A serial number label is located on the Maurice system's front lower right side, on the system base.



Computer Workstation

The PC has two built-in Ethernet ports, one is used for Maurice and the other is available for your company's network. ProteinSimple configures one port to have a fixed IP for a local link connection to the instrument, the other is configurable by users and will typically use a DHCP for dynamic IP. Set the IP address to 172.30.1.2 subnet 255.255.255.0 to connect to Maurice.



Chapter 4: Compass for iCE Overview

Chapter Overview

- Launching Compass for iCE
- Compass for iCE Overview
- Software Menus
- Changing the Compass for iCE Main Window Layout
- Viewing the User Guide
- Visiting the Bio-Techne Academy
- Checking for and Installing New Versions of Compass for iCE
- Viewing Release Notes
- Sending Run Files to Technical Support
- Compass for iCE Version Information
- Directory and File Information

Launching Compass for iCE



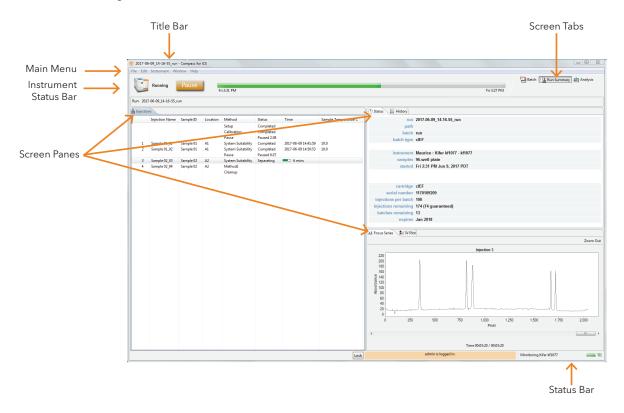
To open Compass for iCE, just double-click the icon on the computer desktop.

Compass for iCE Overview

Compass for iCE has three main screens:

- Batch You'll create and review your batch.
- Run Summary Check out the status of your run.
- Analysis Take a look at the data from your experiment.

Each screen has these components:



Changing the Screen View

To toggle between the Batch, Run Summary and Analysis screens, just click the button in the screen tab located in the upper right corner of the main window.



Batch Screen

The Batch screen is used to create, view, and edit batches. You can assign samples to 96-well plate wells or vials, create and modify methods, customize your injection list and assign methods to each of your injections. The Batch screen is also where you can define how many fractions to collect and which row to start collecting fractions when performing a MauriceFlex Fractionation batch.

File Edit Instrument	Window Help								
	·····						🔛 Batch ᠿ Run Sumn	and the	Anal
Batch: Maurice_CE-SDS	TURBO Reduced	Init Init	ections 🔚 History <u> </u> N	otes		Pause	O Stop It Add III Replicate X Remov		
			Injection Name	Sample ID	Location	Method	Notes		
Layout		1	Sample 01_01	Sample 01	A1	Reduced IgG			
Layout			2 Sample 01_02	Sample 01	A1	Reduced IgG			
5	10°C - C+ Add - CX Rem	ove	3 Sample 01_03	Sample 01	A1	Reduced IgG			
			4 Sample 01_04	Sample 01	A1	Reduced IgG			
C1	C2 Water Sep. Wash Empty		5 Sample 01_05	Sample 01	A1	Reduced IgG			
			6 Sample 01_06	Sample 01	A1	Reduced IgG			
			7 Sample 01_07	Sample 01	A1	Reduced IgG			
			8 Sample 01_08	Sample 01	A1	Reduced IgG			
Wast	Run Run Run		9 Sample 01_09	Sample 01	A1	Reduced IgG			
1 2 3	4 5 6 7 8 9 10 11 12		1(Sample 01_10	Sample 01	A1	Reduced IgG			
			11 Sample 01_11	Sample 01	A1	Reduced IgG			
в			12 Sample 01_12	Sample 01	A1	Reduced IgG			
c (((((((((((((((((((✓ 13	Sample 02_13	Sample 02	A2	Reduced IgG			
POOO			14 Sample 02_14	Sample 02	A2	Reduced IgG			
ECOO			1: Sample 02_15	Sample 02	A2	Reduced IgG			
FOOD			16 Sample 02_16	Sample 02	A2	Reduced IgG			
•			17 Sample 02_17	Sample 02	A2	Reduced IgG			
н			18 Sample 02_18	Sample 02	A2	Reduced IgG			
-			15 Sample 02_19	Sample 02	A2	Reduced IgG			
			20 Sample 02_20	Sample 02	A2	Reduced IgG			
			21 Sample 02_21	Sample 02	A2	Reduced IgG			
			22 Sample 02_22	Sample 02	A2	Reduced IgG			
			2: Sample 02_23	Sample 02	A2	Reduced IgG			
			24 Sample 02_24	Sample 02	A2	Reduced IgG			
Methods									
								New	Rem
Name	Sample Load		Separation						
Reduced IgG	8 sec 3500 Volts		5.5 min 4200 Volts						
Non-reduced IgG	8 sec 3500 Volts		8.0 min 4200 Volts						
MW Markers	8 sec 3500 Volts		8.0 min 4200 Volts						

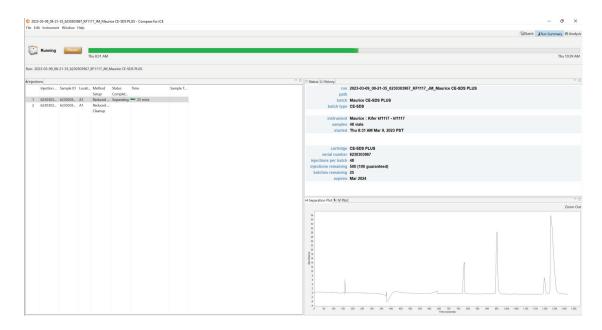
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		Injection		Sample ID	Location	Method	Notes	
" Layout		1 System Si	uit 01	System Suit	A1	Method1		
		2 Peptide N		Peptide Mix	A2	Method1		
🛑 💥 📑	10°C - C Add - C Remove	3 mAb_03		mAb	A3	Method2		
		4 System Se	uit_04	System Suit	A1	Method1		
	FI Cal Water Empty	5 Peptide N		Peptide Mix	A2	Method1		
() Wat		6 mAb_06		mAb	A3	Method2		
A B B C D E F								
Methods								
								New Rem
Name	Separation	Detection	Sample Load (s)		Ampholytes J	Additives		
Method1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures	90	3.38, 10.17				
	1.0 min 1500 Volts, 6.0 min 3000 Volts	6 Exposures	90	4.05, 9.99				
Method2								

	Window Help							🔛 Batch ᠿ Run Su	
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			Injection N		ample ID	Location	Method	Notes	
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-	and the Are				ample 02	A2	IgG		
	10°C 👻 🚺 Add 👻 候 Ren	nove			ample 03 ample 04	A3 A4	lgG lgG		
Methods									
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Name	Separation		Detection	Sample Load (s)	pl Markers	Ampholytes A	dditives		
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E Layout					Fraction 01	B1	.9-					
10°C -	👎 Fractions 🔇 Add 👻 🔇 Remove	-			Fraction 02	B2						
					Fraction 03	B3						
	IC FICal Water Water Empty				Fraction 04	B4						
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					Fraction 06	B6						
					Fraction 07	B7						
					Fraction 08	B8						
	1 2 3 4 5 6 7 8 9 10 11 12				Fraction 09	B9						
Sample A					Fraction 10	B10						
Ki B					Fraction 11	B11						
Catholyte					Fraction 12	B12						
Mobilizer					Fraction 13	C12						
13 1					Fraction 14	C11						
Mobilizer O		-			Fraction 15	C10						
K4 0					Fraction 16	C9						
Water H					Fraction 17	C8 C7						
15					Fraction 18 Fraction 19	C/ C6						
					Fraction 19 Fraction 20	C6						
					Fraction 20 Fraction 21	C3						
					Fraction 22	C4						
					Fraction 23	C2						
••••					Flaction 25	C2						
Methods											New	
Name	Separation	De	etection S	Sample Load (s)	Mobilization	Refocus	Fractions	pl Markers	Ampholytes	Additives	INEW	
lqG	10.0 min 500 Volts, 10.0 min 1000 Volts, 25.0 min 150			20	25.0 min 100	0.0 min 150	45.0 sec 100	7.05, 10.17				
90		· · · · ·	exposure 2		23.0 1111 100	0.0 1111 1 50	45.0 Sec 100	1.03, 10.17				

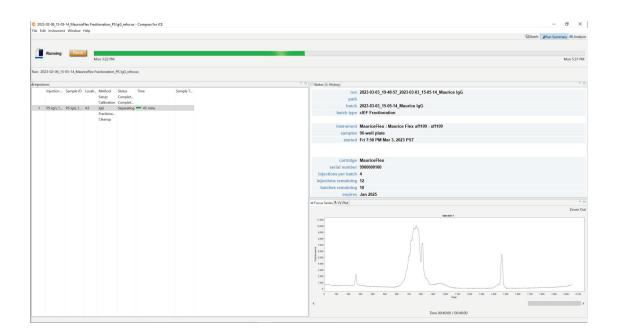
Run Summary Screen

The Run Summary screen is used to monitor status of a batch in progress, view the CE-SDS Separation plot or cIEF, MauriceFlex cIEF and MauriceFlex Fractionation Focus series for each injection and view the current and voltage plots for each injection.



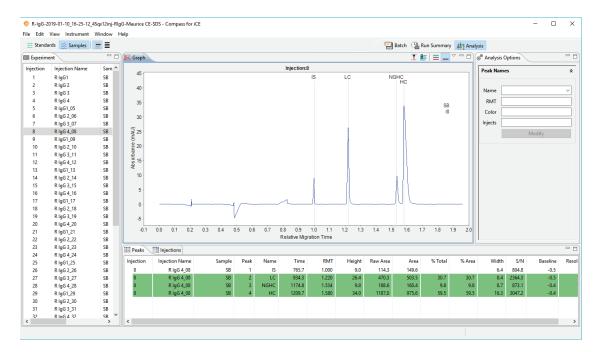
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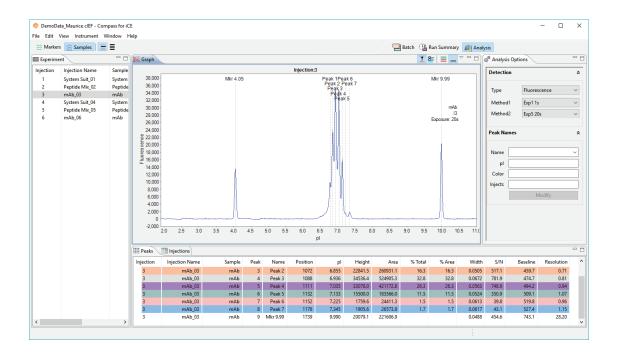
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					Complet			batch 2023.03.03_MauriceFlex.clEF MDG
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2	Seamen	Seagen	43	Cleanup SG.Math	Complet	2023-02-06 13:43:42	10.2	
	ounger().	stagenen	10	Cleanup	Complet_	LOLD OL OU IDIGIAL	TOTAL.	instrument MauriceFlex : Maurice Flex xf1109 - xf1109
3	NIST_05	NIST_05	A4	NIST		2023-02-06 14:38:33	10.3	samples 96-well plate
				Cleanup	Complet		_	started Fri 8:22 PM Mar 3, 2023 PST
4	PS Ig0_1	PS IgG_1	AS	PS IgG Cleanup	Separating	45 mins		
								cartridge MauriceFlex
								serial number 9900000100
								injections per batch 4
								injections remaining 11
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								M Focus Series € (V Plot
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								Time 00-40:00 / 00-40:00
								Time 004000 / 004000

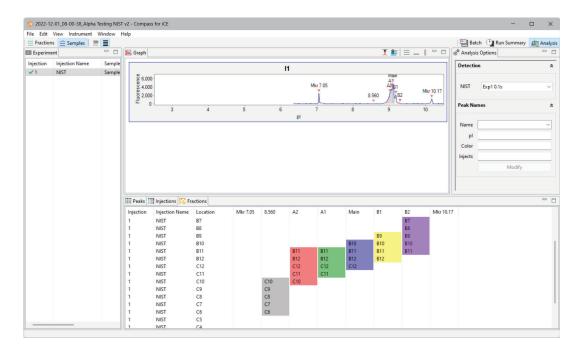


Analysis Screen

The Analysis screen is used to view data from your batch, including the graph view (electropherograms) and a table with your results, and analyze data for completed runs. For MauriceFlex Fractionation batches, you can also view a table predicting where each sample peak is collected into a 96-well plate.







Screen Panes

Each of the Batch, Run Summary and Analysis screens have multiple panes that let you view the individual components of a batch, method or data file. Each pane has a labeled tab and a unique icon. We'll describe panes specific to each screen later in the individual screen sections.

The active pane in a screen is blue. To view a pane, click in the pane or on its tab. The screen panes can be minimized and moved. To return to the default view, select **Default Layout** in the Window menu. The example below shows panes in the Batch screen, and the Graph pane is active:

Experime	ent			尻 Graph
Injection	Sample	Location	Me	

Title Bar

In the title bar you will see the batch file name and the icons that allow the main Compass for iCE window to be minimized, maximized or closed.

ladder assigned_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS - Compass for iCE

Main Menu

Access to various software, instrument and screen operations is available through the main menu. More details on menu commands can be found in "Software Menus" on page 44.

File Edit View Instrument Window Help

Instrument Status Bar

The instrument status bar is used to start batches and cleaning protocols, indicate system status and show run progress. More details on instrument control and status can be found in Chapter 17: "Controlling Maurice, Maurice C., Maurice S. and MauriceFlex".

File Edit Instrument Window Help		
Running Pause	Tue 10:49 AM	Wed 9:39 AM
File Edit Instrument Window Help		
		🗐 🖽 Batch 🖓 Run Summary 🚛 Analysis
Running Pause	Tue 1:50 PM	Tue 2:15 PM

NOTE: You will only see the instrument status bar when Compass for iCE is connected to an instrument. There is no status bar on computer workstations that you're only using for data analysis.

- -

Screen Tab

The screen tab lets you move between Batch, Run Summary or Analysis screens and is located in the upper right corner of the main window. Just click a button to view a screen.



View Bar

The view bar is only displayed in the Analysis screen as part of the main menu, and allows you to switch between viewing standards or sample data for a CE-SDS batch, markers or sample data for a cIEF batch and fractions or sample for a MauriceFlex Fractionation batch. You can also switch between data for a single injection or all injections in the batch, or grouped injection data. View bar options are in "Analysis Options Pane" on page 483 for cIEF and MauriceFlex cIEF applications, page 671 for CE-SDS applications or page 580 for MauriceFlex fractionation application.

🚊 Markers 🚉 Samples 📃 🚍

Compass for iCE Status Bar

The status bar is in the lower right corner of the main window. It displays active software processes and their progress.

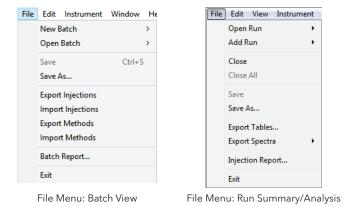
Analyzing: MW ladder as...urice CE-SDS 🛛 🔤 👘

Software Menus

Some of the items in the Compass for iCE main menu are available in specific screens only, and menu commands change depending on which screen is active. You can find menus and commands available for each screen in the Chapter 5: "cIEF Batches", Chapter 7: "MauriceFlex cIEF Batches", Chapter 9: "MauriceFlex Fractionation Batches", Chapter 11: "CE-SDS PLUS Batches", Chapter 13: "Turbo CE-SDS Batches", Chapter 16: "Run Status", Chapter 18: "cIEF Data Analysis", Chapter 20: "CE-SDS Data Analysis", Chapter 19: "MauriceFlex Fractionation Data Analysis".

File Menu

The File menu contains basic file commands. The file menu options change when you change between the Batch View or Run Summary/Analysis tab.



Edit Menu

The Edit menu contains basic editing commands, analysis and preferences options. Specific details on preferences are described in Chapter 21: "Setting Your Preferences".

Edit	View	Instrument	Windo				
	Cut	Ct	rl+X				
	Сору	Ctrl+C					
	Paste	Ct	rl+V				
	Analysis Preferer						

View Menu

The View menu is only available in the Analysis screen, and allows you to change how your data is displayed. For more info on view options check out "Analysis Options Pane" on page 483 for cIEF applications, page 671 for CE-SDS applications or page 580 for Maurice Fractionation and "Using Groups" on page 498 for cIEF applications or page 684 for CE-SDS applications.

/iew Instrument Window	View Instrument Window	View Instrument Window
Selected All	Selected All	Selected All
Standards	Markers	Fractions
Samples	Samples	Samples
Grouping	Grouping	Grouping
View Region	View Region	View Region
Show Hidden	Show Hidden	Show Hidden
CE-SDS Application	Standard cIEF and	MauriceFlex Fractionatior
	MauriceFlex cIEF Application	Application

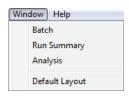
Instrument Menu

The Instrument menu is only available when the software is connected directly to your instrument. You can learn more about instrument control options in Chapter 17: "Controlling Maurice, Maurice C., Maurice S. and MauriceFlex".

File	Edit	Instrument	Window	Help	
		Cartrid	ge Post-Ru	n Cleanup	1
		Cartrid	ge Purge		
	-	Self Te	st		>
1	-	Runs			
Batch	h: Mau	Proper	ties		
	ayout	Update			>
		Discon	nect		

Window Menu

The Window menu lets you to switch between the Batch, Run Summary or Analysis screens, and restore screens to the default layout.



- Batch Displays the Batch screen where you create, view, and edit batches.
- Run Summary Displays the Run Summary screen which lets you view the status of a batch in progress.
- Analysis Displays the Analysis screen that lets you view electropherograms and results and change analysis parameters
- Default Layout Restores the individual panes in the current screen back to their default size and location.

Help Menu

The Help menu gives you access to Help, software updates, release notes and other software info.



- User Guide Displays the User Guide for Maurice, Maurice C., Maurice S, and MauriceFlex.
- **Bio-Techne Academy** Redirects you to the online Bio-Techne Academy where you can watch online training videos for Maurice, register for online workshops and access product collateral.
- Check for Updates Automatically checks to see if a new version of Compass for iCE is available.
- Release Notes Displays the software release notes for the current and prior versions.
- Export Log Sends a zipped log file directly to ProteinSimple Technical Support.
- Send Run File Sends a zipped run file directly to ProteinSimple Technical Support.
- About Compass for iCE Displays the software version and build information.

Changing the Compass for iCE Main Window Layout

You can easily resize the main window and the individual panes in each screen. Screen panes can also be moved outside of the main window.

Resizing the Main Compass for iCE Window

To resize the main window, roll the mouse over a corner or border until the sizing arrow appears. Then just click and drag to resize.

Resizing the Screen Tab

The screen tab can be sized to show all or just some of the screen buttons. To resize, roll the mouse over the left edge of the tab until the sizing arrow appears, then click and drag to resize. If a screen button is hidden, a double arrow will display in the tab. Just click to display and select the hidden screen.

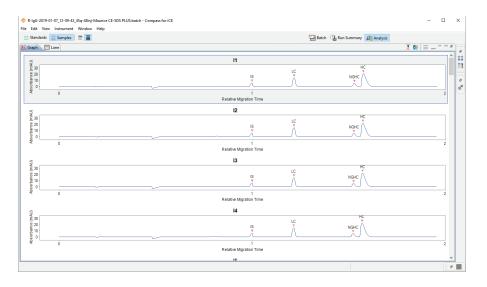


Resizing Screen Panes

- To resize a pane Roll the mouse over the pane border until the sizing arrow appears. Then just click and drag to resize.
- To maximize a pane Click the maximize button in the upper right corner or double-click the tab.

💾 Batch 强 Run Summary 🚛 Analysis		
M	axir	nize

The other panes in the screen will automatically minimize to pane bars in the task area along the window border.



• To restore all minimized panes - Click Restore on the minimized pane bar.



• To restore only one minimized pane - Click the pane icon on the minimized pane bar.



• To restore a maximized pane to its original size - Double-click the tab or right click the tab and click Restore.

Graph		
	Detached	
S	Restore	
₹ E_ 15	Move	+
2 10	Size	•
Lpar 5	Minimize	
Absorbance (mAU) 0 2 01 2	Maximize	
	Close	

• To restore all panes to their original sizes - Select Window in the main menu and click Default Layout.

Changing the Location of Screen Panes

Panes can be moved to different locations within a screen.

• **To move a pane** - Click on its tab and drag it to the new location. As the pane is moved, area guides will display to assist you in choosing a drop location.



Area guides with a black arrow let you know that if the pane is dropped at that location, it will be resized and relocated as an individual pane in that area of the screen.

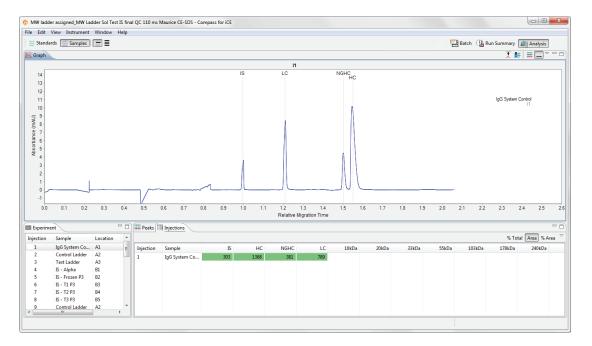


Area guides with a folder let you know that if the pane is dropped at that location, it will be added as a new tab in an area with one or more pane tabs.

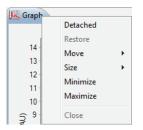


Area guides with a window let you know that if the pane is dropped at that location, it will be a separate window outside the Compass for iCE main window.

This example shows the Analysis screen after moving the Graph pane:



• To detach a pane from the main window - Click on its tab and drag it outside the main Compass for iCE window or right click the tab and click Detached.



- To move a detached pane back inside the main window Right click the tab and deselect Detached.
- To restore all panes to their original locations Select Window in the main menu and click Default Layout.

Restoring the Main Window to the Default Layout

To restore screen pane sizes and locations to the original Compass for iCE layout, select **Window** from the main menu and click **Default Layout**.

Viewing the User Guide

Select Help and click User Guide to view Maurice Systems User Guide.

- If the computer you're using has an internet connection, the latest online version of the User Guide PDF will display.
- If your computer doesn't have an internet connection, you'll first need to download the User Guide PDF from another computer or contact tech support for a copy. Upload the PDF file to the C:\Program Files\Compass for iCE folder to access the User Guide from the Help menu.

Visiting the Bio-Techne Academy

Select **Help** and click **Bio-Techne Academy** to get redirected to this online resource. Registered users can view online training videos, registers for online workshops or watch previous workshops and view instrument collateral. Training videos in Chinese, Korean, Japanese and French are also available. Enter Maurice in the search window to view Maurice-related content only.

Checking for and Installing New Versions of Compass for iCE

The software can automatically check to see if a newer version of software is available. To do this:

- 1. Make sure the computer being used has an active internet connection.
- Select Help and click Check for Updates. If an update is found, a screen will display with the new version that's available.

- 3. Click Finish to start the download and install the update.
- 4. Follow the on-screen instructions to complete the software installation.
- 5. Reboot the computer before using the new version of software.

Viewing Release Notes

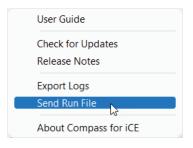
Select **Help** and click **Release Notes** to view feature updates and bug fixes for new and past versions of Compass for iCE. If the computer you're using has an internet connection, the latest online version of the release notes PDF will display. When an internet connection isn't available, the release notes PDF shipped with the original installer for the software will open instead. We recommend you review these notes whenever a software update is installed.

NOTE: You can contact ProteinSimple Technical Support to request the release notes for new versions of Compass for iCE before you install it.

Sending Run Files to Technical Support

If the computer you're using has an internet connection, Compass for iCE can zip and send a run file directly to ProteinSimple Technical Support.

- 1. Open the run file in Compass for iCE.
- 2. Select Help in the main menu and click Send Run File:



3. Enter your Name, Company and E-mail address, and any details in the Comments section:

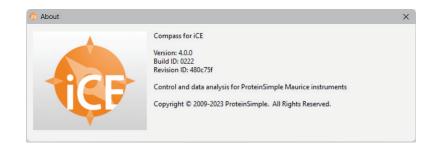
츊 Send Run Fi	le	×
File:	DemoData_Maurice clEF.mbz	
Name:		
Company:]
*Email:]
Instrument:	kf1004]
Comment:		
	Send Cancel	

4. Click Send. When the file upload is complete, the following message displays. Click OK.



Compass for iCE Version Information

Select Help and click About Compass for iCE to view the software version and build number information.



Directory and File Information

The main Compass for iCE directory is located in the **Program Files** folder, and also contains PDF files of the User Guide for Maurice, Maurice C., Maurice S. and MauriceFlex.

	🔄 🖻 🗊 🔨 Sort ~ 🗏	View - ···			
\leftrightarrow \rightarrow \checkmark \uparrow \blacksquare > This PC >	OS (C:) > Program Files > Compass for iCE >	~ C 0	Search Compass fo	r iCE	
✓ ➡ Program Files	Name	Date modified	Туре	Size	
> 🛅 Acrolinx	Configuration	2/23/2023 9:53 AM	File folder		
> 🔁 Adobe	Examples	2/23/2023 9:53 AM	File folder		
Clockify	afeatures	2/23/2023 9:53 AM	File folder		
> 📁 Common Files	🚞 jre	2/23/2023 9:53 AM	File folder		
 Compass for iCE 	p 2	11/9/2022 11:45 AM	File folder		
> 🚞 configuration	Dugins 🔁	2/23/2023 9:53 AM	File folder		
🚞 Examples	templates	11/9/2022 11:45 AM	File folder		
> 🚞 features	Client.policy	2/15/2023 2:26 PM	POLICY File	1 KB	
> 🚞 jre	E Compass for iCE Release Notes.pdf	2/22/2023 3:11 PM	Adobe Acrobat D	1,066 KB	
> 📁 p2	🛃 Compass for iCE User Guide.pdf	7/15/2022 11:18 AM	Adobe Acrobat D	24,630 KB	
> 🚞 plugins	Ompass for iCE.exe	2/22/2023 3:14 PM	Application	418 KB	
> 🚞 templates	Compass for iCE.ini	2/22/2023 3:14 PM	Configuration setti	1 KB	
> 🚞 Dell	\min license.rtf	2/15/2023 2:26 PM	Rich Text Format	21 KB	
DellTPad	server.policy	2/15/2023 2:26 PM	POLICY File	1 KB	

Batch and run files are located in the Documents folder in the User directory on your computer:

🕽 Libraries 4 🗟 Documents	Documents library Compass for ICE				
4 📗 My Documents	Name	Date modified	Date created	Туре	Size
Add-in Express Adobe Clients	Batches New Batches	1/18/2016 5:39 PM 1/13/2016 8:24 PM	1/13/2016 8:24 PM 1/13/2016 8:24 PM	File folder File folder	
Compass for iCE	Runs DemoData Maurice cIEF.mbz	1/17/2016 8:41 PM 1/18/2016 11:38 AM	11/11/2015 4:46 PM	File folder	798

- Batches Folder Contains all batch files that you've saved.
- New Batches Folder Contains Maurice batch template files.
- Runs Folder Contains all batch data files. Data is automatically written to this folder.

NOTE: When a Compass for iCE software update is performed, the template s in the New Batch folder are overwritten. If you have customized these batches, we recommend saving them in a unique subfolder prior to updating the software, then transferring them back to the New Batch folder after the update to avoid losing your customizations.

File Types

These file types are used by Compass for iCE:

- Batch Files Use a *.batch file extension.
- **Run Files** Use a *.mbz file extension. The default file format for run files is Date_Time_BatchName. An example run file name would be 2016-01-28_18-50-53_CE-SDS.mbz.
- Analysis Settings Files Exported analysis settings files use a *.settings file extension.

Chapter 5: CIEF Batches

Chapter Overview

- Overview
- Batch Screen Overview
- Opening a Batch
- Creating a New Batch
- Viewing Replicate Injections
- On-board Mixing (Maurice and Maurice C.)
- Batch History
- Making Changes to a Batch
- Viewing and Editing Batches in Completed Runs
- Copying and Pasting Injection Names or Sample IDs from other Documents
- Importing and Exporting Injections
- Importing and Exporting Methods
- Batch Reports

Overview

Standard cIEF batches can be run on Maurice, Maurice C. or MauriceFlex using a cIEF cartridge.

Batch Screen Overview

You can use the Batch screen to create, view and edit batches. To get to this screen, click the Batch screen tab:

Batch 🖓 Run Summary 🏥 Analysis

Batch Screen Panes

The Batch screen has five panes:

- Layout Displays a map of either the 96-well plate or 48-vial tray of batch sample locations.
- **Injections** Lists the injections, sample ID, sample locations and methods that Maurice, Maurice C. or MauriceFlex will execute for each sample in the batch.
- History Lists all batch file events from initial creation to the most current update.
- Notes Lets you enter specific information about your batch.
- Methods Lets you create methods and enter method parameters used in the batch.

Batch: 2016-01-21_09-46	-39_mAb11_Prep20160121_QC(0)	Injections	🔚 History 🖪 N	lotes					Pause Sto	op 🎁 Add 📗 Re	plicate 🛛 🗶 Remove	• • •
[™] Layout ● 🛞 🚺 10°C <u>M</u> C		1 2 3 4 5 6 7	System Suitability.0 mAb 11 Blank, 20 mAb 11 Ref. Std. 03 mAb 11 Ref. Std. 03 mAb 11 Prep 20160 mAb 11 Prep 20160 mAb 11 Prep 20160 mAb 11 Prep 20160 mAb 11 Ref. Std. 07 mAb 11 Blank_08	1 121_04 121_05 121_06	Sample ID System Suit mAb 11 Bla mAb 11 Ref mAb 11 Pre mAb 11 Pre mAb 11 Pre mAb 11 Ref mAb 11 Ref	nk 5. Std. 20160121 20160121 20160121 5. Std.	Location A1 A2 A3 A4 A4 A4 A3 A2 A2	Method System Suitability mAb Method mAb Method mAb Method mAb Method mAb Method mAb Method mAb Method	Notes			
Methods Name System Suitablity mAb Method	Separation 1.0 min 1500 Volts, 4.5 min 3000 Volts 1.0 min 1500 Volts, 6.0 min 3000 Volts		Detection 5 Exposures 5 Exposures	Sample 55 55	: Load (s)	pl Markers 3.38, 10.17 4.05, 9.99	Ampholyte	s Additives				e New Rem

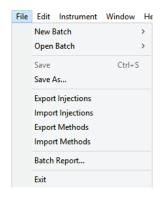
Software Menus Active in the Batch Screen

These main menu items are active in the Batch screen:

- File
- Edit
- Instrument (when the software is connected to Maurice, Maurice C. or MauriceFlex)
- Window
- Help

File Menu

These File menu options are active:



- New Batch Creates a new batch from a starter template.
- Open Batch Opens an existing batch.
- Save/Save As Saves the open batch.
- Export Injections Exports injections from the current batch as a .csv file.
- Import Injections Imports injections into the current batch from a .csv file.
- Export Methods Exports method(s) from the current batch as separate files.
- Import Methods Imports saved method(s) into the current batch.
- Batch Report Exports a table of sample and method details for each injection in the batch as a PDF file.
- Exit Closes Compass for iCE.

Edit Menu

The following Edit menu options are active in the Batch screen:

Edit] Instrument Wind	ow Help	_		
	Cut	Ctrl+X			
	Сору	Ctrl+C	-		.
	Paste	Ctrl+V			In
	Plate Layout	۰.	•	48 Vials	5.0
	Default Analysis			96-well Plate	
	Preferences			Air	- 3

- Cut Cuts the information currently selected.
- Copy Copies the information currently selected.
- **Paste** Pastes the copied information.

NOTE: Cut, Copy and Paste work differently depending on the pane you're in. How and when you can use them is described throughout the chapter.

- Plate Layout Lets you select between a 96-well plate or a 48-vial tray to run samples in.
- Default Analysis Displays the default settings that will be used to analyze the data generated with your batch.
- Default Analysis View Displays the default settings that will used to view the data generated with your batch.
- **Preferences** Lets you set and save your preferences for Access Control, data export, graph colors, grouped data and Twitter settings. See Chapter 13: "Setting Your Preferences" for more information.

Opening a Batch

NOTE: cIEF batches that use the FL458 nm fluorescence detection filter can only be opened in Compass for iCE 2.1 or later.

To open an existing batch:

1. Select File in the main menu and click Open Batch.

File	Edit Instrument	Window	Help
	New Batch	•	
	Open Batch	•	Maurice cIEF 011816
	Save Save As		Maurice CE-SDS sample batch Maurice cIEF Maurice CE-SDS2
	Batch Report		Maurice CE-SDS Gen Meth
	Exit		Browse

- 2. A list of the last five batches opened will display based on the last location found. If the location of the file has changed, you may need to navigate to find the file. Select one of those or click **Browse** to open the Batches folder and select a different one.
- 3. To make changes to the batch, see the steps in "Creating a New Batch" on page 59. When you're done, select File from the main menu and click **Save**.

Creating a New Batch

To create a new batch, we recommend that you use one of the template methods and make any necessary modifications from there.

Step 1 - Open a Template Batch

1. Select File in the main menu and click New Batch:

New Batch > Open Batch > Save Ctrl+S Save As MauriceFlex clEF MauriceFlex clEF MauriceFlex clEF	File	Edit Instrument	Window Help	
Save Ctrl+S Maurice Turbo CE-SDS™ Save As		New Batch	>	Maurice cIEF
Save Ctrl+S MauriceFlex clEF		Open Batch	>	Maurice CE-SDS PLUS
Save As		Save	Ctrl+S	
MauriceFlex Fractionation		Save As		MauriceFlex cIEF
E				

NOTE: Only template batches specific to your Maurice will be available when you are connected to the instrument. Template batches will not appear in the menu if that application type cannot be performed on your instrument.

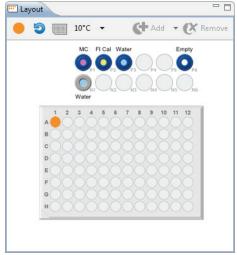
2. Select Maurice cIEF. A batch using the default method will display.

Batch: Maurice cIEF		Injectio	ns 🛛 🔚 History 👖 N	lotes				🕕 Pause 🔘 Stop 🗗 A	dd 📗 Replicat	e 🕌 Remove	• • •
E Layout		1	Injection Name Sample 1_01	Sample ID Sample 1		Location A1	Method System Suitability	Notes			
🛑 🧿 🥅 10°C	- CH Add - CX Remove										
Viete A C C C C C C C C C C C C C C C C C C C											
E C C C C C C C C C C C C C C C C C C C											
E C C C C C C C C C C C C C C C C C C C											New Remo
E F G G G G G G G G G G G G G G G G G G	Separation		Detection	Sample Load (s)	pl Markers	Ampholyte	s Additives				
E C C C C C C C C C C C C C C C C C C C			Detection 5 Exposures	Sample Load (s) 55	pl Markers 3.38, 10.17	Ampholyte	s Additives				
E C C C C C C C C C C C C C C C C C C C	Separation					Ampholyte	s Additives				

Step 2 - Assign Your Samples

The Layout pane shows the default locations of where batch reagent should be placed in your Maurice system's samples and reagents platform, and a map of either the 96-well plate or the 48-vial tray used for samples.

00 C	10°C ▼	C Add	- 🕅 R	emove
	MC FICal V	Vater	Empty	
) O _{P5}	
	Water			
A (2 3 4	5 6	8	
в	OOOC	$) \bigcirc \bigcirc$	\mathcal{O}	
c	OOOC) O O (
D	OOOC	$) \bigcirc \bigcirc$	$\mathbf{)}$	
E	OOOC)))) ()))	
F)	$\tilde{\mathbf{D}}$	



The same reagent locations are used for every batch:

- P1 0.5% Methyl Cellulose with blue pressure cap
- P2 Fluorescence Calibration Standard with blue pressure cap
- P3 Water vial with blue pressure cap
- P6 Empty vial (air) with blue pressure cap
- N1 Water vial with clear screw cap

If you are using Maurice-OBM or Maurice C.-OBM to do on-board mixing:

- N2 Water vial with clear screw cap
- N3 Empty vial with clear screw cap
- M1 6 mL IEF Separation Mix vial
- M2 N/A for 48 samples or less, add a 6 mL IEF Separation Mix vial when running more than 48 samples
- M3 6 mL water vial
- M4 6 mL water vial

NOTE: On-board mixing is only available on Maurice and Maurice C. systems.

1. To assign samples, select 48 vials or a 96-well plate depending on what you're running. Clicking on the vial/plate icon toggles between formats.



2. Select your samples:

To import samples using a saved injections file:

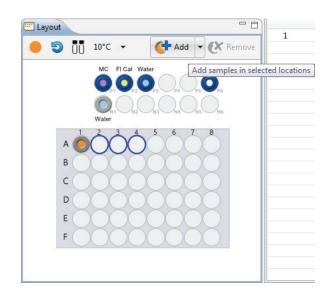
- a. Select File in the main menu and click Import Injections.
- b. Select an injections .csv file and click OK. The imported information will display in the Injections pane.
- c. Skip to step 3 on page 63.

NOTE: For more information on setting up an injections file for import, see "Importing and Exporting Injections" on page 84

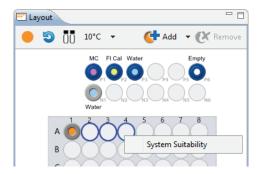
To select samples manually:

• Add samples and select methods later: Use your mouse to highlight the well or vial positions your samples are located in, then click Add. For this example we're using vials.

NOTE: The template batch automatically adds a sample in well or vial A1 by default, but if you don't have a sample in this position you can remove it after you've added new positions for your samples.



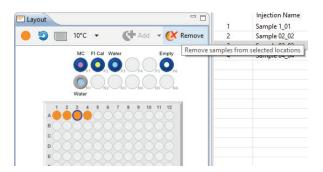
• Add samples with preassigned methods: Highlight the well or vial positions your samples are located in, then right-click and select a method.



Either option of adding samples populates the Injections table:

Injection	ns 🛛 🔚 History 🌃 Notes				🕕 Pause	O Stop	🕇 Add	Replicat	e 🔀 Remove	ŒE) - 0
	Injection Name	Sample ID	Location	Method	Notes						
1	Sample 1_01	Sample 1	A1	System Suitability							
2	Sample 02_02	Sample 02	A2	System Suitability							
3	Sample 03_03	Sample 03	A3	System Suitability							
4	Sample 04_04	Sample 04	A4	System Suitability							

To remove samples, just highlight the ones you want to remove and click **Remove**. They'll also be removed in the Injections table. You can also right-click well(s) or vial(s) in the Layout pane and click **Remove Sample(s)**.



3. Compass for iCE can monitor the current during a separation for you, stop it if an abnormal current profile is detected and reinject the sample for you automatically. Reinjections are enabled by default, but if you don't want to use this feature just click the reinject icon to toggle it off.

NOTES:

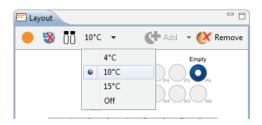
If a sample was reinjected, the injection row will be flagged in the Injections pane in the Run Summary screen. See "Injection Flags" on page 414 for more info.

A maximum of 10 reinjections are allowed per batch.



4. The sample platform is temperature controlled with a default setting of 10 °C. To change the temperature or turn it off, click the **down arrow** next to the temperature and select an option.

NOTE: The two reagent rows are kept at room temperature.



Step 3 - Assign Your Method Parameters

NOTE: We recommend using the default method parameters. Please see the Maurice cIEF Method Development Guide for more information on method optimization.

The Methods pane lists all of the methods used in a batch. You can add and remove methods here and change method parameters.

To import a saved method:

- 1. Select File in the main menu and click Import Method.
- 2. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

To create a new method or make changes to an existing one:

1. In the Methods table, click the first cell in the Name column and enter a new method name if needed.

Name	Separation	Detection	Sample Load (s)	pI Markers	Ampholytes	Additives
Method 1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures	55	3.38, 10.17		

2. Click the first cell in the Separation column, then click the selection button [...] to set the pre-focusing and focusing time (in minutes) and voltage (V).

Methods		ô Separation Profile	
Name	Separation	Add	move
Method1	Voltage 2 Steps	Time (min) Voltage (V	/olts)
		1.0 1500	
		4.5 3000	
		ОК С	ancel

- To change time and voltage parameters: Just click in a cell under Time or Voltage and type the new value(s).
- To add a profile step: Click Add. A new row will be added in the table. Then just type in a load time (in minutes) and voltage value (in V).
- To remove a profile step: Select the row you want to remove and click Remove.

3. Click the first cell in the Detection column the selection button [...] to set your exposure times for absorption and fluorescence detection modes.

ame	Separation	Detection	Add	Remove
lethod1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures 🛄 🗕	Exposure (sec) Type
			0.0050	Absorbance
			3	Fluorescend
			5	Fluorescend
			10	Fluorescend
			20	FL458nm
				Fluorescence
				FL458nm

ОК

Cancel

• To change the exposure time: Just click in a cell under Exposure and type the new value(s) in seconds.

NOTES:

For standard Maurice, Maurice C. and MauriceFlex systems, the first exposure uses Absorbance detection and is a default setting that can't be changed or removed. Fluorescence detections (native fluorescence or FL458 nm) can be changed or removed.

If your Maurice system has the optional 458 nm filter installed, you can choose either the native fluorescence or the FL458 nm fluorescence filter for any of the remaining exposures. The FL458 nm filter enables detection of fluorescence emission at a longer wavelength to analyze molecules other than proteins, such as small molecule drugs in antibody-drug conjugates (ADCs). When used, ratiometric analysis of fluorescence and absorbance data can be applied to support applications including drug-antibody ratio (DAR) analysis.

- To change the fluorescence detection for the exposure: Click in a cell under Type and select an option.
- To add a profile step: Click Add. A new row will be added in the table. Then just type in an exposure time (in seconds). **Optional:** If your Maurice has the FL458 nm filter, you can change the fluorescence detection for the exposure. Click in the Type cell to select an option.
- To remove a profile step: Select the row you want to remove and click Remove.

4. Click the first cell in the Sample Load(s) column and set the load time in seconds.

NOTE: We recommend using the default Sample Load time of 55 seconds. Please contact ProteinSimple Technical Support if you have questions on the Sample Load time to use for your application.

Name	Separation	Detection	Sample Load (s
Method1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures	55

5. Click the first cell in the pI Markers column to select pI markers. Add new markers or remove existing ones then click OK.

NOTE: When you edit the pI markers in the method for a batch, Compass for iCE automatically creates a Markers group in the pI Markers Analysis settings for you.

Atechod1 1.0 min 1500 Volts, 4.5 min 3000 Volts 5 Exposures 55 3.38 10.17 Image: pl Markers: pl Position 3.38 300 10.17 1,700	lame	Separation	Detection	Sample Load (s)	pI Markers		Add	Remove
3.38 300	Method1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures	55	3.38 10.17	\longrightarrow	pI Markers:	
							pI	Position
10.17 1,700							3.38	300
							10.17	1,700

- To change a pI marker and position: Just click in a cell under pI or Position and type the new value(s).
- To add a pI marker: Click Add. A new row will be added in the table. Then just type in a pI and a position (in pixels).
- To remove a pI marker: Select the row you want to remove and click Remove.

6. Optional: Click the first cell in the Ampholytes column and enter the ampholytes you're using.

Name	Separation	Detection	Sample Load (s)	pI Markers	Ampholytes	Additives
Method1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures	55	3.38, 10.17	Pharmalyte 3-10	

7. Optional: Click the first cell in the Additives column and enter any additives you're using.

Name	Separation	Detection	Sample Load (s)	pI Markers	Ampholytes	Additives
Method1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures	55	3.38, 10.17	Pharmalyte 3-10	Urea

- 8. You can now:
 - Click **New** in the upper right corner of the Methods pane to add a new one if you want to use different methods for different samples. Then just repeat the steps above for the new method.
 - Make updates to the remaining methods by repeating the prior steps.
 - Select a method and click **Remove** in the upper right corner of the Methods pane to delete it.

Step 4 - Set Up Your Injections

The Injection pane lists all sample injections for the batch. Any samples that were added in "Step 2 - Assign Your Samples" are automatically added to this list.

NOTE: If you imported injections in Step 2, you can update the injections table and assign methods as needed using the information that follows. Otherwise skip to "Step 5 - Setup On-Board Mixing (Optional)" on page 70.

Selecting an injection in the table also selects the sample the injection will be made from in the plate or vial map in the Layout pane and vice-versa.

atch: Maurice cIEF	📗 Injectio	ons 🔚 History 👖 Not	es		
Layout		Injection Name	Sample ID	Location	Method
	1	Sample 1_01	Sample 1	A1	System Suitability
📄 🔄 📶 10°C 👻 🛛 🚺 Add 👻 🚺 Remove	2	Sample 02_02	Sample 02	A2	System Suitability
	3	Sample 03_03	Sample 03	A3	System Suitability
MC FI Cal Water Empty	4	Sample 04_04	Sample 04	A4	System Suitability
N1 N2 N3 N4 N5 N6					
Water					
1 2 3 4 5 6 7 8 9 10 11 12					
B000000000000					
c0000000000000000000000000000000000000					

1. To add sample names, click the **Sample ID** cell for the injection and type a name.

NOTES:

Sample IDs can be copied from other documents and pasted into Compass for iCE to make batch setup faster. Check out "Copying and Pasting Injection Names or Sample IDs from other Documents" on page 82 for more info.

If you change the sample ID when the default injection name is still being used, the injection name will automatically update to match the sample ID. If you've already changed the injection name manually, updating the sample ID will not update the injection name.

Injection:	s 🛛 📗 History 📑 Notes				🕕 Pause ဝ Stop 🕌 Add 📗 Replicate 🔀 Remove 🕞 🖻 🗖
	Injection Name	Sample ID	Location	Method	Notes
1	Sample 1_01	Product A	A1	System Suitability	
2	Sample 02_02	Sample 02	A2	System Suitability	
3	Sample 03_03	Sample 03	A3	System Suitability	
4	Sample 04_04	Sample 04	A4	System Suitability	

The sample name also displays when you hover the mouse over the sample in the plate or vial map:

Batch: Maurice cIEF	🛄 Injectio	ns 🛛 🔚 History 🚹 Not	es		
I Layout		Injection Name	Sample ID	Location	Method
	1	Product A_01	Product A	A1	System Suitability
🔴 🔄 🥅 10°C 👻 🚺 Add 👻 🚺 Remove	2	Sample 02_02	Sample 02	A2	System Suitability
	3	Sample 03_03	Sample 03	A3	System Suitability
MC FI Cal Water Empty	4	Sample 04_04	Sample 04	Α4	System Suitability
A Product A P					

2. Injection names are automatically set to 'Sample ID_injection number'. To change the name, click the **Injection Name** cell for the injection and type a name. Each injection name must be unique. If they aren't when you save the batch, Compass for iCE highlights any non-unique injection names so you can change them.

Injectio	ns 🛛 🔚 History 👖 Note	s			🕕 Pause 🟮 Stop 👫	Add 📗 Replicate	🔀 Remove	Ð 🖯 🗆
	Injection Name	Sample ID	Location	Method	Notes			
1	Injection 1	Product A	A1	System Suitability				
2	Sample 02_02	Sample 02	A2	System Suitability				
3	Sample 03_03	Sample 03	A3	System Suitability				
4	Sample 04_04	Sample 04	A4	Method2				

NOTE: Changing the injection name won't affect the sample ID.

3. Assign your methods to each injection. Just click the **Method** cell for the injection and select a method from the drop down menu. If you added your samples with pre-assigned methods and don't need to make any changes, skip to the next step.

Injection	ns 🛛 🔚 History 🚺 Notes				🕕 Pause ဝ Stop 🎁 Add 🚻 Replicate 🔀 Remove 🕞 🖻	
	Injection Name	Sample ID	Location	Method	Notes	
1	Injection 1	Product A	A1	System Suitability		
2	Sample 02_02	Sample 02	A2	System Suitability		
3	Sample 03_03	Sample 03	A3	System Suitability		
4	Sample 04_04	Sample 04	A4	Method2	V	
				System Suitability		
				Method2		

Hovering over a method name displays the method parameters:

Injection	s 🔚 History 🌃 Notes				🕕 Pause (🖸 Stop	🕂 Ad	d 📊 Replicat	te 🔀 Remove	ŦĒ	- 0
	Injection Name	Sample ID	Location	Method	Notes						
1	Injection 1	Product A	A1	System Suitab	ability						
2	Sample 02_02	Sample 02	A2	System Suitab System Suitab Separation:	1.0 min 1500	Volts 4	5 min 30	00 Volts			
3	Sample 03_03	Sample 03	A3	System Suitab Detection: 5	5 Exposures	,					
4	Sample 04_04	Sample 04	A4		Sample Load (s): 55						
				pl Markers:	3.38, 10.17						

- 4. You can add or remove injections as needed using a few different options. If you don't need to make any changes here, just skip to the next step.
 - To add sequential replicate injections: Highlight an injection and click **Replicate**. A new injection will be added under the row you selected

njectio	ons 🔚 History <u>T</u> Not	6			🕕 Pause 🟮			maphroot	e p Kentove	
	Injection Name	Sample ID	Location	Method	Notes			Replica	te selected inj	ections (
1	Injection 1	Product A	A1	System Suitability				replied	ne serecce mj	central
2	Sample 02_02	Sample 02	A2	System Suitability						
3	Sample 03_03	Sample 03	A3	System Suitability						
4	Sample 04_04	Sample 04	A4	Method2						
niectic	History TR Not	ec)			O Pause O	Stop 🖁	Add III	Replicat	e 🗼 Remove	
njectio			Location	Method	Pause	Stop 🕌	Add 📗	Replicat	e 🕌 Remove	: 🕀 🖻 '
njectio 1	Injection Name	Sample ID	Location A1	Method System Suitability	Pause Notes	Stop 불	Add	Replicat	e 🕌 Remove	: 🕀 🖻
njectio 1 2	Injection Name Injection 1	Sample ID Product A	Location A1 A2	System Suitability		Stop 🕌	Add	Replicat	e 🕌 Remove	: 🕀 🖻
1 2	Injection Name	Sample ID	A1			Stop 🕌	Add	Replicat	e 🕌 Remove	• • •
1	Injection Name Injection 1 Sample 02_02	Sample ID Product A Sample 02	A1 A2	System Suitability System Suitability		Stop 🕌	Add	Replicat	e 🕌 Remove	• • •

• To add injections at the end of the batch: Click on any sample position in the Layout pane or sample injection in the Injection table and click Add. A new injection using the same sample will be added to the end of the table. Assign the method if needed.

Injection	s 🔚 History 🌃 Notes				🕕 Pause 🛛 Stop	Add 📕 Replicate	🔀 Remove	••	
	Injection Name	Sample ID	Location	Method	Notes	Add injections			
1	Injection 1	Product A	A1	System Suitability		Add Injections			
2	Sample 02_02	Sample 02	A2	System Suitability					
∨ 3	Sample 03_03	Sample 03	A3	System Suitability					
4	Sample 03_04	Sample 03	A3	System Suitability					
5	Sample 04_05	Sample 04	A4	Method2					

• To copy and paste injections: Right-click on an injection in the Injection table and select Copy. Click on the injection number above where you want to insert the copied injection, right click and select Paste. The copied injection will be inserted under the row you selected.

Step 5 - Setup On-Board Mixing (Optional)

If you're using Maurice-OBM or Maurice C.-OBM, you can tell Compass for iCE which samples to automatically mix for you. Up to 96 samples can be on-board mixed in a batch. You can also have a mix of premixed samples and samples to on-board mix in the same batch.

NOTES:

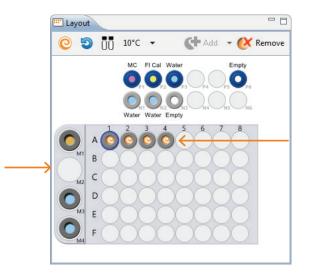
OBM is only availabe on Maurice and Maurice C. systems.

To use the OBM function, you must load 25 μ L of sample in every sample vial or plate well that will be mixed on board. Maurice will automatically mix 25 μ L of each sample with 100 μ L of IEF Separation Mix prior to injection.

- 1. Make sure you've placed the following on-board mixing reagents in Maurice:
 - N2 Water vial with clear screw cap
 - N3 Empty vial with clear screw cap
 - M1 6 mL IEF Separation Mix vial
 - M2 6 mL IEF Separation Mix vial (use only when running more than 48 samples)
 - M3 6 mL water vial
 - M4 6 mL water vial
- 2. The on-board mixing function is disabled by default. Click the on-board mixing icon to toggle it on.



All sample positions will now display the mixing icon, and the on-board mixing reagent vial positions will also display on the left:



The Injection pane will also display a Mix Bottle column showing the position of the IEF Separation Mix vial that will be used for each sample. The vial in the M1 position is used for samples 1–48, and the vial in M2 will automatically display and be used for samples 49–96:

Batch: Maurice cIEF	Injectio	ns 🛛 🔚 History 🌃 Not	es			🕕 Pause 🛛
T Layout		Injection Name	Sample ID	Location	Method	Mix Bottle
	1	Injection 1	Product A	A1	System Suitability	M1
[O] [D] 10°C ▼ (] Add ▼ (X Remove	2	Sample 02_02	Sample 02	A2	System Suitability	M1
	3	Sample 03_03	Sample 03	A3	System Suitability	M1
MC FI Cal Water Empty	4	Sample 03_04	Sample 03	A3	System Suitability	M1
	5	Sample 04_05	Sample 04	A4	Method2	M1
P1 P2 P3 P4 P5 P6						
Water Water Empty						
1 2 3 4 5 6 7 8 9 10 11 12						
M2 000000000000000						
▲ 0000000000000						
M						

Batch: Maurice cIEF	Injection	ns 🛛 🔚 History 🚹 Note	s			🕕 Pause 🛛
Layout	5	Injection Name	Sample ID	Location	Method	Mix Bottle
	40	Sample 38_40	Sample 38	D3	System Suitability	M1
💽 🗐 📖 10°C 👻 🛛 💽 Add 👻 💓 Remov	e 41	Sample 39_41	Sample 39	D4	System Suitability	M1
	- 42	Sample 40_42	Sample 40	D5	System Suitability	M1
MC FI Cal Water Empty	43	Sample 41_43	Sample 41	D6	System Suitability	M1
	44	Sample 42_44	Sample 42	D7	System Suitability	M1
	45	Sample 43_45	Sample 43	D8	System Suitability	M1
	46	Sample 44_46	Sample 44	D9	System Suitability	M1
Water Water Empty	47	Sample 45_47	Sample 45	D10	System Suitability	M1
	48	Sample 46_48	Sample 46	D11	System Suitability	M1
	49	Sample 47_49	Sample 47	D12	System Suitability	M1
900000000000 IM	50	Sample 48_50	Sample 48	E1	System Suitability	M2
00000000000	51	Sample 49_51	Sample 49	E2	System Suitability	M2
	52	Sample 50_52	Sample 50	E3	System Suitability	M2
	53	Sample 51_53	Sample 51	E4	System Suitability	M2
	54	Sample 52_54	Sample 52	E5	System Suitability	M2
Ma	55	Sample 53_55	Sample 53	E6	System Suitability	M2
	56	Sample 54_56	Sample 54	E7	System Suitability	M2
	57	Sample 55_57	Sample 55	E8	System Suitability	M2
(//w	58	Sample 56_58	Sample 56	E9	System Suitability	M2
	59	Sample 57_59	Sample 57	E10	System Suitability	M2
	60	Sample 58_60	Sample 58	E11	System Suitability	M2

3. To turn on-board mixing off for specific samples, select those well(s) or vial(s), right click and select Mixing Off.



The sample positions will display solid orange indicating mixing is off, and the Mix Bottle designation in the Injections pane is removed:

Batch: Maurice cIEF	Injectio	ons 🔚 History 🖪 Not	es			🕕 Pause 🛛 Si
III Layout	1	Injection Name Injection 1	Sample ID Product A	Location A1	Method System Suitability	Mix Bottle M1
② ③ ■ 10°C ▼	2	Sample 02_02	Sample 02	A2	System Suitability	M1
	3	Sample 01_03	Sample 01	A3	System Suitability	
MC FI Call Water Empty	4	Sample 03_04	Sample 03	A4	System Suitability	
Water Water Empty						
1 2 3 4 5 6 7 8 9 10 11 12 M1 0 </td <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>						

Step 6 - Add Programmed Pauses and Stops (Optional)

You can program pauses and stops in the batch to automatically pause or stop after injections even when you aren't in front of Maurice.

To program a pause:

Pauses are helpful when you want to review injection results before continuing with the rest of the batch.

1. Highlight the injection you want to pause at and click Pause. The batch will pause after that injection is complete.

NOTE: Maurice can tweet you when the batch pauses. See "Setting Up Maurice Systems to Send Tweets" on page 764.

Injectio	ons 🛛 🔚 History 👖 N	Votes		op 👫 Add 📊 Re	eplicate 🔀 Remove	• 🕀 🖻 🗖
	Injection Name	Sample ID	Loc Pause	after the selected ir	jection tes	
1	Sample 01_01	Sample 01	A1	Method 1		
2	Sample 02_02	Sample 02	A2	Method 1		
3	Sample 03_03	Sample 03	A3	Method 1		
Injectio	ons 🔚 History 🎹 N	Votes	🕕 Pause 🕒 Sto	op 🕂 Add 📊 Re	eplicate 🔀 Remov	e 🕂 🗖 🗖
Injectio				op 🕌 Add 📗 Re	eplicate 🔀 Remov	e 🕀 🖻 🗖
Injectio	Injection Name	Sample ID	Location	Method		e 🕀 🖻 🗖
1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method Method 1		• • •
Injectio 1 2	Injection Name	Sample ID	Location	Method		e 🕀 🖻 🗖

2. To resume the batch, click **Continue** in the instrument status bar:

Paused	Continue				
		Mon 1:43 PM			

To stop the run after a specific injection:

1. Highlight the injection you want the batch to stop at and click **Stop**. Maurice will continue the batch through the selected injection, then stop the batch and perform end-run cleanup steps.

	Injection Name	Sample ID	Location	Stop after the sel	lected injection	
1	Sample 01_01	Sample 01	A1	Method 1		
2	Sample 02_02	Sample 02	A2	Method 1		
3	Sample 03_03	Sample 03	A3	Method 1		
njecti	ons 📗 History 🏋 N	Votes	🕕 Pause 🗴 Sto	op 👫 Add 📊 Re	plicate 🔀 Remove	• 🕀 🖻
njecti	ons 🔚 History 🌃 N Injection Name	Notes Sample ID	Pause O Sto Location	op 🕂 Add 📗 Re Method	plicate 🔀 Remove	• 🕀 🖻
njecti 1						• 🕀 🖻
	Injection Name	Sample ID	Location	Method		• 🕀 🖻
	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method Method 1		• 🕀 🖻

Data collected for injections completed up to the point where the batch was stopped are saved in the .mbz file.

2. Be sure to complete your normal post-batch procedures.

Step 7 - Add Batch Notes (Optional)

- 1. Click on the Notes pane.
- 2. Click in the notes area and type any information you want to add about your batch.

Injections 🔚 History 🚺 *Notes	- 0
Product testing	

Step 8 - Modify Default Analysis Parameters (Optional)

You can preset the parameters used to analyze data generated with the batch. We recommend using the default parameters for cIEF applications, but if you need to modify parameters:

1. Select Edit from the main menu and click Default Analysis. The following screen will display:

ô Default Analysis: Maurice clEF					_		×
Detection Peak Names	Detection						
Peak Fit Advanced	Method	Absorbance	⊖ Fluorescence				
pl Markers	System	Exposure 1 $$ 0.005 seconds $$ $$ $$	Exposure 1 3 seconds	\sim			
Import Export			ОК	Cancel		Apply	

2. Change the parameters you want to, then click OK. For detailed information on analysis parameters, please refer to "Analysis Settings Overview" on page 528.

Step 9 - Modify Default Analysis View Parameters (Optional)

You can preset the parameters used to display the electropherogram data when the batch is complete. Default Analysis View Parameters must be set before you start the batch and cannot be modified once the batch starts. However, you can still manually change parameters in the Analysis pane using the Graph Options button.

To modify the parameters:

1. Select Edit from the main menu and click Default Analysis View. The following screen will display:

 Matching Peak Names Peak Names Peak Values Fitted Peaks Baseline Fit Overlay FL/ABS Grid Lines Plot Label Sample Method Injection Exposure Injection Name 	
Baseline Fit Overlay FL/ABS Grid Lines Plot Label Sample Method Injection Exposure	
Sample Method Injection Exposure	

2. Change the parameters you want to, then click **Apply**. Click **OK** when you are done changing display parameters. For detailed information on graph view options, please refer to "Customizing the Data Display" on page 509.

Step 10 - Save Your Batch

1. Once all of your sample, method and injection info is entered, select **File > Save**. Enter any comments on the batch if you want, then click **Save**.

츊 Save Batch Comment	×
Batch: Maurice cIEF Comment:	
	Save Cancel

2. Enter a name for your batch then click Save.

Viewing Replicate Injections

Injections with replicates have an arrow next to the injection number. You can expand or collapse the list of replicate injections by toggling the arrow:

	Sample ID	Location	Method		Sample ID	Location	Method
1	Product A	A1	Method1	⊿ 1	Product A	A1	Method
6	Product B	A2	Method1	2	Product A	A1	Method
11	Product C	A3	Method1	3	Product A	A1	Method
12	Product D	A4	Method1	4	Product A	A1	Method
13	Product E	A5	Method1	5	Product A	A1	Method
14	Product A	A6	Method2	⊳ 6	Product B	A2	Method
15	Product B	B1	Method2	11	Product C	A3	Method
16	Product C	B2	Method2	12	Product D	A4	Method
17	Product D	B3	Method2	13	Product E	A5	Method
18	Product E	B4	Method2	14	Product A	A6	Method
19	Test	B5	Method2	15	Product B	B1	Method
20	Test	B6	Method2	16	Product C	B2	Method

• To show all replicate injections in the batch, click the Expand All Injections button.

Injection	s 🛛 🔚 History 👖 Notes				👉 Add 📊 Replicate 🄀 Remove 🕞 🖻 🗖
	Sample ID	Location	Method	Notes	Expand All Inject
a 1	Product A	A1	Method1		
2	Product A	A1	Method1		
3	Product A	A1	Method1		
4	Product A	A1	Method1		
5	Product A	A1	Method1		
a 6	Product B	A2	Method1		
7	Product B	A2	Method1		
8	Product B	A2	Method1		
9	Product B	A2	Method1		
10	Product B	A2	Method1		
11	Product C	A3	Method1		
12	Product D	A4	Method1		
13	Product E	A5	Method1		
14	Product A	A6	Method2		
15	Product B	B1	Method2		
16	Product C	B2	Method2		
17	Product D	B3	Method2		
18	Product E	B4	Method2		
19	Test	B5	Method2		
20	Test	B6	Method2		

• To hide all replicate injections in the batch, click the Collapse All Injections button.

Injectio	ns 🔚 History 🌃 No	otes		🚰 Add 🔛 Replicate 🔀 Remove 😨 🖻 🗖			
	Sample ID	Location	Method	Notes	Collapse All Injecti		
⊳ 1	Product A	A1	Method1				
⊳ 6	Product B	A2	Method1				
11	Product C	A3	Method1				
12	Product D	A4	Method1				
13	Product E	A5	Method1				
14	Product A	A6	Method2				
15	Product B	B1	Method2				
16	Product C	B2	Method2				
17	Product D	B3	Method2				
18	Product E	B4	Method2				
19	Test	B5	Method2				
20	Test	B6	Method2				

T.

On-board Mixing (Maurice and Maurice C.)

Maurice's On-board Mixing function (OBM) can be used to automate preparation of cIEF samples by adding and aspirating the ampholyte mix into your protein samples. OBM is really useful when you need to analyze proteins using platform methods and when your proteins have a limited stability in their sample solution. It also minimizes assay complexity while maximizing mixing accuracy and consistency.

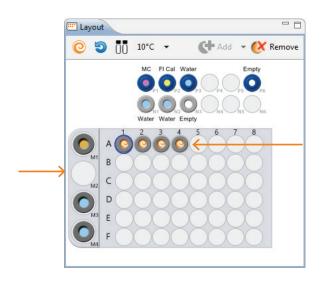
You can use OBM with samples in both 96-well plates and in vials, and on up to 96 samples in a single batch. The mixing protocol uses a fixed set of aspiration volume, speeds, and cycle parameters. The OBM protocol adds 100 µL of IEF Separation Mix to 25 µL of sample so the IEF Separation Mix components should be 1.25x that of the final desired concentration. Reagent positions M1–M4 on Maurice's sample and reagent platform all hold 6 mL vials that are used for on-board mixing.

- M1 and M2: Used for the IEF Separation Mix that contain the ampholytes, methyl cellulose, and excipient components of a cIEF sample solution. M1 is used for samples 1–48 and M2 is used for samples 49–96. The minimum IEF Separation Mix vial volume is 1.5 mL, and the maximum is 6.0 mL.
- M3 and M4: Used for DI water which is used in both aspirating the IEF Separation Mix and cleaning the OBM pipette between sample preparation cycles. Place two full, fresh 6 mL vials of DI water in positions M3 and M4 prior to running an OBM batch.

The on-board mixing function is disabled by default. Click the on-board mixing icon to toggle it on.



All sample positions will now display the mixing icon, and the on-board mixing reagent vial positions will also display on the left:

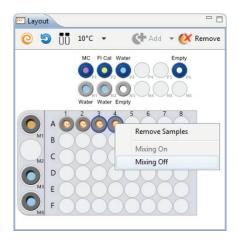


The Injection pane will also display a Mix Bottle column showing the position of the IEF Separation Mix vial that will be used for each sample. The vial in the M1 position is used for samples 1–48, and the vial in M2 will automatically display and be used for samples 49–96:

Batch: Maurice cIEF	Injectio	ns 🔚 History 🌃 Not	es			🕕 Pause 🛛 St
III Layout	1	Injection Name Injection 1	Sample ID Product A	Location A1	Method System Suitability	Mix Bottle M1
O S TOP C ▼ C Add ▼ OK Remove	2	Sample 02_02	Sample 02	A2	System Suitability	M1
	3	Sample 03_03	Sample 03	A3	System Suitability	M1
MC FI Cal Water Empty	4	Sample 03_04	Sample 03	A3	System Suitability	M1
	5	Sample 04_05	Sample 04	A4	Method2	M1
Vater Empty						
1 2 3 4 5 6 7 8 9 10 11 12 A C C C 0 <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>						

Batch: Maurice cIEF	🔢 Injectio	ns 🛛 🔚 History 📧 Not	es			🕕 Pause 🛛 S
Eayout 📃	5	Injection Name	Sample ID	Location	Method	Mix Bottle
	40	Sample 38_40	Sample 38	D3	System Suitability	M1
🙋 🔄 🥅 10°C 👻 🚺 🕂 🚺 🗸 🚺 👘 🕐 Remov	e 41	Sample 39_41	Sample 39	D4	System Suitability	M1
	- 42	Sample 40_42	Sample 40	D5	System Suitability	M1
MC FI Cal Water Empty	43	Sample 41_43	Sample 41	D6	System Suitability	M1
	44	Sample 42_44	Sample 42	D7	System Suitability	M1
	45	Sample 43_45	Sample 43	D8	System Suitability	M1
	46	Sample 44_46	Sample 44	D9	System Suitability	M1
Water Water Empty	47	Sample 45_47	Sample 45	D10	System Suitability	M1
	48	Sample 46_48	Sample 46	D11	System Suitability	M1
	49	Sample 47_49	Sample 47	D12	System Suitability	M1
000000000000	50	Sample 48_50	Sample 48	E1	System Suitability	M2
66666666666	51	Sample 49_51	Sample 49	E2	System Suitability	M2
	52	Sample 50_52	Sample 50	E3	System Suitability	M2
	53	Sample 51_53	Sample 51	E4	System Suitability	M2
	54	Sample 52_54	Sample 52	E5	System Suitability	M2
M3 POODOOOOOOOOOOOO	55	Sample 53_55	Sample 53	E6	System Suitability	M2
	56	Sample 54_56	Sample 54	E7	System Suitability	M2
	57	Sample 55_57	Sample 55	E8	System Suitability	M2
mai	58	Sample 56_58	Sample 56	E9	System Suitability	M2
	59	Sample 57_59	Sample 57	E10	System Suitability	M2
	60	Sample 58_60	Sample 58	E11	System Suitability	M2

To turn on-board mixing off for specific samples, select those well(s) or vial(s), right click and select Mixing Off.



The sample positions will display solid orange indicating mixing is off, and the Mix Bottle designation in the Injections pane is removed:

Batch: Maurice clEF	Injecti	ons 🛛 🔚 History 🚺 Not	es			🕕 Pause 🛛 S
🖾 Layout 📃 🗖	1	Injection Name Injection 1	Sample ID Product A	Location A1	Method System Suitability	Mix Bottle M1
O S 10°C ▼ C Add ▼ (X Remove)	2	Sample 02_02	Sample 02	A2	System Suitability	M1
	3	Sample 01_03	Sample 01	A3	System Suitability	
MC FI Cal Water Empty	4	Sample 03_04	Sample 03	A4	System Suitability	
Water Water Empty						
1 2 3 4 5 6 7 8 9 10 11 12 Model 1 10 10 11 12 10 11 12 Model 10 10 10 11 12 11 12 Model 10 10 10 11 12 <						

Batch History

Clicking on the History pane shows the batch event history, starting with the date and time the batch was created through the most current event. Clicking on a row in the table displays the full event details in the box under the table.

ate	User Name	Message	Comment	
2022-11-15 11:00:0		Batch created using the factory default Maurice cIEF with Compass for iCE Version: 3.0.0-0922		
2022-11-15 11:03:5		Saved as C:\Users\Administrator\Documents\Compass for iCE\New Batches\Maurice PSIgG ref 2M repeat cIEF		
2022-11-15 11:03:5		Save injections and methods changes to C:\Users\Administrator\Documents\Compass for iCE\New Batches\M		
me	2022-11-1	5 11:00:07 User		
essage	Batch cre	ated using the factory default Maurice cIEF with Compass for iCE Version: 3.0.0-0922		
omment				

- Date: Date and time of the batch event.
- User Name: User that initiated the event. User names only display if you're using the Access Control feature to help satisfy the 21CFR Part 11 data security requirements. Go to "Enabling Access Control" on page 781 to learn how to set it up.
- Message: Description of the event that took place.
- **Comment:** Comments entered by the user when the batch was saved.

You can copy the information in the History pane to use in other documents:

- 1. Click the History pane to make sure it's active.
- 2. Click Edit in the main menu and select Copy.
- 3. Open a document and click Paste.

Making Changes to a Batch

1. Select File in the main menu and click Open Batch.

File	Edit Instrument	Window	Help
N	New Batch	•	
C	Open Batch	•	Maurice cIEF 011816
-	New Batch Open Batch Save Save As Batch Report Exit		Maurice CE-SDS sample batch Maurice cIEF Maurice CE-SDS2
B	Batch Report		Maurice CE-SDS Gen Meth
E	ixit		Browse

- 2. A list of the last five batches opened will display based on the last location found. If the location of the file has changed, you may need to navigate to find the file.
 - Select one of these files or click **Browse** to open the Batch folder and select a different one.
 - To open a batch used in a run file, click **Browse**. Go to the Run folder in the Compass for iCE directory and select the run file that uses the batch you want to edit.

Organize Share with Burn	New folder				
 ▲ (⇒ Libraries ▲ 1 Documents 	Documents library Compass for iCE				
4 📗 My Documents	Name	Date modified	Date created	Туре	Size
🎉 Add-in Express	The second se	4 H 0 1001 5 5 70 PL 1			
🎍 Adobe	Batches	1/18/2016 5:39 PM	1/13/2016 8:24 PM	File folder	
Clients	🌽 New Batches	1/13/2016 8:24 PM	1/13/2016 8:24 PM	File folder	
Compass for iCE	🔒 Runs	1/17/2016 8:41 PM	11/11/2015 4:46 PM	File folder	
Batches	DemoData_Maurice cIEF.mbz	1/18/2016 11:38 AM	1/18/2016 11:38 AM	Maurice data file.	798 KI
New Batches					
Runs					

3. To make changes to the batch, see the steps in "Creating a New Batch" on page 59 "Creating a New Batch". Then select File from the main menu and click Save or Save As.

Viewing and Editing Batches in Completed Runs

- 1. Click the Analysis screen and open your run file(s).
- 2. After the run opens, click the Batch screen to view the batch used with the run.

If you opened more than one run file, you can switch between viewing batches for each file. Just click the **down arrow** in the Run box and select the batch you want to view from the drop down list.

Run:	2015-12	2-06_15	-13-01	_Maurice cIEF_Mab11	Te	-		
📟 Laj	2016-01 2015-12	1-21_09 2-06_15	- 46-39 -13-01	_mAb11_Prep2016012 _Maurice cIEF_Mab11	1_Q Tec	C (0) :hRep		- 0
	00	10°C	Ŧ	🗲 Add	*	Ø	Rer	nove

- 3. In completed run files, you can only make edits to the **sample** and **method** names in a batch, and these changes are saved to the run file only. Update sample and method names as needed.
- 4. Click the Analysis screen. Then select File from the main menu and click Save or Save As to save the new changes to the run file.

Copying and Pasting Injection Names or Sample IDs from other Documents

Injection names and Sample IDs can be copied from other documents and pasted into the Injection pane to make batch setup faster.

To paste a list of injection names into the batch:

1. Select the list of injection names in a document (Microsoft[®] Word[®], Excel[®], etc.) and select **Copy** or hold the **Ctrl+C** keys to copy.

	А	В	C
1			
2		My Injection 1	My Sample 1
3		My Injection 2	My Sample 2
4		My Injection 3	My Sample 3
5		My Injection 4	My Sample 4
6		My Injection 5	My Sample 5
7		My Injection 6	My Sample 6
8		My Injection 7	My Sample 7
9		My Injection 8	My Sample 8
10		My Injection 9	My Sample 9
11		My Injection 10	My Sample 10

Chapter 5: cIEF Batches | Copying and Pasting Injection Names or Sample IDs from other Documents

2. Select an injection in the Injection pane, then hold the Ctrl+V keys to paste. You can also select the injection, right click and select Paste.

	Injection Name	Sample ID	Location	Method	Notes	
1	Sample 01_01	Sample 01	A1	System Suitability		
2	Sample 02_02	Sample 02	A2	Method2		
3	Sample 03_03	Sample 03	A3	Method2		
4	Sample 04_04	Sample 04	A4	Method2		
5	Sample 05_05	Sample 05	A5	Method2		
6	Sample 06_06	Sample 06	A6	Method2		
7	Sample 07_07	Sample 07	A7	Method2		
8	Sample 08_08	Sample 08	A8	Method2		
9	Sample 09_09	Sample 09	A9	Method2		
10	Sample 10_10	Sample 10	A10	Method2		
11	Sample 11_11	Sample 11	A11	Method2		
12	Sample 12_12	Sample 12	A12	Method2		

The injection names are pasted into the Injection pane:

	Injection Name	Sample ID	Location	Method	Notes	
1	My Injection 1	Sample 01	A1	System Suitability		
2	My Injection 2	Sample 02	A2	Method2		
3	My Injection 3	Sample 03	A3	Method2		
4	My Injection 4	Sample 04	A4	Method2		
5	My Injection 5	Sample 05	A5	Method2		
6	My Injection 6	Sample 06	A6	Method2		
7	My Injection 7	Sample 07	A7	Method2		
8	My Injection 8	Sample 08	A8	Method2		
9	My Injection 9	Sample 09	A9	Method2		
10	My Injection 10	Sample 10	A10	Method2		
11	Sample 11_11	Sample 11	A11	Method2		
12	Sample 12_12	Sample 12	A12	Method2		

To paste a list of Sample IDs into the batch:

1. Select the list of Sample IDs in a document (Microsoft Word, Excel, etc.) and select **Copy** or hold the **Ctrl+C** keys to copy.

	А	В	С
1			
2		My Injection 1	My Sample 1
3		My Injection 2	My Sample 2
4		My Injection 3	My Sample 3
5		My Injection 4	My Sample 4
6		My Injection 5	My Sample 5
7		My Injection 6	My Sample 6
8		My Injection 7	My Sample 7
9		My Injection 8	My Sample 8
10		My Injection 9	My Sample 9
11		My Injection 10	My Sample 10
12			

2. Select a Sample ID in the Injection pane, then hold the Ctrl+V keys to paste. You can also select the Sample ID, right click and select Paste.

		🕕 Pause 🔍 Stop 👫 Add 📗 Replicate 样 Remove 🖽 🗉										
	Injection Name	Sample ID	Location	Method	Notes							
1	Sample 01_01	Sample 01	A1	System Suitability								
2	Sample 02_02	Sample 02	A2	Method2								
3	Sample 03_03	Sample 03	A3	Method2								
4	Sample 04_04	Sample 04	A4	Method2								
5	Sample 05_05	Sample 05	A5	Method2								
6	Sample 06_06	Sample 06	A6	Method2								
7	Sample 07_07	Sample 07	A7	Method2								
8	Sample 08_08	Sample 08	A8	Method2								
9	Sample 09_09	Sample 09	A9	Method2								
10	Sample 10_10	Sample 10	A10	Method2								
11	Sample 11_11	Sample 11	A11	Method2								
12	Sample 12_12	Sample 12	A12	Method2								
	Sample IL_IL	bumpie 12	7112	methodz								

The Sample IDs are pasted into the Injection pane.

NOTE: If you paste in new sample IDs when the default injection names are still being used, the injection names will automatically update to match the sample ID. If you've already changed the injection names manually, updating the sample IDs will not update the injection names.

	Injection Name	Sample ID	Location	Method	Notes	
1	My Sample 1_01	My Sample 1	A1	System Suitability		
2	My Sample 2_02	My Sample 2	A2	Method2		
3	My Sample 3_03	My Sample 3	A3	Method2		
4	My Sample 4_04	My Sample 4	A4	Method2		
5	My Sample 5_05	My Sample 5	A5	Method2		
6	My Sample 6_06	My Sample 6	A6	Method2		
7	My Sample 7_07	My Sample 7	A7	Method2		
8	My Sample 8_08	My Sample 8	A8	Method2		
9	My Sample 9_09	My Sample 9	A9	Method2		
10	My Sample 10_10	My Sample 10	A10	Method2		
11	Sample 11_11	Sample 11	A11	Method2		
12	Sample 12_12	Sample 12	A12	Method2		

Importing and Exporting Injections

Injections in an open batch or run file can be exported as a separate file. This lets you import the same or a modified set of injections into another batch later, rather than having to enter the information manually.

Exporting Injections

- 1. Open the batch or run you want to export injections from.
- 2. In the Batch screen, select File in the main menu and click Export Injections. The following window displays:

Injections File					
\rightarrow \wedge \uparrow	> Th	is PC → Documents → Compass for iCE → Batches	ڻ ~	Search Batches	م
Organize 🔻 New	w folde	er			== -
a OneDrive	^	Name	Date modified	Туре	Size
This DC		🚯 4Sqx12inj-RlgG-Maurice CE-SDS.batch_Injections.csv	2/10/2019 11:13 PM	Microsoft Excel C	2 KB
This PC		2019-01-08_ clEF_Injections.csv	2/9/2019 3:18 PM	Microsoft Excel C	2 KB
🧊 3D Objects		Dye-ComboCollect_Maurice clEF_Fl.batch_Injections.csv	1/29/2019 8:19 PM	Microsoft Excel C	2 KB
E Desktop					
Documents					
👆 Downloads	- 10				
Music					
Pictures					
📲 Videos					
🏪 OS (C:)					
👝 DATA (D:)					
🕳 Seagate Backu	up				
	~				
File name:	Maur	ice clEF_Fl.batch_Injections.csv			
Save as type:	Text F	ile, comma delimited (*.csv)			
51					
Hide Folders				Save	Cancel
Hide Folders				Save	Cano

- 3. The default directory is Compass for iCE/Batches. Change the directory if needed.
- 4. The default file name will be batchname.batch_Injections.csv. Change the name if needed and click Save.

Creating an Injections File

To create a new injections file .csv, it's easiest to export injections from an existing batch and use that as your template.

- 1. Follow the instructions in "Exporting Injections" above to export injections from an existing cIEF batch.
- 2. Open the .csv file in a program that provides a table/spreadsheet format.
- 3. To add or change injection information:
 - a. Type in a unique name in each cell in the Injection Name column. For replicate injections, type > in front of the injection name, for example: >Injection 1.
 - b. Type in a sample ID, location and method for each injection in their respective columns.
 - c. Optional: Enter a mix bottle (M1 or M2) if on-board mixing will be used for any of the injections. If you leave the mix bottle cell blank, mixing will not be used for that injection.
 - d. Optional: Type in notes if needed.

NOTE: Programmed pauses and stops can't be added in the injections file. They can be added in the Injections pane after importing your injections into Compass for iCE.

	А	В	С	D	E	F
1	Injection Name	Sample ID	Location	Method	Mix Bottle	Notes
2	Inj01	R01_SSPP	E4	System Suitability		
3	Inj02	S01_Her2-A1_None_0M Urea	D1	Method_M458		
4	>Inj02	S01_Her2-A1_None_0M Urea	D1	Method_M458		
5	>Inj02	S01_Her2-A1_None_0M Urea	D1	Method_M458		
6	Inj03	S02_Her2-B5_None_0M Urea	D2	Method_M458		
7	Inj04	S03_Her2-B7_None_0M Urea	D3	Method_M458		
8	Inj05	S04_Her2-A1_CPM_0M Urea	D4	Method_M458		
9	Inj06	S05_Her2-B5_CPM_0M Urea	D5	Method_M458		
10	Inj07	S06_Her2-B7_CPM_0M Urea	D6	Method_M458		
11	Inj08	S07_Her2-A1_CPM_4M Urea	D7	Method_M458		
12	Inj09	S08_Her2-B5_CPM_4M Urea	D8	Method_M458		
13	Inj10	S09_Her2-B7_CPM_4M Urea	D9	Method_M458		

4. Save the .csv file.

Importing Injections

- 1. Open the batch you want to import injections into, or open a new batch.
- 2. Select File in the main menu and click Import Injections.
- 3. Select an injections file (*.csv) and click OK. The imported information will display in the Layout and Injections panes.

NOTE: Imported injections will replace any injections already in the Injections table, they will not append an existing table.

Importing and Exporting Methods

Methods in an open batch or run file can be exported as a separate file. This lets you import the same method into another batch later, rather than having to re-enter method information manually.

Importing a Method

NOTE: Importing a method imports information into the Batch window's Method pane only.

- 1. Open the batch you want to import the method into.
- 2. Select File in the main menu and click Import Method.
- 3. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

Exporting a Method

NOTE: Exporting a method exports information in the Batch window's Method pane only.

- 1. Open the batch you want to export the method from.
- 2. In the Method pane, select the method you want to export. To export more than one method at the same time, hold the Ctrl key to select multiple methods.
- 3. Select File in the main menu and click Export Method. The following window displays:

log Method File			×
🕥 🗸 🖉 « My	Documents + Compass for iCE + Batches	✓ 4 Search Batches	٩
Organize 🔻 New	v folder	· == •	(?)
Favorites Downloads Desktop CneDrive	Name Name No items n	Date modified Type natch your search.	Size
 □ Libraries □ Documents □ Music □ Pictures □ Videos 			
🖳 Computer	 ✓ 		Þ
	Standard Method.method Method File (*.method)		•
Hide Folders		Save Canc	eli

- 4. The default directory is Compass for iCE/Batches. Change the directory if needed.
- 5. Enter a method file name and click Save. The settings will be saved as a *.method file.

Batch Reports

You can export a PDF file of sample and method details for each injection in the batch.

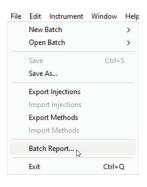
NOTES:

You can have Compass for iCE generate reports for you automatically at the end of each run. See "Setting up Automatic Injection Reports" on page 761 for more information.

Any time a new report is run, it's saved in a separate run folder. Existing reports aren't overwritten.

Chapter 5: cIEF Batches | Batch Reports

- 1. Go to the **Analysis** or **Run Summary** screen, then click **File** > **Open Run** and select a run file (if you don't have one open already).
- 2. After the run opens, go to the **Batch** screen.
- 3. Select File from the main menu and click Batch Report.



4. The report name defaults to the run file name. If you want to change it, type in the Report Name box to make updates.

🍖 Batch Report		×
Run: DemoData_Maurice	cIEF	
Secure PDF		
Report Name:		Browse
DemoData_Maurice clEF		
Location: C:\Users\Docum	ents\Compass for iCE	
	ОК	Cancel

Report PDFs generated by Compass for iCE are secured by default, which means they can be viewed and printed but not modified or renamed. Uncheck **Secure PDF** if you don't want to generate a secure report. To learn more about permissions for secured vs. unsecured reports, see page 800.

5. The Batch Report PDF is exported to the Runs folder in the Compass for iCE directory. It'll be in a folder with the report name used in the prior step. When the reports are done, the folder opens for you automatically.

👺 Favorites 🖉	~	Name	Date modified	Type	Size	
👔 Links		• 2016 01 21 00 45 20 AL11 B 20160121 OC B-t-L 46	1 (24 (2016 1-04 DM			26
My Documents		2016-01-21_09-46-39_mAb11_Prep20160121_QC_Batch.pdf	1/24/2016 1:04 PM	Adobe Acrobat D		20
🎉 Add-in Express						
📙 Adobe						
📙 Clients						
Compass for iCE						
🔰 Batches						
New Batches						
🎍 Runs						
2015-12-06_15-13-01_Maurice cIEF_Mab11_TechR						
2016-01-21_09-46-39_mAb11_Prep20160121_QC_F						
78664 P3 IS 2015-11-30_16-49-49_MW Ladder Sol						

Here's an example Batch Report:

cIEF Batch: Maurice cIEF

Injections

Injection	Injection Name	Sample ID	Location	Method	Notes
1	System Suit_01	System Suit	A1	Method1	
2	Peptide Mix_02	Peptide Mix	A2	Method1	
3	mAb_03	mAb	A3	Method2	
4	System Suit_04	System Suit	A1	Method1	
5	Peptide Mix_05	Peptide Mix	A2	Method1	
6	mAb_06	mAb	A3	Method2	

Methods

Name	Separation	Detection	Sample Load (s)	pl Markers	Ampholytes	Additives
Method1	1.0 min, 1500 Volts	Absorbance, 0.005 sec	90	3.38 pl, 250 pixels		
	4.5 min, 3000 Volts	Fluorescence, 1 sec		10.17 pl, 1700 pixels		
		Fluorescence, 3 sec				
		Fluorescence, 5 sec				
		Fluorescence, 10 sec				
Method2	1.0 min, 1500 Volts	Absorbance, 0.005 sec	90	4.05 pl, 500 pixels		
	6.0 min, 3000 Volts	Fluorescence, 1 sec		9.99 pl, 1700 pixels		
		Fluorescence, 5 sec				
		Fluorescence, 10 sec				
		Fluorescence, 15 sec				
		Fluorescence, 20 sec				

Batch Log

Date	User Name	Message	Comment
10/27/2015 12:01 PM		Batch created using the factory default Maurice cIEF	
10/27/2015 12:11 PM		Save protocol and template changes	Auto-saved

Created By: Andrea Sat 8:27 PM Mar 4, 2023 PST C/Users/Andrea/Documentsi/Compass for /CE/Runs/DemoData_Maurice clEF.mbz Computer: DESKTOP-IFI/I/G05 Software Version: Compass for /CE 4.0.0, Build ID: 0222

Page 1 of 2



Chapter 6: Running cIEF Applications

Chapter Overview

- Overview
- Before You Throw the Switch
- Power Up
- Running cIEF Applications
- Editing a Running Batch
- Post-batch Procedures
- Checking Your Data

Overview

Standard cIEF applications can be run on Maurice, Maurice C. or MauriceFlex systems using a cIEF cartridge.

Before You Throw the Switch

Ensure that everyone using Maurice have:

- Received instruction in general safety practices for laboratories.
- Received instruction in specific safety practices for Maurice.
- Received instruction on handling of biohazards (if biohazardous materials are to be used on Maurice).
- Read and understood all Product Inserts and related Safety Data Sheets (SDS).

Power Up

- 1. Turn on the computer connected to Maurice.
- 2. Turn on Maurice's main power switch.
- 3. Wait for Maurice to initialize. His indicator light will turn from magenta to blue when he's done.
- 4. Double-click the Compass for iCE software icon on the computer desktop to open the application.
- 5. Connect Maurice to Compass for iCE.

Running cIEF Applications

What You'll Need

- Maurice cIEF Cartridges
- Maurice cIEF Method Development Kit (optional)
- Maurice System Suitability Kit (optional)
- Maurice cIEF Fluorescence Calibration Standard
- Maurice cIEF pI Markers (3.38, 4.05, 5.85, 6.14, 7.05, 8.4, 9.50, 9.99, or 10.17)
- 0.5% Methyl Cellulose Solution
- 1% Methyl Cellulose Solution
- iCE Electrolyte Kit
- Deionized (DI) water

• Glass reagent vials, 2 mL



MauriceFlex crimp top glass vial (PN 110-0019, left) and glass reagent vial (PN 046-017, right) Only glass reagent vials (PN 046-017) should be used to prepare cIEF batch reagents.

- · 96-well plate or vials with integrated inserts for samples
- Clear screw caps for vials
- Blue pressure caps for vials
- P10, P20, P200, P1000 pipettes and tips
- Electrolyte pipette
- Vortexer
- Table-top centrifuge with plate adapter or vial adapter (12 mm, 2 mL vials)

IMPORTANT:

Use glass reagent vials, 2 mL (PN 046-017) to prepare cIEF batch reagents.

Step 1: Prep Your Markers, Samples and Reagents

NOTES:

You can prepare your samples to run either in 96-well plates or vials.

If you need to seal the 96-well plate during your run, we recommend the Slit Seal, 96 well plate seal from BioChromato (https://biochromato.com/slit-seal/). It can be used in both absorbance and native fluorescence modes. If you're currently using X-Pierce adhesive film (PN XP-100, Excel Scientific), we recommend using it in absorbance mode only.

System Suitability Peptide Panel (Optional)

NOTES:

Run the System Suitability Peptide Panel when you need to confirm performance on Maurice.

The System Suitability Peptide Panel is lyophilized. Always reseal the foil bag containing the unopened tubes with desiccant to prevent moisture absorption.

- 1. Using scissors, carefully cut the top the package off leaving the sealing strip intact.
- 2. Take out the strip of tubes and cut one clear tube of lyophilized System Suitability Peptide Panel from the strip. Return the remaining tubes to the original package, reseal tightly and store at 2–8 °C.
- 3. Pierce the foil on the tube with a clean pipette tip.
- 4. Add 40 µL of DI water to the tube. Gently resuspend by pipetting up and down to mix.
- 5. Add 160 µL of the System Suitability Test Mix to the freshly reconstituted Peptide Panel. Gently mix by pipetting up and down. Transfer this solution to a 1.5 mL microcentrifuge tube.
- 6. Vortex the tube 3 times, 5 seconds each.
- 7. Centrifuge the tube at 10,000 xg for 3 minutes to sediment any particulates.
- Carefully aspirate the top 160 μL of the solution and pipette it into a sample vial with integrated insert or well of a 96-well plate. You'll want to insert the pipette tip all the way to the bottom of the insert or well when you dispense the solution to avoid introducing bubbles.

NOTE: Make sure to check for and remove any bubbles at the bottom of the sample vial or well.

9. If you're using vials, close the sample vial with a clear screw cap.



Samples

- 1. In a microcentrifuge tube, prepare your sample at a concentration of 1 mg/mL in a final volume of 40 µL in DI water.
- 2. In a separate tube, prepare IEF Separation Mix containing your chosen pI marker(s).

NOTE: Check out the Method Development Guide for suggested IEF Separation Mix recipes.

- 3. Add 160 μ L of IEF Separation Mix to the 40 μ L of your sample.
- 4. Vortex the tube 3 times, 5 seconds each.
- 5. Centrifuge the tube at 10,000 xg for 3 minutes to sediment any particulates
- Carefully aspirate the top 160 μL of the sample and pipette it into your sample vial with integrated insert or well of a 96-well plate by inserting the pipette tip all the way to the bottom to avoid introducing bubbles.

Note: Make sure to check for and remove any bubbles at the bottom of the sample vial or well.

- 7. If you're using vials, close the sample vial with a clear screw cap.
- 8. Spin the plate or sample vials at 1,000 xg for 5 minutes using the appropriate centrifuge adapter.

pl Markers

- 1. Open the vial of lyophilized pI marker by lifting the center tab and gently pulling it back to break the metal seal. Slowly remove the rubber stopper.
- 2. Add 210 μL of DI water to the vial.
- 3. Put the rubber stopper back in the vial and vortex 3 times, 5 seconds each time to completely reconstitute the lyophilized cake. Repeat this step for all pI markers you're using.
- 4. Aliquot 20 µL of each reconstituted pI marker into separate tubes for storage.

NOTES:

Keep your reconstituted pI markers on ice until you're ready to add them to your sample or IEF Separation Mix.

If you'll use the pI markers within a month, store the aliquots at 2-8 °C. Otherwise, store the aliquots at -20 °C. They'll be stable up to 6 months.

5. Use 2 μ L of each pI marker for every 200 μ L of sample.

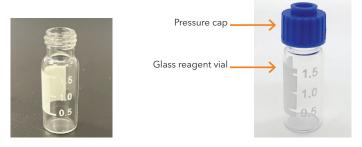
Reagents

IMPORTANT:

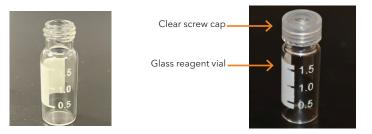
Use glass reagent vials, 2 mL (PN 046-017) to prepare cIEF batch reagents.

NOTE: Don't reuse reagents, vials or the clear screw caps. Always keep the blue pressure caps paired with their respective reagents. If you want to reuse pressure caps, first wash them thoroughly with DI water, soak overnight in DI water, rinse caps thoroughly with DI water again and air dry them before reusing.

1. Pipette 2 mL of 0.5% Methyl Cellulose into a glass reagent vial, label and close with a **blue pressure cap**.



- 2. Pipette 500 µL of Fluorescence Calibration Standard in a glass reagent vial, label and close with a **blue pressure cap**.
- 3. Pipette 2 mL of DI water into a glass reagent vial, label and close with a blue pressure cap.
- 4. Close an empty glass reagent vial with a blue pressure cap.
- 5. Pipette 2 mL of DI water into a glass reagent vial, label and close with a clear screw cap.
- 6. If you will be doing on-board mixing, also prepare the following reagents. If not, skip to the next step.
 - a. Pipette 2 mL of DI water into a glass reagent vial, label and close with a clear screw cap.
 - b. Close an empty glass reagent vial with a clear screw cap.



- c. If you are running 48 samples or less, add 6 mL of IEF Separation Mix to one 6 mL glass reagent vial. For more than 48 samples, prepare two vials.
- d. Add 6 mL of DI water to two 6 mL glass reagent vials.

Step 2: Prep the cIEF Cartridge

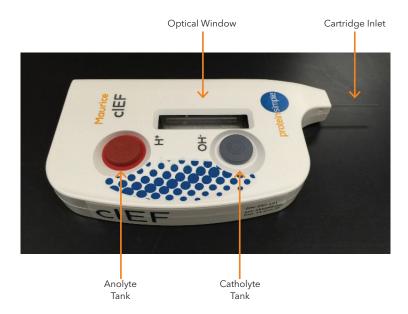
NOTE: A cIEF Cartridge is guaranteed for 100 injections and a maximum of 20 batches. Its RFID will keep track of how many are left for you. The absolute injection limit of the cartridge is 200.

1. Take the cIEF Cartridge out of its packaging. Save the packaging, you'll need it later to store the cartridge.

NOTE: When you remove the cartridge from its packaging, make sure the cartridge inlet doesn't come in contact with any surface.



- 2. Put the cartridge on a flat surface with its electrolyte tanks facing up.
- 3. Remove the stoppers from both electrolyte tanks.



- 4. Add 2 mL of Catholyte solution to the OH- electrolyte tank (white port).
- 5. Add 2 mL Anolyte solution to the H+ electrolyte tank (red port).

NOTE: Make sure you don't overfill the electrolyte tanks.

6. Seal each tank with the rubber stoppers. Use the grey stopper for the OH⁻ tank and the red one for the H⁺ tank. If excess liquid comes out of the tank, make sure to wipe it with a laboratory wipe.



Step 3: Install the Cartridge

1. Open Maurice's door by touching the metal plate on top of the door.



NOTE: The indicator light on Maurice's front panel will blink rapidly as the door disengages.

2. Swing the door open to access the cartridge slot and the reagents and samples platform. The lights on either side of the slot will be **orange**.



- 3. Double check to make sure you've got electrolytes loaded and the tanks are properly sealed with the stoppers.
- 4. Lift the cartridge and hold it vertically using the finger holds on either side, cartridge inlet down, with the cIEF label facing you.
- 5. Gently insert it into the slot. You'll feel the alignment groove on the cartridge align inside the slot when you insert it.



6. Continue to slide the cartridge into the slot until the locking mechanism engages. The lights on either side of the slot will change to **blue** once the cartridge is installed correctly.



Step 4: Load Samples and Reagents

1. Place the reagent vials into their respective positions on the sample and reagents platform:

NOTES:

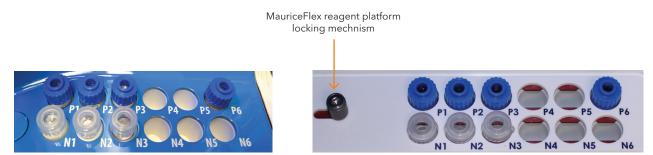
The two reagent rows in Maurice's reagent and sample platform are kept at room temperature.

Pressure caps are blue and have a raised, ringed surface. They should only be used in Reagent Row P. Use reagent vials with clear screw caps in Row N.

IMPORTANT:

Batch reagents should be prepared in glass reagent vials, 2 mL (PN 046-017).

- **P1** 0.5% Methyl Cellulose with **blue pressure cap**
- P2 Fluorescence Calibration Standard with blue pressure cap
- **P3** Water with **blue pressure cap**
- P6 Empty vial (air) with blue pressure cap
- N1 Water with clear screw cap



cIEF reagent platform on Maurice and Maurice C. (left) or MauriceFlex (right).

IMPORTANT:

Reagent vials on MauriceFlex must be locked in place by sliding the locking mechanism from the left to the right before starting a batch. A warning will appear in the Start Run window if they are not locked when you start the batch.

Optional: If you are doing on-board mixing, add these additional reagents:

- N2 Water with clear screw cap
- N3- Empty vial with clear screw cap
- M1 6 mL IEF Separation Mix

- M2 N/A for 48 samples or less, add a 6 mL IEF Separation Mix vial when running more than 48 samples
- M3 6 mL water
- M4 6 mL water

NOTE: On-board mixing is only available on Maurice and Maurice C. systems.

Depending on what you prepared your samples in, put your 96-well sample plate in the metal plate insert or your sample vials in the metal vial insert.

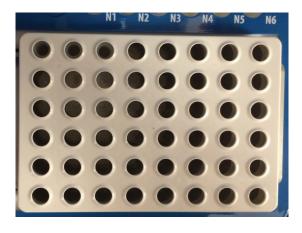


NOTES:

If you need to seal the 96-well plate during your run, we recommend the Slit Seal, 96 well plate seal from BioChromato (https://biochromato.com/slit-seal/). It can be used in both absorbance and native fluorescence modes. If you're currently using X-Pierce adhesive film (PN XP-100, Excel Scientific), we recommend using it in absorbance mode only.

Plate seals should NOT be used when running CE-SDS mode.

Well A1 on the 96-well plate should be in the top left corner of the insert.



2. If you are using a vial tray, place the condensation lid on top of the vials.

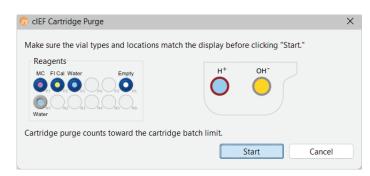
3. Close the instrument door. Maurice locks it automatically.

Step 5: Check for Cartridge Alerts

- 1. If your cartridge was last used in a run with an error you will need to perform a Cartridge Purge. The Maurice system will remind you if a Cartridge Purge is required.
 - a. To purge the cartridge, click the brown **Purge** button in the instrument status bar.



b. Confirm that the required batch reagents are loaded and that the cartridge is prepped. Then click Start.



c. Once the purge is done, perform a Cartridge Post-Run Cleanup by clicking on the brown **Cleanup** button that will appear in the instrument status bar. See step 2 for more info.

NOTE: If there's only one batch left on the cartridge, you'll get a message that it can't be used after purging.

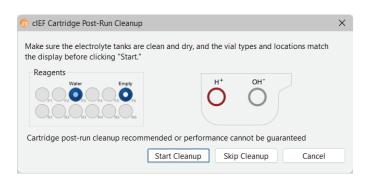
2. If you just completed a Cartridge Purge or if the cartridge you're using did not undergo a cartridge post-run cleanup after the last run, you will be asked if you want to perform a Cartridge Post-Run Cleanup.

To start the Post-Run Cleanup:

- a. Remove the cartridge from Maurice and remove the analyte and catholyte from the cartridge. See "Post-batch Procedures" on page 120 for more info.
- b. Confirm there is a vial of Water (P3) and Air (P6) in place.
- c. Click the brown Cleanup button in the instrument status bar.



d. Click Start Cleanup in the prompt that appears.



NOTE: You can also start a Post-Run Cleanup by selecting **Instrument > Cartridge Post-Run Cleanup**. When you start a Cartridge Post-Run Cleanup from the instrument menu, click **Start** in the prompt that appears to begin the cleanup.

- e. Once the cartridge post-run cleanup is completed, re-prepare the cartridge and install the cartridge in Maurice. See "Step 2: Prep the cIEF Cartridge" on page 96 for more information.
- f. Click on the green **Start** button in the instrument status menu to start the batch.

To start the run without a Post-Run Cleanup:

a. Click the brown Cleanup button in the instrument status bar



b. Click **Skip Cleanup** in the prompt that appears.

or cIEF Cartridge Post-Run Cleanup	×
Make sure the electrolyte tanks are clean and dry, and the vial types and locations match the display before clicking "Start."	
Reagents Water Empty H ⁺ OH ⁻	
Cartridge post-run cleanup recommended or performance cannot be guaranteed	
Start Cleanup Skip Cleanup Cancel	

c. Click **Start** in the Start Run window. The run summary and injection report will record that the cartridge did not undergo a post-run cleanup before starting the batch.

	31-40_Maurice c	EF			
ocation: C:\U					
	sers\Andrea\Doc	uments\Compass for i	iCE\Runs		
omment:					
	Cartridge				
	Type:	cIEF	Injections per Batch :	100	
•	Evnires	Jan 2025	Injections Remaining :		
	Serial Number :		Batches Remaining :		
	Senai Number :	990000100	batches Kemaining :	25	
		100	mended or performance cannot	1.000	

To start the run with a different cartridge:

- a. If necessary, click Cancel in the cIEF Cartridge Post-Run Cleanup window.
- b. Open Maurice's door, remove the first cartridge from Maurice and prepare a second cartridge. See"Step 2: Prep the cIEF Cartridge" on page 96 for more information.

Step 6: Create a Batch

- 1. Launch Compass for iCE.
- 2. Select the Batch tab. This is where you'll enter sample/injection information, methods and batch parameters.

Batch: Maurice cIEF		Injection	ns 🛛 🔚 History 🏋 N	Notes				🕕 Pause 🛛 Stop	Add Replica	ite 🕅 Remove 🖪	• e - C
Layout	- 8	1	Injection Name Sample 1_01	Sample ID Sample 1		Location A1	Method System Suitability	Notes			
🛑 🧐 🏢 10°C	- C - C Remove		Sample 1_01	Sample I		AI	System Suitability				
	FI Cal Water Empty										
0											
Water	4 5 6 7 8 9 10 11 12										
B O O O											
EOOO											
FOOO											
	000000000										
	00000000										
HOOO	00000000										-
HOOO										Ne	
Methods Name	Separation		Detection	Sample Load (s)	pl Markers	Ampholytes	5 Additives			Ne	ew Remov
Methods Name			Detection 5 Exposures	Sample Load (s) 55	pl Markers 3.38, 10.17	Ampholytes	a Additives			Ne	
H Methods	Separation					Ampholytes	Additives			Ne	
Methods Name	Separation					Ampholytes	Additives			Ne	

- 3. To create a batch, make sure your Maurice system is connected to Compass for iCE. Select Instrument and click Connect.
 - a. If your instrument is listed, select your Maurice system and click Connect.
 - b. If your instrument isn't listed, click on the Settings button and connect by typing in your instrument IP address.

Name	Location	Serial Num

To create a new batch:

- On Maurice systems in the main menu, select File > New Batch > Maurice cIEF
- On Maurice C. systems in the main menu, select File > New Batch
- On MauriceFlex systems in the main menu, select File > New Batch > Maurice cIEF

To use an existing batch: In the main menu, select File > Open Batch.

NOTES:

cIEF batches that use the FL458 nm fluorescence detection filter can only be opened in Compass for iCE 2.1 or later.

If you're making changes to an existing batch, follow the steps in this section. Otherwise skip to "Step 7: Start the Batch" on page 116.

File	Edit Instrument	Window H	lelp
	New Batch	>	1
	Open Batch	>	Maurice cIEF
	Save	Ctrl+S	Maurice CE-SDS test samples
	Save As		Maurice CE-SDS
	Export Injections		Maurice CE-SDS PLUS Maurice cIEF 013019
	Export Methods		Browse

4. In the Layout pane, clicking on the vial/plate icon toggles between formats. Select 48 vials or a 96-well plate depending on what you're running.

Eayout	· 🗆	🖭 Layout	- 0
	ove	- ── ゔ ∭ 10°C ▾	🖨 Add 👻 🧭 Remove
MC FI Cal Water Empty			Aster Empty p3 p4 p5 p6 H3 H4 H5 H6
1 2 3 4 5 6 7 8 B 2 3 4 5 6 7 8 B 2 3 4 5 6 7 8 B 2 3 4 5 6 7 8 B 2 3 4 5 6 7 8 B 2 3 4 5 6 7 8 B 2 3 4 5 6 7 8 B 2 3 4 5 6 7 8 C 2 3 4 5 6 7 8 D 2 3 4 5 6 7 8 F 2 3 4 5 6 7 8 F 3 4 5 6 7 8 6 F 3 4 5 6 7 6 6 6 6<		1 2 3 4 5 6 A B C C C C C C C C C C C C C C C C C C	7 8 9 10 11 12 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

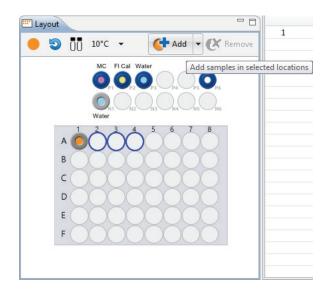
5. Add your samples:

To import samples using a saved injections file:

- a. Select File in the main menu and click Import Injections.
- b. Select an injections .csv file and click OK. The imported information will display in the Injections pane.

NOTE: For more information on setting up an injections file for import, see "Importing and Exporting Injections" on page 84.

To select samples manually: Use your mouse to highlight the well positions for each of your samples, then click Add.



This populates the Injections table:

Injections	5 🔚 History 🏋 Notes				🕕 Pause	O Stop	🕇 Add	Replic	ate 🕌	Remove	Ð (8 - 8
	Injection Name	Sample ID	Location	Method	Notes							
1	Sample 1_01	Sample 1	A1	System Suitability								
2	Sample 02_02	Sample 02	A2	System Suitability								
3	Sample 03_03	Sample 03	A3	System Suitability								
4	Sample 04_04	Sample 04	A4	System Suitability								

6. Compass for iCE can monitor the current during a separation for you, stop it if an abnormal current profile is detected and reinject the sample for you automatically. Reinjections are enabled by default, but if you don't want to use this feature just click the reinject icon to toggle it off.

NOTES:

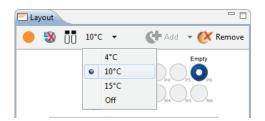
If a sample was reinjected, the injection row will be flagged in the Injections pane in the Run Summary screen. See "Injection Flags" on page 414 for more info.

A maximum of 10 reinjections are allowed per batch.



7. The sample platform is temperature controlled with a default setting of 10 °C. To change the temperature or turn it off, click the **down arrow** next to the temperature and select an option.

NOTE: The two reagent rows are kept at room temperature.



8. Enter your method parameters in the Methods pane.

NOTE: We recommend using the default method parameters. Please see the Maurice cIEF Method Development Guide for more information on method optimization.

To import a saved method:

- a. Select File in the main menu and click Import Method.
- b. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

To create a new method or make changes to an existing one:

a. Click the first cell in the Name column and enter a method name.

Name	Separation	Detection	Sample Load (s)	pI Markers	Ampholytes	Additives
Method 1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures	55	3.38, 10.17		

b. Click the first cell in the Separation column, then click the selection button [...] to set the pre-focusing and focusing time (in minutes) and voltage.

	Separation	
Method1	Voltage 2 Steps	Time (min) Voltage (V
		1.0 1500
		4.5 3000

c. Click the first cell in the Detection column then click the selection button [...] to set your exposure times for absorption and fluorescence detection modes. You can also select between native or FL458 nm fluorescence if the optional FL458 nm filter is installed on your system.

lame	Separation	Detection	Add	Remove
/lethod1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures 🛄	Exposure (see	c) Type
			0.0050	Absorbance
			3	Fluorescence
			5	Fluorescence
			10	Fluorescence
			20	FL458nm
				Fluorescence
				FL458nm

d. Click the first cell in the Sample Load(s) column and set the load time in seconds.

Name	Separation	Detection	Sample Load (s)
Method1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures	55

e. Click the first cell in the pI Markers column to select pI markers. Add new markers or remove existing ones then click OK.

Vame	Separation	Detection	Sample Load (s)	pI Markers		Add	Remove
Method1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures	55	3.38 10.17	\longrightarrow	pI Markers:	
						pI	Position
						3.38	300
						10.17	1,700

ОК

Cancel

f. Optional: Click the first cell in the Ampholytes column and enter the ampholytes you're using.

Volts, 4.5 min 3000 Volts 5 Exposures 55 3.38, 10.17 Pharmalyte 3-10	Name	Separation	Detection	Sample Load (s)	pI Markers	Ampholytes	Additives
	Method1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures	55	3.38, 10.17	Pharmalyte 3-10	

g. Optional: Click the first cell in the Additives column and enter any additives you're using.

1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures				
	5 Exposures	55	3.38, 10.17	Pharmalyte 3-10	Urea

- 9. You can now:
 - Make updates to the remaining methods by repeating the prior steps.
 - Select a method and click **Remove** in the upper right corner of the Methods pane to delete it.
 - Click **New** in the upper right corner of the Methods pane to add a new one if you want to use different methods for different samples. Then just repeat the steps above for the new method.

10. In the Injections pane:

• To add or change sample names: Click the Sample ID cell for the injection and type a name.

NOTES:

Sample IDs can be copied from other documents and pasted into Compass for iCE to make batch setup faster. Check out "Copying and Pasting Injection Names or Sample IDs from other Documents" on page 82 for more info.

If you change the sample ID when the default injection name is still being used, the injection name will automatically update to match the sample ID. If you've already changed the injection name manually, updating the sample ID will not update the injection name.

Injectio	ns 🛛 🔚 History 🚺 Note	es			🕕 Pause 🕒 Stop	🕇 Add 📊 Replicate	e 🔀 Remove	•••
	Injection Name	Sample ID	Location	Method	Notes			
1	Sample 1_01	Product A	A1	System Suitability				
2	Sample 02_02	Sample 02	A2	System Suitability				
3	Sample 03_03	Sample 03	A3	System Suitability				
4	Sample 04_04	Sample 04	A4	System Suitability				

• To change injection names: Click the Injection Name cell for the injection and type a name.

NOTES:

Each injection name must be unique.

Changing the injection name won't affect the sample ID.

II njections	s 🔚 History 👖 Notes			(🕕 Pause	O Stop	🕂 Add	Replic	ate 🔀 Re	move	Ð	۲ L
	Injection Name	Sample ID	Location	Method	Notes							
1	Injection 1	Product A	A1	System Suitability								
2	Sample 02_02	Sample 02	A2	System Suitability								
3	Sample 03_03	Sample 03	A3	System Suitability								
4	Sample 04_04	Sample 04	A4	Method2								

• To assign methods for each injection: Click the Method cell for the injection and select a method from the drop down menu.

Injection	ns 🛛 🔚 History 🌃 Notes				0	Pause 🔘 Stop	🕇 Add	Replicat	te 🔀 Remove	ΞE	9 - 0
	Injection Name	Sample ID	Location	Method	1	Notes					
1	Injection 1	Product A	A1	System Suitability							
2	Sample 02_02	Sample 02	A2	System Suitability							
3	Sample 03_03	Sample 03	A3	System Suitability							
4	Sample 04_04	Sample 04	A4	Method2	~						
				System Suitability							
				Method2							

• To add sequential replicate injections: Highlight an injection and click **Replicate**. A new injection will be added under the row you selected

	Injection Name	Sample ID	Location	Method	Notes			Devil		
1	Injection 1	Product A	A1	System Suitability				керпо	ate selected inj	ections
2	Sample 02_02	Sample 02	A2	System Suitability						
3	Sample 03_03	Sample 03	A3	System Suitability						
4	Sample 04_04	Sample 04	A4	Method2						
Injectio	ns 🔚 History 🏋 Not	es			O Pause (Stop	🕇 Add 💧	Replica	ite 🕌 Removi	: 🕀 🖻
Injectio	ns 🔚 History 🌃 Not	es Sample ID	Location	Method	Pause Notes	Stop	🕂 Add 💧	Replica	ite 🕌 Removi	: 🛨 🖻
Injectio			Location A1	Method System Suitability		Stop	🕂 Add 💧	Replica	ite 🕌 Removi	: 🕀 🖻
Injectio 1 2	Injection Name	Sample ID				Stop	🕹 Add 💧	Replica	ite 🕌 Remov	e 🕂 🗖
1 2	Injection Name Injection 1	Sample ID Product A	A1	System Suitability		Stop	🕂 Add 💧	Neplica 🗌	ite 🕌 Removi	: 🕂 🗖
Injectio	Injection Name Injection 1 Sample 02_02	Sample ID Product A Sample 02	A1 A2	System Suitability System Suitability		Stop	🕂 Add 💧	Replica	ite 🕌 Removi	

• To add injections at the end of the batch: Click on any sample position in the Layout pane or sample injection in the Injection table and click Add. A new injection using the same sample will be added to the end of the table. Assign the method if needed.

Injections	🗼 🔚 History 🚺 Notes				🕕 Pause 🕻	🕽 Stop	🕇 Add 📕 Replica	te 🕌 Remove	Ð	
	Injection Name	Sample ID	Location	Method	Notes		Add injections	1		
1	Injection 1	Product A	A1	System Suitability			ridd Hjeetions	1		
2	Sample 02_02	Sample 02	A2	System Suitability						
✓ 3	Sample 03_03	Sample 03	A3	System Suitability						
4	Sample 03_04	Sample 03	A3	System Suitability						
5	Sample 04_05	Sample 04	A4	Method2						

- To copy and paste injections: Right-click on an injection in the Injection table and select Copy. Click on the injection number above where you want to insert the copied injection, right click and select Paste. The copied injection will be inserted under the row you selected.
- 11. If your Maurice has the on-board mixing (OBM) option, you can tell Compass for iCE which samples to automatically mix for you. Otherwise you can skip to the next step. Up to 96 samples can be on-board mixed in a batch. You can also have a mix of premixed samples and samples to on-board mix in the same batch.

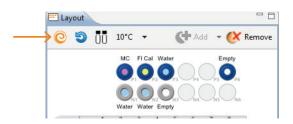
NOTES:

OBM is only available on Maurice and Maurice C. systems.

To use the OBM function, you must load 25 μ L of sample in every sample vial or plate well that will be mixed on board. Maurice will automatically mix 25 μ L of each sample with 100 μ L of IEF Separation Mix prior to injection.

- a. Make sure you've placed the following on-board mixing reagents in Maurice:
- M1 6 mL IEF Separation Mix vial
- M2 6 mL IEF Separation Mix vial (use only when running more than 48 samples)
- M3 6 mL water vial

- M4 6 mL water vial
- b. The on-board mixing function is disabled by default. Click the **on-board mixing icon** to toggle it on.



All sample positions will now display the mixing icon, and the on-board mixing reagent vial positions will also display on the left:

🖭 Layou		
0	00 10°C - C+ Add	🝷 🚺 Remov
	MC FI Cal Water	Empty
) _{P5} O _{P6}
	Water Water Empty	
		7 8
M1	в	\sim
\rightarrow	c	\prec
M2	D	\prec
U _{M3}	E	\prec
		\sim
M4	F () () () () () () () () () () () () ()	

The Injection pane will also display a Mix Bottle column showing the position of the IEF Separation Mix vial that will be used for each sample. The vial in the M1 position is used for samples 1–48, and the vial in M2 will automatically display and be used for samples 49–96:

atch: Maurice cIEF	Injection	ns 🛛 🔚 History 🌃 Not	es			🕕 Pause 🛛 S
🛛 Layout 📃 🗖		Injection Name	Sample ID	Location	Method	Mix Bottle
	1	Injection 1	Product A	A1	System Suitability	M1
💽 🔄 🥅 10°C 👻 🚺 Add 👻 🚺 Remove	2	Sample 02_02	Sample 02	A2	System Suitability	M1
	3	Sample 03_03	Sample 03	A3	System Suitability	M1
MC FI Cal Water Empty	4	Sample 03_04	Sample 03	A3	System Suitability	M1
	5	Sample 04_05	Sample 04	A4	Method2	M1
P1 P2 P3 P4 P5 P6						
Water Water Empty						
1 2 3 4 5 6 7 8 9 10 11 12						
MI						
M2 000000000000000000000000000000000000						
M3 F000000000000000000000000000000000000						
• 0000000000000000						
- M4]						

Batch: Maurice cIEF	Injection	s 🛛 🔚 History 👖 Note	s			🕕 Pause 🛛 Sto
🖽 Layout 👘 🗖	5	Injection Name	Sample ID	Location	Method	Mix Bottle
	40	Sample 38_40	Sample 38	D3	System Suitability	M1
🙋 🗐 🥅 10°C 👻 🚺 Add 👻 🚺 Remove	41	Sample 39_41	Sample 39	D4	System Suitability	M1
	- 42	Sample 40_42	Sample 40	D5	System Suitability	M1
MC FI Cal Water Empty	43	Sample 41_43	Sample 41	D6	System Suitability	M1
	44	Sample 42_44	Sample 42	D7	System Suitability	M1
	45	Sample 43_45	Sample 43	D8	System Suitability	M1
	46	Sample 44_46	Sample 44	D9	System Suitability	M1
Water Water Empty	47	Sample 45_47	Sample 45	D10	System Suitability	M1
	48	Sample 46_48	Sample 46	D11	System Suitability	M1
	49	Sample 47_49	Sample 47	D12	System Suitability	M1
	50	Sample 48_50	Sample 48	E1	System Suitability	M2
66666666666	51	Sample 49_51	Sample 49	E2	System Suitability	M2
	52	Sample 50_52	Sample 50	E3	System Suitability	M2
A A	53	Sample 51_53	Sample 51	E4	System Suitability	M2
	54	Sample 52_54	Sample 52	E5	System Suitability	M2
	55	Sample 53_55	Sample 53	E6	System Suitability	M2
	56	Sample 54_56	Sample 54	E7	System Suitability	M2
	57	Sample 55_57	Sample 55	E8	System Suitability	M2
	58	Sample 56_58	Sample 56	E9	System Suitability	M2
	59	Sample 57_59	Sample 57	E10	System Suitability	M2
	60	Sample 58_60	Sample 58	E11	System Suitability	M2

c. To turn on-board mixing off for specific samples, select those well(s) or vial(s), right click and select Mixing Off.



The sample positions will display solid orange indicating mixing is off, and the Mix Bottle designation in the Injections pane is removed:

Batch: Maurice cIEF	III Injectio	ons 🔚 History 📶 Not	es			🕕 Pause 🛛 S
Layout	1	Injection Name Injection 1	Sample ID Product A	Location A1	Method System Suitability	Mix Bottle M1
○ ⑤ 10°C ▼ C+ Add ▼ CX Remove	2	Sample 02_02	Sample 02	A1 A2	System Suitability System Suitability	M1
	3	Sample 01_03	Sample 02	A2 A3	System Suitability	IVII
MC FI Cal Water Empty		Sample 03_04	Sample 03	A3 A4	System Suitability	
O. 1	4	Sample 05_04	Sample US	744	System Suitability	
1 2 4 5 6 7 8 9 10 11 12 M1 0 </td <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>						

12. Add programmed pauses or stops in the batch to automatically pause or stop after injections (optional).

• **To program a pause:** Highlight the injection you want to pause at and click **Pause**. The batch will pause after that injection is complete. To resume the batch, click **Continue** in the instrument status bar.

Injectio	ons 🛛 📗 History 🔽 N	lotes		p 👫 Add 📗 Re	eplicate 🛛 🗱 Remove	• • •
	Injection Name	Sample ID	Loc Pause	after the selected ir	njection tes	
1	Sample 01_01	Sample 01	A1	Method 1		
2	Sample 02_02	Sample 02	A2	Method 1		
3	Sample 03_03	Sample 03	A3	Method 1		
••••) I I I I I I I I I I I I I I I I I I I)		- Maria III B		□
Injectio	- , -			p 🚰 Add 🛄 Re	eplicate 🔀 Remove	• 🕀 🖻 🗖
Injectio	Injection Name Sample 01 01	lotes Sample ID Sample 01	Pause Sto Location A1			• • •
	Injection Name	Sample ID	Location	Method		• • • •
1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method Method 1		

• To stop the run after a specific injection: Highlight the injection you want the batch to stop at and click Stop. Maurice will continue the batch through the selected injection, then stop the batch and perform end-run cleanup steps.

Injectio	ons 🛛 🔚 History 🚹 N	Votes	U Pause 🖸 Sto	p 📑 Add 📗 Rej	plicate 🔀 Remove	• •
	Injection Name	Sample ID	Location	Stop after the sele	ected injection	
1	Sample 01_01	Sample 01	A1	Method 1		
2	Sample 02_02	Sample 02	A2	Method 1		
3	Sample 03_03	Sample 03	A3	Method 1		
Injectio	ons 🛛 🔚 History 🏋 N	Notes	🕕 Pause 🛛 Sto	p 🚰 Add 📕 Rej	plicate 🔀 Remove	. 🗄 🖻
Injectio			Pause Sto Location	p 🕂 Add 📕 Rej	plicate 🔀 Remove	• 🕀 🖻
Injectio 1	Injection Name Sample 01 01	Notes Sample ID Sample 01				: 🕀 🖻
	Injection Name	Sample ID	Location	Method		: 🕀 🖻
1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method Method 1		: 🖣 🗖

13. Click on the Notes pane, then click in the notes area and type any information you want to add about your batch (optional).



- 14. You can preset the parameters used to analyze data generated with the batch (optional). We recommend using the default parameters for cIEF applications, but if you want to modify parameters:
 - a. Select Edit from the main menu and click Default Analysis. The following screen will display:

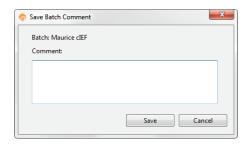
ô Default Analysis: Maurice clEF							×
Detection Peak Names	Detection						
Peak Fit Advanced	Method	Absorbance) Fluorescence				
pl Markers	System	Exposure 1 0.005 seconds $$	Exposure 1 3 seconds	\sim			
Import Export			ОК	Car	ncel	Apply	/

b. Change the parameters you want to, then click **OK**. For detailed information on analysis parameters, please refer to "Analysis Settings Overview" on page 528.

- 15. You can preset the parameters used to view data when the batch is complete (optional). Default Analysis View Parameters must be set before you start the batch and cannot be modified once the batch starts. However, you can still manually change parameters in the Analysis pane using the Graph Options button:
 - a. Select Edit from the main menu and click Default Analysis View. The following screen will display:

 Matching Peak Names Peak Names Peak Values 	
Fitted Peaks Baseline Fit Overlay FL/ABS Grid Lines	
Plot Label Sample Method Injection Exposure	
Injection Name	

- b. Change the parameters you want to, then click OK. For detailed graph view options, please refer to "Customizing the Data Display" on page 509.
- 16. Once all of your sample, method and injection info is entered, select File > Save. Enter any comments on the batch if you want, then click Save.



17. Enter a name for your batch then click Save.

Step 7: Start the Batch

1. Make sure Maurice is connected to Compass for iCE. If he isn't, select **Instrument** and click **Connect**. Then select your Maurice system and click **Connect**.

2. Click on the green Start button to start your batch.

NOTE: An alert may appear if the wronge cartridge is installed or if a cartridge post-run cleanup or cartridge purge is recommended. See "Step 5: Check for Cartridge Alerts" on page 101 for more information.



3. If you have made any changes, you will be asked to save your batch before starting the run. Click Save

ô Save	: batch X	(
?	The batch must be saved before starting. Save the batch?	
	Save Cancel	

- 4. The Start Run box shows you the number of injections and batches remaining on your cartridge. Make sure you still have enough injections left before you start the run. If not, prep a new cartridge.
- 5. Click in the **Results File name** box if you want to change the default run file name. Otherwise just leave it as is.

ô Start Run					X
Batch: Mauri	ce cIEF				
Results file na	me:				Browse
2016-09-07_1	0-20-39_Maurice cIEF				
Location: C:	\Users\atu\Documents\(Compass for iCE\Runs			
Comment:					
	Cartridge				
	Type: cIEF	:	Injections per Batch :	100	
	Expires : Dec	2016	Injections Remaining :	124 (24 guaranteed)	
	Serial Number: 1151	1219325	Batches Remaining :	11	
				Start	Cancel

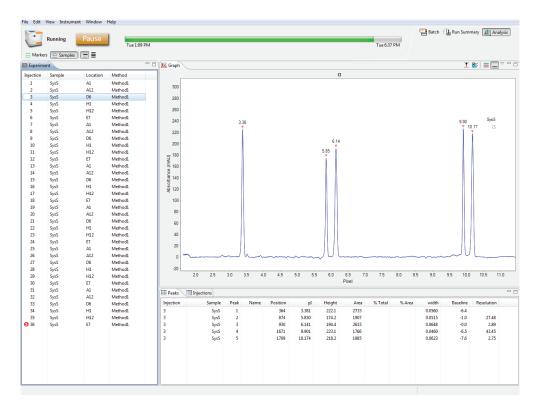
- 6. If you don't want to save the file to the default Runs folder, click Browse to select a different location.
- 7. Enter any run details you'd like in the Comments box (optional).
- 8. Click Start to start the run.

NOTE: The indicator light on Maurice's front panel will pulse slowly while he's running the batch.

To monitor the progress of your batch, click the **Run Summary** tab. See Chapter 16: "Run Status" for more details.

It is betweet Wides Het Image: Bill is betweet Wides He	\$ 2017-0	5-09_14-16-55_run	- Compass for	iCE					
by extensive by	File Edit			ļ	ii 2:31 PM				
Suppletion Single D Location Method Single X Time Single X Sin	Run: 201	7-06-09 14-16-55 r	un						
Injection Name Sample D Location Method State Time Sample Tempentore C 1 Sample D, Di Sample D, Samp									P Status History
1 Sample 01_01 Sample 01_01 All System Subable V Completed 2017-66-90 164139 10.0 2 Sample 02_02 Sample 02_02<			Sample ID	Location	Method	Status	Time	Sample Temperature C	
 3 Sample 02,93 Sample 02, A2 Sparm Subbitivy Sparating 6 mins 4 Sample 02,94 Sample 02, A2 Monod Ceanop 4 Monod Ceanop<td></td><td></td><td></td><td></td><td>Calibration Pause System Suitability System Suitability</td><td>Completed Paused 2:38 Completed Completed</td><td></td><td></td><td>path batch run batch type cIEF</td>					Calibration Pause System Suitability System Suitability	Completed Paused 2:38 Completed Completed			path batch run batch type cIEF
4 Sample 02,04 Sa	3	Sample 02 03	Sample 02	A2			6 mins		
seial number 11/01/20/9 injections remaining 13 expires Jan 2018 MM Focus Serie: In View 300 100 100 100 100 100 100 100 100 100					Method1	separating			
Zoom Dut injection 3 200 100 100 100 100 100 100 100									serial number 1170109209 injections per batch 100 injections remaining 174 (74 guaranteed) batches remaining 13
200 100 100 0 250 550 750 1.5									
Lock admin is logged in.									200 100 100 100 100 100 100 100
								Lock	admin is logged in.

To view results, analyze results or change analysis parameters on completed injections while the batch is still running, click the **Analysis** tab. See Chapter 18: "cIEF Data Analysis" for more details.



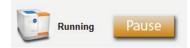
When your batch is complete, you can view electropherograms for all injections in the Analysis tab, and all batch and injection details in the Run Summary tab.

NOTE: If you'd like Maurice to let you know when your run is done, you can set him up to tweet you. Go to "Setting Up Maurice Systems to Send Tweets" on page 764 for more info.

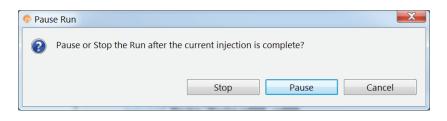
Editing a Running Batch

You can pause a batch after it's started to make updates or add samples and reagents.

1. Select Instrument > Pause or select the Pause button.



2. Click Pause in the pop-up window.



The Pause button will change to Continue but Maurice's status will stay at Running until Compass for iCE completes the current injection.



- You can now make these edits to the batch:
 - Add sample(s)
 - Add injection(s) to the end of the batch
 - · Modify injections that haven't completed and aren't greyed out
 - Create a new method
 - Update the method. Once a method is run it can only be updated. Highlight the method you want to edit and click **Update** in the Methods pane. The software will copy the parameters into a new method that you can modify.

3. When Maurice completes the current injection, his status will change to Paused and the progress bar will turn yellow.

NOTE: Maurice's status light will change from a pulsing blue to a blue pulse with magenta flashes which means he's paused the run.

17 24	Paused	Continue	-	
_			Mon 1:43 PM	

The status in the Injection pane also changes to Paused and the pause duration updates live. You can now open the instrument door to:

- · Add new samples
- Add on-board mixing reagents if the paused batch was set up to do on-board mixing and your Maurice has this
 option.

IMPORTANT

The door must be closed within 15 minutes of opening it to avoid potential assay performance issues.

NOTE: If the door is open for more than 30 seconds, a white light near the cartridge will start to flash and a warning message displays in Compass for iCE until the door is closed.

4. To continue the batch, click **Continue**. Changes you made to the batch are saved and Maurice will continue with the next sample injection.

Post-batch Procedures

When the batch is done:

- 1. Open Maurice's door. The lights on either side of the cartridge slot will be **orange** as Maurice will have already disengaged the cartridge.
- 2. Remove your sample. Leave the Water (P3) and Air (P6) vials in place if your cartridge still has injections left since they will be needed for the post-run cleanup step. Remove the remaining reagent vials.

3. Gently pull out the cartridge making sure the cartridge inlet doesn't come into contact with any surface.



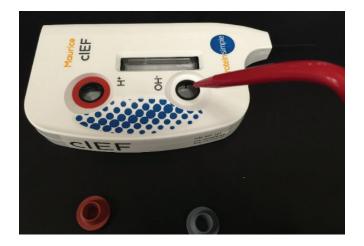
If you're at 100 injections, you've reached the limit of guaranteed performance for the cartridge. To dispose of a finished cartridge, put it in its original packing and discard it per your institution's safety and waste disposal guidelines. Discard any remaining reagent vials.

NOTE: Disposal of cartridges, sample plates and vials depends on the samples you ran. If you aren't sure what your sample origins are, we recommend you dispose of everything in biohazard waste.

If the cartridge will be used again, clean up and store the cartridge:

- a. Put the cartridge on a flat surface with its electrolyte tanks facing up.
- b. Remove the stoppers from both the electrolyte tanks.
- c. Using an electrolyte pipette or low vacuum, aspirate the solutions from each tank.
- d. Fill each tank with 2 mL DI water, then aspirate it out. Repeat this rinse 3 times.

NOTE: Make sure not to get any liquid on the cartridge's optical window.



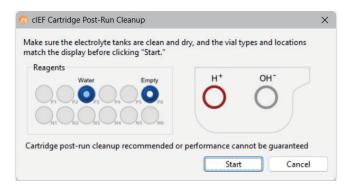
e. Aspirate all the remaining liquid and make sure that the tanks are dry.

NOTE: If you are using Compass for iCE v3.0.0, go to step f. If you are using an earlier version of Compass for iCE, remove all the reagent vials and skip to step k.

- f. Put the stoppers back on the tanks and install the cartridge in Maurice.
- g. Verify there is at least 1.5 mL of DI water in the Water (P3) vial and air in the empty (P6) vial.
- h. Click on the brown **Cleanup** button in the Instrument Status Bar or select **Instrument** and **Cartridge Post-Run Cleanup** in the Compass main menu.

		Instrument Window Help
		Start
		Cartridge Post-Run Cleanup
		Cartridge Purge
Ready	Cleanup	Self Test >
-		Runs
		Properties
		Update >
		Disconnect

i. You'll get the following message. Click Start. It'll only take 6 minutes.



- j. Open Maurice's door. Gently pull out the cartridge making sure the cartridge inlet doesn't come in contact with any surface.
- k. Remove the reagent vials.
- 1. Leave the stoppers off to allow the tanks to air dry.
- m. Put the cartridge and stoppers back in the protective packaging and store at room temperature.

!WARNING! SHARPS HAZARD

The capillary inlet of the cartridge may present a potential sharps hazard. Dispose of used cartridges according to your organizations health and safety regulations.



!WARNING! BIOHAZARD

Cartridges, sample plates and vials should be handled by procedures recommended in the CDC/NIH manual: Biosafety in Microbiological and Biomedical Laboratories (BMBL). The manual is available from the U.S. Government Printing Office or online at http://www.cdc.gov/biosafety/publications/bmbl5/.

Depending on the samples used, the cartridges, plates and vials may constitute a chemical or a biohazard. Dispose of the cartridges, plates and vials in accordance with good laboratory practices and local, state/ provincial, or national environmental and health regulations. Read and understand the Safety Data Sheets (SDSs) provided by the manufacturers of the chemicals in the waste content before you store, handle, or dispose of chemical waste.

Checking Your Data

Compass for iCE detects your sample protein and pI marker peaks and reports results automatically. But, we always recommend you review your data using the steps in this section as a good general practice to make sure your results are accurate. If you see a data warning in the Experiment pane, these steps will also help you identify and correct any issues.

Step 1: Select Your Detection Mode

- 1. Go to the Analysis screen and open your run (if it isn't already open).
- 2. The data displays in absorbance mode by default. If you want to look at fluorescence data instead, select Edit from the main menu and click Analysis. In the Analysis window, select Detection in the left sidebar, then click Fluorescence in the Detection page.

e filter text	Detection			⇔ ◄ ⇔
Advanced Detection Peak Fit	Method	Ø Absorbance	Fluorescence	
Peak Names pI Markers	System Suitablity	Exposure 1 0.005 seconds 👻	Exposure 3 10 seconds 🔻	
	mAb Method	Exposure 1 0.005 seconds 🔻	Exposure 4 20 seconds 🔻	

Step 2: Check Your pl Markers

To make sure your pI markers are identified correctly:

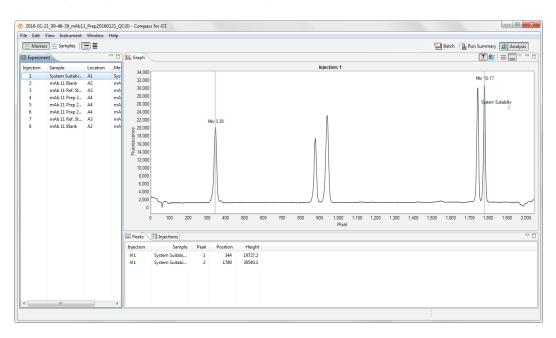
- 1. Go to the Analysis screen.
- 2. Click Markers in the View bar.



3. Click the View Selected icon in the View bar.

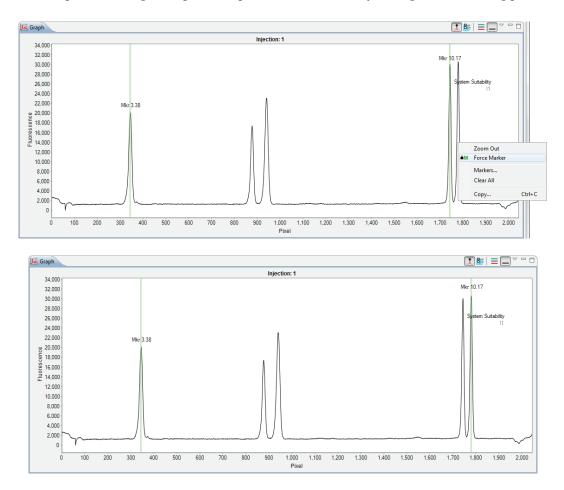
File	Edit	View	Instrume	ent	Window
Ē	Marke	ers 🚊	Samples		∎∎
				1	`

- 4. Click Injection 1 in the Experiment pane.
- 5. Check that your pI markers in the electropherogram have been correctly identified. Each marker peak will have a green vertical line running through it and be labeled Mkr. They're also identified with an **M** in the Peaks table.



6. If your pI markers aren't identified correctly, here's how to manually correct them:

To set an unidentified peak as a pI marker: Right-click the peak in the electropherogram or Peaks table and select **Force Marker**. Compass will assign that peak as a pI marker, and correctly reassign the remaining pI marker peaks.

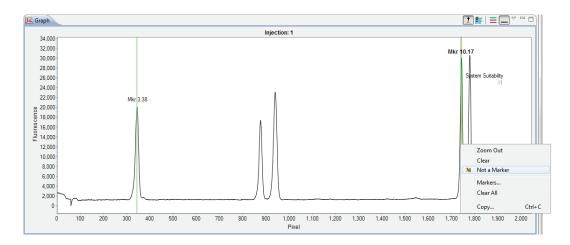


A lock icon indicating the pI marker was set manually will display next to the peak in the Peaks table and a check mark will appear next to the injection in the Experiment pane to show a manual correction was made.

Peaks	Injections			
Injection	Sample	Peak	Position	Height
1	System Suitabi	14	1315	1315.8
1	System Suitabi	15	1422	1433.6
1	System Suitabi	16	1549	1627.6
M1	System Suitabi	17	1743	29396.8
1	System Suitabi	18	1780	30540.1
1	System Suitabi	19	1959	1399.5
1	System Suitabi	20	2018	1470.4
	-,			

NOTE: To remove pI marker peak assignments that were made manually, right click on the peak in the electropherogram or Peaks table and click **Clear**. To clear all the manual settings for the injection, click **Clear** All.

If an incorrect peak is identified as a pI marker: Right-click the peak in the electropherogram or Peaks table and select **Not a Marker**. Compass should correctly reassign the remaining peaks as pI markers and update the Peaks table.



7. Repeat the previous steps for the remaining pI marker peaks as needed in the current injection and for all other injections to make sure all your pI markers are identified correctly.

Step 3: Checking Sample Peaks

All detected peaks will be labeled automatically with the calculated protein pI.

NOTE: The reported protein pI in Compass may vary slightly from predicted pIs based on sample, buffer, and method conditions.

To make sure your sample proteins are identified correctly:

1. Click **Samples** in the View bar.



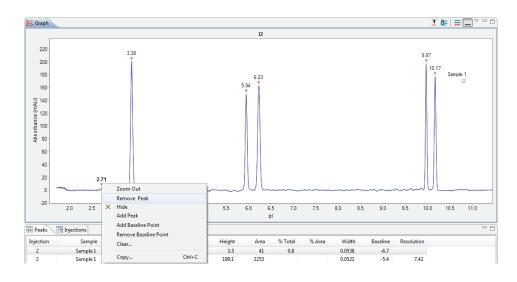
2. Click the View Selected icon in the View bar.

File	Edit	View	Instrument	Window
Ħ	Marke	ers 🚘	Samples	∎≣
				 ^

3. Click Injection 1 in the Experiment pane.

4. If your sample peaks aren't identified correctly, here's how to manually correct them:

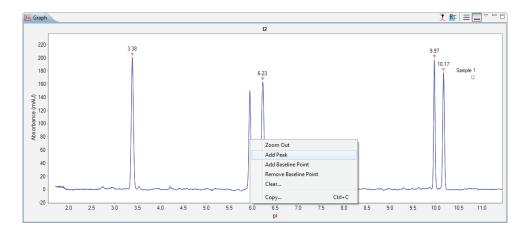
If a peak is incorrectly identified as a sample peak: Right-click the peak in the electropherogram or Peaks table and select **Remove Peak**. Compass will no longer identify it as a sample peak in the electropherogram and the peak data will be removed in the results table.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

Injection	Sample	Location	Method
√ 1	Sample 1	A1	Method1
2	Sample 1	A1	Method1
3	Sample 1	A1	Method1
4	Sample 1	A1	Method1
5	Sample 1	A1	Method1

To identify a peak as a sample peak: Right-click the peak in the electropherogram or Peaks table and select Add Peak. Compass will calculate and display the results for the peak in the results table and identify the peak in the electropherogram.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

Experime	ent		- 0
Injection	Sample	Location	Method
✓1	Sample 1	A1	Method1
2	Sample 1	A1	Method1
3	Sample 1	A1	Method1
4	Sample 1	A1	Method1
5	Sample 1	A1	Method1

NOTE: To remove sample peak assignments that were made manually and go back to the original peak data, right-click the peak in the electropherogram and select **Clear**.

5. Repeat the previous steps for the remaining injections to make sure all sample peaks are correctly identified.

Step 4: Assigning Peak Names

Compass can also optionally identify and automatically name sample peaks using user-specified peak name settings. For more information on how to do this, see "Manual Peak Integration" on page 474.

Chapter 7: MauriceFlex cIEF Batches

Chapter Overview

- Overview
- Batch Screen Overview
- Opening a Batch
- Creating a New Batch
- Viewing Replicate Injections
- Batch History
- Making Changes to a Batch
- Viewing and Editing Batches in Completed Runs
- Copying and Pasting Injection Names or Sample IDs from other Documents
- Importing and Exporting Injections
- Importing and Exporting Methods
- Batch Reports

Overview

MauriceFlex cIEF batches can be run on MauriceFlex systems using a cIEF Fractionation cartridge.

NOTES:

We recommend first optimizing methods with cIEF batches using a cIEF cartridge on Maurice, Maurice C. or MauriceFlex. Then, use recommendations in the MauriceFlex cIEF Fractionation Method Development Guide for tips to modify the method for a MauriceFlex cIEF batch using a cIEF Fractionation cartridge on MauriceFlex to confirm successful method transfer before performing a MauriceFlex Fractionation batch.

On-board mixing is not available on MauriceFlex.

Batch Screen Overview

You can use the Batch screen to create, view and edit batches. To get to this screen, click the Batch screen tab:

💾 Batch 强 Run Summary 🏥 Analysis

Batch Screen Panes

The Batch screen has five panes:

- Layout Displays a map of the 96-well plate for MauriceFlex cIEF batch sample locations. Batch reagent locations are also displayed.
- **Injections** Lists the injections, sample ID, sample locations and methods that MauriceFlex will execute for each sample in the batch.
- History Lists all batch file events from initial creation to the most current update.
- Notes Lets you enter specific information about your batch.
- Methods Lets you create methods and enter method parameters used in the batch.

	ment Window Help								
								🖽 Batch 🔮 Run	Summary 🎄 Anal
atch: MauriceFlex	cIEF III	Injections	s 🔚 Histo	ory 🃧 Notes					
							(🕽 Pause 🖸 Stop 🗜 Add 📗 Replic	ate 🕅 Remove 🕞
1 Layout			Injection	Name Sa	imple ID	Locatio	n Method	Notes	
10°C	- C Add - C Remove		Sample 0		mple 01	A1	IgG		
MC	FI Cal Water Water Empty								
-									
1	2 3 4 5 6 7 8 9 10 11 12								
Sample									
Catholyte									
O P	00000000000								
Water	00000000000								
KS HO									
Methods									
									New Remo
Name	Separation	Det	tection	Sample Load	pl Markers	Ampholyt A	dditives		
gG	10.0 min 500 Volts, 10.0 min 1000 Volts, 2	5 1 E	xposure	20	7.05, 10.17				

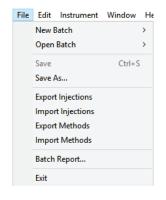
Software Menus Active in the Batch Screen

These main menu items are active in the Batch screen:

- File
- Edit
- Instrument (when the software is connected to MauriceFlex)
- Window
- Help

File Menu

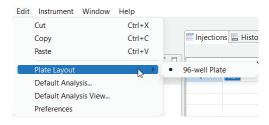
These File menu options are active:



- New Batch Creates a new batch from a starter template.
- Open Batch Opens an existing batch.
- Save/Save As Saves the open batch.
- Export Injections Exports injections from the current batch as a .csv file.
- Import Injections Imports injections into the current batch from a .csv file.
- Export Methods Exports method(s) from the current batch as separate files.
- Import Methods Imports saved method(s) into the current batch.
- Batch Report Exports a table of sample and method details for each injection in the batch as a PDF file.
- Exit Closes Compass for iCE.

Edit Menu

The following Edit menu options are active in the Batch screen:



- Cut Cuts the information currently selected.
- Copy Copies the information currently selected.
- **Paste** Pastes the copied information.

NOTE: Cut, Copy and Paste work differently depending on the pane you're in. How and when you can use them is described throughout the chapter.

- Plate Layout Indicates a 96-well plate will be used to run samples.
- Default Analysis Displays the default settings that will be used to analyze the data generated with your batch.
- Default Analysis View Displays the default settings that will used to view the data generated with your batch.
- **Preferences** Lets you set and save your preferences for Access Control, data export, graph colors, grouped data and Twitter settings. See Chapter 21: "Setting Your Preferences" for more information.

Opening a Batch

To open an existing batch:

1. Select File in the main menu and click Open Batch.

File	Edit Instrument	Window Help		
	New Batch	>		
	Open Batch	> (Maurice FLEX cIEF batch 20221214	
	Save Save As	Ctrl+S	Maurice_CE-SDS_TURBO_Reduced DemoData_Maurice clEF Maurice CE-SDS PLUS	
	Export Injections Import Injections Export Methods		Maurice FLEX clEF batch Browse	Ctrl+O

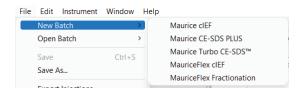
- 2. A list of the last five batches opened will display based on the last location found. If the location of the file has changed, you may need to navigate to find the file. Select one of those or click **Browse** to open the Batches folder and select a different one.
- 3. To make changes to the batch, see the steps in "Creating a New Batch" on page 133. When you're done, select File from the main menu and click Save.

Creating a New Batch

To create a new batch, we recommend that you use one of the template methods and make any necessary modifications from there.

Step 1 - Open a Template Batch

1. Select File in the main menu and click New Batch:

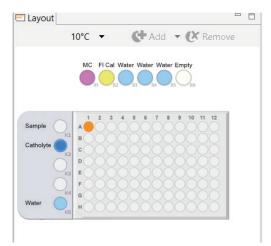


NOTE: Only template batches specific to your Maurice system will be available when you are connected to the instrument. Template batches will not appear in the menu if that application type cannot be performed on your instrument.

- log MauriceFlex cIEF Compass for iCE \times File Edit Instrument Window Help 💾 Batch 🔮 Run Summary 🚛 Analysis 🎹 Injections 🔛 History 耳 Notes Batch: MauriceFlex clEF ❶ Pause ● Stop 🕅 Add 📗 Replicate 🕅 Re • • 🖭 Layout Injection Name Sample ID Location Method Notes CH Add - CX Re 10°C ▼ 1 Sample 01 01 Sample 01 A1 lgG Empty Samp Methods New Remove Detection Sample Load ... pl Markers Ampholyt... Additives Name Separation IgG 10.0 min 500 Volts, 10.0 min 1000 Volts, 25.... 1 Exposure 20 7.05, 10.17
- 2. Select MauriceFlex cIEF. A batch using the default method will display.

Step 2 - Assign Your Samples

The Layout pane shows the default locations of where batch reagent should be placed in the fractionation adapter.



The same reagent locations are used for every batch:

- R1 0.5% Methyl Cellulose
- R2 Fluorescence Calibration Standard
- R3 Water vial

- R4 Water vial
- R5 Water vial
- R6 Empty vial (air)
- K2 Catholyte Solution
- K5 Water vial
- 1. Select your samples:

To import samples using a saved injections file:

- a. Select File in the main menu and click Import Injections.
- b. Select an injections .csv file and click OK. The imported information will display in the Injections pane.
- c. Skip to step 2 on page 136.

NOTE: For more information on setting up an injections file for import, see "Importing and Exporting Injections" on page 150.

To select samples manually:

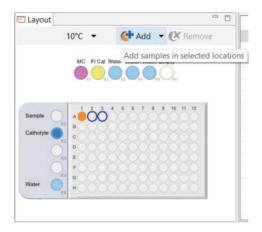
• Add samples and select methods later: Use your mouse to highlight the well or vial positions your samples are located in, then click Add.

NOTES:

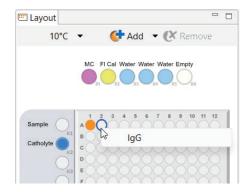
The template batch automatically adds a sample in well A1 by default.

Samples can be assigned to any well in the 96-well plate or in postion K1 of the fractionation adapter if the sample is prepared in a vial.

The maximum number of injections per batch for a MauriceFlex cIEF batch is four.



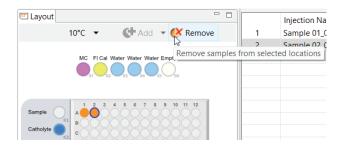
• Add samples with preassigned methods: Highlight the well or vial positions your samples are located in, then right-click and select a method.



Either option of adding samples populates the Injections table:

Inject	ions 🔚 History 🎩 Not	tes						-	
				Pause O Stop	🗼 🛃 Add	I 📕 Replicate	🔀 Remove	Ŧ	Ξ
	Injection Name	Sample ID	Location	Method	N	otes			
1	Sample 01_01	Sample 01	A1	IgG					
2	Sample 02_02	Sample 02	A2	IgG					
3	Sample 03_03	Sample 03	A3	IgG					

To remove samples, just highlight the ones you want to remove and click **Remove**. They'll also be removed in the Injections table. You can also right-click well(s) or vial(s) in the Layout pane and click **Remove Sample(s)**.



2. The 96-well plate on the fractionation adapter is temperature controlled with a default setting of 10 °C. To change the temperature or turn it off, click the **down arrow** next to the temperature and select an option.

NOTE: The reagent row (R) is kept at room temperature while the reagent column (K) and sample plate are temperature controlled.



Step 3 - Assign Your Method Parameters

NOTE: We recommend using the default method parameters. Please see the MauriceFlex cIEF Fractionation Method Development Guide for more information on method optimization.

The Methods pane lists all of the methods used in a batch. You can add and remove methods here and change method parameters.

To import a saved method:

- 1. Select File in the main menu and click Import Method.
- 2. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

To create a new method or make changes to an existing one:

1. In the Methods table, click the first cell in the Name column and enter a new method name if needed.

Methods							
							New Re
Name	Separation	Detection	Sample Load	pl Markers	Ampholyt	Additives	
lgG	10.0 min 500 Volts, 10.0 min 1000 Volts, 25	1 Exposure	20	7.05, 10.17			

2. Click the first cell in the Separation column, then click the selection button [...] to set the pre-focusing and focusing time (in minutes) and voltage (V). You can also set the Detection Interval (in minutes) and Exposure (in seconds) to adjust how often an image is taken using the listed Exposure time.

Method	ts		o Separation	Profile	
			Ade	tt	Remove
Name	Separation		 Time (min)	Voltage (Volts)	
gG	Voltage 3 Steps		10.0	500	
90		and the second se	10.0	1000	
		•0	25.0	1500	
			Detection Int Exposure(sec	terval(min) 5.0 .) 0.1	
				ОК	Cancel

- To change time and voltage parameters: Just click in a cell under Time or Voltage and type the new value(s).
- To change the detection interval or exposure parameters: Click on the field and type the new value(s).

- To add a profile step: Click Add. A new row will be added in the table. Then just type in a separation time (in minutes) and voltage value (in V).
- To remove a profile step: Select the row you want to remove and click Remove.
- 3. Click the first cell in the Detection column the selection button [...] to set your fluoresence detection time for the final focused image.

Methods					o Detection Profile	
					Add	Remove
Name	Separation	Detection		\longrightarrow	Exposure (sec)	Туре
gG	10.0 min 500 Volts, 10.0 min 100	1 Exposures	Ģ		0.2	Fluorescence
			3		0.2	Hubitstellee

- To change the exposure time: Just click in a cell under Exposure and type the new value(s) in seconds.
- To add a profile step: Click Add. A new row will be added in the table. Then just type in an exposure time (in seconds).
- To remove a profile step: Select the row you want to remove and click Remove.
- 4. Click the first cell in the Sample Load(s) column and set the load time in seconds.

NOTE: We recommend using the default Sample Load time of 20 seconds. Please contact ProteinSimple Technical Support if you have questions on the Sample Load time to use for your application.

Methods			
Name	Separation	Detection	Sample Load
IgG	10.0 min 500 Volts, 10.0 min 1000 Volts, 25	1 Exposure	20

5. Click the first cell in the pI Markers column to select pI markers. Add new markers or remove existing ones then click OK.

NOTE: When you edit the pI markers in the method for a batch, Compass for iCE automatically creates a Markers group in the pI Markers Analysis settings for you.

Name	Separation	Detection	Sample Load	pl Markers 7.05, 10.17	erros		Add	Remove
IgG	10.0 min 500 Volts, 10.0 min 10	1 Exposure	20	7.05, 10.17	73	\rightarrow	pl Markers:	
							pl	Position
							7.05	300
							10.17	1,900
							_	

- To change a pI marker and position: Just click in a cell under pI or Position and type the new value(s).
- **To add a pI marker:** Click **Add**. A new row will be added in the table. Then just type in a pI and a position (in pixels).
- To remove a pI marker: Select the row you want to remove and click Remove.
- 6. Optional: Click the first cell in the Ampholytes column and enter the ampholytes you're using.

Name	Separation	Detection	Sample Load (s)	pl Markers	Ampholytes	Additives		
							_	
lgG	10.0 min 500 Volts, 10.0 min 1000 Vol	1 Exposure	20	7.05, 10.17	Pharmalyte 3-10	Urea		

7. Optional: Click the first cell in the Additives column and enter any additives you're using.

Methods							
_						New	Remove
Name	Separation	Detection	Sample Load (s)	pl Markers	Ampholytes	Additives	
lgG	10.0 min 500 Volts, 10.0 min 1000 Volts, 25.0	1 Exposure	20	7.05, 10.17	Pharmalyte	Urea	

- 8. You can now:
 - Click **New** in the upper right corner of the Methods pane to add a new one if you want to use different methods for different samples. Then just repeat the steps above for the new method.
 - Make updates to the remaining methods by repeating the prior steps.
 - Select a method and click Remove in the upper right corner of the Methods pane to delete it.

Step 4 - Set Up Your Injections

The Injection pane lists all sample injections for the batch. Any samples that were added in "Step 2 - Assign Your Samples" are automatically added to this list.

NOTE: If you imported injections in Step 2, you can update the injections table and assign methods as needed using the information that follows.

Selecting an injection in the table also selects the sample the injection will be made from in the plate or vial map in the Layout pane and vice-versa.

Batch: MauriceFlex clEF	Injection	ns 🔚 History 👖 Notes	5				- 0
					🕕 Pause 🖸 Stop 🎁 /	Add 📗 Replicate 🔀 Remove	H
🖾 Layout 📃 🗖		Injection Name	Sample ID	Location	Method	Notes	
10°C 👻 🛛 🐨 🧭 Remove	1	Sample 01_01	Sample 01	A1	lgG		
	2	Sample 02_02	Sample 02	A2	lgG		
MC FI Cal Water Water Empty	3	Sample 03_03	Sample 03	A3	IgG		
Sample III 2 3 4 5 6 7 8 9 10 11 12 Catholyse Catholyse							

1. To add sample names, click the **Sample ID** cell for the injection and type a name.

NOTES:

Sample IDs can be copied from other documents and pasted into Compass for iCE to make batch setup faster. Check out "Copying and Pasting Injection Names or Sample IDs from other Documents" on page 149 "for more info.

If you change the sample ID when the default injection name is still being used, the injection name will automatically update to match the sample ID. If you've already changed the injection name manually, updating the sample ID will not update the injection name.

Injecti	ons 📗 History 🚺 Notes					
		🕕 Pause 🛛 Sto	op 👉 Add 📊 Repli	cate 🔀 Remove	Ŧ	Ξ
	Injection Name	Sample ID	Location	Method		
1	Sample 01_01	Sample 01	A1	IgG		
2	Sample 02_02	Molecule X	A2	IgG		
3	Sample 03_03	Sample 03	A3	IgG		

The sample name also displays when you hover the mouse over the sample in the plate map:

					🕕 Pause 🛛 Stop	📌 Add 📊 Replie	cate 🔀 Remove 📑
Layout				Injection Name	Sample ID	Location	Method
	10°C 👻	🗲 Add 📼 候 Remove	1	Sample 01_01	Sample 01	A1	lgG
	10 0	Contract Contractor	2	Sample 02_02	Molecule X	A2	lgG
			3	Sample 03_03	Sample 03	A3	IgG
		R3 R4 R5 R6					
Sample	1 2 3 4 A	5 6 7 8 9 10 11 12					

2. Injection names are automatically set to 'Sample ID_injection number'. To change the name, click the **Injection Name** cell for the injection and type a name. Each injection name must be unique. If they aren't when you save the batch, Compass for iCE highlights any non-unique injection names so you can change them.

		🕕 Pause 🛛 Sto	p 👫 Add 📊 Repli	cate 🔀 Remove 👍
	Injection Name	Sample ID	Location	Method
1	Sample 01_01	Sample 01	A1	IgG
2	lgG	Sample 02	A2	lgG
3	Sample 03_03	Sample 03	A3	IgG

NOTE: Changing the injection name won't affect the sample ID.

3. Assign your methods to each injection. Just click the **Method** cell for the injection and select a method from the drop down menu. If you added your samples with pre-assigned methods and don't need to make any changes, skip to the next step.

	ons 🔚 History 👖 Notes			Stop 🕂 Add 📊 Replicate		
	Injection Name	Sample ID	Location	Method	Notes	
1	Sample 01_01	Sample 01	A1	IgG		
2	Molecule X_02	Molecule X	A2	lgG		
3	Sample 03_03	Sample 03	A3	lgG		
				Method2		

Hovering over a method name displays the method parameters:

Injections	🔚 History 👖 Notes			🕕 Pause 🛛 Stop 🏌 A	Add 📊 Replicate 🔀 Remove 🕞 🖻 🗖
1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method IgG	Notes
2	Molecule X_02	Molecule X	A2	Method2	
3	Sample 03_03	Sample 03	A3	Ig Method2 Separation: 10.0 min 500 Detection: 1 Exposure Sample Load (s): 20 pl Markers: 7.05, 10.17	Volts, 10.0 min 1000 Volts, 25.0 min 1500 Volts

- 4. You can add or remove injections as needed using a few different options. If you don't need to make any changes here, just skip to the next step.
 - To add sequential replicate injections: Highlight an injection and click **Replicate**. A new injection will be added under the row you selected

Injectio	ns 🔚 History <u> N</u> otes		🕕 Pause 🛛	Stop 🛃 Add	Replicate 🔀 Rer	nove 📑	⊟ " [
	Injection Name	Sample ID	Location	Method	Replicate select	ted iniecti	ons i
1	Sample 01_01	Sample 01	A1	IgG			
2	Molecule X_02	Molecule X	A2	Method2			
3	Sample 03_03	Sample 03	A3	lgG			
Injection	ns 🔚 History 🏋 Notes		🕕 Pause 🔘	Stop 🕂 Add 📊	Replicate 🔀 Ren	nove 🕀	E - E
Injectior	hs History T Notes						8 - 5
Injection	Injection Name	Sample ID	Location	Method	Replicate 🕌 Ren Notes		E - E
Injection 1 V 2							
1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method IgG			8 - 6

• To add injections at the end of the batch: Click on any sample position in the Layout pane or sample injection in the Injection table and click Add. A new injection using the same sample will be added to the end of the table. Assign the method if needed.

1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Methe Add injections	Notes
2	Molecule X_02	Molecule X	A2	Method2	
3	Sample 03_03	Sample 03	A3	IgG	

• To copy and paste injections: Right-click on an injection in the Injection table and select Copy. Click on the injection number above where you want to insert the copied injection, right click and select Paste. The copied injection will be inserted under the row you selected.

Step 5 - Add Programmed Pauses and Stops (Optional)

You can program pauses and stops in the batch to automatically pause or stop after injections even when you aren't in front of MauriceFlex.

Note: The cartridge cleanup is performed at the end of the batch and after an injection. A programmed pause will occur after the injection before the cartridge cleanup starts.

To program a pause:

Pauses are helpful when you want to review injection results before continuing with the rest of the batch.

1. Highlight the injection you want to pause at and click **Pause**. The batch will pause after that injection is complete.

NOTE: MauriceFlex can tweet you when the batch pauses. See "Setting Up Maurice Systems to Send Tweets" on page 764.

Inject	tions 🔚 History 🎵 Not	es							E
			0	Pause 🛛 Stop	🕇 Add	Replicate	🔀 Remove	Ŧ	
	Injection Name	Sample ID	Location	Me Pause afte	er the sele	ected injection			
1	Sample 01_01	Sample 01	A1	lgG		,			
2	Sample 02_02	Sample 02	A2	lgG					
3	Sample 03_03	Sample 03	A3	lgG					
Inject	tions 🔚 History ᅚ Not	es							E
Inject	tions 🔚 History 耳 Not	es	0	Pause 💿 Stop	🕂 Add	Replicate	Remove		_
Inject	tions 🔚 History ᅚ Not	es Sample ID	0 Location	Pause O Stop Method	H Add	Replicate Notes	Remove		_
Inject					it Add		Kemove		
	Injection Name	Sample ID	Location	Method	H Add		Remove		
1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method IgG	Add		K Remove		_

2. To resume the batch, click **Continue** in the instrument status bar:



To stop the run after a specific injection:

1. Highlight the injection you want the batch to stop at and click **Stop**. MauriceFlex will continue the batch through the selected injection, then stop the batch and perform end-run cleanup steps.

nject	tions 📗 History 👖 Not	tes							E
			0	Pause O Stop	🕇 🕂 Add	Replicate	🔀 Remove	e 🕀	Į
	Injection Name	Sample ID	Location	Method 13	Stop afte	r the selected	injection I		
1	Sample 01_01	Sample 01	A1	lgG	Stop unte	T the selected	injection		
2	Sample 02_02	Sample 02	A2	IgG					
3	Sample 03_03	Sample 03	A3	IgG					
nject	ions 🔚 History 🎹 Not	es							ľ
nject	ions 🔚 History 🏋 Not	es	0	Pause 🖸 Stop	🕂 Add	Replicate	Remove		
nject	ions 🔚 History 🎵 Not	Sample ID	U Location	Pause O Stop Method	• 🕌 Add	Replicate Notes	Kemove		
nject 1					d 🕂 Add		Remove		
nject 1 2	Injection Name	Sample ID	Location	Method	d 👫 Add		Kemove		
1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method IgG	Add 🕂		Kemove		_
1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method IgG IgG	Add 🕂		Kemove		

Data collected for injections completed up to the point where the batch was stopped are saved in the .mbz file.

2. Be sure to complete your normal post-batch procedures.

Step 6 - Add Batch Notes (Optional)

- 1. Click on the Notes pane.
- 2. Click in the notes area and type any information you want to add about your batch.

III Injections 🔚 History 🍞 Notes	
Product testing	

Step 7 - Modify Default Analysis Parameters (Optional)

You can preset the parameters used to analyze data generated with the batch. We recommend using the default parameters for MauriceFlex cIEF applications, but if you need to modify parameters:

1. Select Edit from the main menu and click Default Analysis. The following screen will display:

o Default Analysis: Ma	uriceFlex cIEF			×
Detection Peak Names	Detection			
Peak Fit				
Advanced pl Markers				
	IgG Exposure 1 0.2 seconds ~			
Import	Export OK	Cancel	Apply	
	UN UN	Cancer	Apply	

2. Change the parameters you want to, then click OK. For detailed information on analysis parameters, please refer to "Analysis Settings Overview" on page 528.

Step 8 - Modify Default Analysis View Parameters (Optional)

You can present the parameters used to display the electropherogram data when the batch is complete. Default Analysis View Parameters must be set before you start the batch and cannot be modified once the batch starts. However, you can still manually change parameters in the Analysis pane using the Graph Options button.

To modify the parameters:

1. Select Edit from the main menu and click Default Analysis View. The following screen will display:

o Default Analysis View Mau	uriceFlex cIEF			2	×
Graph View Options	Graph View Options Matching Peak Names Peak Names Peak Values Fitted Peaks Baseline Fit Grid Lines Plot Label Sample Method Injection Exposure Injection Name				
	OK Car	ncel	4	Apply	

2. Change the parameters you want to, then click **Apply**. Click **OK** when you are done changing display parameters. For detailed information on graph view options, please refer to "Customizing the Data Display" on page 509.

Step 9 - Save Your Batch

1. Once all of your sample, method and injection info is entered, select **File > Save**. Enter any comments on the batch if you want, then click **Save**.

🧒 Save Batch Comment	×
Batch: MauriceFlex clEF Comment:	
Save Car	ncel

2. Enter a name for your batch then click Save.

Viewing Replicate Injections

Injections with replicates have an arrow next to the injection number. You can expand or collapse the list of replicate injections by toggling the arrow:

	Injection Name	Sample ID	Location	Method		Injection Name	Sample ID	Location	Method
1	Sample 01_01	Sample 01	A1	lgG	✓ 1	Sample 01_01	Sample 01	A1	lgG
4	Sample 02_02	Sample 02	A2	lgG	2	Sample 01_02	Sample 01	A1	IgG
					3	Sample 01_03	Sample 01	A1	IgG
					4	Sample 02_02	Sample 02	A2	lgG

• To show all replicate injections in the batch, click the Expand All Injections button.

Injectio	ons 🔚 History 🖪 Not	es				♥□
			🕕 Pause	e 🖸 Stop 🖁	🖡 Add 📗 Replicate 🔀	Remove 🖳 🖻
	Injection Name	Sample ID	Location	Method	Notes	Expand all injections
~ 1	Sample 01_01	Sample 01	A1	IgG		
2	Sample 01_02	Sample 01	A1	lgG		
3	Sample 01_03	Sample 01	A1	lgG		
4	Sample 02_02	Sample 02	A2	lgG		

• To hide all replicate injections in the batch, click the Collapse All Injections button.

Injecti	ons 🔚 History 耳 Not	es					- 🖌	•
			🕕 Paus	e 🖸 Stop 🎁	Add 📗 Replicate	🔀 Remove		
	Injection Name	Sample ID	Location	Method	Notes		hi	al Collapse all injections
> 1	Sample 01_01	Sample 01	A1	IgG				
4	Sample 02_02	Sample 02	A2	lgG				

Batch History

Clicking on the History pane shows the batch event history, starting with the date and time the batch was created through the most current event. Clicking on a row in the table displays the full event details in the box under the table.

Date	User Name	Message	Comment	
2023-01-13 14:49:08	3	Started run: 2023-01-13_14-49-17_MauriceFlex clEF_user manual Batch: MauriceFlex clEF.batch from Compass for iCE v4.0.0-0110	5221108010	
> 2023-01-16 13:12:12	2	Saved analysis and methods changes from Compass for iCE v4.0.0-0113		
ime	2023-01-13 1	4:49:08 User		
/lessage		2023-01-13_14-49-17_MauriceFlex clEF_user manual Batch: MauriceFlex clEF.batch from Compass for iCE v4.0.0-0110		
Comment	5221108010			

- Date: Date and time of the batch event.
- User Name: User that initiated the event. User names only display if you're using the Access Control feature to help satisfy the 21CFR Part 11 data security requirements. Go to "Enabling Access Control" on page 781 to learn how to set it up.
- Message: Description of the event that took place.
- **Comment:** Comments entered by the user when the batch was saved.

You can copy the information in the History pane to use in other documents:

- 1. Click the History pane to make sure it's active.
- 2. Click Edit in the main menu and select Copy.
- 3. Open a document and click Paste.

Making Changes to a Batch

1. Select File in the main menu and click Open Batch.

Open Batch	Maurice FLEX clEF batc				
Save Ctrl Save As	+S Maurice_CE-SDS_TURB DemoData_Maurice cIE Maurice CE-SDS PLUS				
Export Injections		Maurice FLEX clEF batch			
Import Injections Export Methods	Browse	Ctrl+C			
Import Methods					

- 2. A list of the last five batches opened will display based on the last location found. If the location of the file has changed, you may need to navigate to find the file.
 - Select one of these files or click **Browse** to open the Batch folder and select a different one.
 - To open a batch used in a run file, click **Browse**. Go to the Run folder in the Compass for iCE directory and select the run file that uses the batch you want to edit.

Organize ▼ Share with ▼ Burn New	v folder				
 Libraries Documents 	Documents library Compass for iCE				
4 📗 My Documents	Name	Date modified	Date created	Туре	Size
Add-in Express Adobe	Batches	1/18/2016 5:39 PM	1/13/2016 8:24 PM	File folder	
Dients	🍌 New Batches	1/13/2016 8:24 PM	1/13/2016 8:24 PM	File folder	
Compass for iCE	Runs	1/17/2016 8:41 PM	11/11/2015 4:46 PM	File folder	
Batches	DemoData Maurice cIEF.mbz	1/18/2016 11:38 AM	1/18/2016 11:38 AM	Maurice data file.	798 K

3. To make changes to the batch, see the steps in "Creating a New Batch" on page 133. Then select File from the main menu and click **Save** or **Save As**.

Viewing and Editing Batches in Completed Runs

- 1. Click the Analysis screen and open your run file(s).
- 2. After the run opens, click the Batch screen to view the batch used with the run.

If you opened more than one run file, you can switch between viewing batches for each file. Just click the **down arrow** in the Run box and select the batch you want to view from the drop down list.

Run:	2015-1	2-06_15	-13-0	1_Maurice cIEF_Mab11_Te ╺
🖭 Laj	2016-0	L-21_09 2-06_15	- 46-3 9	9_mAb11_Prep20160121_QC(0)
	00	10°C	•	🗲 Add 🕞 🧭 Remove

- 3. In completed run files, you can only make edits to the **sample** and **method** names in a batch, and these changes are saved to the run file only. Update sample and method names as needed.
- 4. Click the Analysis screen. Then select File from the main menu and click Save or Save As to save the new changes to the run file.

Copying and Pasting Injection Names or Sample IDs from other Documents

Injection names and Sample IDs can be copied from other documents and pasted into the Injection pane to make batch setup faster.

To paste a list of injection names into the batch:

1. Select the list of injection names in a document (Microsoft[®] Word[®], Excel[®], etc.) and select **Copy** or hold the **Ctrl+C** keys to copy.

А	В	С
	My Injection 1	My Sample 1
	My Injection 1	My Sample 2
	My Injection 1	My Sample 3
	My Injection 1	My Sample 4
		My Injection 1 My Injection 1 My Injection 1 My Injection 1

2. Select an injection in the Injection pane, then hold the Ctrl+V keys to paste. You can also select the injection, right click and select Paste.

Injecti	ons 📗 History <u> II</u> Notes	0	🕕 Pause 🖸 Stop 🕌 Add 📗 Replicate 🔀 Remove 🕞 📄			
	Injection Name	Sample ID	Location	Method	Notes	
1	Sample 01_01	Sample 01	A1	IgG		
2	Sample 02_02	Sample 02	A2	IgG		
3	Sample 03_03	Sample 03	A3	IgG		
4	Sample 04_04	Sample 04	A4	lgG		

The injection names are pasted into the Injection pane:

Injections	s 🔚 History 📑 Notes	l III	Pause 🖸 Stop 🎁	Add 📗 Replicate	e 🔀 Remove 🕀 🖻 🗖
	Injection Name	Sample ID	Location	Method	Notes
1	My Injection 1	Sample 01	A1	lgG	
2	My Injection 2	Sample 02	A2	lgG	
3	My Injection 3	Sample 03	A3	IgG	
4	My Injection 4	Sample 04	A4	IgG	

To paste a list of Sample IDs into the batch:

1. Select the list of Sample IDs in a document (Microsoft Word, Excel, etc.) and select **Copy** or hold the **Ctrl+C** keys to copy.

	А	В	С
1			
2			My Sample 1
3		My Injection 1	My Sample 2
4		My Injection 1	My Sample 3
5		My Injection 1	My Sample 4
G			

2. Select a Sample ID in the Injection pane, then hold the Ctrl+V keys to paste. You can also select the Sample ID, right click and select Paste.

s 🔚 History 🚹 Notes	0	Pause 🖸 Stop 🎼	Add Replicate	🔀 Remove 🕀 🖻 🗖
Injection Name	Sample ID	Location	Method	Notes
Sample 01_01	Sample 01	A1	IgG	
Sample 02_02	Sample 02	A2	IgG	
Sample 03_03	Sample 03	A3	IgG	
Sample 04_04	Sample 04	A4	lgG	
	Injection Name Sample 01_01 Sample 02_02 Sample 03_03	Injection Name Sample ID Sample 01_01 Sample 01 Sample 02_02 Sample 02 Sample 03_03 Sample 03	Injection Name Sample ID Location Sample 01_01 Sample 01 A1 Sample 02_02 Sample 02 A2 Sample 03_03 Sample 03 A3	Injection Name Sample ID Location Method Sample 01_01 Sample 01 A1 IgG Sample 02_02 Sample 02 A2 IgG Sample 03_03 Sample 03 A3 IgG

The Sample IDs are pasted into the Injection pane.

NOTE: If you paste in new sample IDs when the default injection names are still being used, the injection names will automatically update to match the sample ID. If you've already changed the injection names manually, updating the sample IDs will not update the injection names.

Injectio	ons 🔚 History <u> Notes</u>	🕕 Pat	use 🟮 Stop 🏌	Add Replicate	🗙 Remove 🕀 🖻 🗖
	Injection Name	Sample ID	Location	Method	Notes
1	My Sample 1_01	My Sample 1	A1	lgG	
2	My Sample 2_02	My Sample 2	A2	IgG	
3	My Sample 3_03	My Sample 3	A3	IgG	
4	My Sample 4_04	My Sample 4	A4	IgG	

Importing and Exporting Injections

Injections in an open batch or run file can be exported as a separate file. This lets you import the same or a modified set of injections into another batch later, rather than having to enter the information manually.

Exporting Injections

- 1. Open the batch or run you want to export injections from.
- 2. In the Batch screen, select File in the main menu and click Export Injections. The following window displays:

or Injections File				×
$\leftarrow \rightarrow \checkmark \uparrow$	Compass for iCE > Batches	~ C	Q Search Batches	
Organize 🔻 Ne	w folder		≣	• 3
> 📒 Desktop	Name	Date modified	Туре	Size
> 📑 Documents	MauriceFlex Fractionation 20221223_Inje	1/2/2023 2:55 PM	Microsoft Excel C	1 KB
> 🛓 Downloads				
> 🕖 Music	1			
> 🔀 Pictures	1			
> 🚺 Videos				
🗸 📮 This PC				
File <u>n</u> ame:	MauriceFlex clEF_Injections.csv			~
Save as <u>t</u> ype:	Text File, comma delimited (*.csv)			~
∧ Hide Folders			Save	Cancel

- 3. The default directory is Compass for iCE/Batches. Change the directory if needed.
- 4. The default file name will be batchname.batch_Injections.csv. Change the name if needed and click Save.

Creating an Injections File

To create a new injections file .csv, it's easiest to export injections from an existing batch and use that as your template.

- 1. Follow the instructions in "Exporting Injections" above to export injections from an existing cIEF batch.
- 2. Open the .csv file in a program that provides a table/spreadsheet format.
- 3. To add or change injection information:
 - a. Type in a unique name in each cell in the Injection Name column. For replicate injections, type > in front of the injection name, for example: >Injection 1.
 - b. Type in a sample ID, location and method for each injection in their respective columns.
 - c. Optional: Type in notes if needed.

NOTES:

Mix bottles are not used for MauriceFlex cIEF batches. Compass for iCE ignores this column when importing injections into a MauriceFlex cIEF batch.

Programmed pauses and stops can't be added in the injections file. They can be added in the Injections pane after importing your injections into Compass for iCE.

1 Injection Name Sample ID Location Method Mix Bottle 2 Inj01 R01_SSPP A1 Method_M458 3 Inj02 S01_Her2_A1_None_0 M Urea A2 Method_M458		А	В	С	D	E	F
·	1	Injection Name	Sample ID	Location	Method	Mix Bottle	Notes
3 Inj02 S01_Her2_A1_None_0 M Urea A2 Method_M458	2	Inj01	R01_SSPP	A1	Method_M458		
	3	Inj02	S01_Her2_A1_None_0 M Urea	A2	Method_M458		
4 >Inj02 S01_Her2_A1_None_0 M Urea A2 Method_M458	4	>Inj02	S01_Her2_A1_None_0 M Urea	A2	Method_M458		

4. Save the .csv file.

Importing Injections

- 1. Open the batch you want to import injections into, or open a new batch.
- 2. Select File in the main menu and click Import Injections.
- 3. Select an injections file (*.csv) and click OK. The imported information will display in the Layout and Injections panes.

NOTE: Imported injections will replace any injections already in the Injections table, they will not append an existing table.

Importing and Exporting Methods

Methods in an open batch or run file can be exported as a separate file. This lets you import the same method into another batch later, rather than having to re-enter method information manually.

Importing a Method

NOTE: Importing a method imports information into the Batch window's Method pane only.

- 1. Open the batch you want to import the method into.
- 2. Select File in the main menu and click Import Method.
- 3. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

Exporting a Method

NOTE: Exporting a method exports information in the Batch window's Method pane only.

- 1. Open the batch you want to export the method from.
- 2. In the Method pane, select the method you want to export. To export more than one method at the same time, hold the Ctrl key to select multiple methods.
- 3. Select File in the main menu and click Export Method. The following window displays:

log Method File			×
🕥 🗸 🖉 « My	Documents + Compass for iCE + Batches	✓ 4 Search Batches	٩
Organize 🔻 New	v folder	· == •	(?)
Favorites Downloads Desktop CneDrive	Name Name No items n	Date modified Type natch your search.	Size
 □ Libraries □ Documents □ Music □ Pictures □ Videos 			
🖳 Computer	 ✓ 		Þ
	Standard Method.method Method File (*.method)		•
Hide Folders		Save Canc	eli

- 4. The default directory is Compass for iCE/Batches. Change the directory if needed.
- 5. Enter a method file name and click Save. The settings will be saved as a *.method file.

Batch Reports

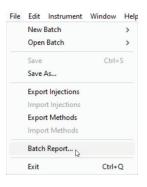
You can export a PDF file of sample and method details for each injection in the batch.

NOTES:

You can have Compass for iCE generate reports for you automatically at the end of each run. See "Setting up Automatic Injection Reports" for more information.

Any time a new report is run, it's saved in a separate run folder. Existing reports aren't overwritten.

- 1. Go to the **Analysis** or **Run Summary** screen, then click **File** > **Open Run** and select a run file (if you don't have one open already).
- 2. After the run opens, go to the **Batch** screen.
- 3. Select File from the main menu and click **Batch Report**.



4. The report name defaults to the run file name. If you want to change it, type in the Report Name box to make updates.

😨 Batch Report		×
Run: 2023-01-13_14-49-17_MauriceFlex clEF_user manual		
Secure PDF		
Report Name:	Browse	
2023-01-13_14-49-17_MauriceFlex clEF_user manual		
$\label{eq:location: C:UsersAndrea} Location: C: Users Andrea Documents Compass for iCE Runs$		
ОК	Cancel	

Report PDFs generated by Compass for iCE are secured by default, which means they can be viewed and printed but not modified or renamed. Uncheck **Secure PDF** if you don't want to generate a secure report. To learn more about permissions for secured vs. unsecured reports, see page 800.

5. The Batch Report PDF is exported to the Runs folder in the Compass for iCE directory. It'll be in a folder with the report name used in the prior step. When the reports are done, the folder opens for you automatically.

🚡 Favorites	^	Name	Date modified	Туре	Size	
📝 Links		2016-01-21_09-46-39_mAb11_Prep20160121_QC_Batch.pdf	1/24/2016 1:04 PM	Adobe Acrobat D		26
My Documents		2010-01-21_09-40-35_IIIA011_PTep20100121_QC_Batch.pdf	1/24/2010 1:04 PW	Adobe Acrobat D		20
🎉 Add-in Express						
퉬 Adobe						
Clients						
퉬 Compass for iCE						
Batches						
🐌 New Batches						
🐌 Runs						
2015-12-06_15-13-01_Maurice cIEF_Mab11_Techl	R					
2016-01-21_09-46-39_mAb11_Prep20160121_QC_	F					
78664 P3 IS 2015-11-30_16-49-49_MW Ladder Sol	-					

Here's an example Batch Report:

cIEF Batch: MauriceFlex cIEF

[Injection	Injection Name	Sample ID	Location	Method	Notes
	1	sys suit_01	sys suit	A3	system suit_1	
[2	sys suit_02	sys suit	A3	system suit_2	

Methods

Name	Separation	Detection	Sample Load (s)	pl Markers	Ampholytes	Additives
system suit_1	10.0 min, 500 Volts	Fluorescence, 0.2 sec	20	3.38 pl, 350 pixels		
	10.0 min, 1000 Volts			10.17 pl, 1900 pixels		
	10.0 min, 1500 Volts					
	Detection					
	Exposure: 0.2 sec					
	Interval: 5.0 min					
system suit_2	10.0 min, 500 Volts	Fluorescence, 0.2 sec	20	3.38 pl, 350 pixels		
	10.0 min, 1000 Volts			10.17 pl, 1900 pixels		
	10.0 min, 2000 Volts					
	Detection					
	Exposure: 0.2 sec					
	Interval: 5.0 min					

Batch Log

Date	User Name	Message	Comment
2023-01-13 14:07:35		Batch created using the factory default MauriceFlex cIEF with Compass for iCE Version: 4.0.0-0110	
2023-01-13 14:09:23		Saved as C:\Users\xiaojing.shen\Documents\Compass for iCE\Batches\MauriceFlex cIEF.batch from Compass for iCE v4.0.0-0110	

Created By: Andrea Thu 3:56 PM Feb 23, 2023 PST (SECURED) C:UsersiAndrea/Documents/Compass for ICE/Runs/2023-01-13_14-49-17_Maurice/Fiex cIEF_user manual.mbz Computer: DESKTOP-1FM7G05 Software Version: Compass for ICE 4.0.0, Build ID:0222

Page 1 of 2



cIEF Batch: MauriceFlex cIEF

Date	User Name	Message	Comment
2023-01-13 14:09:23		Save injections and methods changes to C:\Users\viaojing.shen\Documents\Compass for iCE\Batches\MauriceFlex clFE batch from Compass for iCF v4 0 -0-0110	
2023-01-13 14:49:17		Save injections changes to C:\Users\xiaojing.shen\Documents\Compass for iCE\Batches\MauriceFlex clEF.batch from Compass for iCE v4.0.0-0110	
2023-01-13 14:56:45 2023-01-13 14:57:55		Runtime injections changes Runtime methods changes	

Center for Anten Te 3.55 PUT PC 31, 2023 2021 (dCUVID2) CUMARADERIZODOWINGCOMPARTICIPATION (dCUVID2) CUMARA (dCUVID2) (dCUVID2) Compart: DESITOR-MATODS COMPARE: DESITOR-MATODS Page 3 of 2 Page 3 of 2

Chapter 8: Running MauriceFlex cIEF Applications

Chapter Overview

- Overview
- Before You Throw the Switch
- Power Up
- Running MauriceFlex cIEF Applications
- Editing a Running Batch
- Post-batch Procedures
- Checking Your Data

Overview

MauriceFlex cIEF applications can be run on MauriceFlex system using a cIEF Fractionation cartridge.

NOTES:

We recommend first optimizing methods with cIEF batches using a cIEF cartridge on Maurice, Maurice C. or MauriceFlex. Then, use recommendations in the MauriceFlex cIEF Fractionation Method Development Guide for tips to modify the method for a MauriceFlex cIEF batch using a cIEF Fractionation cartridge on MauriceFlex to confirm successful method transfer before performing a MauriceFlex Fractionation batch.

cIEF Fractionation cartridges support 15 injections.

On-board mixing is not available on MauriceFlex.

Before You Throw the Switch

Ensure that everyone using MauriceFlex have:

- · Received instruction in general safety practices for laboratories.
- Received instruction in specific safety practices for MauriceFlex.
- Received instruction on handling of biohazards (if biohazardous materials are to be used on MauriceFlex).
- Read and understood all Product Inserts and related Safety Data Sheets (SDS).

Power Up

- 1. Turn on the computer connected to MauriceFlex.
- 2. Turn on MauriceFlex's main power switch.
- 3. Wait for MauriceFlex to initialize. His indicator light will turn from magenta to blue when he's done.
- 4. Double-click the Compass for iCE software icon on the computer desktop to open the application.
- 5. Connect MauriceFlex to Compass for iCE.

Running MauriceFlex cIEF Applications

What You'll Need

- MauriceFlex cIEF Fractionation Cartridges
- MauriceFlex cIEF Fractionation Method Development Kit (optional)

- Maurice cIEF Fluorescence Calibration Standard
- Maurice cIEF pI Markers (3.38, 4.05, 5.85, 6.14, 7.05, 8.4, 9.50, 9.99, or 10.17)
- 0.5% Methyl Cellulose Solution
- 1% Methyl Cellulose Solution
- iCE Electrolyte Kit
- Deionized (DI) water
- MauriceFlex glass crimp top reagent vials, 2 mL



MauriceFlex glass crimp top reagent vial (PN 110-0019, left) and glass reagent vial (PN 046-017, right) Only MauriceFlex glass crimp top reagent vials (PN 110-0019) should be used to prepare MauriceFlex cIEF batch reagents.

- MauriceFlex glass vials with insert, 0.3 mL for the Fluorescence Calibration Standard
- 96-well plate for samples
- P10, P20, P200, P1000 pipettes and tips
- Electrolyte pipette
- Vortexer
- Table-top centrifuge with plate adapter or vial adapter (12 mm, 2 mL vials)

IMPORTANT:

Use MauriceFlex glass crimp top reagent vials, 2 mL (PN 110-0019) and glass vials with insert, 0.3 mL (PN 110-0018) to prepare MauriceFlex cIEF batch reagents.

Step 1: Prep Your Markers, Samples and Reagents

NOTES:

You can prepare your samples in a 96-well plate or vial.

Samples

- 1. In a microcentrifuge tube, prepare your sample at a concentration of 2.5 10 mg/mL in a final volume of 25μ L in DI water.
- 2. In a separate tube, prepare IEF Separation Mix containing your chosen pI marker(s).

NOTES:

Check out the MauriceFlex cIEF Fractionation Method Development Guide for suggested IEF Separation Mix recipes.

If you are running a method optimized for cIEF analysis, increase the concentration of arginine and both pI markers in your IEF Separation Mix. Check out the MauriceFlex cIEF Fractionation Method Development Guide for more information.

- 3. Add 100 μ L of IEF Separation Mix to the 25 μ L of your sample.
- 4. Thoroughly vortex the sample to mix completely.
- 5. Centrifuge the tube at 13,000 xg for 5 minutes to remove air bubbles and sediment any particulates.
- 6. Carefully aspirate the top 100 μL of the sample and pipette it into a well in a 96-well plate by inserting the pipette tip all the way to the bottom to avoid introducing bubbles.
- 7. Spin the plate for 5 minutes at 1000 xg using a centrifuge plate adapter.

NOTES:

If you're preparing sample in a sample vial with insert, 0.2 mL (PN 046-083), increase the sample and IEF Separation Mix volumes in steps 1–3 by 3-fold and transfer a minimum of 300 µL of sample to the vial.

Make sure to check for and remove any bubbles at the bottom of the well.

pl Markers

- 1. Open the vial of lyophilized pI marker by lifting the center tab and gently pulling it back to break the metal seal. Slowly remove the rubber stopper.
- 2. Add 210 µL of DI water to the vial.
- 3. Put the rubber stopper back in the vial and vortex 3 times, 5 seconds each time to completely reconstitute the lyophilized cake. Repeat this step for all pI markers you're using.

4. Aliquot 20 µL of each reconstituted pI marker into separate tubes for storage.

NOTES:

Keep your reconstituted pI markers on ice until you're ready to add them to your sample or IEF Separation Mix.

If you'll use the pI markers within a month, store the aliquots at 2-8 °C. Otherwise, store the aliquots at -10 °C to -30 °C. They'll be stable up to 6 months.

5. Use 4 μ L of each pI marker for every 200 μ L of sample.

Reagents

IMPORTANT:

Use MauriceFlex crimp top glass reagent vials, 2 mL (PN 110-0019) and glass vials with insert, 0.3 mL (PN 110-0018) to prepare MauriceFlex cIEF batch reagents. Glass reagent vials, 2 mL (PN 046-017) should only be used when running a standard cIEF or CE-SDS batch.

NOTE: Don't reuse reagents or vials

1. Pipette 350 µL of Fluorescence Calibration Standard in a MauriceFlex glass vial with insert, 0.3 mL (PN 110-0018) and label.



2. Pipette 2 mL of 0.5% Methyl Cellulose into a MauriceFlex crimp top glass reagent vial and label.



- 3. Prepare four vials of water by pipetting 2 mL of DI water into a MauriceFlex crimp top glass reagent vial (PN 110-0019). Label the vials.
- 4. Pipette 2 mL of Catholyte solution to a MauriceFlex crimp top glass reagent vial and label.
- 5. Label an empty MauriceFlex crimp top glass reagent vial.

NOTES:

Make sure you don't overfill the vials, especially the methyl cellulose vial, to avoid introducing bubbles to your run. Wipe excess liquid at the mouth of the vial with a laboratory wipe.

Vials do not need to be capped.

Step 2: Load Samples and Reagents

1. Open MauriceFlex's door by touching the metal plate on top of the door.



NOTE: The indicator light on MauriceFlex's front panel will blink rapidly as the door disengages.

2. Swing the door open to access the cartridge slot and the reagents and samples platform. The lights on either side of the slot will be orange.

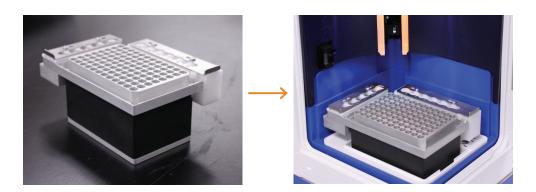


3. Install the fractionation adapter in MauriceFlex.

NOTES:

Remove all the vials in rows P and N of the reagent platform before installing the fractionation adapter if a CE-SDS or standard cIEF application was previously performed.

When installing the fractionation adapter, confirm the adapter is seated and sitting flat in MauriceFlex.



4. Place the reagent vials into their respective positions on the fractionation adapter.

IMPORTANT:

Reagent vials on MauriceFlex must be locked in place before starting a batch. The vial locking mechanism default state is locked. Pull the locking mechanism on Row R to the right and the locking mechanism on Column K down to unlock and place vials in the fractionation adapter. Release the locking mechanism to lock the vials in place.

If the fractionation adapter locking mechanism does not spring back upon release, check that all the vials are seated.

NOTES:

The reagent row (R) on the fractionation adapter is kept at room temperature. The reagent column (K) and sample plate are temperature controlled.

MauriceFlex cIEF batch reagents should be prepared in 2 mL crimp top glass vials (PN 110-0019) and glass vials with insert, 0.3 mL (110-0018).

Vials do not need to be capped before placing them on the fractionation adapter.

- R1 0.5% Methyl Cellulose
- R2 Fluorescence Calibration Standard
- **R3** Water
- **R4** Water

- **R5** Water
- **R6** Empty vial (air)
- K2 Catholyte Solution
- K5 Water



5. Place your 96-well sample plate on the Fractionation Adapter. Well A1 should be in the top left corner of the adapter.



Step 3: Prep the cIEF Fractionation Cartridge

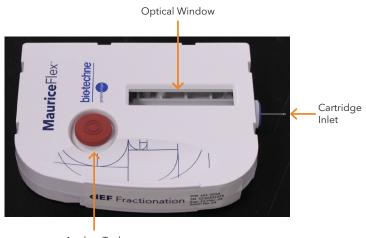
NOTE: A cIEF Fractionation Cartridge supports a maximum of 15 injections and a maximum of 15 batches. Its RFID will keep track of how many are left for you.

1. Take the cIEF Fractionation Cartridge out of its packaging. Save the packaging, you'll need it later to store the cartridge.

NOTE: When you remove the cartridge from its packaging, make sure the cartridge inlet doesn't come in contact with any surface.



- 2. Put the cartridge on a flat surface with the electrolyte tank facing up.
- 3. Remove the stopper from the anolyte tank.



Anolyte Tank

4. Add 2 mL Anolyte Solution to the H⁺ electrolyte tank (red port).

NOTE: Make sure you don't overfill the electrolyte tanks.

5. Seal the Anolyte tank with the rubber stopper. If excess liquid comes out of the tank, make sure to wipe it with a laboratory wipe.



Step 4: Install the Cartridge

- 1. Double check to make sure you've got anolyte loaded and the tank is properly sealed with the stopper.
- 2. Lift the cartridge and hold it vertically using the finger holds on either side, cartridge inlet down, with the cIEF Fractionation label facing you.
- 3. Gently insert it into the slot. You'll feel the alignment groove on the cartridge align inside the slot when you insert it.



4. Continue to slide the cartridge into the slot until the locking mechanism engages. The lights on either side of the slot will change to **blue** once the cartridge is installed correctly.



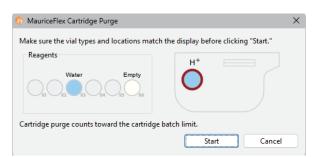
5. Close the instrument door. MauriceFlex locks it automatically.

Step 5: Check for Cartridge Alerts

- 1. If your cartridge was last used in a run with an error, you will need to perform a Cartridge Purge. MauriceFlex will remind you if a Cartridge Purge is required.
 - a. To purge the cartridge, click the brown **Purge** button in the instrument status bar.



b. Confirm that the required batch reagents are loaded and that the cartridge is prepped. Then click Start.



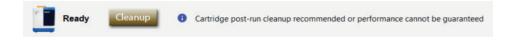
c. Once the purge is done, perform a Cartridge Post-Run Cleanup by clicking on the brown **Cleanup** button that will appear in the instrument status bar. See step 2 for more information.

NOTE: If there's only one batch left on the cartridge, you'll get a message that it can't be used after purging.

2. If you just completed a Cartridge Purge or if the cartridge you're using did not undergo a cartridge post-run cleanup after the last run, you will be asked if you want to perform a Cartridge Post-Run Cleanup.

To start the Post-Run Cleanup:

- a. Remove the cartridge from MauriceFlex and remove the anolyte. See "Post-batch Procedures" on page 182 for more information.
- b. Confirm there is a vial of Water (P3) and Air (P6) in place
- c. Click the brown Cleanup button in the instrument status bar.



d. Click **Start Cleanup** in the prompt that appears.

Make sure the electrolyte tank is clean display before clicking on "Start."	and dry, and the	e vial types a	nd locations r	match the
Reagents	(^{⊪•}		
Cartridge post-run cleanup recommer	ded or perform	ance cannot	be guarantee	ed

NOTE: You can also start a Post-Run Cleanup by selecting **Instrument > Cartridge Post-Run Cleanup**. When you start a Cartridge Post-Run Cleanup from the instrument menu, click **Start** in the prompt that appears to begin the cleanup.

- e. Once the cartridge post-run cleanup is completed, re-prepare the cartridge and install the cartridge in MauriceFlex. See "Step 3: Prep the cIEF Fractionation Cartridge" on page 163 for more information.
- f. Click on the green Start button in the instrument status menu to start the batch.

To start the run without a Post-Run Cleanup:

a. Click the brown Cleanup button in the instrument status bar



b. Click Skip Cleanup in the prompt that appears.



c. Click **Start** in the Start Run window. The run summary and injection report will record that the cartridge did not undergo a post-run cleanup before starting the batch.

😚 Start Run				\times
Batch: MauriceFlex clEF				
Results file name :			Brov	vse
2023-03-13_16-58-19_Ma	auriceFlex cIEF			
Location: C:\Users\Andre	a\Documents\Compass for i	CE\Runs		
Comment:				
Cartridge				
_	Type: MauriceFlex	Injections per Batch: 4		
	pires : Jan 2025	Injections Remaining : 9		
	nber: 9900000100	Batches Remaining: 4		
 Cartrie 	dge post-run cleanup recom	mended or performance cannot be g	uaranteed	
			Start Cancel	

To start the run with a different cartridge:

- a. If necessary, click Cancel in the cIEF Fractionation Cartridge Post-Run Cleanup window.
- b. Open MauriceFlex's door, remove the first cartridge from MauriceFlex and prepare a second cartridge. See "Step 3: Prep the cIEF Fractionation Cartridge" on page 163 for more information.

Step 6: Create a Batch

1. Launch Compass for iCE.

2. Select the Batch tab. This is where you'll enter sample/injection information, methods and batch parameters.

File Eult Inst	rument Window Help						: En (De	Run Summary 🚛 Analy
Batch: MauriceFl	ex cIEE	Injections 🛄 H	story 🌃 Notes				Batch C.	Kun Summary 🚛 Analy
aten. waaneen		injections and in				(DPause OStop 🗗 Add 🖩 Re	aplicate 🕅 Remove 🗔
Layout 10°	C → C Add → C Remove	Injection 1 Sample		ample ID ample 01	Locatio A1	n Method IgG	Notes	
(C Fi Cal Water Water Empty							
Sample A Catholyte K1 K2 K2 K2 K3 K4 K4 K4 K4 K4 K4 K4 K4 K4 K4 K4 K4 K4								
Methods								
								New Remo
Name IgG	Separation 10.0 min 500 Volts, 10.0 min 1000 Volts, 2	Detection 5 1 Exposure		pl Markers 7.05, 10.17	Ampholyt A	dditives		

- 3. To create a batch, make sure MauriceFlex is connected to Compass for iCE. Select Instrument and click Connect.
 - a. If your instrument is listed, select your MauriceFlex system and click Connect.
 - b. If your instrument isn't listed, click on the Settings button and connect by typing in your instrument IP address.

lame	Location	Serial Num

To create a new batch:

• In the main menu, select File > New Batch > MauriceFlex cIEF

File	Edit Instrument	Window Help	
	New Batch	>	Maurice cIEF
	Open Batch	>	Maurice CE-SDS PLUS
	Save	Ctrl+S	Maurice Turbo CE-SDS™
	Save As	Carro	MauriceFlex cIEF
	Save As		MauriceFlex Fractionation

To use an existing batch: In the main menu, select File > Open Batch.

NOTE: If you're making changes to an existing batch, follow the steps in this section. Otherwise skip to "Step 7: Start the Batch" on page 178.

ile Edit Instrument	Window Help	p
New Batch	>	
Open Batch	> (Maurice FLEX cIEF batch 20221214
Save Save As	Ctrl+S	Maurice_CE-SDS_TURBO_Reduced 43 DemoData_Maurice cIEF Maurice CE-SDS PLUS
Export Injections		Maurice FLEX cIEF batch
Import Injections Export Methods	-	Browse Ctrl+C

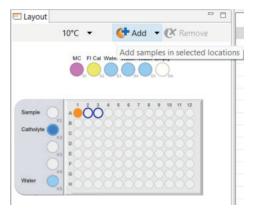
4. Add your samples:

To import samples using a saved injections file:

- a. Select File in the main menu and click Import Injections.
- b. Select an injections .csv file and click OK. The imported information will display in the Injections pane.

NOTE: For more information on setting up an injections file for import, see "Importing and Exporting Injections" on page 150.

To select samples manually: Use your mouse to highlight the well positions for each of your samples, then click Add.



This populates the Injections table:

Inject	ions 🔚 History 🎵 Not	tes				
				🕕 Pause 🛛 Stop	o 👫 Add 📗 Replicate 🔀 Remov	e 🕀 🖻
	Injection Name	Sample ID	Location	Method	Notes	
1	Sample 01_01	Sample 01	A1	lgG		
2	Sample 02_02	Sample 02	A2	lgG		
3	Sample 03_03	Sample 03	A3	lgG		

5. The fractionation adapter is temperature controlled with a default setting of 10 °C. To change the temperature or turn it off, click the **down arrow** next to the temperature and select an option.

NOTE: The reagent row (R) is kept at room temperature. The reagent column (K) and sample plate are temperature controlled.



6. Enter your method parameters in the Methods pane.

NOTE: We recommend using the default method parameters. Please see the MauriceFlex cIEF Fractionation Method Development Guide for more information on method optimization.

To import a saved method:

- a. Select File in the main menu and click Import Method.
- b. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

To create a new method or make changes to an existing one:

a. Click the first cell in the Name column and enter a method name.

Methods							
							New F
Name	Separation	Detection	Sample Load	pl Markers	Ampholyt	Additives	
lgG	10.0 min 500 Volts, 10.0 min 1000 Volts, 25	1 Exposure	20	7.05, 10.17			

b. Click the first cell in the Separation column, then click the selection button [...] to set the pre-focusing and focusing time (in minutes) and voltage (V). You can also set the Detection Interval (in minutes) and Exposure (in seconds) to adjust how often an image is taken using the listed Exposure time.

Method	s		💮 Separation	Profile	×
			Ado	e e e e e e e e e e e e e e e e e e e	Remove
Name	Separation		 Time (min)	Voltage (Volts)	
lgG	Voltage 3 Steps		10.0	500	
igo		- Contraction of the second se	10.0	1000	
		- 0	25.0	1500	
			14		
			Detection Int	erval(min) 5.0	
			Exposure(sec	0.1	
			Exposure(sec)	
				ОК	Cancel

c. Click the first cell in the Detection column the selection button [...] to set your fluoresences detection time for the final focused image.

Name Separation Detection IgG 10.0 min 500 Volts, 10.0 min 100 1 Exposures	Remove
Exposure	
LaG 10.0 min 500 Volts 10.0 min 100 1 Exposures	Tura
	sec) Type Fluorescen
6.2	Fluorescen

d. Click the first cell in the Sample Load(s) column and set the load time in seconds.

News	Concention	Detection	Completed
Name	Separation	Detection	Sample Load
lgG	10.0 min 500 Volts, 10.0 min 1000 Volts, 25	1 Exposure	20

Chapter 8: Running MauriceFlex clEF Applications | Running MauriceFlex clEF Applications

e. Click the first cell in the pI Markers column to select pI markers. Add new markers or remove existing ones then click OK.

pi minecia pl 7.05	pl Position	Name	Separation	Detection	Sample Load			Add	Remove
7.05	7.05 300	lgG	10.0 min 500 Volts, 10.0 min 10	1 Exposure	20	7.05, 10.17	\rightarrow	pl Markers:	
								pl	Position
10.17	10.17 1,900							7.05	300
								10.17	1,900

f. Optional: Click the first cell in the Ampholytes column and enter the ampholytes you're using.

Methods								- 0
							New	Remove
Name	Separation	Detection	Sample Load (s)	pl Markers	Ampholytes	Additives		
lgG	10.0 min 500 Volts, 10.0 min 1000 Vol	1 Exposure	20	7.05, 10.17	Pharmalyte 3-10	Urea		

g. Optional: Click the first cell in the Additives column and enter any additives you're using.

Methods							- 8
						New	Remove
Name	Separation	Detection	Sample Load (s)	pl Markers	Ampholytes	Additives	
lgG	10.0 min 500 Volts, 10.0 min 1000 Volts, 25.0	1 Exposure	20	7.05, 10.17	Pharmalyte	Urea	

- 7. You can now:
 - Make updates to the remaining methods by repeating the prior steps.
 - Select a method and click **Remove** in the upper right corner of the Methods pane to delete it.
 - Click **New** in the upper right corner of the Methods pane to add a new one if you want to use different methods for different samples. Then just repeat the steps above for the new method.
- 8. In the Injections pane:
 - To add or change sample names: Click the Sample ID cell for the injection and type a name.

NOTES:

Sample IDs can be copied from other documents and pasted into Compass for iCE to make batch setup faster. Check out "Copying and Pasting Injection Names or Sample IDs from other Documents" on page 149 for more info.

If you change the sample ID when the default injection name is still being used, the injection name will automatically update to match the sample ID. If you've already changed the injection name manually, updating the sample ID will not update the injection name.

Injecti	ons 🔚 History 👖 Notes					
		🕕 Pause 🛛 S	op 🚏 Add 📊 Repl	icate 🔀 Remove	Ŧ	E
	Injection Name	Sample ID	Location	Method		
1	Sample 01_01	Sample 01	A1	IgG		
2	Sample 02_02	Molecule X	A2	lgG		
3	Sample 03_03	Sample 03	A3	IgG		

• To change injection names: Click the Injection Name cell for the injection and type a name.

NOTES:

Each injection name must be unique.

Changing the injection name won't affect the sample ID.

		🕕 Pause 🔘	Stop 📑 Add 📊 Repli	cate 🔀 Remove	Ŧ
	Injection Name	Sample ID	Location	Method	
1	Sample 01_01	Sample 01	A1	IgG	
2	lgG	Sample 02	A2	IgG	
3	Sample 03_03	Sample 03	A3	IgG	

• To assign methods for each injection: Click the Method cell for the injection and select a method from the drop down menu.

	ons 🔚 History 👖 Notes			Stop 👫 Add 📊 Replicate		
	Injection Name	Sample ID	Location	Method	Notes	
1	Sample 01_01	Sample 01	A1	lgG		
2	Molecule X_02	Molecule X	A2	IgG		
3	Sample 03_03	Sample 03	A3	IgG]	
				Method2		

• To add sequential replicate injections: Highlight an injection and click **Replicate**. A new injection will be added under the row you selected

	Injection Name	Sample ID	Location	Method	Replicate selected i	njections
1	Sample 01_01	Sample 01	A1	IgG	-	-
2	Molecule X_02	Molecule X	A2	Method2		
3	Sample 03 03	Sample 03	A3	IgG		
Injectio	ns 🔚 History 🚺 Notes		🕕 Pause 🖸	Stop 👫 Add 📕 Re	plicate 🔀 Remove	• 🕀 🖻 🗖
Injectio	ns 🔚 History 🌃 Notes	Sample ID	Pause	Stop 🕂 Add 📕 Re Method	plicate 🔀 Remove Notes	• • • •
Injectio		Sample ID Sample 01				• • •
1	Injection Name	·	Location	Method		• 🛨 🖻 🗖
Injectio	Injection Name Sample 01_01	Sample 01	Location A1	Method IgG		• • •

• To add injections at the end of the batch: Click on any sample position in the Layout pane or sample injection in the Injection table and click Add. A new injection using the same sample will be added to the end of the table. Assign the method if needed.

ingection	ns 📗 History 🚺 Notes		U Pause U	Stop 👫 Add 📊 Replicate	Kemove	• E	
1	Injection Name Sample 01 01	Sample ID Sample 01	Location A1	Methe Add injections	Notes		
2	Molecule X_02	Molecule X	A2	Method2			
3	Sample 03_03	Sample 03	A3	lgG			

- To copy and paste injections: Right-click on an injection in the Injection table and select Copy. Click on the injection number above where you want to insert the copied injection, right click and select Paste. The copied injection will be inserted under the row you selected.
- 9. Add programmed pauses or stops in the batch to automatically pause or stop after injections (optional).
 - **To program a pause:** Highlight the injection you want to pause at and click **Pause**. The batch will pause after that injection is complete. To resume the batch, click **Continue** in the instrument status bar.

Inject	ions 🔚 History 🎩 Not	tes							E
			0	Pause 🖸 Stop				e 🕀	1
	Injection Name	Sample ID	Location	Me Pause aft	er the sele	ected injection	n l		
1	Sample 01_01	Sample 01	A1	lgG		,			
2	Sample 02_02	Sample 02	A2	IgG					
3	Sample 03_03	Sample 03	A3	IgG					
Inject	ions 🔚 History 頂 Not	tes							
Inject	ions 🔚 History 🏋 Not	tes	0	Pause 🖸 Stop) 🕂 Add	Replicate	K Remove		
Inject	ions 🔚 History 🎵 Not	sample ID	0 Location	Pause O Stop Method	🕴 🕂 Add	Replicate Notes	Remove		_
Inject					🛛 🏕 Add		Remove		_
	Injection Name	Sample ID	Location	Method) 🕂 Add		Remove		_
1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method IgG) 🕂 Add		Kemove		
1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method IgG IgG			K Remove		

NOTE: A cleanup step will occur after each injection on the MauriceFlex cartridge. A programmed pause will occur after the injection completes but before the cleanup step begins.

• To stop the run after a specific injection: Highlight the injection you want the batch to stop at and click Stop. MauriceFlex will continue the batch through the selected injection, then stop the batch and perform end-run cleanup steps.

Inject	tions 📗 History 🎩 Not	tes							E
			0	Pause O Sto	op 👫 Add	Replicate	🔀 Remove	• =	Į
	Injection Name	Sample ID	Location	Method		r the selected	injection I		
1	Sample 01_01	Sample 01	A1	IgG	Stop unto	a the selected	injection		
2	Sample 02_02	Sample 02	A2	IgG					
3	Sample 03_03	Sample 03	A3	lgG					
Inject	ions 🔚 History ፲ Not	tes						-	
Inject	ions 🔚 History 🏋 Not	tes	0	Pause 🟮 Sto	op 🕂 Add	Replicate	Remove		
Inject	ions 🔚 History 🌃 Not	sample ID	0 Location	Pause O Sto Method	op 🎁 Add	Replicate Notes	Remove		
Inject					op 🎁 Add		Kemove		
Inject 1 2	Injection Name	Sample ID	Location	Method	p 🎁 Add		Remove		
1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method IgG	op 達 Add		Remove		
1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method IgG IgG	op 🎼 Add		K Remove		

10. Click on the **Notes** pane, then click in the notes area and type any information you want to add about your batch (optional).

Injections 🔚 History 📑 *Notes		- 0
Product testing		

11. You can preset the parameters used to analyze data generated with the batch (optional). We recommend using the default parameters for MauriceFlex cIEF applications, but if you want to modify parameters:

Detection	Detection					
Peak Names Peak Fit Advanced					 	
pl Markers	IgG	Exposure 1	0.2 seconds	~		

a. Select Edit from the main menu and click Default Analysis. The following screen will display:

- b. Change the parameters you want to, then click **OK**. For detailed information on analysis parameters, please refer to "Analysis Settings Overview" on page 528.
- 12. You can preset the parameters used to view data when the batch is complete (optional). Default Analysis View Parameters must be set before you start the batch and cannot be modified once the batch starts. However, you can still manually change parameters in the Analysis pane using the Graph Options button:
 - a. Select Edit from the main menu and click Default Analysis View. The following screen will display:

😚 Default Analysis View MauriceFlex clEF – 🗆 🗙						
Graph View Options	Graph View Options					
	 Matching Peak Names Peak Names Peak Values Fitted Peaks Baseline Fit Grid Lines Plot Label Sample Method Injection Exposure Injection Name 					
	OK Cancel	Apply				

- b. Change the parameters you want to, then click OK. For detailed information on graph view options, please refer to "Customizing the Data Display" on page 509.
- 13. Once all of your sample, method and injection info is entered, select File > Save. Enter any comments on the batch if you want, then click Save.

😨 Save Batch Comment 🛛 💈					
Batch: MauriceFle	ex cIEF				
Comment:					
	Save	Cancel			

14. Enter a name for your batch then click Save.

Step 7: Start the Batch

- 1. Make sure MauriceFlex is connected to Compass for iCE. If he isn't, select **Instrument** and click **Connect**. Then select your MauriceFlex system and click **Connect**.
- 2. Click on the green Start button to start your batch.

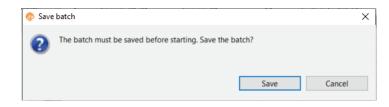
NOTES:

An alert may appear if the wronge cartridge is installed or if a cartridge post-run cleanup or cartridge purge is recommended. See "Step 5: Check for Cartridge Alerts" for more information.

An alert may appear if you are starting a MauriceFlex cIEF batch and have not installed the fractionation adapter. See "Adapter and Insert Alerts" on page 403 for more information.



3. If you have made any changes, you will be asked to save your batch before starting the run. Click Save.



- 4. The Start Run box shows you the number of injections and batches remaining on your cartridge. Make sure you still have enough injections left before you start the run. If not, prep a new cartridge.
- 5. Click in the **Results File name** box if you want to change the default run file name. Otherwise just leave it as is.

😚 Start Run						×
Batch: 2023-	03-03_MauriceFle	x cIEF MDG				
Results file nar	ne:					Browse
2023-03-03_2	0-22-13_2023-03-03	_MauriceFlex clEF M	IDG			
Location: C:\	Users\Andrea\Doc	uments\Compass fo	r iCE\Runs			
Comment:						
	Cartridge					
	Type :	MauriceFlex	Injections per Batch :	4		
and the second	Expires :	Jan 2025	Injections Remaining :	11		
	Serial Number :	9900000100	Batches Remaining :	8		
				Sta	rt	Cancel

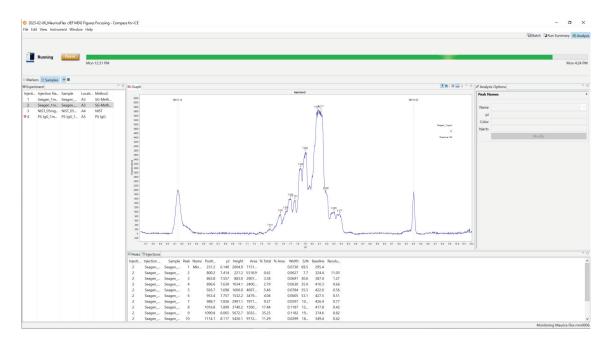
- 6. If you don't want to save the file to the default Runs folder, click Browse to select a different location.
- 7. Enter any run details you'd like in the Comments box (optional).
- 8. Click Start to start the run.

NOTE: The indicator light on MauriceFlex's front panel will pulse slowly while he's running the batch.

To monitor the progress of your batch, click the Run Summary tab. See Chapter 16: "Run Status" for more details.

				jures Focusini	g - Compass fo	IT ICE		- σ
File E	dit Instrumer	nt Window	Help					🗟 Batch 🛄 Run Summery, 40
	Running	Pau						
				Mon 12:31 P	141			Mon 4:
Run: 2	2023-02-06_M	lauriceFlex cll	EF MDG	Figures Focus	ing			
å Injec	tions							□ [I] Status]
	Injection	Sample ID	Locati.			Time	Sample T	run 2023-03-03_20-22-13_2023-03-03_MauriceFlex cIEF MDG
				Setup	Complet.			path
1	Sanaan	Seagen	42		Complet_	2023-02-06 12:48:52	10.0	batch 2023-03-03_MauriceFlex cIEF MDG
	sugar	Stoffil	~	Cleanup	Complet.	LULD OF 00 12/40/32	1900	batch type cIEF Fractionation
2	Seagen	Seagen	A3			2023-02-06 13:43:42	10.2	
				Cleanup	Complet.			instrument MauriceFlex : Maurice Flex xf1109 - xf1109
3	NIST_05	NIST_05	A4	NIST		2023-02-06 14:38:33	10.3	samples 96-well plate
	201-01	DC LLC A	45	Cleanup	Complet. Separating	17	_	started Fri 8:22 PM Mar 3, 2023 PST
4	PS IgG_1	PS Igo_1	AS	PS IgG Cleanup	separating •	40 mins		
				Creanop				
								cartridge MauriceFlex
								serial number 990000100
								injections per batch 4
								injections remaining 11
								batches remaining 8
								expires Jan 2025
								A Foon Striet IN M Plot
								Al hous Series & W Rot
								Zoo Naactore 4
								11300
								1000
								800
								400 200 200
								200
								8 198 286 308 400 598 800 100 800 1006 1,006 1,000 1,000 1,000 1,000 1,000 1,000 1,000 1,000 1,000 1,000 1,000 2,000
								Puer
								<
								Time 00:40:00 / 00:40:00

To view results, analyze results or change analysis parameters on completed injections while the batch is still running, click the **Analysis** tab. See Chapter 18: "cIEF Data Analysis" for more details.



When your batch is complete, you can view electropherograms for all injections in the Analysis tab, and all batch and injection details in the Run Summary tab.

NOTE: If you'd like MauriceFlex to let you know when your run is done, you can set him up to tweet you. Go to "Setting Up Maurice Systems to Send Tweets" on page 764 for more info.

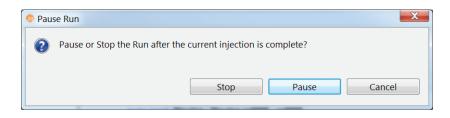
Editing a Running Batch

You can pause a batch after it's started to make updates or add samples and reagents.

1. Select **Instrument** > **Pause** or select the **Pause** button.



2. Click Pause in the pop-up window.



The Pause button will change to Continue but MauriceFlex's status will stay at Running until Compass for iCE completes the current injection.



- You can now make these edits to the batch:
 - Add sample(s)
 - Add injection(s) to the end of the batch
 - · Modify injections that haven't completed and aren't greyed out
 - Create a new method
 - Update the method. Once a method is run it can only be updated. Highlight the method you want to edit and click **Update** in the Methods pane. The software will copy the parameters into a new method that you can modify.
- 3. When MauriceFlex completes the current injection, his status will change to Paused and the progress bar will turn yellow.

NOTE: MauriceFlex's status light will change from a pulsing blue to a blue pulse with magenta flashes which means he's paused the run.

Paused	Continue	-	
		Mon 1:43 PM	

The status in the Injection pane also changes to Paused and the pause duration updates live. You can now open the instrument door to:

• Add new samples

IMPORTANT

The door must be closed within 15 minutes of opening it to avoid potential assay performance issues.

NOTE: If the door is open for more than 30 seconds, a white light near the cartridge will start to flash and a warning message displays in Compass for iCE until the door is closed.

4. To continue the batch, click **Continue**. Changes you made to the batch are saved and MauriceFlex will continue with the next sample injection.

Post-batch Procedures

When the batch is done:

- 1. Open MauriceFlex's door. The lights on either side of the cartridge slot will be **orange** as MauriceFlex will have already disengaged the cartridge.
- 2. Remove your sample. Leave the Water (P3) and Air (P6) vials in place if your cartridge still has injections left since they will be needed for the post-run cleanup step. Remove the remaining reagent vials.

NOTE: You can remove reagent vials from the MauriceFlex fractionation adapter when the locking mechanism is pulled to the right (row R) or pulled down (column K). Release the mechanism to lock remaining vials in place before starting the Post-Run Cleanup.

3. Gently pull out the cartridge making sure the cartridge inlet doesn't come into contact with any surface.



If you're at 15 injections, you've reached the limit of supported injections for the cartridge. To dispose of a finished cartridge, put it in its original packing and discard it per your institution's safety and waste disposal guidelines. Discard any remaining reagent vials.

NOTE: Disposal of cartridges, sample plates and vials depends on the samples you ran. If you aren't sure what your sample origins are, we recommend you dispose of everything in biohazard waste.

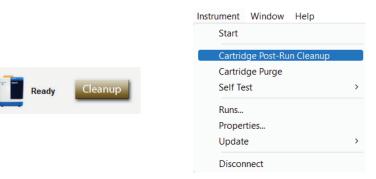
If the cartridge will be used again, clean up and store the cartridge:

- a. Put the cartridge on a flat surface with its electrolyte tank facing up.
- b. Remove the stoppers from the Anolyte tank.
- c. Using an electrolyte pipette or low vacuum, aspirate the solution from the tank.
- d. Fill the tank with 3 mL DI water, then aspirate it out. Repeat this rinse 2 more times.

NOTE: Make sure not to get any liquid on the cartridge's optical window.



- e. Aspirate all the remaining liquid and make sure that the tank is dry.
- f. Put the stopper back on the tank and install the cartridge in MauriceFlex.
- g. Verify there is at least 2 mL of DI water in the Water (P3) vial and air in the empty (P6) vial.
- h. Click on the brown **Cleanup** button in the Instrument Status Bar or select **Instrument** and **Cartridge Post-Run Cleanup** in the Compass main menu.



i. You'll get the following message. Click Start. It'll only take 6 minutes.

😨 Flex Cartridge Post-Run Cleanup	\times
Make sure the electrolyte tank is clean and dry, and the vial types and locations match the display before clicking on "Start."	
Reagents Water Empty R1 R2 R3 R8 R5 R5 R5 R5 R5 R5 R5 R5 R5 R5 R5 R5 R5 R5 R5 R5 R	
Cartridge post-run cleanup recommended or performance cannot be guaranteed Start Cancel	

- j. Open MauriceFlex's door. Gently pull out the cartridge making sure the cartridge inlet doesn't come in contact with any surface.
- k. Remove the reagent vials.
- 1. Leave the stopper off to allow the tank to air dry.
- m. Put the cartridge and stopper back in the protective packaging and store at room temperature.

!WARNING! SHARPS HAZARD

The capillary inlet of the cartridge may present a potential sharps hazard. Dispose of used cartridges according to your organizations health and safety regulations.



!WARNING! BIOHAZARD

Cartridges, sample plates and vials should be handled by procedures recommended in the CDC/NIH manual: Biosafety in Microbiological and Biomedical Laboratories (BMBL). The manual is available from the U.S. Government Printing Office or online at http://www.cdc.gov/biosafety/publications/bmbl5/.

Depending on the samples used, the cartridges, plates and vials may constitute a chemical or a biohazard. Dispose of the cartridges, plates and vials in accordance with good laboratory practices and local, state/ provincial, or national environmental and health regulations. Read and understand the Safety Data Sheets (SDSs) provided by the manufacturers of the chemicals in the waste content before you store, handle, or dispose of chemical waste.

Checking Your Data

Compass for iCE detects your sample protein and pI marker peaks and reports results automatically. But, we always recommend you review your data using the steps in this section as a good general practice to make sure your results are accurate. If you see a data warning in the Experiment pane, these steps will also help you identify and correct any issues.

Chapter 8: Running MauriceFlex cIEF Applications | Checking Your Data

Step 1: Check Your pl Markers

To make sure your pI markers are identified correctly:

- 1. Go to the **Analysis** screen.
- 2. Click Markers in the View bar.



3. Click the View Selected icon in the View bar.

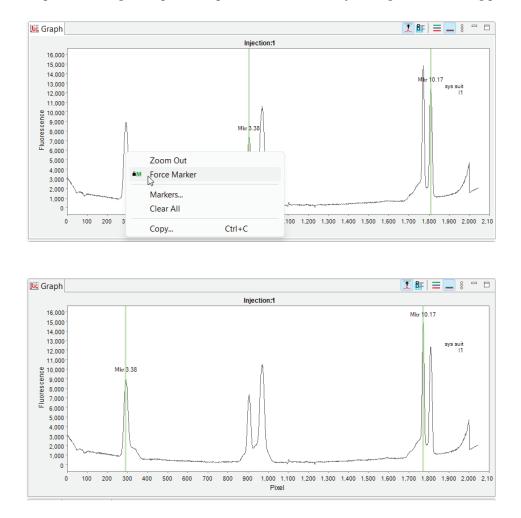
File	Edit	View	Instrume	ent	Window
Ē	Mark	ers 🚊	Samples		∎∎
				1	↑

- 4. Click Injection 1 in the Experiment pane.
- 5. Check that your pI markers in the electropherogram have been correctly identified. Each marker peak will have a green vertical line running through it and be labeled Mkr. They're also identified with an **M** in the Peaks table.

🗄 Markers	😤 Samples									
I Experim	ent	- 0	😹 Graph							
Injection	Injection Name	e Sample						Inject	ion:1	
1	sys suit_01	sys suit	16.000							
⊘ 2	sys suit_02	sys suit	15,000 - 14,000 - 13,000 - 12,000 - 10,000 - 0,000 - 5,000 - 5,000 - 4,000 - 3,000 - 2,000 - 1,000 - 0,000 -	M	or 3 38			N		Her 10.17 systait
			0	100 200	300 400 50	0 600	700 80	00 900	1.000 1.100 1.200 1.300 1.400 Pixel	1.500 1.600 1.700 1.800 1.900 2.000 2.10
			III Peaks	Injections						- 0
			Injection M1 M1	Injection N sys suit_01 sys suit_01	Sample sys suit sys suit	Peak 1 2	Position 291.9 1809.5	Height 8908.1 12338.3		

6. If your pI markers aren't identified correctly, here's how to manually correct them:

To set an unidentified peak as a pI marker: Right-click the peak in the electropherogram or Peaks table and select **Force Marker**. Compass will assign that peak as a pI marker, and correctly reassign the remaining pI marker peaks.

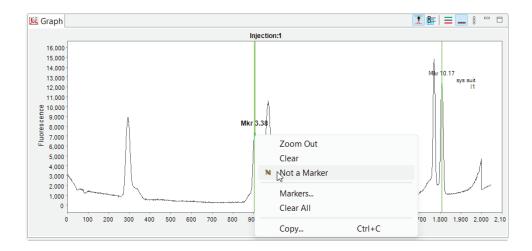


A lock icon indicating the pI marker was set manually will display next to the peak in the Peaks table and a check mark will appear next to the injection in the Experiment pane to show a manual correction was made.

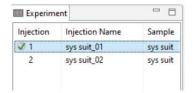
Injection 1	Injection Name sys suit_01	Sample sys suit
∛ 2	sys suit_02	sys suit
	Injection 1 2	1 sys suit_01

NOTE: To remove pI marker peak assignments that were made manually, right click on the peak in the electropherogram or Peaks table and click **Clear**. To clear all the manual settings for the injection, click **Clear** All.

If an incorrect peak is identified as a pI marker: Right-click the peak in the electropherogram or Peaks table and select **Not a Marker**. Compass should correctly reassign the remaining peaks as pI markers and update the Peaks table.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.



7. Repeat the previous steps for the remaining pI marker peaks as needed in the current injection and for all other injections to make sure all your pI markers are identified correctly.

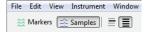
Step 2: Checking Sample Peaks

All detected peaks will be labeled automatically with the calculated protein pI.

NOTE: The reported protein pI in Compass may vary slightly from predicted pIs based on sample, buffer, and method conditions.

To make sure your sample proteins are identified correctly:

1. Click **Samples** in the View bar.

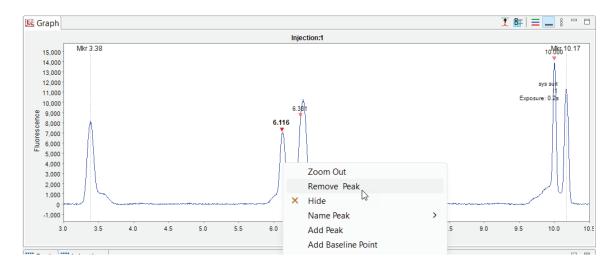


2. Click the View Selected icon in the View bar.



- 3. Click Injection 1 in the Experiment pane.
- 4. If your sample peaks aren't identified correctly, here's how to manually correct them:

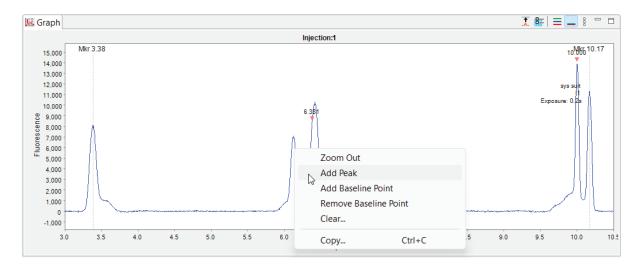
If a peak is incorrectly identified as a sample peak: Right-click the peak in the electropherogram or Peaks table and select **Remove Peak**. Compass will no longer identify it as a sample peak in the electropherogram and the peak data will be removed in the results table.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

🔳 Experim	ient -	
Injection	Injection Name	San
✓1	sys suit_01	sys
2	sys suit_02	sys :

To identify a peak as a sample peak: Right-click the peak in the electropherogram or Peaks table and select Add Peak. Compass will calculate and display the results for the peak in the results table and identify the peak in the electropherogram.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

Experiment 🛛 🗆							
Injection Name	San						
sys suit_01	sys						
sys suit_02	sys :						
	Injection Name sys suit_01						

NOTE: To remove sample peak assignments that were made manually and go back to the original peak data, right-click the peak in the electropherogram and select **Clear**.

5. Repeat the previous steps for the remaining injections to make sure all sample peaks are correctly identified.

Step 3: Assigning Peak Names

Compass can also optionally identify and automatically name sample peaks using user-specified peak name settings. For more information on how to do this, see "Manual Peak Integration" on page 547.

Chapter 9: MauriceFlex Fractionation Batches

Chapter Overview

- Overview
- Batch Screen Overview
- Opening a Batch
- Creating a New Batch
- Viewing Fractions To Be Collected
- Batch History
- Making Changes to a Batch
- Viewing and Editing Batches in Completed Runs
- Copying and Pasting an Injection Name or Sample ID from other Documents
- Importing and Exporting an Injection
- Importing and Exporting Methods
- Batch Reports

Overview

MauriceFlex Fractionation batches can be run on MauriceFlex systems using a cIEF Fractionation cartridge.

NOTES:

We recommend first optimizing methods with cIEF batches using a cIEF cartridge on Maurice, Maurice C. or MauriceFlex. Then, use recommendations in the MauriceFlex cIEF Fractionation Method Development Guide to modify the method for a MauriceFlex cIEF batch using a cIEF Fractionation cartridge on MauriceFlex to confirm successful method transfer before performing a MauriceFlex Fractionation batch.

Batch Screen Overview

You can use the Batch screen to create, view and edit batches. To get to this screen, click the Batch screen tab:

Batch 🖓 Run Summary 🏥 Analysis

Batch Screen Panes

The Batch screen has five panes:

- Layout Displays a map of the 96-well plate for MauriceFlex Fractionation batch sample locations. Batch reagent locations are also displayed.
- **Injections** Lists the injections, sample ID, sample locations and methods that MauriceFlex will execute for each sample in the batch.
- History Lists all batch file events from initial creation to the most current update.
- Notes Lets you enter specific information about your batch.
- Methods Lets you create methods and enter method parameters used in the batch.

	Fractionation - Compass for iCE rument Window Help										
The Lone mot	anene window help							:	Batch 🔮 Run	Summary 🕮 🧸	Analys
Batch: MauriceFl	ex Fractionation	ections 🛄 His	tory 📧 Notes						butter og nam		- (
aten. maaneen		test the	,				O Paul	e OSton b	🕈 Add 📗 Replic	ate 🛛 🗶 Remove	
🗉 Layout		Injection	Name S	ample ID	Locati	ion Metho		Notes	e noo minopre	ACC REPARENTO VC	
10°C 👻 🧕	Fractions C Add - C Remove - 1	Sample		ample 01	A1	lgG		notes			
Add • C Remove		Sumple		raction 01	B1	igo					
				raction 02	B2						
				raction 03	B3						
	WC FI Cal Water Water Water Empty			raction 04	B4						
				raction 05	B5						
				raction 06	B6						
				raction 07	B7						
Sample A A A A A A A A A A A A A A A A A A A			F	raction 08	B8						
			F	raction 09	B9						
Catholyte			F	raction 10	B10						
Mobilizer O			F	raction 11	B11						
Mobilizer			Fi	raction 12	B12						
K4 g			F	raction 13	C12						
Water H			Fi	raction 14	C11						
			-	10 A.C.	C40						
Methods											
										New R	lemo
Name	Separation	Detection	Sample Load	Mobilizati	Refocus	Fractions	pl Markers	Ampholyt	Additives		
lgG	10.0 min 500 Volts, 10.0 min 1000 Volts, 25	1 Exposure	20	25.0 min 1	0.0 min 1	45.0 sec 1	7.05, 10.17				
-											

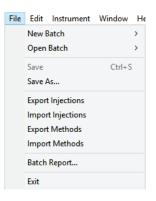
Software Menus Active in the Batch Screen

These main menu items are active in the Batch screen:

- File
- Edit
- Instrument (when the software is connected to MauriceFlex)
- Window
- Help

File Menu

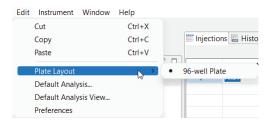
These File menu options are active:



- New Batch Creates a new batch from a starter template.
- Open Batch Opens an existing batch.
- Save/Save As Saves the open batch.
- Export Injections Exports injections from the current batch as a .csv file.
- Import Injections Imports injections into the current batch from a .csv file.
- Export Methods Exports method(s) from the current batch as separate files.
- Import Methods Imports saved method(s) into the current batch.
- Batch Report Exports a table of sample and method details for each injection in the batch as a PDF file.
- Exit Closes Compass for iCE.

Edit Menu

The following Edit menu options are active in the Batch screen:



- Cut Cuts the information currently selected.
- Copy Copies the information currently selected.
- **Paste** Pastes the copied information.

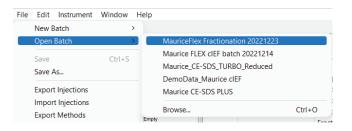
NOTE: Cut, Copy and Paste work differently depending on the pane you're in. How and when you can use them is described throughout the chapter.

- Plate Layout Indicates a 96-well plate will be used to run samples.
- Default Analysis Displays the default settings that will be used to analyze the data generated with your batch.
- Default Analysis View Displays the default settings that will used to view the data generated with your batch.
- **Preferences** Lets you set and save your preferences for Access Control, data export, graph colors, grouped data and Twitter settings. See Chapter 21: "Setting Your Preferences" for more information.

Opening a Batch

To open an existing batch:

1. Select File in the main menu and click Open Batch.



- 2. A list of the last five batches opened will display based on the last location found. If the location of the file has changed, you may need to navigate to find the file. Select one of those or click **Browse** to open the Batches folder and select a different one.
- 3. To make changes to the batch, see the steps in "Creating a New Batch" on page 194. When you're done, select File from the main menu and click Save.

Creating a New Batch

To create a new batch, we recommend that you use one of the template methods and make any necessary modifications from there.

Chapter 9: MauriceFlex Fractionation Batches | Creating a New Batch

Step 1 - Open a Template Batch

1. Select File in the main menu and click New Batch:

New Batch	>	Maurice cIFF
Open Batch	>	Maurice CE-SDS PLUS
Save	Ctrl+S	Maurice Turbo CE-SDS™
Save As	Curro	MauriceFlex clEF
Save As		MauriceFlex Fractionation
From a state for the state of a		

NOTE: Only template batches specific to your Maurice will be available when you are connected to the instrument. Template batches will not appear in the menu if that application type cannot be performed on your instrument.

2. Select MauriceFlex Fractionation A batch using the default method will display.

File Edit Inst	rument Window Help										
								1	Batch 🕒 Rur	n Summary 🥼	Analy
Batch: MauriceFl	ex Fractionation	njections 🔚 Hist	tory 👖 Notes								-
							O Paus	e 🖸 Stop 🖁	Add 📗 Repli	cate 🕅 Remove	•
🛙 Layout		Injection	Name Sa	ample ID	Locatio	on Metho	d	Notes			
10°C - Fractions C+ Add - CX Remove	🕈 Fractions 🔇 Add 👻 🔇 Remove 🔍 🗸	1 Sample	01_01 Sa	ample 01	A1	IgG					
			Fr	action 01	B1	-					
			Fr	action 02	B2						
			Fr	action 03	B3						
	MC FI Cal Water Water Empty		Fr	action 04	B4						
			Fr	action 05	B5						
			Fr	action 06	B6						
	1 2 3 4 5 6 7 8 9 10 11 12		Fr	action 07	B7						
Sample A • • • • • • • • • • • • •			Fr	action 08	B8						
			Fr	action 09	B9						
			Fr	action 10	B10						
Mobilizer			Fr	action 11	B11						
Mobilizer 🔴 F	000000000000000000000000000000000000000		Fr	action 12	B12						
Water	000000000000		Fr	action 13	C12						
KS H			Fr	action 14	C11						
			-	10 A.C.	C40						_
Methods											-
										New F	(emc
Name	Separation	Detection	Sample Load	Mobilizati	Refocus	ractions	pl Markers	Ampholyt	Additives		
lgG	10.0 min 500 Volts, 10.0 min 1000 Volts, 25	1 Exposure	20	25.0 min 1	0.0 min 1	45.0 sec 1	7.05, 10.17				

Step 2 - Assign Your Samples

The Layout pane shows the default locations of where batch reagent should be placed in the fractionation adapter.

] Layout							-	
	10°C	•	📑 Fr	actions	CT A	dd 🔫 (K Re	move
		MC	FI Cal Wat	er Water	Water En	R6		
Sample	<u>О</u> кі	A	2 3 4	5 6	7 8 9	10 11	12	
Catholyte	() K2						3	
Mobilizer	() (K3							
Mobilizer	() (K4	FŎ					ŏІ	
Water		H					8	
		1						

The same reagent locations are used for every batch:

- R1 0.5% Methyl Cellulose
- R2 Fluorescence Calibration Standard
- R3 Water vial
- R4 Water vial
- R5 Water vial
- R6 Empty vial (air)
- K2 Catholyte Solution
- K3 Mobilizer Solution (5 mM ammonium acetate)
- K4 Mobilizer Solution (5 mM ammonium acetate)
- K5 Water vial
- 1. Select your sample:

To import a sample using a saved injections file:

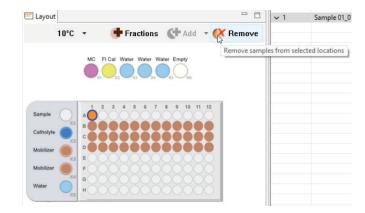
- a. Select File in the main menu and click Import Injections.
- b. Select an injections .csv file and click OK. The imported information will display in the Injections pane.
- c. Skip to step 3 on page 199.

NOTE: For more information on setting up an injections file for import, see "Importing and Exporting an Injection" on page 214.

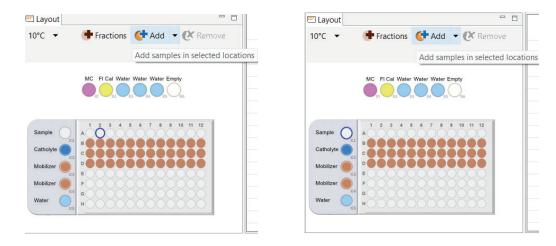
To change the sample location manually and select the method later:

NOTE: The template batch automatically adds the sample in well A1 by default. You can change the sample location to any well in row A or to position K1 if your sample is in a Maurice sample vial with integrated insert.

a. In the Layout pane, highlight well A1 and click **Remove**. The sample will also be removed from the Injections table. You can also right-click on the well and click **Remove Sample**.

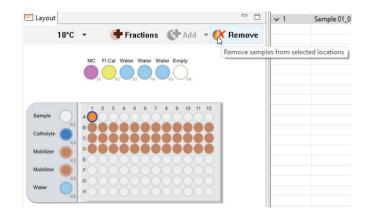


b. Use your mouse to highlight the well in Row A that your sample is located in or position K1, then click Add. The Injections table will automatically update

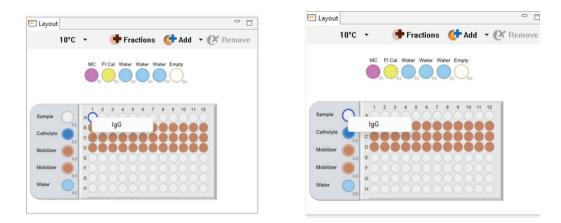


To change the sample location with preassigned methods:

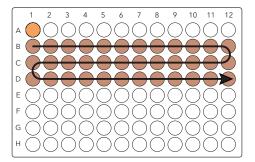
a. Highlight well A1 and click **Remove**. The sample will also be removed from the Injections table. You can also rightclick on the well and click **Remove Sample**.



b. Highlight the well your sample is located in or position K1, then right-click and select a method. The Injections table will automatically update.



2. Select where sample peak fractions will be collected in the 96-well plate. All fraction collection starts in column 1 and will be collected in a serpentine pattern. You can define which row to start collecting fractions and how many fractions to collect.



NOTES:

The sample location must first be defined before fraction locations can be assigned.

A minimum of 24 fractions must be collected.

To assign fraction collection locations:

- a. In the Layout pane, click Fractions.
- b. A prompt will appear. In the Start Row pulldown, select the row to start collecting fractions.

6 Fractions		×
Start Row:	В	~
Number of fractions:	В	
	C D	
ОК	E	
	F	
	G	

c. In the **Number of fractions** field, type the number of fractions to collect or use the arrows to increase or decrease the number of fractions.

6 Fractions		×
Start Row:	В	~
Number of fractions:	24	
ОК	Cancel	Defaults

NOTE: The number entered will be highlighted in red if the number is below the minimum (24) or higher than the available wells on the plate based on where you start collecting fractions.

- d. Click Defaults to reset fields to default settings.
- e. Click OK. The plate map in the Layout pane and the Injections list will automatically update.
- 3. The 96-well plate on the fractionation adapter is temperature controlled with a default setting of 10 °C. To change the temperature or turn it off, click the **down arrow** next to the temperature and select an option.

NOTE: The reagent row (R) is kept at room temperature while the reagent column (K) and sample plate are temperature controlled.



Step 3 - Assign Your Method Parameters

NOTE: We recommend using the default method parameters. Please see the Maurice cIEF Fractionation Method Development Guide for more information on method optimization.

The Methods pane lists all of the methods used in a batch. You can add and remove methods here and change method parameters.

To import a saved method:

- 1. Select File in the main menu and click Import Method.
- 2. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

To create a new method or make changes to an existing one:

1. In the Methods table, click the first cell in the Name column and enter a new method name if needed.

Method	s									- 6
									New	Remov
Name	Separation	Detection	Sample Load	Mobilizati	Refocus	Fractions	pl Markers	Ampholyt	Additives	
lgG	10.0 min 500 Volts, 1	1 Exposure	20	25.0 min 1	0.0 min 150	45.0 sec 1	7.05, 10.17			

2. Click the first cell in the Separation column, then click the selection button [...] to set the pre-focusing and focusing time (in minutes) and voltage (V). You can also set the Detection Interval (in minutes) and Exposure (in seconds) to adjust how often an image is taken using the listed Exposure time.

gG Voltage 3 Steps	/oltage (Volts)
G Voltage 3 Steps	
	00
25.0	000
	500
Detection Interval (min)	5.0
Exposure (sec)	0.2

- To change time and voltage parameters: Just click in a cell under Time or Voltage and type the new value(s).
- To change the detection interval or exposure parameters: Click on the field and type the new value(s).
- **To add a profile step:** Click **Add**. A new row will be added in the table. Then just type in a load time (in minutes) and voltage value (in V).
- To remove a profile step: Select the row you want to remove and click Remove.

- 3. The Detection Profile exposure setting is linked to and defined by the Separation step and cannot be changed.
- 4. Click the first cell in the Sample Load(s) column and set the load time in seconds.

NOTE: We recommend using the default Sample Load time of 20 seconds. Please contact ProteinSimple Technical Support if you have questions on the Sample Load time to use for your application.

Name	Separation	Detection	Sample Load (s)
lgG	10.0 min 500 Volts, 1	1 Exposure	20

5. Click the first cell in the Mobilization column, then click selection button [...] to set the mobilization time (in minutes) and voltage (V). You can also set the Detection Interval (in minutes) and Exposure (in seconds) to adjust how often an image is taken using the listed Exposure time.

Methods						💮 Mobilization Profile		×
Name	Separation	Detection	Sample Load	Mobilization		Time (min)	Voltage (Volts)	
IgG	10.0 min 500 Volts,	1 Exposure		25.0 min 1000 Vo	\longrightarrow	25.0	1000	
				43				
						Detection Interval (min)	1.0	
						Exposure (sec)	0.2	
						ОК	Cancel	

- To change time and voltage parameters: Just click in a cell under Time or Voltage and type the new value(s).
- To change the detection interval or exposure parameters: Click on the field and type the new value(s).

6. An optional refocusing step can be added right before fraction collection to improve fraction resolution. Click the first cell in the Refocus column, then click the selection button [...] to set the refocusing time (in minutes).

NOTES:

The Compass for iCE fraction peak predictor will not be availabe if a refocusing step is added to the method. A warning will disply in the refocus profile and Start Run window and will be recorded in the run summary when then time parameter is changed.

The refocusing step volage is linked and defined by the Separation step and cannot be changed.

Refer to the MauriceFlex cIEF Fractionation Method Development Guide for refocusing times and voltage setting tips.

Name Separation Detection Sample Load Mobiliza IgG 10.0 min 500 Volts, 1 1 Exposure 20 25.0 min	ti Refocus 1 0.0 min 1500	Time (min)	Voltage (Volts) 1500
IgG 10.0 min 500 Volts, 1 1 Exposure 20 25.0 min	1 0.0 min 150(0.0	1500
IgG 10.0 min 500 Volts, 1 1 Exposure 20 25.0 min			1500
	T 0.0 mm 1300	\rightarrow	
	45		
	Lef	Detection Interval (r	min) 1.0
		Exposure (sec)	0.2
			OK Cancel

- To change time: Just click in a cell under Time and type the new value(s).
- 7. Click the first cell in the Fractions column, then click the selection button [...] to set the fraction collection time (in seconds) and voltage (V).

NOTE: The voltage, detection interval and exposure settings are linked to and defined by the Mobilization step settings and cannot be changed.

Name	Separation	Detection	Sample Load	Mohilizati	Pofocus	Fractions		Time (sec)	Voltage (Volts)	
								45	1000	
lgG	10.0 min 500 Volts, 10	1 Exposure	20	25.0 min 1	0.0 min 1	45.0 sec 1	\rightarrow			
						10				
								Detection Interval (min)	1.0	
								Exposure (sec)	0.2	
								Exposure (see)	0.4	

• To change time parameters: Just click in a cell under Time and type the new value(s).

8. Click the first cell in the pI Markers column to select pI markers. Add new markers or remove existing ones then click OK.

NOTE: When you edit the pI markers in the method for a batch, Compass for iCE automatically creates a Markers group in the pI Markers Analysis settings for you.

ame	Separation	Detection	Sample Load			Fractions	pl Markers		Add	Remove	
5	10.0 min 500 Volts, 10	1 Exposure	20	25.0 min 1	0.0 min 1	45.0 sec 1	7.05, 10.17	\rightarrow	pl Markers:		
									pl	Position	
									7.05	300	
									10.17	1,900	
									-		

- To change a pI marker and position: Just click in a cell under pI or Position and type the new value(s).
- **To add a pI marker:** Click **Add**. A new row will be added in the table. Then just type in a pI and a position (in pixels).
- To remove a pI marker: Select the row you want to remove and click Remove.
- 9. Optional: Click the first cell in the Ampholytes column and enter the ampholytes you're using.

Methods								
						1		1
Name	Separation	Detection	Sample Load	Mobilizati	Refocus	Fractions	pl Markers	Ampholytes
lgG	10.0 min 500 Volts	1 Exposure	20	25.0 min 1	0.0 min 1	45.0 sec 1	7.05, 10.17	Pharmalyte 3-10

10. Optional: Click the first cell in the Additives column and enter any additives you're using.

Methods									1	- 8
									New Rei	move
Name	Separation	Detection	Sample Load	Mobilizati	Refocus	Fractions	pl Markers	Ampholytes	Additives	
IgG	10.0 min 500 Volts, 10.0	1 Exposure	20	25.0 min 1	0.0 min 1	45.0 sec 1	7.05, 10.17	Pharmalyte 3-10	Urea	

11. You can now:

- Click **New** in the upper right corner of the Methods pane to add a new one if you want to use different methods for different samples. Then just repeat the steps above for the new method.
- Make updates to the remaining methods by repeating the prior steps.
- Select a method and click Remove in the upper right corner of the Methods pane to delete it.

Step 4 - Set Up Your Injection

The Injection pane lists information for the batch sample injection and lists fractionation collection locations in the 96-well plate.

Injection	ons 🔚 History 🚹 Notes			18.0	-	E
		🕕 Pause 🛛 Stop 👫 Add	Replicate	Remove 🕺	Ŧ	E
	Injection Name	Sample ID	Location	Method		
v 1	Sample 01_01	Sample 01	A1	IgG		
		Fraction 01	B1			
		Fraction 02	B2			
		Fraction 03	B3			
		Fraction 04	B4			
		Fraction 05	B5			
		Fraction 06	B6			
		Fraction 07	B7			
		Fraction 08	B8			
		Fraction 09	B9			
		Fraction 10	B10			
	Fraction 11	B11				
	Fraction 12	B12				
		Fraction 13	C12			
		Fraction 14	C11			
		Fraction 15	C10			
		Fraction 16	C9			
		Fraction 17	C8			
		Fraction 18	C7			
		Fraction 19	C6			
		Fraction 20	C5			
		Fraction 21	C4			
		Fraction 22	C3			
		Fraction 23	C2			
		Fraction 24	C1			
		Fraction 25	D1			
		n 11 nn	00			

NOTE: If you imported the injection in Step 2, you can update the injections table and assign a method as needed using the information that follows.

1. To change the sample name, click the **Sample ID** cell and type a name.

NOTES:

A Sample ID can be copied from other documents and pasted into Compass for iCE to make batch setup faster. Check out "Copying and Pasting an Injection Name or Sample ID from other Documents" on page 213 for more info.

If you change the sample ID when the default injection name is still being used, the injection name will automatically update to match the sample ID. If you've already changed the injection name manually, updating the sample ID will not update the injection name.

	tions 🔚 History 🌃 Not		Pause	Stop 🖟 Add 📗 R	enlicate 🔀 Remove	Ŧ	F
	Injection Name	Sample ID	Location	Method	Notes		
× 1	Sample 01_01	Sample 01	A1	lgG			1
		Fraction 01	B1				1
		Fraction 02	B2				
		Fraction 03	B3				

The sample name also displays when you hover the mouse over the sample in the plate map:

Batch: Mauri	ceFlex Fractionation	Inject	ions 🔚 History 🃧 Notes	5			
		_			🕕 Pause 🤇	Stop 🖟 Add	🖩 Replicate 🔀 Remove 🖽
🖽 Layout		_	Injection Name	Sample ID	Location	Method	Notes
10°C 🔻	🕂 Fractions 🔇 🕈 Add 🕞 😻 Remove	∨ 1	Sample 01_01	Sample 01	A1	IgG	
				Fraction 01	B1		
				Fraction 02	B2		
				Fraction 03	B3		
	MC FI Cal Water Water Empty			Fraction 04	B4		
	R1 R2 R3 R4 R5 R6			Fraction 05	B5		
				Fraction 06	B6		
	1 2 3 4 5 6 7 8 9 10 11 12			Fraction 07	B7		
Sample	AR00000000000			Fraction 08	B8		
Catholyte	Sample 01			Fraction 09	B9		
· •				Fraction 10	B10		
Mobilizer 🔵				Fraction 11	B11		

2. The Injection name is automatically set to 'Sample ID_injection number'. To change the name, click the Injection Name cell and type a name. The injection name must be unique. If it isn't when you save the batch, Compass for iCE highlights any non-unique injection names so you can change them.

Inject	ions 🔚 History 🌃 No	tes				- 0
			🕕 Pause 🤇	Stop 🖟 Add 🖁	Replicate 🛛 🔀 Remove	•
	Injection Name	Sample ID	Location	Method	Notes	
∨ 1	Sample 01_01	Sample 01	A1	IgG		
		Fraction 01	B1			
		Fraction 02	B2			_

NOTE: Changing the injection name won't affect the sample ID.

3. Assign your methods to each injection. Just click the **Method** cell for the injection and select a method from the drop down menu. If you added your samples with pre-assigned methods and don't need to make any changes, skip to the next step.

ingect	ions 📗 History 🎵 Not	100				
			U Pause	Stop 🕼 Add 🔟 F	Replicate 🛛 🔀 Remove	
	Injection Name	Sample ID	Location	Method	Notes	
1	Sample 01_01	Sample 01	A1	lgG		
		Fraction 01	B1	lgG		
		Fraction 02	B2	Method2		
		Fraction 03	B3	6		

Hovering over a method name displays the method parameters:

📗 Injed	ctions 🔚 History I	Notes								
				0	Pause 🛛 Stop	🖟 Add 📗 i	Replicate	🔀 Remove	Ŧ	Ξ
	Injection Name	Sample ID	Location	Method	Notes					
v 1	Sample 01_01	Sample 01	A1	IgG					_	
		Fraction 01	B1	lgG						
		Fraction 02	B2	Separation: 10.0 mi		.0 min 1000 V	olts, 25.0	min 1500 Vo	lts	
		Fraction 03	B3	Detection: 1 Expose Sample Load (s): 20						
		Fraction 04	B4	pl Markers: 7.05, 10						
		Fraction 05	B5	Ampholytes: Pharm						
		Fraction 06	B6	Additives: Urea	,					
		Fraction 07	B7						_	

Step 5 - Add Programmed Pauses and Stops (Optional)

You can program pauses and stops in the batch to automatically pause or stop after injections even when you aren't in front of MauriceFlex.

Note: The cartridge cleanup is performed at the end of the batch and after an injection. A programmed pause will occur after the injection before the cartridge cleanup starts.

To program a pause:

Pauses are helpful when you want to review injection results before continuing with the rest of the batch.

1. Highlight the injection you want to pause at and click **Pause**. The batch will pause after that injection is complete.

NOTE: MauriceFlex can tweet you when the batch pauses. See "Setting Up Maurice Systems to Send Tweets" on page 764.

🛄 Injec	tions 🔚 History 耳	Notes			- 0
				O Pause O Stop I Add III Replicate K Remove	Ð
	Injection Name	Sample ID	Location	Method Pause after the selected injection	
> 1	Sample 01_01	Sample 01	A1	IgG	

Injec	tions 🔚 History 👖	Notes								
				Pause	O Stop	🕇 Ad	d 📗 Replicate	🔀 Remove	Ŧ	Ξ
	Injection Name	Sample ID	Location	Method		1	Notes			
> 1	Sample 01_01	Sample 01	A1	IgG						
				Pause						

2. To resume the batch, click **Continue** in the instrument status bar:

Paused	Continue		
		Mon 1:43 PM	

To stop the run after a specific injection:

1. Highlight the injection you want the batch to stop at and click **Stop**. Maurice will continue the batch through the selected injection, then stop the batch and perform end-run cleanup steps.

🛛 Injec	tions 🔚 History 🔳	Notes							- 0
				Pause	Stop	🕂 Add	📗 Replicate	🔀 Remove	Ð
	Injection Name	Sample ID	Location	Method	Sto	op after t	he selected in	jection	
> 1	Sample 01_01	Sample 01	A1	IgG	_				
Injec	ctions 🔚 History 耳	Notes	1	1					- 0
Injec	tions 🔚 History 耳	Notes		Pause	• Stop	🗗 Add	III Replicate	Remove	
Injec	tions 🔚 History 🗊	Notes Sample ID	Location	Pause Method	O Stop		Replicate	Remove	
Injec			Location A1		O Stop			¦× Remove	
Injec	Injection Name	Sample ID		Method	O Stop			Kemove Remove	

Data collected for injections completed up to the point where the batch was stopped are saved in the .mbz file.

2. Be sure to complete your normal post-batch procedures.

Step 6 - Add Batch Notes (Optional)

- 1. Click on the Notes pane.
- 2. Click in the notes area and type any information you want to add about your batch.

Injections III History T *Notes Product testing	- 0
Product testing	

Step 7 - Modify Default Analysis Parameters (Optional)

You can preset the parameters used to analyze data generated with the batch. We recommend using the default parameters for MauriceFlex Fractionation applications, but if you need to modify parameters:

1. Select Edit from the main menu and click Default Analysis. The following screen will display:

or Default Analysis: MauriceF	lex Fractionation		×
Detection Peak Names Peak Fit Advanced	Detection		
pl Markers	IgG Exposure 1 0.2 seconds v		
Import Exp	OK Cancel	Apply	

2. Change the parameters you want to, then click OK. For detailed information on analysis parameters, please refer to "Analysis Settings Overview" on page 620.

Step 8 - Modify Default Analysis View Parameters (Optional)

You can preset the parameters used to display the electropherogram data when the batch is complete. Default Analysis View Parameters must be set before you start the batch and cannot be modified once the batch starts. However, you can still manually change parameters in the Analysis pane using the Graph Options button.

To modify the paramters:

1. Select Edit from the main menu and click Default Analysis View. The following screen will display:

Graph View Options	Graph View Options			
	 Matching Peak Names Peak Names Peak Values 			
	 Fitted Peaks Baseline Fit Grid Lines 			
	Plot Label Sample Method Injection Exposure Injection Name			
	ОК	Cancel	Appl	

2. Change the parameters you want to, then click **Apply**. Click **OK** when you are done changing display parameters. For detailed information on on graph view options, please refer to "Customizing the Data Display" on page 603.

Step 9 - Save Your Batch

1. Once all of your sample, method and injection info is entered, select **File > Save**. Enter any comments on the batch if you want, then click **Save**.

🤠 Save Batch Comment	×
Batch: MauriceFlex Fractionation 20221223 Comment:	
Commence	
	-
Save Cancel	

2. Enter a name for your batch then click Save.

Viewing Fractions To Be Collected

An arrow will appear next to the injection number. Toggle the arrow to expand or collapse the list of fractions that will be collected.

Injections	🔚 History 👖 Notes	🕕 Pause 🛛 Stop	Add 📗	Replicate 볹	Injections	🔚 History 👖 Notes	🕕 Pause 🛛 Sto	p ∭≓ Add ∭	Replicat
	Injection Name	Sample ID	Location	Method		Injection Name	Sample ID	Location	Metho
> 1 Si	Sample 01_01	Sample 01	A1	IgG	✓ 1	Sample 01_01	Sample 01	A1	IgG
							Fraction 01	B1	
							Fraction 02	B2	
							Fraction 03	B3	
							Fraction 04	B4	
							Fraction 05	B5	

• To show all fractions collected in the batch, click the Expand All Injections button.

				🕕 Pause 🖸 Sto	p 🖟 Add 📗 Replicate 😿 Rei	move 🛒 🖻
	Injection Name	Sample ID	Location	Method	Notes	Expand all injectio
1	Sample 01_01	Sample 01	A1	lgG		Expand an injectio
		Fraction 01	B1			
		Fraction 02	B2			
		Fraction 03	B3			
		Fraction 04	B4			
		Fraction 05	B5			
		Fraction 06	B6			

• To hide all fractions collected in the batch, click the Collapse All Injections button.

III Injec	ctions 🔚 History 耳	Notes					- 4	•
				🕕 Pause 🕻	🕽 Stop 🖟 Add 📗 Replie	ate 🔀 Remove	EĘ	
	Injection Name	Sample ID	Location	Method	Notes			Collapse all injections
> 1	Sample 01_01	Sample 01	A1	lgG				contapse an injections
								-
								-

.

Batch History

Clicking on the History pane shows the batch event history, starting with the date and time the batch was created through the most current event. Clicking on a row in the table displays the full event details in the box under the table.

Date	User Name	Message	Comment	
2022-11-08 11:48:4	4	Batch created using the factory default Maurice Flex Fractions with Compass for iCE Version: 4.0.0-1102		
2022-11-08 11:56:	1	Saved as C:\Users\xiaojing.shen\Desktop\Maurice Flex Fractions.batch from Compass for iCE v4.0.0-1102		
2022-11-08 11:56:	1	Save injections and methods changes to C:\Users\xiaojing.shen\Desktop\Maurice Flex Fractions.batch from Co		
ime	2022-11-0	18 11:48:41 User		
lessage		ated using the factory default Maurice Flex Fractions with Compass for iCE Version: 4.0.0-1102		
Comment				

- Date: Date and time of the batch event.
- User Name: User that initiated the event. User names only display if you're using the Access Control feature to help satisfy the 21CFR Part 11 data security requirements. Go to "Enabling Access Control" on page 781 to learn how to set it up.
- Message: Description of the event that took place.
- **Comment:** Comments entered by the user when the batch was saved.

You can copy the information in the History pane to use in other documents:

- 1. Click the **History** pane to make sure it's active.
- 2. Click Edit in the main menu and select Copy.
- 3. Open a document and click Paste.

Making Changes to a Batch

1. Select File in the main menu and click Open Batch.

File	Edit Instrument	Window H	elp		
	New Batch	>			
	Open Batch	\rightarrow		MauriceFlex Fractionation 20221223	
	Save Save As	Ctrl+S		Maurice FLEX clEF batch 20221214 Maurice_CE-SDS_TURBO_Reduced DemoData Maurice clEF	
	Export Injections Import Injections			Maurice CE-SDS PLUS	Ctrl+0
	Export Methods		Empty	biowse	Er

- 2. A list of the last five batches opened will display based on the last location found. If the location of the file has changed, you may need to navigate to find the file.
 - Select one of these files or click Browse to open the Batch folder and select a different one.
 - To open a batch used in a run file, click **Browse**. Go to the Run folder in the Compass for iCE directory and select the run file that uses the batch you want to edit.

Organize 👻 Share with 👻 Burn	New folder				
 ▲ Contraction ▲ Documents 	Documents library Compass for iCE				
4 📗 My Documents	Name	Date modified	Date created	Туре	Size
Add-in Express	Batches	1/18/2016 5:39 PM	1/13/2016 8:24 PM	File folder	
🎍 Adobe	New Batches	1/13/2016 8:24 PM	1/13/2016 8:24 PM	File folder	
Clients	Runs	1/17/2016 8:41 PM	11/11/2015 4:46 PM	File folder	
Compass for iCE Batches	DemoData_Maurice clEF.mbz	1/18/2016 11:38 AM	1/18/2016 11:38 AM	Maurice data file.	798 K
 Batches New Batches Runs 					

3. To make changes to the batch, see the steps in "Creating a New Batch" on page 194. Then select File from the main menu and click **Save** or **Save As**.

Viewing and Editing Batches in Completed Runs

- 1. Click the Analysis screen and open your run file(s).
- 2. After the run opens, click the Batch screen to view the batch used with the run.

If you opened more than one run file, you can switch between viewing batches for each file. Just click the **down arrow** in the Run box and select the batch you want to view from the drop down list.

Run:	2015-12	2-06_15	-13-01	1_Maurice cIEF_Mab11	Te	•		
🖭 Laj	2016-01	-21_09 2-06_15	- 46-3 9	9_mAb11_Prep2016012 L_Maurice cIEF_Mab11	1_Q _Teo	C(0) :hRep		
	00	10°C	*	🗲 Add	*	Ø	Rem	iove

3. In completed run files, you can only make edits to the **sample** and **method** names in a batch, and these changes are saved to the run file only. Update sample and method names as needed.

4. Click the Analysis screen. Then select File from the main menu and click Save or Save As to save the new changes to the run file.

Copying and Pasting an Injection Name or Sample ID from other Documents

An injection name and Sample ID can be copied from other documents and pasted into the Injection pane to make batch setup faster.

To paste an injection name into the batch:

1. Select the injection name in a document (Microsoft[®],Word[®], Excel[®], etc.) and select **Copy** or hold the **Ctrl+C** keys to copy.



2. Select the injection cell in the Injection pane, then hold the Ctrl+V keys to paste. You can also select the injection, right click and select Paste.

Injections	🔚 History 👖 Notes	🕕 Pause 🛛 S	top 🖟 Add 📗 I	Replicate 🔀 Remove	• • • •
	Injection Name	Sample ID	Location	Method	Notes
v 1	Sample 01_01	Sample 01	A1	IgG	
		Fraction 01	B1		
		Fraction 02	B2		

The injection name is pasted into the Injection pane:

Injections	🔚 History 👖 Notes	🕕 Pause 🛛 🛈 Sto	p ⊯ Add ∭ I	Replicate 🕌 Remove	F C C
	Injection Name	Sample ID	Location	Method	Notes
v 1	My Injection 1	Sample 01	A1	lgG	
		Fraction 01	B1		
		Fraction 02	B2		

To paste a Sample ID into the batch:

1. Select the Sample ID in a document (Microsoft[®], Word[®], Excel[®], etc.) and select **Copy** or hold the **Ctrl+C** keys to copy.

	А	В	С
1			
2		My Injection 1	My Sample 1
3			

2. Select a Sample ID in the Injection pane, then hold the Ctrl+V keys to paste. You can also select the Sample ID, right click and select Paste.

Injections	🔚 History 👖 Notes	🕕 Pause 🛛 Stop	🕂 Add 📗	Replicate	🔀 Remove	Ŧ	₿ "	
	Injection Name	Sample ID	Location	Method		1	Notes	
v 1	Sample 01_01	Sample 01	A1	IgG				11
		Fraction 01	B1					
			12222					

The Sample ID is pasted into the Injection pane.

NOTE: If you paste in a new sample ID when the default injection name is still being used, the injection name will automatically update to match the sample ID. If you've already changed the injection name manually, updating the sample IDwill not update the injection names.

🔚 History <u> N</u> otes	🕕 Pause 🛛 🛈 Sto	p 🖟 Add 🔤 F	Replicate 🛛 🔀 Remove	• • • •
Injection Name	Sample ID	Location	Method	Notes
My Sample 1_01	My Sample 1	A1	lgG	
	Fraction 01	B1		
	Injection Name	Injection Name Sample ID My Sample 1_01 My Sample 1	Injection Name Sample ID Location My Sample 1_01 My Sample 1 A1	Injection Name Sample ID Location Method My Sample 1_01 My Sample 1 A1 IgG Fraction 01 B1

Importing and Exporting an Injection

An injections in an open batch or run file can be exported as a separate file. This lets you import the same or modified injection into another batch later, rather than having to enter the information manually.

Exporting an Injection

- 1. Open the batch or run you want to export the injection from.
- 2. In the Batch screen, select File in the main menu and click Export Injections. The following window displays:

$\leftrightarrow \rightarrow \checkmark \uparrow$	Compass for iCE > Batches	~ C	Q Search Batches	
Organize 🔻 Ne	w folder		Ξ	• 0
> 📒 Desktop	Name	Date modified	Туре	Size
> 📔 Documents	; MauriceFlex Fractionation 20221223_Inje	1/2/2023 2:55 PM	Microsoft Excel C	1 K
> 🛓 Downloads				
> 🕖 Music	1			
> 🔀 Pictures				
> 💽 Videos				
🗸 📮 This PC				
· · · · · · · · · · · · · · · · · · ·				
File <u>n</u> ame:	MauriceFlex clEF_Injections.csv			
	Text File, comma delimited (*.csv)			

- 3. The default directory is Compass for iCE/Batches. Change the directory if needed.
- 4. The default file name will be batchname.batch_Injections.csv. Change the name if needed and click Save.

Creating an Injection File

To create a new injection file .csv, it's easiest to export the injection from an existing batch and use that as your template.

- 1. Follow the instructions in "Exporting an Injection" above to export the injection from an existing cIEF batch.
- 2. Open the .csv file in a program that provides a table/spreadsheet format.
- 3. To add or change injection information:
 - a. Type in a unique name in each cell in the Injection Name column.
 - b. Type in a sample ID, location and method for each injection in their respective columns.
 - c. Optional: Type in notes if needed.

NOTES:

Mix bottles are not used for MauriceFlex cIEF batches. Compass for iCE ignores this column when importing injections into a MauriceFlex cIEF batche.

Programmed pauses and stops can't be added in the injections file. They can be added in the Injections pane after importing your injections into Compass for iCE.

	А	В	С	D	E	F
1	Injection Name	Sample ID	Location	Method	Mix Bottle	Notes
2	Inj01	R01_SSPP	E4	System Suitability		

4. Save the .csv file.

Importing an Injection

- 1. Open the batch you want to import the injection into, or open a new batch.
- 2. Select File in the main menu and click Import Injections.
- 3. Select an injections file (*.csv) and click OK. The imported information will display in the Layout and Injections panes.

NOTE: The imported injection will replace any injections already in the Injections table, they will not append an existing table.

Importing and Exporting Methods

Methods in an open batch or run file can be exported as a separate file. This lets you import the same method into another batch later, rather than having to re-enter method information manually.

Importing a Method

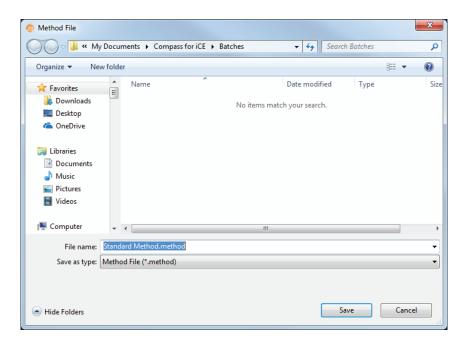
NOTE: Importing a method imports information into the Batch window's Method pane only.

- 1. Open the batch you want to import the method into.
- 2. Select File in the main menu and click Import Method.
- 3. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

Exporting a Method

NOTE: Exporting a method exports information in the Batch window's Method pane only.

- 1. Open the batch you want to export the method from.
- 2. In the Method pane, select the method you want to export. To export more than one method at the same time, hold the Ctrl key to select multiple methods.
- 3. Select File in the main menu and click Export Method. The following window displays:



- 4. The default directory is Compass for iCE/Batches. Change the directory if needed.
- 5. Enter a method file name and click Save. The settings will be saved as a *.method file.

Batch Reports

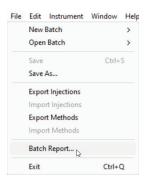
You can export a PDF file of sample and method details for each injection in the batch.

NOTES:

You can have Compass for iCE generate reports for you automatically at the end of each run. See "Setting up Automatic Injection Reports" on page 761 for more information.

Any time a new report is run, it's saved in a separate run folder. Existing reports aren't overwritten.

- Go to the Analysis or Run Summary screen, then click File > Open Run and select a run file (if you don't have one open already).
- 2. After the run opens, go to the Batch screen.
- 3. Select File from the main menu and click Batch Report.



4. The report name defaults to the run file name. If you want to change it, type in the Report Name box to make updates.

Batch Report		
Run: 2022-12-01_08-00-38_Alp	ha Testing NIST v2	
Secure PDF		
Report Name:		Browse
2022-12-01_08-00-38_Alpha Test	ing NIST v2	
Location: C:\Users\Andrea\Docu	ments\Compass for iCE	\Runs

Report PDFs generated by Compass for iCE are secured by default, which means they can be viewed and printed but not modified or renamed. Uncheck **Secure PDF** if you don't want to generate a secure report. To learn more about permissions for secured vs. unsecured reports, see page 800.

5. The Batch Report PDF is exported to the Runs folder in the Compass for iCE directory. It'll be in a folder with the report name used in the prior step. When the reports are done, the folder opens for you automatically.

🛓 Favorites	~	Name	Date modified	Туре	Size	
🐺 Links		2016-01-21_09-46-39_mAb11_Prep20160121_QC_Batch.pdf	1/24/2016 1:04 PM	Adobe Acrobat D		26 K
My Documents		2010-01-21_09-40-39_mAb11_Prep20100121_QC_batch.pdf	1/24/2010 1:04 PIVI	Adobe Acrobat D		20 K
🌗 Add-in Express						
🌗 Adobe						
퉬 Clients						
🐌 Compass for iCE						
퉬 Batches						
퉬 New Batches						
퉬 Runs						
2015-12-06_15-13-01_Maurice clEF_Mab11_TechR						
2016-01-21_09-46-39_mAb11_Prep20160121_QC_F						
78664 P3 IS 2015-11-30_16-49-49_MW Ladder Sol ⁻						

Here's an example Batch Report:

MauriceFlex Fractionation Batch: Alpha Testing NIST

Injection	Injection Name	Sample ID	Location	Method	Notes
				NIST	Notes
1	NIST	Sample 01	A1	NIST	
		Fraction 01	B1		
		Fraction 02	B2		
		Fraction 03	B3		
		Fraction 04	B4		
		Fraction 05	B5		
		Fraction 06	B6		
		Fraction 07	B7		
		Fraction 08	B8		
		Fraction 09	B9		
		Fraction 10	B10		
		Fraction 11	B11		
		Fraction 12	B12		
		Fraction 13	C12		
		Fraction 14	C11		
		Fraction 15	C10		
		Fraction 16	C9		
		Fraction 17	C8		
		Fraction 18	C7		
		Fraction 19	C6		
		Fraction 20	C5		
		Fraction 21	C4		
		Fraction 22	C3		
		Fraction 23	C2		
		Fraction 24	C1		

Created By. Andrea Fri 9:24 AM Feb 24, 2023 PST (SECURED) C'UlserNAdretaDocumenti/Compass for (CERuns)2022-1201, 08-00-38_Alpha Testing NIST v2.mbz Computer: DESNT04-FIAI7030 Software Version: Compass for (CE 4.0.0, Build ID: 0222





MauriceFlex Fractionation Batch: Alpha Testing NIST

Methods

Γ	Name	Separation	Detection	Sample Load (s)	Mobilization	Refocus	Fractions	pl Markers
1	IIST	10.0 min, 500 Volts	Fluorescence, 0.1 sec	30	25.0 min 1000 Volts	0.0 min 1500 Volts	45.0 sec 1000 Volts	7.05 pl, 300 pixels
		10.0 min, 1000 Volts			Detection	Detection	Detection	10.17 pl, 1800 pixels
		25.0 min, 1500 Volts			Exposure: 0.1 sec	Exposure: 0.1 sec	Exposure: 0.1 sec	
		Detection			Interval: 1.0 min	Interval: 1.0 min	Interval: 1.0 min	
		Exposure: 0.1 sec						
		Interval: 5.0 min						

Methods (continued)

Name	Ampholytes	Additives
NIST		

Batch Log

Date	User Name	Message	Comment
2022-11-04 08:07:40		Batch created using the factory default Maurice Flex Fractions with Compass for iCE Version: 4.0.0-1102	
2022-11-04 08:33:39		Saved as Z:\shared\ppd\science\r&d science\team members\mason\Flex Cartridge Validation - Backup\Alpha Testing\Alpha Testing NIST.batch from Compass for iCE v4.0.0-102	
2022-11-04 08:33:39		Save injections changes to Z'shared/ppd/scienceir&d scienceiteam members/mason/Flex Cartridge Validation - Backup/Alpha Testing/Alpha Testing NIST batch from Compass for iCE v4.0.0-1102	

Created By: Andrea Fri 9:24 AM Feb 24, 2023 PST (SECURED) C1UberNardreaDcoumentbiOcmpass for (CERuns)2022-1201, 06:00-38, Alpha Testing NIST v2.mbz Comparter: DESATOP-IFM0703

Page 2 of 2



Chapter 10: Running MauriceFlex Fractionation Applications

Chapter Overview

- Overview
- Before You Throw the Switch
- Power Up
- MauriceFlex Fractionation Workflow
- Running MauriceFlex Fractionation Applications
- Editing a Running Batch
- Post-batch Procedures
- Checking Your Data

Overview

MauriceFlex Fractionation applications can be run on MauriceFlex system using a cIEF Fractionation cartridge. You can then confirm which fractions contain the desired peak by running a standard cIEF batch on a Maurice, Maurice C. or MauriceFlex system with a cIEF cartridge before mass spectrometry analysis.

NOTES:

We recommend first optimizing methods with cIEF batches using a cIEF cartridge on Maurice, Maurice C. or MauriceFlex. Then, use recommendations in the MauriceFlex cIEF Fractionation Method Development Guide for tips to modify the method for a MauriceFlex cIEF batch using a cIEF Fractionation cartridge on MauriceFlex to confirm successful method transfer before performing a MauriceFlex Fractionation batch.

cIEF Fractionation cartridges support 15 injections.

On-board mixing is not available on MauriceFlex.

Before You Throw the Switch

Ensure that everyone using MauriceFlex have:

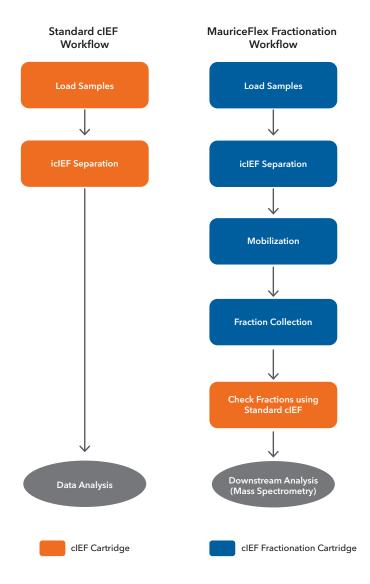
- Received instruction in general safety practices for laboratories.
- Received instruction in specific safety practices for MauriceFlex.
- Received instruction on handling of biohazards (if biohazardous materials are to be used on MauriceFlex).
- Read and understood all Product Inserts and related Safety Data Sheets (SDS).

Power Up

- 1. Turn on the computer connected to MauriceFlex.
- 2. Turn on MauriceFlex's main power switch.
- 3. Wait for MauriceFlex to initialize. His indicator light will turn from magenta to blue when he's done.
- 4. Double-click the Compass for iCE software icon on the computer desktop to open the application.
- 5. Connect MauriceFlex to Compass for iCE.

MauriceFlex Fractionation Workflow

Perform a MauriceFlex Fractionation batch to isolate specific peaks of interest from your Maurice cIEF electropherogram. Then run your fractions using a cIEF batch to confirm the peak identity and purity in your fraction before mass spectrometry analysis.



Comparison of standard cIEF and MauriceFlex Fractionation applications.

Running MauriceFlex Fractionation Applications

What You'll Need

- MauriceFlex cIEF Fractionation Cartridges
- MauriceFlex cIEF Fractionation Method Development Kit (optional)
- Maurice cIEF Fluorescence Calibration Standard
- Maurice cIEF pI Markers (3.38, 4.05, 5.85, 6.14, 7.05, 8.4, 9.50, 9.99, or 10.17)
- 0.5% Methyl Cellulose Solution
- 1% Methyl Cellulose Solution
- iCE Electrolyte Kit
- Deionized (DI) water
- MauriceFlex glass crimp top reagent vials, 2 mL



MauriceFlex glass crimp top reagent vial (PN 110-0019, left) and glass reagent vial (PN 046-017, right) Only MauriceFlex glass crimp top reagent vials (PN 110-0019) should be used to prepare MauriceFlex Fractionation batch reagents.

- Glass vials with insert, 0.3 mL for the Fluorescence Calibration Standard 96-well plate for samples
- P10, P20, P200, P1000 pipettes and tips
- Electrolyte pipette
- Vortexer
- Table-top centrifuge with plate adapter or vial adapter (12 mm, 2 mL vials)

IMPORTANT:

Use MauriceFlex glass crimp top reagent vials, 2 mL (PN 110-0019) and glass vials with insert, 0.3 mL (PN 110-0018) to prepare MauriceFlex Fractionation batch reagents.

Step 1: Prep Your Markers, Samples and Reagents

NOTE: You can prepare your samples in a 96-well plate or vial.

Mobilizer Solution

1. Add 20 µL of 2 M Ammonium Acetate to 8 mL of DI or LC-MS grade water and mix thoroughly.

NOTE: Use LC-MS grade water if fractions will be directly analyzed by mass spectrometry.

2. Store the prepared Mobilizer Solution on ice until ready to dispense in the 96-well plate.

Samples

- 1. In a microcentrifuge tube, prepare your sample at a concentration of 2.5–10 mg/mL in a final volume of 25 μL in DI water.
- 2. In a separate tube, prepare IEF Separation Mix containing your chosen pI marker(s).

NOTES:

Check out the MauriceFlex cIEF Fractionation Method Development Guide for suggested IEF Separation Mix recipes.

If you are running a method optimized for cIEF analysis, increase the concentration of arginine and both pI markers in your IEF Separation Mix. Check out the MauriceFlex cIEF Fractionation Method Development Guide for more information.

- 3. Add 100 μ L of IEF Separation Mix to the 25 μ L of your sample.
- 4. Thoroughly vortex the sample to mix completely.
- 5. Centrifuge the tube at 13,000 xg for 5 minutes to remove air bubbles and sediment any particulates.
- 6. Carefully aspirate the top 100 μL of the sample and pipette it into a well in a 96-well plate by inserting the pipette tip all the way to the bottom to avoid introducing bubbles.
- 7. Pipette 30 µL of Mobilizer Solution (5 mM ammonium acetate) to each fraction well in a 96-well plate as defined by your MauriceFlex Fractionation batch. The number of wells will depend on the number of fractions being collected.
- 8. Spin the plate for 5 minutes at 1000 xg using a centrifuge plate adapter.

NOTES:

If you're preparing sample in a sample vial with insert, 0.2 mL (PN 046-083), increase the sample and IEF Separation Mix volumes in steps 1–3 by 3-fold and transfer a minimum of 300 μ L of sample to the vial.

Make sure to check for and remove any bubbles at the bottom of the well.

pl Markers

- 1. Open the vial of lyophilized pI marker by lifting the center tab and gently pulling it back to break the metal seal. Slowly remove the rubber stopper.
- 2. Add 210 μ L of DI water to the vial.
- 3. Put the rubber stopper back in the vial and vortex 3 times, 5 seconds each time to completely reconstitute the lyophilized cake. Repeat this step for all pI markers you're using.
- 4. Aliquot 20 µL of each reconstituted pI marker into separate tubes for storage.

NOTES:

Keep your reconstituted pI markers on ice until you're ready to add them to your sample or IEF Separation Mix.

If you'll use the pI markers within a month, store the aliquots at 2-8 °C. Otherwise, store the aliquots at -10 °C to -30 °C. They'll be stable up to 6 months.

5. Use 4 μ L of each pI marker for every 200 μ L of sample.

Reagents

IMPORTANT:

Use MauriceFlex crimp top glass reagent vials, 2 mL (PN 110-0019) and glass vials with insert, 0.3 mL (PN 110-0018) to prepare MauriceFlex Fractionation batch reagents. Glass reagent vials, 2 mL (PN 046-017) should only be used when running a standard cIEF or CE-SDS batch.

NOTE: Don't reuse reagents or vials

1. Pipette 350 µL of Fluorescence Calibration Standard in a MauriceFlex glass vial with insert, 3 mL (PN 110-0018) and label.



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2. Pipette 2 mL of 0.5% Methyl Cellulose into a MauriceFlex crimp top glass reagent vial and label.



- 3. Pipette 2 mL of DI water into four MauriceFlex crimp top glass reagent vials. Label the vials.
- 4. Pipette 2 mL of Catholyte solution to a MauriceFlex crimp top glass reagent vial and label.
- 5. Pipette 2 mL of Mobilizer Solution (5 mM ammonium acetate) into two MauriceFlex crimp top glass reagent vials. Label the vials.
- 6. Label an empty MauriceFlex crimp top glass reagent vial.

NOTES:

Make sure you don't overfill the vials, especially the methyl cellulose vial, to avoid introducing bubbles to your run. Wipe excess liquid at the mouth of the vial with a laboratory wipe.

Vials do not need to be capped.

Step 2: Load Samples and Reagents

1. Open MauriceFlex's door by touching the metal plate on top of the door.



NOTE: The indicator light on MauriceFlex's front panel will blink rapidly as the door disengages.

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2. Swing the door open to access the cartridge slot and the reagents and samples platform. The lights on either side of the slot will be **orange**.

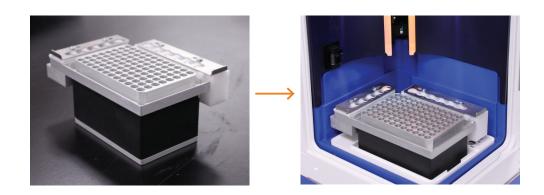


3. Install the fractionation adapter in MauriceFlex.

NOTES:

Remove all the vials in rows P and N of the reagent platform before installing the fractionation adapter if a CE-SDS or standard cIEF application was previously performed.

When installing the fractionation adapter, confirm the adapter is seated and sitting flat in MauriceFlex.



4. Place the reagent vials into their respective positions on the fractionation adapter.

IMPORTANT:

Reagent vials on MauriceFlex must be locked in place before starting a batch. The vial locking mechanism default state is locked. Pull the locking mechanism on Row R to the right and the locking mechanism on Column K down to unlock and place vials in the fractionation adapter. Release the locking mechanism to lock the vials in place.

NOTES:

The reagent row (R) on the fractionation adapter is kept at room temperature. The reagent column (K) and sample plate are temperature controlled.

MauriceFlex Fractionation batch reagents should be prepared in 2 mL crimp top glass vials (PN 110-0019) and glass vials with insert, 0.3 mL (110-0018).

Vials do not need to be capped before placing them on the fractionation adapter.

- **R1** 0.5% Methyl Cellulose
- R2 Fluorescence Calibration Standard
- R3 Water
- R4 Water
- R5 Water
- R6 Empty vial (air)
- K2 Catholyte Solution
- K3 Mobilizer Solution (5 mM Ammonium Acetate)
- K4 Mobilizer Solution (5 mM Ammonium Acetate)
- K5 Water



5. Place your 96-well sample plate on the fractionation adapter. Well A1 should be in the top left corner of the adapter.



Step 3: Prep the cIEF Fractionation Cartridge

NOTE: A cIEF Fractionation Cartridge supports a maximum of 15 injections and a maximum of 15 batches. Its RFID will keep track of how many are left for you.

1. Take the cIEF Fractionation Cartridge out of its packaging. Save the packaging, you'll need it later to store the cartridge.

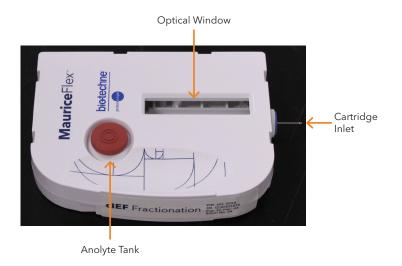
NOTE: When you remove the cartridge from its packaging, make sure the cartridge inlet doesn't come in contact with any surface.



2. Put the cartridge on a flat surface with the electrolyte tank facing up.

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3. Remove the stopper from the Anolyte tank.



4. Add 2 mL Anolyte Solution to the H⁺ electrolyte tank (red port).

NOTE: Make sure you don't overfill the electrolyte tanks.

5. Seal the Anolyte tank with the rubber stopper. If excess liquid comes out of the tank, make sure to wipe it with a laboratory wipe.



Step 4: Install the Cartridge

- 1. Double check to make sure you've got anolyte loaded and the tank is properly sealed with the stoppers.
- 2. Lift the cartridge and hold it vertically using the finger holds on either side, cartridge inlet down, with the cIEF Fractionation label facing you.
- 3. Gently insert it into the slot. You'll feel the alignment groove on the cartridge align inside the slot when you insert it.



4. Continue to slide the cartridge into the slot until the locking mechanism engages. The lights on either side of the slot will change to **blue** once the cartridge is installed correctly.



5. Close the instrument door. MauriceFlex locks it automatically.

Step 5: Check for Cartridge Alerts

- 1. If your cartridge was last used in a run with an error, you will need to perform a Cartridge Purge. The Maurice system will remind you if a Cartridge Purge is required.
 - a. To purge the cartridge, click the brown **Purge** button in the instrument status bar.

Ready	Purge	🛕 Cartridge purge required after a run error

b. Confirm that the required reagents are loaded and that the cartridge is prepped. Then click Start.

🔞 MauriceFlex Cartridge Purge	×
Make sure the vial types and locations match the disp	ay before clicking "Start."
Reagents	ł+
Water Empty	
Cartridge purge counts toward the cartridge batch lin	t.
	Start Cancel

c. Once the purge is done, perform a Cartridge Post-Run Cleanup by clicking on the brown **Cleanup** button that will appear in the instrument status bar. See step 2 for more info.

NOTE: If there's only one batch left on the cartridge, you'll get a message that it can't be used after purging.

2. If you just completed a Cartridge Purge or if the cartridge you're using did not undergo a cartridge post-run cleanup after the last run, you will be asked if you want to perform a Cartridge Post-Run Cleanup.

To start the Post-Run Cleanup:

- a. Remove the cartridge from MauriceFlex and remove the Anolyte from the cartridge. See "Post-batch Procedures" on page 248 for more information.
- b. Confirm there is a vial of Water (P3) and Air (P6) in place.
- c. Click the brown **Cleanup** button in the instrument status bar.

Ready Cleanup	0	Cartridge post-run cleanup recommended or performance cannot be guaranteed
---------------	---	--

d. Click Start Cleanup in the prompt that appears.

Make sure the electrolyte tank is cl display before clicking on "Start."	ean and dry, and the	e vial types and locati	ons match the
Reagents Water Empty	(H. C	
Cartridge post-run cleanup recom	mended or perform	ance cannot be guara	anteed Cancel

NOTE: You can also start a Post-Run Cleanup by selecting **Instrument > Cartridge Post-Run Cleanup**. When you start a Cartridge Post-Run Cleanup from the instrument menu, click **Start** in the prompt that appears to begin the cleanup.

- e. Once the cartridge post-run cleanup is completed, re-prepare the cartridge and install the cartridge in MauriceFlex. See "Step 3: Prep the cIEF Fractionation Cartridge" on page 229 for more information.
- f. Click on the green **Start** button in the instrument status menu to start the batch.

To start the run without a Post-Run Cleanup:

a. Click the brown Cleanup button in the instrument status bar



b. Click Skip Cleanup in the prompt that appears.

Make sure the electrolyte tank match the display before click		d the vial types	and locations
Reagents Water	Empty RS R6	H⁺ O	
Cartridge post-run cleanup re	commended or per	formance cann	ot be guaranteed

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c. Click **Start** in the Start Run window. The run summary and injection report will record that the cartridge did not undergo a post-run cleanup before starting the batch.

Results file r	name :				Brows
2023-02-24	_20-14-29_MauriceFl	ex Fractionation			
Location:	C:\Users\Andrea\Doc	uments\Compass for i	CE\Runs		
Comment:					
	Cartridge				
	Type :	MauriceFlex			
1 m	Expires :	Jan 2025	Injections Remaining :	13	
_	Serial Number :	9900000100	Batches Remaining :	12	
	-				
	Cartridge p	ost-run cleanup recom	mended or performance cannot	be guaranteed	

To start the run with a different cartridge:

- a. If necessary, click Cancel in the cIEF Fractionation Cartridge Post-Run Cleanup window.
- b. Open MauriceFlex's door, remove the first cartridge from MauriceFlex and prepare a second cartridge. See "Step 3: Prep the cIEF Fractionation Cartridge" on page 229 for more information.

Step 6: Create a Batch

- 1. Launch Compass for iCE.
- 2. Select the Batch tab. This is where you'll enter sample/injection information, methods and batch parameters.

File Edit Instru	iment Window Help										
								: 🔤	Batch 🕒 Rur	Summary	Analy
Batch: MauriceFle	x Fractionation	III Injection	ıs 🔛 History	T Notes							-
							Pause	O Stop 🖟	Add 📗 Repli	cate 🔀 Rem	iove 🗉
🗄 Layout	- E	1	Injection Nar	ne Sampl	e ID	Location	Method	١	Votes		
10°C 👻 📑	Fractions 🗲 Add 👻	× 1	Sample 01_0	1 Sampl	e 01	A1	IgG				
Kemove				Fractio	n 01	B1					
s kenove				Fractio	n 02	B2					
	FI Cal Water Water Water Empty			Fractio		B3					
				Fractio		B4					
	R1 R2 R3 R4 R5 R6			Fractio		B5					
	1 2 3 4 5 6 7 8 9 10 11 12			Fractio		B6					
				Fractio		B7					
Sample A				Fractio		B8					
Catholyte				Fractio		B9					
Mobilizer				Fractio		B10					
K3 E	0000000000000			Fractio		B11					
Mobilizer				Fractio		B12					
Water				Fractio		C12					
				Fractio	n 14	C11					
Methods											
										Nev	N Rem
Name	Separation		Detection	Sample Load	Mobilizati	Refocus	Fractions	pl Markers	Ampholyt	Additives	
IqG	10.0 min 500 Volts, 10.0 min 10	000 Volts. 25	1 Exposure	20	25.0 min 1	0.0 min 1	45.0 sec 1	7.05, 10.17			
-											

- 3. To create a batch, make sure MauriceFlex is connected to Compass for iCE. Select Instrument and click Connect.
 - a. If your instrument is listed, select your MauriceFlex system and click Connect.
 - b. If your instrument isn't listed, click on the Settings button and connect by typing in your instrument IP address.

	Serial Num		

To create a new batch:

• In the main menu, select File > New Batch > MauriceFlex Fractionation

File	Edit Instr	rument	Window	Help	
	New Batch			>	Maurice cIEF
	Open Batch	1		>	Maurice CE-SDS PLUS
	Save		Ctrl+S		Maurice Turbo CE-SDS™
	Save As		Curro		MauriceFlex cIEF
	Save As				MauriceFlex Fractionation
	Export Inject	tions			

To use an existing batch: In the main menu, select File > Open Batch.

NOTE: If you're making changes to an existing batch, follow the steps in this section. Otherwise skip to "Step 7: Start the Batch" on page 244.

ile	Edit Instrument	Window Help		
	New Batch	>		
	Open Batch	>	MauriceFlex Fractionation 20221223	
	Save	Ctrl+S	Maurice FLEX cIEF batch 20221214	
	Save As	caro	Maurice_CE-SDS_TURBO_Reduced Maurice CE-SDS PLUS	
	Export Injections		Maurice FLEX cIEF batch 20221218	
	Import Injections			
	Export Methods		Browse	Ctrl+0

4. Add your sample:

To import a sample using a saved injection file:

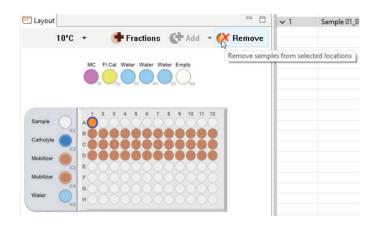
a. Select File in the main menu and click Import Injections.

b. Select an injection .csv file and click OK. The imported information will display in the Injections pane.

NOTE: For more information on setting up an injections file for import, see "Importing and Exporting an Injection" on page 214.

To change the sample location manually:

a. In the Layout pane, highlight well A1 and click **Remove**. The sample will also be removed from the Injections table. You can also right-click on the well and click **Remove Sample**.

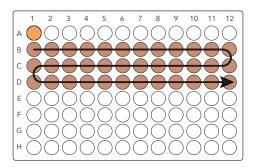


b. Use your mouse to highlight the well your sample is located in or position K1, then click **Add**. The Injections table will automatically update.

🖭 Layout		🖭 Layout	
10°C Fractions	C Remove	10°C ▼ 📑	Fractions C Add V C Remove
	Add samples in selected locations		Add samples in selected locations
MC FI Cal Wate	Water Water Empty		C FI Cal Water Water Water Empty
Sample Catholyte Mobilizer Water Katholyte K		Sample Original Catholyte Origin	

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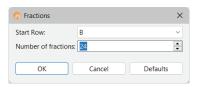
5. Assign fraction collection locations. Fraction collection starts in column 1 of the Start Row and will be collected in a serpentine pattern.



- a. In the Layout pane, click Fractions.
- b. A prompt will appear. In the Start Row pulldown, select the row to start collecting fractions.



c. In the **Number of fractions** field, type the number of fractions to collect or use the arrows to increase or decrease the number of fractions.



NOTE: The number entered will be highlighted in red if it is below the minimum (24) or higher than the available wells on the plate based on where you start collecting fractions.

- d. Click **Defaults** to reset fields to default settings.
- e. Click OK. The plate map in the Layout pane and the Injections list will automatically update.

6. The fractionation adapter is temperature controlled with a default setting of 10 °C. To change the temperature or turn it off, click the **down arrow** next to the temperature and select an option.

NOTE: The reagent row (R) is kept at room temperature. The reagent column (K) and sample plate are temperature controlled.



7. Enter your method parameters in the Methods pane.

NOTE: We recommend using the default method parameters. Please see the MauriceFlex cIEF Fractionation Method Development Guide for more information on method optimization.

To import a saved method:

- a. Select File in the main menu and click Import Method.
- b. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

To create a new method or make changes to an existing one:

a. Click the first cell in the Name column and enter a method name.

Method	s										
	New F										
Name	Separation	Detection	Sample Load	Mobilizati	Refocus	Fractions	pl Markers	Ampholyt	Additives		
lgG	10.0 min 500 Volts, 1	1 Exposure	20	25.0 min 1	0.0 min 150	45.0 sec 1	7.05, 10.17				

b. Click the first cell in the Separation column, then click the selection button [...] to set the pre-focusing and focusing time (in minutes) and voltage (V). You can also set the Detection Interval (in minutes) and Exposure (in seconds) to adjust how often an image is taken using the listed Exposure time.

			Add	Remove
Vame	Separation		Time (min)	Voltage (Volts)
			 10.0	500
lgG	Voltage 3 Steps		10.0	1000
		Lsi	25.0	1500
			Detection Interval (min)	5.0
			Exposure (sec)	0.2

- c. The Detection Profile exposure setting is linked to and defined by the Separation step and cannot be changed.
- d. Click the first cell in the Sample Load(s) column and set the load time in seconds.

Name	Separation	Detection	Sample Load (s)
lgG	10.0 min 500 Volts, 1	1 Exposure	20

e. Click the first cell in the Mobilization column, then click the selection button [...] to set the mobilization time (in minutes) and voltage. You can also set the Detection Interval (in minutes) and Exposure (in seconds) to adjust how often an image is taken using the listed Exposure time.

Methods						or Mobilization Profile		
Name	Separation	Detection	Sample Load	Mobilization		Time (min)	Voltage (Volts)	
lgG	10.0 min 500 Volts,	1 Exposure	20	25.0 min 1000 Vo	\longrightarrow			
				6				
						Detection Interval (min)	10	
						Exposure (sec)	0.2	
						ОК	Cance	

f. Optional: Click on the first cell on the Refocus column, then click the selection button [...] to set the refocusing time (in minutes) and voltage.

NOTES:

The Compass for iCE fraction peak predictor is available but not applicable if a refocusing step is added to the method. A warning will disply in the refocus profile and Start Run window and will be recorded in the run summary when then time parameter is changed.

Refer to the MauriceFlex cIEF Fractionation Method Development Guide for refocusing times and voltage setting tips.

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g. Click the first cell in the pI Markers column to select pI markers. Add new markers or remove existing ones then click **OK**.

ame	Separation	Detection	Sample Load	Mobilizati	Refocus	Fractions	pl Markers		Add	Remove
G	10.0 min 500 Volts, 10	1 Exposure	20	25.0 min 1	0.0 min 1	45.0 sec 1	7.05, 10.17	\longrightarrow	pl Markers:	
									pl	Position
									7.05	300
									10.17	1,900
									-	

h. Optional: Click the first cell in the Ampholytes column and enter the ampholytes you're using.

Methods								
Name	Separation	Detection	Sample Load			Fractions	pl Markers	
IgG	10.0 min 500 Volts	1 Exposure	20	25.0 min 1	0.0 min 1	45.0 sec 1	7.05, 10.17	Pharmalyte 3-10

i. Optional: Click the first cell in the Additives column and enter any additives you're using.

Methods										
									New Re	mov
Name	Separation	Detection	Sample Load	Mobilizati	Refocus	Fractions	pl Markers	Ampholytes	Additives	
lgG	10.0 min 500 Volts, 10.0	1 Exposure	20	25.0 min 1	0.0 min 1	45.0 sec 1	7.05, 10.17	Pharmalyte 3-10	Urea	

8. You can now:

- Make updates to the remaining methods by repeating the prior steps.
- Select a method and click Remove in the upper right corner of the Methods pane to delete it.
- Click **New** in the upper right corner of the Methods pane to add a new one if you want to use different methods for different samples. Then just repeat the steps above for the new method.

9. In the Injections pane:

• To change the sample name: Click the Sample ID cell and type a name.

NOTES:

The Sample ID can be copied from other documents and pasted into Compass for iCE to make batch setup faster. Check out "Copying and Pasting an Injection Name or Sample ID from other Documents" on page 213 for more info.

If you change the sample ID when the default injection name is still being used, the injection name will automatically update to match the sample ID. If you've already changed the injection name manually, updating the sample ID will not update the injection name.

			🕕 Pause 🤇	Stop 🖟 Add 📗 R	leplicate 🛛 🔀 Remove	Ŧ
	Injection Name	Sample ID	Location	Method	Notes	
× 1	Sample 01_01	Sample 01	A1	lgG		
		Fraction 01	B1			
		Fraction 02	B2			
		Fraction 03	B3			

• To change the injection name: Click the Injection Name cell and type a name.

NOTES:

The injection name must be unique.

Changing the injection name won't affect the sample ID.

Inject	ions 🔚 History 🌃 Not	tes				- 6
			🕕 Pause 🤇	Stop 🖟 Add 📗 F	Replicate 🛛 🔀 Remove	Ð
	Injection Name	Sample ID	Location	Method	Notes	
∨ 1	Sample 01_01	Sample 01	A1	IgG		
		Fraction 01	B1			
		Fraction 02	B2			

• To assign a methods for the injection: Click the Method cell and select a method from the drop down menu.

Inject	ions 🔚 History 🎩 Not	ies				- 0
			🕕 Pause 🤇	Stop 🖟 Add 📗	Replicate 🔀 Remov	e 🕀 🖻
	Injection Name	Sample ID	Location	Method	Notes	
× 1	Sample 01_01	Sample 01	A1	IgG		
		Fraction 01	B1	lgG		
		Fraction 02	B2	Method2		
		Fraction 03	B3	l	v	

Add a programmed pause or stop in the batch to automatically pause or stop after fractions have been collected (optional).

• **To program a pause:** Highlight the injection and click **Pause**. The batch will pause after fractions for that injection have been collected. To resume the batch, click **Continue** in the instrument status bar.

				🛛 Pause 🖸 Stop 👫 Add 📗 Replicate 🔀	Remove 🕀
	Injection Name	Sample ID	Location	Method Pause after the selected injection	
> 1	Sample 01_01	Sample 01	A1	lgG	
Injec	tions 🔚 History 耳	Notes			
Injec	tions 🔚 History 🎵	Notes		🛛 Pause 🗿 Stop 🏕 Add 📗 Replicate 🗱	
Injec	tions 🔚 History T	Notes Sample ID	Location	O Pause O Stop II Add III Replicate IX Method Notes	
Injec			Location A1		

• **To program a stop:** Highlight the injection and click **Stop**. MauriceFlex will continue the batch through fraction collection, then stop the batch and perform end-run cleanup steps.

Injec	tions 🔚 History 耳	Notes							- 6
				Pause	Stop	🖟 Add	📗 Replicate	🔀 Remove	Ŧ
	Injection Name	Sample ID	Location	Method	Sto	p after t	he selected in	jection	
1	Sample 01_01	Sample 01	A1	lgG	_				
Injec	tions 🔚 History 🕇	Notes							- [
Injec	tions 🔚 History 🎵	Notes		Pause	O Stop	🚰 Add	Replicate	Remove	
Injec	tions 🔚 History T	Notes Sample ID	Location	Pause Method	• Stop		Replicate	Remove	
-			Location A1		O Stop			Remove	
Injec	Injection Name	Sample ID		Method	O Stop			k Remove	

10. Click on the Notes pane, then click in the notes area and type any information you want to add about your batch (optional).



- 11. You can preset the parameters used to analyze data generated with the batch (optional). We recommend using the default parameters for MauriceFlex Fractionation applications, but if you want to modify parameters:
 - a. Select Edit from the main menu and click Default Analysis. The following screen will display:

o Default Analysis: Maurice	Flex Fractionation		×
Detection Peak Names Peak Fit Advanced pl Markers	Detection		
pr maneco	IgG Exposure 1 0.2 seconds ~		
Import Exp	ort OK Cancel	Apply	

- b. Change the parameters you want to, then click **OK**. For detailed information on analysis parameters, please refer to "Analysis Settings Overview" on page 620.
- 12. You can preset the parameters used to display the electropherogram data when the batch is complete. Default Analysis View Parameters must be set before you start the batch and cannot be modified once the batch starts. However, you can still manually change parameters in the Analysis pane using the Graph Options button:Select Edit from the main menu and click Default Analysis View. The following screen will display:

o Default Analysis View Maur	iceFlex Fractionation	-		×
Graph View Options	Graph View Options Graph View Options Matching Peak Names Peak Names Peak Values Fitted Peaks Baseline Fit Grid Lines Plot Label Sample Method Injection Exposure Injection Name			×
	ОК	Cancel	Apply	y

- a. Change the parameters you want to, then click **OK**. For detailed information on graph view options, please refer to "Customizing the Data Display" on page 603.
- 13. Once all of your sample, method and injection info is entered, select File > Save. Enter any comments on the batch if you want, then click Save.

🕼 Save Batch Comment	×
Batch: MauriceFlex Fractionation 20221223 Comment:	
Save	Cancel

14. Enter a name for your batch then click Save.

Step 7: Start the Batch

- 1. Make sure MauriceFlex is connected to Compass for iCE. If he isn't, select **Instrument** and click **Connect**. Then select your MauriceFlex system and click **Connect**.
- 2. Click on the green Start button to start your batch.

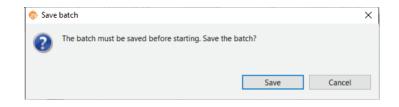
NOTES:

An alert may appear if the wrong cartridge is installed or if a cartridge post-run cleanup or cartridge purge is recommended. See "Step 5: Check for Cartridge Alerts" on page 232 for more information.

An alert may appear if you are starting a MauriceFlex Fractionation batch and have not installed the fractionation adapter. See "Adapter and Insert Alerts" on page 403 for more information.



3. If you have made any changes, you will be asked to save your batch before starting the run. Click **Save**.



- 4. The Start Run box shows you the number of injections and batches remaining on your cartridge. Make sure you still have enough injections left before you start the run. If not, prep a new cartridge.
- 5. Click in the Results File name box if you want to change the default run file name. Otherwise just leave it as is.

😨 Start Run						×
Batch: Mauric	eFlex Fractionatio	on				
Results file nan	ne:					Browse
2023-02-24_21	-34-46_MauriceFle	x Fractionation				
Location: C:\	Users\Andrea\Doc	uments\Compass for	iCE\Runs			
Comment:						
	Catila					
	Cartridge					
1.00		MauriceFlex				
17 Mar.	Expires :		Injections Remaining :			
_	Serial Number :	9900000100	Batches Remaining :	12		
				Star	t	Cancel

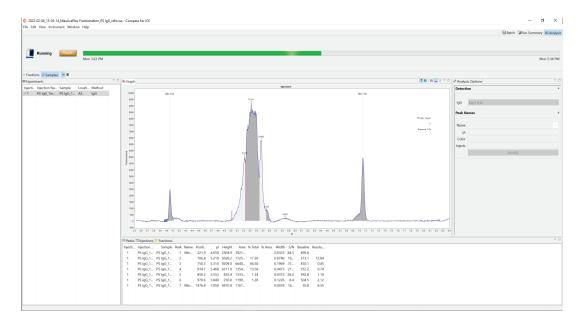
- 6. If you don't want to save the file to the default Runs folder, click Browse to select a different location.
- 7. Enter any run details you'd like in the Comments box (optional).
- 8. Click Start to start the run.

NOTE: The indicator light on MauriceFlex's front panel will pulse slowly while he's running the batch.

To monitor the progress of your batch, click the **Run Summary** tab. See Chapter 16: "Run Status" for more details.

e Edit Instrumen	-14_MauriceFlex Fit Window Help					
						Batch 'Likun Summary' 《Anal
Running	Pause	Mon 3:22 PM				Mos 5371
n: 2023-02-06_15	-05-14_MauriceFle	Fractionation	PS IgG_refocus			
njections						C 0 Status History
	Sample ID Loca	i Method	Status Ti	me	Sample T	run 2023/03/03_19/48-57_2023/03/03_15/05-14_Maurice IgG
		Setup	Complet			path
1 201-01	PS lgG_1 A3	Calibration	Complet Separating	Af union	_	batch 2023-03-03_15-05-14_Maurice IgG
· P3 Ig0_1	13 Igu_1 A3	Fractiona.	-paraong	47 880		batch type cIEF Fractionation
		Cleanup				instrument MauriceFlex : Maurice Flex xt1109 - xt1109
						samples 96-well plate
						started Fri 7:50 PM Mar 3, 2023 PST
						cartridge MauricoFlex
						serial number 990000100
						injections per batch 4
						injections remaining 12
						batches remaining 10
						expires Jan 2025
						# Focus Series 8: W Plot
						Zoom
						Name in the second se
						x.007
						8.000
						± 2000
						2 A000
						1009
						2.000
						1.000
						a a 100 200 800 400 900 800 900 800 900 100 100 100 100 100 100 100 100 1
						Peel
						e

To view results, analyze results or change analysis parameters on completed injections while the batch is still running, click the **Analysis** tab. See Chapter 19: "MauriceFlex Fractionation Data Analysis" for more details.



When your batch is complete, you can view electropherograms for the sample injection and mobilization in the Analysis tab, and all batch and injection details in the Run Summary tab.

NOTE: If you'd like MauriceFlex to let you know when your run is done, you can set him up to tweet you. Go to "Setting Up Maurice Systems to Send Tweets" on page 764 for more info.

Editing a Running Batch

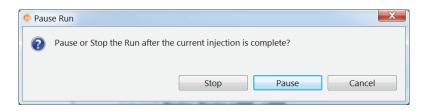
You can pause a batch after it's started to make updates or add samples and reagents.

1. Select **Instrument** > **Pause** or select the **Pause** button.



NOTE: MauriceFlex can only be paused during a run after the calibration step or after the injection has completed.

2. Click Pause in the pop-up window.



The Pause button will change to Continue but MauriceFlex's status will stay at Running until Compass for iCE completes the current injection.



- You can now make these edits to the batch:
 - Change the Sample Name
 - Change the Injection Name
 - Modify the injection if it isn't greyed out
 - Create a new method
 - Update the method.
- 3. When MauriceFlex completes the current injection, his status will change to Paused and the progress bar will turn yellow.

NOTE: MauriceFlex's status light will change from a pulsing blue to a blue pulse with magenta flashes which means he's paused the run.



The status in the Injection pane also changes to Paused and the pause duration updates live. You can now open the instrument door.

IMPORTANT

The door must be closed within 15 minutes of opening it to avoid potential assay performance issues.

NOTE: If the door is open for more than 30 seconds, a white light near the cartridge will start to flash and a warning message displays in Compass for iCE until the door is closed.

4. To continue the batch, click **Continue**. Changes you made to the batch are saved and MauriceFlex will continue with the batch.

Post-batch Procedures

When the batch is done:

- 1. Open MauriceFlex's door. The lights on either side of the cartridge slot will be **orange** as MauriceFlex will have already disengaged the cartridge.
- 2. Remove and save the 96-well plate. Collected fractions will be used to for further analysis.

IMPORTANT:

We recommend that you seal the plate to prevent evaporation if the fractions will not be used immediately.

NOTE: Check out the MauriceFlex cIEF Fractionation Method Development guide for more info on how confirm the identity and purity of peaks collected in your fractions using a Maurice cIEF batch.

3. If the sample was prepared in a vial, remove your sample. Leave the Water (P3) and Air (P6) vials in place if your cartridge still has injections left since they will be needed for the post-run cleanup step. Remove the remaining reagent vials.

NOTE: You can remove reagent vials from the MauriceFlex fractionation adapter when the locking mechanism is pulled to the right (row R) or pulled down (column K). Release the mechanism to lock remaining vials in place before starting the Post-Run Cleanup.

4. Gently pull out the cartridge making sure the cartridge inlet doesn't come into contact with any surface.



If you're at 15 injections, you've reached the limit of supported injections for the cartridge. To dispose of a finished cartridge, put it in its original packing and discard it per your institution's safety and waste disposal guidelines. Discard any remaining reagent vials.

NOTE: Disposal of cartridges, sample plates and vials depends on the samples you ran. If you aren't sure what your sample origins are, we recommend you dispose of everything in biohazard waste.

If the cartridge will be used again, clean up and store the cartridge:

- a. Put the cartridge on a flat surface with its electrolyte tank facing up.
- b. Remove the stoppers from the Anolyte tank.
- c. Using an electrolyte pipette or low vacuum, aspirate the solutions from the tank.
- d. Fill the tank with 3 mL DI water, then aspirate it out. Repeat this rinse 2 more times.

NOTE: Make sure not to get any liquid on the cartridge's optical window.



- e. Aspirate all the remaining liquid and make sure that the tank is dry.
- f. Put the stopper back on the tank and install the cartridge in MauriceFlex.
- g. Verify there is at least 2 mL of DI water in the Water (P3) vial and air in the empty (P6) vial.
- h. Click on the brown **Cleanup** button in the Instrument Status Bar or select **Instrument** and **Cartridge Post-Run Cleanup** in the Compass main menu.

	Instrument Window Help
	Start
	Cartridge Post-Run Cleanup
	Cartridge Purge
Ready Cleanup	Self Test >
	Runs
	Properties
	Update >
	Disconnect

i. You'll get the following message. Click Start. It'll only take 6 minutes.

😨 Flex Cartridge Post-Run Cleanup	×
Make sure the electrolyte tank is clean and dry, and the vial types and locations match the display before clicking on "Start."	
Reagents Water Empty Bib Diz Diz Diz Dia Dis Dis	
Cartridge post-run cleanup recommended or performance cannot be guaranteed Start Cancel	

- j. Open MauriceFlex's door. Gently pull out the cartridge making sure the cartridge inlet doesn't come in contact with any surface.
- k. Remove the reagent vials.
- 1. Leave the stopper off to allow the tank to air dry.

m. Put the cartridge and stopper back in the protective packaging and store at room temperature.

!WARNING! SHARPS HAZARD

The capillary inlet of the cartridge may present a potential sharps hazard. Dispose of used cartridges according to your organizations health and safety regulations.



!WARNING! BIOHAZARD

Cartridges, sample plates and vials should be handled by procedures recommended in the CDC/NIH manual: Biosafety in Microbiological and Biomedical Laboratories (BMBL). The manual is available from the U.S. Government Printing Office or online at http://www.cdc.gov/biosafety/publications/bmbl5/.

Depending on the samples used, the cartridges, plates and vials may constitute a chemical or a biohazard. Dispose of the cartridges, plates and vials in accordance with good laboratory practices and local, state/ provincial, or national environmental and health regulations. Read and understand the Safety Data Sheets (SDSs) provided by the manufacturers of the chemicals in the waste content before you store, handle, or dispose of chemical waste.

Checking Your Data

Compass for iCE detects your sample protein, fraction and pI marker peaks and reports results automatically. But, we always recommend you review your data using the steps in this section as a good general practice to make sure your results are accurate. If you see a data warning in the Experiment pane, these steps will also help you identify and correct any issues.

Check your data in the Analysis screen.

- When you select Fractions in the View bar, you'll see:
 - The focused injected sample (I1) where you can make sure the pI markers for your sample are identified correctly.
 - Mobilization electropherograms (T0, T1, T2, etc) that show the sample moving off of the capillary- where you can confirm all the peaks in the mobilization electropherograms are correctly identified.
- When you select Samples in the view bar, you'll see:
 - The focused, injection sample (I1) where you can make sure peaks in your sample injection are identified correctly and where you can name the peaks. Named peaks will automatically be updated in the mobilzation electropherogram in the Fractions view bar.

Step 1: Check the pI Markers for the Injected Sample

To make sure your pI markers are identified correctly:

- 1. Go to the Analysis screen.
- 2. Click Fractions in the View bar.

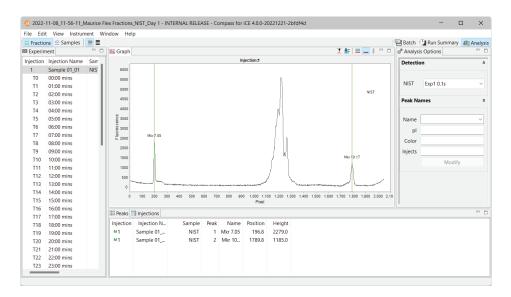
File	Edit	View	Instrument	W	Window	
±	Fracti	ons	🚖 Samples	1	=	Ξ

3. Click the View Selected icon in the View bar.



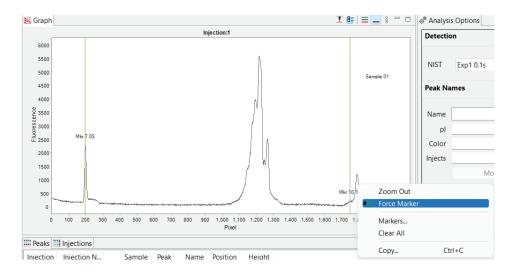
4. Click Injection 1 in the Experiment pane.

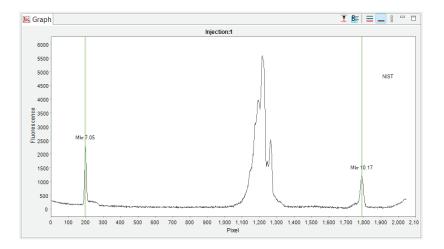
5. Check that your pI markers in the electropherogram have been correctly identified. Each marker peak will have a green vertical line running through it and be labeled Mkr. They're also identified with an M in the Peaks table.



6. If your pI markers aren't identified correctly, here's how to manually correct them:

To set an unidentified peak as a pI marker: Right-click the peak in the electropherogram or Peaks table and select **Force Marker**. Compass will assign that peak as a pI marker, and correctly reassign the remaining pI marker peaks.



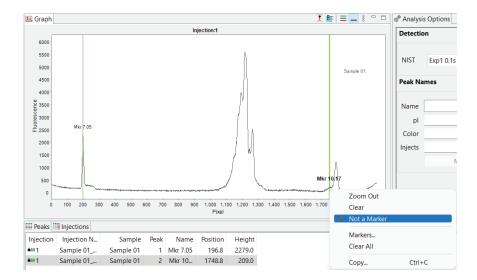


A lock icon indicating the pI marker was set manually will display next to the peak in the Peaks table and a check mark will appear next to the injection in the Experiment pane to show a manual correction was made.

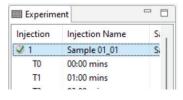


NOTE: To remove pI marker peak assignments that were made manually, right click on the peak in the electropherogram or Peaks table and click **Clear**. To clear all the manual settings for the injection, click **Clear** All.

If an incorrect peak is identified as a pI marker: Right-click the peak in the electropherogram or Peaks table and select Not a Marker. Compass should correctly reassign the remaining peaks as pI markers and update the Peaks table.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.



Step 2: Checking Sample Peaks

All detected peaks in your injected sample will be labeled automatically with the calculated protein pI.

NOTE: The reported protein pI in Compass may vary slightly from predicted pIs based on sample, buffer, and method conditions.

To make sure peaks in your sample injection are identified correctly:

1. Click **Samples** in the View bar.

File	Edit	View	Instrument	W	/indo	w
: 🗮 I	racti	ons	🚖 Samples		=	≣

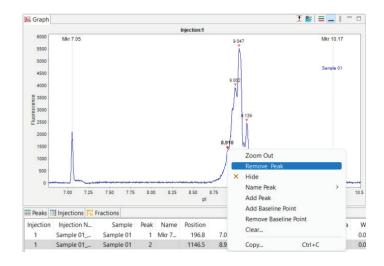
2. Click the View Selected icon in the View bar.

File	Edit	View	Instrument	Window
ヨ	Fracti	ons	${\simeq}$ Samples	
				1

3. Click Injection 1 in the Experiment pane.

4. If your sample peaks aren't identified correctly, here's how to manually correct them:

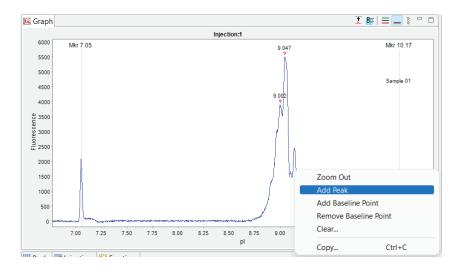
If a peak is incorrectly identified as a sample peak: Right-click the peak in the electropherogram or Peaks table and select **Remove Peak**. Compass will no longer identify it as a sample peak in the electropherogram and the peak data will be removed in the results table.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

Injection	Injection Name	Samp
√1	Sample 01_01	Samp

To identify a peak as a sample peak: Right-click the peak in the electropherogram or Peaks table and select Add Peak. Compass will calculate and display the results for the peak in the results table and identify the peak in the electropherogram.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

💷 Experim	ent	
Injection	Injection Name	Samp
√1	Sample 01_01	Samp

NOTE: To remove sample peak assignments that were made manually and go back to the original peak data, right-click the peak in the electropherogram and select **Clear**.

5. Repeat the previous steps to make sure all sample peaks are correctly identified.

Step 3: Assigning Sample Peak Names

Compass can also optionally identify and name sample peaks in the focused injection sample using user-specified peak name settings. For more information on how to do this, see "Manual Peak Integration" on page 637.

Step 4: Checking Peaks in the Mobilization Electropherograms

All detected peaks in the mobilization electropherograms will be labeled automatically with either the pixel position or peak name as defined in Peak Names.

To make sure peaks in the mobilization electropherograms are identified correctly:

1. Click **Fractions** in the View bar.



2. Click the View Selected icon in the View bar.

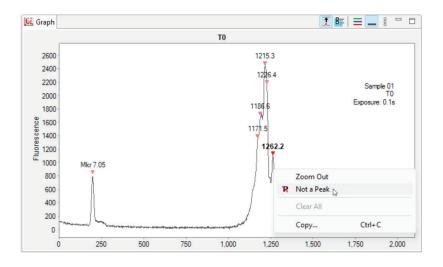
File	Edit	View	Instrument	Window
曲	Fracti	ons	🚖 Samples	
				$\mathbf{\Lambda}$

3. Click T0 in the Experiment pane.

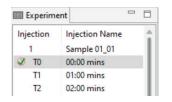
🚊 Fraction	s 🚖 Samples 🛛 🚍	
Experime	ent	- 6
Injection	Injection Name	Sam
1	Sample 01_01	Samj
TO	00:00 mins	
T1	01:00 mins	
T2	02:00 mins	

4. If the peaks aren't identified correctly, here's how to manually correct them:

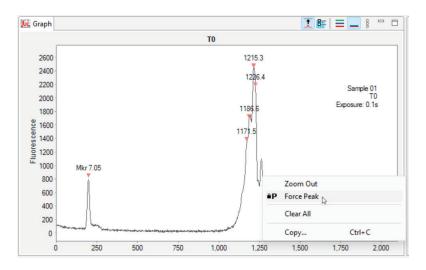
If a peak is incorrectly identified: Right-click the peak in the electropherogram or Peaks table and select **Not a Peak**. Compass will no longer identify it as a peak in the mobilization electropherogram and the peak data will be removed in the results table.



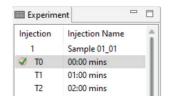
A check mark will appear next to the mobilization electropherogram in the Experiment pane to indicate a manual correction was made.



To identify a peak: Right-click the peak in the electropherogram and select **Force Peak**. Compass will calculate and display the results for the peak in the results table and identify the peak in the electropherogram.



A check mark will appear next to the mobilization electropherogram in the Experiment pane to indicate a manual correction was made.



NOTE: To remove sample peak assignments that were made manually and go back to the original peak data, right-click the peak in the electropherogram and select **Clear**.

5. Repeat the previous steps to make sure all peaks are correctly identified.

Step 5: Assigning Peak Names in the Mobilization Electropherograms

Existing peak names assigned to the focused injection sample are automatically updated in the mobilization electropherogram and can be manually adjusted. For more information on how to do this, see page 601.

Chapter 11: CE-SDS PLUS Batches

Chapter Overview

- Overview
- Batch Screen Overview
- Opening a Batch
- Creating a New Batch
- Viewing Replicate Injections
- Batch History
- Making Changes to a Batch
- Viewing and Editing Batches in Completed Runs
- Copying and Pasting Injection Names or Sample IDs from other Documents
- Importing and Exporting Injections
- Importing and Exporting Methods
- Batch Reports

Overview

Maurice CE-SDS PLUS batches can be run on Maurice, Maurice S., or MauriceFlex systems using a CE-SDS PLUS cartridge.

Batch Screen Overview

You can use the Batch screen to create, view, and edit batches. To get to this screen, click the Batch screen tab:

Batch 🖓 Run Summary 🏥 Analysis

Batch Screen Panes

The Batch screen has five panes:

- Layout Displays a map of either the 96-well plate or 48-vial tray of batch sample locations.
- **Injections** Lists the injections, sample ID, sample locations and methods that Maurice or Maurice S. will execute for each sample in the batch.
- History Lists all batch file events from initial creation to the most current update.
- Notes Lets you enter specific information about your batch.
- Methods Lets you create methods and enter method parameters used in the batch.

							💾 Batch 🔮 Run Sum	-
Batch: Maurice Cl	E-SDS PLUS	Inject	ions 🔚 History 🌃 Notes			D = 1		
Layout			1 6 6 7 6 1991				🕽 Stop 🔮 Add 📗 Replicate	🕅 Remove 🔳
			Injection Name	Sample ID	Location		Notes	
🗐 🗓 10°C	- Ct Add - Ct Remove	1	IgG System Control_01		A1	Method 1		
c	1 C2 Water Sep. Wash Empty	2	Control Ladder_02	Sample 02	A2	Method 2		
6		3	Test Ladder_03	Sample 03	A3	Method 2		
Wah Wah A 2 3 4 5 5 7 8 B 2 2 3 4 5 5 7 8 C D C D E		4	IS - Alpha_04	Sample 04	B1	Method 1		
		5	IS - Alpha_05	Sample 08	B2	Method 2		
		6	IS - Beta_06	Sample 05	B3	Method 1		
		7	IS - Beta_07	Sample 06	B4	Method 2		
		8	IS - Gamma_08	Sample 07	B5	Method 1		
		9	IS - Gamma_09	Sample 09	B6	Method 2		
		10	IgG System Control_10	Sample 01	A1	Method 1		
		11	Control Ladder_11	Sample 02	A2	Method 2		
		12	Test Ladder_12	Sample 03	A3	Method 2		
		13	IS - Alpha_13	Sample 04	B1	Method 1		
FUL		14	IS - Alpha_14	Sample 08	B2	Method 2		
		15	IS - Beta_15	Sample 05	B3	Method 1		
Methods								
Wiethous								New Remov
Name	Sample Load		Separation					New Remo
Method 1	20 sec 4600 Volts		0.1 min 1150 Volts, 0.1 mir	2450 Volte 25.0				
Method 2	20 sec 4600 Volts		0.1 min 1150 Volts, 0.1 min					
Wethou 2	20 Sec 4000 Volts		0.11111111130 voits, 0.11111	1 3430 VOILS, 30.0				

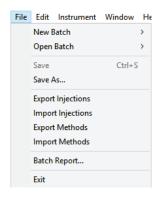
Software Menus Active in the Batch Screen

These main menu items are active in the Batch screen:

- File
- Edit
- Instrument (when the software is connected to Maurice, Maurice S. or MauriceFlex)
- Window
- Help

File Menu

These File menu options are active:



- New Batch Creates a new batch from a starter template.
- Open Batch Opens an existing batch.
- Save/Save As Saves the open batch.
- Export Injections Exports injections from the current batch as a .csv file.
- Import Injections Imports injections into the current batch from a .csv file.
- Export Methods Exports method(s) from the current batch as separate files.
- Import Methods Imports saved method(s) into the current batch.
- Batch Report Exports a table of sample and method details for each injection in the batch as a PDF file.
- Exit Closes Compass for iCE.

Edit Menu

The following Edit menu options are active in the Batch screen:

Edit] Instrument Windo	w Help	_	
	Cut	Ctrl+X		
	Сору	Ctrl+C		(,
	Paste	Ctrl+V		In
	Plate Layout	•	•	48 Vials
	Default Analysis			96-well Plate
	Preferences			Air

- Cut Cuts the information currently selected.
- Copy Copies the information currently selected.
- **Paste** Pastes the copied information.

NOTE: Cut, Copy and Paste work differently depending on the pane you're in. How and when you can use them is described throughout the chapter.

- Plate Layout Lets you select between a 96-well plate or a 48-vial tray to run samples in.
- Default Analysis Displays the default settings that will be used to analyze the data generated with your batch.
- **Default Analysis View** Displays the default settings that will used to view the data generated with your batch.
- **Preferences** Lets you set and save your preferences for Access Control, data export, graph colors, grouped data and Twitter settings. See Chapter 21, "Setting Your Preferences" for more information.

Opening a Batch

To open an existing batch:

1. Select File in the main menu and click Open Batch.

File	Edit Instrument	Wir	ndow Help
	New Batch	•	
	Open Batch	×	Platform CE-SDS2
	Save		Platform CE-SDS1
	Save As		Maurice CE-SDS3
			Maurice CE-SDS2
	Batch Report		Maurice CE-SDS1
	Exit		Browse

- 2. A list of the last five batches opened will display based on the last location found. If the location of the file has changed, you may need to navigate to find the file. Select one of those or click **Browse** to open the Batches folder and select a different one.
- 3. To make changes to the batch, see the steps in "Creating a New Batch". When you're done, select File from the main menu and click **Save**.

Creating a New Batch

To create a new batch, we recommend that you use one of the template methods and make any necessary modifications from there.

Step 1 - Open a Template Batch

1. Select File in the main menu and click New Batch:

ile Edit Instrur	ment Window Help)
New Batch	>	Maurice cIEF
Open Batch	>	Maurice CE-SDS PLUS
Save	Ctrl+S	Maurice Turbo CE-SDS™
Save As	Currs	MauriceFlex clEF
Save As		MauriceFlex Fractionation
Export Injecti	ons	

NOTE: Only template batches specific to your Maurice will be available when you are connected to the instrument. Template batches will not appear in the menu if that application type cannot be performed on your instrument.

2. Select Maurice CE-SDS PLUS. A batch using the default method will display.

							Batch 🕒 Run Summary 🏭 Analy
Batch: Maurice CE-SDS	PLUS	Injections	🔚 History 🚺 Notes		0	Pause 🖸 Stop 😫 Add	d 📗 Replicate 🕌 Remove 📑 🖻 🗖
	- 0	1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method Reduced IgG	Notes
10°C	• C Add • C Remove						
() Was	C2 Valuer Sep. Wash Empty Image: Separation of the separation of						
E C C C C C C C C C C C C C C C C C C C							
E F G G G G G G G G G G G G G G G G G G							
E F							
	Sample Load 20 see 4600 Volts		Separation 25.0 min 5750 Volts				New Ram

Step 2 - Assign Your Samples

The Layout pane shows the default locations of where batch reagent should be placed in your Maurice system's samples and reagents platform, and a map of either the 96-well plate or the 48-vial tray used for samples.

CH Add - C Remove

I Layout	Layout
3 00 10°C ▼ C Add ▼ C Remove	🗐 🥅 10°C 🔻
C1 C2 Water Sep. Wash Empty C1 C2 Water Sep. C1 C2 W	C1 C2
1 2 3 4 5 6 7 8 A 2 3 4 5 6 7 8 B 2 3 4 5 6 7 8 C 2 3 4 5 6 7 8 C 3 4 5 6 7 8 D 3 4 5 6 7 8 F 3 4 5 6 7 8 F 3 4 5 6 7 8	1 2 3 4 6 B 0 0 0 0 C 0 0 0 0 E 0 0 0 0 F 0 0 0 0 H 0 0 0 0

The same reagent locations are used for every batch:

- P1 Conditioning Solution 1 with orange pressure cap
- P2 Conditioning Solution 2 with orange pressure cap
- **P3** DI water with orange pressure cap
- P4 Separation Matrix with orange pressure cap
- P5 Wash Solution vial with orange pressure cap
- **P6** Empty vial (air) with orange pressure cap
- N1 Wash Solution vial with clear screw cap
- N2 Wash Solution vial with clear screw cap
- N4 Running Buffer Bottom with clear screw cap
- 1. To assign samples, select a 96-well plate or 48 vials depending on what you're running. Clicking on the vial/plate icon toggles between formats.



2. Select your samples:

To import samples using a saved injections file:

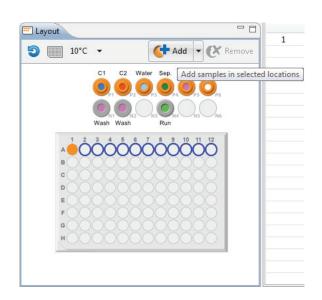
- a. Select File in the main menu and click Import Injections.
- b. Select an injections .csv file and click OK. The imported information will display in the Injections pane.
- c. Skip to step 3 page 266.

NOTE: For more information on setting up an injections file for import, see "Importing and Exporting Injections" on page 281.

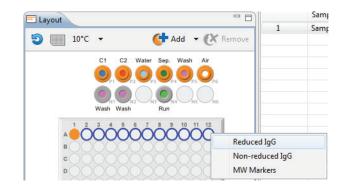
To select samples manually:

• Add samples and select methods later: Use your mouse to highlight the well or vial positions your samples are located in, then click Add. For this example we're using a 96-well plate.

NOTE: The template batch automatically adds a sample in well or vial A1 by default, but if you don't have a sample in this position you can remove it after you've added new positions for your samples.



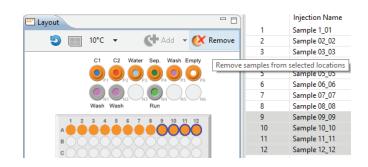
• Add samples with preassigned methods: Highlight the well or vial positions your samples are located in, then right-click and select a method.



Either option of adding samples populates the Injections table:

	Injection Name	Sample ID	Location	Method	Notes			
1	Sample 1_01	Sample 1	A1	Reduced IgG				
2	Sample 02_02	Sample 02	A2	Reduced IgG				
3	Sample 03_03	Sample 03	A3	Reduced IgG				
4	Sample 04_04	Sample 04	A4	Reduced IgG				
5	Sample 05_05	Sample 05	A5	Reduced IgG				
6	Sample 06_06	Sample 06	A6	Reduced IgG				
7	Sample 07_07	Sample 07	A7	Reduced IgG				
8	Sample 08_08	Sample 08	A8	Reduced IgG				
9	Sample 09_09	Sample 09	A9	Reduced IgG				
10	Sample 10_10	Sample 10	A10	Reduced IgG				
11	Sample 11_11	Sample 11	A11	Reduced IgG				
12	Sample 12_12	Sample 12	A12	Reduced IgG				

To remove samples, just highlight the ones you want to remove and click **Remove**. They'll also be removed in the Injections table. You can also right-click well(s) or vial(s) in the Layout pane and click **Remove Sample(s)**.



3. Compass for iCE can monitor the current during a separation for you, stop it if an abnormal current profile is detected and reinject the sample for you automatically. Reinjections are enabled by default, but if you don't want to use this feature just click the reinject icon to toggle it off.

NOTES:

If a sample was reinjected, the injection row will be flagged in the Injections pane in the Run Summary screen. See "Injection Flags" on page 414for more info.

A maximum of 10 reinjections are allowed per batch.



4. The sample platform is temperature controlled with a default setting of 10 °C. To change the temperature or turn it off, click the **down arrow** next to the temperature and select an option.

NOTE: The two reagent rows are kept at room temperature.



Step 3 - Assign Your Method Parameters

NOTE: There are three default methods. We recommend using the default method parameters for the listed sample types. Please see the Maurice CE-SDS Application Guide for more information on method optimization.

The Methods pane lists all of the methods used in a batch. You can add and remove methods here and change method parameters.

To import a saved method:

- 1. Select File in the main menu and click Import Method.
- 2. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

To create a new method or make changes to an existing one:

1. In the Methods table, click the first cell in the Name column and enter a new method name if needed.

Name	Sample Load	Separation
Reduced IgG	20 sec 4600 Volts	25.0 min 5750 Volts
Non-reduced IgG	20 sec 4600 Volts	35.0 min 5750 Volts
MW Markers	20 sec 4600 Volts	30.0 min 5750 Volts

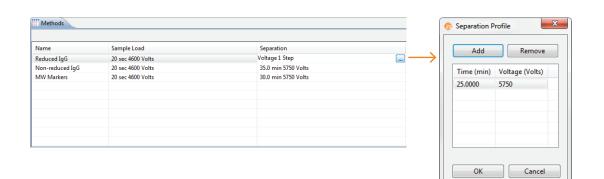
2. Click the first cell in the Sample Load column, then click the selection button [...] to set your sample load profile time (in seconds) and voltage.

Methods		🔞 Sample Load Profile
Name	Sample Load	Add Remove
Reduced IgG	Voltage 1 Step	Time (s) Voltage (Volts)
Non-reduced IgG	20 sec 4600 Volts	20 4600
MW Markers	20 sec 4600 Volts	20 1000
		OK Cancel

- To change time and voltage parameters: Just click in a cell under Time or Voltage and type the new value(s).
- **To add a profile step:** Click **Add**. A new row will be added in the table. Then just type in a load time (in seconds) and voltage value.
- To remove a profile step: Select the row you want to remove and click Remove.

3. Click the first cell in the Separation column the selection button [...] to set your separation profile parameters (in minutes) and voltage.

NOTE: Run your reduced IgG samples and IgG Standard for 25 minutes and the CE-SDS MW Markers for 35 minutes. Run your non-reduced IgG samples and IgG Standard for 35 minutes. The default separation voltage for all sample types is 5750 volts.



- To change time and voltage parameters: Just click in a cell under Time or Voltage and type the new value(s).
- To add a profile step: Click Add. A new row will be added in the table. Then just type in a load time (in seconds) and voltage value.
- To remove a profile step: Select the row you want to remove and click Remove.
- 4. You can now:
 - Click **New** in the upper right corner of the Methods pane to add a new one if you want to use different methods for different samples. Then just repeat the steps above for the new method.
 - Make updates to the remaining methods by repeating the prior steps.
 - Select a method and click Remove in the upper right corner of the Methods pane to delete it.

Step 4 - Set Up Your Injections

The Injection pane lists all sample injections for the batch. Any samples that were added in Step 2 - Assign Your Samples are automatically added to this list.

NOTE: If you imported injections in Step 2, you can update the injections table and assign methods as needed using the information that follows. Otherwise skip to "Step 5 - Add Programmed Pauses and Stops (Optional)" on page 272.

Selecting an injection in the table also selects the sample the injection will be made from in the plate or vial map in the Layout pane and vice-versa.

tch: Maurice CE-SDS	Injection	ns 🛛 🔚 History 📑 Note	es		
Layout 🖓 🗖		Injection Name	Sample ID	Location	Method
	1	Sample 1_01	Sample 1	A1	Reduced IgG
🏐 📖 10°C 👻 📢 Add 👻 🚺 Remove	2	Sample 02_02	Sample 02	A2	Reduced IgG
	3	Sample 03_03	Sample 03	A3	Reduced IgG
C1 C2 Water Sep. Wash Empty	4	Sample 04_04	Sample 04	A4	Reduced IgG
	5	Sample 05_05	Sample 05	A5	Reduced IgG
	6	Sample 06_06	Sample 06	A6	Reduced IgG
	7	Sample 07_07	Sample 07	A7	Reduced IgG
Wash Wash Run	8	Sample 08_08	Sample 08	A8	Reduced IgG
1 2 3 4 5 6 7 8 9 10 11 12	9	Sample 09_09	Sample 09	A9	Reduced IgG
	10	Sample 10_10	Sample 10	A10	Reduced IgG
80000000000000	11	Sample 11_11	Sample 11	A11	Reduced IgG
c 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	12	Sample 12_12	Sample 12	A12	Reduced IgG

1. To add sample names, click the **Sample ID** cell for the injection and type a name.

NOTES:

Sample IDs can be copied from other documents and pasted into Compass for iCE to make batch setup faster. Check out "Copying and Pasting Injection Names or Sample IDs from other Documents" on page 279 for more info.

If you change the sample ID when the default injection name is still being used, the injection name will automatically update to match the sample ID. If you've already changed the injection name manually, updating the sample ID will not update the injection name.

	Injection Name	Sample ID	Location	Method	Notes			
1	Sample 1_01	Product A	A1	Reduced IgG				
2	Sample 02_02	Sample 02	A2	Reduced IgG				
3	Sample 03_03	Sample 03	A3	Reduced IgG				
4	Sample 04_04	Sample 04	A4	Reduced IgG				
5	Sample 05_05	Sample 05	A5	Reduced IgG				
6	Sample 06_06	Sample 06	A6	Reduced IgG				
7	Sample 07_07	Sample 07	A7	Reduced IgG				
8	Sample 08_08	Sample 08	A8	Reduced IgG				
9	Sample 09_09	Sample 09	A9	Reduced IgG				
10	Sample 10_10	Sample 10	A10	Reduced IgG				
11	Sample 11_11	Sample 11	A11	Reduced IgG				
12	Sample 12_12	Sample 12	A12	Reduced IgG				

The sample name also displays when you hover the mouse over the sample in the plate or vial map:

tch: Maurice CE-SDS PLUS		ns 🔚 History 🚹 Notes		·	Pause 🖸 Stop 👫 Add
		Injection Name	Sample ID	Location	Method
Layout 🗖 🗖	1	Product A_01	Product A	A1	Reduced IgG
	2	Sample 02_02	Sample 02	A2	Reduced IgG
10°C • C • Add • C Remove	3	Sample 03_03	Sample 03	A3	Reduced IgG
C1 C2 Water Sep. Wash Empty	4	Sample 04_04	Sample 04	A4	Reduced IgG
	5	Sample 05_05	Sample 05	A5	Reduced IgG
	6	Sample 06_06	Sample 06	A6	Reduced IgG
	7	Sample 07_07	Sample 07	A7	Reduced IgG
NI NZ NJ N4 NS N6	8	Sample 08_08	Sample 08	A8	Reduced IgG
Wash Wash Run	9	Sample 09_09	Sample 09	A9	Reduced IgG
1 2 3 4 5 6 7 8 9 10 11 12	10	Sample 10_10	Sample 10	A10	Reduced IgG
	11	Sample 11_11	Sample 11	A11	Reduced IgG
B Product A	12	Sample 12_12	Sample 12	A12	Reduced IgG

2. Injection names are automatically set to 'Sample ID_injection number'. To change the name, click the **Injection Name** cell for the injection and type a name. Each injection name must be unique. If they aren't when you save the batch, Compass for iCE highlights any non-unique injection names so you can change them.

	Injection Name	Sample ID	Location	Method	Notes			
1	njection 1	Product A	A1	Reduced IgG				
2	Sample 02_02	Sample 02	A2	Reduced IgG				
3	Sample 03_03	Sample 03	A3	Reduced IgG				
4	Sample 04_04	Sample 04	A4	Reduced IgG				
5	Sample 05_05	Sample 05	A5	Reduced IgG				
6	Sample 06_06	Sample 06	A6	Reduced IgG				
7	Sample 07_07	Sample 07	A7	Reduced IgG				
8	Sample 08_08	Sample 08	A8	Reduced IgG				
9	Sample 09_09	Sample 09	A9	Reduced IgG				
10	Sample 10_10	Sample 10	A10	Reduced IgG				
11	Sample 11_11	Sample 11	A11	Reduced IgG				
12	Sample 12_12	Sample 12	A12	Reduced IgG				

NOTE: Changing the injection name won't affect the sample ID.

3. Assign your methods to each injection. Just click the **Method** cell for the injection and select a method from the drop down menu. If you added your samples with pre-assigned methods and don't need to make any changes, skip to the next step.

Injections	🔚 History 🖪 Notes				C	Pause	O Stop	<table-cell-rows> Add</table-cell-rows>	Rep	licate	🔀 Remove	Ŧ	8 7	
	Injection Name	Sample ID	Location	Method		Notes								
1	Injection 1	Product A	A1	Reduced IgG	¥									
2	Sample 02_02	Sample 02	A2	Reduced IgG										
3	Sample 03_03	Sample 03	A3	Non-reduced IgG										
4	Sample 04_04	Sample 04	A4	MW Markers										
5	Sample 05_05	Sample 05	A5	Reduced IgG										
6	Sample 06_06	Sample 06	A6	Reduced IgG										
7	Sample 07_07	Sample 07	A7	Reduced IgG										
8	Sample 08_08	Sample 08	A8	Reduced IgG										

Hovering over a method name displays the method parameters:

Injectio	ons 🛛 🔚 History 👖 Not	es			🕕 Pause 🕻
	Injection Name	Sample ID	Location	Method	Notes
1	Injection 1	Product A	A1	Non-reduced InC	_
2	Sample 02_02	Sample 02	A2	Reduce Non-reduced IgC	j
3	Sample 03_03	Sample 03	A3	Reduce Sample Load: 20 Reduce Separation: 35.0	min 5750 Volts
4	Sample 04_04	Sample 04	A4	Reducea igo	111 51 50 1013
5	Sample 05_05	Sample 05	A5	Reduced IgG	

- 4. You can add or remove injections as needed using a few different options. If you don't need to make any changes here, just skip to the next step.
 - To add sequential replicate injections: Highlight an injection and click **Replicate**. A new injection will be added under the row you selected

	Injection Name	Sample ID	Location	Method	Notes		Po	plicate selected i	niections. I
1	Injection 1	Product A	A1	Non-reduced IgG			IVC.	plicate selected	njections
2	Sample 02_02	Product B	A2	Reduced IgG					
3	Product C_03	Product C	A3	Reduced IgG					
4	Product D_04	Product D	A4	Reduced IgG					
5	Product E_05	Product E	A5	Reduced IgG					
6	Product F 06	Product F	A6	Reduced IgG					
Injectio	- Ilitary T Nat	<u></u>			D Daura (Stop III :	Vdd III Penli	cata IN Remov	
Injectio		es				Stop 🗗	Add 📗 Repli	cate 🛛 🗶 Remov	/e 🕀 🖻
Injectio	Injection Name	es Sample ID	Location	Method	D Pause (Notes	🕽 Stop 🗜 /	Add 📗 Repli	cate 🕌 Remov	re 🛨 🖻 🗖
1	Injection Name Injection 1	es Sample ID Product A	Location A1	Method Non-reduced IgG		🕽 Stop 🗗 /	Add 📗 Repli	cate 🕅 Remov	re 🕀 🖻 🗖
Injectio 1 2	Injection Name	es Sample ID	Location	Method		🕽 Stop 🕻 /	Add ∭ Repli	cate 🕅 Remov	~e 🕀 🖻 🗖
1 2	Injection Name Injection 1	es Sample ID Product A	Location A1	Method Non-reduced IgG		🕽 Stop 👉 /	Add 📗 Repli	cate 🛛 🗶 Remov	~ 🕀 🖻 🗖
1 2	Injection Name Injection 1 Sample 02_02	Sample ID Product A Product B	Location A1 A2	Method Non-reduced IgG Reduced IgG		🕽 Stop 👉 /	Add 📗 Repli	cate 🛛 🗶 Remov	re 🛨 🖻 🗖
3	Injection Name Injection 1 Sample 02_02 Product C_03	Sample ID Product A Product B Product C	Location A1 A2 A3	Method Non-reduced IgG Reduced IgG Reduced IgG		🕽 Stop 🕌)	∆dd ∦ Repli	cate [🗶 Remov	re 🖣 🖻 🗖

• To add injections at the end of the batch: Click on any sample position in the Layout pane or sample injection in the Injection table and click Add. A new injection using the same sample will be added to the end of the table. Assign the method if needed.

Injection	is 🛛 🔚 History 👖 Notes				🕕 Pause 🖸 Stop 🕌 Add 🚻 Replicate 🕌 Remove 🕀 🖻
	Injection Name	Sample ID	Location	Method	Notes Add injections
1	Injection 1	Product A	A1	Non-reduced IgG	Additigetions
2	Product B_02	Product B	A2	Reduced IgG	
> 3	Product C_03	Product C	A3	Reduced IgG	
5	Product D_05	Product D	A4	Reduced IgG	
6	Product E_06	Product E	A5	Reduced IgG	
7	Product F_07	Product F	A6	Reduced IgG	
8	Product G_08	Product G	A7	Reduced IgG	
9	Product H_09	Product H	A8	Reduced IgG	
10	Product H1_10	Product H1	A9	Reduced IgG	
11	Product H2_11	Product H2	A10	Reduced IgG	
12	Product H3_12	Product H3	A11	Reduced IgG	
13	Product H4_13	Product H4	A12	Reduced IgG	

• To copy and paste injections: Right-click on an injection in the Injection table and select Copy. Click on the injection number above where you want to insert the copied injection, right click and select Paste. The copied injection will be inserted under the row you selected.

Step 5 - Add Programmed Pauses and Stops (Optional)

You can program pauses and stops in the batch to automatically pause or stop after injections even when you aren't in front of Maurice.

To program a pause:

Pauses are helpful when you want to review injection results before continuing with the rest of the batch.

1. Highlight the injection you want to pause at and click **Pause**. The batch will pause after that injection is complete.

NOTE: Maurice can tweet you when the batch pauses. See "Setting Up Maurice Systems to Send Tweets" on page 764.

	Injection Name	Sample ID	Log Pau	se after the selected in	jection tes	
1	Sample 01_01	Sample 01	A1	Method 1		
2	Sample 02_02	Sample 02	A2	Method 1		
3	Sample 03_03	Sample 03	A3	Method 1		
Injectio	ons 🔄 🔚 History 🃭 I	Notes	🕕 Pause 🕻	Stop 🕂 Add 📗	Replicate 🔀 F	Remove 🕀 🗄
Injecti						Remove 🕀 🗄
Injectio	ons 🔚 History 🚹 Injection Name	Notes Sample ID	Pause C		Replicate 🔀 F Notes	Remove 🕀 🗄
Injectio						Remove 🕀 🗄
Injectio 1 2	Injection Name	Sample ID	Locati	on Method		Remove 📻 🗄
Injectio 1 2	Injection Name Sample 01_01	Sample ID Sample 01	Locati A1	on Method Method 1		Remove 🕀 🗄

2. To resume the batch, click Continue in the instrument status bar:

Paused	Continue		
		Mon 1:43 PM	

To stop the run after a specific injection:

1. Highlight the injection you want the batch to stop at and click **Stop**. Maurice will continue the batch through the selected injection, then stop the batch and perform end-run cleanup steps.

	Injection Name	Sample ID	Location	Stop after the sel	ected injection		
1	Sample 01_01	Sample 01	A1	Method 1			
2	Sample 02_02	Sample 02	A2	Method 1			
3	Sample 03_03	Sample 03	A3	Method 1			
Injecti	ons 🛛 🔚 History 👖 N	lotes	🕕 Pause 🛛 Sto	p 🎁 Add 📊 Re	plicate 🔀 Remove	: 🕂	6
njecti			Pause Sto	p 🕂 Add 📕 Re	plicate 🔀 Remove Notes	• 🕀	8
njecti 1	ons History T N Injection Name Sample 01 01	Sample ID Sample 01				: 🛨	8
	Injection Name	Sample ID	Location	Method		: =	
-	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method Method 1		: Ŧ	8

Data collected for injections completed up to the point where the batch was stopped are saved in the .mbz file.

2. Be sure to complete your normal post-batch procedures.

Step 6 - Add Batch Notes (Optional)

- 1. Click on the **Notes** pane.
- 2. Click in the notes area and type any information you want to add about your batch.

Injections 🔚 History 🎵 *Notes	
Product testing	

Step 7 - Modify Default Analysis Parameters (Optional)

You can preset the parameters used to analyze data generated with the batch. We recommend using the default parameters for CE-SDS PLUS applications, but if you need to modify parameters:

1. Select Edit from the main menu and click Default Analysis. The following screen will display:

Analysis Group	5	Markers		
Standards		Internal Standard Time 750 Seconds Markers Injection no markers		
Add	Pomovo	MW (kDa) 10	RMT 1	
Add	Kentove	20	1.15	
Apply Default		33	1.3	
			1.5	
Standards		103	1.8	
Apply Override	:		2.05	
	Group Standards	270	2.4	
		Add	Remove	
Add	Remove			
	Standards Add Apply Default: Standards Apply Override Apply To Sample	Add Remove Apply Default: Standards Apply Override: Apply To Group Sample Standards	Analysis divulus Internal Standard Time 750 Standards Internal Standard Time 750 Add Remove Apply Default 0 Standards 10 Standards 103 Apply Override: 103 Apply To Group Sample Standards Add F	

2. Change the parameters you want to, then click OK. For detailed information on analysis parameters, please refer to "Analysis Settings Overview" on page 713

Step 8 - Modify Default Analysis View Parameters (Optional)

You can preset the parameters used to display the graph and lane view data when the batch is complete. Default Analysis View Parameters must be set before you start the batch and cannot be modified once the batch starts. However, you can still manually change parameters in the Analysis pane using the Graph View Options and Lane View Options buttons.

To modify the parameters:

1. Select Edit from the main menu and click Default Analysis View. The following screen will display:

o Default Analysis View Mau	urice CE-SDS PLUS		×
Graph View Options Lane View Options	Graph View Options Matching Peak Names Peak Names Peak Values Fitted Peaks Baseline Fit Grid Lines Plot Label Sample Method Injection Injection Name		
	OK Cancel	Apply	

2. Change the parameters you want to, then click Apply. Click OK when you are done changing display parameters. For detailed information on graph and lane view options, please refer to "Customizing the Data Display" on page 695.

Step 9 - Save Your Batch

1. Once all of your sample, method and injection info is entered, select **File > Save**. Enter any comments on the batch if you want, then click **Save**.

Batch: Maurice CE-SDS PLUS	
Comment:	
L	

2. Enter a name for your batch then click Save.

Viewing Replicate Injections

Injections with replicates have an arrow next to the injection number. You can expand or collapse the list of replicate injections by toggling the arrow:

	Sample ID	Location	Method		Sample ID	Location	Method
1	Product A A	A1	Non-reduced IgG	1	Product A	A1	Non-reduced IgG
2	Product A /	A2	Reduced IgG	⊿ 2	Product A	A2	Reduced IgG
7	Product B /	A3	Non-reduced IgG	3	Product A	A2	Reduced IgG
8	Product B A	A4	Reduced IgG	4	Product A	A2	Reduced IgG
⊳ 9	Product C A	A5	Non-reduced IgG	5	Product A	A2	Reduced IgG
13	Product C A	A6	Reduced IgG	6	Product A	A2	Reduced IgG
14	Product D A	A7	Reduced IgG	7	Product B	A3	Non-reduced IgG
15	Product E /	A8	Reduced IgG	8	Product B	A4	Reduced IgG
16	Product F A	A9	Reduced IgG	⊳ 9	Product C	A5	Non-reduced IgG
17	Product G	A10	Non-reduced IgG	13	Product C	A6	Reduced IgG
18	Product H /	A11	Non-reduced IgG	14	Product D	A7	Reduced IgG
19	Markers /	A12	MW Markers	15	Product E	A8	Reduced IgG

• To show all replicate injections in the batch, click the Expand All Injections button.

Injection	s 🛛 🔚 History 👖 *Notes				👫 Add 🚻 Replicate 🔀 Remove 🕞 🖻 🗖
	Sample ID	Location	Method	Notes	Expand All Injecti
1	Product A	A1	Non-reduced IgG		Expand An Inject
a 2	Product A	A2	Reduced IgG		
3	Product A	A2	Reduced IgG		
4	Product A	A2	Reduced IgG		
5	Product A	A2	Reduced IgG		
6	Product A	A2	Reduced IgG		
7	Product B	A3	Non-reduced IgG		
8	Product B	A4	Reduced IgG		
a 9	Product C	A5	Non-reduced IgG		
10	Product C	A5	Non-reduced IgG		
11	Product C	A5	Non-reduced IgG		
12	Product C	A5	Non-reduced IgG		
13	Product C	A6	Reduced IgG		
14	Product D	A7	Reduced IgG		
15	Product E	A8	Reduced IgG		
16	Product F	A9	Reduced IgG		
17	Product G	A10	Non-reduced IgG		
18	Product H	A11	Non-reduced IgG		
19	Markers	A12	MW Markers		

• To hide all replicate injections in the batch, click the **Collapse All Injections** button.

					\downarrow
Injectio	ns 🛛 🔚 History 👖 *Notes			📂 Add 🚻 Replicate 🔀 Remove 🗊 📄 🗖 🗖	
	Sample ID I	Location	Method	Notes	Collapse All Injection
1	Product A A	A1	Non-reduced IgG		
⊳ 2	Product A A	A2	Reduced IgG		
7	Product B A	A3	Non-reduced IgG		
8	Product B A	A4	Reduced IgG		
⊳ 9	Product C A	A5	Non-reduced IgG		
13	Product C A	A6	Reduced IgG		
14	Product D A	Α7	Reduced IgG		
15	Product E A	A8	Reduced IgG		
16	Product F A	A9	Reduced IgG		
17	Product G A	A10	Non-reduced IgG		
18	Product H A	A11	Non-reduced IgG		
19	Markers A	A12	MW Markers		

Batch History

Clicking on the History pane shows the batch event history, starting with the date and time the batch was created through the most current event. Clicking on a row in the table displays the full event details in the box under the table.

Date	User Name	Message	Comment	
2019-01-07	10:17:2	Batch created using the factory default Maurice CE-SDS PLUS with Compass for iCE Version: 2.1.0-1219		
2019-01-07	10:26:1	Save Batch changes from Compass for iCE v2.1.0-1219		
2019-01-07	10:20:0	Saved as Z:\Shared\PPD\Science\R&D Science\team members\Irina\Shaun\FT Cartridge\assays\4Sq-16inj-Ma		
2019-01-07	10:26:1	Saved as Z:\Shared\PPD\Science\R&D Science\team members\Irina\Shaun\FT Cartridge\assays\4Sq-16inj-Ma		
2019-01-07	10:20:0	Save injections changes from Compass for iCE v2.1.0-1219		
2019-01-07	12:06:2	Save injections changes from Compass for iCE v2.1.0-1219		
ime	2019-01-0	7 10:17:22 User		
/essage	Batch cre	ated using the factory default Maurice CE-SDS PLUS with Compass for iCE Version: 2.1.0-1219		
Comment				
Johnnellt				

- Date: Date and time of the batch event.
- User Name: User that initiated the event. User names only display if you're using the Access Control feature to help satisfy the 21CFR Part 11 data security requirements. Go to "Enabling Access Control" on page 781 to learn how to set it up.
- Message: Description of the event that took place.
- **Comment:** Comments entered by the user when the batch was saved.

You can copy the information in the History pane to use in other documents:

- 1. Click the History pane to make sure it's active.
- 2. Click Edit in the main menu and select Copy.
- 3. Open a document and click Paste.

Making Changes to a Batch

1. Select File in the main menu and click Open Batch.

File	Edit Instrument	Wi	ndow Help
	New Batch	►	
	Open Batch	•	Platform CE-SDS2
	Save		Platform CE-SDS1
	Save As		Maurice CE-SDS3
			Maurice CE-SDS2
	Batch Report		Maurice CE-SDS1
	Exit		Browse

- 2. A list of the last five batches opened will display based on the last location found. If the location of the file has changed, you may need to navigate to find the file.
 - Select one of these files or click Browse to open the Batch folder and select a different one.
 - To open a batch used in a run file, click **Browse**. Go to the Run folder in the Compass for iCE directory and select the run file that uses the batch you want to edit.

	lder				
🖥 Libraries 🖹 Documents	Documents library Compass for iCE				
My Documents Add-in Express	Name	Date modified	Date created	Туре	Size
Add-in Express	Batches	1/18/2016 5:39 PM	1/13/2016 8:24 PM	File folder	
Addbe Addbe Elients	🐌 New Batches	1/13/2016 8:24 PM	1/13/2016 8:24 PM	File folder	
Compass for iCE	🐌 Runs	1/17/2016 8:41 PM	11/11/2015 4:46 PM	File folder	
Batches	DemoData_Maurice cIEF.mbz	1/18/2016 11:38 AM	1/18/2016 11:38 AM	Maurice data file.	798 H

3. To make changes to the batch, see the steps in "Creating a New Batch" on page 84. Then select File from the main menu and click Save or Save As.

Viewing and Editing Batches in Completed Runs

- 1. Click the Analysis screen and open your run file(s).
- 2. After the run opens, click the Batch screen to view the batch used with the run.

If you opened more than one run file, you can switch between viewing batches for each file. Just click the **down arrow** in the Run box and select the batch you want to view from the drop down list.

File	Edit	Instrum	ent W	indow	Help		
1							
1							
Run:	KF10	06_s-CE	-SDS Pro	oduct B		-	
۳	ay KF10 KF10	06_s-CE	- <mark>SDS</mark> -SDS Pro	oduct B			
		10°C			🕻 Add	-	Remove

- 3. In completed run files, you can only make edits to the **sample** and **method** names in a batch, and these changes are saved to the run file only. Update sample and method names as needed.
- 4. Click the Analysis screen. Then select File from the main menu and click Save or Save As to save the new changes to the run file.

Copying and Pasting Injection Names or Sample IDs from other Documents

Injection names and Sample IDs can be copied from other documents and pasted into the Injection pane to make batch setup faster.

To paste a list of injection names into the batch:

1. Select the list of injection names in a document (Microsoft[®] Word[®], Excel[®], etc.) and select **Copy** or hold the **Ctrl+C** keys to copy.

	А	В	C
1			
2		My Injection 1	My Sample 1
3		My Injection 2	My Sample 2
4		My Injection 3	My Sample 3
5		My Injection 4	My Sample 4
6		My Injection 5	My Sample 5
7		My Injection 6	My Sample 6
8		My Injection 7	My Sample 7
9		My Injection 8	My Sample 8
10		My Injection 9	My Sample 9
11		My Injection 10	My Sample 10

2. Select an injection in the Injection pane, then hold the Ctrl+V keys to paste. You can also select the injection, right click and select Paste.

	Injection Name	Sample ID	Location	Method	Notes	
1	Sample 01_01	Sample 01	A1	System Suitability		
2	Sample 02_02	Sample 02	A2	Method2		
3	Sample 03_03	Sample 03	A3	Method2		
4	Sample 04_04	Sample 04	A4	Method2		
5	Sample 05_05	Sample 05	A5	Method2		
6	Sample 06_06	Sample 06	A6	Method2		
7	Sample 07_07	Sample 07	A7	Method2		
8	Sample 08_08	Sample 08	A8	Method2		
9	Sample 09_09	Sample 09	A9	Method2		
10	Sample 10_10	Sample 10	A10	Method2		
11	Sample 11_11	Sample 11	A11	Method2		
12	Sample 12_12	Sample 12	A12	Method2		

The injection names are pasted into the Injection pane:

	Injection Name	Sample ID	Location	Method	Notes	
1	My Injection 1	Sample 01	A1	System Suitability		
2	My Injection 2	Sample 02	A2	Method2		
3	My Injection 3	Sample 03	A3	Method2		
4	My Injection 4	Sample 04	A4	Method2		
5	My Injection 5	Sample 05	A5	Method2		
6	My Injection 6	Sample 06	A6	Method2		
7	My Injection 7	Sample 07	A7	Method2		
8	My Injection 8	Sample 08	A8	Method2		
9	My Injection 9	Sample 09	A9	Method2		
10	My Injection 10	Sample 10	A10	Method2		
11	Sample 11_11	Sample 11	A11	Method2		
12	Sample 12_12	Sample 12	A12	Method2		

To paste a list of Sample IDs into the batch:

1. Select the list of Sample IDs in a document (Microsoft Word, Excel, etc.) and select **Copy** or hold the **Ctrl+C** keys to copy.

	А	В	С	
1				
2		My Injection 1	My Sample 1	
3		My Injection 2	My Sample 2	
4		My Injection 3	My Sample 3	
5		My Injection 4	My Sample 4	
6		My Injection 5	My Sample 5	
7		My Injection 6	My Sample 6	
8		My Injection 7	My Sample 7	
9		My Injection 8	My Sample 8	
10		My Injection 9	My Sample 9	
11		My Injection 10	My Sample 10	
12				

2. Select a Sample ID in the Injection pane, then hold the Ctrl+V keys to paste. You can also select the Sample ID, right click and select Paste.

				U Pa	use 🖸 Stop 👫 Add 📗 Replic	ate 🕅 Remove 🗄
	Injection Name	Sample ID	Location	Method	Notes	
1	Sample 01_01	Sample 01	A1	System Suitability		
2	Sample 02_02	Sample 02	A2	Method2		
3	Sample 03_03	Sample 03	A3	Method2		
4	Sample 04_04	Sample 04	A4	Method2		
5	Sample 05_05	Sample 05	A5	Method2		
6	Sample 06_06	Sample 06	A6	Method2		
7	Sample 07_07	Sample 07	A7	Method2		
8	Sample 08_08	Sample 08	A8	Method2		
9	Sample 09_09	Sample 09	A9	Method2		
10	Sample 10_10	Sample 10	A10	Method2		
11	Sample 11_11	Sample 11	A11	Method2		
12	Sample 12_12	Sample 12	A12	Method2		

The Sample IDs are pasted into the Injection pane.

NOTE: If you paste in new sample IDs when the default injection names are still being used, the injection names will automatically update to match the sample ID. If you've already changed the injection names manually, updating the sample IDs will not update the injection names.

	Injection Name	Sample ID	Location	Method	Notes	
1	My Sample 1_01	My Sample 1	A1	System Suitability		
2	My Sample 2_02	My Sample 2	A2	Method2		
3	My Sample 3_03	My Sample 3	A3	Method2		
4	My Sample 4_04	My Sample 4	A4	Method2		
5	My Sample 5_05	My Sample 5	A5	Method2		
6	My Sample 6_06	My Sample 6	A6	Method2		
7	My Sample 7_07	My Sample 7	A7	Method2		
8	My Sample 8_08	My Sample 8	A8	Method2		
9	My Sample 9_09	My Sample 9	A9	Method2		
10	My Sample 10_10	My Sample 10	A10	Method2		
11	Sample 11_11	Sample 11	A11	Method2		
12	Sample 12_12	Sample 12	A12	Method2		

Importing and Exporting Injections

Injections in an open batch or run file can be exported as a separate file. This lets you import the same or a modified set of injections into another batch later, rather than having to enter the information manually.

Exporting Injections

- 1. Open the batch or run you want to export injections from.
- 2. In the Batch screen, select File in the main menu and click Export Injections. The following window displays:

💮 Injections File				×
$\leftarrow \rightarrow \land \uparrow$	This PC Documents Compass for iCE Batches	ٽ ~	Search Batches	م
Organize 🔻 Nev	folder			== • ?
a OneDrive	^ Name	Date modified	Туре	Size
This PC	2019-01-08_ clEF_Injections.csv	2/9/2019 3:18 PM	Microsoft Excel C	2 KB
Inis PC 3D Objects	Dye-ComboCollect_Maurice clEF_FI.batch_Injections.csv	1/29/2019 8:19 PM	Microsoft Excel C	2 KB
Desktop				
Documents				
Downloads				
👌 Music				
Pictures				
😽 Videos				
🟪 OS (C:)				
👝 DATA (D:)				
👝 Seagate Backu				
r	•			
L	4Sqx12inj-RIgG-Maurice CE-SDS.batch_Injections.csv			
Save as type:	ext File, comma delimited (*.csv)			~
∧ Hide Folders			Save	Cancel

- 3. The default directory is Compass for iCE/Batches. Change the directory if needed.
- 4. The default file name will be batchname.batch_Injections.csv. Change the name if needed and click Save.

Creating an Injections File

To create a new injections file .csv, it's easiest to export injections from an existing batch and use that as your template.

- 1. Follow the instructions in Exporting Injections above to export injections from an existing CE-SDS PLUS batch.
- 2. Open the .csv file in a program that provides a table/spreadsheet format.
- 3. To add or change injection information:
 - a. Type in a unique name in each cell in the Injection Name column. For replicate injections, type > in front of the injection name, for example: >Injection 1.
 - b. Type in a sample ID, location and method for each injection in their respective columns.
 - c. Optional: Type in notes if needed.

NOTES:

Mix bottle is not used for CE-SDS PLUS batches. Compass for iCE ignores this column when importing injections into CE-SDS PLUS batches.

Programmed pauses and stops can't be added in the injections file. They can be added in the Injections pane after importing your injections.

	А	В	С	D	E	F
1	Injection Name	Sample ID	Location	Method	Mix Bottle	Notes
2	R IgG1	SB	B2	Reduced IgG		
3	R IgG 2	SB	B3	Reduced IgG		
4	>R IgG 2	SB	B3	Reduced IgG		
5	>R IgG 2	SB	B3	Reduced IgG		
6	R IgG 3	SB	C2	Reduced IgG		
7	R IgG 4	SB	C3	Reduced IgG		
8	R IgG1_05	SB	B2	Reduced IgG		
9	R IgG 2_06	SB	B3	Reduced IgG		
10	R IgG 3_07	SB	C2	Reduced IgG		

4. Save the .csv file.

Importing Injections

- 1. Open the batch you want to import injections into, or open a new batch.
- 2. Select File in the main menu and click Import Injections.
- 3. Select an injections file (*.csv) and click OK. The imported information will display in the Layout and Injections panes.

NOTE: Imported injections will replace any injections already in the Injections table, they will not append an existing table.

Importing and Exporting Methods

Methods in an open batch or run file can be exported as a separate file. This lets you import the same method into another batch later, rather than having to re-enter method information manually.

Importing a Method

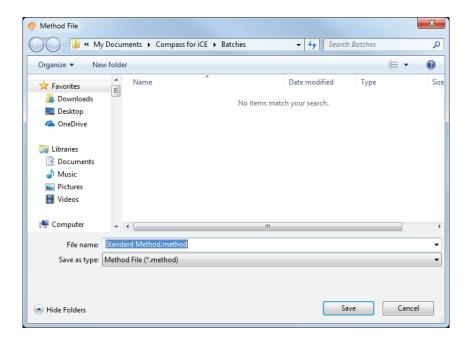
NOTE: Importing a method imports information into the Batch window's Method pane only.

- 1. Open the batch you want to import the method into.
- 2. Select File in the main menu and click Import Method.
- 3. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

Exporting a Method

NOTE: Exporting a method exports information in the Batch window's Method pane only.

- 1. Open the batch you want to export the method from.
- 2. In the Method pane, select the method you want to export. To export more than one method at the same time, hold the Ctrl key to select multiple methods.
- 3. Select File in the main menu and click Export Method. The following window displays:



- 4. The default directory is Compass for iCE/Batches. Change the directory if needed.
- 5. Enter a method file name and click Save. The settings will be saved as a *.method file.

Batch Reports

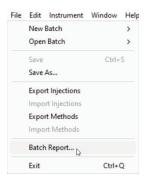
You can export a PDF file of sample and method details for each injection in the batch.

NOTES:

You can have Compass for iCE generate reports for you automatically at the end of each run. See ""Setting up Automatic Injection Reports" on page 761 for more information.

Any time a new report is run, it's saved in a separate run folder. Existing reports aren't overwritten.

- Go to the Analysis or Run Summary screen, then click File > Open Run and select a run file (if you don't have one open already).
- 2. After the run opens, go to the **Batch** screen.
- 3. Select File from the main menu and click Batch Report.



4. The report name defaults to the run file name. If you want to change it, type in the **Report Name** box to make updates.

¢	Batch Report	\times
	Run: R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch	
	Secure PDF	
	Report Name: Browse	
	R-lgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch	
	Location: C:\Users\Documents\Compass for iCE	
	OK Cancel	

Report PDFs generated by Compass for iCE are secured by default, which means they can be viewed and printed but not modified or renamed. Uncheck **Secure PDF** if you don't want to generate a secure report. To learn more about permissions for secured vs. unsecured reports, see page 800.

5. The Batch Report PDF is exported to the Runs folder in the Compass for iCE directory. It'll be in a folder with the report name used in the prior step. When the reports are done, the folder opens for you automatically.

Organize Include in library Share with	Burn	New folder			
🛛 🉀 Favorites	*	Name	Date modified	Туре	Size
😺 Links 4 頂 My Documents		📜 78664 P3 IS 2015-11-30_16-49-49_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS_Batch.pdf	1/18/2016 3:57 PM	Adobe Acrobat D	33 KI
🌗 Add-in Express					
📔 Adobe					
D Clients					
4 🌗 Compass for iCE					
퉬 Assays					
퉬 Batches					
🎉 New Assays					
퉬 New Batches					
4 퉲 Runs					
퉬 2015-12-06_15-13-01_Maurice cIEF_Mab11_TechR					
🍌 78664 P3 IS 2015-11-30_16-49-49_MW Ladder Sol					

Here's an example Batch Report:

Injection	Injection Name	Sample ID	Location	Method	Sample Load	Separation
1	R IgG1	SB	B2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
2	R IgG 2	SB	B3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
3	R IgG 3	SB	C2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
4	R IgG 4	SB	C3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
5	R IgG1_05	SB	B2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
6	R IgG 2_06	SB	B3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
7	R lgG 3_07	SB	C2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
8	R IgG 4_08	SB	C3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
9	R lgG1_09	SB	B2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
10	R IgG 2_10	SB	B3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
11	R IgG 3_11	SB	C2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
12	R IgG 4_12	SB	C3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
13	R lgG1_13	SB	B2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
14	R lgG 2_14	SB	B3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
15	R lgG 3_15	SB	C2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
16	R lgG 4_16	SB	C3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
17	R lgG1_17	SB	B2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
18	R lgG 2_18	SB	B3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
19	R lgG 3_19	SB	C2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
20	R IgG 4_20	SB	C3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
21	R lgG1_21	SB	B2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
22	R IgG 2_22	SB	B3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
23	R IgG 3_23	SB	C2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
24	R IgG 4_24	SB	C3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
25	R lgG1_25	SB	B2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
26	R IgG 2_26	SB	B3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
27	R lgG 3_27	SB	C2	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts
28	R IgG 4_28	SB	C3	Reduced IgG	20 sec 4600 Volts	25.0 min, 5750 Volts

CE-SDS Batch: 4Sqx12inj-RIgG-Maurice CE-SDS

Created By: Jacquelyn Sat 4:47 PM Feb 2, 2019 CST Software Version: 2.1.0, Build ID: 0130 C:Users/Jacquelyn/Documents/Clients/ProteinSimple/Maurice/User Guide/Rev 12 edits/Data from Andrea - no edits/R-igG-2019-01-10_16-25-12_4Sqx12inj-RIgG-Maurice CE-

Creates c, . C:Users/Jacquelyn/Documents/Lines SDS.mbz Computer: DESKTOP-C7FPQGB

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User Guide for Maurice, Maurice C. Maurice S. and MauriceFlex

CE-SDS Batch: 4Sqx12inj-RIgG-Maurice CE-SDS

Batch Log

Date	User Name	Message	Comment
2019-01-10 16:22:44		Batch created using the factory default Maurice CE-SDS with Compass for iCE	
		Version: 2.1.0-1219	
2019-01-10 16:25:08		Saved as C:\Users\ikazakova\Documents\Compass for iCE\Batches\4Sqx12inj-	
		RIgG-Maurice CE-SDS.batch from Compass for iCE v2.1.0-1219	
2019-01-10 16:25:08		Save injections changes from Compass for iCE v2.1.0-1219	

Created By: Jacquelyn Sat 447 PM Feb 2, 2019 CST Software Version: 2.1.0, Build ID: 0130 C'UlsersUlaquelynDocumentSIDientSiProtenSimple/MauriceUlser Guide/Rev 12 edits/Data from Andrea - no edits/R-IgG-2019-01-10_16-26-12_4Sqr.12ny-RigG-Maurice CE-Software Computer: DESKTOP-C7FP0GB Page 3 of 3



User Guide for Maurice, Maurice C. Maurice S. and MauriceFlex

Chapter 12: Running CE-SDS PLUS Applications

Chapter Overview

- Overview
- Before You Throw the Switch
- Power Up
- Running CE-SDS PLUS Applications
- Editing a Running Batch
- Post-batch Procedures
- Checking Your Data

Overview

CE-SDS PLUS applications can be run on Maurice, Maurice S. and MauriceFlex systems with a CE-SDS PLUS cartridge.

Before You Throw the Switch

Ensure that everyone using Maurice have:

- Received instruction in general safety practices for laboratories.
- Received instruction in specific safety practices for Maurice.
- Received instruction on handling of biohazards (if biohazardous materials are to be used on Maurice).
- Read and understood all Product Inserts and related Safety Data Sheets (SDS).

Power Up

- 1. Turn on the computer connected to Maurice.
- 2. Turn on Maurice's main power switch.
- 3. Wait for Maurice to initialize. His indicator light will turn from magenta to blue when he's done.
- 4. Double-click the Compass for iCE software icon on the computer desktop to open the application.
- 5. Connect Maurice to Compass for iCE.

Running CE-SDS PLUS Applications

What You'll Need

- Maurice CE-SDS PLUS Application Kit which include:
 - Maurice CE-SDS PLUS Cartridges
 - Cartridge Cleaning Vials
 - Separation Matrix
 - Running Buffer (Top and Bottom)
 - CE-SDS PLUS 1X Sample Buffer
 - Wash Solution
 - Conditioning Solutions (1 and 2)
 - 25X Internal Standard

- Glass reagent vials, 2 mL
- 96-well plates
- Clear screw caps for vials
- Orange pressure caps for vials
- Maurice CE-SDS IgG Standard (optional)
- Maurice CE-SDS MW Markers (optional)
- β -mercaptoethanol (β ME, >98% = 14.2 M) for reducing conditions
- · Iodoacetamide (IAM, 250 mM) for alkylation at non-reducing conditions
- Deionized (DI) water
- Sample vials with integrated inserts for samples (optional)
- P10, P20, P200, P1000 and pipette tips
- Water bath or thermocycler
- Vortexer
- Table-top centrifuge with plate adapter or vial adapter (12 mm, 2 mL vials)

Step 1: Prep Your Internal Standard, Samples and Reagents

NOTE: You can prepare your samples to run either in 96-well plates or vials. Using 96-well plates is the default method.

Internal Standard

NOTES:

The Internal Standard is lyophilized. Always reseal the foil bag containing the unopened tubes with desiccant to prevent moisture absorption.

Aliquot the reconstituted solution into appropriately sized vials and store at -70 to -90 °C for long term storage. For short-term storage (< 1 week), the solution can be stored at 2-8 °C.

Prepare the Internal Standard in the same buffer as your sample.

- 1. Open the vial of lyophilized 25X Internal Standard by lifting the center tab and gently pulling it back to break the metal seal. Then slowly remove the rubber stopper.
- Reconstitute by adding 240 μL of 1X Sample Buffer. Pipette up and down a few times to mix thoroughly. This results in a 25X Internal Standard solution.

NOTE: Don't vortex the reconstituted Internal Standard during prep.

Sample Prep Under Reducing Conditions

NOTES:

Prepare a minimum of 50 µL of sample for a CE-SDS PLUS batch.

Reduced IgG Sample

1. In a microcentrifuge tube, dilute your IgG sample with 1X Sample Buffer to a concentration of 0.25-1.00 mg/mL in a final volume of 50 μ L.

NOTE: Dilute at least 1:1 with CE-SDS PLUS 1X Sample Buffer.

- 2. Add 2 µL of reconstituted 25X Internal Standard for every 50 µL of sample volume.
- 3. Add 2.5 μ L of 14.2 M β -mercaptoethanol for every 50 μ L of sample volume.
- 4. Mix thoroughly.

NOTE: Heating in the presence of SDS linearizes the protein and allows for SDS binding. The reducing agents break up inter- and intra-molecular disulfide bonds.

- 5. Centrifuge the tube and heat the mixture in a water bath or thermocycler at 70 °C for 10 minutes.
- 6. Put the tube on ice for 5 minutes.
- 7. Vortex briefly and spin down.

Reduced IgG Standard (Optional)

NOTES:

The IgG Standard is lyophilized. Always reseal the foil bag containing the unopened tubes with desiccant to prevent moisture absorption.

Prepare the reduced IgG Standard in CE-SDS PLUS 1X Sample Buffer.

1. Using scissors, carefully cut the top of the foil package, leaving the sealing strip intact.

- 2. Take out the strip of tubes and carefully cut one pink tube of lyophilized IgG Standard from the strip. Put the unopened tubes back in the package, seal tightly and store at 2-8 °C.
- 3. Pierce the foil on the tube with a clean pipette tip.
- 4. Reconstitute the IgG Standard with 50 μL of 1X Sample Buffer. Gently resuspend by pipetting the solution up and down. Transfer the solution to a microcentrifuge tube.
- 5. Add 2 µL of reconstituted 25X Internal Standard.
- 6. Add 2.5 μ L of 14.2 M β -mercaptoethanol.
- 7. Mix thoroughly by vortex.
- 8. Centrifuge the tube and heat mixture in a water bath or thermocycler at 70 °C for 10 minutes.
- 9. Put the tube on ice for 5 minutes.
- 10. Vortex briefly and spin down.

CE-SDS Molecular Weight (MW) Markers (Optional)

NOTES:

The CE-SDS MW Markers are lyophilized. Always reseal the foil bag containing the unopened tubes with desiccant to prevent moisture absorption.

Prepare the MW Markers in CE-SDS PLUS 1X Sample Buffer.

- 1. Using scissors, carefully cut the top of the foil package leaving the sealing strip intact.
- 2. Take out the strip of tubes and carefully cut one green tube of lyophilized CE-SDS MW Markers from the strip. Put the unopened tubes back in the package, seal tightly and store at 2-8 °C.
- 3. Pierce the foil on the tube with a clean pipette tip.
- Reconstitute the CE-SDS MW Markers with 50 μL of 1X Sample Buffer. Gently resuspend by pipetting the solution up and down. Transfer the solution to a microcentrifuge tube.
- 5. Add 2 µL of reconstituted 25X Internal Standard.
- 6. Add 2.5 μ L of 14.2 M β -mercaptoethanol.
- 7. Mix thoroughly.
- 8. Centrifuge the tube and heat the mixture in a water bath or thermocycler at 70 °C for 10 minutes.
- 9. Put the tube on ice for 5 minutes.
- 10. Vortex briefly and spin down.

Spin Samples, Standards and CE-SDS MW Markers

If you're using a 96-well plate:

- 1. Transfer 50 µL of each of your samples, IgG Standard and CE-SDS MW Markers to their designated wells in a 96-well plate.
- 2. Cover the plate with a lid and spin for 10 minutes at 1000 xg in a centrifuge with a plate adapter.
- 3. Pop any bubbles in the samples with a clean pipette tip.

If you're using vials:

- 1. Transfer 50 μL of each of your samples, IgG Standard and CE-SDS MW Markers to their designated sample vials with insert, 0.2 mL.
- 2. Close the vials with a clear screw cap.
- 3. Place the vials in a centrifuge using a vial adapter (12 mm, 2 mL vials) and spin for 10 minutes at 1000 xg.



Sample Prep Under Non-reducing Conditions

Alkylation Reagent

NOTES:

We use a 250 mM solution of iodoacetamide (IAM) as an alkylating reagent.

Prepare a fresh 250 mM solution of iodoacetamide in DI water before use.

- 1. Weigh out 46 mg of IAM directly into a 1.5 mL microcentrifuge tube.
- 2. Add 1 mL of DI water to the tube and mix thoroughly.

Non-reduced IgG Sample

NOTE: Prepare a minimum of 50 µL of sample for a CE-SDS PLUS batch.

1. In a microcentrifuge tube, dilute your IgG sample with 1X Sample Buffer to a concentration of 0.25-1.0 mg/mL in a final volume of 50 µL.

NOTE: Dilute at least 1:1 with CE-SDS PLUS 1X Sample Buffer.

- 2. Add 2 µL of reconstituted 25X Internal Standard for every 50 µL of sample volume.
- 3. Add 2.5 μ L of 250 mM IAM for every 50 μ L of sample volume.
- 4. Mix thoroughly.
- 5. Centrifuge the tube and heat the mixture in a water bath or thermocycler at 70 °C for 10 minutes.
- 6. Put the tube on ice for 5 minutes.
- 7. Vortex briefly and spin down.

Non-reduced IgG Standard (Optional)

NOTES:

The IgG Standard is lyophilized. Always reseal the foil bag containing the unopened tubes with desiccant to prevent moisture absorption.

Prepare the non-reduced IgG Standard in CE-SDS PLUS 1X Sample Buffer.

- 1. Using scissors, carefully cut the top of the foil package, leaving the sealing strip intact.
- 2. Take out the strip of tubes and carefully cut one pink tube of lyophilized IgG Standard from the strip. Put the unopened tubes back in the package, seal tightly and store at 2-8 °C.
- 3. Pierce the foil on the tube with a clean pipette tip.
- 4. Reconstitute the IgG Standard with 50 μL of 1X Sample Buffer. Gently resuspend by pipetting the solution up and down. Transfer the solution to a microcentrifuge tube.
- 5. Add 2 µL of reconstituted 25X Internal Standard.
- 6. Add 2.5 μL of 250 mM IAM.
- 7. Mix thoroughly by vortex.

NOTE: Heating in the presence of SDS linearizes the protein and allows for SDS binding. The alkylating agents prevent disulfide-bond scrambling catalyzed by free sulfhydryl groups. This minimizes the appearance of fragments under non-reducing conditions.

8. Centrifuge the tube and heat mixture in a water bath or thermocycler at 70 °C for 10 minutes.

- 9. Put the tube on ice for 5 minutes.
- 10. Vortex briefly and spin down.

Spin Samples and Standards

If you're using a 96-well plate:

- 1. Transfer 50 µL of each of your samples and IgG Standard to their designated wells in a 96-well plate.
- 2. Cover the plate with a lid and spin for 10 minutes at 1000 xg in a centrifuge with a plate adapter.
- 3. Pop any bubbles in the samples with a clean pipette tip.

If you're using vials:

- 1. Transfer 50 µL of your samples and IgG Standard to their designated sample vials with insert, 0.2 mL.
- 2. Close the vials with a clear screw cap.
- 3. Place the vials in a centrifuge using vial adapter (12 mm, 2 mL vials) and spin for 10 minutes at 1000 xg.

Reagents

IMPORTANT:

Use glass reagent vials, 2 mL (PN 046-017) to prepare CE-SDS PLUS batch reagents.

NOTE: Don't reuse reagents, vials or the clear screw caps. Always keep the orange pressure caps paired with their respective reagents. If you want to reuse pressure caps, first wash them thoroughly with DI water, soak overnight in DI water, rinse caps thoroughly with DI water again and air dry them before reusing.

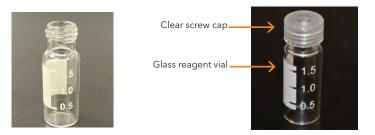
1. Pipette 1.5 mL of Conditioning Solution 1 into a glass reagent vial, label and close with an orange pressure cap.





- 2. Pipette 1.5 mL of Conditioning Solution 2 into a glass reagent vial, label and close with an orange pressure cap.
- 3. Pipette 1.0 mL of Wash Solution into a glass reagent vial, label each and close with an orange pressure cap.

4. Pipette 1.5 mL of Wash Solution into two glass reagent vials, label each and close the vials with clear screw caps.



- 5. Pipette 1 mL of Separation Matrix into a glass reagent vial, label and close with an orange pressure cap.
- 6. Pipette 1 mL of Running Buffer Bottom into one glass reagent vial, label and close with a clear screw cap.
- 7. Pipette 1.5 mL of DI water into a glass reagent vials, label and close with an orange pressure cap.
- 8. Close an empty glass reagent vial with an orange pressure cap.

Step 2: Prep the Cartridge

NOTES:

A CE-SDS PLUS Cartridge is guaranteed for 100 injections, with a maximum of 48 injections per batch and a maximum of 25 batches. The absolute injection limit of the cartridge is 500.

1. Take the CE-SDS PLUS Cartridge out of its packaging. Save the packaging, you'll need it later to store the cartridge.

NOTE: When you remove the cartridge from its packaging, make sure the cartridge inlet doesn't come in contact with any surface.



2. Pull the cartridge insert out of the cartridge.



3. Grab a fresh vial of Top Running Buffer from 2-8 °C storage and slide it into the cartridge insert so that the metal pin on the side of the vial is facing out. Press the vial up until it is completely inside the cartridge insert.

NOTES:

The Top Running Buffer vial should be stored at 2-8 °C when not in use.

The Top Running Buffer vial has metal pins on either side, so no specific orientation is necessary.

Once you've inserted the Top Running Buffer vial, the cartridge insert and the cartridge **must** be kept in an upright position at all times.



4. Slide the cartridge insert back into the cartridge.



Step 3: Install the Cartridge

1. Open Maurice's door by touching the metal plate on top of the door.



NOTE: The indicator light on Maurice's front panel will blink rapidly as the door disengages.

2. Swing the door open to access the cartridge slot and the reagents and samples platform. The lights on either side of the slot will be **orange**.



- 3. Lift the cartridge and hold it vertically using the finger holds on either side, cartridge inlet down, with the CE-SDS PLUS label facing you.
- 4. Gently insert it into the slot. You'll feel the alignment groove on the cartridge align inside the slot when you insert it.



5. Continue to slide the cartridge into the slot until the locking mechanism engages. The lights on either side of the slot will change to **blue** once the cartridge is installed correctly.



Step 4: Load Samples and Reagents

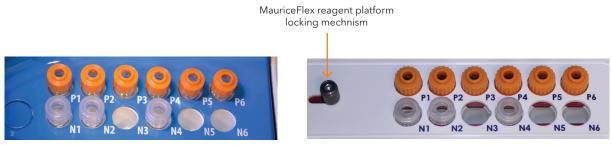
1. Place the reagent vials into their respective positions in the sample and reagents platform:

NOTES:

The two reagent rows in Maurice's reagent and sample platform are kept at room temperature.

Pressure caps are orange and have a raised, ringed surface. They should only be used in Reagent Row P. Use reagent vials with clear screw caps in Row N.

- P1 Conditioning Solution 1 with orange pressure cap
- P2 Conditioning Solution 2 with orange pressure cap
- **P3** DI water with orange pressure cap
- P4 Separation Matrix with orange pressure cap
- **P5** Wash Solution with orange pressure cap
- P6 Empty vial (air) with orange pressure cap
- N1 Wash Solution with clear screw cap
- N2 Wash Solution with clear screw cap
- N4 Running Buffer Bottom with clear screw cap



CE-SDS PLUS reagent platform on Maurice and Maurice S. (left) or MauriceFlex (right).

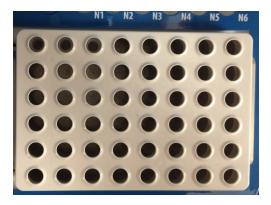
MPORTANT:

Reagent vials on MauriceFlex must be locked in place by sliding the locking mechanism from the left to the right before starting a batch. A warning will appear in the Start Run window if they are not locked when you start the batch.

2. Depending on what you prepared your samples in, put your 96-well sample plate in the metal plate insert or your sample vials in the metal vial insert. If you have a lid on the 96-well sample plate, be sure to remove it before closing the instrument door!

NOTE: Well A1 on the 96-well plate should be in the top left corner of the insert.

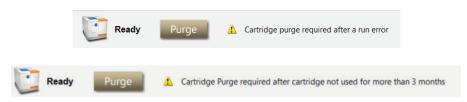
3. If you are using a vial tray, place the condensation lid on top of the vials.



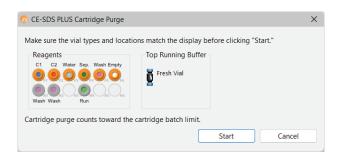
4. Close the instrument door. Maurice locks it automatically.

Step 5: Check for Cartridge Alerts

- 1. If your cartridge was last used in a run with an error or if it has not been used in the last three months, you will need to perform a Cartridge Purge. The Maurice system will remind you if a Cartridge Purge is required.
 - a. To purge the cartridge, click the brown Purge button in the instrument status bar.



b. Load the reagents required for the cartridge purge and ensure the cartridge is prepped. Then click Start.



c. Once the purge is done, perform a Cartridge Post-Run Cleanup by clicking on the brown **Cleanup** button that will appear in the instrument status bar. See step 2 for more info.

NOTE: If there's only one batch left on the cartridge, you'll get a message that it can't be used after purging.

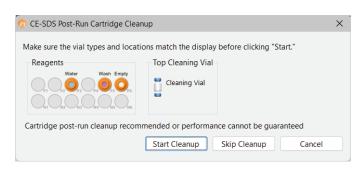
2. If you just completed a Cartridge Purge or if the cartridge you're using did not undergo a cartridge post-run cleanup after the last run, you will be asked if you want to perform a Cartridge Post-Run Cleanup.

To start the Post-Run Cleanup:

- a. Remove the cartridge from Maurice, remove the cartridge insert and check the saturation sensor in the back of the cartridge insert. See "Post-batch Procedures" on page 316 for more information.
- b. Replace the Top Running Buffer vial with a Cleaning Vial in the cartridge insert.
- c. Slide the cartridge insert back into the cartridge.
- d. Re-install the cartridge in Maurice.
- e. Confirm there is a vial of Water (P3), Wash Solution (P5) and Air (P6) in place.
- f. Click the brown Cleanup button in the instrument status bar.



g. Click Start Cleanup in the prompt that appears.

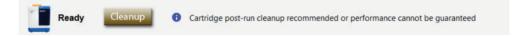


NOTE: You can also start a Post-Run Cleanup by selecting **Instrument > Cartridge Post-Run Cleanup**. When you start a Cartridge Post-Run Cleanup from the instrument menu, click **Start** in the prompt that appears to begin the cleanup.

- h. Once the cartridge post-run cleanup is completed, re-prepare the cartridge and install the cartridge in Maurice. See "Step 2: Prep the Cartridge" on page 295 for more information.
- i. Click on the green Start button in the instrument status menu to start the batch.

To start the run without a Post-Run Cleanup:

a. Click the brown Cleanup button in the instrument status bar



b. Click Skip Cleanup in the prompt that appears.



c. Click **Start** in the Start Run window. The run summary and injection report will record that the cartridge did not undergo a post-run cleanup before starting the batch.

💮 Start Run			×
Batch: Mauri	ice CE-SDS PLUS		
Results file na	ame :		Browse
2023-02-08_	15-17-10_Maurice CE-SDS PLUS		
Location: C:	\Users\Andrea\Documents\Compass for	r iCE\Runs	
Comment:			
	Cartridge		
	Type: CE-SDS PLUS	Injections per Batch : 48	
· •	Expires : Jan 2025	Injections Remaining: 439 (39 guaranteed)
_	Serial Number: 000000001	Batches Remaining: 16	
	Cartridge post-run cleanup recon	mmended or performance cannot be guaranteed	
		Start	Cancel

To start the run with a different cartridge:

- a. If necessary, click Cancel in the CE-SDS PLUS Cartridge Post-Run Cleanup window.
- b. Open Maurice's door, remove the first cartridge from Maurice and prepare a second cartridge. See"Step 2: Prep the Cartridge" on page 295 for more information.

Step 6: Create a Batch

- 1. Launch Compass for iCE.
- 2. Select the Batch tab. This is where you'll enter sample/injection information, methods and batch parameters.

Batch: Maurice CE-SI	DS PLUS	Inject	ions 🔚 History 🌃 Not	tes				-	
						O F	ause 🖸 Stop 🖟 Add 📗 R	eplicate 🕅 Remove 🦷	Ð
🖺 Layout	- 0		Injection Name	Sample ID	Location	Method	Notes		
🧿 🧾 10°C ·	- CH Add - CK Remove	1	Sample 01_01	Sample 01	A1	Reduced IgG			
	C2 Water Sep. Wash Empty C2 Sep. Constraints (C)								
1 2 3 4 A Image: Constraint of the second sec									
Methods									-
								New Rem	no۱
Name	Sample Load		Separation						
Reduced IgG	20 sec 4600 Volts		25.0 min 5750 Volts						
Non-reduced IgG	20 sec 4600 Volts		35.0 min 5750 Volts						
MW Markers	20 sec 4600 Volts		35.0 min 5750 Volts						

- 3. To create a batch, make sure your Maurice system is connected to Compass for iCE. Select Instrument and click Connect.
 - a. If your instrument is listed, select your Maurice system and click Connect.
 - b. If your instrument isn't listed, click on the Settings button and connect by typing in your instrument IP address.

ame	Location	Serial Num

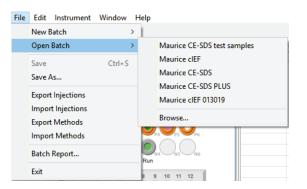
To create a new batch:

• In the main menu, select File > New Batch > Maurice CE-SDS Plus.

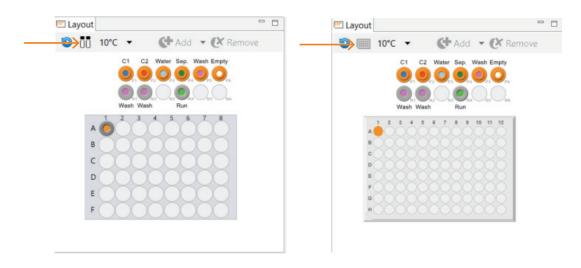
File	Edit Instrument	Window Hel	p
	New Batch	>	Maurice cIEF
	Open Batch	>	Maurice CE-SDS PLUS
	Save	Ctrl+S	Maurice Turbo CE-SDS™
	Save As		MauriceFlex clEF MauriceFlex Fractionation
	Export Injections		

To use an existing batch: In the main menu, select File > Open Batch.

NOTE: If you're making changes to an existing batch, follow the steps in this section. Otherwise skip to "Step 7: Start the Batch" on page 312.



4. In the Layout pane, clicking on the vial/plate icon toggles between formats. Select a 96-well plate or 48 vials depending on what you're running.



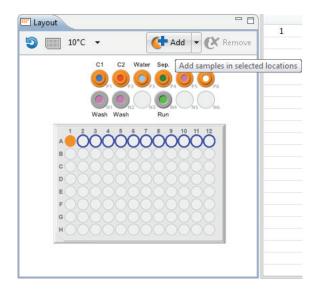
5. Add your samples:

To import samples using a saved injections file:

- a. Select File in the main menu and click Import Injections.
- b. Select an injections .csv file and click OK. The imported information will display in the Injections pane.

NOTE: For more information on setting up an injections file for import, see "Importing and Exporting Injections" on page 281.

To select samples manually: Use your mouse to highlight the well positions for each of your samples, then click Add.



This populates the Injections table:

Injections	🔚 History 👖 Notes				🕕 Pause	O Stop	🕂 Add	Replicat	e 🔀 Remove	Ŧ	
	Injection Name	Sample ID	Location	Method	Notes						
1	Sample 1_01	Sample 1	A1	Reduced IgG							
2	Sample 02_02	Sample 02	A2	Reduced IgG							
3	Sample 03_03	Sample 03	A3	Reduced IgG							
4	Sample 04_04	Sample 04	A4	Reduced IgG							
5	Sample 05_05	Sample 05	A5	Reduced IgG							
6	Sample 06_06	Sample 06	A6	Reduced IgG							
7	Sample 07_07	Sample 07	A7	Reduced IgG							
8	Sample 08_08	Sample 08	A8	Reduced IgG							
9	Sample 09_09	Sample 09	A9	Reduced IgG							
10	Sample 10_10	Sample 10	A10	Reduced IgG							
11	Sample 11_11	Sample 11	A11	Reduced IgG							
12	Sample 12_12	Sample 12	A12	Reduced IgG							

6. Compass for iCE can monitor the current during a separation for you, stop it if an abnormal current profile is detected and reinject the sample for you automatically. Reinjections are enabled by default, but if you don't want to use this feature just click the reinject icon to toggle it off.

NOTES:

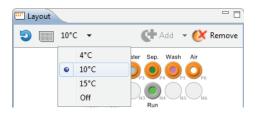
If a sample was reinjected, the injection row will be flagged in the Injections pane in the Run Summary screen. See "Injection Flags" on page 414 for more info.

A maximum of 10 reinjections are allowed per batch.



7. The sample platform is temperature controlled with a default setting of 10 °C. To change the temperature or turn it off, click the **down arrow** next to the temperature and select an option.

NOTE: The two reagent rows are kept at room temperature.



8. Enter your method parameters in the pane.

NOTE: There are three default methods. We recommend using the default method parameters for the listed samples. Please see the Maurice CE-SDS Application Guide for more information on method optimization.

To import a saved method:

- a. Select File in the main menu and click Import Method.
- b. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

To create a new method or make changes to an existing one:

a. Click the first cell in the Name column and enter a new method name if needed.

Name	Sample Load	Separation
Reduced IgG	20 sec 4600 Volts	25.0 min 5750 Volts
Non-reduced IgG	20 sec 4600 Volts	35.0 min 5750 Volts
MW Markers	20 sec 4600 Volts	30.0 min 5750 Volts

b. Click the first cell in the Sample Load column, then click then click the selection button [...] to set your load profile time (in seconds) and voltage.

Methods		😚 Sample Load Profile
Name	Sample Load	Add Remove
Reduced IgG	Voltage 1 Step	Time (s) Voltage (Volts)
Non-reduced IgG	20 sec 4600 Volts	20 4600
MW Markers	20 sec 4600 Volts	
		OK Cancel

c. Click the first cell in the Separation column then click the selection button [...] to set your separation time (in minutes) and voltage.

NOTE: Run your reduced IgG samples and IgG Standard for 25 minutes and the CE-SDS MW Markers for 35 minutes. Run your non-reduced IgG samples and IgG Standard for 35 minutes. The default separation voltage for all sample types is 5750 volts.

Name	Sample Load	Separation		Add	Remove
Reduced IgG	20 sec 4600 Volts	Voltage 1 Step	$\square \longrightarrow$		
Non-reduced IgG	20 sec 4600 Volts	35.0 min 5750 Volts		Time (min)	Voltage (Volts)
MW Markers	20 sec 4600 Volts	30.0 min 5750 Volts			-
				25.0000	5750

9. You can now:

- Make updates to the remaining methods by repeating the prior steps.
- Select a method and click Remove in the upper right corner of the Methods pane to delete it.
- Click New in the upper right corner of the Methods pane to add a new one if you want to use different methods for different samples. Then just repeat the steps above for the new method.

10. In the Injections pane:

• To add or change sample names: Click the Sample ID cell for the injection and type a name.

NOTES:

Sample IDs can be copied from other documents and pasted into Compass for iCE to make batch setup faster. Check out "Copying and Pasting Injection Names or Sample IDs from other Documents" on page 103 for more info.

If you change the sample ID when the default injection name is still being used, the injection name will automatically update to match the sample ID. If you've already changed the injection name manually, updating the sample ID will not update the injection name.

Injectio	ons 🔚 History 🖪 Notes				🕕 Pause 🔵 Stop 🛔	Add Replicate	🔀 Remove	
	Injection Name	Sample ID	Location	Method	Notes			
1	Sample 1_01	Product A	A1	Reduced IgG				
2	Sample 02_02	Sample 02	A2	Reduced IgG				
3	Sample 03_03	Sample 03	A3	Reduced IgG				
4	Sample 04_04	Sample 04	A4	Reduced IgG				
5	Sample 05_05	Sample 05	A5	Reduced IgG				
6	Sample 06_06	Sample 06	A6	Reduced IgG				
7	Sample 07_07	Sample 07	A7	Reduced IgG				
8	Sample 08_08	Sample 08	A8	Reduced IgG				
9	Sample 09_09	Sample 09	A9	Reduced IgG				
10	Sample 10_10	Sample 10	A10	Reduced IgG				
11	Sample 11_11	Sample 11	A11	Reduced IgG				
12	Sample 12_12	Sample 12	A12	Reduced IgG				

• To change injection names: Click the Injection Name cell for the injection and type a name.

NOTES:

Each injection name must be unique.

Changing the injection name won't affect the sample ID.

Injectio	ns 🛛 🔚 History 👖 Note	es			🕕 Pause ဝ Stop 👫 Add 📗 Replicate 🔀 Remove 🕞 😑 🖯
	Injection Name	Sample ID	Location	Method	Notes
1	njection 1	Product A	A1	Reduced IgG	
2	Sample 02_02	Sample 02	A2	Reduced IgG	
3	Sample 03_03	Sample 03	A3	Reduced IgG	
4	Sample 04_04	Sample 04	A4	Reduced IgG	
5	Sample 05_05	Sample 05	A5	Reduced IgG	
6	Sample 06_06	Sample 06	A6	Reduced IgG	
7	Sample 07_07	Sample 07	A7	Reduced IgG	
8	Sample 08_08	Sample 08	A8	Reduced IgG	
9	Sample 09_09	Sample 09	A9	Reduced IgG	
10	Sample 10_10	Sample 10	A10	Reduced IgG	
11	Sample 11_11	Sample 11	A11	Reduced IgG	
12	Sample 12_12	Sample 12	A12	Reduced IgG	

• To assign methods for each injection: Click the Method cell for the injection and select a method from the drop down menu.

	🔚 History 👖 Notes				0	Pause	O Stop	🕂 Add	Replica	ate	🔀 Remove	Ŧ	3 " 6
	Injection Name	Sample ID	Location	Method		Notes							
1	Injection 1	Product A	A1	Reduced IgG	¥								
2	Sample 02_02	Sample 02	A2	Reduced IgG									
3	Sample 03_03	Sample 03	A3	Non-reduced IgG									
4	Sample 04_04	Sample 04	A4	MW Markers	_								
5	Sample 05_05	Sample 05	A5	Reduced IgG									
6	Sample 06_06	Sample 06	A6	Reduced IgG									
7	Sample 07_07	Sample 07	A7	Reduced IgG									
8	Sample 08_08	Sample 08	A8	Reduced IgG									

• To add sequential replicate injections: Highlight an injection and click **Replicate**. A new injection will be added under the row you selected

Injections	🔚 History 👖 Notes				🕕 Pause 🛛 Stop	👫 Add 📗 Replicate 🔀 Remove 🕞 📄 🗖 🗖
	Injection Name	Sample ID	Location	Method	Notes	Replicate selected injections
1	Injection 1	Product A	A1	Non-reduced IgG		·
2	Sample 02_02	Product B	A2	Reduced IgG		
3	Product C_03	Product C	A3	Reduced IgG		
4	Product D_04	Product D	A4	Reduced IgG		
5	Product E_05	Product E	A5	Reduced IgG		
6	Product F_06	Product F	A6	Reduced IgG		

Injections 🔚 History 👖 Notes							🕌 Add	📗 Repli	cate	🔀 Remove	E (3 - 0
	Injection Name	Sample ID	Location	Method	Notes							
1	Injection 1	Product A	A1	Non-reduced IgG								
2	Sample 02_02	Product B	A2	Reduced IgG								
∨ 3	Product C_03	Product C	A3	Reduced IgG								
4	Product C_04	Product C	A3	Reduced IgG								
5	Product D_05	Product D	A4	Reduced IgG								
6	Product E_06	Product E	A5	Reduced IgG								

• To add injections at the end of the batch: Click on any sample position in the Layout pane or sample injection in the Injection table and click Add. A new injection using the same sample will be added to the end of the table. Assign the method if needed.

Injection Name Sample ID Location Method Notes 1 Injection 1 Product A A1 Non-reduced IgG 2 Product B_02 Product B A2 Reduced IgG 3 Product C_03 Product C A3 Reduced IgG 5 Product D_05 Product D A4 Reduced IgG	•
1 Injection 1 Product A A1 Non-reduced IgG 2 Product B_02 Product B A2 Reduced IgG > 3 Product C_03 Product C A3 Reduced IgG 5 Product D_05 Product D A4 Reduced IgG	
> 3 Product C_03 Product C A3 Reduced IgG 5 Product D_05 Product D A4 Reduced IgG	
5 Product D_05 Product D A4 Reduced IgG	
6 Product E_06 Product E A5 Reduced IgG	
7 Product F_07 Product F A6 Reduced IgG	
8 Product G_08 Product G A7 Reduced IgG	
9 Product H_09 Product H A8 Reduced IgG	
10 Product H1_10 Product H1 A9 Reduced IgG	
11 Product H2_11 Product H2 A10 Reduced IgG	
12 Product H3_12 Product H3 A11 Reduced IgG	
13 Product H4_13 Product H4 A12 Reduced IgG	

• To copy and paste injections: Right-click on an injection in the Injection table and select Copy. Click on the injection number above where you want to insert the copied injection, right click and select Paste. The copied injection will be inserted under the row you selected.

11. Add programmed pauses or stops in the batch to automatically pause or stop after injections (optional).

• **To program a pause:** Highlight the injection you want to pause at and click **Pause**. The batch will pause after that injection is complete. To resume the batch, click **Continue** in the instrument status bar.

Injectio	ons 🛛 🔚 History 🚺 N	lotes	U Pause	top 👫 Add 📊	Replicate	Remove	E E
	Injection Name	Sample ID		e after the selected	d injection	tes	
1	Sample 01_01	Sample 01	A1	Method 1	-	-	
2	Sample 02_02	Sample 02	A2	Method 1			
3	Sample 03_03	Sample 03	A3	Method 1			
Iniecti	ions 🔲 History 🎹	Notes	O Pause	Stop 🕂 Add	Replic	ate 🔀 Rem	iove 🗐
Injecti	ons 🔚 History 🏋 Injection Name	Notes Sample ID	Pause	Stop 🕂 Add	Replic	cate 🔀 Rem	iove 🗐
Injecti 1					Replic		iove 🗐
	Injection Name	Sample ID	Locatio	on Method	Replic		iove 🗐
-	Injection Name Sample 01_01	Sample ID Sample 01	Locatio A1	on Method Method 1	Replic		iove 🕂

• To stop the run after a specific injection: Highlight the injection you want the batch to stop at and click Stop. Maurice will continue the batch through the selected injection, then stop the batch and perform end-run cleanup steps.

	Injection Name	Sample ID	Location	Stop after the sel	ected injection		
1	Sample 01_01	Sample 01	A1	Method 1			
2	Sample 02_02	Sample 02	A2	Method 1			
3	Sample 03_03	Sample 03	A3	Method 1			
Injecti	ons 🛛 🔚 History 👖 N	Votes	🕕 Pause 🕒 Sto	op 🕂 Add 📊 Re	plicate 🕌 Remov	e 🕀 🤅	3 -
Injecti			Pause O Sto Location	op 🚰 Add 📗 Re	plicate 🕌 Remov	e 🕂 🤅	3
Injecti 1	ons History T N Injection Name Sample 01 01	Notes Sample ID Sample 01				e 🕀 [3
	Injection Name	Sample ID	Location	Method		e 🕀 🤅	3
-	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method Method 1		e \Xi [3 -

12. Click on the Notes pane, then click in the notes area and type any information you want to add about your batch (optional).



13. You can preset the parameters used to analyze data generated with the batch (optional). We recommend using the default parameters for CE-SDS PLUS applications, but if you want to modify parameters:

Aarkers Peak Names	Markers			
eak Names Peak Fit	Analysis Group	IS	Markers	
Advanced Signal Processing	Standards		Internal Standard Time 75	0 Seconds
			Markers Injection no mark	ers 🗸
			MW (kDa)	RMT
	Add	Remove	10	1
			20	1.15
	Apply Default		33	1.3
	Apply Default:		55	1.5
	Standards		<u> </u>	1.8
	Apply Override	5:	178	2.05
	Apply To	Group	270	2.4
	Sample	Standards		
			Add	Remove
	Add	Remove		

a. Select Edit from the main menu and click Default Analysis. The following screen will display:

b. Change the parameters you want to, then click **OK**. For detailed information on analysis parameters, please refer to "Analysis Settings Overview" on page 713.

- 14. You can preset the parameters used to view data when the batch is complete (optional). Default Analysis View Parameters must be set before you start the batch and cannot be modified once the batch starts. However, you can still manually change parameters in the Analysis pane using the Graph Options button:
 - a. Select Edit from the main menu and click Default Analysis View. The following screen will display:

of Default Analysis View Ma	urice CE-SDS PLUS			×
Graph View Options Lane View Options	Graph View Options Graph View Options Antering Peak Names Peak Names Peak Values Fitted Peaks Baseline Fit Grid Lines Plot Label Sample Method Injection Injection Name			×
	ОК С	Cancel	Apply	

- b. Change the parameters you want to, then click OK. For detailed information on analysis parameters, please refer to "Customizing the Data Display" on page 695.
- 15. Once all of your sample, method and injection info is entered, select File > Save. Enter any comments on the batch if you want, then click Save.

😨 Save Batch Comment		×
Batch: Maurice CE-SDS PLUS Comment:		
ŕ		
	Save	Cancel

16. Enter a name for your batch then click Save.

Step 7: Start the Batch

1. Make sure Maurice is connected to Compass for iCE. If he isn't, select **Instrument** and click **Connect**. Then select your Maurice system and click **Connect**.

2. Click **Start** to start your batch.

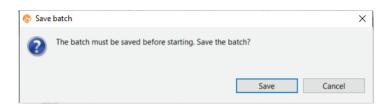
NOTES:

An alert may appear if the wrong cartridge is installed or if a cartridge post-run cleanup or cartridge purge is recommended. See page "Step 5: Check for Cartridge Alerts" on page 300 for more information.

An alert may appear if the wrong adapter is installed or if you are starting a CE-SDS PLUS batch on MauriceFlex and have not locked the reagent vials in place. See "Adapter and Insert Alerts" on page 403 for more information.



3. You will be asked to save your batch before starting the run. Click **Save**.



- 4. The Start Run box shows you the number of injections and batches remaining on your cartridge. Make sure you still have enough injections left before you start the run. If not, prep a new cartridge.
- 5. Click in the **Results File name** box if you want to change the default run file name. Otherwise just leave it as is.

	×
Batch: Maurice CE-SDS PLUS	
Results file name :	Browse
2023-02-10_20-16-12_Maurice CE-SDS PLUS	
Location: C:\Users\Andrea\Documents\Compass for iCE\Runs	
Comment:	
Cartridge	
Type: CE-SDS PLUS Injections per Batch: 48	
Expires : Jan 2025 Injections Remaining : 439 (39 guaranteed)	
Serial Number : 0000000001 Batches Remaining : 20	
Description of the second seco	
Start Ca	ncel

6. If you don't want to save the file to the default Runs folder, click Browse to select a different location.

- 7. Enter any run details you'd like in the Comments box (optional).
- 8. Click **Start** to start the run.

NOTE: The indicator light on Maurice's front panel will pulse slowly while he's running the batch.

To monitor the progress of your batch, click the Run Summary tab. See Chapter 16: "Run Status" for more details.

		3967_KF1117_JM_Ma	urice CE-SDS	PLUS - Compass for	ICE		- ø ×
ile Edit Instru	ment Window	Help					Summary 4 Analys
						A BORU TUR	Summary en Analys
C Runni	ng Paus		_				
		Thu 8:31 AM	4				Thu 10:39 AM
un: 2023-03-0	9_08-21-35_623	0303967_KF1117_JN	(Maurice CE-	SDS PLUS			
Injections						° □	0
	n Sample ID	Locati Method	Status	Time	Sample T	run 2023-03-09_08-21-35_6230303967_KF1117_JM_Maurice CE-SDS PLUS	
		Setup	Complet.			path	
	3 6230303			= 25 mins		batch Maurice CE-SDS PLUS	
2 62303	13 6230303					batch type CE-SOS	
		Cleanup					
						instrument Maurice : Kifer kf1117 - kf1117	
						samples 48 viais	
						started Thu 8:31 AM Mar 9, 2023 PST	
						cartridge CE-SDS PLUS	
						serial number 6230303967	
						injections per batch 48	
						injections remaining 500 (100 guaranteed)	
						batches remaining 25	
						expires Mar 2024	
						aA Separation Plot	
							Zoom O
						3	- E
						14 27	1
						3	
						2	
						27	
						1 H	
						4 HO LO	
						* 0	
						10	
						0 50 100 158 209 256 308 300 468 550 550 600 169 776 758 500 550 500 50 100 1100 1.000 1.1	3 1,250 1,300 1,350

To view results, analyze results or change analysis parameters on completed injections while the batch is still running, click the **Analysis** tab. See Chapter 20: "CE-SDS Data Analysis" for more details.

File Edit	View Instrument	Window	Help														
0	Running	Pause	Tue 10:49 AM									Wed 9:39		💾 Batch	ျှို့ Run Sur	nmary 📠 A	nalysis
🗮 Standar	rds 🚊 Samples																
Experime	ent			💹 Graph											3	: 8 F ≡ 🗖] ~ - 0
Injection	Sample	Location	Method							16	5						
1	MW ladder	A1	Method3	55													
2	IgG2B-R	B1	Method1										1.31				
3	hSAP IgG-R	C1	Method1	50									1.31				
4	IgG2B-NR	D1	Method2														
5	hSAP-IgG-NR	E1	Method2	45													
6	IgG2B-R	B1	Method1													IgG2B-R	
7	hSAP IgG-R	C1	Method1	40												16	
8	IgG2B-NR	D1	Method2													10	
9	hSAP-IgG-NR	E1	Method2	35													
10	MW ladder	A1	Method3														
11	IgG2B-R	B1	Method1														
12	hSAP IgG-R	C1	Method1	1 S 31													
\varTheta 13	IgG2B-NR	D1	Method2	E													
🕴 14	hSAP-IgG-NR	E1	Method2	2 25 1													
🕴 15	IgG2B-R	81	Method1	Ę.													
16	hSAP IgG-R	C1	Method1	(UMM) 30 · 25 · 20 ·													
17	IgG2B-NR	D1	Method2														
18	hSAP-IgG-NR	E1	Method2	15													
😆 19	MW ladder	A1	Method3														
3 20	IgG2B-R	81	Method1	10					1								
3 21	hSAP IgG-R	C1	Method1														
22	IgG2B-NR	D1	Method2	5 -				1									
🙆 23	hSAP-IgG-NR	E1	Method2														
🕴 24	IgG2B-R	B1	Method1	0	/	1/2		~~ [
25	hSAP IgG-R	C1	Method1		\sim	V											
26	IgG2B-NR	D1	Method2	-5													
😏 27	hSAP-IgG-NR	E1	Method2														
28	MW ladder	A1	Method3	-10													
🙆 29	IgG2B-R	B1	Method1	0.2	2 0.3 0	.4	0.5 (0.6 0.7	0.8	0.9		1.1 1.2	1.3	1.4	1.5	1.6 1.1	7 1.8
\varTheta 30	hSAP IgG-R	C1	Method1							Relative	Migration Tir	ne					
😆 31	IgG2B-NR	D1	Method2	Peaks	Injections												
6 32	hSAP-IgG-NR	E1	Method2				_		_	_	_			_			
6 33	IgG2B-R	81	Method1	Injection	Sample	Peak	Name	Time	RMT	Height	Raw Area	Area	% Total	% Area	width	Baseline	Resolutio
<mark>69</mark> 34	hSAP IgG-R	C1	Method1	6	IgG2B-R	1		1061.8	1.307	49.2	1385	1304.3	100.0		10.5	0.8	
😆 35	IgG2B-NR	D1	Method2														
€ 36	hSAP-IgG-NR	E1	Method2														
<mark>€</mark> 37	MW ladder	A1	Method3														

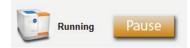
When your batch is complete, you can view electropherograms for all injections in the Analysis tab, and all batch and injection details in the Run Summary tab.

NOTE: If you'd like Maurice to let you know when your run is done, you can set him up to tweet you. Go to "Setting Up Maurice Systems to Send Tweets" on page 764 for more info.

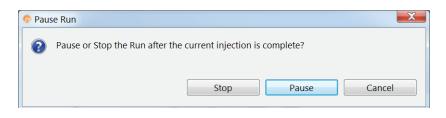
Editing a Running Batch

You can pause a batch after it's started to make updates or add samples and reagents.

1. Select Instrument > Pause or select the Pause button.



2. Click Pause in the pop-up window.



The Pause button will change to Continue but Maurice's status will stay at Running until Compass for iCE completes the current injection or calibration.



- You can now make these edits to the batch:
 - Add sample(s)
 - Add injection(s) to the end of the batch
 - · Modify injections that haven't completed and aren't greyed out
 - Create a new method
 - Update the method. Once a method is run it can only be updated. Highlight the method you want to edit and click **Update** in the Methods pane. The software will copy the parameters into a new method that you can modify.

3. When Maurice completes the current injection, his status will change to Paused and the progress bar will turn yellow.

NOTE: Maurice's status light will change from a pulsing blue to a blue pulse with magenta flashes which means he's paused the run.

	Paused	Continue		
_			Mon 1:43 PM	

The status in the Injection pane also changes to Paused and the pause duration updates live. You can now open the instrument door to:

• Add new samples

IMPORTANT

The door must be closed within 15 minutes of opening it to avoid potential assay performance issues.

NOTE: If the door is open for more than 30 seconds, a white light near the cartridge will start to flash and a warning message displays in Compass for iCE until the door is closed.

4. To continue the batch, click **Continue**. Changes you made to the batch are saved and Maurice will continue with the next sample injection.

NOTE: The D2 lamp is turned off for safety reasons when the door is opened. Once the batch is continued, Maurice will pause for seven additional minutes before the next injection to let the lamp re-stabilize. During that time, the batch status in Compass for iCE will display injection loading.

Post-batch Procedures

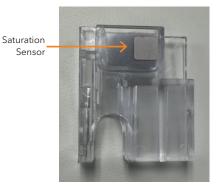
When the batch is done:

- 1. Open Maurice's door. The lights on either side of the cartridge slot will be **orange** as Maurice will have already disengaged the cartridge.
- 2. If you're using the optional Maurice Filter Kit to contain βME odor, cover the 96-well sample plate immediately with a plate lid.
- 3. Remove your samples. Leave the Water (P3), Wash Solution (P5), and Air (P6) vials in place if your cartridge still has injections left since they will be needed for the cartridge post-run cleanup step. Discard the remaining reagent vials.
- 4. Gently pull out the cartridge making sure the cartridge inlet doesn't come into contact with any surface.

NOTE: If you see any separation matrix sticking to the capillary inlet, soak it in DI water for 5 minutes. Then wipe it using a lint-free laboratory wipe that's been moistened with DI water.



- 5. Pull the cartridge insert out.
- 6. Remove the Top Running Buffer vial and dispose of it according to your institution's safety and waste disposal guidelines.
- 7. Check the saturation sensor on the back of the cartridge insert. If it's red, you'll need to use a new cartridge insert for your next batch. If the saturation sensor isn't red, you can keep using the current cartridge insert with that cartridge.



NOTE: Don't dispose of the cartridge insert unless the saturation sensor is red.

If you're at 100 injections, you've reached the limit of guaranteed performance for the CE-SDS PLUS cartridge. To dispose of a finished cartridge, put it in its original packing and discard it along with the cartridge insert and the Top Running Buffer vial per your institution's safety and waste disposal guidelines. Discard the cleaning vial you've used with that cartridge too.

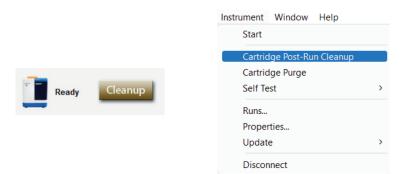
NOTE: Disposal of cartridges, sample plates and vials depends on the samples you ran. If you aren't sure what your sample origins are, we recommend you dispose of everything in biohazard waste.

If the cartridge will be used again, clean up and store the cartridge:

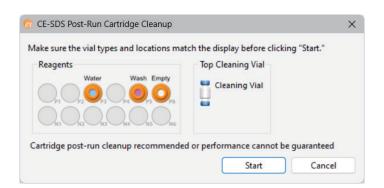
- a. Verify that there is 1.5 mL of DI water in the Water (P3) vial, 1.5 mL of Wash Solution in the Wash Solution (P5) vial, and air in the empty (P6) vial.
- b. Insert a Cleaning Vial into the cartridge insert.



- c. Slide the cartridge insert back into the cartridge.
- d. Insert the cartridge in Maurice.
- e. Click on the brown **Cleanup** button in the Instrument Status Bar or select **Instrument** and **Cartridge Post-Run Cleanup** in the Compass main menu.



f. You'll get the following message. Click **Start**. It'll only take six minutes.



- g. Once the cleanup procedure is done, discard the reagent vials and remove the cartridge.
- h. Pull the insert from the cartridge.
- i. Remove the Cleaning Vial and push the empty insert back into the cartridge.

NOTE: The cleaning vial is paired with the cartridge and can be used for a maximum of five Cartridge Cleanup cycles of that cartridge. Dispose of the cleaning vial when you dispose of the cartridge. Don't use it with other cartridges.

j. Put the cartridge back in its protective packaging and store it at room temperature.

!WARNING! SHARPS HAZARD

The capillary inlet of the cartridge may present a potential sharps hazard. Dispose of used cartridges according to your organizations health and safety regulations.



!WARNING! BIOHAZARD

Cartridges, sample plates and vials should be handled by procedures recommended in the CDC/NIH manual: Biosafety in Microbiological and Biomedical Laboratories (BMBL). The manual is available from the U.S. Government Printing Office or online at http://www.cdc.gov/biosafety/publications/bmbl5/.

Depending on the samples used, the cartridges, plates and vials may constitute a chemical or a biohazard. Dispose of the cartridges, plates and vials in accordance with good laboratory practices and local, state/ provincial, or national environmental and health regulations. Read and understand the Safety Data Sheets (SDSs) provided by the manufacturers of the chemicals in the waste content before you store, handle, or dispose of chemical waste.

Checking Your Data

Compass for iCE detects your sample proteins, CE-SDS MW Markers and Internal Standard peaks and reports results automatically. But, we always recommend you review your data using the steps in this section as a good general practice to make sure your results are accurate. If you see a data warning in the Experiment pane, these steps will also help you identify and correct any issues.

Step 1: Check Your Internal Standard

To make sure your Internal Standard is identified correctly:

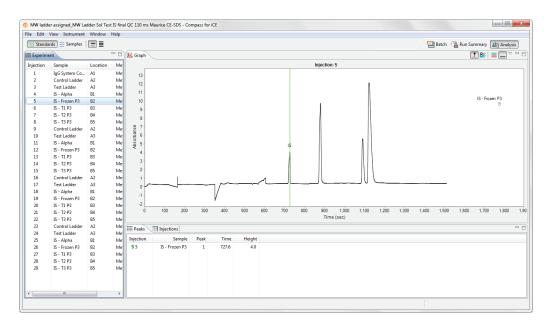
- 1. Go to the Analysis screen and open your run (if it isn't already open).
- 2. Click Standards in the View bar.

File	Edit	View	Instrument	Window
Ħ	Stand	ards	🔆 Samples	

3. Click the View Selected icon in the View bar.

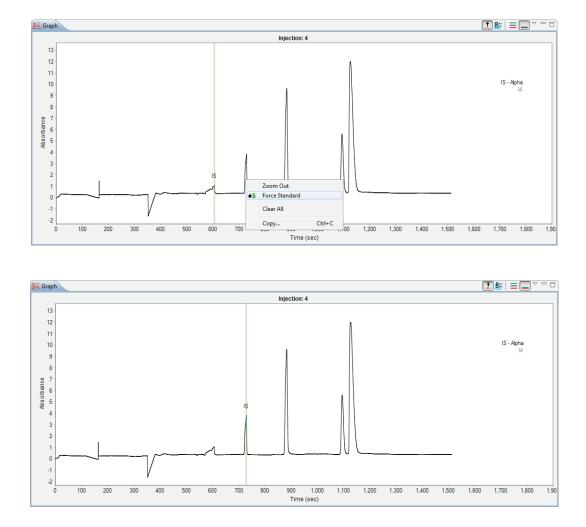
File	Edit	View	Instrument	W	/indow
Ē	Stand	lards	E Samples		∎≣
				1	

- 4. Click Injection 1 in the Experiment pane.
- 5. Check that your Internal Standard in the electropherogram has been correctly identified. It'll be labeled IS and will have a green vertical line running through it. The Internal Standard is also identified with an **S** in the Peaks table.



6. If your Internal Standard isn't identified correctly, here's how to manually correct it:

To set an unidentified peak as the Internal Standard: Right-click the peak in the electropherogram or Peaks table and select **Force Standard**. Compass will assign that peak as the Internal Standard.

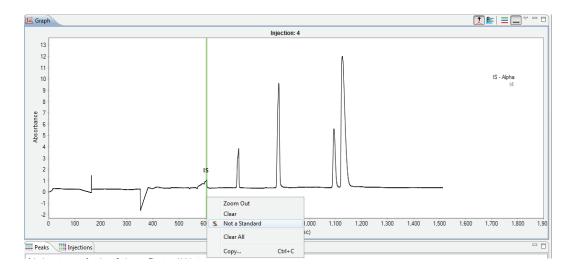


A lock icon indicating the Internal Standard was set manually will display next to the peak in the Peaks table and a check mark will appear next to the injection in the Experiment pane to show a manual correction was made.

Peaks III Injections				Experim	ent			
Injection	Sample	Peak	Time	Height	Injection	Sample	Location	М
1	Sample 1	11	548.2	115.1	Ø 1	Sample 1	A1	М
1	Sample 1	12	557.7	115.2	2	Sample 1	A1	М
1	Sample 1	13	572.0	134.0	3	Sample 1	A1	М
1	Sample 1	14	583.5	149.7	4	Sample 1	A1	Μ
≜S 1	Sample 1	15	590.6	190.0	5	Sample 1	A1	М
1	Sample 1	16	710.8	230.3	6	Sample 1	A1	Μ
1	Sample 1	17	714.6	278.5	7	Sample 1	A1	М

NOTE: To remove an Internal Standard peak assignment that was made manually, right click on the peak in the electropherogram or Peaks table and click **Clear**. To clear all the manual settings for the injection, click **Clear** All.

If an incorrect peak is identified as the Internal Standard: Right-click the peak in the electropherogram or Peaks table and select Not a Standard.



A check mark will appear next to the injection in the Experiment pane to show a manual correction was made.

Experiment 🛛 🗖						
Injection	Sample	Location	Method			
V 1	Sample 1	A1	Method1			
2	Sample 1	A1	Method1			
3	Sample 1	A1	Method1			
4	Sample 1	A1	Method1			
5	Sample 1	A1	Method1			
6	Sample 1	A1	Method1			
7	Sample 1	A1	Method1			

7. Repeat the previous steps for all other injections to make sure your Internal Standard is identified correctly.

Step 2: Set Your Molecular Weight (MW) Markers

NOTE: You'll only need to do this if you ran the CE-SDS MW Markers. If you didn't, you can skip to the next section.

Compass reports the relative migration time (RMT) of your sample in the Peaks table. If you also want to know the relative molecular weight of your sample, you can run the CE-SDS MW Markers as one of your injections.

You'll see these sizing markers when you run the CE-SDS MW Markers: 10, 20, 33, 55, 103, 178, and 270 kDa.

To get MW data:

1. Click **Samples** in the View bar.

File	Edit	View	Instrument	Window
Ħ	Stand	ards [Samples	∎∎

2. Select Edit from the main menu and click Analysis. In the Analysis window, select Markers in the left sidebar. Then click the Markers Injection drop down menu to select the injection you ran your CE-SDS MW Markers in.

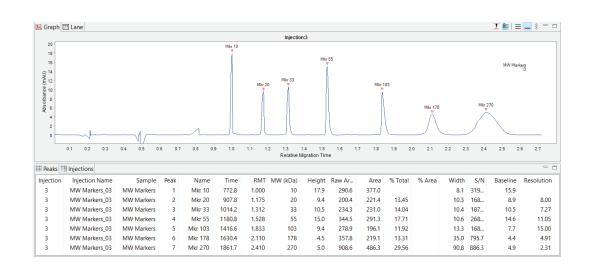
Markers Peak Names	Markers					
Peak Fit Advanced	Analysis Groups		Markers			
Signal Processing	Standards		Internal Standard Time 750 Markers Injection no markers	Seconds		
			no markers MW 2	RMT		
			3	1		
	Add	Remove	20	1.15		
			33	1.3		
	Apply Default:		103	1.8		
	Standards	~	178	2.05		
	Apply Override:		270	2.4		
	Apply To Sample	Group Standards				
			Add	Remove		
	Ado	Remove				

3. The default Maurice CE-SDS MW Markers molecular weights and relative migration time (RMT) values are already populated in the table. If you'd like to use these values, skip to the next step. If you're using different markers, click in the MW and RMT cells to type new values, click a row and select **Remove** to delete, or click Add to add a new one.

MW (kDa	a) RMT
15	1
2	0 1.15
3	3 1.3
5	5 1.5
10	3 1.8
17	8 2.05
27	0 2.4

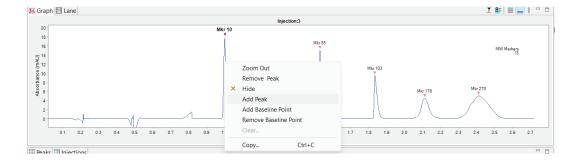
4. Click OK to close the Analysis window. Compass will automatically assign the molecular weights to your makers and label them Mkr. A MW (kDa) column will also now display in the Peaks table.





5. It's always a good idea to verify that all your CE-SDS MW Markers are identified correctly. Here's how to manually correct them:

To set an unidentified peak as a MW Marker: Right-click the peak in the electropherogram or Peaks table and select **Add Peak**. Compass will assign that peak as a MW Marker, and correctly reassign the remaining marker peaks.

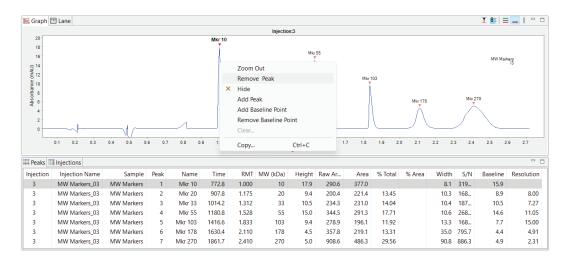


A check mark will appear next to the injection in the Experiment pane to show a manual correction was made.

Experiment 🗖 🗖					
Injection	Sample	Location	Me		
1	IgG System Co	A1	Me		
✓2	Control Ladder	A2	Me		
3	Test Ladder	A3	Me		
4	IS - Alpha	B1	Me		

NOTE: To remove MW Marker peak assignments that were made manually, right click on the peak in the electropherogram or Peaks table and click **Clear**.

If an incorrect peak is identified as a MW Marker: Right-click the peak in the electropherogram or Peaks table and select **Remove Peak**. Compass should correctly reassign the remaining peaks as markers and update the Peaks table.



A check mark will appear next to the injection in the Experiment pane to show a manual correction was made.

Experime	Experiment 🛛 🖓									
Injection	Sample	Location	Me							
1	IgG System Co	A1	Me							
✓2	Control Ladder	A2	Me							
3	Test Ladder	A3	Me							
4	IS - Alpha	B1	Me							

Step 3: Checking Sample Peaks

All detected peaks will be labeled automatically with the RMT (default) or apparent MW (if the CE-SDS MW Markers were run).

To make sure your sample proteins are identified correctly:

1. Click **Samples** in the View bar.

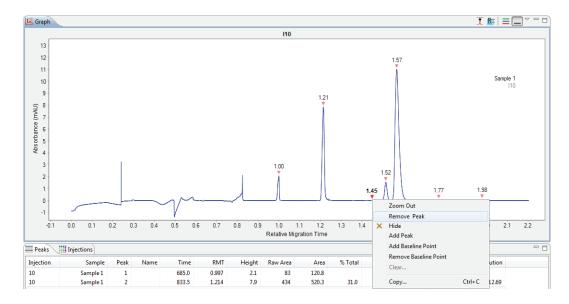
File	Edit	View	Instrument	Window
Ħ	Stand	ards [Samples	≣≡

2. Click the View Selected icon in the View bar.



- 3. Click Injection 1 in the Experiment pane.
- 4. If your sample peaks aren't identified correctly, here's how to manually correct them:

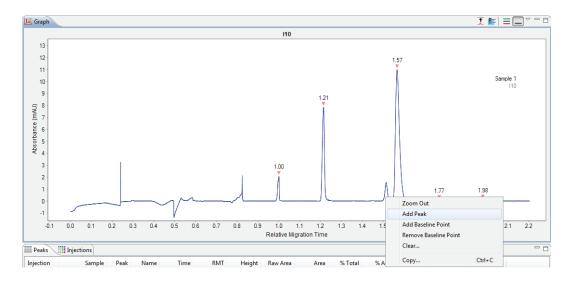
If a peak is incorrectly identified as a sample peak: Right-click the peak in the electropherogram or Peaks table and select **Remove Peak**. Compass will no longer identify it as a sample peak in the electropherogram and the peak data will be removed in the results table.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

Experiment 🗖 🗖								
Injection	Sample	Location	Method					
1	Sample 1	A1	Method1					
2	Sample 1	A1	Method1					
3	Sample 1	A1	Method1					
4	Sample 1	A1	Method1					
5	Sample 1	A1	Method1					
6	Sample 1	A1	Method1					
7	Sample 1	A1	Method1					
8	Sample 1	A1	Method1					
9	Sample 1	A1	Method1					
√ 10	Sample 1	A1	Method1					
11	Sample 1	A1	Method1					
12	Sample 1	A1	Method1					

To identify a peak as a sample peak: Right-click the peak in the electropherogram or Peaks table and select Add Peak. Compass will calculate and display the results for the peak in the results table and identify the peak in the electropherogram.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

Experiment 🗖 🗖								
Injection	Sample	Location	Method					
1	Sample 1	A1	Method1					
2	Sample 1	A1	Method1					
3	Sample 1	A1	Method1					
4	Sample 1	A1	Method1					
5	Sample 1	A1	Method1					
6	Sample 1	A1	Method1					
7	Sample 1	A1	Method1					
8	Sample 1	A1	Method1					
9	Sample 1	A1	Method1					
√ 10	Sample 1	A1	Method1					
11	Sample 1	A1	Method1					
12	Sample 1	A1	Method1					

NOTE: To remove sample peak assignments that were made manually and go back to the original peak data, right-click the peak in the electropherogram and select **Clear**.

5. Repeat the previous steps for the remaining injections to make sure all sample peaks are correctly identified.

Step 4: Assigning Peak Names

Compass can also optionally identify and automatically name sample peaks using user-specified peak name settings. For more information on how to do this, see "Manual Peak Integration" on page 739.

Chapter 13: Turbo CE-SDS Batches

Chapter Overview

- Overview
- Batch Screen Overview
- Opening a Batch
- Creating a New Batch
- Viewing Replicate Injections
- Batch History
- Making Changes to a Batch
- Viewing and Editing Batches in Completed Runs
- Copying and Pasting Injection Names or Sample IDs from other Documents
- Importing and Exporting Injections
- Importing and Exporting Methods
- Batch Reports

Overview

Maurice Turbo CE-SDS batches can be run on Maurice, Maurice S., or MauriceFlex systems using a Turbo CE-SDS cartridge.

Batch Screen Overview

You can use the Batch screen to create, view, and edit batches. To get to this screen, click the Batch screen tab:

🖽 Batch 强 Run Summary 🏼 🏥 Analysis

Batch Screen Panes

The Batch screen has five panes:

- Layout Displays a map of either the 96-well plate or 48-vial tray of batch sample locations.
- **Injections** Lists the injections, sample ID, sample locations and methods that Maurice or Maurice S. will execute for each sample in the batch.
- History Lists all batch file events from initial creation to the most current update.
- Notes Lets you enter specific information about your batch.
- Methods Lets you create methods and enter method parameters used in the batch.

o Maurice CE-SDS T	URBO - INTERNAL RELEASE - Compass	for iCE 4.0).0-20221221-2bfdf4d					-		×	
File Edit Instrumer	nt Window Help										
							1	Batch 🔮 Run Sun	ımary 🏨 A		
Batch: Maurice CE-SD	S TURBO	📰 Injections 🖺 History T Notes 🔍 🗖									
						Pause	O Stop 🕌	Add 📕 Replicate	🔀 Remove	. 🗉 🖻	
🖭 Layout			Injection Name	Sample ID	Location	Method	Notes				
🗐 🚺 10°C 🔻	🗲 Add 👻 🐼 Remove	1	Sample 01_01	Sample 01	A1	Reduced IgG					
C1 (Sample 02_02	Sample 02	A2	Reduced IgG					
0		3	Sample 03_03	Sample 03	A3	Reduced IgG					
Wash	Run Run Run										
P											
E											
Methods						1				- 0	
									New R	lemove	
Name Sample Load		1	Separation								
Reduced IgG 8 sec 3500 Volts			5.5 min 4200 Volts								
Non-reduced IgG	8 sec 3500 Volts	4	8.0 min 4200 Volts								
MW Markers	8 sec 3500 Volts	1	8.0 min 4200 Volts								

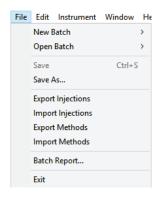
Software Menus Active in the Batch Screen

These main menu items are active in the Batch screen:

- File
- Edit
- Instrument (when the software is connected to Maurice, Maurice S. or MauriceFlex)
- Window
- Help

File Menu

These File menu options are active:



- New Batch Creates a new batch from a starter template.
- Open Batch Opens an existing batch.
- Save/Save As Saves the open batch.
- Export Injections Exports injections from the current batch as a .csv file.
- Import Injections Imports injections into the current batch from a .csv file.
- Export Methods Exports method(s) from the current batch as separate files.
- Import Methods Imports saved method(s) into the current batch.
- Batch Report Exports a table of sample and method details for each injection in the batch as a PDF file.
- Exit Closes Compass for iCE.

Edit Menu

The following Edit menu options are active in the Batch screen:

Edit] Instrument Windo	w Help	_	
	Cut	Ctrl+X		
	Сору	Ctrl+C		(,
	Paste	Ctrl+V		In
	Plate Layout	•	•	48 Vials
	Default Analysis			96-well Plate
	Preferences			Air

- Cut Cuts the information currently selected.
- Copy Copies the information currently selected.
- **Paste** Pastes the copied information.

NOTE: Cut, Copy and Paste work differently depending on the pane you're in. How and when you can use them is described throughout the chapter.

- Plate Layout Lets you select between a 96-well plate or a 48-vial tray to run samples in.
- Default Analysis Displays the default settings that will be used to analyze the data generated with your batch.
- **Default Analysis View** Displays the default settings that will used to view the data generated with your batch.
- **Preferences** Lets you set and save your preferences for Access Control, data export, graph colors, grouped data and Twitter settings. See Chapter 21, "Setting Your Preferences" for more information.

Opening a Batch

To open an existing batch:

1. Select **File** in the main menu and click **Open Batch**.

File	Edit Instrument	Wir	ndow Help
	New Batch		
	Open Batch	•	Platform CE-SDS2
	Save		Platform CE-SDS1
	Save As		Maurice CE-SDS3 Maurice CE-SDS2
	Batch Report		
	baten neportan		Maurice CE-SDS1
1	Exit		Browse

2. A list of the last five batches opened will display based on the last location found. If the location of the file has changed, you may need to navigate to find the file. Select one of those or click **Browse** to open the Batches folder and select a different one.

3. To make changes to the batch, see the steps in "Creating a New Batch". When you're done, select File from the main menu and click **Save**.

Creating a New Batch

To create a new batch, we recommend that you use one of the template methods and make any necessary modifications from there.

Step 1 - Open a Template Batch

1. Select File in the main menu and click New Batch:

le Edit Instrume	nt Window Help	i de la construcción de la constru
New Batch	>	Maurice cIEF
Open Batch	>	Maurice CE-SDS PLUS
Save	Ctrl+S	Maurice Turbo CE-SDS™
Save As	Cuita	MauriceFlex clEF
Save As		MauriceFlex Fractionation
Export Injections		

NOTE: Only template batches specific to your Maurice will be available when you are connected to the instrument. Template batches will not appear in the menu if that application type cannot be performed on your instrument.

2. Select Maurice Turbo CE-SDS. A batch using the default method will display.

	ent Window Help								
	G						💾 Batch 🖓 Run S		alys
Batch: Maurice CE-S	DS TURBO	Inject	ions 🔛 History 🌃 Not	tes					
🗉 Layout							ause 🖸 Stop 🛱 Add 📗 Replica	ite 🕅 Remove 🛛	æ
2 ayout 10°C		1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method Reduced IgG	Notes		
C1	C2 Water Sep. Wash Empty								
1 2 3 4 B 0 0 0 C 0 0 0 E 0 0 0 F 0 0 0 H 0 0 0									
Methods								e	-
								New Ren	no
Name Reduced IgG	Sample Load 8 sec 3500 Volts		Separation 5.5 min 4200 Volts						
Non-reduced IgG	8 sec 3500 Volts	8.0 min 4200 Volts							
MW Markers	8 sec 3500 Volts		8.0 min 4200 Volts						

Step 2 - Assign Your Samples

The Layout pane shows the default locations of where batch reagent should be placed in your Maurice system's samples and reagents platform, and a map of either the 96-well plate or the 48-vial tray used for samples.

יו 🛄 🌔	0°C ₹	CT Add	• 🕻 Rem	ove
		Vater Sep. Wa	sh Empty	
	Wash	Run Ru		
1 1		7 8 9 1		
B				
cOC			DOO	
DOC				
E				
			388	
HOC				



The same reagent locations are used for every batch:

- **P1** Conditioning Solution 1 with orange pressure cap
- P2 Conditioning Solution 2 with orange pressure cap
- **P3** DI water with **orange pressure cap**
- **P4** Separation Matrix with **orange pressure cap**
- **P5** Wash Solution vial with orange pressure cap
- **P6** Empty vial (air) with orange pressure cap
- N1 Wash Solution vial with clear screw cap
- N4 Running Buffer Bottom with clear screw cap
- N5 Running Buffer Bottom with clear screw cap
- N6 Running Buffer Bottom with clear screw cap
- 1. To assign samples, select a 96-well plate or 48 vials depending on what you're running. Clicking on the vial/plate icon toggles between formats.



2. Select your samples:

To import samples using a saved injections file:

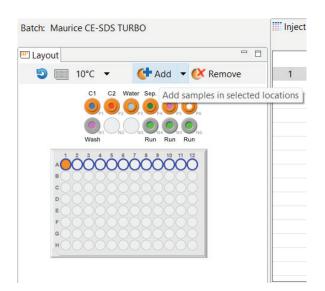
- a. Select File in the main menu and click Import Injections.
- b. Select an injections .csv file and click OK. The imported information will display in the Injections pane.
- c. Skip to step 3 on page 336.

NOTE: For more information on setting up an injections file for import, see "Importing and Exporting Injections" on page 350.

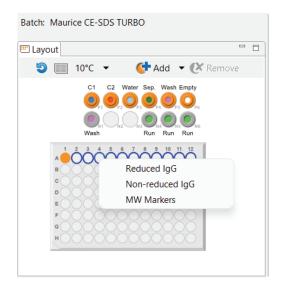
To select samples manually:

• Add samples and select methods later: Use your mouse to highlight the well or vial positions your samples are located in, then click Add. For this example we're using a 96-well plate.

NOTE: The template batch automatically adds a sample in well or vial A1 by default, but if you don't have a sample in this position you can remove it after you've added new positions for your samples.



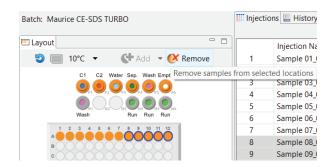
• Add samples with preassigned methods: Highlight the well or vial positions your samples are located in, then right-click and select a method.



Either option of adding samples populates the Injections table:

	Injection Name	Sample ID	Location	Method	Notes			
1	Sample 1_01	Sample 1	A1	Reduced IgG				
2	Sample 02_02	Sample 02	A2	Reduced IgG				
3	Sample 03_03	Sample 03	A3	Reduced IgG				
4	Sample 04_04	Sample 04	A4	Reduced IgG				
5	Sample 05_05	Sample 05	A5	Reduced IgG				
6	Sample 06_06	Sample 06	A6	Reduced IgG				
7	Sample 07_07	Sample 07	A7	Reduced IgG				
8	Sample 08_08	Sample 08	A8	Reduced IgG				
9	Sample 09_09	Sample 09	A9	Reduced IgG				
10	Sample 10_10	Sample 10	A10	Reduced IgG				
11	Sample 11_11	Sample 11	A11	Reduced IgG				
12	Sample 12_12	Sample 12	A12	Reduced IgG				

To remove samples, just highlight the ones you want to remove and click **Remove**. They'll also be removed in the Injections table. You can also right-click well(s) or vial(s) in the Layout pane and click **Remove Sample(s)**.



3. Compass for iCE can monitor the current during a separation for you, stop it if an abnormal current profile is detected and reinject the sample for you automatically. Reinjections are enabled by default, but if you don't want to use this feature just click the reinject icon to toggle it off.

NOTES:

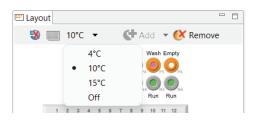
If a sample was reinjected, the injection row will be flagged in the Injections pane in the Run Summary screen. See "Injection Flags" on page 414 for more info.

A maximum of 10 reinjections are allowed per batch.



4. The sample platform is temperature controlled with a default setting of 10 °C. To change the temperature or turn it off, click the **down arrow** next to the temperature and select an option.

NOTE: The two reagent rows are kept at room temperature.



Step 3 - Assign Your Method Parameters

NOTE: There are three default methods. We recommend using the default method parameters for the listed sample types. Please see the Maurice CE-SDS Application Guide for more information on method optimization.

The Methods pane lists all of the methods used in a batch. You can add and remove methods here and change method parameters.

To import a saved method:

- 1. Select File in the main menu and click Import Method.
- 2. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

To create a new method or make changes to an existing one:

1. In the Methods table, click the first cell in the Name column and enter a new method name if needed.

Methods			New Remove
Name	Sample Load	Separation	New Renove
Reduced IgG	8 sec 3500 Volts	5.5 min 4200 Volts	
Non-reduced IgG	8 sec 3500 Volts	8.0 min 4200 Volts	
MW Markers	8 sec 3500 Volts	8.0 min 4200 Volts	

2. Click the first cell in the Sample Load column, then click the selection button [...] to set your sample load profile time (in seconds) and voltage.

			Add	Remove	
Name	Sample Load				
Reduced IgG	Voltage 1 Step)	Time (sec)	Voltage (Volts)	
Non-reduced IgG	8 sec 3500 Volts		8	3500	
MW Markers	8 sec 3500 Volts				

- To change time and voltage parameters: Just click in a cell under Time or Voltage and type the new value(s).
- To add a profile step: Click Add. A new row will be added in the table. Then just type in a load time (in seconds) and voltage value.
- To remove a profile step: Select the row you want to remove and click Remove.

3. Click the first cell in the Separation column the selection button [...] to set your separation profile parameters (in minutes) and voltage.

NOTE: Run your reduced IgG samples for 5.5 minutes and your non-reduced IgG samples, IgG Standard and CE-SDS MW Markers for 8.0 minutes. The default separation voltage for all sample types is 4200 volts.

Remove tage (Volts)
tage (Volts)
tage (Volts)
0
ř

- To change time and voltage parameters: Just click in a cell under Time or Voltage and type the new value(s).
- To add a profile step: Click Add. A new row will be added in the table. Then just type in a load time (in seconds) and voltage value.
- To remove a profile step: Select the row you want to remove and click Remove.
- 4. You can now:
 - Click New in the upper right corner of the Methods pane to add a new one if you want to use different methods for different samples. Then just repeat the steps above for the new method.
 - Make updates to the remaining methods by repeating the prior steps.
 - Select a method and click Remove in the upper right corner of the Methods pane to delete it.

Step 4 - Set Up Your Injections

The Injection pane lists all sample injections for the batch. Any samples that were added in *Step 2 - Assign Your Samples* are automatically added to this list.

NOTE: If you imported injections in Step 2, you can update the injections table and assign methods as needed using the information that follows. Otherwise skip to "Step 5 - Add Programmed Pauses and Stops (Optional)" on page 341.

Selecting an injection in the table also selects the sample the injection will be made from in the plate or vial map in the Layout pane and vice-versa.

Batch: Maurice CE-SDS TURBO	Injection	is 🔚 History 👖 Notes					- 8
					Pause	O Stop 👫 Add 📗 Replicate	🔀 Remove 🗉 🖻
E Layout		Injection Name	Sample ID	Location	Method	Notes	
😵 📖 10°C 🔻 🛛 🚷 🐨 🐼 Remove	1	Sample 01_01	Sample 01	A1	Reduced IgG		
C1 C2 Water Sep. Wash Empty	2	Sample 02_02	Sample 02	A2	Reduced IgG		
	3	Sample 03_03	Sample 03	A3	Reduced IgG		
P1 P2 P3 P4 P5 P6	4	Sample 04_04	Sample 04	A4	Reduced IgG		
	5	Sample 05_05	Sample 05	A5	Reduced IgG		
Wash Run Run	6	Sample 06_06	Sample 06	A6	Reduced IgG		
1 2 3 4 5 6 7 8 9 10 11 12	7	Sample 07_07	Sample 07	A7	Reduced IgG		
	8	Sample 08_08	Sample 08	A8	Reduced IgG		
	~	- · · · · · · · · · · · · · · · · · · ·			a		

1. To add sample names, click the **Sample ID** cell for the injection and type a name.

NOTES:

Sample IDs can be copied from other documents and pasted into Compass for iCE to make batch setup faster. Check out "Copying and Pasting Injection Names or Sample IDs from other Documents" on page 348 for more info.

If you change the sample ID when the default injection name is still being used, the injection name will automatically update to match the sample ID. If you've already changed the injection name manually, updating the sample ID will not update the injection name.

	Injection Name	Sample ID	Location	Method	Notes			_
	-				Notes			
1	Sample 1_01	Product A	A1	Reduced IgG				
2	Sample 02_02	Sample 02	A2	Reduced IgG				
3	Sample 03_03	Sample 03	A3	Reduced IgG				
4	Sample 04_04	Sample 04	A4	Reduced IgG				
5	Sample 05_05	Sample 05	A5	Reduced IgG				
6	Sample 06_06	Sample 06	A6	Reduced IgG				
7	Sample 07_07	Sample 07	A7	Reduced IgG				
8	Sample 08_08	Sample 08	A8	Reduced IgG				
9	Sample 09_09	Sample 09	A9	Reduced IgG				
10	Sample 10_10	Sample 10	A10	Reduced IgG				
11	Sample 11_11	Sample 11	A11	Reduced IgG				
12	Sample 12_12	Sample 12	A12	Reduced IgG				

The sample name also displays when you hover the mouse over the sample in the plate or vial map:

Batch: Maurice CE-SDS TURBO	Injections	🔚 History 👖 Notes	0	Pause 🛛 Stop	👫 Add 🚻 Rep
		Injection Name	Sample ID	Location	Method
🖫 Layout 📃 🗖	1	Product A_01	Product A	A1	Reduced IgG
	2	Sample 02_02	Sample 02	A2	Reduced IgG
🏐 📖 10°C 👻 💽 🔂 🐨 🚱 🐑	3	Sample 03_03	Sample 03	A3	Reduced IgG
C1 C2 Water Sep. Wash Empty	4	Sample 04_04	Sample 04	A4	Reduced IgG
	5	Sample 05_05	Sample 05	A5	Reduced IgG
	6	Sample 06_06	Sample 06	A6	Reduced IgG
	7	Sample 07_07	Sample 07	A7	Reduced IgG
NI N2 N3 N4 N5 N6	8	Sample 08_08	Sample 08	A8	Reduced IgG
Wash Run Run Run	9	Sample 09_09	Sample 09	A9	Reduced IgG
1 2 3 4 5 6 7 8 9 10 11 12	10	Sample 10_10	Sample 10	A10	Reduced IgG
	11	Sample 11_11	Sample 11	A11	Reduced IgG
B Product A	12	Sample 12_12	Sample 12	A12	Reduced IgG

2. Injection names are automatically set to 'Sample ID_injection number'. To change the name, click the **Injection Name** cell for the injection and type a name. Each injection name must be unique. If they aren't when you save the batch, Compass for iCE highlights any non-unique injection names so you can change them.

	Injection Name	Sample ID	Location	Method	Notes			
1	njection 1	Product A	A1	Reduced IgG				
2	Sample 02_02	Sample 02	A2	Reduced IgG				
3	Sample 03_03	Sample 03	A3	Reduced IgG				
4	Sample 04_04	Sample 04	A4	Reduced IgG				
5	Sample 05_05	Sample 05	A5	Reduced IgG				
6	Sample 06_06	Sample 06	A6	Reduced IgG				
7	Sample 07_07	Sample 07	A7	Reduced IgG				
8	Sample 08_08	Sample 08	A8	Reduced IgG				
9	Sample 09_09	Sample 09	A9	Reduced IgG				
10	Sample 10_10	Sample 10	A10	Reduced IgG				
11	Sample 11_11	Sample 11	A11	Reduced IgG				
12	Sample 12_12	Sample 12	A12	Reduced IgG				

NOTE: Changing the injection name won't affect the sample ID.

3. Assign your methods to each injection. Just click the **Method** cell for the injection and select a method from the drop down menu. If you added your samples with pre-assigned methods and don't need to make any changes, skip to the next step.

Injections	🔚 History 🌆 Notes				0	Pause	O Stop	🕂 Add	Replic	ate	🔀 Remove	Ŧ	8 -	, 🗆
	Injection Name	Sample ID	Location	Method		Notes								
1	Injection 1	Product A	A1	Reduced IgG	¥									
2	Sample 02_02	Sample 02	A2	Reduced IgG										
3	Sample 03_03	Sample 03	A3	Non-reduced IgG										
4	Sample 04_04	Sample 04	A4	MW Markers	_									
5	Sample 05_05	Sample 05	A5	Reduced IgG										
6	Sample 06_06	Sample 06	A6	Reduced IgG										
7	Sample 07_07	Sample 07	A7	Reduced IgG										
8	Sample 08_08	Sample 08	A8	Reduced IgG										

Hovering over a method name displays the method parameters:

Injecti	ons 🔚 History 👖 Notes		🕕 Pause 🛛 Stoj	o 📌 Add 📊 Replicate 🔀 Re
	Injection Name	Sample ID	Location	Method No
1	Product A_01	Product A	A1	Reduced lag
2	Sample 02_02	Sample 02	A2	R Reduced IgG
3	Sample 03_03	Sample 03	A3	R Separation: 5.5 min 4200 Volts
4	Sample 04_04	Sample 04	A4	Reduced igo
5	Sample 05 05	Sample 05	A5	Reduced InG

- 4. You can add or remove injections as needed using a few different options. If you don't need to make any changes here, just skip to the next step.
 - To add sequential replicate injections: Highlight an injection and click **Replicate**. A new injection will be added under the row you selected

			1							
	Injection Name	Sample ID	Location	Method	Notes			Replic	ate selected in	jections
1	Injection 1	Product A	A1	Non-reduced IgG						
2	Sample 02_02	Product B	A2	Reduced IgG						
3	Product C_03	Product C	A3	Reduced IgG						
4	Product D_04	Product D	A4	Reduced IgG						
5	Product E_05	Product E	A5	Reduced IgG						
6	Product F 06	Product F	A6	Reduced IgG						
Injectio	ns History T Nat	<u>_</u>		headed igo	n Pause	O Stop	⊨ ∆da W	Renlicate	Remove	
Injectio		es	Leasting			O Stop	🕇 Add 📗	Replicate	e 🕌 Remove	
Injectio	Injection Name	es Sample ID	Location	Method	Pause Notes	O Stop	Add	Replicate	e 🕌 Remove	• 🕀 🖻 🗖
1	Injection Name Injection 1	es Sample ID Product A	A1	Method Non-reduced IgG		O Stop 🕻	► Add 🕌	Replicate	e 🕌 Remove	• 🕀 🖻
Injectio 1 2	Injection Name	es Sample ID		Method		O Stop 🕻	🕈 Add 🛔	Replicate	e 🕌 Remove	: 🕀 🖻
1 2	Injection Name Injection 1	es Sample ID Product A	A1	Method Non-reduced IgG		O Stop	🖡 Add 🛔	Replicate	e 🕌 Remove	
1 2	Injection Name Injection 1 Sample 02_02	es Sample ID Product A Product B	A1 A2	Method Non-reduced lgG Reduced lgG		O Stop 🛓	🕈 Add 🕌	Replicate	e 🛛 🎘 Remove	: 🕀 🗖
/ 3	Injection Name Injection 1 Sample 02_02 Product C_03	sample ID Product A Product B Product C	A1 A2 A3	Method Non-reduced IgG Reduced IgG Reduced IgG		O Stop 🛓	🕇 Add 🕌	Replicate	e 🕌 Remove	• • •

• To add injections at the end of the batch: Click on any sample position in the Layout pane or sample injection in the Injection table and click Add. A new injection using the same sample will be added to the end of the table. Assign the method if needed.

Injection	is 🛛 🔚 History 👖 Notes				🕕 Pause 🖸 Stop 🕌 Add 🚻 Replicate 🕌 Remove 🕀 🖻
	Injection Name	Sample ID	Location	Method	Notes Add injections
1	Injection 1	Product A	A1	Non-reduced IgG	Additigenous
2	Product B_02	Product B	A2	Reduced IgG	
> 3	Product C_03	Product C	A3	Reduced IgG	
5	Product D_05	Product D	A4	Reduced IgG	
6	Product E_06	Product E	A5	Reduced IgG	
7	Product F_07	Product F	A6	Reduced IgG	
8	Product G_08	Product G	A7	Reduced IgG	
9	Product H_09	Product H	A8	Reduced IgG	
10	Product H1_10	Product H1	A9	Reduced IgG	
11	Product H2_11	Product H2	A10	Reduced IgG	
12	Product H3_12	Product H3	A11	Reduced IgG	
13	Product H4_13	Product H4	A12	Reduced IgG	

• To copy and paste injections: Right-click on an injection in the Injection table and select Copy. Click on the injection number above where you want to insert the copied injection, right click and select Paste. The copied injection will be inserted under the row you selected.

Step 5 - Add Programmed Pauses and Stops (Optional)

You can program pauses and stops in the batch to automatically pause or stop after injections even when you aren't in front of Maurice.

To program a pause:

Pauses are helpful when you want to review injection results before continuing with the rest of the batch.

1. Highlight the injection you want to pause at and click **Pause**. The batch will pause after that injection is complete.

NOTE: Maurice can tweet you when the batch pauses. See "Setting Up Maurice Systems to Send Tweets" on page 764.

	Injection Name	Sample ID	Loc Pau	se after the selected inject	tion tes
1	Sample 01_01	Sample 01	A1	Method 1	
2	Sample 02_02	Sample 02	A2	Method 1	
3	Sample 03_03	Sample 03	A3	Method 1	
Injectio	ons 🔚 History 🌃	Notes	🕕 Pause 🕻	Stop 🅕 Add 📗 Re	plicate 🕌 Remove 🕞 (
Injectio	- , -				plicate 🔀 Remove 📺 (Notes
Injectio	ons History 🏋 Injection Name Sample 01 01	Notes Sample ID Sample 01	Pause Locati A1		

2. To resume the batch, click **Continue** in the instrument status bar:

-	Paused	Continue	_	
			Mon 1:43 PM	

To stop the run after a specific injection:

1. Highlight the injection you want the batch to stop at and click **Stop**. Maurice will continue the batch through the selected injection, then stop the batch and perform end-run cleanup steps.

njecti	ons 🛛 🔚 History 🚹 N	NOTES	🕕 Pause 🚺 Sto		replicate	He Kelliove	a.	8
	Injection Name	Sample ID	Location	Stop after the	selected in	jection		
1	Sample 01_01	Sample 01	A1	Method 1				
2	Sample 02_02	Sample 02	A2	Method 1				
3	Sample 03_03	Sample 03	A3	Method 1				
njectio	ons 🔚 History 🌃 N	Votes	🕕 Pause 🕒 Sto	p 🕂 Add 📊	Replicate	🔀 Remove	Ŧ	6 -
injectio			Pause O Sto Location	p 🕌 Add 📊		Remove	Ŧ	8
injectio	Injection Name	Sample ID					Ŧ	8
			Location	Method			Ŧ	8
-	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method Method 1			Ŧ	8 5

Data collected for injections completed up to the point where the batch was stopped are saved in the .mbz file.

2. Be sure to complete your normal post-batch procedures.

Step 6 - Add Batch Notes (Optional)

- 1. Click on the Notes pane.
- 2. Click in the notes area and type any information you want to add about your batch.

Injections 🔛 History 🚺 *Notes	
Product testing	

Step 7 - Modify Default Analysis Parameters (Optional)

You can preset the parameters used to analyze data generated with the batch. We recommend using the default parameters for Turbo CE-SDS applications, but if you need to modify parameters:

1. Select Edit from the main menu and click Default Analysis. The following screen will display:

or Default Analysis: Maurice	CE-SDS TURBO					×
Markers	Markers					
Peak Names Peak Fit Advanced Signal Processing	Analysis Groups Standards		Markers Internal Standard Time	170	Seconds	
			Markers Injection no m	narkers ~]	
			MW (kDa)		RMT	
	Add	Remove	10		1	
			20		1.15	
	Apply Default:		33		1.3	
	Standards	~	55		1.5	
	Stanuarus	· ·	103		1.8	
	Apply Override:		178		2.05	
	Apply To	Group	270		2.4	
	Sample	Standards				
	Add	Remove	Add	Remov	e	
Import Exp	ort		OK Can	icel	Apply	
				(1997	

2. Change the parameters you want to, then click OK. For detailed information on analysis parameters, please refer to "Analysis Settings Overview" on page 713.

Step 8 - Modify Default Analysis View Parameters (Optional)

You can preset the parameters used to display the graph and lane view data when the batch is complete. Default Analysis View Parameters must be set before you start the batch and cannot be modified once the batch starts. However, you can still manually change parameters in the Analysis pane using the Graph View Options and Lane View Options buttons.

To modify the parameters:

1. Select Edit from the main menu and click Default Analysis View. The following screen will display:

📀 Default Analysis View Mau	urice CE-SDS TURBO			×
Graph View Options Lane View Options	urice CE-SDS TURBO Graph View Options Matching Peak Names Peak Names Peak Values Fitted Peaks Baseline Fit Grid Lines Plot Label Sample			×
	Method Injection Injection Name OK Cancel		Apply	

2. Change the parameters you want to, then click Apply. Click OK when you are done changing display parameters. For detailed information on data display parameters, please refer to "Customizing the Data Display" on page 695.

Step 9 - Save Your Batch

1. Once all of your sample, method and injection info is entered, select **File > Save**. Enter any comments on the batch if you want, then click **Save**.

o Save Batch Comm	nent	×
Batch: Maurice CE Comment:	-SDS TURBO	
I		
	Save	Cancel
	bare	

2. Enter a name for your batch then click Save.

Viewing Replicate Injections

Injections with replicates have an arrow next to the injection number. You can expand or collapse the list of replicate injections by toggling the arrow:

	Sample ID	Location	Method		Sample ID	Location	Method
1	Product A /	A1	Non-reduced IgG	1	Product A	A1	Non-reduced IgG
2	Product A /	A2	Reduced IgG	⊿ 2	Product A	A2	Reduced IgG
7	Product B /	A3	Non-reduced IgG	3	Product A	A2	Reduced IgG
8	Product B A	A4	Reduced IgG	4	Product A	A2	Reduced IgG
⊳ 9	Product C A	A5	Non-reduced IgG	5	Product A	A2	Reduced IgG
13	Product C A	A6	Reduced IgG	6	Product A	A2	Reduced IgG
14	Product D A	A7	Reduced IgG	7	Product B	A3	Non-reduced IgG
15	Product E /	A8	Reduced IgG	8	Product B	A4	Reduced IgG
16	Product F A	A9	Reduced IgG	⊳ 9	Product C	A5	Non-reduced IgG
17	Product G	A10	Non-reduced IgG	13	Product C	A6	Reduced IgG
18	Product H /	A11	Non-reduced IgG	14	Product D	A7	Reduced IgG
19	Markers /	A12	MW Markers	15	Product E	A8	Reduced IgG

• To show all replicate injections in the batch, click the Expand All Injections button.

Injection	s 🔚 History 👖 *Notes				🕂 Add 📊 Replicate 🧩 Remove 🕞 🖻 🗖
	Sample ID	Location	Method	Notes	Expand All Inject
1	Product A	A1	Non-reduced IgG		Expand An article
a 2	Product A	A2	Reduced IgG		
3	Product A	A2	Reduced IgG		
4	Product A	A2	Reduced IgG		
5	Product A	A2	Reduced IgG		
6	Product A	A2	Reduced IgG		
7	Product B	A3	Non-reduced IgG		
8	Product B	A4	Reduced IgG		
a 9	Product C	A5	Non-reduced IgG		
10	Product C	A5	Non-reduced IgG		
11	Product C	A5	Non-reduced IgG		
12	Product C	A5	Non-reduced IgG		
13	Product C	A6	Reduced IgG		
14	Product D	A7	Reduced IgG		
15	Product E	A8	Reduced IgG		
16	Product F	A9	Reduced IgG		
17	Product G	A10	Non-reduced IgG		
18	Product H	A11	Non-reduced IgG		
19	Markers	A12	MW Markers		

• To hide all replicate injections in the batch, click the Collapse All Injections button.

Injectio	ons 🛛 🔚 History 🚺 *Not	tes			👉 Add 📊 Replicate 📝 Remove 🕞 📄 🗖
	Sample ID	Location	Method	Notes	Collapse All Inject
1	Product A	A1	Non-reduced IgG		
⊳ 2	Product A	A2	Reduced IgG		
7	Product B	A3	Non-reduced IgG		
8	Product B	A4	Reduced IgG		
> 9	Product C	A5	Non-reduced IgG		
13	Product C	A6	Reduced IgG		
14	Product D	A7	Reduced IgG		
15	Product E	A8	Reduced IgG		
16	Product F	A9	Reduced IgG		
17	Product G	A10	Non-reduced IgG		
18	Product H	A11	Non-reduced IgG		
19	Markers	A12	MW Markers		

Batch History

Clicking on the History pane shows the batch event history, starting with the date and time the batch was created through the most current event. Clicking on a row in the table displays the full event details in the box under the table.

🛄 Injections 🔚 Histor	y 📧 Notes			- 0
Date	User Name	Message	Comment	
2022-01-17 14:28:1		Batch created using the factory default Maurice CE-SDS TURBO with Compass for iCE Version: 3.0.0-0114		
2022-01-17 14:29:4		Saved as C:\Users\hxu\Documents\Compass for iCE\Batches\Maurice CE-SDS TURBO_D1-8_96x.batch fro		
2022-01-17 14:29:4		Save injections changes to C:\Users\hxu\Documents\Compass for iCE\Batches\Maurice CE-SDS TURBO		
Time 20	022-01-17 14	28:14 User		
Message B	atch created	using the factory default Maurice CE-SDS TURBO with Compass for iCE Version: 3.0.0-0114		
Comment				

- Date: Date and time of the batch event.
- User Name: User that initiated the event. User names only display if you're using the Access Control feature to help satisfy the 21CFR Part 11 data security requirements. Go to "Enabling Access Control" on page 781 to learn how to set it up.
- Message: Description of the event that took place.
- **Comment:** Comments entered by the user when the batch was saved.

You can copy the information in the History pane to use in other documents:

- 1. Click the History pane to make sure it's active.
- 2. Click Edit in the main menu and select Copy.
- 3. Open a document and click Paste.

Making Changes to a Batch

1. Select File in the main menu and click Open Batch.

File	Edit Instrument	Wir	ndow Help
	New Batch	+	
	Open Batch	•	Platform CE-SDS2
	Save		Platform CE-SDS1
	Save As		Maurice CE-SDS3
			Maurice CE-SDS2
	Batch Report		Maurice CE-SDS1
	Exit		Browse

- 2. A list of the last five batches opened will display based on the last location found. If the location of the file has changed, you may need to navigate to find the file.
 - Select one of these files or click Browse to open the Batch folder and select a different one.
 - To open a batch used in a run file, click **Browse**. Go to the Run folder in the Compass for iCE directory and select the run file that uses the batch you want to edit.

Organize ▼ Share with ▼ Burn New f	older				
🕽 Libraries 4 🗎 Documents	Documents library Compass for ICE				
My Documents	Name	Date modified	Date created	Туре	Size
🎍 Add-in Express	Batches	1/18/2016 5:39 PM	1/13/2016 8:24 PM	File folder	
Adobe Clients	闄 New Batches	1/13/2016 8:24 PM	1/13/2016 8:24 PM	File folder	
Compass for iCE	🕌 Runs	1/17/2016 8:41 PM	11/11/2015 4:46 PM	File folder	
Batches	DemoData Maurice cIEF.mbz	1/18/2016 11:38 AM	1/18/2016 11:38 AM	Maurice data file.	798

3. To make changes to the batch, see the steps in "Creating a New Batch" on page 332. Then select File from the main menu and click **Save** or **Save As**.

Viewing and Editing Batches in Completed Runs

- 1. Click the Analysis screen and open your run file(s).
- 2. After the run opens, click the Batch screen to view the batch used with the run.

If you opened more than one run file, you can switch between viewing batches for each file. Just click the **down arrow** in the Run box and select the batch you want to view from the drop down list.

File	Edit	Instrum	ent \	Vindow	Help		
1							
	_					_	
Run:	KF10	06_s-CE	-SDS Pi	roduct B		-	
E La	KF10	06_s-CE	SDS	oduct B			
	KF10	06_s-CE	-SDS Pr	oduct B			
		10°C	*		🕻 Add	Ŧ	🕻 Remove

- 3. In completed run files, you can only make edits to the **sample** and **method** names in a batch, and these changes are saved to the run file only. Update sample and method names as needed.
- 4. Click the Analysis screen. Then select File from the main menu and click Save or Save As to save the new changes to the run file.

Copying and Pasting Injection Names or Sample IDs from other Documents

Injection names and Sample IDs can be copied from other documents and pasted into the Injection pane to make batch setup faster.

To paste a list of injection names into the batch:

1. Select the list of injection names in a document (Microsoft[®] Word[®], Excel[®], etc.) and select **Copy** or hold the **Ctrl+C** keys to copy.

	А	В	C
1			
2		My Injection 1	My Sample 1
3		My Injection 2	My Sample 2
4		My Injection 3	My Sample 3
5		My Injection 4	My Sample 4
6		My Injection 5	My Sample 5
7		My Injection 6	My Sample 6
8		My Injection 7	My Sample 7
9		My Injection 8	My Sample 8
10		My Injection 9	My Sample 9
11		My Injection 10	My Sample 10

2. Select an injection in the Injection pane, then hold the Ctrl+V keys to paste. You can also select the injection, right click and select Paste.

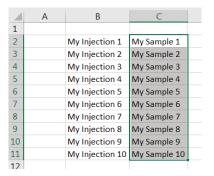
Sample 01_01 Sample 01 A1 System Suitability 2 Sample 02_02 Sample 02 A2 Method2 3 Sample 03_03 Sample 03 A3 Method2 4 Sample 04_04 Sample 04 A4 Method2 5 Sample 05_05 Sample 05 A5 Method2 6 Sample 06_06 Sample 06 A6 Method2 7 Sample 07_07 Sample 07 A7 Method2 8 Sample 08_08 Sample 09 A9 Method2 9 Sample 10_10 Sample 10 A10 Method2 10 Sample 11 Sample 11 A11 Method2		Injection Name	Sample ID	Location	Method	Notes	
Sample 03_03 Sample 03 A3 Method2 4 Sample 04_04 Sample 04 A4 Method2 5 Sample 05_05 Sample 05 A5 Method2 6 Sample 06_06 Sample 06 A6 Method2 7 Sample 07_07 Sample 07 A7 Method2 8 Sample 08_08 Sample 08 A8 Method2 9 Sample 09_09 Sample 09 A9 Method2 10 Sample 10_10 Sample 10 A10 Method2		Sample 01_01	Sample 01	A1	System Suitability		
Sample 04_04 Sample 04 A4 Method2 5 Sample 05_05 Sample 05 A5 Method2 5 Sample 06_06 Sample 06 A6 Method2 7 Sample 07_07 Sample 07 A7 Method2 8 Sample 08_08 Sample 08 A8 Method2 9 Sample 09_09 Sample 09 A9 Method2 10 Sample 10_10 Sample 10 A10 Method2	2	Sample 02_02	Sample 02	A2	Method2		
Sample 05_05 Sample 05 A5 Method2 6 Sample 06_06 Sample 06 A6 Method2 7 Sample 07_07 Sample 07 A7 Method2 8 Sample 08_08 Sample 08 A8 Method2 9 Sample 09_09 Sample 09 A9 Method2 10 Sample 10_10 Sample 10 A10 Method2	1	Sample 03_03	Sample 03	A3	Method2		
Sample 06_06 Sample 06 A6 Method2 7 Sample 07_07 Sample 07 A7 Method2 8 Sample 08_08 Sample 08 A8 Method2 9 Sample 09_09 Sample 09 A9 Method2 10 Sample 10_10 Sample 10 A10 Method2	ļ	Sample 04_04	Sample 04	A4	Method2		
A Method2 8 Sample 07_07 Sample 07 A7 Method2 8 Sample 08_08 Sample 08 A8 Method2 9 Sample 09_09 Sample 09 A9 Method2 10 Sample 10_10 Sample 10 A10 Method2	;	Sample 05_05	Sample 05	A5	Method2		
Sample 08_08 Sample 08 A8 Method2 9 Sample 09_09 Sample 09 A9 Method2 10 Sample 10_10 Sample 10 A10 Method2	5	Sample 06_06	Sample 06	A6	Method2		
9 Sample 09_09 Sample 09 A9 Method2 10 Sample 10_10 Sample 10 A10 Method2		Sample 07_07	Sample 07	A7	Method2		
10 Sample 10_10 Sample 10 A10 Method2	3	Sample 08_08	Sample 08	A8	Method2		
)	Sample 09_09	Sample 09	A9	Method2		
11 Sample 11 11 Sample 11 A11 Method2	.0	Sample 10_10	Sample 10	A10	Method2		
	1	Sample 11_11	Sample 11	A11	Method2		

The injection names are pasted into the Injection pane:

				🕕 Pa	ause 🗴 Stop 👫 Add 📗 Repli	cate 样 Remove 🗉
	Injection Name	Sample ID	Location	Method	Notes	
1	My Injection 1	Sample 01	A1	System Suitability		
2	My Injection 2	Sample 02	A2	Method2		
3	My Injection 3	Sample 03	A3	Method2		
4	My Injection 4	Sample 04	A4	Method2		
5	My Injection 5	Sample 05	A5	Method2		
6	My Injection 6	Sample 06	A6	Method2		
7	My Injection 7	Sample 07	A7	Method2		
8	My Injection 8	Sample 08	A8	Method2		
9	My Injection 9	Sample 09	A9	Method2		
10	My Injection 10	Sample 10	A10	Method2		
11	Sample 11_11	Sample 11	A11	Method2		
12	Sample 12_12	Sample 12	A12	Method2		
12	Sumple 12_12	Sumple 12	A12	Wiethouz		

To paste a list of Sample IDs into the batch:

1. Select the list of Sample IDs in a document (Microsoft Word, Excel, etc.) and select **Copy** or hold the **Ctrl+C** keys to copy.



2. Select a Sample ID in the Injection pane, then hold the Ctrl+V keys to paste. You can also select the Sample ID, right click and select Paste.

🕛 Pause 오 Stop 🖟 Add 📗 Replicate 🔀 Remove 🐵 🖻								
	Injection Name	Sample ID	Location	Method	Notes			
1	Sample 01_01	Sample 01	A1	System Suitability				
2	Sample 02_02	Sample 02	A2	Method2				
3	Sample 03_03	Sample 03	A3	Method2				
4	Sample 04_04	Sample 04	A4	Method2				
5	Sample 05_05	Sample 05	A5	Method2				
6	Sample 06_06	Sample 06	A6	Method2				
7	Sample 07_07	Sample 07	A7	Method2				
8	Sample 08_08	Sample 08	A8	Method2				
9	Sample 09_09	Sample 09	A9	Method2				
10	Sample 10_10	Sample 10	A10	Method2				
11	Sample 11_11	Sample 11	A11	Method2				
12	Sample 12_12	Sample 12	A12	Method2				

The Sample IDs are pasted into the Injection pane.

NOTE: If you paste in new sample IDs when the default injection names are still being used, the injection names will automatically update to match the sample ID. If you've already changed the injection names manually, updating the sample IDs will not update the injection names.

	Injection Name	Sample ID	Location	Method	Notes	
1	My Sample 1_01	My Sample 1	A1	System Suitability		
2	My Sample 2_02	My Sample 2	A2	Method2		
3	My Sample 3_03	My Sample 3	A3	Method2		
4	My Sample 4_04	My Sample 4	A4	Method2		
5	My Sample 5_05	My Sample 5	A5	Method2		
6	My Sample 6_06	My Sample 6	A6	Method2		
7	My Sample 7_07	My Sample 7	A7	Method2		
8	My Sample 8_08	My Sample 8	A8	Method2		
9	My Sample 9_09	My Sample 9	A9	Method2		
10	My Sample 10_10	My Sample 10	A10	Method2		
11	Sample 11_11	Sample 11	A11	Method2		
12	Sample 12_12	Sample 12	A12	Method2		

Importing and Exporting Injections

Injections in an open batch or run file can be exported as a separate file. This lets you import the same or a modified set of injections into another batch later, rather than having to enter the information manually.

Exporting Injections

- 1. Open the batch or run you want to export injections from.
- 2. In the Batch screen, select File in the main menu and click Export Injections. The following window displays:

Injections File				×
$\leftarrow \rightarrow \neg \uparrow$	Search Batches	Q		
Organize 🔻 Nev	v folder			== - ?
a OneDrive	^ Name	Date modified	Туре	Size
This PC	2019-01-08_ cIEF_Injections.csv	2/9/2019 3:18 PM	Microsoft Excel C	2 KB
This PC 3D Objects	Dye-ComboCollect_Maurice clEF_Fl.batch_Injections.csv	1/29/2019 8:19 PM	Microsoft Excel C	2 KB
E Desktop				
Documents				
👆 Downloads				
👌 Music				
Pictures				
Videos				
🏪 OS (C:)				
🔜 DATA (D:)				
🕳 Seagate Backu	p			
	~			
File name:	4Sqx12inj-RlgG-Maurice CE-SDS.batch_Injections.csv			~
Save as type:	Text File, comma delimited (*.csv)			~
∧ Hide Folders			Save	Cancel

- 3. The default directory is Compass for iCE/Batches. Change the directory if needed.
- 4. The default file name will be batchname.batch_Injections.csv. Change the name if needed and click Save.

Creating an Injections File

To create a new injections file .csv, it's easiest to export injections from an existing batch and use that as your template.

- 1. Follow the instructions in Exporting Injections above to export injections from an existing Turbo CE-SDS batch.
- 2. Open the .csv file in a program that provides a table/spreadsheet format.
- 3. To add or change injection information:
 - a. Type in a unique name in each cell in the Injection Name column. For replicate injections, type > in front of the injection name, for example: >Injection 1.
 - b. Type in a sample ID, location and method for each injection in their respective columns.

c. Optional: Type in notes if needed.

NOTES:

Mix bottle is not used for Turbo CE-SDS batches. Compass for iCE ignores this column when importing injections into Turbo CE-SDS batches.

Programmed pauses and stops can't be added in the injections file. They can be added in the Injections pane after importing your injections.

	А	В	C	D	E	F
1	Injection Name	Sample ID	Location	Method	Mix Bottle	Notes
2	R IgG1	SB	B2	Reduced IgG		
3	R IgG 2	SB	B3	Reduced IgG		
4	>R IgG 2	SB	B3	Reduced IgG		
5	>R IgG 2	SB	B3	Reduced IgG		
6	R IgG 3	SB	C2	Reduced IgG		
7	R IgG 4	SB	C3	Reduced IgG		
8	R IgG1_05	SB	B2	Reduced IgG		
9	R IgG 2_06	SB	B3	Reduced IgG		
10	R IgG 3 07	SB	C2	Reduced IgG		

4. Save the .csv file.

Importing Injections

- 1. Open the batch you want to import injections into, or open a new batch.
- 2. Select File in the main menu and click Import Injections.
- 3. Select an injections file (*.csv) and click OK. The imported information will display in the Layout and Injections panes.

NOTE: Imported injections will replace any injections already in the Injections table, they will not append an existing table.

Importing and Exporting Methods

Methods in an open batch or run file can be exported as a separate file. This lets you import the same method into another batch later, rather than having to re-enter method information manually.

Importing a Method

NOTE: Importing a method imports information into the Batch window's Method pane only.

1. Open the batch you want to import the method into.

- 2. Select File in the main menu and click Import Method.
- 3. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

Exporting a Method

NOTE: Exporting a method exports information in the Batch window's Method pane only.

- 1. Open the batch you want to export the method from.
- 2. In the Method pane, select the method you want to export. To export more than one method at the same time, hold the Ctrl key to select multiple methods.
- 3. Select File in the main menu and click Export Method. The following window displays:

💮 Method File					×
○○ - ○ ● ≪ M	ly Documents 🕨 Compass for	r iCE 🕨 Batches	✓ Search	n Batches	م
Organize 🔻 Ne	ew folder				
★ Favorites ↓ Downloads ↓ Desktop ▲ OneDrive	Name	No items mat	Date modified tch your search.	Туре	Size
 □ Libraries □ Documents → Music □ Pictures ■ Videos 					
🖳 Computer					•
File name: Save as type:	Standard Method.method Method File (*.method)				•
Hide Folders			Sa	ive	Cancel

- 4. The default directory is Compass for iCE/Batches. Change the directory if needed.
- 5. Enter a method file name and click Save. The settings will be saved as a *.method file.

Batch Reports

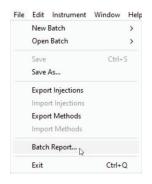
You can export a PDF file of sample and method details for each injection in the batch.

NOTES:

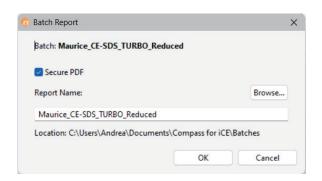
You can have Compass for iCE generate reports for you automatically at the end of each run. See "Setting up Automatic Injection Reports" on page 761 for more information.

Any time a new report is run, it's saved in a separate run folder. Existing reports aren't overwritten.

- Go to the Analysis or Run Summary screen, then click File > Open Run and select a run file (if you don't have one open already).
- 2. After the run opens, go to the **Batch** screen.
- 3. Select File from the main menu and click Batch Report.



4. The report name defaults to the run file name. If you want to change it, type in the **Report Name** box to make updates.



Report PDFs generated by Compass for iCE are secured by default, which means they can be viewed and printed but not modified or renamed. Uncheck **Secure PDF** if you don't want to generate a secure report. To learn more about permissions for secured vs. unsecured reports, see page 800.

5. The Batch Report PDF is exported to the Runs folder in the Compass for iCE directory. It'll be in a folder with the report name used in the prior step. When the reports are done, the folder opens for you automatically.

Organize Include in library Share with	Burn	New folder				
Favorites	*	Name	Date modified	Туре	Size	
📝 Links		78664 P3 IS 2015-11-30 16-49-49 MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS Batch.pdf	1/18/2016 3:57 PM	Adobe Acrobat D		33 K
My Documents			1,10,2010 5157 1111	//dobe//crobat bill		
퉬 Add-in Express						
🌗 Adobe						
Description of the second s						
4 퉬 Compass for iCE						
퉬 Assays						
퉬 Batches						
퉬 New Assays						
퉬 New Batches						
4 퉬 Runs						
2015-12-06_15-13-01_Maurice cIEF_Mab11_TechR	t					
퉬 78664 P3 IS 2015-11-30_16-49-49_MW Ladder Sol						

Here's an example Batch Report:

	CE-SDS Batch: Maurice_CE-SDS_TURBO_Reduced								
Injection	Injection Name	Sample ID	Location	Method	Sample Load	Separation			
1	Sample 01_01	Sample 01	A1	Reduced IgG	8 sec 3500 Volts	5.5 min, 4200 Volts			
13	Sample 02_13	Sample 02	A2	Reduced IgG	8 sec 3500 Volts	5.5 min, 4200 Volts			
25	Sample 03_25	Sample 03	A3	Reduced IgG	8 sec 3500 Volts	5.5 min, 4200 Volts			
37	Sample 04_37	Sample 04	A4	Reduced IgG	8 sec 3500 Volts	5.5 min, 4200 Volts			
49	Sample 05_49	Sample 05	A5	Reduced IgG	8 sec 3500 Volts	5.5 min, 4200 Volts			
61	Sample 06_61	Sample 06	A6	Reduced IgG	8 sec 3500 Volts	5.5 min, 4200 Volts			
73	Sample 07_73	Sample 07	A7	Reduced IgG	8 sec 3500 Volts	5.5 min, 4200 Volts			
85	Sample 08 85	Sample 08	A8	Reduced IgG	8 sec 3500 Volts	5.5 min, 4200 Volts			

Andrea Sat 11:58 PM Feb 25, 2023 PST (SECURED) drea/Documents/Compass for /CEBatches/Maurice_CE-SDS_TURBO_Reduced.batch DESKTOP-IFM/7G05 Software Version: Compass for ICE 4.0.0, Build ID: 0222

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User Guide for Maurice, Maurice C. Maurice S. and MauriceFlex

CE-SDS Batch: Maurice_CE-SDS_TURBO_Reduced

Batch Log

Date	User Name	Message	Comment
2022-12-14 10:22:35		Saved as C:\Users\Andrea\Documents\Compass for iCE\Batches\Maurice_CE- SDS_TURBO_Reduced.batch from Compass for iCE v4.0.0-1102	
2022-12-14 10:22:35		Save Batch changes to C:\Users\Andrea\Documents\Compass for ICE\Batches\Maurice_CE-SDS_TURBO_Reduced.batch from Compass for iCE v4.0.0-1102	

Created By: Andrea Sat 11:58 PM Feb 25, 2023 PST (SECURED) C:Users/AndreaDocuments(Compass for ICEBatches/Maurice_CE-SDS_TURBO_Reduced batch Computer: DESKTOP-IFMTG05 Software Version: Compass for ICE 4.0.0, Build ID: 0222

Page 2 of 2



Chapter 14: Running Turbo CE-SDS Applications

Chapter Overview

- Overview
- Before You Throw the Switch
- Power Up
- Running Turbo CE-SDS Applications
- Editing a Running Batch
- Post-batch Procedures
- Checking Your Data

Overview

Turbo CE-SDS applications can be run on Maurice, Maurice S. or MauriceFlex systems with a Turbo CE-SDS cartridge.

Before You Throw the Switch

Ensure that everyone using Maurice have:

- Received instruction in general safety practices for laboratories.
- Received instruction in specific safety practices for Maurice.
- Received instruction on handling of biohazards (if biohazardous materials are to be used on Maurice).
- Read and understood all Product Inserts and related Safety Data Sheets (SDS).

Power Up

- 1. Turn on the computer connected to Maurice.
- 2. Turn on Maurice's main power switch.
- 3. Wait for Maurice to initialize. His indicator light will turn from magenta to blue when he's done.
- 4. Double-click the Compass for iCE software icon on the computer desktop to open the application.
- 5. Connect Maurice to Compass for iCE.

Running Turbo CE-SDS Applications

What You'll Need

- Maurice Turbo CE-SDS Application Kit which include:
 - Maurice Turbo CE-SDS Cartridges
 - Separation Matrix
 - Turbo CE-SDS Running Buffer Bottom
 - CE-SDS or CE-SDS PLUS 1X Sample Buffer
 - Wash Solution
 - Conditioning Solutions (1 and 2)
 - 25X Internal Standard
 - Glass reagent vials, 2 mL

- 96-well plates
- Clear screw caps for vials
- Orange pressure caps for vials
- Maurice CE-SDS IgG Standard (optional)
- Maurice CE-SDS MW Markers (optional)
- β -mercaptoethanol (β ME, >98% = 14.2 M) for reducing conditions
- Optional: Sodium hypochlorite solution (10-15%), for neutralizing β-mercaptoethanol (Sigma PN 425044)
- · Iodoacetamide (IAM, 250 mM) for alkylation at non-reducing conditions
- Deionized (DI) water
- Sample vials with integrated inserts for samples (optional)
- P10, P20, P200, P1000 and pipette tips
- Water bath or thermocycler
- Vortexer
- Table-top centrifuge with plate adapter or vial adapter (12 mm, 2 mL vials)

Step 1: Prep Your Internal Standard, Samples and Reagents

NOTE: You can prepare your samples to run either in 96-well plates or vials. Using 96-well plates is the default method.

Internal Standard

NOTES:

The Internal Standard is lyophilized. Always reseal the foil bag containing the unopened tubes with desiccant to prevent moisture absorption.

Aliquot the reconstituted solution into appropriately sized vials and store at -70 to -90 °C for long term storage. For short-term storage (< 1 week), the solution can be stored at 2-8 °C.

Prepare the Internal Standard in the same buffer as your sample.

- 1. Open the vial of lyophilized 25X Internal Standard by lifting the center tab and gently pulling it back to break the metal seal. Then slowly remove the rubber stopper.
- Reconstitute by adding 240 μL of 1X Sample Buffer. Pipette up and down a few times to mix thoroughly. This results in a 25X Internal Standard solution.

NOTE: Don't vortex the reconstituted Internal Standard during prep.

Sample Prep Under Reducing Conditions

NOTES:

Prepare a minimum of 100 µL of sample for a Turbo CE-SDS batch.

Reduced IgG Sample

NOTE: If you are sample limited and running a Turbo CE-SDS batch, prepare your sample in a final volume of 50 μ L and dilute the denatured sample 1:1 in DI water to bring the volume to 100 μ L.

1. In a microcentrifuge tube, dilute your IgG sample with 1X Sample Buffer to a concentration of 0.25-1.00 mg/mL in a final volume of 100 μ L.

NOTE: Dilute at least 1:1 with with either CE-SDS 1X Sample Buffer or CE-SDS PLUS 1X Sample Buffer.

- 2. Add 2 μ L of reconstituted 25X Internal Standard for every 50 μ L of sample volume.
- 3. Add 2.5 μ L of 14.2 M β -mercaptoethanol for every 50 μ L of sample volume.
- 4. Mix thoroughly.

NOTE: Heating in the presence of SDS linearizes the protein and allows for SDS binding. The reducing agents break up inter- and intra-molecular disulfide bonds.

- 5. Centrifuge the tube and heat the mixture in a water bath or thermocycler at 70 °C for 10 minutes.
- 6. Put the tube on ice for 5 minutes.
- 7. Vortex briefly and spin down.

Reduced IgG Standard (Optional)

NOTES:

The IgG Standard is lyophilized. Always reseal the foil bag containing the unopened tubes with desiccant to prevent moisture absorption.

Prepare the reduced IgG Standard in either CE-SDS 1X Sample Buffer or CE-SDS PLUS 1X Sample Buffer.

- 1. Using scissors, carefully cut the top of the foil package, leaving the sealing strip intact.
- 2. Take out the strip of tubes and carefully cut one pink tube of lyophilized IgG Standard from the strip. Put the unopened tubes back in the package, seal tightly and store at 2-8 °C.
- 3. Pierce the foil on the tube with a clean pipette tip.
- 4. Reconstitute the IgG Standard with 50 μL of 1X Sample Buffer. Gently resuspend by pipetting the solution up and down. Transfer the solution to a microcentrifuge tube.
- 5. Add 2 µL of reconstituted 25X Internal Standard.
- 6. Add 2.5 μ L of 14.2 M β -mercaptoethanol.
- 7. Mix thoroughly by vortex.
- 8. Centrifuge the tube and heat mixture in a water bath or thermocycler at 70 °C for 10 minutes.
- 9. Put the tube on ice for 5 minutes.
- 10. Vortex briefly and spin down.

CE-SDS Molecular Weight (MW) Markers (Optional)

NOTES:

The CE-SDS MW Markers are lyophilized. Always reseal the foil bag containing the unopened tubes with desiccant to prevent moisture absorption.

Prepare the MW Markers in either CE-SDS 1X Sample Buffer or CE-SDS PLUS 1X Sample Buffer.

- 1. Using scissors, carefully cut the top of the foil package leaving the sealing strip intact.
- 2. Take out the strip of tubes and carefully cut one green tube of lyophilized CE-SDS MW Markers from the strip. Put the unopened tubes back in the package, seal tightly and store at 2-8 °C.
- 3. Pierce the foil on the tube with a clean pipette tip.
- 4. Reconstitute the CE-SDS MW Markers with 50 µL of 1X Sample Buffer. Gently resuspend by pipetting the solution up and down. Transfer the solution to a microcentrifuge tube.
- 5. Add 2 µL of reconstituted 25X Internal Standard.
- 6. Add 2.5 μ L of 14.2 M β -mercaptoethanol.
- 7. Mix thoroughly.
- 8. Centrifuge the tube and heat the mixture in a water bath or thermocycler at 70 °C for 10 minutes.
- 9. Put the tube on ice for 5 minutes.
- 10. Vortex briefly and spin down.

Spin Samples, Standards and CE-SDS MW Markers

If you're using a 96-well plate:

- 1. Transfer 100 µL of each of your samples, IgG Standard and CE-SDS MW Markers to their designated wells in a 96-well plate.
- 2. Cover the plate with a lid and spin for 10 minutes at 1000 xg in a centrifuge with a plate adapter.
- 3. Pop any bubbles in the samples with a clean pipette tip.

If you're using vials:

- 1. Transfer 100 µL of each of your samples, IgG Standard and CE-SDS MW Markers to their designated sample vials with insert, 0.2 mL.
- 2. Close the vials with a clear screw cap.
- 3. Place the vials in a centrifuge using a vial adapter (12 mm, 2 mL vials) and spin for 10 minutes at 1000 xg.



Sample Prep Under Non-reducing Conditions

Alkylation Reagent

NOTES:

We use a 250 mM solution of iodoacetamide (IAM) as an alkylating reagent.

Prepare a fresh 250 mM solution of iodoacetamide in DI water before use.

- 1. Weigh out 46 mg of IAM directly into a 1.5 mL microcentrifuge tube.
- 2. Add 1 mL of DI water to the tube and mix thoroughly.

Non-reduced IgG Sample

NOTES:

Prepare a minimum of 100 μ L of sample for a Turbo CE-SDS batch.

If you are sample limited and running a Turbo CE-SDS batch, prepare your sample in a final volume of 50 μ L and dilute the denatured sample 1:1 in DI water to bring the volume to 100 μ L.

1. In a microcentrifuge tube, dilute your IgG sample with 1X Sample Buffer to a concentration of 0.25-1.0 mg/mL in a final volume of 50 μL.

NOTE: Dilute at least 1:1 with CE-SDS 1X Sample Buffer or CE-SDS PLUS 1X Sample Buffer.

- 2. Add 2 µL of reconstituted 25X Internal Standard for every 50 µL of sample volume.
- 3. Add 2.5 µL of 250 mM IAM for every 50 µL of sample volume.
- 4. Mix thoroughly.
- 5. Centrifuge the tube and heat the mixture in a water bath or thermocycler at 70 °C for 10 minutes.
- 6. Put the tube on ice for 5 minutes.
- 7. Vortex briefly and spin down.

Non-reduced IgG Standard (Optional)

NOTES:

The IgG Standard is lyophilized. Always reseal the foil bag containing the unopened tubes with desiccant to prevent moisture absorption.

Prepare the non-reduced IgG Standard in in either CE-SDS 1X Sample Buffer or CE-SDS PLUS 1X Sample Buffer.

- 1. Using scissors, carefully cut the top of the foil package, leaving the sealing strip intact.
- 2. Take out the strip of tubes and carefully cut one pink tube of lyophilized IgG Standard from the strip. Put the unopened tubes back in the package, seal tightly and store at 2-8 °C.
- 3. Pierce the foil on the tube with a clean pipette tip.
- 4. Reconstitute the IgG Standard with 50 μL of 1X Sample Buffer. Gently resuspend by pipetting the solution up and down. Transfer the solution to a microcentrifuge tube.
- 5. Add 2 µL of reconstituted 25X Internal Standard.
- 6. Add 2.5 µL of 250 mM IAM.

7. Mix thoroughly by vortex.

NOTE: Heating in the presence of SDS linearizes the protein and allows for SDS binding. The alkylating agents prevent disulfide-bond scrambling catalyzed by free sulfhydryl groups. This minimizes the appearance of fragments under non-reducing conditions.

- 8. Centrifuge the tube and heat mixture in a water bath or thermocycler at 70 °C for 10 minutes.
- 9. Put the tube on ice for 5 minutes.
- 10. Vortex briefly and spin down.

Spin Samples and Standards

If you're using a 96-well plate:

- 1. Transfer 100 µL of each of your samples and IgG Standard to their designated wells in a 96-well plate.
- 2. Cover the plate with a lid and spin for 10 minutes at 1000 xg in a centrifuge with a plate adapter.
- 3. Pop any bubbles in the samples with a clean pipette tip.

If you're using vials:

- 1. Transfer 100 µL of your samples and IgG Standard to their designated sample vials with insert, 0.2 mL.
- 2. Close the vials with a clear screw cap.
- 3. Place the vials in a centrifuge using vial adapter (12 mm, 2 mL vials) and spin for 10 minutes at 1000 xg.

Reagents

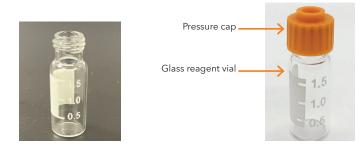
IMPORTANT:

Use glass reagent vials, 2 mL (PN 046-017) to prepare Turbo CE-SDS batch reagents.

NOTE: Don't reuse reagents, vials or the clear screw caps. Always keep the orange pressure caps paired with their respective reagents. If you want to reuse pressure caps, first wash them thoroughly with DI water, soak overnight in DI water, rinse caps thoroughly with DI water again and air dry them before reusing.

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1. Pipette 1.5 mL of Conditioning Solution 1 into a glass reagent vial, label and close with an orange pressure cap.



- 2. Pipette 1.5 mL of Conditioning Solution 2 into a glass reagent vial, label and close with an orange pressure cap.
- 3. Pipette 1.0 mL of Wash Solution into a glass reagent vial, label each and close with an orange pressure cap.
- 4. Pipette 1.5 mL of Wash Solution into a glass reagent vial, label each and close with a clear screw caps.



Clear screw cap	
Glass reagent vial	
5	1.5
	1.0
	0.0

- 5. Pipette 1 mL of Separation Matrix into a glass reagent vial, label and close with an **orange pressure cap**.
- 6. Pipette 1 mL of Running Buffer Bottom into three glass reagent vials, label each and close with a clear screw cap.
- 7. Pipette 1.5 mL of DI water into a glass reagent vials, label and close with an orange pressure cap.
- 8. Close an empty glass reagent vial with an orange pressure cap.

Step 2: Prep the Cartridge

NOTES:

A Turbo CE-SDS cartridge is guaranteed for 100 injections, with a maximum of 96 injections per batch and a maximum of 25 batches.

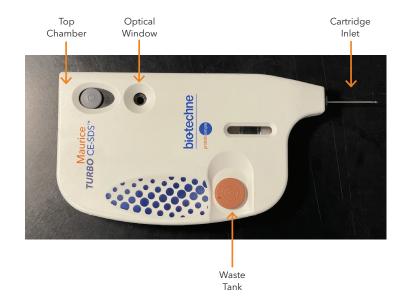
Prepare your samples and reagents before preparing the cartridge. Allowing the Separation Matrix to sit in the cartridge too long may result in cartridge clogs.

1. Take the Turbo CE-SDS Cartridge out of its packaging. Save the packaging, you'll need it later to store the cartridge.

NOTE: When you remove the cartridge from its packaging, make sure the cartridge inlet doesn't come in contact with any surface.



2. Place the cartridge on a flat surface and remove the stopper from the Top Chamber.



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3. Add 750 µL of Separation Matrix to the Top Chamber.



- 4. Pop any visible bubbles with a clean pipet tip.
- 5. Firmly close the chamber with the stopper.
- 6. Ensure the Waste Tank is firmly closed with the stopper.

Step 3: Install the Cartridge

1. Open Maurice's door by touching the metal plate on top of the door.



NOTE: The indicator light on Maurice's front panel will blink rapidly as the door disengages.

2. Swing the door open to access the cartridge slot and the reagents and samples platform. The lights on either side of the slot will be **orange**.



- 3. Lift the cartridge and hold it vertically using the finger holds on either side, cartridge inlet down, with the Turbo CE-SDS label facing you.
- 4. Gently insert it into the slot. You'll feel the alignment groove on the cartridge align inside the slot when you insert it.



5. Continue to slide the cartridge into the slot until the locking mechanism engages. The lights on either side of the slot will change to **blue** once the cartridge is installed correctly.



Step 4: Load Samples and Reagents

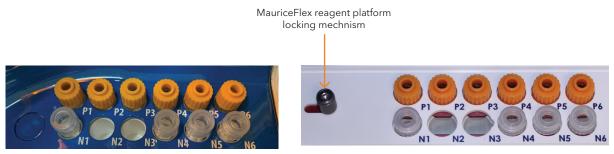
1. Place the reagent vials into their respective positions in the sample and reagents platform:

NOTES:

The two reagent rows in Maurice's reagent and sample platform are kept at room temperature.

Pressure caps are orange and have a raised, ringed surface. They should only be used in Reagent Row P. Use reagent vials with clear screw caps in Row N.

- P1 Conditioning Solution 1 with orange pressure cap
- P2 Conditioning Solution 2 with orange pressure cap
- **P3** DI water with orange pressure cap
- **P4** Separation Matrix with **orange pressure cap**
- **P5** Wash Solution with orange pressure cap
- P6 Empty vial (air) with orange pressure cap
- N1 Wash Solution with clear screw cap
- N4 Turbo Running Buffer Bottom with clear screw cap
- N5 Turbo Running Buffer Bottom with clear screw cap
- N6 Turbo Running Buffer Bottom with clear screw cap



Turbo CE-SDS reagent platform on Maurice and Maurice S. (left) or MauriceFlex (right).

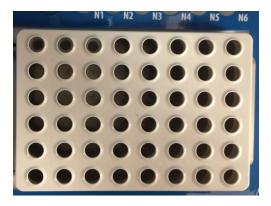
IMPORTANT:

Reagent vials on MauriceFlex must be locked in place by sliding the locking mechanism from the left to the right before starting a batch. A warning will appear in the Start Run window if they are not locked when you start the batch.

2. Depending on what you prepared your samples in, put your 96-well sample plate in the metal plate insert or your sample vials in the metal vial insert. If you have a lid on the 96-well sample plate, be sure to remove it before closing the instrument door!

NOTE: Well A1 on the 96-well plate should be in the top left corner of the insert.

3. If you are using a vial tray, place the condensation lid on top of the vials.



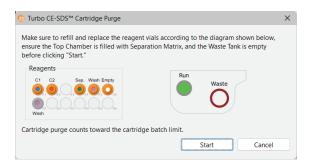
4. Close the instrument door. Maurice locks it automatically.

Step 5: Check for Cartridge Alerts

- 1. If your cartridge was last used in a run with an error or if it has not been used in the last three months, you will need to perform a Cartridge Purge. The Maurice system will remind you if a Cartridge Purge is required.
 - a. To purge the cartridge, click the brown **Purge** button in the instrument status bar.



b. Confirm that the required batch reagents are loaded and that the the cartridge is prepped. Then click Start.



c. Once the purge is done, perform a Cartridge Post-Run Cleanup by clicking on the brown **Cleanup** button that will appear in the instrument status bar. See step 2 for more info.

NOTE: If there's only one batch left on the cartridge, you'll get a message that it can't be used after purging.

2. If you just completed a Cartridge Purge or if the cartridge you're using did not undergo a cartridge post-run cleanup after the last run, you will be asked if you want to perform a Cartridge Post-Run Cleanup.

To start the Post-Run Cleanup:

- a. Remove the cartridge from Maurice and remove the Separation Matrix from the Top Chamber and any liquid from the Waste tank from the cartridge. See ""Post-batch Procedures" on page 385 for more info.
- b. Confirm there is a vial of Water (P3), Wash Solution (P5) and Air (P6) in place,
- c. Click the brown Cleanup button in the instrument status bar.



- d. Re-install the cartridge in Maurice.
- e. Click Start Cleanup in the prompt that appears.

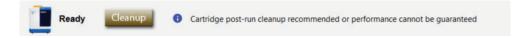


NOTE: You can also start a Post-Run Cleanup by selecting **Instrument > Cartridge Post-Run Cleanup**. When you start a Cartridge Post-Run Cleanup from the instrument menu, click **Start** in the prompt that appears to begin the cleanup.

- f. Once the cartridge post-run cleanup is completed, re-prepare the cartridge and install the cartridge in Maurice. See "Step 2: Prep the Cartridge" on page 364 for more information.
- g. Click on the green **Start** button in the instrument status menu to start the batch.

To start the run without a Post-Run Cleanup:

a. Click the brown Cleanup button in the instrument status bar



b. Click **Skip Cleanup** in the prompt that appears.



c. Click **Start** in the Start Run window. The run summary and injection report will record that the cartridge did not undergo a post-run cleanup before starting the batch.

Batch: Ma	urice CE-SDS TURBO		
Results file	name :		Browse
2023-02-0	08_20-16-46_Maurice CE-SDS TURBO		
Location:	C:\Users\Andrea\Documents\Compass for iCE	\Runs	
Comment:			
.onment.			
	Cartridge		
	Cartridge Type∶Turbo CE-SDS™	Injections per Batch : 48	
	-	Injections per Batch : 48 Injections Remaining : (39 guaranteed)	
1	Type : Turbo CE-SDS™		
	Type : Turbo CE-SDS™ Expires : Jan 2025 Serial Number : 000000001	Injections Remaining : (39 guaranteed) Batches Remaining : 15	
	Type : Turbo CE-SDS™ Expires : Jan 2025 Serial Number : 000000001	Injections Remaining : (39 guaranteed)	
1	Type : Turbo CE-SDS™ Expires : Jan 2025 Serial Number : 000000001	Injections Remaining : (39 guaranteed) Batches Remaining : 15	
	Type : Turbo CE-SDS™ Expires : Jan 2025 Serial Number : 000000001	Injections Remaining : (39 guaranteed) Batches Remaining : 15	

To start the run with a different cartridge:

- a. If necessary, click Cancel in the Turbo CE-SDS Cartridge Post-Run Cleanup window.
- b. Open Maurice's door, remove the first cartridge from Maurice and prepare a second cartridge. See"Step 2: Prep the Cartridge" on page 364 for more information.

Step 6: Create a Batch

1. Launch Compass for iCE.

2. Select the Batch tab. This is where you'll enter sample/injection information, methods and batch parameters.

Maurice CE-SDS File Edit Instrum	ent Window Help								
rite Edit Institutio	ent window help					E Rate	h 🔮 Run Summi	any de A	halveie
Batch: Maurice CE-SI		III Iniec	tions 🔛 History 頂 Not	PS		- m batt		ary and r	
baten. Waanee ee si	55 10180				O Pa	use 🛛 Stop 🗜 Add	I Replicate	Remove	E E
🖭 Layout	- 8		Injection Name	Sample ID		Method	Notes	Turrova	
🧐 🏢 10°C 🔻	🗲 Add 👻 🧭 Remove	1	Sample 01_01	Sample 01	A1	Reduced IgG			
	C2 View Sign. Wash Empty 								
Methods								New R	
Name	Sample Load		Separation					New R	
Reduced IgG	8 sec 3500 Volts		5.5 min 4200 Volts						
Non-reduced IgG	8 sec 3500 Volts		8.0 min 4200 Volts						
MW Markers	8 sec 3500 Volts		8.0 min 4200 Volts						

- 3. To create a batch, make sure your Maurice system is connected to Compass for iCE. Select Instrument and click Connect.
 - a. If your instrument is listed, select your Maurice system and click Connect.
 - b. If your instrument isn't listed, click on the Settings button and connect by typing in your instrument IP address.

lame	Location Serial	Num

To create a new batch:

• In the main menu, select File > New Batch > Maurice Turbo CE-SDS.

File	Edit Instrument	Window He	p	
	New Batch	>	Maurice cIEF	
	Open Batch	>	Maurice CE-SDS PLUS	
	Save	Ctrl+S	Maurice Turbo CE-SDS™	
	Save As	Curro	MauriceFlex clEF	
			MauriceFlex Fractionation	
	Export Injections			

To use an existing batch: In the main menu, select File > Open Batch.

NOTE: If you're making changes to an existing batch, follow the steps in this section. Otherwise skip to "Step 7: Start the Batch" on page 381.

File	Edit Instrur	ment Window	Help		
	New Batch		>		
	Open Batch		>	Maurice CE-SDS TURBO	
	Save Save As	Ctrl+S		2023-03-03_MauriceFlex cl Maurice CE-SDS PLUS MauriceFlex Fractionation	
	Export Injecti Import Injecti Export Metho Import Metho	ions ids		Maurice clEF_Simulator Browse	Ctrl+O
	Batch Report.		Run	1	
	Exit	Ctrl+C			

4. In the Layout pane, clicking on the vial/plate icon toggles between formats. Select a 96-well plate or 48 vials depending on what you're running.

📟 Layout	- D	ayout	
🍑 🥅 10°C 🔹 🕻 Add 🗸 🕻	K Remove	→ 10°C -	C Add - C Remove
C1 C2 Water Sep. Water C1 C2 Water Sep. Water C2 C2 Water Sep. Water C2 C2 Water Sep. Water C2 C2 Water Sep. Water Sep. Water C2 C2 Water Sep. Water	Empty Po Po Run		Water Sep. Wash Empty
1 2 3 4 5 6 7 8 9 10 11 B 0 <td></td> <td>A 2 3 B 0 0 0 D 0 0 F 0 0</td> <td></td>		A 2 3 B 0 0 0 D 0 0 F 0 0	

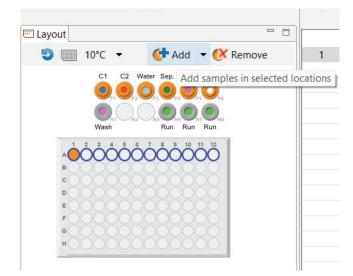
5. Add your samples:

To import samples using a saved injections file:

- a. Select File in the main menu and click Import Injections.
- b. Select an injections .csv file and click OK. The imported information will display in the Injections pane.

NOTE: For more information on setting up an injections file for import, see "Importing and Exporting Injections" on page 350.

To select samples manually: Use your mouse to highlight the well positions for each of your samples, then click Add.



This populates the Injections table:

Injectio	ns 🔚 History 👖 Notes				🕕 Pause 🔘 Stop 🎁 Add 📗 Replicate 🧩 Remov	e 🕀 🖻 🗖 🕻
	Injection Name	Sample ID	Location	Method	Notes	
1	Sample 1_01	Sample 1	A1	Reduced IgG		
2	Sample 02_02	Sample 02	A2	Reduced IgG		
3	Sample 03_03	Sample 03	A3	Reduced IgG		
4	Sample 04_04	Sample 04	A4	Reduced IgG		
5	Sample 05_05	Sample 05	A5	Reduced IgG		
6	Sample 06_06	Sample 06	A6	Reduced IgG		
7	Sample 07_07	Sample 07	A7	Reduced IgG		
8	Sample 08_08	Sample 08	A8	Reduced IgG		
9	Sample 09_09	Sample 09	A9	Reduced IgG		
10	Sample 10_10	Sample 10	A10	Reduced IgG		
11	Sample 11_11	Sample 11	A11	Reduced IgG		
12	Sample 12_12	Sample 12	A12	Reduced IgG		

6. Compass for iCE can monitor the current during a separation for you, stop it if an abnormal current profile is detected and reinject the sample for you automatically. Reinjections are enabled by default, but if you don't want to use this feature just click the reinject icon to toggle it off.

NOTES:

If a sample was reinjected, the injection row will be flagged in the Injections pane in the Run Summary screen. See "Injection Flags" on page 414 for more info.

A maximum of 10 reinjections are allowed per batch.



- 7. The sample platform is temperature controlled with a default setting of 10 °C. To change the temperature or turn it off, click the **down arrow** next to the temperature and select an option.
 - **NOTE:** The two reagent rows are kept at room temperature.



8. Enter your method parameters in the pane.

NOTE: There are three default methods. We recommend using the default method parameters for the listed samples. Please see the Maurice CE-SDS Application Guide for more information on method optimization.

To import a saved method:

- a. Select File in the main menu and click Import Method.
- b. Select a method file (*.method) and click OK. The imported information will display in the Method pane.

To create a new method or make changes to an existing one:

a. Click the first cell in the Name column and enter a new method name if needed.

Methods			P 0
			New Remove
Name	Sample Load	Separation	
Reduced IgG	8 sec 3500 Volts	5.5 min 4200 Volts	
Non-reduced IgG	8 sec 3500 Volts	8.0 min 4200 Volts	
MW Markers	8 sec 3500 Volts	8.0 min 4200 Volts	

b. Click the first cell in the Sample Load column, then click then click the selection button [...] to set your load profile time (in seconds) and voltage.

Methods				Sample Load Pro	file	×
Name	Sample Load			Add	Remove	
Reduced IgG	Voltage 1 Step)	\rightarrow	Time (sec)	Voltage (Volts)	
Non-reduced IgG	8 sec 3500 Volts			8	3500	
MW Markers	8 sec 3500 Volts					
				OK	Cancel	

c. Click the first cell in the Separation column then click the selection button [...] to set your separation time (in minutes) and voltage.

NOTE: Run your reduced IgG samples for 5.5 minutes and your non-reduced IgG samples, IgG Standard and CE-SDS MW Markers for 8.0 minutes. The default separation voltage for all sample types is 4200 volts.

Methods			@ S	eparation Profil	2	2
Name	Sample Load	Separation		Add	Remove	
Reduced IgG	8 sec 3500 Volts	Voltage 1 Step				
Non-reduced IgG	8 sec 3500 Volts	8.0 min 4200 Volts	Ti	me (min)	Voltage (Volts)	
MW Markers	8 sec 3500 Volts	8.0 min 4200 Volts	5.	5	4200	
				-		
						_
				OK	Cancel	

9. You can now:

- Make updates to the remaining methods by repeating the prior steps.
- Select a method and click Remove in the upper right corner of the Methods pane to delete it.
- Click **New** in the upper right corner of the Methods pane to add a new one if you want to use different methods for different samples. Then just repeat the steps above for the new method.

10. In the Injections pane:

• To add or change sample names: Click the Sample ID cell for the injection and type a name.

NOTES:

Sample IDs can be copied from other documents and pasted into Compass for iCE to make batch setup faster. Check out "Copying and Pasting Injection Names or Sample IDs from other Documents" on page 103 for more info.

If you change the sample ID when the default injection name is still being used, the injection name will automatically update to match the sample ID. If you've already changed the injection name manually, updating the sample ID will not update the injection name.

njectio	ns 🔚 History 🚹 Note				Under U	Stop 👫 Add	HH replicate	Re nemove	
	Injection Name	Sample ID	Location	Method	Notes				
1	Sample 1_01	Product A	A1	Reduced IgG					
2	Sample 02_02	Sample 02	A2	Reduced IgG					
3	Sample 03_03	Sample 03	A3	Reduced IgG					
4	Sample 04_04	Sample 04	A4	Reduced IgG					
5	Sample 05_05	Sample 05	A5	Reduced IgG					
6	Sample 06_06	Sample 06	A6	Reduced IgG					
7	Sample 07_07	Sample 07	A7	Reduced IgG					
8	Sample 08_08	Sample 08	A8	Reduced IgG					
9	Sample 09_09	Sample 09	A9	Reduced IgG					
10	Sample 10_10	Sample 10	A10	Reduced IgG					
11	Sample 11_11	Sample 11	A11	Reduced IgG					
12	Sample 12_12	Sample 12	A12	Reduced IgG					

• To change injection names: Click the Injection Name cell for the injection and type a name.

NOTES:

Each injection name must be unique.

Changing the injection name won't affect the sample ID.

	Injection Name	Sample ID	Location	Method	Notes				
1	njection 1	Product A	A1	Reduced IgG					
2	Sample 02_02	Sample 02	A2	Reduced IgG					
3	Sample 03_03	Sample 03	A3	Reduced IgG					
4	Sample 04_04	Sample 04	A4	Reduced IgG					
5	Sample 05_05	Sample 05	A5	Reduced IgG					
6	Sample 06_06	Sample 06	A6	Reduced IgG					
7	Sample 07_07	Sample 07	A7	Reduced IgG					
8	Sample 08_08	Sample 08	A8	Reduced IgG					
9	Sample 09_09	Sample 09	A9	Reduced IgG					
10	Sample 10_10	Sample 10	A10	Reduced IgG					
11	Sample 11_11	Sample 11	A11	Reduced IgG					
12	Sample 12_12	Sample 12	A12	Reduced IgG					

• To assign methods for each injection: Click the Method cell for the injection and select a method from the drop down menu.

	🔚 History 👖 Notes				0	Pause	O Stop	🕂 Add	Replica	ate	🔀 Remove	Ŧ	3 " 6
	Injection Name	Sample ID	Location	Method		Notes							
1	Injection 1	Product A	A1	Reduced IgG	¥								
2	Sample 02_02	Sample 02	A2	Reduced IgG									
3	Sample 03_03	Sample 03	A3	Non-reduced IgG									
4	Sample 04_04	Sample 04	A4	MW Markers	_								
5	Sample 05_05	Sample 05	A5	Reduced IgG									
6	Sample 06_06	Sample 06	A6	Reduced IgG									
7	Sample 07_07	Sample 07	A7	Reduced IgG									
8	Sample 08_08	Sample 08	A8	Reduced IgG									

• To add sequential replicate injections: Highlight an injection and click **Replicate**. A new injection will be added under the row you selected

Injection	s 🔚 History 👖 Notes				🕕 Pause 🟮 Stop 🛔	🕈 Add 📗 Replicate 🔀 Remove 🕤 📄 🗖 🗋
	Injection Name	Sample ID	Location	Method	Notes	Replicate selected injections
1	Injection 1	Product A	A1	Non-reduced IgG		
2	Sample 02_02	Product B	A2	Reduced IgG		
3	Product C_03	Product C	A3	Reduced IgG		
4	Product D_04	Product D	A4	Reduced IgG		
5	Product E_05	Product E	A5	Reduced IgG		
6	Product F_06	Product F	A6	Reduced IgG		

Injection:	s 🛛 🔚 History 📶 Notes				O Pause	O Stop	🕌 Add	📗 Repli	cate	🔀 Remove	E (3 - 0
	Injection Name	Sample ID	Location	Method	Notes							
1	Injection 1	Product A	A1	Non-reduced IgG								
2	Sample 02_02	Product B	A2	Reduced IgG								
∨ 3	Product C_03	Product C	A3	Reduced IgG								
4	Product C_04	Product C	A3	Reduced IgG								
5	Product D_05	Product D	A4	Reduced IgG								
6	Product E_06	Product E	A5	Reduced IgG								

• To add injections at the end of the batch: Click on any sample position in the Layout pane or sample injection in the Injection table and click Add. A new injection using the same sample will be added to the end of the table. Assign the method if needed.

📗 Injectio	ns 🛛 🔚 History 👖 Notes				🕕 Pause	O Stop	🕂 Add	Replicate	🔀 Remove	ΞE
	Injection Name	Sample ID	Location	Method	Notes		Add in	jections		
1	Injection 1	Product A	A1	Non-reduced IgG			Add II	Jections		
2	Product B_02	Product B	A2	Reduced IgG						
> 3	Product C_03	Product C	A3	Reduced IgG						
5	Product D_05	Product D	A4	Reduced IgG						
6	Product E_06	Product E	A5	Reduced IgG						
7	Product F_07	Product F	A6	Reduced IgG						
8	Product G_08	Product G	A7	Reduced IgG						
9	Product H_09	Product H	A8	Reduced IgG						
10	Product H1_10	Product H1	A9	Reduced IgG						
11	Product H2_11	Product H2	A10	Reduced IgG						
12	Product H3_12	Product H3	A11	Reduced IgG						
13	Product H4_13	Product H4	A12	Reduced IgG						

• To copy and paste injections: Right-click on an injection in the Injection table and select Copy. Click on the injection number above where you want to insert the copied injection, right click and select Paste. The copied injection will be inserted under the row you selected.

11. Add programmed pauses or stops in the batch to automatically pause or stop after injections (optional).

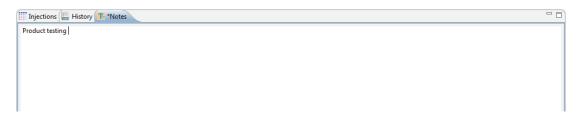
• **To program a pause:** Highlight the injection you want to pause at and click **Pause**. The batch will pause after that injection is complete. To resume the batch, click **Continue** in the instrument status bar.

Injecti	ons 🛛 🔚 History 👖 N	lotes 🤇		top 👫 Add 📗	Replicate	🔀 Remove	: 🕀 I	
	Injection Name	Sample ID	Log Paus	e after the selecte	ed injection	tes		
1	Sample 01_01	Sample 01	A1	Method 1	-	-		
2	Sample 02_02	Sample 02	A2	Method 1				
3	Sample 03_03	Sample 03	A3	Method 1				
Injecti	ons 🔚 History 🌆 I	Notes	Pause	Stop 🕂 Add	Replic	ate 🔀 Rem	iove [ŧ 🖻 🗖
Injecti	ons 🔚 History 🏋 Injection Name	Notes Sample ID	Pause		Replic	ate 🕌 Rem	iove [ŧ 🖻 🗖
Injecti							iove [ŧ 🖯 🗖
	Injection Name	Sample ID	Locatio	n Method			iove [ŧ 6 ⁻
1	Injection Name Sample 01_01	Sample ID Sample 01	Locatio A1	n Method Method 1			iove [ŧ E ⁻

• To stop the run after a specific injection: Highlight the injection you want the batch to stop at and click Stop. Maurice will continue the batch through the selected injection, then stop the batch and perform end-run cleanup steps.

Injectio	ons 🛛 🔚 History 🚹 N	Notes	🕕 Pause 🚺 Stop	🔒 🕂 Add 📗 Rep	licate 🕌 Remove	Ŧ	8
	Injection Name	Sample ID	Location	Stop after the sele	cted injection		
1	Sample 01_01	Sample 01	A1	Method 1			
2	Sample 02_02	Sample 02	A2	Method 1			
3	Sample 03_03	Sample 03	A3	Method 1			
Iniectio	ons 🔚 History 🎹 N	Notes	🕕 Pause 🗯 🖸 Stop	o 🕂 Add 📕 Rep	licate 🔀 Remove	Ŧ	R -
Injectio	ons 🔚 History 🏋 M	Notes Sample ID	Pause OStop Location	p 👫 Add 📊 Rep Method	licate 🕌 Remove Notes	Ŧ	8
Injectio						Ŧ	•
Injectio 1 2	Injection Name	Sample ID	Location	Method		Ŧ	8
1	Injection Name Sample 01_01	Sample ID Sample 01	Location A1	Method Method 1		Ŧ	8

12. Click on the Notes pane, then click in the notes area and type any information you want to add about your batch (optional).



13. You can preset the parameters used to analyze data generated with the batch (optional). We recommend using the default parameters for Turbo CE-SDS applications, but if you want to modify parameters:

Markers Peak Names	Markers		
₽eak Names ₽eak Fit Advanced Signal Processing	Analysis Groups	Markers	
	Standards	Internal Standard Time 170	Secon
		Markers Injection no markers	~
		MW (kDa)	RMT
	Add Remove	10	1
		20	1.15
	Apply Default:	33	1.3 1.5
	Standards	× 103	1.5
		178	2.05
	Apply Override:	270	2.4
	Apply To Group		
	Sample Standards		
		Add Rem	ove
	Add Remove		

a. Select Edit from the main menu and click Default Analysis. The following screen will display:

b. Change the parameters you want to, then click **OK**. For detailed information on analysis parameters, please refer to "Analysis Settings Overview" on page 713.

Chapter 14: Running Turbo CE-SDS Applications | Running Turbo CE-SDS Applications

- 14. You can preset the parameters used to display the graph and lane view data when the batch is complete. Default Analysis View Parameters must be set before you start the batch and cannot be modified once the batch starts. However, you can still manually change parameters in the Analysis pane using the Graph Options and Lane Options buttons:
 - a. Select Edit from the main menu and click Default Analysis View. The following screen will display:

o Default Analysis View Ma	urice CE-SDS TURBO			×
Graph View Options Lane View Options	Graph View Options Matching Peak Names Peak Names Peak Values Fitted Peaks Baseline Fit Grid Lines Plot Label Sample Method Injection Injection Name			
	OK Cano	;el	Apply	

- b. Change the parameters you want to, then click **OK**. For detailed information on graph and lane view options, please refer to "Customizing the Data Display" on page 695.
- 15. Once all of your sample, method and injection info is entered, select File > Save. Enter any comments on the batch if you want, then click Save.

o Save Batch Con	nment	×
Batch: Maurice C Comment:	CE-SDS TURBO	
I		
	Save	Cancel

16. Enter a name for your batch then click Save.

Step 7: Start the Batch

- 1. Make sure Maurice is connected to Compass for iCE. If he isn't, select **Instrument** and click **Connect**. Then select your Maurice system and click **Connect**.
- 2. Click **Start** to start your batch.

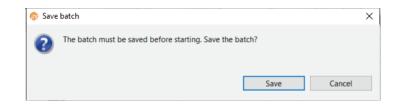
NOTES:

An alert may appear if the wrong cartridge is installed or if a cartridge post-run cleanup or cartridge purge is recommended. See "Step 5: Check for Cartridge Alerts" on page 369 for more information.

An alert may appear if the wrong adapter is installed or if you are starting a Turbo CE-SDS batch on MauriceFlex and have no locked the reagent vials in place. See "Adapter and Insert Alerts" on page 403 for more information.



3. You will be asked to save your batch before starting the run. Click Save.



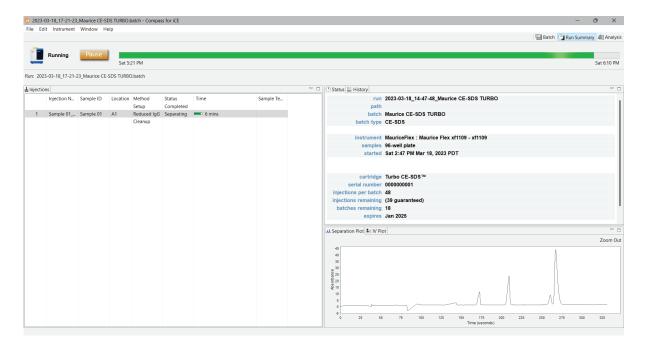
- 4. The Start Run box shows you the number of injections and batches remaining on your cartridge. Make sure you still have enough injections left before you start the run. If not, prep a new cartridge.
- 5. Click in the Results File name box if you want to change the default run file name. Otherwise just leave it as is.

Batch: Ma	urice CE-SDS TURBO				
Results file	name :				Browse
2023-02-0	8_20-16-46_Maurice C	E-SDS TURBO			
Location:	C:\Users\Andrea\Docu	uments\Compass for iCE	Runs		
Comment:					
.omment.					
	Cartridge				
	-	Turbo CE-SDS™	Injections per Batch :	48	
1	-		Injections per Batch : Injections Remaining :		
1	Type :	Jan 2025		(39 guaranteed)	
	Type : Expires : Serial Number :	Jan 2025 0000000001	Injections Remaining :	(39 guaranteed) 15	
	Type : Expires : Serial Number :	Jan 2025 0000000001	Injections Remaining : Batches Remaining :	(39 guaranteed) 15	

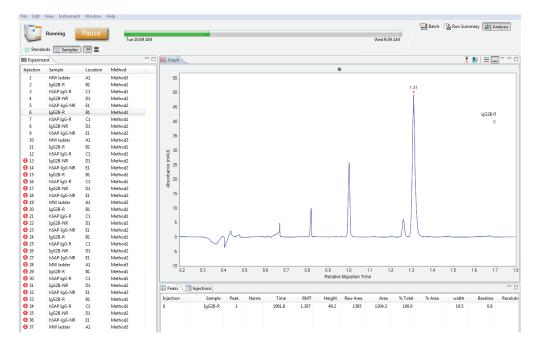
- 6. If you don't want to save the file to the default Runs folder, click Browse to select a different location.
- 7. Enter any run details you'd like in the Comments box (optional).
- 8. Click **Start** to start the run.

NOTE: The indicator light on Maurice's front panel will pulse slowly while he's running the batch.

To monitor the progress of your batch, click the **Run Summary** tab. See Chapter 16: "Run Status" for more details.



To view results, analyze results or change analysis parameters on completed injections while the batch is still running, click the **Analysis** tab. See Chapter 20: "CE-SDS Data Analysis" for more details.



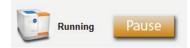
When your batch is complete, you can view electropherograms for all injections in the Analysis tab, and all batch and injection details in the Run Summary tab.

NOTE: If you'd like Maurice to let you know when your run is done, you can set him up to tweet you. Go to "Setting Up Maurice Systems to Send Tweets" on page 764 for more info.

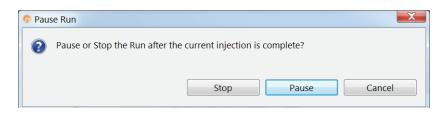
Editing a Running Batch

You can pause a batch after it's started to make updates or add samples and reagents.

1. Select Instrument > Pause or select the Pause button.



2. Click Pause in the pop-up window.



The Pause button will change to Continue but Maurice's status will stay at Running until Compass for iCE completes the current injection or calibration.



- You can now make these edits to the batch:
 - Add sample(s)
 - Add injection(s) to the end of the batch
 - · Modify injections that haven't completed and aren't greyed out
 - Create a new method
 - Update the method. Once a method is run it can only be updated. Highlight the method you want to edit and click **Update** in the Methods pane. The software will copy the parameters into a new method that you can modify.

3. When Maurice completes the current injection, his status will change to Paused and the progress bar will turn grey.

NOTE: Maurice's status light will change from a pulsing blue to a blue pulse with magenta flashes which means he's paused the run.

 Paused	Continue		
		Mon 1:43 PM	

The status in the Injection pane also changes to Paused and the pause duration updates live. You can now open the instrument door to:

• Add new samples

IMPORTANT

The door must be closed within 15 minutes of opening it to avoid potential assay performance issues.

NOTE: If the door is open for more than 30 seconds, a white light near the cartridge will start to flash and a warning message displays in Compass for iCE until the door is closed.

4. To continue the batch, click **Continue**. Changes you made to the batch are saved and Maurice will continue with the next sample injection.

NOTE: The D2 lamp is turned off for safety reasons when the door is opened. Once the batch is continued, Maurice will pause for 7 additional minutes before the next injection to let the lamp re-stabilize. During that time, the batch status in Compass for iCE will display injection loading.

Post-batch Procedures

When the batch is done:

- 1. Open Maurice's door. The lights on either side of the cartridge slot will be **orange** as Maurice will have already disengaged the cartridge.
- 2. If you're using the optional Maurice Filter Kit to contain βME odor, cover the 96-well sample plate immediately with a plate lid.
- 3. Remove your samples. Leave the Water (P3), Wash Solution (P5), and Air (P6) vials in place if your cartridge still has injectsion left as they will be needed for the cartridge post-run cleanup step. Discard the remaining reagent vials.
- 4. Gently pull out the cartridge making sure the cartridge inlet doesn't come into contact with any surface.

NOTE: If you see any separation matrix sticking to the capillary inlet, soak it in DI water for 5 minutes. Then wipe it using a lint-free laboratory wipe that's been moistened with DI water.



If you're at 100 injections, you've reached the limit of guaranteed performance for the Turbo CE-SDS cartridge (note this is not necessarily the maximum injection limit). The cartridge will not be usable after 25 batches. To dispose of a finished cartridge, put it in its original packing and discard it per your institution's safety and waste disposal guidelines.

NOTE: Disposal of cartridges, sample plates and vials depends on the samples you ran. If you aren't sure what your sample origins are, we recommend you dispose of everything in biohazard waste.

If the cartridge will be used again, clean up and store the cartridge:

- a. Put the cartridge on a flat surface and remove the stopper from the Waste Tank.
- b. Tilt the cartridge so that all the liquid flows toward the Waste Tank opening, and aspirate out all of the liquid.

Optional: Before aspirating out the liquid, add 200 μ L of sodium hypochlorite solution (10-15%) to neutralize β -mercaptoethanol, then aspirate out all the liquid.

- c. Remove the stopper from the Top Chamber and aspirate out all the liquid.
- d. Dispense 2.7 mL of DI water into the Top Chamber to fill it. Aspirate out all the liquid. Repeat 2 more times.

NOTE: Tilt the cartridge so that all the liquid flows toward the Top Chamber opening while aspirating.

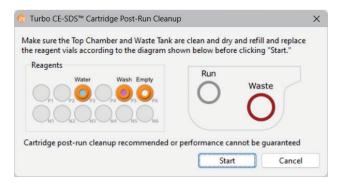
e. Aspirate out all the remaining liquid. Use the transparent back of the Top Chamber to check if any liquid remains visible. Residual liquid can be removed at this point by tilting the cartridge.



- f. Verify that there is 1.5 mL of DI water in the Water (P3) vial, 1.5 mL of Wash Solution in the Wash Solution (P5) vial and air in the empty (P6) vial.
- g. Place the stoppers on the empty Waste Tank and Top Chamber. They should be firmly closed.
- h. Insert the cartridge in Maurice
- i. Click on the brown **Cleanup** button in the Instrument Status Bar or select **Instrument** and **Cartridge Post-Run Cleanup** in the Compass main menu.

		Instrument Window Help
		Start
		Cartridge Post-Run Cleanup
		Cartridge Purge
Ready	Cleanup	Self Test >
		Runs
		Properties
		Update >
		Disconnect

j. You'll get the following message. Click Start. It'll only take 7 minutes.



k. Once the cleanup procedure is done, discard the reagent vials and remove the cartridge.

NOTES:

Keep cartridge upright while transporting.

See page 401 for information on what to do if a cartridge clog is detected during the Post-Run Cleanup.

- 1. Place the cartridge on a flat surface and remove the stopper from the Waste Tank.
- m. Tilt the cartridge so that all the liquid flows toward the Waste Tank opening, and aspirate out. Leave the stopper off to allow to air dry.
- n. Remove the stopper from the Top Chamber and aspirate out all visible liquid. Leave the stopper off to allow to air dry.
- o. Put the cartridge and stoppers in its protective packaging and store at room temperature.

!WARNING! SHARPS HAZARD

The capillary inlet of the cartridge may present a potential sharps hazard. Dispose of used cartridges according to your organizations health and safety regulations.



!WARNING! BIOHAZARD

Cartridges, sample plates and vials should be handled by procedures recommended in the CDC/NIH manual: Biosafety in Microbiological and Biomedical Laboratories (BMBL). The manual is available from the U.S. Government Printing Office or online at http://www.cdc.gov/biosafety/publications/bmbl5/.

Depending on the samples used, the cartridges, plates and vials may constitute a chemical or a biohazard. Dispose of the cartridges, plates and vials in accordance with good laboratory practices and local, state/ provincial, or national environmental and health regulations. Read and understand the Safety Data Sheets (SDSs) provided by the manufacturers of the chemicals in the waste content before you store, handle, or dispose of chemical waste.

Checking Your Data

Compass for iCE detects your sample proteins, CE-SDS MW Markers and Internal Standard peaks and reports results automatically. But, we always recommend you review your data using the steps in this section as a good general practice to make sure your results are accurate. If you see a data warning in the Experiment pane, these steps will also help you identify and correct any issues.

Step 1: Check Your Internal Standard

To make sure your Internal Standard is identified correctly:

1. Go to the Analysis screen and open your run (if it isn't already open).

2. Click Standards in the View bar.

File	Edit	View	Instrument	Window
Ē	Stand	ards	🔆 Samples	≣∎

3. Click the View Selected icon in the View bar.

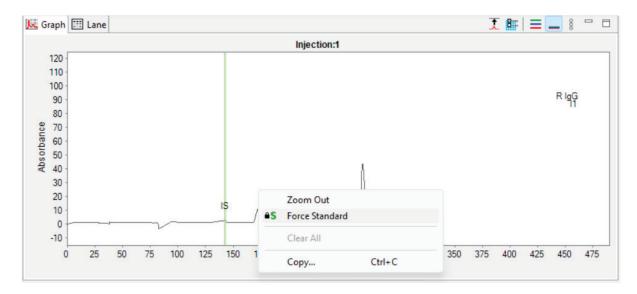
File	Edit	View	Instrumer	nt Window
Ē	Stand	ards	🚊 Samples	
				\uparrow

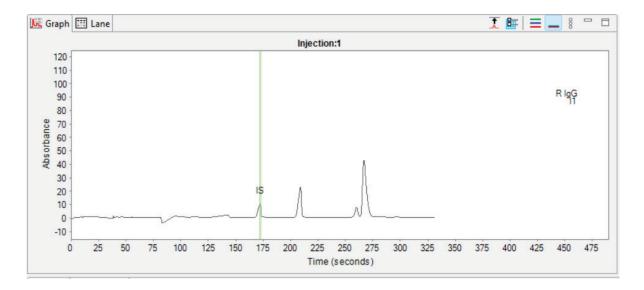
- 4. Click Injection 1 in the Experiment pane.
- 5. Check that your Internal Standard in the electropherogram has been correctly identified. It'll be labeled IS and will have a green vertical line running through it. The Internal Standard is also identified with an **S** in the Peaks table.

💮 Maurice	_CE-SDS_TURBO_R	ed-NonR	ed - Compass	s for iCE													-		×
File Edit View Instrument Window Help																			
🚊 Standard	😂 Standards 🖄 Samples 🛛 🚍 🗮 🔛 Summary 🚛 Analysis																		
Experime	nt	- 0	🛵 Graph	🖽 Lane							1 📴	=_	8 -	· 🗆	⊕ [®] Ana	alysis Op	tions		- 0
Injection	Injection Name	San					Injectio	n:1							Peak	Names			*
Ø 1	R lgG_01	RIg	120																
2	NR TRF_02	NR	110													_			
3	NR TRF_03	NR													Nan	ne			~
4	NR TRF_04	NR	100 -										1-0		RN	TN			
5	NR IgG_05	NR	90 -									n	lgG I1		Col				_
6	NR TRF_06	NR	80 -																
7	NR TRF_07	NR													Injec	cts			
8	NR TRF_08	NR	م 70 ·														Mo	dify	
9	R lgG_09	RIg	Absorbance																
10	NR TRF_10	NR	50 ·																
11	NR TRF_11	NR	Abs																
12	NR TRF_12	NR	40					1											
13	NR IgG_13	NR	30 -																
14	NR TRF_14	NR	20 -			- L	6	1											
15	NR TRF_15	NR	220			IS		11											
16	NR TRF_16	NR	10			1		0											
17	R lgG_17	Rlg	0-			~~/													
18	NR TRF_18	NR	-10 -																
19	NR TRF_19	NR	-10																
20	NR TRF_20	NR	0	25 50 75	100 125 1	50 175		250 275	300 325	350 37	5 400	425 4	450 4	75					
21	NR IgG_21	NR					Time	(seconds)											
22	NR TRF_22	NR	[III Dealer]	Injections															- 0
23	NR TRF_23	NR	HI Peaks																
24	NR TRF_24	NR	Injection	Injection Name	Sample	Peak	Time	Height											
25	R IgG_25	Rlg	AS 1	R lgG_01	R IgG	1	172.4	9.3											
26	NR TRF_26	NR																	
27	NR TRF_27	NR																	
28	NR TRF_28	NR																	
29	NR IgG_29	NR																	
30	NR TRF_30	NR																	
31	NR TRF 31	NR																	
	_																		

6. If your Internal Standard isn't identified correctly, here's how to manually correct it:

To set an unidentified peak as the Internal Standard: Right-click the peak in the electropherogram or Peaks table and select **Force Standard**. Compass will assign that peak as the Internal Standard.



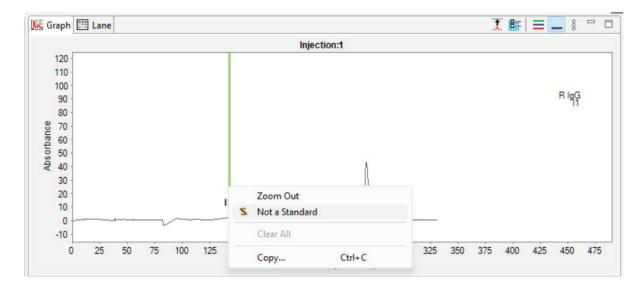


A lock icon indicating the Internal Standard was set manually will display next to the peak in the Peaks table and a check mark will appear next to the injection in the Experiment pane to show a manual correction was made.

njection	Sample	Peak
1	Sample 1	11
1	Sample 1	12
1	Sample 1	13
1	Sample 1	14
S 1	Sample 1	15
1	Sample 1	16
1	Sample 1	17

NOTE: To remove an Internal Standard peak assignment that was made manually, right click on the peak in the electropherogram or Peaks table and click **Clear**. To clear all the manual settings for the injection, click **Clear** All.

If an incorrect peak is identified as the Internal Standard: Right-click the peak in the electropherogram or Peaks table and select Not a Standard.



A check mark will appear next to the injection in the Experiment pane to show a manual correction was made.

Experiment 🛛 🗖						
Injection	Sample	Location	Method			
Ø 1	Sample 1	A1	Method1			
2	Sample 1	A1	Method1			
3	Sample 1	A1	Method1			
4	Sample 1	A1	Method1			
5	Sample 1	A1	Method1			
6	Sample 1	A1	Method1			
7	Sample 1	A1	Method1			

7. Repeat the previous steps for all other injections to make sure your Internal Standard is identified correctly.

Step 2: Set Your Molecular Weight (MW) Markers

NOTE: You'll only need to do this if you ran the CE-SDS MW Markers. If you didn't, you can skip to the next section.

Compass reports the relative migration time (RMT) of your sample in the Peaks table. If you also want to know the relative molecular weight of your sample, you can run the CE-SDS MW Markers as one of your injections.

You'll see these sizing markers when you run the CE-SDS MW Markers: 10, 20, 33, 55, 103, 178, and 270 kDa.

Chapter 14: Running Turbo CE-SDS Applications | Checking Your Data

To get MW data:

1. Click **Samples** in the View bar.

File	Edit	View	Instrument	Window	
Ħ	Stand	ards	Samples	∎∎	

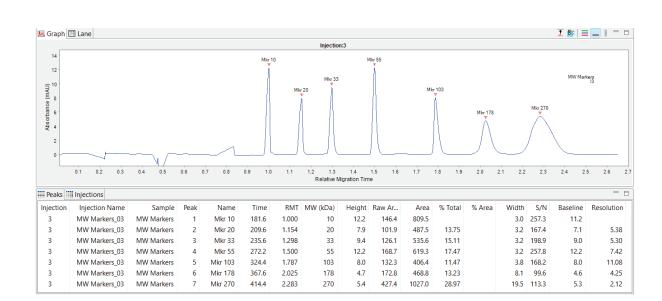
2. Select Edit from the main menu and click Analysis. In the Analysis window, select Markers in the left sidebar. Then click the Markers Injection drop down menu to select the injection you ran your CE-SDS MW Markers in.

/larkers	Markers			
eak Names eak Fit Idvanced	Analysis Groups		Markers	
Signal Processing	Standards		Internal Standard Time 150	Seconds
			Markers Injection no markers	
			MW 12	RMT
	Add	Remove	3 4 5	1 1.15
	Apply Default:		67	1.3
	Standards		8 9	1.8
	Apply Override:		10 11 12	2.4
	Apply To Sample	Group Standards	13 14 15 16	
			18 19 20 21	emove
	Add	Remove		

3. The default Maurice CE-SDS MW Markers molecular weights and relative migration time (RMT) values are already populated in the table. If you'd like to use these values, skip to the next step. If you're using different markers, click in the MW and RMT cells to type new values, click a row and select **Remove** to delete, or click **Add** to add a new one.

Markers Injection 2	\checkmark
MW (kDa)	RMT
15	1
20	1.15
33	1.3
55	1.5
103	1.8
178	2.05
270	2.4
Add	Remove

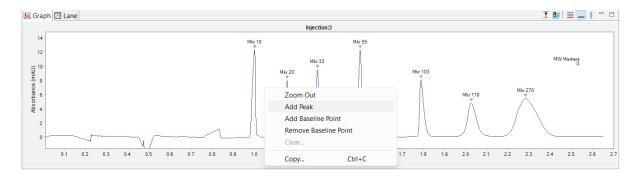
4. Click OK to close the Analysis window. Compass will automatically assign the molecular weights to your makers and label them Mkr. A MW (kDa) column will also now display in the Peaks table.



NOTE: The Mkr 10 peak is also the Internal Standard in every sample.

5. It's always a good idea to verify that all your CE-SDS MW Markers are identified correctly. Here's how to manually correct them:

To set an unidentified peak as a MW Marker: Right-click the peak in the electropherogram or Peaks table and select **Add Peak**. Compass will assign that peak as a MW Marker, and correctly reassign the remaining marker peaks.

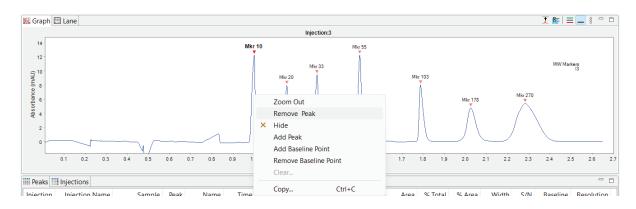


A check mark will appear next to the injection in the Experiment pane to show a manual correction was made.

Experiment 🛛 🗖					
Injection	Sample	Location	Me		
1	IgG System Co	A1	Me		
√ 2	Control Ladder	A2	Me		
3	Test Ladder	A3	Me		
4	IS - Alpha	B1	Me		

NOTE: To remove MW Marker peak assignments that were made manually, right click on the peak in the electropherogram or Peaks table and click **Clear**.

If an incorrect peak is identified as a MW Marker: Right-click the peak in the electropherogram or Peaks table and select **Remove Peak**. Compass should correctly reassign the remaining peaks as markers and update the Peaks table.



A check mark will appear next to the injection in the Experiment pane to show a manual correction was made.

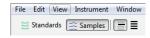
Experiment 🗖 🗖					
Injection	Sample	Location	Me		
1	IgG System Co	A1	Me		
✓2	Control Ladder	A2	Me		
3	Test Ladder	A3	Me		
4	IS - Alpha	B1	Me		

Step 3: Checking Sample Peaks

All detected peaks will be labeled automatically with the RMT (default) or apparent MW (if the CE-SDS MW Markers were run).

To make sure your sample proteins are identified correctly:

1. Click **Samples** in the View bar.

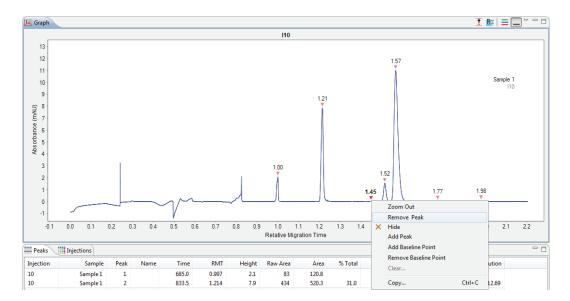


2. Click the View Selected icon in the View bar.

File E	dit Vie	w Instrument	Window
⊞ s	tandards	🚖 Samples	≣≡
			$\mathbf{\Lambda}$

- 3. Click Injection 1 in the Experiment pane.
- 4. If your sample peaks aren't identified correctly, here's how to manually correct them:

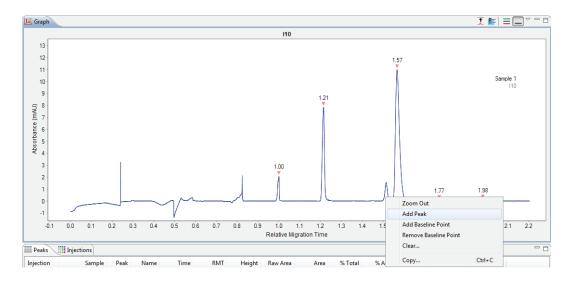
If a peak is incorrectly identified as a sample peak: Right-click the peak in the electropherogram or Peaks table and select **Remove Peak**. Compass will no longer identify it as a sample peak in the electropherogram and the peak data will be removed in the results table.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

Experiment 🗖 🗖				
Injection	Sample	Location	Method	
1	Sample 1	A1	Method1	
2	Sample 1	A1	Method1	
3	Sample 1	A1	Method1	
4	Sample 1	A1	Method1	
5	Sample 1	A1	Method1	
6	Sample 1	A1	Method1	
7	Sample 1	A1	Method1	
8	Sample 1	A1	Method1	
9	Sample 1	A1	Method1	
✓ 10	Sample 1	A1	Method1	
11	Sample 1	A1	Method1	
12	Sample 1	A1	Method1	

To identify a peak as a sample peak: Right-click the peak in the electropherogram or Peaks table and select Add Peak. Compass will calculate and display the results for the peak in the results table and identify the peak in the electropherogram.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

Experiment 🖓 🗖				
Injection	Sample	Location	Method	
1	Sample 1	A1	Method1	
2	Sample 1	A1	Method1	
3	Sample 1	A1	Method1	
4	Sample 1	A1	Method1	
5	Sample 1	A1	Method1	
6	Sample 1	A1	Method1	
7	Sample 1	A1	Method1	
8	Sample 1	A1	Method1	
9	Sample 1	A1	Method1	
√ 10	Sample 1	A1	Method1	
11	Sample 1	A1	Method1	
12	Sample 1	A1	Method1	

NOTE: To remove sample peak assignments that were made manually and go back to the original peak data, right-click the peak in the electropherogram and select **Clear**.

5. Repeat the previous steps for the remaining injections to make sure all sample peaks are correctly identified.

Step 4: Assigning Peak Names

Compass can also optionally identify and automatically name sample peaks using user-specified peak name settings. For more information on how to do this, see "Manual Peak Integration" on page 739.

Chapter 15: Cartridge and Adapter Alerts

Chapter Overview

- Overview
- Cartridge Alerts
- Adapter and Insert Alerts
- Compass Alerts

Overview

Maurice will double check that everythign is set up properly when you install your cartridge, start your batch or pause your run.

Cartridge Alerts

Cartridge Maintenance

An alert may appear when you install your cartridge in Maurice if a cartridge purge or cartridge post-run cleanup is recommended for your cartridge.

- If you install a cIEF or cIEF Fractionation cartridge that was used previously in a run that had an error, or a CE-SDS PLUS or Turbo CE-SDS cartridge that has not been used in 3 months or was used previously in a run that had an error, an alert that a cartridge purge is required will appear next to a brown Purge button. Run a cartridge post-run cleanup after performing a cartridge purge.
 - See "Step 5: Check for Cartridge Alerts" for cIEF applications, page 166 for MauriceFlex cIEF applications, page 232 for MauriceFlex Fractionation applications, page 300 for CE-SDS PLUS applications, and page 369 for Turbo CE-SDS applications for more information.

C Ready	Purge	🛕 Cartridge I	Purge required after cartridge not used for more than 3 mo	onths
Read	y Purge	🛕 Cartridge	e Purge required after cartridge not used for more than 3 mo	nths
	Ready	Purge	▲ Cartridge purge required after a run error	
	Ready	Purge	Cartridge purge required after a run error	

- If you install a cartridge that did not undergo a post-run cleanup after the last batch, an alert will appear next to a brown Cleanup button recommending you perform a cartridge post-run cleanup. The green Start button will appear after successful cleanup.
 - See page 120 for cIEF applications, page 182 for MauriceFlex cIEF applications, page 248 for MauriceFlex Fractionation applications, page 316 for CE-SDS PLUS applications, and page 385 for Turbo CE-SDS applications for more information.

Ready Cleanup Cartridge post-run cleanup recommended or performance cannot be guarant	ranteed
--	---------

Chapter 15: Cartridge and Adapter Alerts | Cartridge Alerts

If you start the batch without performing the post-run clean up, a warning will appear in the Start Run window.

2023-02-08_15-	17.10 Maurice C			
	17-10_ivlaurice C	E-SDS PLUS		
Location: C:\Us	ers\Andrea\Docu	uments\Compass for iC	E\Runs	
Comment:				
	Cartridge			
_	Type :	CE-SDS PLUS	Injections per Batch :	48
177 179	Expires :	Jan 2025	Injections Remaining :	439 (39 guaranteed)
	Serial Number :	000000001	Batches Remaining :	16

A warning that the post-run cleanup was not performed will appear at the bottom of the Run Summary pane if you proceed with the batch without running the post-run cleanup.

🕑 Status 🔚 History		
run	2023-03-13_21-41-29_Maurice clEF_2023 03 12	
path		
batch	Maurice cIEF_2023 03 12	
batch type	cIEF	
instrument	MauriceFlex : Maurice Flex xf1109 - xf1109	
samples	96-well plate	
started	Mon 9:41 PM Mar 13, 2023 PDT	
cartridge	cIEF	
serial number	990000100	
injections per batch	100	
injections remaining	119 (99 guaranteed)	
batches remaining	20	
expires	Jan 2025	
	Cartridge post-run cleanup not performed after previous run	

Chapter 15: Cartridge and Adapter Alerts | Cartridge Alerts

The warning will also be recorded in the Cartridge Properties and Injection Report.

	ce Flex xf1109			
Location : Michae	el's Maurice Sim	ulator		
	Type : Maur	iceFlex	Network Name :	192.168.1.80
Serial 1	Number: xf110)9	Network Address :	192.168.1.80
Instrument S	oftware : 4.2.20	022.11.03.21.24.04.1	o15d551f6	
Instrument Date ar	nd Time : 2023	-02-09 16:30:16 -08	3:00	Set to PC time
Expires : J Serial Number : (Injections Rema Batches Rema	ining: (39 guarante ining: 13
	Batch	Date	Injections	
	1	1 Sep 2018	48	
	2	4 Sep 2018	cleanup	•
	3	4 Sep 2018	12	
	_	4 Sep 2018 5 Sep 2018	cleanup	
	3			

	Model	Maurice OBM
	Instrument S/N	kf1147
	Software Version	Compass for iCE 3.0.0, Build ID: 0124
	Firmware Version	4.1.2021.12.09.23.23.49.55b8e524f
	Tray Type	96-well plate
	Cartridge Type	Turbo CE-SDS™
	Cartridge S/N	8211213001
	Cartridge Expiration	Dec 2022
	Injections Remaining	(4 guaranteed)
	Batches Remaining	20
\longrightarrow	Warning	Cartridge post-run cleanup not performed after previous run

At the end of your batch, an alert will appear next to a brown Cleanup button reminding you to perform a cartridge post-run cleanup. The green start button will appear after successful cleanup.

Ready	Cleanup	0	Cartridge post-run cleanup recommended or performance cannot be guaranteed

- If the cartridge post-run cleanup was stopped during the cleanup or did not complete successfully, and error will appear next to a yellow Reset button.
 - Click the yellow **Reset** button to clear the error.
 - You can try running the post-run cleanup again, start a run without the cleanup or prepare another cartridge to use for your run.
 - The error will be recorded in the Run Summary Status pane and Cartridge properties.

	Error Reset Error: Clean failed:	U
		🕑 Status 🔛 History
,	Cleaning	run
		path
	Cleaning	batch
	CE-SDS	batch type
	Maurice : Maurice Simulator - kf9991	instrument
	96-well plate	samples
	Mon 2:15 PM Apr 18, 2022 PDT	started
	Mon 2:15 PM Apr 18, 2022 PDT	stopped
	Clean failed:	error
	CE-SDS PLUS	cartridge
	000000001	serial number
	48	injections per batch
	439 (39 guaranteed)	injections remaining
	18	batches remaining
	Jan 2025	expires
~		

• If the cartridge post-run cleanup for your Turbo CE-SDS cartridge completed successfully but a clog is detected, an error will appear next to the Reset button and in the Run Summary Status pane.

When this happens

- Purge the cartridge. See page 369 for more information
- Perform a post-run cleanup and store the cartridge. See page 385 for more information on performing a post-run cleanup and storing the cartridge.
- If the purge or the post-run cleanup is not successful, contact Technical Support.

Cartridge Prep

An alert will appear in the Start Run window to ensure the cartridge has been correctly prepped.

Results file	name :				Bro
2023-02-0	9 20-44-20 Maurice Cl	E-SDS PLUS			
Location:	C:\Users\Andrea\Docu	ments\Compass for iC	E\Runs		
Comment:					
comment.					
	Cartridge				
	-	CE-SDS PLUS	Injections per Batch :	48	
17 1 1	-		Injections per Batch : Injections Remaining :		
	Type : 0	Jan 2025		439 (39 guaranteed)	
	Type : 0 Expires : J	Jan 2025	Injections Remaining :	439 (39 guaranteed)	

Cartridge Type

An alert will appear in the Start Run window if the cartridge type that is installed in Maurice does not match your batch type. You will not be able to start the batch until the correct cartridge is installed.

			6
Results file	name :		E
2023-02-0	9_20-40-28_Maurice CE-SDS PLUS		
Location:	C:\Users\Andrea\Documents\Compass for iC	E\Runs	
Commont			
Comment:	Catildaa		
Comment:	Cartridge		
Comment:	Cartridge Type∶Turbo CE-SDS™	Injections per Batch : 48	
Comment:	-	Injections per Batch : 48 Injections Remaining : (39 guarantee	:d)
Comment:	Type : Turbo CE-SDS™	Injections Remaining: (39 guarantee	:d)
Comment:	Type : Turbo CE-SDS™ Expires : Jan 2025		:d)
Comment:	Type : Turbo CE-SDS™ Expires : Jan 2025	Injections Remaining : (39 guarantee Batches Remaining : 13	:d)

You will also see an alert in the Start Run window if no cartridge is detected. You will not be able to start the batch until a cartridge is installed.

Adapter and Insert Alerts

Maurice will check to ensure the correct sample or vial insert or adapter is installed before you start a batch or if you restart a paused batch.

Alerts when Starting a Batch

Alerts will appear in the Start Run window.

Results file	name :			B
2023-02-0	3_16-32-39_MauriceFlex Fractionation			
Location:	C:\Users\lavanya.telukuntla\Documents\Co	mpass for iCE\Runs		
Comment:				
	Cartridge			
Ň	Cartridge Type : MauriceFlex Expires : Jan 2025	Injections Remaining :	9 (9 guaranteed)	
	Type : MauriceFlex	Injections Remaining : Batches Remaining :		
	Type : MauriceFlex Expires : Jan 2025	Batches Remaining :		

If you are running a standard cIEF or CE-SDS application on Maurice, Maurice C. and Maurice S., Compass for iCE will check to make sure that:

- The metal plate insert is installed if your sample is prepared in a 96-well plate.
- The metal vial insert is installed if your samples are prepared in vials.

If you are running a standard cIEF or CE-SDS application on MauriceFlex, Compass for iCE will check to make sure that:

- The fractionation adapter is not installed.
- The metal plate insert is installed if your sample is prepared in a 96-well plate.
- The metal vial insert is installed if your samples are prepared in vials.
- The reagent vials are locked in the reagent platform.

If you are running a MauriceFlex cIEF or MauriceFlex Fractionation application on MauriceFlex, Compass for iCE will check to make sure that:

• The fractionation adapter is installed.

Alerts when Pausing a Batch

Alerts may appear when your batch is paused and click the yellow Continue button. .

• When you pause a standard cIEF or CE-SDS batch, an alert may appear if correct metal insert is not detected.

-			This batch requires a fractionation adapter, not a plate	
Paused	Continue	Wed 2:34 PM		Wed 3:33 PM

• When you pause a running MauriceFlex batch, an alert may also appear if the batch reagent vials are not locked or if the fractionation adapter is not detected.

The vials must be locked before continuing the run.	
Mon 1:44 PM	Mon 2:07 PM
This batch requires a sample plate, not a fractionation adapter	
Paused Continue	
Wed 2:36 PM	Wed 3:00 PM

Compass Alerts

A Compass Alert window may appear during the Cartridge Post-Run Clean, Cartridge Purge, Cartridge Self-Test and Instrument Self-Test if you have the wrong cartridge, insert or adapter installed.

When performing a Cartridge Post-Run Cleanup, Compass Alerts will remind you to:



- Install a cartridge
- Lock reagent vials when cleaning a cIEF, CE-SDS PLUS or Turbo CE-SDS cartridge on MauriceFlex
- Install the fractionation adapter when cleaning a cIEF Fractionation cartridge on MauriceFlex
- Remove the fractionation adapter when cleaning a cIEF, CE-SDS PLUS or Turbo CE-SDS cartridge on MauriceFlex

When performing a Cartridge Purge, Compass Alerts will remind you to:



- Install a cartridge
- Lock reagent vials when purging a cIEF, CE-SDS PLUS or Turbo CE-SDS cartridge on MauriceFlex
- Install the fractionation adapter when purging a cIEF Fractionation cartridge on MauriceFlex
- Remove the fractionation adapter when purging a cIEF, CE-SDS PLUS or Turbo CE-SDS cartridge on MauriceFlex

When performing a Cartridge Self-Test, Compass Alerts will remind you to:



- Install a cartridge
- Lock reagent vials when testing a cIEF, CE-SDS PLUS or Turbo CE-SDS cartridge on MauriceFlex
- Remove the fractionation adapter when testing cartridges on MauriceFlex

When performing an Instrument Self-Test, Compass Alerts will remind you to:



- Remove the cartridge
- Remove the fractionation adapter when testing MauriceFlex

Chapter 16: Run Status

Chapter Overview

- Run Summary Screen Overview
- Opening Run Files
- Batch Injection Information
- Run Status Information
- Viewing the Injection Focus Series (cIEF, MauriceFlex cIEF, MauriceFlex Fractionation Only)
- Viewing the Fractionation Focus Series (MauriceFlex Fractionation Only)
- Viewing the Separation Plot (CE-SDS PLUS and Turbo CE-SDS Only)
- Current and Voltage Plots
- Run History
- Viewing Multiple Events
- Viewing Run Errors or Warnings
- Injection Reports
- Switching Between Open Run Files
- Closing Run Files

Run Summary Screen Overview

You can use the Run Summary screen to monitor the status of a batch in progress, see the CE-SDS PLUS and Turbo CE-SDS separation or cIEF, MauriceFlex cIEF and MauriceFlex Fractionation Focus series for your injections or the current and voltage plots for each injection. To get to this screen, click the **Run Summary** screen tab:



Run Summary Screen Panes

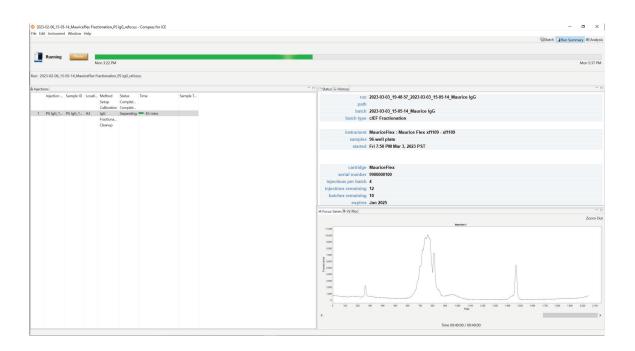
The Run Summary screen has five panes:

- **Injections** Lists the sample IDs, sample locations and methods used for each injection in the run. It also shows the status of the current injection if a run is in progress.
- Status Displays run file information and the current status of a run if one's in progress.
- History Running history of all run file events from when the run was first started to the most current analysis update.
- Separation Plot (CE-SDS PLUS and Turbo CE-SDS only)- Lets you view the raw protein separation in the capillary for each injection.
- Focus Series (cIEF, MauriceFlex cIEF and MauriceFlex Fractionation only) Lets you view the recorded focusing of proteins along the pH gradient in the capillary for each injection.
- IV Plot Lets you view plots of the total current and voltage measured during the separation for each injection.

hen zelze 49 gek 21-35 gezolosoff / STITTZ_MM. Maurice CE-SDS PLUS				117_JM_Mau	rice CE-SDS	PLUS - Compass for	iCE				- o ×
Ib. 231 M Db. 231 MULL Db	File Edit Instr	rument Wind	low Help							🗟 Bath 🕼	tun Summary Al Analysi
Applicione Service 1 620002 2 620002 3 620002 4 60000 5 60000 5 60000 6 60000 <	-									-	Thu 10:39 AM
ipedion. Semple D. Loud. Mediod Buth Inter Semple T. Consel. i 42000. 42000. 41 Beloed: Separator 2 Series 2 42000. 42000. 41 Beloed: Separator 2 Series 2 42000. 42000. 41 Beloed: Separator 2 Series 3 400 Minute: CE-505 PLUS 1 Beloed: Minute: CE-505 PLUS 1 Beloe: Minute: CE-505 PLUS 2 Beloe: Minute: CE-505 PLUS 1 Beloe: Minute: CE-505	Run: 2023-03-	09_08-21-35	6230303967	_KF1117_JM	Maurice CE-	SDS PLUS					
Stage Company Stages Company Stages	di Injections							 • • St	atus 🗮 History		- e
1 020000, 42000, A1 NoticedSpectra per binne 2 02000, 42000, A1 NoticedSpectra per binne 4 02000, 42000, A1 NoticedSpectra per binne 4 02000, 4200, A1 Notice CESOS 4 02000, 4200, A1 Notice 4 02000, 4200, A1 Notice CESOS 4 02000, 4200, A1 Notice 5 02000, 4200, A1 Notice CESOS 4 02000, 4200, A1 Notice 5 0200, 4200, A1 Notice 4 0200, 4200, A1 Notice 5 0200, 4200, A1 Notice 5 0200, 4200, A1 Notice 6 0200, 4000, A1 A1 6 0200, A1 A1 7 0200, A1 A1 7 0200, A1 A1 8 0200, A1 A1 8 0200, A1 A1 8 0200, A1 A	Inject	ion Samp	le ID Locati			Time	Sample T			2023-03-09_08-21-35_6230303967_KF1117_JM_Maurice CE-SDS PLUS	
Centop Comp	1 6230	303 62303	03 A1	Reduced	Separating	25 mins				Maurice CE-SDS PLUS	
samples 44 vials startide Tru 8-31 AM Mar 9, 2023 PST cartridge CE-805 PLUS setal number 6230303977 injections prenaiting 25 batches remaining 25 separation Piol Hir Mitel Total Control Piol Hir Mitel Total C	2 6230	303 62303	03 A1								
samples 44 vials startide Tru 8-31 AM Mar 9, 2023 PST cartridge CE-805 PLUS setal number 6230303977 injections prenaiting 25 batches remaining 25 separation Piol Hir Mitel Total Control Piol Hir Mitel Total C									instrument	Maurice : Kifer kf1117 - kf1117	
cartidge CE-905 PLUS setal number 623030597 injections per bath. 48 injections remaining 25 batcher remaining 25 at Separation Riv Hr Mit Zoom O									samples 4	48 vials	
sectors provide a sector of the VP Rel									started 1	Thu 8:31 AM Mar 9, 2023 PST	
Injections prevaiding 25 batches remaining 25 at Sparator Rol Mr Mai Sparator Rol Mr Mai									cartridge (CE-SDS PLUS	
telectors remaining 25 express Mar 2024									serial number	6230303967	
Latcher remaining 25 expires Mar 2024											
expires Mar 2024											
At Separation Pict M: V Pict Zoom O											
									expires	Mar 2024	
								M. Se	eparation Plot		-
											Zoom Oi
0 50 100 105 200 200 300 400 450 500 155 400 455 500 155 400 155 200 155 400 155 200 155 100 150 100 1100 1100 1200 12								Assertance			

6 2017-06	i-09_14-16-55_run	- Compass for	ICE					
File Edit	Instrument Wi	ndow Help						
0	Running	Pause	F	ri 2:31 PM				편 Batch [] 문un Summary] 4頁 Analysis Fri 3:27 PM
Run: 2017	7-06-09_14-16-55_r	un						
L Injectio	ns							🕑 Status 🔚 History
	Injection Name	Sample ID	Location	Method	Status	Time	Sample Temperature C	run 2017-06-09_14-16-55_run
				Setup	Completed			path
				Calibration Pause	Completed Paused 2:38			batch run
1	Sample 01_01	Sample 01	A1	System Suitability	Completed	2017-06-09 14:41:59	10.0	batch type cIEF
2	Sample 01_02	Sample 01	A1	System Suitability	Completed	2017-06-09 14:50:53		
				Pause	Paused 0:27			instrument Maurice : Kifer kf1077 - kf1077
3	Sample 02_03	Sample 02	A2 A2	System Suitability Method1	Separating	6 mins		samples 96-well plate
4	Sample 02_04	Sample 02	AZ	Cleanup				started Fri 2:31 PM Jun 9, 2017 PDT
				cicanop				
								cartridge cIEF
								serial number 1170109209
								injections per batch 100
								injections remaining 174 (74 guaranteed)
								batches remaining 13
								expires Jan 2018
								🛄 Focus Series 🕹 IV Plot
								Zoom Out
								Injection 3
								220
								200
								100
								041 041 120 120 04 04 04 04 04
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								0 250 500 750 1,000 1,250 1,500 1,750 2,000
								Pixel
								۲
								Time 00:03:30 / 00:03:30
							Lock	admin is logged in.

2023-02-06_Maure	iceFlex cIEF MDG Fi	gures Focusing -	Compass for iCE		- Ø
	C THINGH THEP				🖼 Batch 🛄 Run Summary 🐗 An
Running	Pause	-			
Running		Mon 12:31 PM			Mon #24
an: 2023-02-06_M	uriceFlex cIEF MDG	Figures Focusing	3		
Injections					° □ 0 Sahus ≣ History
	Sample ID Locati	Mathod S	itatus Time	Sample T	- January
injection	Sample ID Locati		Complet	Sample I	run 2023-03-03_20-22-13_2023-03-03_MauriceFlex cIEF MDG
		Calibration C			path batch 2023.03.03_MauriceFlex cIEF MDG
1 Seagen	Seagen A3		Complet. 2023-02-06 12:48:52	10.0	batch 2023-03-03 monotometex cere muss
	2 (200)		Complet		batch type citer Fractionation
2 Seagen	Seagen A3		Complet 2023-02-06 13:43:42 Complet	10.2	instrument MauriceFlex : Maurice Flex x11109 - x11109
3 NIST_05	NIST 05 A4		Complet 2023-02-06 14:38:33	10.3	instrument maunceriex imaunce riex xinus - xinus samples 96-well plate
			Complet.		samples 36-wein prate startred Fri 8-22 PM Mar 3, 2023 PST
4 PS lgG_1	PS IgG_1 AS		eparating 💳 45 mins		stated FI 6.22 FM mai 5, 2023 F31
		Cleanup			
					cartridge MauriceFlex
					serial number 99000100
					injections per batch 4
					injectors per outer •
					batches remaining 8
					expires Jan 2025
					Zoom
					1000 Bigetter 4
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					5000 mm
					194 550 C
					5 000 4 4400
					and the second s
					0 100 200 500 400 500 500 700 800 1000 1,100 1,200 1,5
					Peel
					< c
					Time 00x40:00 / 00x40:00



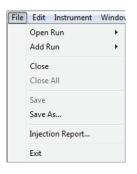
Software Menus Active in the Run Summary Screen

These main menu items are active in the Run Summary screen:

- File
- Edit
- Instrument (when the software is connected to an instrument)
- Window
- Help

File Menu

These File menu options are active:



- Open Run Opens a run file.
- Add Run Lets you open and view other run files besides the one that's already open.
- Close Closes the run file currently being viewed.
- Close All Closes all open run files.
- Save/Save As If you made changes in the Analysis screen before you went to the Run Summary screen, this saves your changes to the run file.
- **Injection Report** Exports the raw and analyzed data, IV plot, peaks table, sample and system info for individual injections as PDF files. You can also export the run history with all analysis events.
- Exit Closes Compass for iCE.

Edit Menu

These Edit menu options are active:

Edit	Instrument	Window	He
	Cut	Ctrl+X	
	Сору	Ctrl+C	
	Paste	Ctrl+V	
	Preferences		

- Copy Copies the information in the History pane so you can paste it into other documents.
- **Preferences** Lets you set and save your preferences for Access Control, data export, graph colors, grouped data and Twitter settings. See Chapter 21: "Setting Your Preferences" for more information.

Opening Run Files

You can open one run file or multiple files at the same time to compare information between runs.

Opening One Run File

1. Select File in the main menu and click Open Run.

Edit View Instrument	Window Help
Open Run 🕨	MW ladder assigned_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS
Add Run 🕨	2016-01-14_09-53-54_Maurice cIEF Ab dilution
Close	3160106286 KF1011 DG 2016-01-15_15-25-52_Maurice CE-SDS
Close All	3160106284 KF1011 DG 2016-01-15_12-42-55_Maurice CE-SDS
Close / III	3160106283 KF1011 DG 2016-01-14_18-50-33_Maurice CE-SDS
Save	1151120281-KF1007-BP-2015-12-04_10-17-58_2015Dec3_QC_plateA1_Maurice cIEF
Save As	1151120284-KF1007-BP-RERUN-2015-12-04_12-48-18_2015Dec3_QC_plateA1_Maurice cIEF
Export Tables	1151120284-KF1007-BP-2015-12-04_11-21-51_2015Dec3_QC_plateA1_Maurice cIEF
Export Spectra	1151120284-KF1007-BP-2015-12-04_12-16-51_2015Dec3_QC_plateA1_Maurice cIEF
Injection Report	KF1007_C1151214314_1X 2015-12-29_14-15-45_cIEF_VialA1_Maurice cIEF
Exit	Browse

2. A list of the last 10 runs opened will display. Select one of these runs or click **Browse** to open the Runs folder and select a different file.

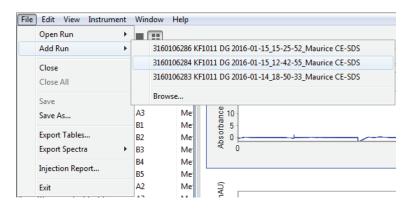
Opening Multiple Run Files

1. To open the first run file, select File in the main menu and click Open Run.

Edit View Instrum	nent W	'indow Help
Open Run	•	MW ladder assigned_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS
Add Run	•	2016-01-14_09-53-54_Maurice cIEF Ab dilution
Close		3160106286 KF1011 DG 2016-01-15_15-25-52_Maurice CE-SDS
Close All		3160106284 KF1011 DG 2016-01-15_12-42-55_Maurice CE-SDS
Close All		3160106283 KF1011 DG 2016-01-14_18-50-33_Maurice CE-SDS
Save		1151120281-KF1007-BP-2015-12-04_10-17-58_2015Dec3_QC_plateA1_Maurice cIEF
Save As		1151120284-KF1007-BP-RERUN-2015-12-04_12-48-18_2015Dec3_QC_plateA1_Maurice cIEF
Export Tables		1151120284-KF1007-BP-2015-12-04_11-21-51_2015Dec3_QC_plateA1_Maurice cIEF
Export Spectra	•	1151120284-KF1007-BP-2015-12-04_12-16-51_2015Dec3_QC_plateA1_Maurice cIEF
Injection Report		KF1007_C1151214314_1X 2015-12-29_14-15-45_cIEF_VialA1_Maurice cIEF
		Browse
Exit		

2. A list of the last 10 runs opened will display. Select one of these runs or click **Browse** to open the Runs folder and select a different file.

3. To open another run file, select File in the main menu and click Add Run.



- 4. A list of runs will display. You can only open a run that uses a similar application as the run that's already open (cIEF with MauriceFlex cIEF, MauriceFlex Fractionation only, or CE-SDS PLUS with Turbo CE-SDS), so the run files displayed are only for that application. Select one of these runs or click **Browse** to open the Runs folder and select a different file.
- 5. Repeat the last two steps to open additional runs.

Batch Injection Information

The Injections pane lists the system protocols (Setup and Cleanup) and injections performed during the run.

ction Name

stem Suitabi...

mAb 11 Blank... mAb 11 Ref. St...

Sample ID

mAb 11 Blank mAb 11 Ref. St...

Location Method

A2

A3

Setup

. Calibration

System S...

mAb Me..

mAb Me...

Injections

IgG System Co Control Ladde Test Ladder_03 IS - Alpha_04 IS - Frozen P3	lgG System Co Control Ladder Test Ladder IS - Alpha	A1 A2 A3	Setup Method1 Method2	Completed Completed	
Control Ladde Test Ladder_03 IS - Alpha_04	Control Ladder Test Ladder	A2		Completed	
Test Ladder_03 IS - Alpha_04	Test Ladder		Method2		
IS - Alpha_04		4.2	iniculou2	Completed	
	IS - Alpha	Ab	Method2	Completed	
IS - Frozen P3		B1	Method1	Completed	
	IS - Frozen P3	B2	Method1	Completed	
IS - T1 P3_06	IS - T1 P3	B3	Method1	Completed	
IS - T2 P3_07	IS - T2 P3	B4	Method1	Completed	
IS - T3 P3_08	IS - T3 P3	B5	Method1	Completed	
Control Ladde	Control Ladder	A2	Method2	Completed	
Test Ladder_10	Test Ladder	A3	Method2	Completed	
IS - Alpha_11	IS - Alpha	B1	Method1	Completed	
IS - Frozen P3	IS - Frozen P3	B2	Method1	Completed	
			Condition	Completed	
IS - T1 P3_13	IS - T1 P3	B3	Method1	Completed	
IS - T2 P3_14	IS - T2 P3	B4	Method1	Completed	
IS - T3 P3_15	IS - T3 P3	B5	Method1	Completed	
Control Ladde	Control Ladder	A2	Method2	Completed	
Test Ladder_17	Test Ladder	A3	Method2	Completed	
IS - Alpha_18	IS - Alpha	B1	Method1	Completed	
IS - Frozen P3	IS - Frozen P3	B2	Method1	Completed	
IS - T1 P3_20	IS - T1 P3	B3	Method1	Completed	
IS - T2 P3_21	IS - T2 P3	B4	Method1	Completed	
IS - T3 P3_22	IS - T3 P3	B5	Method1	Completed	
Control Ladde	Control Ladder	A2	Method2	Completed	
Test Ladder_24	Test Ladder	A3	Method2	Completed	
			Condition	Completed	
IS - Alpha_25	IS - Alpha	B1	Method1	Completed	
IS - Frozen P3	IS - Frozen P3	B2	Method1	Completed	
IS - T1 P3_27	IS - T1 P3	B3	Method1	Completed	•
	IS - T3 P3_08 Control Ladde Text Ladder.10 IS - Alpha_11 IS - Frozen P3 IS - T1 P3_13 IS - T2 P3_14 IS - T3 P3_15 Control Ladder. Text Ladder_17 IS - Alpha_18 IS - Frozen P3 IS - T1 P3_20 IS - T2 P3_21 Control Ladde Text Ladder_24 IS - Alpha_25 IS - Frozen P3	IS - T3 P3_08 IS - T3 P3 Control Ladder. Control Ladder Text Ladder, ID Text Ladder IS - Facen P3 IS - Alpha IS - Frozen P3 IS - Facen P3 IS - T1 P3 IS - T1 P3 IS - T1 P3 IS - T1 P3 IS - T2 P3, IA IS - T2 P3 IS - T3 P3 Control Ladder Text Ladder, TJ Text Ladder Text Ladder, TJ Text Ladder Text Ladder, TJ Text Ladder For P3, P3, IS IS - T3 P3 Control Ladder IS - Frozen P3, IS IS - T2 P3, 2U IS - T3 P3 Control Ladder, T2 P3, IS IS - T3 P3 Control Ladder, 2U Control Ladder IS - Alpha, 2U IS - T3 P3 Control Ladder, 2U Control Ladder IS - Alpha, IS S - Alpha IS - Frozen P3, IS - Frozen P3 S - Alpha	S - T3 P3_08 S - T3 P3 B5 Control Ladder. Control Ladder A2 Text Ladder. Control Ladder A3 IS - Alpha B1 B1 IS - Finzen P3 IS - T1 P3 B3 IS - T1 P3_11 IS - T1 P3 B3 IS - T1 P3_13 IS - T1 P3 B3 IS - T2 P3_14 IS - T2 P3 B4 IS - T3 P3_15 IS - T1 P3 B3 IS - T2 P3_14 IS - T2 P3 B4 IS - T3 P3_15 IS - T3 P3 B5 Control Ladder. Control Ladder A3 IS - Forcen P3 IS - Forcen P3 B2 IS - T1 P3_20 IS - T1 P3 B4 IS - T1 P3_20 IS - T1 P3 B4 IS - T3 P3_21 IS - T2 P3 B4 IS - T3 P3_22 IS - T3 P3 B5 Control Ladder. Control Ladder A3 IS - Alpha_25 IS - Alpha B1 IS - Forcen P3 IS - Alpha B2 IS - T1 P3_27 IS -	S - T3 P3_08 IS - T3 P3 B5 Method1 Control Laddec. Control Ladder A2 Method2 Test Ladder. Test Ladder A3 Method2 IS - Alpha, 11 IS - Alpha B1 Method2 IS - Frozen P3 IS - Frozen P3 B2 Method1 IS - TP3, 13 IS - T1 P3 B3 Method1 IS - T2 P3, 14 IS - T2 P3 B4 Method1 IS - T2 P3, 15 IS - T2 P3 B4 Method1 IS - T2 P3, 15 IS - T2 P3 B4 Method1 Control Ladder. Control Ladder A2 Method1 IS - Frozen P3 IS - Frozen P3 B2 Method1 IS - Frozen P3 IS - T2 P3 B4 Method1 IS - T2 P3, 21 IS - T2 P3 B4 Method1 IS - T3 P3, 22 IS - T3 P3 B5 Method1 IS - T2 P3, 21 IS - T3 P3 B5 Method1 IS - T3 P3, 22 IS - T3 P3 B5 Method1 Control Ladder	S - T3 P3_08 IS - T3 P3 B5 Method1 Completed Control Ladder. Comtrol Ladder A2 Method2 Completed S - Alpha, 11 IS - Alpha B1 Method2 Completed IS - Frozen P3 IS - Frozen P3 B2 Method1 Completed S - T1 P3, 13 IS - T1 P3 B3 Method1 Completed S - T2 P3, 14 IS - T2 P3 B4 Method1 Completed Control Ladder. Control Ladder A2 Method1 Completed Control Ladder. Control Ladder A3 Method1 Completed IS - T2 P3, 14 IS - Alpha B1 Method1 Completed Control Ladder. Control Ladder A3 Method2 Completed IS - Frozen P3 IS - Frozen P3 B2 Method1 Completed IS - Frozen P3 IS - T2 P3 B4 Method1 Completed IS - T2 P3, 20 IS - T1 P3 B3 Method1 Completed IS - T2 P3, 21 IS - T2 P3 B4 Method1 Completed IS - T3 P3, 22 IS - T3 P3 B5 Method1 Completed Control Ladder. Control Ladder A3 Method2

 mab
 11
 Prep 2...
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 A4

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 mAb Me... mAb Me... mAb Me... mAb Me... Completed Completed Completed Completed mAb 11 Blank... mAb 11 Blank Δ: mAb Me... Cleanup Completed Completed Injections Injection Name Sample ID Location 1 Sample 01_01 Sample 01 A1

Status

Completed Completed Completed

Completed

Completed

Standard cIEF

Cleanup Completed MauriceFlex Fractionation

Method

Calibrat

NIST

Fractionat

Setup

Status

Completed

Completer

Completed

ction N... Sample ID

MauriceFlex cIEF

sys suit_01 sys suit

sys suit_02

- Each injection includes information on:
 - Injection name
 - Sample ID
 - Sample location
 - Method
 - Run status
 - Time of injection
 - Sample temperature
- Clicking on an injection displays its data in the Focus Series (cIEF, MauriceFlex cIEF and MauriceFlex Fractionation) or Separation (CE-SDS PLUS and Turbo CE-SDS) and IV Plot panes. Hovering over a method name displays the method parameters:

🔟 Injecti	Injections										
	Sample ID	Location	Method	Status	^						
			Setup	Completed		р					
1	IgG System Co	A1	Method1	Method1		· · · · ·					
2	Control Ladder	A2	Method2	Sample Load: 20 sec 460	0 Volts						
3	Test Ladder	A3	Method2			Volts, 25.0 min 5750 Volts					

Injections								
	Sample ID	Location	Method	Status				
			Setup Calibration	Completed Completed				
1	mAb11 Sample 1	A1	Method1	Completed				
2 3 4 5	mAb11 Sample 2 mAb11 Sample 3 mAb11 Sample 4 mAb11 Sample 5	A2 A3 A4 A5	Method1 Separation: 1.0 Detection: 6 Exp Sample Load: 90 pI Markers: 4.05) seconds				

For runs in progress, the Status column displays:

- Running for Setup, Conditioning (CE-SDS only) and Cleanup protocols that are in progress
- Loading or Separating for injections in progress. Once the separation starts, a status bar displays next to the injection so you know when the separation will be done. Hovering your mouse over the progress bar tells you the time left for the injection.
- Completed for Setup, Conditioning and Cleanup protocols and injections that are done.

	Sample ID	Locat	Method	Status	*
			Setup	Completed	
1	MW Ladder	A1	MW Markers	Separating	
2	IgG-R	A8	Reduced IgG		5 mins remaining

For MauriceFlex Fractionation runs in progress, the fractionation step Status column additionally displays:

- Mobilizing for when Mobilization solution is being applied to the cartridge.
- Refocusing for when the optional refocusing step is being applied
- Eluting (Fractionation number) for when protein is mobilizing off of the capillary and being collected into fraction wells on the 96-well plate. The fraction being collected in the series will be noted in parenthesis.

Injection Flags

If Compass for iCE detects a potential injection issue, a flag icon will display next to the injection row in the Injections pane.

Past cartridge injection limit notification - This means the injection is over the guaranteed number of injections for the cartridge. Roll your mouse over the icon to display details.

占 Injecti	ons	
	Sample ID	Locat
3	0.5% Tween	A3
4	TBST	A4
<u> </u>	SB	A1
🔒 Pas	t cartridge injec	tion limit
4 7	0.5% Tween	A3

Reinjection notification - This means an abnormal current profile is detected, so the separation was stopped and the sample was reinjected. The second injection always runs to completion even if the current drops again. Roll your mouse over the icon to display details.



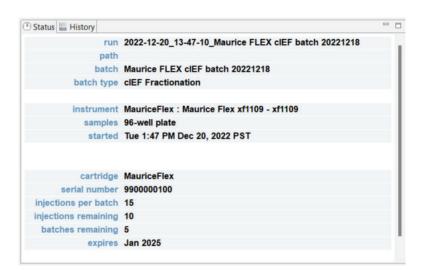
Run Status Information

The Status pane shows info specific to each run file:

- Run file name and path (directory location)
- Batch name and type
- Instrument and serial number
- Type of sample tray used
- Run start/complete date and time
- Type of cartridge
- Cartridge serial number
- Cartridge batch injection limit, injections/batches remaining and expiration date
- Recorded run errors or warning. See "Viewing Run Errors or Warnings" on page 424 for more information.

Status 🔚 History		-
run	2021-12-15_11-35-24_Maurice CE-SDS TURBO_96_Inj	
path	C:\Users\User\Documents\Compass for iCE\Runs	
batch	Maurice CE-SDS TURBO_8_Inj	
batch type	CE-SDS	
instrument	Maurice : Maurice kf1147 - kf1147	
samples	96-well plate	
started	Wed 11:35 AM Dec 15, 2021 PST	
completed	Thu 1:39 AM Dec 16, 2021 PST	
cartridge	Turbo CE-SDS™	
serial number	8211213001	
injections per batch	96	
injections remaining	(4 guaranteed)	
batches remaining	20	
expires	Dec 2022	

Status 🔚 History		- 0
run	2021-07-28_14-35-03_2021_0503_Maurice CE-SDS PLUS	
path	C:\Users\User\Documents\Compass for iCE\Runs	
batch	2021_0503_Maurice CE-SDS PLUS	
batch type	CE-SDS	
instrument	Maurice : Maurice kf1018 - kf1018	
samples	48 vials	
started	Wed 2:33 PM Jul 28, 2021 PDT	
completed	Wed 5:13 PM Jul 28, 2021 PDT	
cartridge	CE-SDS PLUS	
serial number	6210115849	
injections per batch	48	
injections remaining	358 (0 guaranteed)	
batches remaining	19	
ovniree	Jan 2022	



Status 🔚 History		-	E
run	2022-11-08_11-56-11_Maurice Flex Fractions		
path	C:\Users\User\Documents\Compass for iCE\Runs		
batch	Maurice Flex Fractions		
batch type	cIEF Fractionation		
instrument	MauriceFlex : Maurice Flex kf1884 - kf1884		
samples	96-well plate		
started	Tue 11:56 AM Nov 8, 2022 PST		
completed	Tue 1:55 PM Nov 8, 2022 PST		
cartridge	MauriceFlex		
serial number	5221012106		
injections per batch	1		
injections remaining	11		
batches remaining	10		
expires	Oct 2023		

🕑 Status 📗 History	
run	KF0002_clEF1160607664_2016-08-09_12-01-50_mAB high low
path	<u>C:\Users\User\Documents\Compass for iCE\Runs</u>
batch	mAB high low_OBM Validation
batch type	cIEF
instrument	Maurice : Maurice kf0002 - kf0002
samples	96-well plate
started	Tue 2:02 PM Aug 9, 2016 CDT
completed	Wed 1:48 AM Aug 10, 2016 CDT
cartridge	cIEF
serial number	1160607664
injections per batch	100
injections remaining	60 (60 guaranteed)
batches remaining	9
expires	Jun 2017

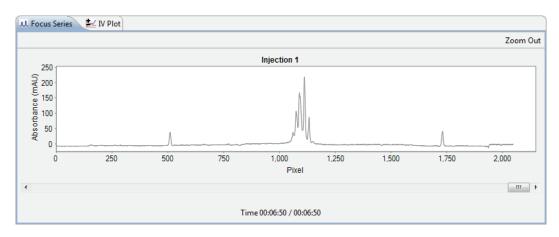
- To go to the run file directory location Double click the path hyperlink, or right-click and select Open Directory.
- **To copy the path** Right-click on the path hyperlink and click **Copy Path**. The path can then be copied into documents. The path can also be copied into the Windows Explorer address bar to launch Compass for iCE and open the run file automatically.

Viewing the Injection Focus Series (cIEF, MauriceFlex cIEF, MauriceFlex Fractionation Only)

You can view your proteins focusing along the pH gradient in the capillary for each injection in the Focus Series pane.

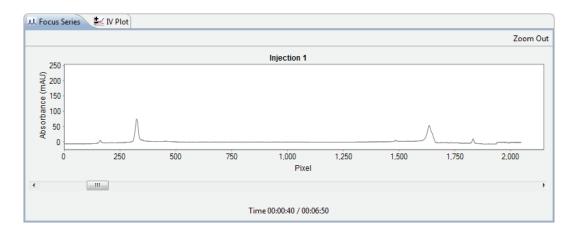
NOTE: The Focus Series y-axis displays in absorbance for a standard cIEF assay and fluorescence for a MauriceFlex cIEF and MauriceFlex Fractionation run.

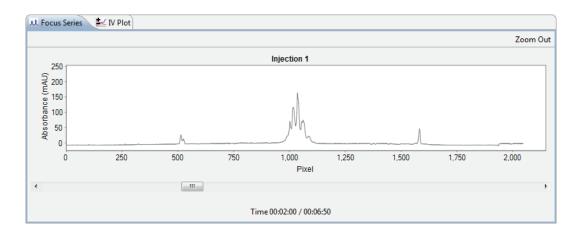
- 1. Select an injection in the Injections pane.
- 2. Click the Focus Series pane. It'll display the final focusing plot:



Chapter 16: Run Status | Viewing the Fractionation Focus Series (MauriceFlex Fractionation Only)

3. To view the focusing as it happened, drag the slider bar under the plot to the left or right. To view it frame by frame, click the left/right arrows.





- To zoom in on an area of the plot Hold the mouse button down and draw a box around the area with the mouse.
- To zoom out Click Zoom Out in the upper right corner of the pane.

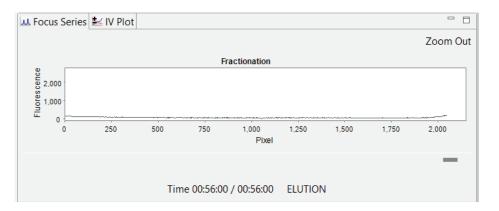
NOTE: Focus Series data for a run in progress won't be available until the injection is executing. Once it starts, the plot displays data up to the current point in time.

Viewing the Fractionation Focus Series (MauriceFlex Fractionation Only)

You can view your separated protein peaks mobilizing out of the capillary in the Focus Series pane.

1. Select the Fractionation step in the Method column in the Injections pane.

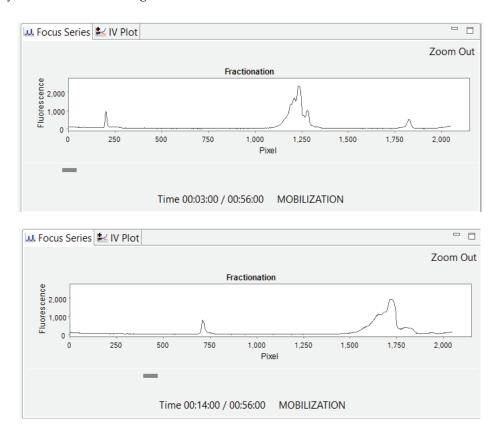
Chapter 16: Run Status | Viewing the Fractionation Focus Series (MauriceFlex Fractionation Only)



2. Click the Focus Series pane. It will display the final focusing plot:

NOTE: The fractionation status is updated next to Focus Series timestamp.

3. To view separated protein peak mobilization as it happened, drag the slider bar under the plot to the left or right. To view it frame by frame, click the left/right arrows.



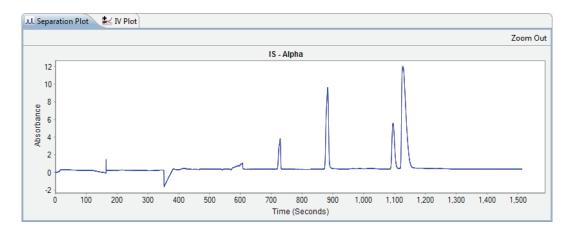
- To zoom in on an area of the plot Hold the mouse button down and draw a box around the area with the mouse.
- To zoom out Click Zoom Out in the upper right corner of the pane.

NOTE: Focus Series data for the fractionation step progress won't be available until the IEF separation is complete and mobilization/fractionation is executing. Once it starts, the plot displays data up to the current point in time.

Viewing the Separation Plot (CE-SDS PLUS and Turbo CE-SDS Only)

You can view your protein separation in the capillary for each injection in the Separation Plot pane.

- 1. Select an injection in the Injections pane.
- 2. Click the Separation Plot pane. It'll display a plot of the raw separation data.



- To zoom in on an area of the plot Hold the mouse button down and draw a box around the area with the mouse.
- To zoom out Click Zoom Out in the upper right corner of the pane.

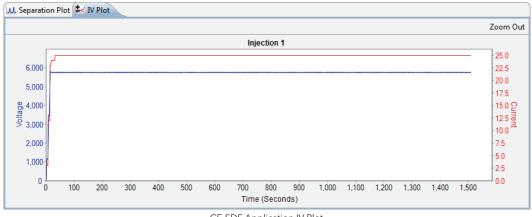
NOTE: Separation data for a run in progress won't be available until the injection is executing. Once it starts, the plot displays data up to the current point in time.

Current and Voltage Plots

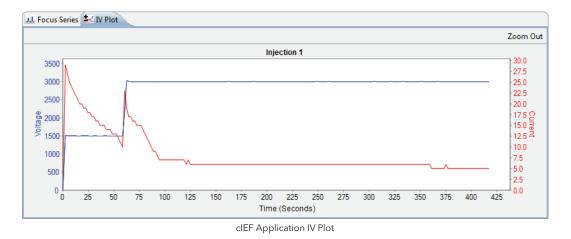
To view plots of the total current and voltage measured during an injection:

1. Select an injection in the Injections pane.

2. Click the IV Plot pane.



CE-SDS Application IV Plot



😐 Focus Series 🛃 IV Plot - -Zoom Out 1200 40 35 1000 30 25 Current 20 (uA) Voltage () 400 10 200 5 0 0 250 500 750 1,000 1,250 1,500 1,750 2,000 2,250 2,500 2,750 3,000 3,250 3,500 Time (seconds)

Fractionation Application Mobilization/Fractionation IV Plot

The blue Y-axis and plot shows the run voltage in volts (V), and the red Y-axis and plot shows the run current in microamps (µA). The X-axis displays time in seconds.

- To zoom in on an area of the plot Hold the mouse button down and draw a box around the area with the mouse.
- To zoom out Click Zoom Out in the upper right corner of the pane.

NOTE: IV Plots for a run in progress won't be available until the injection is executing. Once it starts, the plot displays in real time.

Run History

The History pane shows the run file event history, starting with the date and time the run was started through the most current analysis event. Clicking on a row in the table displays the full event details in the box under the table.

Date	User Name	Message	Comment	
12/06/2015 3:13 PM		Started run: 2015-12-06_15-13-01_Maurice cIEF		
b 12/08/2015 10:43 AM		Saved analysis changes		
12/08/2015 3:21 PM		Saved analysis changes		
12/09/2015 12:31 PM		Saved analysis changes		
12/14/2015 2:23 PM		Saved analysis changes		
01/05/2016 4:39 PM		Saved analysis changes		
	2015 3:13 PM	User 15-13-01_Maurice cIEF_Mab11_TechRep_Assay: Maur		

🕑 Status 🔝 History				
Date	User Name	Message	Comment	
11/30/2015 4:50 PM		Started run: 78664 P3 IS 2015-11-30_16-49-49_M		
> 12/01/2015 11:19 A	N	Saved analysis changes		
> 12/28/2015 6:25 PM		Saved as MW ladder assigned_MW Ladder Sol Te		
	0/2015 4:50 PM	User		
fessage Star	ted run: 78664 P3 IS	2015-11-30_16-49-49_MW Ladder Sol Test IS final QC	110 ms Maurice CE-SDS	Assay: MW Ladder Sol Test IS
Comment				

- **Date:** Date and time of the run event.
- User Name: User that initiated the event. User names only display if you're using the Access Control feature to help satisfy the 21CFR Part 11 data security requirements.

- Message: Description of the event that took place.
- **Comment:** Comments entered by the user when the batch was saved.

Viewing Multiple Events

Items in the table with multiple analysis events have an arrow next to the date and time. You can view or hide these details by toggling the arrow:

Date	User Name	Message	Comment
12/06/2015 3:13 PM		Started run: 2015-12-06_15-13-01_Maurice cIEF_Mab11_TechRep_Assay: Mauric	
a 12/08/2015 10:43 AM		Saved analysis changes	
		Changed 1 from "Exposure 1 1 seconds" to "Exposure 3 20 seconds"	
		Changed select: type from absorption to fluorescence	
		Changed Peak Fit Analysis Settings Peak Fit: Range Maximum from 11.0 to 10.1	
		Changed Peak Fit Analysis Settings Peak Fit: Range Minimum from 2.0 to 4.0	
> 12/08/2015 3:21 PM		Saved analysis changes	
> 12/09/2015 12:31 PM		Saved analysis changes	
> 12/14/2015 2:23 PM		Saved analysis changes	
01/05/2016 4:39 PM		Saved analysis changes	
	015 10:43 AM analysis changes	User	

• To view details for all items with multiple analysis events in the run, click the Expand All button.

Status 🔚 History				Ē
ate	User Name	Message	Comment	Expand
12/06/2015 3:13 PM		Started run: 2015-12-06_15-13-01_Maurice cIEF_Mab11_TechRep Assay: Mauric		
12/08/2015 10:43 AM		Saved analysis changes		
		Changed 1 from "Exposure 1 1 seconds" to "Exposure 3 20 seconds"		
		Changed select: type from absorption to fluorescence		=
		Changed Peak Fit Analysis Settings Peak Fit: Range Maximum from 11.0 to 10.1		
		Changed Peak Fit Analysis Settings Peak Fit: Range Minimum from 2.0 to 4.0		
12/08/2015 3:21 PM		Saved analysis changes		
		Added Peak Names Apply Settings "apply Peak Names 1 to all"		
		Added Peak Names Group Peak Names 1		
		Control Area: 10000.0		
		Control Reference Capillary: mAb11 Sample 1		
		Protein name: Peak1 pl: 6 Color: 32512 Range: 0.1 Control: false Show: true		
		Protein name: Peak2 pI: 6 Color: 32512 Range: 0.1 Control: false Show: true		
		Protein name: Peak3 pl: 6 Color: 32512 Range: 0.1 Control: false Show: true		
		Protein name: Peak4 pI: 6 Color: 32512 Range: 0.1 Control: false Show: true		
		Protein name: Peak5 pI: 6 Color: 32512 Range: 0.1 Control: false Show: true		
		Protein name: Peak6 pl: 6 Color: 32512 Range: 0.1 Control: false Show: true		
		Protein name: Peak7 pI: 7 Color: 32512 Range: 0.1 Control: false Show: true		
		Protein name: Peak8 pI: 7 Color: 32512 Range: 0.1 Control: false Show: true		
		Protein name: Peak9 pl: 7 Color: 32512 Range: 0.1 Control: false Show: true		
		Changed Peak Fit Analysis Settings Peak Fit: Range Maximum from 10.1 to 7.5		

• To hide all items with multiple analysis events, click the **Collapse All** button.

🕑 Status 📙 History				
Date	User Name	Message	Comment	Collapse A
12/06/2015 3:13 PM		Started run: 2015-12-06_15-13-01_Maurice cIEF_Mab11_TechRep Assay: Mauric		
12/08/2015 10:43 AM		Saved analysis changes		
12/08/2015 3:21 PM		Saved analysis changes		
12/09/2015 12:31 PM		Saved analysis changes		
12/14/2015 2:23 PM		Saved analysis changes		
01/05/2016 4:39 PM		Saved analysis changes		

Copying History Info

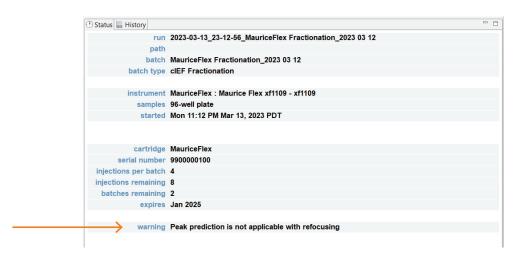
You can copy the information in the History pane to use in other documents:

- 1. Click the History pane to make sure it's active.
- 2. Click Edit in the main menu and select Copy.
- 3. Open a document and click Paste.

Viewing Run Errors or Warnings

If an error or warning is detected during the run it will display in the Status pane. You may need to scroll down to view errors or warnings specific to the cartridge.

🕑 Status 🔚 History	
run	KF0002_cIEF1160607664_2016-08-09_12-01-50_mAB high low_OBM Validation
path	C\Users\User\Documents\Compass for iCE\Runs
batch	mAB high low_OBM Validation
batch type	cIEF
instrument	Maurice : Maurice kf0002 - kf0002
samples	96-well plate
started	Tue 2:02 PM Aug 9, 2016 CDT
completed	Wed 1:48 AM Aug 10, 2016 CDT
warning	Detected chamber temp 35.2C, 03:13:48 PM above control range (16.0C - 28.0C)
cartridge	cIEF
serial number	1160607664
injections per batch	100
injections remaining	60 (60 guaranteed)
batches remaining	9
expires	Jun 2017



Injection Reports

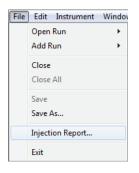
You can export PDF files of the raw and analyzed data, IV plot, peaks table, sample and system info for individual or all injections in a run file. You can also export the run history with all analysis events.

NOTES:

You can have Compass for iCE generate reports for you automatically at the end of each run. See"Setting up Automatic Injection Reports" on page 761 for more information.

Any time a new report is run, it's saved in a separate run folder. Existing reports aren't overwritten.

- 1. Click **File > Open Run** and select a run file.
- 2. If you want reports for all injections, skip to the next step. Otherwise, select the injection in the Injection pane that you want a report for.
- 3. Select File from the main menu in either screen and click Injection Report.



- 4. In the Injection Reports window:
 - a. Choose either Selected injections or All injections.
 - b. Select Analysis log if you want a run history report with all analysis events.
 - c. Select Batch Report if you want to include the sample and method details for each injection in the batch.
 - d. Select Fitted peaks if you want to show peak fitting in the electropherograms.
 - e. Report PDFs generated by Compass for iCE are secured by default, which means they can be viewed and printed but not modified or renamed. Uncheck **Secure PDF** if you don't want to generate a secure report. To learn more about permissions for secured vs. unsecured reports, see page 800.
 - f. The report name defaults to the run file name. If you want to change it, type in the Report Name box to make updates.
 - g. Click OK.

	>
4Sq-48inj-Maurice CE-SDS PLU	S.batch
Analysis log	
Batch report	
Fitted peaks	
В	rowse
inj-Maurice CE-SDS PLUS.batch	
pass for iCE	
ОК С	ancel
	Batch report Fitted peaks Inj-Maurice CE-SDS PLUS.batch ppass for iCE

5. Individual injection report PDF(s) and a combined injection report PDF are exported to the Runs folder in the Compass for iCE directory. They'll be in a folder with the report name used in the prior step. When the reports are done, the folder opens for you automatically.

😻 Dropbox	^ □ Name	Date modified	Туре	Size
O Dia	R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_combined_injection_report.pdf	7/20/2020 9:11 PM	Adobe Acrobat D	5,032 K
OneDrive	R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_1_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108 k
This PC	R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_2_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	105 H
👕 3D Objects	R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_3_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108 H
Desktop	R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_4_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108 H
Documents	R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_5_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108 H
Add-in Express	R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_6_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	106
	R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_7_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108
Adobe	R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_8_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108
CIDFont	R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_9_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	109
CMap	R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_10_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	109 H
Compass for iCE	R-lgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_11_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108

Example Analysis and Injection Report: CE-SDS

Run File R-IgG-2019-01-10_16-25-12_4Sqx12inj-RIgG-Maurice CE-SDS

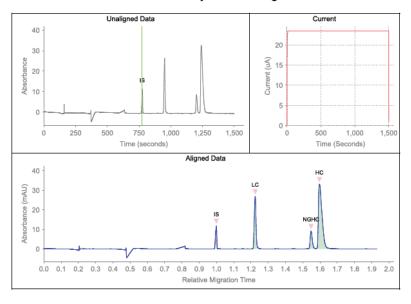
Analysis Log

Date	User Name	Message	Comment
2019-01-10 17:25:27		Started run: R-IgG-2019-01-10_16-25-12_4Sqx12inj-RIgG-Maurice CE-SDS Batch: 4Sqx12inj- RIgG-Maurice CE-SDS.batch	3180910338
2019-01-14 10:39:07		Saved analysis and methods changes from Compass for iCE v2.1.0-1219	
		Added Peak Names Apply Settings "apply IgG to all"	
		Added Peak Names Group IgG	
		Protein name: LC RMT: 1.21 Color: 32512 Range: 0.1	
		Protein name: NGHC RMT: 1.54 Color: 32512 Range: 0.05	
		Protein name: HC RMT: 1.58 Color: 32512 Range: 0.1	

Created By: Jacquelyn Sarl 4:17 PM Feb 2, 2019 CST Software Version: 2.1.0, Build ID: 0130 C:UsersJacquelynDocuments/Clients/ProtenSimple/Maurice/User Guide/Rev 12 edist/Data from Andrea - no edist/R-igG-2019-01-10_16-25-12_4Squ12inj-RigG-Maurice/CE-Software Version: 2.1.0, Build ID: 0130 C:UsersJacquelynDocuments/Clients/ProteinSimple/Maurice/User Guide/Rev 12 edist/Data from Andrea - no edist/R-igG-2019-01-10_16-25-12_4Squ12inj-RigG-Maurice/CE-Software Version: 2.1.0, Build ID: 0130 C:UsersJacquelynDocuments/Clients/ProteinSimple/Maurice/User Guide/Rev 12 edist/Data from Andrea - no edist/R-igG-2019-01-10_16-25-12_4Squ12inj-RigG-Maurice/CE-Software Version: 2.1.0, Build ID: 0130 C:UsersJacquelynDocuments/Clients/ProteinSimple/Maurice/User Guide/Rev 12 edist/Data from Andrea - no edist/R-igG-2019-01-10_16-25-12_4Squ12inj-RigG-Maurice/CE-Software Version: 2.1.0, Build ID: 0130 C:UsersJacquelynDocuments/Clients/ProteinSimple/Maurice/User Guide/Rev 12 edist/Data from Andrea - no edist/R-igG-2019-01-10_16-25-12_4Squ12inj-RigG-Maurice/CE-Software Version: 2.1.0, Build ID: 0130 C:UsersJacquelynDocuments/Clients/ProteinSimple/Maurice/User Guide/Rev 12 edist/Data from Andrea - no edist/R-igG-2019-01-10_16-25-12_4Squ12inj-RigG-Maurice/CE-Software Version: 2.1.0, Build ID: 0130 C:UsersJacquelynDocuments/Clients/ProteinSimple/Maurice/User Guide/Rev 12 edist/Data from Andrea - no edist/R-igG-2019-01-10_16-25-12_4Squ12inj-RigG-Maurice/CE-Software Version: 2.1.0, Build ID: 0130 C:UsersJacquelynDocuments/Clients/ProteinSimple/Rev 12 edist/Data from Andrea - no edist/R-igG-2019-01-10_16-25-12_4Squ12inj-RigG-Maurice/CE-Software Version: 2.1.0, Build ID: 0130 C:UsersJacquelynDocuments/Clients/ProteinSimple/Rev 2.1.0, Build ID: 0130 C:UsersJacquelynDocuments/Clients/ProteinSimple/Re



User Guide for Maurice, Maurice C., Maurice S. and MauriceFlex



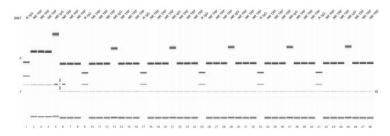
Uncontrolled Injection 1: R IgG1

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		NS.

Peak	Name	Time	RMT	Height	Raw Area	Area	%Total	%Area	Width	S/N	Baseline	Resolution
1	IS	776.7	1.000	11.7	164.6	212.4			7.0	658.6	-0.6	
2	LC	951.3	1.225	26.8	498.5	524.1	30.5	30.5	8.8	1507.3	-0.6	15.02
3	NGHC	1202.7	1.549	9.1	205.6	170.8	9.9	9.9	10.2	510.5	-0.6	17.58
4	HC	1240.2	1.597	33.1	1273.4	1021.8	59.5	59.5	17.9	1859.6	-0.6	1.98

Created By: Jacquetyn Sat 4:47 PM Feb 2, 2019 CST Software Version: 2.1.0, Build ID: 0130	
C:Users/Jacquelyn/Documents/Cients/ProteinSimple/Maurice/User Guide/Rev 12 edits/Data from Andrea - no edits/R-igG-2019-01-10_15-25-12_48qr12inj-RigG-Maurice CE-	
8D6.mbz	proteinsimple
Computer: DE6KTOP-C7FPQGB	classes toru
Page 1 of 2	

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						P2 84 05 1

Createl By: Andrea Mon 8:28 PM Apr 25, 2022 PDT (SECURED) Criberti-Workstocuments/Compass tor ICERandMaurice_TURED_CE=508_ResHonRed.ntax Computer: DEBKTOP-1PM/P005 Boftware Version: Compass for ICE 3.00, Build D: 0218 Page 1 of 199



Uncontrolled Injection 1: R IgG1

Sample Information

Injection Name	R lgG1
Sample ID	SB
Location	Plate Well B2
Batch Name	4Sqx12inj-RlgG-Maurice CE-SDS
Run Started	Thu 5:25 PM Jan 10, 2019 CST
Run Completed	Fri 8:07 PM Jan 11, 2019 CST
Date Acquired	Thu 6:08 PM Jan 10, 2019 CST
Run Error	None
Reinjection	No

Injection Conditions

Guaranteed Injection	Yes						
Focus Period 1	5750V for 25.0 min						
Sample Load	20 sec 4600 Volts						
Tray Temperature	9.1°C						

Maurice Settings						
Model	Maurice OBM					
Instrument S/N	kf1077					
Software Version	2.1.0, Build ID: 0130					
Firmware Version	3.1.2019.01.04.20.16.20.5eb707f					
Tray Type	96-well plate					
Cartridge Type	CE-SDS					
Cartridge S/N	3180910338					
Cartridge Expiration	Sep 2019					
Injections Remaining	152 (52 guaranteed)					
Batches Remaining	24					

Created By: Jacquelyn 8at 447 PM Feb 2, 2019 C6T Software Venion: 2 10, Bulid D: 0130 C-UbenJacquelyn/Documents/Cients/ProteinSimple/Maur/ce/Darr OulderRev 12 edit/Data from Andres - no edits/Prig0-2019-01-10_16-26-12_48qrt3ny-Rig Software	proteinsimple
Computer: DESKTOP-C7FPQ0B Page 2 of 2	a binden ber barre

Example Analysis and Injection Report: cIEF

Run File DemoData_Maurice cIEF

Analysis Log

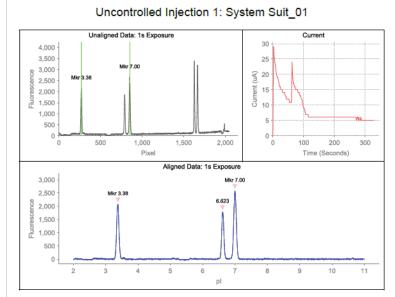
Date	User Name	Message	Comment
2015-10-27 12:11:27		Started run: 2015-10-27_12-11-12_Maurice cIEF Batch: Maurice cIEF.batch	
2015-10-27 14:46:00		Saved analysis changes	
		Changed MethodName Method Exposure from "Exposure 1 Absorbance 0.005 seconds" to	
		"Exposure 1 Fluorescence 1 seconds"	
		Changed MethodName Method Exposure from "Exposure 1 Absorbance 0.005 seconds" to	
		"Exposure 5 Fluorescence 20 seconds"	
		Added Standards Apply Override "apply Standards 3 to Method1"	
		Added Standards 3	
		pl Marker pl: 3.38 Position: 250	
		pl Marker pl: 7 Position: 800	
2015-10-27 14:54:00		Save run file	

Created By: Andrea Mon 11:05 PM Mar 13, 2023 PDT (SECURED) C'UbersUberDocumenta/Compass for /CERuns/DemoData_Maurice DE/mbz Computer: DESTOP-IRM/C60

Page 1 of 2



User Guide for Maurice, Maurice C., Maurice S. and MauriceFlex



	Fluorescence Peaks: 1s Exposure										
Peak	Name	Position	pl	Height	Area	%Total	%Area	Width	S/N	Baseline	Resolution
1	Mkr 3.38	270.1	3.380	2067.9	28502.1			0.0807	112.6	52.7	
2		791.0	6.623	1785.9	22868.7	100.00		0.0750	97.2	41.1	24.56
3	Mkr 7.00	851.9	7.000	2580.0	39590.9			0.0898	140.5	41.0	2.71

Created By: Andrea Mon 11:05 FM Mar 13, 2023 PDT (ISECURED) C'UlwerfUlerDocument/Dompass for (DERuer/DemoDiel, Mauton of Fratz Computer: DEBKTOR-IFM7005 Software Version: Company for ICE 4.0.0, Build ID: 0222 Page 1 of 4

protein simple

Uncontrolled Injection 1: System Suit_01

Sample Information

Injection Name	System Suit_01	
Sample ID	System Suit	
Location	Plate Well A1	
Batch Name	Maurice cIEF	
Run Started	ue 12:11 PM Oct 27, 2015 PDT	
Run Completed	e 1:17 PM Oct 27, 2015 PDT	
Date Acquired	ue 12:17 PM Oct 27, 2015 PDT	
Run Error	None	
Reinjection	No	

Injection Conditions

Guaranteed Injection	Yes
On-board Mixing	Off
Focus Period 1	1500V for 1.0 min
Focus Period 2	3000V for 4.5 min
Sample Load Duration	90.0 Seconds
pl marker 1	3.38
pl marker 2	7.0
Tray Temperature	Not Available

Maurice Settings				
Model	Maurice OBM			
Instrument S/N	kf1004			
Software Version	Compass for iCE 4.0.0, Build ID: 0222			
Firmware Version	2.0.2015.10.20.20.35.52.681a5af			
Tray Type	48 vials			
Cartridge Type				
Cartridge S/N				
Cartridge Expiration				
Injections Remaining				
Batches Remaining				

Created By: Andrea Mon 11:05 PM Mar 13, 2023 PDT (SECURED) D: Warr/Uwe/Document/Dicingeas for ICE 4.0.0, Build ID: 0222 Software Version: Compass for ICE 4.0.0, Build ID: 0222 Page 2 of 4



Example Analysis and Injection Report: MauriceFlex Fractionation

Run File 2023-03-14_14-03-04_MauriceFlex Fractionation_PS IgG_refocus

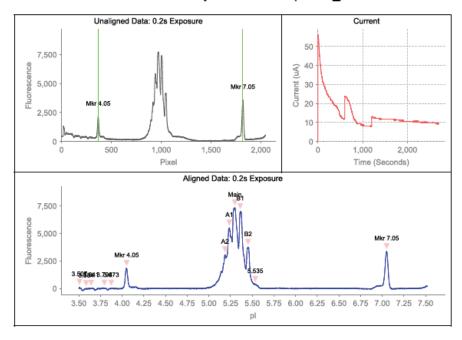
Analysis Log

Date	User Name	Message	Comment
2023-03-14 14:08:37		Started run: 2023-03-14_14-03-04_MauriceFlex Fractionation_PS IgG_refocus Batch: MauriceFlex Fractionation(1).batch from Compass for iCE v4.0.0-0222	5230202259
2023-03-15 16:39:29		Saved analysis changes from Compass for iCE v4.0.0-0222	
		Added Peak Names Group Peak Group 1	
		Protein name: Main pl: 5.3 Color: 32512 Range: 0.05	
		Added Peak Names Apply Settings "apply Peak Group 1 to all"	
		Added Protein B1 to Peak Names Group Peak Group 1	
		name: B1	
		pl: 5.363	
		Color: 32512	
		Range: 0.05	
		Added Protein B2 to Peak Names Group Peak Group 1	
		name: B2	
		pl: 5.452	
		Color: 32512	
		Range: 0.05	
		Added Protein A1 to Peak Names Group Peak Group 1	
		name: A1	
		pl: 5.235	
		Color: 32512	
		Range: 0.05	
		Added Protein A2 to Peak Names Group Peak Group 1	
		name: A2	
		pl: 5.187	
		Color: 32512	
		Range: 0.05	

Page 1 of 2

Oreated By: Andrea Sun 8.11 PM Mar 19, 2023 POT (SECURED) C1UserNadreaDestate/2023.03.14, 14-03-04_Maurice/Fex Fractanation_PS (pG_refocus mbc Computer: DESTOR-FIM/ROG





Uncontrolled Injection 1: Sample 01_01

Fluorescence Peaks: 0.2s Exposure

Peak	Name	Position	pl	Height	Area	%Total	%Area	Width	S/N	Baseline	Resolution
1		105.9	3.507	-13.8	0.0			0.0021	-0.5	521.5	
2		143.2	3.584	-68.8	0.0			0.0000	-2.7	474.1	43.93
3		170.7	3.641	36.0	118.3	0.02		0.0070	1.4	412.1	9.62
4		244.7	3.794	38.2	38.2	0.01		0.0000	1.5	332.9	25.92
5		283.1	3.873	-50.4	0.0			0.0041	-2.0	311.1	22.60
6	Mkr 4.05	368.6	4.050	1837.6	31693.9			0.0319	71.3	276.8	5.77
7	A2	918.4	5.187	3068.6	82235.5	11.24	11.4	0.0561	119.0	279.3	15.20
8	A1	941.6	5.235	5506.2	154682.1	21.14	21.4	0.0724	213.6	307.4	0.44
9	Main	973.5	5.300	7339.0	213113.7	29.13	29.5	0.0733	284.7	335.3	0.53
10	B1	1003.5	5.363	6999.9	187342.2	25.61	25.9	0.0526	271.6	363.9	0.58
11	B2	1046.6	5.452	3752.7	85249.6	11.65	11.8	0.0418	145.6	387.0	1.11
12		1087.0	5.535	413.5	8781.7	1.20		0.0478	16.0	396.7	1.10
13	Mkr 7.05	1819.8	7.050	3367.0	71575.3			0.0390	130.6	168.8	20.56

Uncontrolled Injection 1: Sample 01_01

Peak Predictions

Peak	Name	Predicted Wells
1	3.507	G3, G4, G5, G6, G7, G8
2	3.584	G1, G2, G3, G4, G5, G8
3	3.641	F1, G1, G2, G3, G4, G5
4	3.794	F4, F3, F2, F1, G1, G2, G3
5	3.873	F5, F4, F3, F2, F1, G1
6	Mkr 4.05	F8, F7, F6, F5, F4, F3
7	A2	E2, E3, E4, E5, E6, E7
8	A1	E1, E2, E3, E4, E5, E6
9	Main	
10	B1	E1, E2, E3, E4, E5, E6
11	B2	E1, E2, E3, E4, E5
12	5.535	E3, E4, E5, E6, E7, E8
13	Mkr 7.05	

Uncontrolled Injection 1: Sample 01_01

Sample Information

Injection Name	Sample 01_01
Sample ID	Sample 01
Location	Plate Well A3
Batch Name	MauriceFlex Fractionation(1)
Run Started	Tue 2:08 PM Mar 14, 2023 PDT
Run Completed	Tue 4:30 PM Mar 14, 2023 PDT
Date Acquired	Tue 2:22 PM Mar 14, 2023 PDT
Run Error	None
Reinjection	No

Injection Conditions

Guaranteed Injection	Yes
On-board Mixing	Off
Focus Period 1	500V for 10.0 min
Focus Period 2	1000V for 10.0 min
Focus Period 3	1500V for 25.0 min
Detection Exposure	0.2 sec
Detection Interval	5.0 min
Sample Load Duration	20.0 Seconds
pl marker 1	4.05
pl marker 2	7.05
Tray Temperature	10.0°C

Fractionation Conditions

Mobilization	000 Volts for 45.0 min	
Refocus	1500 Volts for 5.0 min	
Fractions	1000 Volts for 25.0 sec	
Detection Exposure	0.2 sec	
Detection Interval	1.0 min	

Maurice Settings

Model	auriceFlex	
Instrument S/N	mm0006	
Software Version	Compass for iCE 4.0.0, Build ID: 0222	
Firmware Version	2023.02.09.22.55.08.12f36498b	
Tray Type	well plate	
Cartridge Type	lauriceFlex	
Cartridge S/N	5230202259	

Uncontrolled Injection 1: Sample 01_01

Cartridge Expiration	Feb 2024
Injections Remaining	13 (13 guaranteed)
Batches Remaining	13
Warning	Cartridge post-run cleanup not performed after previous run
Warning	Peak prediction is not applicable with refocusing

Switching Between Open Run Files

If you've got more than one run file open, you can switch between viewing the run information in each.

1. Click the down arrow in the Run box.

File I	Edit Instrument Window Help
Run:	3160106286 KF1011 DG 2016-01-15_15-25-52_Maurice CE 💌
ulu Inie	3160106283 KF1011 DG 2016-01-14_18-50-33_Maurice CE-SDS 3160106284 KF1011 DG 2016-01-15_12-42-55_Maurice CE-SDS
<u> </u>	3160106284 KF1011 DG 2016-01-15_12-42-55_Maurice CE-SDS
	3160106286 KF1011 DG 2016-01-15_15-25-52_Maurice CE-SDS

2. Select the run you want to view from the drop down list.

Closing Run Files

If you've got more than one run file open, you can close just one file or all the open files at the same time.

- To close the run file being viewed Select File from the main menu and click Close.
- To close all open run files Select File from the main menu and click Close All.

Chapter 17: Controlling Maurice, Maurice C., Maurice S. and MauriceFlex

Chapter Overview

- Instrument Control
- Stopping a Run
- Status Modes
- Shutdown
- Instrument Software (Embedded) Updates
- Instrument Self Test
- Viewing and Changing System Properties
- Checking Cartridge Status
- Cartridge Self-Test
- Instrument Reports
- Viewing Log Files
- Sending a Log File to Technical Support

Instrument Control

The Instrument menu lets you to control Maurice, Maurice C., Maurice S. and MauriceFlex

Instrument	Window	Help	
Cartrid	lge Post-Ru	n Cleanup	
Cartrid	lge Purge		
Self Te	st		>

NOTE: Instrument menu options are only active when you've got a computer with Compass for iCE software connected directly to your Maurice system.

Starting a Run

To start your run, click the **Start** button in the Batch screen. You can also start a run by selecting **Instrument** in the main menu and clicking **Start**. For more info on creating and starting batches check out

- Chapter 6: "Running cIEF Applications"
- Chapter 8: "Running MauriceFlex cIEF Applications"
- Chapter 10: "Running MauriceFlex Fractionation Applications"
- Chapter 12: "Running CE-SDS PLUS Applications"
- Chapter 14: "Running Turbo CE-SDS Applications"

Cartridge Purge

You'll want to run the Cartridge Purge any time you have to stop a run manually or if the run stops because of an error. You'll also want to run the Cartridge Purge if your CE-SDS PLUS or Turbo CE-SDS cartridge hasn't been used in more than 3 months.

Make sure Maurice's door is closed and a cartridge is installed before you run the Cartridge Purge.

1. Compass for iCE will alert you that a Cartridge Purge is recommended. Click on the brown **Purge** button in the instrument status bar. You can also select **Instrument > Cartridge Purge** in the main menu.

2. Click Start.

NOTE: The Cartridge Purge counts toward the batch limit. If there's only one batch left on the cartridge, you'll get a message that it can't be used after purging.

clEF Cartridge Purge	× CommuniceFlex Cartridge Purge ×
Make sure the vial types and locations match the display before clicking "Start." Reagents MC FIC4 Water Empty Water OH" OH" OH" Water OH"	Make sure the vial types and locations match the display before clicking "Start." Reagents Water Empty Back Back Back Back Back Back Back Back
Cartridge purge counts toward the cartridge batch limit.	Cartridge purge counts toward the cartridge batch limit.
😨 CE-SDS PLUS Cartridge Purge	X 🕼 Turbo CE-SDS [™] Cartridge Purge
CE-SDS PLUS Cartridge Purge Make sure the vial types and locations match the display before clicking "Start." Reagents CI CF Ware Seo, Wash Energy Wash Wash Reagents Wash Wash Reagents Cartridge purge counts toward the cartridge batch limit. Start Cancel	Make sure to refill and replace the reagent vials according to the diagram shown below, ensure the Top Chamber is filled with Separation Matrix, and the Waste Tank is empty before clicking "Start."
Make sure the vial types and locations match the display before clicking "Start." Reagents Top Running Buffer Critical Water Step, Wash Emery Wash Wash Reagents Top Running Buffer Fresh Vial Cartridge purge counts toward the cartridge batch limit.	Make sure to refill and replace the reagent vials according to the diagram shown below, ensure the Top Chamber is filled with Separation Matrix, and the Waste Tank is empty before clicking "Start."

The Cartridge Purge for CE-SDS PLUS or Turbo CE-SDS Cartridges takes about 30 minutes, cIEF Cartridges take a little over 10 minutes and the cIEF Fractionation Cartridge takes about 6 minutes.

6 2023-02	-26_10-06-26_Ma	urice CE-SDS TURB	O Cartridge P	urge.batch - Co	mpass for iCE			- 0	×
File Edit	Instrument Win	dow Help							
								📑 Batch 💽 Run Summary 🗸	Analysis
	Running	Pause	Sun 10:06	AM				Sun	10:27 AM
Run: 2023-0	2-26_10-06-26_Ma	surice CE-SDS TURE	O Cartridge P	urge.batch					
Injections						- 0	🕑 Status 🔚 History		- 0
	Injection Name	Sample ID	Location	Method	Status	Time	run	2023-02-26_10-06-26_Maurice CE-SDS TURBO Cartridge Purge.batch	
				Cleanup	Loading	21 mins	path		
							batch	Maurice CE-SDS TURBO Cartridge Purge	
							batch type	CE-SDS	
							instrument	MauriceFlex : Maurice Flex xf1109 - xf1109	
							samples	96-well plate	
							started	Sun 10:06 AM Feb 26, 2023 PST	

ile Edi	t Instrument	Window H	elp									
									Batch	🕒 Run Sumn	nary 🏨	Ana
-	Running	Pause						1				
-		-	Tue 1:	31 PM							Tue	1:37
1: 2022	2-12-20_13-31-	14_MauriceFlex	Cartridge F	Purge								
		14_MauriceFlex	Cartridge F	Purge			🕑 Status 🛄 History					3
		14_MauriceFlex			Status	Time	🕐 Status 🔚 History		2022-12-20_13-31-14_Mauric	eFlex Cartri	idge Pu	_
	ns			5	Status Loading		🕑 Status 🔚 History			eFlex Cartri	idge Pu	_
	ns			Method		Time	🕐 Status 🔚 History	run			idge Pu	_
n: 2022	ns			Method		Time		run path batch			idge Pu	_

- 3. Once the purge is done, perform a Cartridge Post-Run Cleanup:
 - cIEF Cartridges: Follow the "Post-batch Procedures" instructions on page 120.
 - **cIEF Fractionation Cartridges**: Follow the "Post-batch Procedures" instructions on page 182 for a MauriceFlex cIEF batch and page 248 for a MauriceFlex Fractionation batch.
 - CE-SDS Plus Cartridges: Follow the "Post-batch Procedures" instructions on page 316.
 - Turbo CE-SDS Cartridges: Follow the "Post-batch Procedures" instructions on page 385.
- 4. Once the Cartridge Post-Run Cleanup is completed:

If you'll be starting a new run right away, prep the cartridge.

- cIEF Cartridges: Follow the "Step 2: Prep the Cartridge" instructions on page 96.
- **cIEF Fractionation Cartridges**: Follow the Step 2: Prep the Cartridge" instructions on page 163 for a MauriceFlex cIEF batch and page 229 for a MauriceFlex Fractionation batch.
- CE-SDS Plus Cartridges: Follow the "Step 2: Prep the Cartridge" instructions on page 295.
- Turbo CE-SDS Cartridges: Follow the "Step 2: Prep the Cartridge" instructions on page 364.

If you won't be starting a new run:

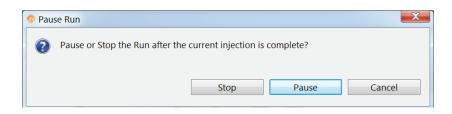
- cIEF Cartridges: Place the cartridge and stoppers in its protective packaging and store at room temperature.
- **cIEF Fractionation Cartridges**: Place the cartridge and stopper in its protective packaging and store at room temperature.
- CE-SDS Plus Cartridges: Place the cartridge in its protective packaging and store at room temperature.
- **Turbo CE-SDS Cartridges**: Place the cartridge and stoppers in its protective packaging and store at room temperature.

Stopping a Run

1. To stop a run after the current injection, you can either select **Instrument** > **Stop**, or click the **Pause** button:



2. If you clicked Pause, select Stop in the pop-up window.



Maurice will stop the run after the current injection is complete and then save the data for the completed instead in the .mbz file. After stopping the run, perform a Cartridge Post-Run Cleanup:

- cIEF Cartridges: Follow the "Post-batch Procedures" instructions on page 120.
- **cIEF Fractionation Cartridges**: Follow the "Post-batch Procedures" instructions on page 182 for a MauriceFlex cIEF batch and page 248 for a MauriceFlex Fractionation batch.
- CE-SDS Plus Cartridges: Follow the "Post-batch Procedures" instructions on page 316.
- Turbo CE-SDS Cartridges: Follow the "Post-batch Procedures" instructions on page 385.
- 3. Once the post-run cleanup is done:

If you'll be starting a new run right away, prep the cartridge:

- cIEF Cartridges: Follow the "Step 2: Prep the Cartridge" instructions on page 96.
- **cIEF Fractionation Cartridges**: Follow the Step 2: Prep the Cartridge" instructions on page 163 for a MauriceFlex cIEF batch and page 229 for a MauriceFlex Fractionation batch.
- CE-SDS Plus Cartridges: Follow the "Step 2: Prep the Cartridge" instructions on page 295.
- Turbo CE-SDS Cartridges: Follow the "Step 2: Prep the Cartridge" instructions on page 364.

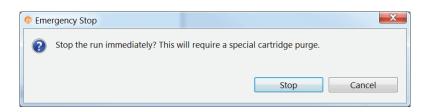
If you won't be starting a new run:

- cIEF Cartridges: Place the cartridge and stoppers in its protective packaging and store at room temperature.
- **cIEF Fractionation Cartridges**: Place the cartridge and stopper in its protective packaging and store at room temperature.

- CE-SDS Plus Cartridges: Place the cartridge in its protective packaging and store at room temperature.
- **Turbo CE-SDS Cartridges:** Place the cartridge and stoppers in its protective packaging and store at room temperature.

Emergency Stop

- 1. To stop a run immediately, select Instrument > Emergency Stop.
- 2. Click **Stop** in the pop up window:



Maurice will stop once it's safe to avoid damaging the cartridge. Data for completed injections will be saved in the .mbz file.

- 3. Perform a Cartridge Purge. Click the brown Purge button in the instument status bar or select Instrument > Cartridge Purge.
- 4. When the cartridge purge is done, perform a Cartridge Post-Run Cleanup:
 - cIEF Cartridges: Follow the "Post-batch Procedures" instructions on page 120.
 - **cIEF Fractionation Cartridges**: Follow the "Post-batch Procedures" instructions on page 182 for a MauriceFlex cIEF batch and page 248 for a MauriceFlex Fractionation batch.
 - CE-SDS Plus Cartridges: Follow the "Post-batch Procedures" instructions on page 316.
 - Turbo CE-SDS Cartridges: Follow the "Post-batch Procedures" instructions on page 385.
- 5. Once the Cartridge Post-Run Cleanup is completed: If you'll be starting a new run right away, prep the cartridge:
 - cIEF Cartridges: Follow the "Step 2: Prep the Cartridge" instructions on page 96.
 - **cIEF Fractionation Cartridges**: Follow the Step 2: Prep the Cartridge" instructions on page 163 for a MauriceFlex cIEF batch and page 229 for a MauriceFlex Fractionation batch.
 - CE-SDS Plus Cartridges: Follow the "Step 2: Prep the Cartridge" instructions on page 295.
 - Turbo CE-SDS Cartridges: Follow the "Step 2: Prep the Cartridge" instructions on page 364.

If you won't be starting a new run:

- cIEF Cartridges: Place the cartridge and stoppers in its protective packaging and store at room temperature.
- **cIEF Fractionation Cartridges**: Place the cartridge and stopper in its protective packaging and store at room temperature.
- CE-SDS Plus Cartridges: Place the cartridge in its protective packaging and store at room temperature.
- **Turbo CE-SDS Cartridges:** Place the cartridge and stoppers in its protective packaging and store at room temperature.

Status Modes

The instrument status bar displays status, buttons and progress bars depending on what Maurice, Maurice C. or Maurice S. are doing.

- Ready/Start button The instrument is ready and a batch is loaded. Click Start to begin a run.
- Not Ready/Reset button The instrument isn't ready and needs to reinitialize. Click Reset to start the initialization protocol.
- **Running/Pause button** The instrument is running. The run name, time it started and when it will be done show in the run progress bar. Click **Pause** to pause or stop the run.
- **Cleaning/Stop button** The instrument is running a cleaning protocol. The time the cleaning protocol started and when it will be done show in the run progress bar.
- Error/Reset button There's an error. Go to the Status pane in the Run Summary screen to view details. When you've fixed the source of the error, click Reset.

Shutdown

Close Compass for iCE software. Maurice can stay on unless he won't be used for an extended period.

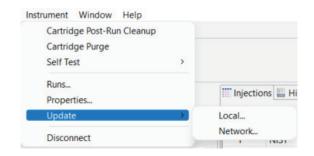
Chapter 17: Controlling Maurice, Maurice C., Maurice S. and MauriceFlex | Instrument Software (Embedded) Updates

Instrument Software (Embedded) Updates

To check for embedded software updates:

If you're on the network:

1. Select Instrument > Update, then select Network.



2. The following screen displays. Click Update.

🌝 Maurice Flex kf9992 Software update	\times
Installed Version: 4.2.2023.01.27.11.04.49.89331	3c5b
Latest Version: 4.2.2023.02.09.22.55.08.12f36	498b
Update embedded software?	
Update Cancel	l -

If you're not on the network:

- 1. Call ProteinSimple Technical Support or your FAS for assistance on getting the latest update.
- 2. Copy the new embedded software file onto Maurice's computer.
- 3. Select Instrument > Update, then select Local.

Instrument Window Help		
Cartridge Post-Run Cleanup		
Cartridge Purge		
Self Test	>	
Runs	-	[****] [10]
Properties		Injections 🔛 Hi
Update	>	Local
Disconnect		Network

4. Browse to the location of the embedded software file, select it and click OK.

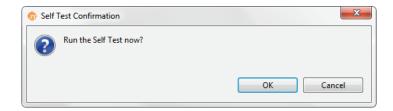
5. The following screen displays. Click Update.

Maurice Flex kf9992 Software update	×
Installed Version: 4.2.2023.01.27.11.04.49.893313c58 Latest Version: 4.2.2023.02.09.22.55.08.12f36498b	-
Update embedded software?	`
Update Cancel	

Instrument Self Test

Maurice, Maurice C., Maurice S. and MauriceFlex can run a series of self tests for you to make sure they're operating properly.

- 1. To start the test, select Instrument > Self Test > Instrument.
- 2. The following screen displays. Click OK.



The test takes approximately 11 minutes.

😨 Self Test - Compass for iCE		
Eile Edit Instrument Window Help		
Testing Stop Tue 12:44 PM	담 Batch 强 Run Sum Tue 12:55 PM	
Run: Self Test		
∎ Injections	🕑 Status 📲 History	
Sample ID Locat Method Status	run Self Test	<u>^</u>
Sample ID Locat Method Status	path	
	batch Self Test	

NOTES:

We recommend running the self test before you start a run.

An alert may appear if a cartridge is installed. Remove the cartridge to start the Instrument Self-Test.

Results will automatically display once the test's done. You can also view current or past self test results anytime by selecting **Instrument > Properties** and clicking **Test Log**. See "Self Test Logs" on page 470 for more info.

Viewing and Changing System Properties

Selecting Instrument > Properties displays your system properties. They include:

- System Name
- System Location
- Instrument Type
- Serial number
- Instrument software version (firmware)
- Network name and address
- Date and time of the instrument clock
- Adapter block currently in use
- Number of hours on the Deuterium (UV) lamp
- Current sample chiller temperature

Location :	ice kf0010			
	Type: Mau Number: kf00 Software: 3.1.2		Network Name : Network Address : 14.682d616	
Instrument Date ar	nd Time: 2018	8-11-12 10:52:46	08:00	Set to PC time
Adapter Bloc D2 Lamp Run Tim Cartridge Type : Expires :	cE-SDS PLUS		Sample Chiller : 19.4 Injections per Batch : njections Remaining :	48
Serial Number :	5181106034		Batches Remaining :	24
	Batch	Date	Injection	
	1	9 Nov 2018 9 Nov 2018	48 cleanur	

• To change the system name or location: Click in the name or location boxes and enter your new info, then click OK.

• To sync the instrument clock with the computer: Click Set to PC time and then restart Compass for iCE and your Maurice system.

Name :	Maurice Flex	xf1109				
Location :	192.168.56.0	1				
	Тур	e: Maur	iceFlex	Network Name :	192.168.56.103	
	Serial Numbe	er: xf110	19	Network Address :	192.168.56.103	
Instru	ument Softwar	e: 4.2.20	022.11.03.21.24.04.b	15d551f6		
Instrument	Date and Tim	e: 2023	-02-10 21:20:06 -08	:00	Set to PC time	
Adap	ter Block : via	als		er clicking on "Set to F Sample Chiller : 10.0		
D2 Lamp I	Run Time: 85	hours				
Cartridge						
	Type: CE-SDS			Injections per B		
	pires : Jan 202			Injections Remaining: 439 (39 guaran		
Serial Nun	nber: 000000	00001		Batches Remai	ning: 20	
		Batch	Date	Injections		
		1	1 Sep 2018	48		
		2	4 Sep 2018	cleanup		
		3	4 Sep 2018	12		
		4	5 Sep 2018	cleanup		
		5	1 Oct 2018	1		
			1 Oct 2010			

Checking Cartridge Status

If you've got a cartridge installed in the system, you can see its serial number, the injections and batches it still has available, and a history of batches and injections its run to date. To view this info, select **Instrument** > **Properties**.

	Maurice kf9	991				
Location :	192.168.56.	101				
	Ту	pe: Maur	ice OBM	Network Name :	192	2.168.56.101
	Serial Numb			Network Address :	192	2.168.56.101
Instru	ument Softwa	are: 4.1.20	022.02.17.22.34.36.3	30f0b19e		
Instrument	Date and Tir	me: 2022	02-18 16:08:15 -08	:00		Set to PC time
D2 Lamp I Cartridge	Run Time : 1	62 hours		Sample Chiller : 10.		
	Type: Turbo pires: Dec 2			Injections per		1: 96 1: (50 guaranteed)
	nber: 82112			Batches Rema		
		Batch	Date	Injections	^	
		1	22 Dec 2021	cleanup		
		2	13 Jan 2022	0		
		3	13 Jan 2022	error		
		4	14 Jan 2022	0		
		1.		1	~	
					warra	anty may be voided

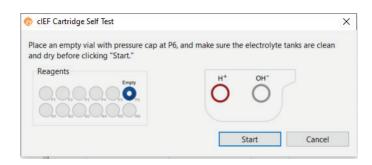
- cIEF, CE-SDS PLUS, and cIEF Fractionation Cartridges will display the number of injections, number of guaranteed injections and number of batches remaining.
- Turbo CE-SDS Cartridges will only display the number of guaranteed injections and batches remaining.
- A warning will appear if a Cartridge Purge or Cartridge Post-Run Cleanup is required.
- The number remaining injections and batches will automatically update as follows:
 - The injections remaining will decrease by one as each injection completes.
 - The batches remaining will decrease by one when a Cartridge Purge is performed on a cIEF, CE-SDS PLUS or Turbo CE-SDS cartridge.
 - The batches and injections remaining will both decrease by one when a Cartridge Purge is performed on a cIEF Fractionation cartridge.
 - The batches and injections remaining will not change when a Cartridge Post-Run Cleanup is performed on all cartridges.

Cartridge Self-Test

You can run a series of self-tests on your cIEF, cIEF Fractionation, CE-SDS PLUS, or Turbo CE-SDS cartridge to make sure they're operating properly.

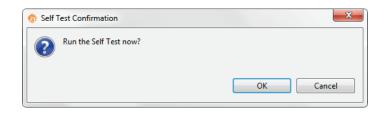
To perform a Cartridge Self-Test on a cIEF cartridge:

- 1. Confirm the electrolyte tanks are clean and dry.
- 2. Place an empty vial with a **blue pressure cap** in position P6.



3. Select Instrument > Self Test > Cartridge.

4. The following screen displays. Click **OK**.



The test takes 3-8 minutes. Results will automatically display once the test's done. You can also view current and past self test results anytime by selecting **Instrument > Properties** and clicking **Test Log**. See "Self Test Logs" on page 470 for more information.

To perform a Cartridge Self-Test on a cIEF Fractionation cartridge:

- 1. Remove the Fractionation Adapter.
- 2. Confirm the Anolyte tank is clean and dry.

or MauriceFlex Cartridge Self Test	×
Make sure the electrolyte tanks are clean a	nd dry before clicking "Start."
Reagents	H*
000000	Ο
	Start Cancel

- 3. Select Instrument > Self Test > Cartridge.
- 4. The following screen displays. Click OK.

log Self Test Confirmation	x
Run the Self Test now?	
	OK Cancel

5. The test takes 3-8 minutes. Results will automatically display once the test's done. You can also view current and past self test results anytime by selecting **Instrument > Properties** and clicking **Test Log**. See "Self Test Logs" on page 470 for more information.

To perform a Cartridge Self-Test on a CE-SDS PLUS cartridge:

- 1. Remove the top Running Buffer and Cleaning vial.
- 2. Place an empty vial with an **orange pressure cap** in position P6.



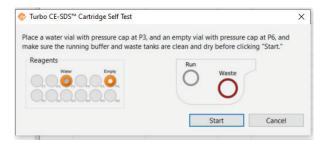
- 3. Select Instrument > Self Test > Cartridge.
- 4. The following screen displays. Click **OK**.

ô Self 1	Test Confirmation	×
?	Run the Self Test now?	
		OK Cancel

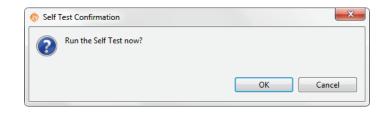
The test takes 3-8 minutes. Results will automatically display once the test's done. You can also view current and past self test results anytime by selecting **Instrument > Properties** and clicking **Test Log**. See "Self Test Logs" on page 470 for more information.

To perform a Cartridge Self-Test on a Turbo CE-SDS cartridge:

- 1. Confirm the Running Buffer and Waste Tanks are clean and dry.
- 2. Place an vial of water with an **orange pressure cap** in position P3 and an empty vial with an **orange pressure cap** in position P6.



- 3. Select Instrument > Self Test > Cartridge.
- 4. The following screen displays. Click **OK**.



The test takes 3-8 minutes. Results will automatically display once the test's done. You can also view current and past self test results anytime by selecting **Instrument > Properties** and clicking **Test Log**. See "Self Test Logs" on page 470 for more information.

Instrument Reports

When Compass for iCE is connected to a Maurice system, you can generate an instrument report that includes instrument and cartridge info, self test records and details and command logs.

- 1. To run the report select **Instrument > Properties**.
- 2. Click Report. The Instrument Report window displays:

	Com	nand lo	og a				
Details for inserted cartridge		mman	-	entrie			
Self-tests Instrument I Cartridge	Show	entries	starti	ing fro	m:		
Last 10 tests	4			pril 20			•
Self-test detail Last test only	27 3 10 17 24	Mon 28 4 11 18 25	29 5 12 19 26	Wed 30 6 13 20 27		Fri 1 8 15 22 29	Sat 2 9 16 23 30
Report:	1	2	3	4	5	6	7 Brows
Maurice-kf1125_2022-04-08_10-36							
Location: C:\Users\unguyen\Document:	s\Compass for	iCE\ln	oK	nent_R	eport	Can	

- 3. Select the information you want included in the report. You can change the location where the report saves by clicking **Browse**.
- 4. Click OK. The Instrument Report PDF is exported to the folder specified. Once the report is done, the folder opens for you automatically.

NOTE: Report PDFs generated by Compass for iCE are secured. They can be viewed and printed but can't be modified or renamed.

Example Instrument Report

Maurice kf1026

Instrument

Name	Maurice kf1026
Location	
Туре	Maurice
Serial Number	kf1026
Instrument Software	4.2.2023.01.13.02.16.24.6f5300503
Adapter Block	plate
D2 Lamp Run Time (hours)	1201
Sample Chiller (°C)	25.3

Cartridge

Туре	cIEF
Expires	Mar 2024
Serial Number	000000001
Injections per Batch	100
Injections Remaining	200
Injections Guaranteed	100
Batches Remaining	20

Chapter 17: Controlling Maurice, Maurice C., Maurice S. and MauriceFlex | Instrument Reports

Instrument Self Test Summary - Last 10 Tests

Test Date	Status	Instrument Software	Username
2022-12-13 11:42	FAILED	4.2.2022.12.02.18.45.42.23a67ef7c	
2022-11-17 10:00	PASSED	4.1.2022.06.29.21.58.35.b9d03b73d	
2022-05-23 11:37	STOPPED	4.1.2022.05.11.05.58.39.c54f50194	
2021-03-17 20:54	PASSED	4.0.2020.07.11.04.16.13.ded2bc3	
2021-03-17 18:26	PASSED	4.0.2020.07.11.04.16.13.ded2bc3	
2021-02-08 18:07	PASSED	4.0.2020.07.11.04.16.13.ded2bc3	
2021-02-08 16:59	FAILED	4.0.2020.07.11.04.16.13.ded2bc3	
2021-02-04 17:05	PASSED	4.0.2020.07.11.04.16.13.ded2bc3	
2020-06-14 22:42	PASSED	3.1.2019.02.11.18.58.45.34dd4a5	
2020-05-25 18:21	PASSED	3.1.2019.02.11.18.58.45.34dd4a5	

Instrument Self Test Details

Self Test Date: 2022-12-13 11:42

Instrument Software: 4.2.2022.12.02.18.45.42.23a67ef7c

Name	Start	Result	Failure Reason
Vacuum Vent	11:42:49	PASSED	
Vacuum Leak	11:41:24	PASSED	
Unregulated Vac level	11:40:59	PASSED	
Temp Sensors	11:40:58	PASSED	
Pressure Vent	11:40:48	PASSED	
Pressure Leak	11:39:31	PASSED	
Low Vacuum Function	11:39:11	PASSED	
High Voltage	11:39:00	PASSED	
Temp Sensor Variance	11:38:58	PASSED	
Tray Move	11:37:07	PASSED	
Tray Jog	11:37:03	PASSED	
Tray Home	11:37:01	PASSED	
Tray Encoders	11:36:58	PASSED	
NFC Service	11:36:55	PASSED	
Disk Storage	11:36:54	PASSED	

Self Test Date: 2022-11-17 10:00

Instrument Software: 4.1.2022.06.29.21.58.35.b9d03b73d

Name	Start	Result	Failure Reason
Sample Cooler	09:59:53	PASSED	
Sample Coolant Pump	09:59:52	PASSED	
Chamber Heater	09:59:15	PASSED	
Chamber Temperature Spec	09:59:14	PASSED	
Ambient Temperature Spec	09:59:13	PASSED	
Point Detector Light	09:58:32	PASSED	
Point Detector Dark	09:58:07	PASSED	
D2 Lamp On	09:57:36	PASSED	
Image Quality	09:57:12	PASSED	
Filter Wheel Move	09:56:44	PASSED	
Filter Wheel Home	09:56:42	PASSED	
Dark Masters	09:56:41	PASSED	
Camera	09:56:39	PASSED	
Vacuum Vent	09:56:34	PASSED	
Vacuum Leak	09:55:08	PASSED	
Unregulated Vac level	09:54:43	PASSED	
Temp Sensors	09:54:42	PASSED	
Pressure Vent	09:54:33	PASSED	
Pressure Leak	09:53:15	PASSED	
Low Vacuum Function	09:52:55	PASSED	
High Voltage	09:52:44	PASSED	
Temp Sensor Variance	09:52:43	PASSED	
Tray Move	09:51:12	PASSED	
Tray Jog	09:51:08	PASSED	
Tray Home	09:51:06	PASSED	
Tray Encoders	09:51:03	PASSED	
NFC Service	09:51:00	PASSED	

Disk Storage	PASSED

Self Test Date: 2022-05-23 11:37

Instrument Software: 4.1.2022.05.11.05.58.39.c54f50194

Username:

Name	Start	Result	Failure Reason
Tray Move	11:35:59	PASSED	
Tray Jog	11:35:55	PASSED	
Tray Home	11:35:53	PASSED	
Tray Encoders	11:35:50	PASSED	
NFC Service	11:35:47	PASSED	
Disk Storage	11:35:46	PASSED	

Self Test Date: 2021-03-17 20:54

Instrument Software: 4.0.2020.07.11.04.16.13.ded2bc3

Name	Start	Result	Failure Reason
Sample Cooler	12:54:03	PASSED	
Sample Coolant Pump	12:54:02	PASSED	
Chamber Heater	12:53:01	PASSED	
Chamber Temperature Spec	12:53:00	PASSED	
Ambient Temperature Spec	12:52:59	PASSED	
Point Detector Light	12:52:18	PASSED	
Point Detector Dark	12:51:53	PASSED	
D2 Lamp On	12:51:22	PASSED	
Camera UV Illumination	12:51:15	PASSED	
Image Quality	12:50:52	PASSED	
Filter Wheel Move	12:50:24	PASSED	
Filter Wheel Home	12:50:23	PASSED	
Dark Masters	12:50:22	PASSED	
Camera	12:50:19	PASSED	
Vacuum Vent	12:50:14	PASSED	

Vacuum Leak	12:48:48	PASSED	
Unregulated Vac level	12:48:23	PASSED	
Temp Sensors	12:48:22	PASSED	
Pressure Vent	12:48:13	PASSED	
Pressure Leak	12:46:51	PASSED	
Low Vacuum Function	12:46:30	PASSED	
High Voltage	12:46:19	PASSED	
Temp Sensor Variance	12:46:18	PASSED	
Tray Move	12:44:47	PASSED	
Tray Jog	12:44:43	PASSED	
Tray Home	12:44:41	PASSED	
Tray Encoders	12:44:38	PASSED	
NFC Service	12:44:35	PASSED	
Disk Storage	12:44:34	PASSED	

Self Test Date: 2021-03-17 18:26

Instrument Software: 4.0.2020.07.11.04.16.13.ded2bc3

Name	Start	Result	Failure Reason
Sample Cooler	10:25:28	PASSED	
Sample Coolant Pump	10:25:27	PASSED	
Chamber Heater	10:24:28	PASSED	
Chamber Temperature Spec	10:24:27	PASSED	
Ambient Temperature Spec	10:24:26	PASSED	
Point Detector Light	10:23:45	PASSED	
Point Detector Dark	10:23:20	PASSED	
D2 Lamp On	10:22:50	PASSED	
Camera UV Illumination	10:22:39	PASSED	
Image Quality	10:22:17	PASSED	
Filter Wheel Move	10:21:48	PASSED	
Filter Wheel Home	10:21:47	PASSED	
Dark Masters	10:21:46	PASSED	

Camera	10:21:44	PASSED	
Vacuum Vent	10:21:38	PASSED	
Vacuum Leak	10:20:13	PASSED	
Unregulated Vac level	10:19:48	PASSED	
Temp Sensors	10:19:47	PASSED	
Pressure Vent	10:19:37	PASSED	
Pressure Leak	10:18:17	PASSED	
Low Vacuum Function	10:17:56	PASSED	
High Voltage	10:17:45	PASSED	
Temp Sensor Variance	10:17:44	PASSED	
Tray Move	10:16:14	PASSED	
Tray Jog	10:16:10	PASSED	
Tray Home	10:16:08	PASSED	
Tray Encoders	10:16:05	PASSED	
NFC Service	10:16:02	PASSED	
Disk Storage	10:16:01	PASSED	

Self Test Date: 2021-02-08 18:07

Instrument Software: 4.0.2020.07.11.04.16.13.ded2bc3

Name	Start	Result	Failure Reason
Sample Cooler	11:06:32	PASSED	
Sample Coolant Pump	11:06:31	PASSED	
Chamber Heater	11:05:32	PASSED	
Chamber Temperature Spec	11:05:31	PASSED	
Ambient Temperature Spec	11:05:30	PASSED	
Point Detector Light	11:04:49	PASSED	
Point Detector Dark	11:04:24	PASSED	
D2 Lamp On	11:03:53	PASSED	
Camera UV Illumination	11:03:43	PASSED	
Image Quality	11:03:20	PASSED	
Filter Wheel Move	11:02:52	PASSED	

Filter Wheel Home	11:02:51	PASSED	
Dark Masters	11:02:50	PASSED	
Camera	11:02:48	PASSED	
Vacuum Vent	11:02:43	PASSED	
Vacuum Leak	11:01:17	PASSED	
Unregulated Vac level	11:00:52	PASSED	
Temp Sensors	11:00:51	PASSED	
Pressure Vent	11:00:40	PASSED	
Pressure Leak	10:59:18	PASSED	
Low Vacuum Function	10:58:57	PASSED	
High Voltage	10:58:46	PASSED	
Temp Sensor Variance	10:58:45	PASSED	
Tray Move	10:57:14	PASSED	
Tray Jog	10:57:11	PASSED	
Tray Home	10:57:09	PASSED	
Tray Encoders	10:57:05	PASSED	
NFC Service	10:57:00	PASSED	
Disk Storage	10:56:59	PASSED	

Self Test Date: 2021-02-08 16:59

Instrument Software: 4.0.2020.07.11.04.16.13.ded2bc3

Name	Start	Result	Failure Reason
Sample Cooler	09:59:09	PASSED	
Sample Coolant Pump	09:59:08	PASSED	
Chamber Heater	09:58:42	PASSED	
Chamber Temperature Spec	09:58:41	FAILED	Detected chamber temp 24.6C, 09:58:41 AM below control range (27.0C - 32.5C)
Ambient Temperature Spec	09:58:40	PASSED	
Point Detector Light	09:57:58	PASSED	
Point Detector Dark	09:57:33	PASSED	
D2 Lamp On	09:57:03	PASSED	
Camera UV Illumination	09:56:55	FAILED	Dark image must be darker than Fluorescence image

Image Quality	09:56:54	FAILED	Camera temperature reads -47.14; must read -40.00 or below to test image quality. Ensure camera has had sufficient time to cool before re-running test.
Filter Wheel Move	09:56:25	PASSED	
Filter Wheel Home	09:56:24	PASSED	
Dark Masters	09:56:23	PASSED	
Camera	09:56:20	PASSED	
Vacuum Vent	09:56:15	PASSED	
Vacuum Leak	09:54:50	PASSED	
Unregulated Vac level	09:54:24	PASSED	
Temp Sensors	09:54:23	PASSED	
Pressure Vent	09:54:14	PASSED	
Pressure Leak	09:52:53	PASSED	
Low Vacuum Function	09:52:32	PASSED	
High Voltage	09:52:21	PASSED	
Temp Sensor Variance	09:52:20	PASSED	
Tray Move	09:50:50	PASSED	
Tray Jog	09:50:46	PASSED	
Tray Home	09:50:44	PASSED	
Tray Encoders	09:50:41	PASSED	
NFC Service	09:50:38	PASSED	
Disk Storage	09:50:37	PASSED	

Self Test Date: 2021-02-04 17:05

Instrument Software: 4.0.2020.07.11.04.16.13.ded2bc3

Name	Start	Result	Failure Reason
Sample Cooler	10:04:33	PASSED	
Sample Coolant Pump	10:04:32	PASSED	
Chamber Heater	10:03:45	PASSED	
Chamber Temperature Spec	10:03:44	PASSED	
Ambient Temperature Spec	10:03:43	PASSED	
Point Detector Light	10:03:02	PASSED	
Point Detector Dark	10:02:37	PASSED	

D2 Lamp On	10:02:07	PASSED	
Camera UV Illumination	10:01:57	PASSED	
Image Quality	10:01:34	PASSED	
Filter Wheel Move	10:01:06	PASSED	
Filter Wheel Home	10:01:04	PASSED	
Dark Masters	10:01:03	PASSED	
Camera	10:01:01	PASSED	
Vacuum Vent	10:00:55	PASSED	
Vacuum Leak	09:59:30	PASSED	
Unregulated Vac level	09:59:05	PASSED	
Temp Sensors	09:59:04	PASSED	
Pressure Vent	09:58:54	PASSED	
Pressure Leak	09:57:32	PASSED	
Low Vacuum Function	09:57:12	PASSED	
High Voltage	09:57:01	PASSED	
Temp Sensor Variance	09:56:59	PASSED	
Tray Move	09:55:29	PASSED	
Tray Jog	09:55:25	PASSED	
Tray Home	09:55:23	PASSED	
Tray Encoders	09:55:20	PASSED	
NFC Service	09:55:17	PASSED	
Disk Storage	09:55:16	PASSED	

Self Test Date: 2020-06-14 22:42

Instrument Software: 3.1.2019.02.11.18.58.45.34dd4a5

Name	Start	Result	Failure Reason
Sample Cooler	14:41:41	PASSED	
Sample Coolant Pump	14:41:40	PASSED	
Chamber Heater	14:40:59	PASSED	
Chamber Temperature Spec	14:40:58	PASSED	
Ambient Temperature Spec	14:40:57	PASSED	

Point Detector Light	14:40:16	PASSED	
Point Detector Dark	14:39:51	PASSED	
D2 Lamp On	14:39:20	PASSED	
Camera UV Illumination	14:39:10	PASSED	
Image Quality	14:38:47	PASSED	
Filter Wheel Move	14:38:19	PASSED	
Filter Wheel Home	14:38:18	PASSED	
Dark Masters	14:38:17	PASSED	
Camera	14:38:14	PASSED	
Vacuum Vent	14:38:08	PASSED	
Vacuum Leak	14:36:43	PASSED	
Unregulated Vac level	14:36:18	PASSED	
Temp Sensors	14:36:17	PASSED	
Pressure Vent	14:36:07	PASSED	
Pressure Leak	14:34:46	PASSED	
Low Vacuum Function	14:34:26	PASSED	
High Voltage	14:34:15	PASSED	
Temp Sensor Variance	14:34:14	PASSED	
Tray Move	14:32:43	PASSED	
Tray Jog	14:32:40	PASSED	
Tray Home	14:32:38	PASSED	
Tray Encoders	14:32:35	PASSED	
NFC Service	14:32:32	PASSED	
Disk Storage	14:32:31	PASSED	

Self Test Date: 2020-05-25 18:21

Instrument Software: 3.1.2019.02.11.18.58.45.34dd4a5

Name	Start	Result	Failure Reason
Sample Cooler	10:21:01	PASSED	
Sample Coolant Pump	10:21:00	PASSED	
Chamber Heater	10:20:03	PASSED	
Chamber Temperature Spec	10:20:02	PASSED	

Chapter 17: Controlling Maurice, Maurice C., Maurice S. and MauriceFlex | Instrument Reports

Maurice kf1026

Ambient Temperature	10:20:01	PASSED	
Spec Point Detector Light	10:19:21	PASSED	
-	10:19:21	PASSED	
Point Detector Dark	10:18:56	PASSED	
D2 Lamp On	10:18:26	PASSED	
Camera UV Illumination	10:18:15	PASSED	
Image Quality	10:17:52	PASSED	
Filter Wheel Move	10:17:24	PASSED	
Filter Wheel Home	10:17:23	PASSED	
Dark Masters	10:17:22	PASSED	
Camera	10:17:21	PASSED	
Vacuum Vent	10:17:15	PASSED	
Vacuum Leak	10:15:50	PASSED	
Unregulated Vac level	10:15:25	PASSED	
Temp Sensors	10:15:24	PASSED	
Pressure Vent	10:15:14	PASSED	
Pressure Leak	10:13:52	PASSED	
Low Vacuum Function	10:13:32	PASSED	
High Voltage	10:13:20	PASSED	
Temp Sensor Variance	10:13:19	PASSED	
Tray Move	10:11:49	PASSED	
Tray Jog	10:11:45	PASSED	
Tray Home	10:11:44	PASSED	
Tray Encoders	10:11:40	PASSED	
NFC Service	10:11:36	PASSED	
Disk Storage	10:11:35	PASSED	

Cartridge Self Test Summary - Last 10 Tests

Test Date	Status	Cartridge S/N	Instrument Software	Username
2022-11-30 09:51	PASSED	8220511003	4.2.2022.11.23.21.59.20.d530e42a9	
2022-11-29 10:43	PASSED	8220511003	4.2.2022.11.23.21.59.20.d530e42a9	
2022-11-28 10:13	PASSED	8220511003	4.2.2022.11.23.21.59.20.d530e42a9	
2022-11-17 10:43	PASSED	8220615870	4.2.2022.11.07.17.15.11.3643af972	
2022-07-01 13:44	PASSED	8220503001	4.1.2022.06.29.21.58.35.b9d03b73d	admin
2022-06-30 17:47	PASSED	8220503001	4.1.2022.06.29.21.58.35.b9d03b73d	
2022-06-30 17:37	FAILED	8220503001	4.1.2022.06.29.21.58.35.b9d03b73d	
2022-06-30 11:07	PASSED	8220503001	4.1.2022.06.29.21.58.35.b9d03b73d	
2022-06-07 10:50	PASSED	8220503001	4.1.2022.05.26.18.36.41.aa06fd9b0	
2022-05-24 13:06	PASSED	8220503001	4.1.2022.05.11.05.58.39.c54f50194	admin

Cartridge Self Test Details

Self Test Date: 2022-11-30 09:51

Instrument Software: 4.2.2022.11.23.21.59.20.d530e42a9

Username:

Cartridge S/N: 8220511003

Name	Start	Result	Failure Reason
Cartridge Clog	09:44:13	PASSED	

Self Test Date: 2022-11-29 10:43

Instrument Software: 4.2.2022.11.23.21.59.20.d530e42a9

Username:

Cartridge S/N: 8220511003

Name	Start	Result	Failure Reason
Cartridge Clog	10:36:01	PASSED	

Self Test Date: 2022-11-28 10:13

Instrument Software: 4.2.2022.11.23.21.59.20.d530e42a9

Username:

Cartridge S/N: 8220511003

	Name Start Result Failure Reason
--	----------------------------------

	Ca	artridge Clog	10:06:17	PASSED	
--	----	---------------	----------	--------	--

Self Test Date: 2022-11-17 10:43

Instrument Software: 4.2.2022.11.07.17.15.11.3643af972

Username:

Cartridge S/N: 8220615870

	Name	Start	Result	Failure Reason
[Cartridge Clog	10:36:03	PASSED	

Self Test Date: 2022-07-01 13:44

Instrument Software: 4.1.2022.06.29.21.58.35.b9d03b73d

Username: admin

Cartridge S/N: 8220503001

Name	Start	Result	Failure Reason
Cartridge Clog	13:37:22	PASSED	

Self Test Date: 2022-06-30 17:47

Instrument Software: 4.1.2022.08.29.21.58.35.b9d03b73d

Username:

Cartridge S/N: 8220503001

Name	Start	Result	Failure Reason
Cartridge Clog	17:40:49	PASSED	

Self Test Date: 2022-06-30 17:37

Instrument Software: 4.1.2022.06.29.21.58.35.b9d03b73d

Username:

Cartridge S/N: 8220503001

Name	Start	Result	Failure Reason
Cartridge Clog	17:30:38		Mean reading with water 2287078.1, mean with air 2288837.3, diff 0.01%, minimum 10.0%

Self Test Date: 2022-06-30 11:07

Instrument Software: 4.1.2022.06.29.21.58.35.b9d03b73d

Username:

Cartridge S/N: 8220503001

Name	Start	Result	Failure Reason
Cartridge Clog	11:00:45	PASSED	

Self Test Date: 2022-06-07 10:50

Instrument Software: 4.1.2022.05.26.18.36.41.aa06fd9b0

Username:

Cartridge S/N: 8220503001

Name	Start	Result	Failure Reason
Cartridge Clog	10:43:28	PASSED	

Self Test Date: 2022-05-24 13:06

Instrument Software: 4.1.2022.05.11.05.58.39.c54f50194

Username: admin

Cartridge S/N: 8220503001

Name	Start	Result	Failure Reason
Cartridge Clog	12:59:36	PASSED	

Created By: Inverse Multicrife Mon 1.00 PM Mer 13, 2023 PDT Bothwere Version: Compense for ICE 4.0.0, Build ID: 0222 Marzina M1028 Computer: USBJD-3A/782J3-L Page 14 of 14



User Guide for Maurice, Maurice C., Maurice S. and MauriceFlex

Viewing Log Files

Runs Log

To see a history of all runs your system has performed, select **Instrument > Runs**:

Name	Date	Size	1
2016-01-13_10-08-00_DreamTeam_Maurice CE-SDS	2016-01-13 16:00	1113474	Ξ
C1151214313_KF1003_2016-01-12_16-33-15_testseal_b	2016-01-12 21:49	4648357	
Uyendreamteam_Pilot3_2016-01-12_14-06-57_Saletrai	2016-01-12 15:11	795319	
2016-01-11_14-31-03_Training CE-SDS_20160111.mbz	2016-01-11 22:28	1619048	
2016-01-11_11-56-48_Applications Training cIEF_2016	2016-01-11 13:08	863362	
2016-01-08_15-05-43_Maurice CE-SDS_vialA1_48inj_K	2016-01-09 17:54	5446827	
2016-01-08_14-22-48_Maurice CE-SDS_vialA1_48inj_K	2016-01-08 14:31	110276	
c1151214313_kf1003_2016-01-07_13-44-59_embedded	2016-01-07 17:44	3365976	
C3151130102_strippedTip_Pilot3_2016-01-07_08-27-3	2016-01-07 11:56	583646	
C3151130102_StrippedTip_Pilot3_hSAP_2016-01-06_1	2016-01-06 22:09	1144978	
C1151124296_200Xpilot_Pilot3_2016-01-06_13-53-19	2016-01-06 14:47	621451	
C1151124301_Pilot200X_Pilot3_2016-01-06_12-43-59	2016-01-06 13:37	680781	
2016-01-06_11-16-23_Maurice cIEF 0106-1151214313	2016-01-06 12:26	863623	
C3151130104_3weeksRT_Pilot3_2016-01-05_14-48-36	2016-01-05 18:17	1771836	
C1151124297_3weeksRT_Pilot3_2016-01-05_12-50-39	2016-01-05 14:26	1329760	
C1151124304_3weeksRT_Pilot3_2016-01-05_11-12-10	2016-01-05 12:47	1322010	
C1151124299_3weeks37C_Pilot3_2016-01-05_10-47-23	2016-01-05 11:11	347173	
C1151120277_3weeks37C_Pilot3_2016-01-05_09-10-35	2016-01-05 10:46	1318208	
C3151130102_2weeksRT_Pilot3_2016-01-04_16-33-22	2016-01-04 20:02	1771347	
C3151130105_3weeks37C_Pilot3_2016-01-04_12-47-07	2016-01-04 16:16	1772422	
C3151130103_3weeks37C_Pilot3_2016-01-04_09-04-25	2016-01-04 12:33	1772022	-
Open	Save Dele	te Cancel	

- To open a run file: Select a run file from the list and click Open.
- To save a run file: Select a run file from the list and click Save. This lets you save a copy of a completed run or one in progress to either a USB drive or the local computer.
- **To delete a run file:** Select a run file from the list and click **Delete**. The run file will be deleted from the history and from the Run file in the Compass for iCE directory.

Chapter 17: Controlling Maurice, Maurice C., Maurice S. and MauriceFlex | Sending a Log File to Technical Support

Sending a Log File to Technical Support

If the computer you're using has an internet connection, Compass for iCE can zip and send a log file directly to ProteinSimple Technical Support.

- 1. Connect to an instrument.
- 2. Select **Help** in the main menu and click **Export Logs**.

User Guide
Check for Updates
Release Notes
Export Logs
Send Run File
About Compass for iCE

3. A window will display where you can enter information. The email and instrument fields are required.

🔞 Get Log File	5	×
Name:		
Company:		
*Email:		
*Instrument:		
Comment:		
		•
Se	end Save Cancel	

4. Click Send. When the file upload is complete, the following message displays. Click OK.

Send Run File		×
I	Upload completed	
	ОК	

5. Click **Save** to save the file directly to the computer. A window will display where you can enter a file name for the zipped log file.

Chapter 17: Controlling Maurice, Maurice C., Maurice S. and MauriceFlex | Sending a Log File to Technical Support

Instrument Log

- 1. Select **Instrument** > **Properties**.
- 2. Click Logs. The Instrument Logs window displays:

Self Tests	Status	Cartridge S/N	^	Command Log
2022-01-12 16:16	FAILED	8211213001		-
2022-01-10 09:55	FAILED	990000100		Instrument Log
2022-01-10 09:11	FAILED	9900000100		All Logs
2022-01-09 20:59	FAILED	9900000100		-
2022-01-05 16:48	FAILED	9900000100		
2021-12-07 14:08	FAILED	9900000100		
2021-12-05 18:00	FAILED	9900000100		
2021-12-03 12:29	FAILED	000000001		
2021-11-18 16:06	FAILED			
2021-11-15 14:41	STOPPED			
2021-11-10 14:00	FAILED			
2021-11-10 10:56	FAILED			
2016-09-07 11:48	STOPPED			
2016-03-03 16:46	STOPPED			
2016-03-03 15:05	FAILED			
2016-03-03 14:45	STOPPED			
2016-03-03 14:36	FAII FD		~	
		View	,	ОК

3. Click Instrument Log.

		 cellbio.network.log_exceptio 	ns - ERROR - Node:CalibrationToolI(
Traceback (most rec			
response = wrapp	ed_callback(request, *callbac	ck_args, **callback_kwargs)	o/core/handlers/base.py", line 111, ii
hrc = nodescalib	orationToolIO.manifoldVacH	lighRawCounts() #I DONT TH	o/network/console/kifer/device/calil INK RAW COUNTS IS ACTUALYL WH
return selfnodeR	lead(_ADRS_MANIFOLD_VAC	CUUM_HIGH, [®] manifoldVacHi	
raise NodeError(se	elfdevName, "Read:"+fieldN	Name, _ERROR_NO_ACK)	o/device/can/BaseNode.py", line 240
		nanifoldVacHighSensor, No A	
2015-12-11 13:24:34,	500 - PoolThread-django-7 -		nTooIIO - ERROR - Read:manifoldVa ns - ERROR - Node:CalibrationTooII(
	bedded-control/local/lib/py		o/core/handlers/base.py", line 111, ii
	ed_callback(request, *callbac		
			o/network/console/kifer/device/calil
			INK RAW COUNTS IS ACTUALYL WH
		2000 HIGH, "manifoldVacHid	o/device/kifer/CalibrationToolIO.py"
			p/device/can/BaseNode.py", line 240
	elfdevName, "Read:"+fieldN		/ device/ carl/ baservoue.py , line 240
		nanifoldVacHighSensor, No A	rk
			nToolIO - ERROR - Read:manifoldVa
			ns - ERROR - Node:CalibrationToolI
Traceback (most rec		5- 1	
File "/usr/share/em	bedded-control/local/lib/py	ython2.7/site-packages/djang	o/core/handlers/base.py", line 111, i
response = wrapp	ed_callback(request, *callbac	ck_args, **callback_kwargs)	
			o/network/console/kifer/device/calil
			INK RAW COUNTS IS ACTUALYL WH
			o/device/kifer/CalibrationToolIO.py"
		CUUM_HIGH, "manifoldVacHig	
raise NodeError(se	elfdevName, "Read:"+field	Name, _ERROR_NO_ACK)	o/device/can/BaseNode.py", line 240
		nanifoldVacHighSensor, No A	
			nToolIO - ERROR - Read:manifoldVa
		 cellbio.network.log_exceptio 	ns - ERROR - Node:CalibrationToolI
Traceback (most rec			
	ed_callback(request, *callbac		o/core/handlers/base.py", line 111, i
•	III		+

4. Click Save File As to save a copy of the log file.

Chapter 17: Controlling Maurice, Maurice C., Maurice S. and MauriceFlex | Sending a Log File to Technical Support

Self Test Logs

- 1. Select **Instrument > Properties**.
- 2. Click Logs. A list of dates each self test was run displays:

Self Tests	Status	Cartridge S/N	^	Command Log
2022-01-12 16:16	FAILED	8211213001		-
2022-01-10 09:55	FAILED	9900000100		Instrument Log
2022-01-10 09:11	FAILED	9900000100		All Logs
2022-01-09 20:59	FAILED	9900000100		
2022-01-05 16:48	FAILED	9900000100		
2021-12-07 14:08	FAILED	9900000100		
2021-12-05 18:00	FAILED	9900000100		
2021-12-03 12:29	FAILED	000000001		
2021-11-18 16:06	FAILED			
2021-11-15 14:41	STOPPED			
2021-11-10 14:00	FAILED			
2021-11-10 10:56	FAILED			
2016-09-07 11:48	STOPPED			
2016-03-03 16:46	STOPPED			
2016-03-03 15:05	FAILED			
2016-03-03 14:45	STOPPED			
2016-03-03 14:36	FAILED		~	

3. Select a test date in the list and click View to see the individual test results:

Name	Start	Duration (s	Result	Failure Reason	
Door Motor	15:58:40	4.017	PASSED		
Sample Cooler	15:58:14	21.173	PASSED		
Sample Coolant Pump	15:58:13	0.004	PASSED		
Chamber Heater	15:57:27	45.265	PASSED		
Chamber Temperature Spec	15:57:26	0.006	PASSED		
Ambient Temperature Spec	15:57:25	0.003	PASSED		
Point Detector Light	15:56:37	45.295	PASSED		
Point Detector Dark	15:56:29	7.243	PASSED		
Image Quality	15:56:10	16.155	PASSED		
Filter Wheel Move	15:55:59	9.966	PASSED		
Filter Wheel Home	15:55:58	0.221	PASSED		
Dark Masters	15:55:57	0.004	PASSED		
Camera	15:55:54	1.624	PASSED		
Vacuum Leak	15:54:27	84.568	PASSED		
Unregulated Vac level	15:54:02	24.053	PASSED		
Temp Sensors	15:54:01	0.009	PASSED		
Pressure Vent	15:53:39	21.491	PASSED		

Name	Start	Duration (s	Result	Failure Reason
Camera	15:55:54	1.624	PASSED	
Vacuum Leak	15:54:27	84.568	PASSED	
Unregulated Vac level	15:54:02	24.053	PASSED	
Temp Sensors	15:54:01	0.009	PASSED	
Pressure Vent	15:53:39	21.491	PASSED	
Pressure Leak	15:52:11	86.997	PASSED	
Low Vacuum Function	15:51:49	21.012	PASSED	
D2 Lamp On	15:51:19	28.182	PASSED	
High Voltage	15:51:08	10.057	PASSED	
Temp Sensor Variance	15:51:07	0.053	PASSED	
Tray Move	15:49:51	71.486	PASSED	
Tray Jog	15:49:44	6.935	PASSED	
Tray Home	15:49:42	0.775	PASSED	
Tray Encoders	15:49:34	6.597	PASSED	
NFC Service	15:49:31	0.000	PASSED	
Disk Storage	15:49:30	0.000	PASSED	
				Save File As Cancel

4. Click Save File As to save a copy of the test log file.

Command Log

- 1. Select **Instrument > Properties** to display your system's properties.
- 2. Click Logs. The Instrument Logs window displays:

Self Tests	Status	Cartridge S/N	^	Command Log
2022-01-12 16:16	FAILED	8211213001		
2022-01-10 09:55	FAILED	9900000100		Instrument Log
2022-01-10 09:11	FAILED	9900000100		All Logs
2022-01-09 20:59	FAILED	9900000100		
2022-01-05 16:48	FAILED	9900000100		
2021-12-07 14:08	FAILED	9900000100		
2021-12-05 18:00	FAILED	9900000100		
2021-12-03 12:29	FAILED	000000001		
2021-11-18 16:06	FAILED			
2021-11-15 14:41	STOPPED			
2021-11-10 14:00	FAILED			
2021-11-10 10:56	FAILED			
2016-09-07 11:48	STOPPED			
2016-03-03 16:46	STOPPED			
2016-03-03 15:05	FAILED			
2016-03-03 14:45	STOPPED			
2016-03-03 14:36	FAILED		~	

3. Click Command Log. A list of system commands displays:

)ate	User Name	Message	Comment	1
01/19/2016 2:12 PM	Service	performUpgrade		
01/19/2016 4:38 PM	rd	Started run: 2016-01-19_16-38-36_Maurice CE-SD		
01/20/2016 8:58 AM	rd	Started cleanup		
01/20/2016 10:43 AM	rd	Started run: cIEF1151219320_KF1004_seal test_co		
01/20/2016 3:11 PM	Ipriya	Started run: cIEF1151219320_KF1004_on board mi		
01/21/2016 10:14 AM	hxu	Started run: 2016-01-21_10-14-17_Maurice CE-SD		
01/22/2016 12:57 PM	atu	Started run: 2016-01-22_12-57-57_Maurice CE-SD		
01/25/2016 8:34 AM	bpurandare	Started cleanup		
01/26/2016 7:44 AM	bpurandare	Started run: 2016-01-26_07-44-10_6X_test-cartrid		
01/26/2016 12:22 PM	bpurandare	Started cleanup		
01/26/2016 1:07 PM	ikazakova	Started run: C3151201218-NewCondVial-PIN_201		
01/27/2016 9:35 AM	ikazakova	Started cleanup		
01/27/2016 10:19 AM	ikazakova	Started run: C3151218250-NewCondVial-PIN-201		
01/27/2016 5:09 PM	ikazakova	Stopped run		
01/27/2016 5:13 PM	ikazakova	Started run: C3151218250-OLDVial-NO_PIN-2016		
01/28/2016 9:32 AM	ikazakova	Started cleanup		
ime 01/27/2010 Iessage Started ru		User ikazakova DLDVial-NO PIN-2016-01-27 17-12-51_24inj-A5A6-Ma	urice CE-SDS Accave	
omment				
			Done	_

Chapter 18: CIEF Data Analysis

Chapter Overview

- Analysis Screen Overview
- Opening Run Files
- How Run Data is Displayed
- Viewing Run Data
- Data Notifications and Warnings
- Checking Your Results
- Naming Peaks
- Group Statistics
- Copying Results Tables and Graphs
- Exporting Run Files
- Changing Sample Protein Identification
- Changing the Electropherogram View
- Closing Run Files
- Analysis Settings Overview
- Detection Settings
- Peak Names Settings
- Peak Fit Analysis Settings
- Manual Peak Integration

- Advanced Analysis Settings
- pI Markers Analysis Settings
- Injection Reports
- Importing and Exporting Analysis Settings

Analysis Screen Overview

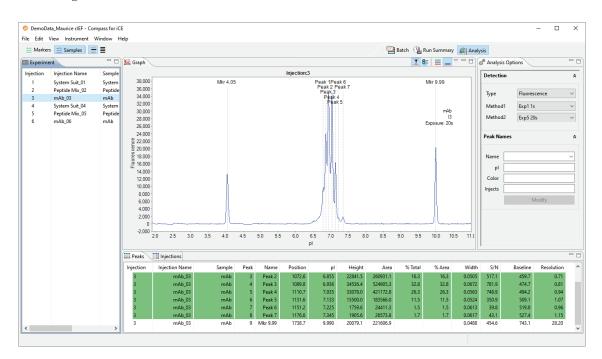
You can use the Analysis screen to view electropherograms and tabulated results for your injections. If any post-run analysis is needed, you can do it here too. To get to this screen, click the **Analysis** screen tab:

Batch 🕒 Run Summary 🚛 Analysis

Analysis Screen Panes

The Analysis screen has four panes:

- Experiment Lists the injection number, sample IDs, sample locations and methods for each injection in the run and lets you get a quick view of method parameters.
- Graph Displays the electropherograms for sample proteins or pI markers.
- Peaks Shows the tabulated results for sample proteins and pI markers.
- **Injections** Displays a list of the sample proteins Compass for iCE names automatically using the user-defined peak name analysis parameters.
- Analysis Options Lets you view absorbance or fluorescence data for the run and view, change and add new custom
 peak name settings.



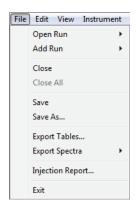
Software Menus Active in the Analysis Screen

These main menu items are active in the Analysis Screen:

- File
- Edit
- View
- Instrument (when Compass for iCE is connected to Maurice, Maurice C. or MauriceFlex.)
- Window
- Help

File Menu

These File menu options are active:



- Open Run Opens a run file.
- Add Run Lets you open and view other run files besides the one that's already open.
- **Close** Closes the run file currently being viewed.
- Close All Closes all open run files.
- Save/Save As If you made changes in the Analysis screen before you went to the Run Summary screen, this saves your changes to the run file.
- Export Tables Exports the results for all injections in the run in .txt format.
- Export Spectra Exports the raw and analyzed data traces and background for each injection in the run in .txt or .cdf format.
- **Injection Report** Exports the raw and analyzed data, IV plot, peaks table, sample and system info for individual injections as PDF files. You can also export the run history with all analysis events.
- Exit Closes Compass for iCE.

Edit Menu

These Edit menu options are active:

Edit	View	Instrument	Windo
	Cut	Ct	rl+X
	Сору	Cti	l+C
	Paste	Ct	rl+V
	Analysi Prefere		

- **Copy** Lets you copy data shown in the graph, lane, peaks or injections pane. See "Copying Results Tables and Graphs" on page 501 for more information.
- Analysis Displays the analysis settings used to analyze the run data and lets you change them as needed. See "Analysis Settings Overview" on page 528 for more information.
- **Preferences** Lets you set and save your preferences for data export, graph colors, grouped data and Twitter settings. See Chapter 21: "Setting Your Preferences" for more information.

View Menu

These View menu options are active:



- Selected (Single View) Displays the data for only the injections selected.
- All (Multiple View) Displays data for all injections so you can scroll through them.
- Markers Lets you view data just for the pI markers in your injections.
- Samples Lets you view data just for sample proteins in your injections.
- Grouping Displays data for injection groups.
- View Region Lets you change the x-axis range of the data displayed.
- Show Hidden- Shows injections that are hidden from the data view.

Opening Run Files

You can open one run file or multiple files at the same time to compare information between runs.

NOTE: cIEF run files that use the FL458 nm fluorescence detection filter can only be opened in Compass for iCE 2.1 or later.

Opening One Run File

1. Select **File** in the main menu and click **Open Run**.

e Edit View Instrumen	t Window Help
Open Run	2016-01-21_09-46-39_mAb11_Prep20160121_QC(0)
Add Run	2015-12-06_15-13-01_Maurice cIEF_Mab11_TechRep
Close	MW ladder assigned_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS
Close All	MW ladder assigned_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS2
ciose nii	3160106284 KF1011 DG 2016-01-15_12-42-55_Maurice CE-SDS
Save	3160106283 KF1011 DG 2016-01-14_18-50-33_Maurice CE-SDS
Save As	3160106286 KF1011 DG 2016-01-15_15-25-52_Maurice CE-SDS
Export Tables	2016-01-14_09-53-54_Maurice cIEF Ab dilution
Export Spectra	1151120281-KF1007-BP-2015-12-04_10-17-58_2015Dec3_QC_plateA1_Maurice cIEF
Intention Depart	1151120284-KF1007-BP-RERUN-2015-12-04_12-48-18_2015Dec3_QC_plateA1_Maurice cIEF
Injection Report	Browse
Exit	510WSE

2. A list of the last 10 runs opened will display. Select one of these runs or click **Browse** to open the Runs folder and select a different file.

Opening Multiple Run Files

1. To open the first run file, select File in the main menu and click Open Run.

File Edit View Instrument	Window Help
Open Run 🕨	2016-01-21_09-46-39_mAb11_Prep20160121_QC(0)
Add Run 🕨	2015-12-06_15-13-01_Maurice cIEF_Mab11_TechRep
Close	MW ladder assigned_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS
Close All	MW ladder assigned_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS2
closeria	3160106284 KF1011 DG 2016-01-15_12-42-55_Maurice CE-SDS
Save	3160106283 KF1011 DG 2016-01-14_18-50-33_Maurice CE-SDS
Save As	3160106286 KF1011 DG 2016-01-15_15-25-52_Maurice CE-SDS
Export Tables	2016-01-14_09-53-54_Maurice cIEF Ab dilution
Export Spectra	1151120281-KF1007-BP-2015-12-04_10-17-58_2015Dec3_QC_plateA1_Maurice cIEF
Injection Report	1151120284-KF1007-BP-RERUN-2015-12-04_12-48-18_2015Dec3_QC_plateA1_Maurice cIEF
Exit	Browse

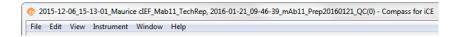
2. A list of the last 10 runs opened will display. Select one of these runs or click **Browse** to open the Runs folder and select a different file. If the run selected is not a cIEF batch, an alert will appear.



3. To open another run file, select File in the main menu and click Add Run.

File Edit View Instrument	Window Help
Open Run 🕨	n ::
Add Run 🕨	2016-01-21_09-46-39_mAb11_Prep20160121_QC(0)
Close Close All	1151120281-KF1007-BP-2015-12-04_10-17-58_2015Dec3_QC_plateA1_Maurice clEF 1151120284-KF1007-BP-RERUN-2015-12-04_12-48-18_2015Dec3_QC_plateA1_Maurice clEF
Save Save As	Browse A3
Export Tables Export Spectra	A5 E A6 A7
Injection Report Exit	A8 A1

- 4. A list of cIEF runs will display. Select one of these runs or click **Browse** to open the Runs folder and select a different file.
- 5. When a run is added, its data appends to the open run file and displays as a second set of injections in all screen panes. The second run file name also appears in the title bar:



6. Repeat the last two steps to add additional runs.

How Run Data is Displayed

Data in the run file is organized for easy review.

Experiment Pane: Batch Injection Information

The Experiment pane lists all the injections performed in the run, which samples were used for each, the sample location in the 96-well plate or 48-vial tray for cIEF batches and in the 96-well plate for MauriceFlex cIEF batches and the method used.

1	System Suitability	System Suitabi	A1	System Suitabl
✓ 2	mAb 11 Blank_02	mAb 11 Blank	A2	mAb Method
√ 3	mAb 11 Ref. Std03	mAb 11 Ref. St	A3	mAb Method
√ 4	mAb 11 Prep 2016	mAb 11 Prep 2	A4	mAb Method
✓ 5	mAb 11 Prep 2016	mAb 11 Prep 2	A4	mAb Method
√ 6	mAb 11 Prep 2016	mAb 11 Prep 2	A4	mAb Method
√7	mAb 11 Ref. Std07	mAb 11 Ref. St	A3	mAb Method
√8	mAb 11 Blank_08	mAb 11 Blank	A2	mAb Method

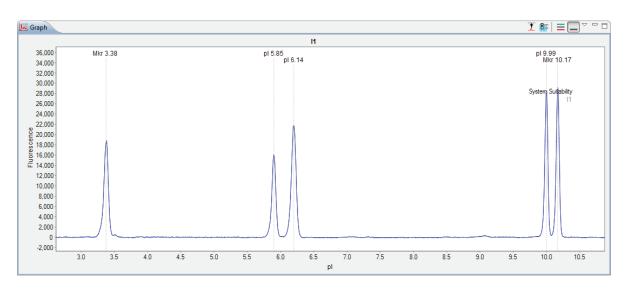
- To view all columns Use the scroll bar or click Maximize in the upper right corner.
- To resize columns Roll the mouse over a column border until the sizing arrow appears, then click and drag to resize.
- To view method parameters Hover the mouse over a method name.

Experime	ent			🗖 🗖 🔀 Graph
Injection	Injection Name	Sample	Location	Method
1	System Suitability	System Suitabi	A1	System Suitabl 36.000 Mkr 3.38
✓2	mAb 11 Blank_02	mAb 11 Blank	A2	mAb
✓ 3	mAb 11 Ref. Std03	mAb 11 Ref. St	A3	mAb Method Separation: 1.0 min 1500 Volts, 6.0 min 3000 Volts
√ 4	mAb 11 Prep 2016	mAb 11 Prep 2	A4	mAb Detection: 5 Exposures
✓ 5	mAb 11 Prep 2016	mAb 11 Prep 2	A4	mAb Sample Load (s): 90
✓ 6	mAb 11 Prep 2016	mAb 11 Prep 2	A4	mAb pl Markers: 4.05, 9.99
√7	mAb 11 Ref. Std07	mAb 11 Ref. St	A3	mAb Method 24,000
✓ 8	mAb 11 Blank_08	mAb 11 Blank	A2	mAb Method 22,000

NOTE: Data notification icons will display in the Injection column if Compass for iCE detects a potential analysis issue or data was manually modified by the user. For more information see "Data Notifications and Warnings" on page 411.

Graph Pane: Electropherogram Data

The Graph pane displays the electropherogram(s) for sample proteins or pI markers depending on the view options you've selected.



You can get more info on graph view options in "Changing the Electropherogram View" on page 507.

Peaks Pane: Calculated Results

The Peaks pane shows the tabulated results for your sample proteins or pI markers. Each row in the table has the individual results for each peak detected in an injection. Results shown will either be for one injection or multiple injections, samples or pI markers depending on the view options you're using. Check out "Analysis Options Pane" on page 483 for more info.

Peaks	Injections													- 6
Injection	Injection Name	Sample	Peak	Name	Position	pl	Height	Area	% Total	% Area	Width	S/N	Baseline	Resolution ^
3	mAb 11 Ref. St	mAb 11 Ref. St	1	Mkr 4.05	542	4.050	8657.5	129440			0.0594	183.1	176.4	
3	mAb 11 Ref. St	mAb 11 Ref. St	2	Peak1	1082	6.554	548.3	7585	0.5	0.5	0.0621	11.6	84.7	24.28
3	mAb 11 Ref. St	mAb 11 Ref. St	3	Peak2	1107	6.668	1503.9	53212	3.4	3.4	0.1294	31.8	83.1	0.70
3	mAb 11 Ref. St	mAb 11 Ref. St	4	Peak3	1139	6.811	7171.3	111929	7.1	7.1	0.0730	151.7	80.8	0.83
3	mAb 11 Ref. St	mAb 11 Ref. St	5	Peak4	1158	6.881	19395.5	293503	18.6	18.6	0.0745	410.3	79.2	0.56
3	mAb 11 Ref. St	mAb 11 Ref. St	6	Peak5	1177	6.968	28124.1	465924	29.5	29.5	0.0959	595.0	77.5	0.60
3	mAb 11 Ref. St	mAb 11 Ref. St	7	Peak6	1199	7.066	32407.9	438220	27.7	27.7	0.0551	685.6	75.3	0.76 ~
<														>

NOTES:

Peaks that Compass for iCE names automatically with user-defined peak name settings are color-coded.

When the Markers view is selected, the information in the Peaks table includes only injection, sample, peak, position and height. pI markers the software has identified are marked with an M.

- To view all rows Use the scroll bar or click Maximize in the upper right corner.
- To resize columns Roll the mouse over a column border until the sizing arrow appears, then click and drag to resize.

The following results and info are listed in the Peaks table:

- Injection Injection number.
- **Injection name** If injection names were entered in the batch, those names will display here. Otherwise the default 'SampleID_injection number' name will display.
- **Sample** If sample names were entered in the batch, those names will display here. Otherwise, Sample (default name) will display.
- Peak Peaks are numbered in order of detection.
- **Name** Displays peaks Compass for iCE named automatically using the user-defined peak name analysis parameters. These cells are blank if the software wasn't able to name the peak or if you didn't enter naming parameters.
- Position Peak location in pixels.
- pI Displays the calculated peak pI based on the migration time of the peak to the pI markers.
- Height The calculated peak height.
- Area Displays the count of the pixel values for dropped line fit and the area of the curve fit for gaussian fit.
- % Total Displays the peak area ratio compared to the sum of all peak areas. This value results from dividing the individual peak area by the sum of all peak areas for the injection and multiplying by 100.
- % Area Displays the calculated percent area for the named peak compared to all named peaks. This value results from dividing the individual peak area by the sum of all named peak areas for the injection and multiplying by 100 (shown for named peak sample data only).
- Width Displays the calculated peak width (sample data only).
- **S**/**N** Displays the calculated signal to noise. The signal to noise ratio is reported for each peak based on the noise in the injection and the height of the peak. S/N = 2 x peak height / noise. For the injection noise calculation, the peak to peak noise is calculated by fitting a quadratic to the test region and taking the difference between the max signal above the fit, and the minimum signal below the fit. A fit is used to mitigate the effect of drift in the signal that would give a falsely high noise value. The software looks for the quietest 50 point region in the entire injection excluding 50 points at each end. The test region is approximately 5 times a typical peak width (FWHM).
- Baseline Displays the raw baseline signal of each peak.
- **Resolution** Displays resolution of the peak compared to neighboring peaks. Two peaks that are baseline resolved will have a resolution value of 1.5. Smaller values means the peaks are not completely resolved, larger values mean the peaks are fully resolved.

Injections Pane: User-Specified Peak Names

The Injections pane shows tabulated results for sample proteins Compass for iCE labels automatically using user-defined peak name settings. Each row in the table shows the individual results for the named peaks detected in each injection.

											% Total	Area	% Area
njection	Injection Name	Sample	pl 3.38	pl 5.85	pl 6.14	pl 9.99	pl 10.17	Peak1	Peak2	Peak3	Peak4		Peak5
	mAb 11 Ref. St	mAb 11 Ref. St						7585	53212	111929	293503	4	465924
	mAb 11 Prep 2	mAb 11 Prep 2						6155	48840	101900	240940	4	451857

NOTES:

Peaks that Compass for iCE names automatically with user-defined peak name settings are color-coded.

When the Markers view is selected, the information in the Injections table includes only injection, sample and the positions of the pI marker (Mkr) peaks.

- To view all rows Use the scroll bar or click Maximize in the upper right corner.
- To resize columns Roll the mouse over a column border until the sizing arrow appears, then click and drag to resize.

The following results and info are listed in the Injections table:

- Injection Injection number.
- Injection name If injection names were entered in the batch, those names will display here. Otherwise the default 'SampleID_injection number' name will display.
- **Sample** If sample names were entered in the batch, those names will display here. Otherwise, Sample (default name) will display.
- **Peak Name Columns** An individual column per peak name will display for every peak identified by name or as a pI marker peak in the run data. Cells for injections in these columns will be blank if Compass for iCE didn't find peaks automatically using the user-defined peak name analysis and maker parameters (or none were entered).
 - To view peak area in the peak name columns (default) Select Area in the upper right corner of the pane. This displays calculated peak area for the individual peak only.
 - To view % total in the peak name columns This displays the calculated percent area for the named peak compared to all named peaks. This value results from dividing the individual peak area by the sum of all named peak areas for the injection and multiplying by 100.

NOTE: The sum of the named peak percentages can be less than 100% if some peaks aren't named.

											% Total	Area % Area
Injection	Injection Name	Sample	pl 3.38	pl 5.85	pl 6.14	pl 9.99	pl 10.17	Peak1	Peak2	Peak3	Peak4	Peak
3	mAb 11 Ref. St	mAb 11 Ref. St						0.5	3.4	7.1	18.6	29.5
4	mAb 11 Prep 2	mAb 11 Prep 2						0.4	3.4	7.2	17.0	31.8
<												

• To view % area in the peak name columns - This displays the peak area ratio compared to the sum of all named peak areas. This value results from dividing the individual peak area by the sum of all peak areas for the injection and multiplying by 100.

											% Total	Area % Area
njection	Injection Name	Sample	pl 3.38	pl 5.85	pl 6.14	pl 9.99	pl 10.17	Peak1	Peak2	Peak3	Peak4	Peak5
	mAb 11 Ref. St	mAb 11 Ref. St						0.5	3.4	7.1	18.6	29.5
	mAb 11 Prep 2	mAb 11 Prep 2						0.4	3.4	7.2	17.0	31.8

Analysis Options Pane

The Analysis Options pane gives you a quick way to view data for different exposures and add peak names without having to open and edit the run's analysis settings.

• Detection - Lets you choose to view absorbance or fluorescence data for the run and select different fluorescence exposures. For more details see "Switching Between Absorbance and Fluorescence Exposures (For Standard cIEF Runs only)" on page 490.

• Peak names - Lets you view, change and add new custom peak name settings for sample proteins. You can apply peak name settings to all, selected, or specified injections. For details on how to use this option, go to "Naming Peaks" on page 493.

Detection		\$
Туре	Fluorescence	~
Method1	Exp1 1s	\sim
Method2	Exp5 20s	~
Peak Name	5	*
Name		~
pl		
Color		
Injects		
	Modify	

Viewing Run Data

The Analysis screen lets you view data for just one injection, specific injections or all injections in the run. Each run file has data for the sample peaks and the pI markers detected in each injection.

Switching Between Samples and Markers Data Views

Here's how you switch between viewing data for your samples and pI markers:

• To view sample data - Click Samples in the View bar or select View in the main menu and click Samples.

File	Edit	View	Instrument	Window
Ħ	Marke	ers 🚊	Samples	≣∎

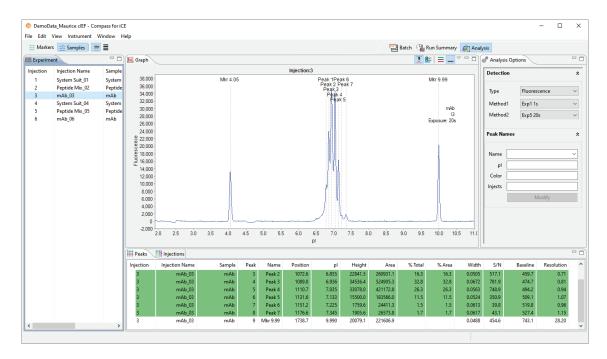
- Data in this view is for sample peaks only.
- The graph displays electropherograms with a y-axis of either Absorbance units (mAU) or Fluorescence units and an x-axis of pI. Go to "Peak Fit Analysis Settings" on page 539 for more info on how to change the detection method to view absorbance, native fluorescence or FL458 fluorescence data.

NOTES:

The FL458 nm fluorescence filter is only available on Maurice, Maurice C. and MauriceFlex systems with the option installed. One MauriceFlex systems, the FL458 nm fluorescence filter is only available for standard cIEF batches.

The FL458 nm filter enables detection of fluorescence emission at a longer wavelength to analyze molecules other than proteins, such as small molecule drugs in antibody-drug conjugates (ADCs). When used, ratiometric analysis of fluorescence and absorbance data can be applied to support applications including drug-antibody ratio (DAR) analysis.

• Results for each peak are shown in the Peaks and Injections panes.

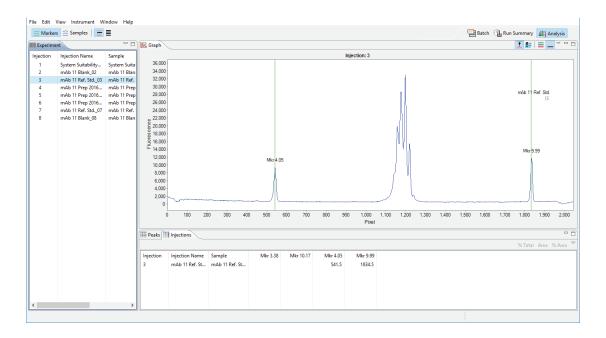


For information on checking and identifying sample peaks, see "Checking Your Data" on page 123 for standard cIEF runs and page 184 for MauriceFlex cIEF runs.

• To view pI marker data - Click Markers in the View bar or select View in the main menu and click Markers.

File	Edit	View	Instrume	ent	Window
Ē	Marke	ers 🚖	Samples		∎≣

- Data in this view is for analyzing pI markers only. These are the pI markers you add to your samples during prep.
- The graph displays electropherograms with a y-axis of either Absorbance units (mAU) or Fluorescence units and an x-axis of pixels. Go to "Peak Fit Analysis Settings" on page 539 for more info on how to change the detection method to view either absorbance or native fluorescence data.
- pI markers are identified in the Peaks pane with an **M** and as Mkr in the Injections pane.

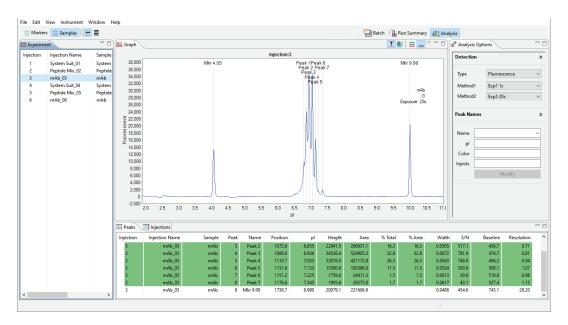


For information on checking and identifying the pI marker peaks, see "Checking Your Data" on page 123 for standard cIEF runs and page 184 for MauriceFlex cIEF runs.

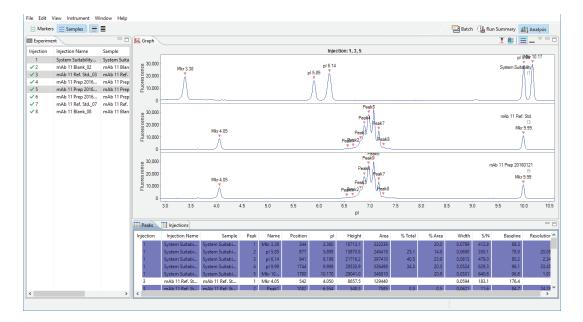
Selecting and Displaying Injection Data

You can view data from one, multiple, or all injections at once.

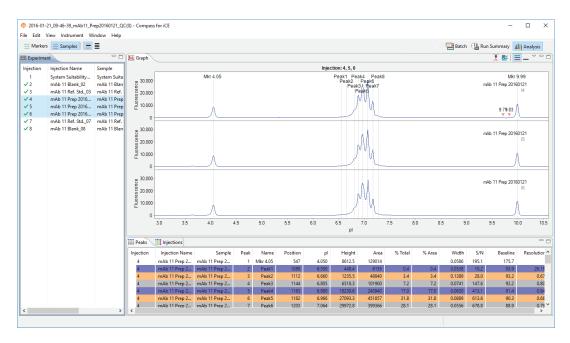
• **To look at data for one injection** - Click an injection row in the Experiment pane. Data for just that injection displays in the graph and tables.



• **To look at data for specific injections** - Hold the **Ctrl** key and select just the injection rows you want to view in the Experiment pane. Data for only the injections selected display in the graph and tables.



• To look at data for sequential injections - Select the first injection row in the Experiment pane that you want to view, then hold the Shift key and select the last. This selects all rows between the two injections. Data for only the injections selected display in the graph and tables.



• To look at data for all injections - Just click View All in the View bar. Data for all injections displays in the graph and tables.

File	Edit	View	Instrument	Window
Ħ	Marke	ers 🚘	Samples	
				, i

Switching Between Selected and All Views of Injections

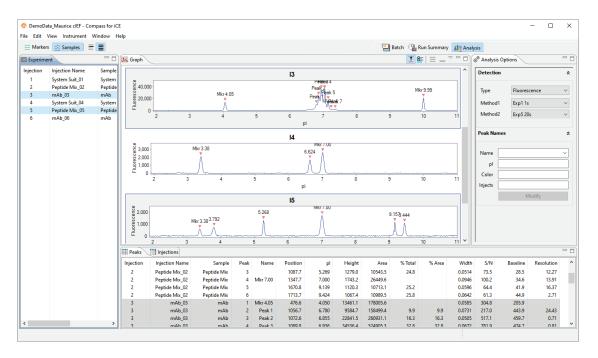
You can switch between displaying run data in a selected, per-injection format or all injections in a multi-injection format.

• To view data per in a per-injection format - Click Selected View in the View bar or select View in the main menu and click Selected.



Data for the injection row(s) selected in the Experiment pane:

- Displays with electropherograms either overlaid or stacked in the Graph pane depending on the option you've got chosen.
- Shows only results for the selected row(s) in the Peaks and Injections panes.

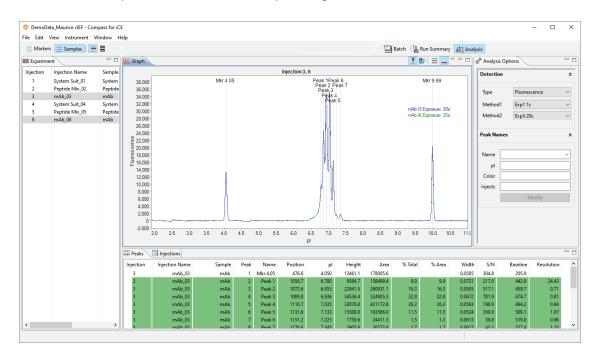


• To view data in a multi-injection format - Click View All in the View bar or select View in the main menu and click All:



Data for the injection row(s) :

- Displays with the injections in the Graph pane in stacked view.
- Graph pane will scroll to the injection when selected in the Experiment pane.
- Shows the results for injections in the Peaks and Injections panes.



Hiding Injection Data

You can hide injection data from the view if needed.

• To hide injections - Select the injection rows you want to hide in the Experiment pane, then right click one and select Hide.

Experim	ent	- 8
Injection	Injection Name	Sample
1	System Suitability	System Suita
✓2	mAb 11 Blank_02	mAb 11 Blan
✓ 3	mAb 11 Ref. Std03	mAb 11 Ref.
√ 4	mAb 11 Prep 2016	mAb 11 Prep
✓ 5	mAb 11 Prep 2016	mAb 11 Prep
√ 6	mAb 11 Prep 2016	mAb 11 Prep
√ 7	mAh 11 Ref Std 07	mAb 11 Ref.
√8	🗙 Hide	mAb 11 Blan
	Clear	

Data for the injections will be hidden in all data views and results tables.

• To view hidden injections - Select View in the main menu and click Show Hidden. Hidden rows will become visible again in all panes, and are marked with an X in the Experiment pane.

Experime	ent	- 8
Injection	Injection Name	Sample
1	System Suitability	System Suita
✓ 2	mAb 11 Blank_02	mAb 11 Blan
×3	mAb 11 Ref. Std03	mAb 11 Ref.
√ 4	mAb 11 Prep 2016	mAb 11 Prep
✓ 5	mAb 11 Prep 2016	mAb 11 Prep
√6	mAb 11 Prep 2016	mAb 11 Prep
X 7	mAb 11 Ref. Std07	mAb 11 Ref.
✓ 8	mAb 11 Blank_08	mAb 11 Blan

• To unhide injections - Select the hidden row(s). Right click on one and click Unhide.

Switching Between Absorbance and Fluorescence Exposures (For Standard cIEF Runs only)

You can choose to display either absorbance or fluorescence data for your standard cIEF run in the Analysis Options pane. Changing detection methods is not an option for MauriceFlex cIEF runs.

NOTES:

You can also change the detection method and exposure in the analysis settings for the run. See "Detection Settings" on page 529 for more information.

Detection options in the Analysis pane are disabled during a run and when Compass for iCE is reanalyzing data.

• To change the detection method - Click the down arrow in the Type field and select Absorbance or Fluorescence.

5	
	*
Absorbance	×
Absorbance Fluorescence	~
Exp1 0.005s	~
Exp1 0.005s	~
Exp1 0.005s	\sim
Exp1 0.005s	~
	Absorbance Absorbance Fluorescence Exp1 0.005s Exp1 0.005s Exp1 0.005s

• To change the exposure used for the sample data displayed - Click the down arrow in one of the exposure fields and select an exposure setting.

a [®] Analysis Options	5	
Detection		*
Туре	Fluorescence	\sim
System	Exp1 3s	\sim
Method_Fl	Exp1 3s Exp2 5s	
Method_M458	Exp3 10s Exp4 20s FL458nm	•
PS_FI	Exp1 3s	\sim
PS_M458	Exp1 3s FL458nm	\sim

NOTES:

You'll only be able to choose exposures for the detection method currently selected.

The number of exposures taken and exposure times shown are specified in the method when you set up your batch. They can't be changed after the run has executed.

The Absorbance exposure at 0.005 seconds is an instrument default exposure setting for standard cIEF runs. No other absorbance exposures are available.

The FL458 nm fluorescence filter is only available on Maurice and Maurice C. systems with the option installed. It is only available on MauriceFlex systems with the option installed when running a batch with a cIEF cartridge.

Data Notifications and Warnings

If Compass for iCE detects a potential data issue, a notification or warning icon will display next to the injection row in the Experiment pane.



Manual correction of sample data notification - This means the sample data was manually changed by a user, for example to add or remove a sample peak. Roll your mouse over the icon to display the type of modification that was made.

- ·	system surrounty	~	system suitable
✓2	mAb 11 Blank	A2	mAb Method
✓ 3	mAb 11 Ref. Std.	A3	mAb Method
✓4	mAb 11 Prep 20160121	A4	mAb Method
✓ 5 Peak	Fit Manual rep 20160121	A4	mAb Method

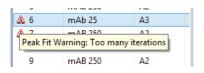
Markers warning - This means one or more of the pI markers may not be identified properly. You can fix this by manually identifying the pI marker using the steps in ""Step 2: Check Your pI Markers" on page 124. for standard cIEF runs and page 185 for MauriceFlex cIEF runs. Roll your mouse over the icon to display warning details.

W 10	mAb 25	A3
W 11	mAB 250	A2
🖗 12	mAb 25	A3
Markers E	rror: Not Found	A1
14	SS	A1
🚳 15	SS	A1

Manual correction of markers data notification - This means a user changed the pI marker data manually. Roll your mouse over the icon to display the type of modification that was made.

Injection	Sample	Location	Method	•
V 1	mAb11 Sample 1	A1	Method1	
2	mAh11 Sample 2	A2	Method1	
3	Markers Manual ble 3	A3	Method1	

Peak fit warning - Means that a peak can't be fit properly. This can sometimes be caused when a broad peak is fitted as multiple narrow peaks. Changing the peak width can help in this case. The warning is also caused by very small peaks around main peaks, or small peaks that are close to the end of the separation range. You can often fix this by removing the peak(s) using the steps in "Step 3: Checking Sample Peaks" on page 126 for standard cIEF runs and page 187 for MauriceFlex cIEF runs. Roll your mouse over the icon to display warning details.



Checking Your Results

If you see a data warning in the Experiment pane, these steps will also help you identify and correct any issues. Compass for iCE detects your sample protein and pI marker peaks and reports results automatically. But, we always recommend you review your data using the steps in this section as a good general practice to make sure your results are accurate. Please see the step by step procedure in "Checking Your Data" on page 123 for standard cIEF runs and page 184 for MauriceFlex cIEF runs to do this.If you see a data warning in the Experiment pane, these steps will also help you identify and correct any issues.

Naming Peaks

NOTE: Analysis screen options will let you add a new peak name, its pI, identifying color for peak tables and what injections it applies to. If you need to remove peak names, add peak name analysis settings groups or set pI ranges, you can do that in the run analysis settings. For more info go to "Peak Names Settings" on page 532.

Adding New Peak Names in the Analysis Options Pane

1. Click the down arrow in the Name field and select New.

Peak Na	mes		*
Name	I		~
pl	Peak1 Peak2		
Color	Peak3 Peak4		
Injects	Peak5		
	[New]	Modify	

2. Type a name.

Peak Names 🌣				
Name	mAB1 v			
pl	6.0			
Color				
Injects	All			
	Create			

3. Click in the pI field and enter the pI value of your sample protein.

Peak Na	mes	*
Name	mAB1	~
pl	6.78	
Color		
Injects	All	
	Create	2

4. Click on the Color field to display the color selection box.

Peak Na	imes 🎗	Color
Name pl Color Injects	mAB1 ~ 6.78	Basic colors:
	Create	Custom colors: Define Custom Colors >> OK Cancel

5. The color you pick is used to identify the sample protein peak in the Peaks and Injections panes in the Analysis screen. Click a color or define a custom color and click OK. The color selection will update in the field:

	*
mAB1	~
6.78	
All	
Create	
	All

6. Click in the Injects field:

To apply the new peak name to all injections - leave the default setting of All.

To apply the new peak name to specific injections - enter individual injections separated by commas (for example 2, 5, 8), a range of injections (for example 3-15) or a combination of both (for example 8, 10, 12-15). You can also click the tool tip for more examples.

Peak Na	imes	*
Name	mAB1	~
Cold Fo	ection descriptor r example, 3, 5-10	
Injects	All	
	Create	

To apply the new peak name to specific run data - type the first letter of a method, sample name, well or vial location. Compass for iCE will search the run data and display a list of matching options for you to choose from. Alternatively you can highlight the text in the Injects cell, hit **Delete**, then select an option from the drop down list.

Peak Na	Peak Names		Peak Na	mes	*
Name	Peak1	~	Name	Peak1	~
pl	6.0		pl	6.0	
Color			Color		
Injects N	Method		Injects		
	Method1			4	2
	Method2			All	
				Method1	
				Method2 System Suit	
				Peptide Mix	
				mAb	
			,	A1	
				A2	- E
h S/	N Resolutio	n	dth S/	N A3	Resolution

- Injection Applies the peak name to the injection.
- All Applies the peak name to all injections.
- **Methods** All methods in the run file display in the list. Selecting a method applies the peak name to all injections that used that method.
- **Sample names** All sample names in the run file display in the list, otherwise the default name of Sample shows. Selecting a sample name applies the peak name to all injections that used that sample name.
- Wells or vials The well or vial numbers currently selected will display in the list. Selecting a well or vial number applies the peak name to all injections that used that well or vial.

7. Click Create to save changes.

NOTE: To clear the new peak name information you've entered without saving changes, just delete the peak name in the Name field.

The named peak will be identified with a peak name label in the electropherogram and color-coded in the Peaks and Injections panes:



Adding Peak Names from the Graph or Peaks Table

NOTE: Analysis screen options will let you change an existing peak name, its pI, identifying color in peak tables and what injections it applies to. If you need to remove peak names, add peak name analysis settings groups or set pI ranges, you can do that in the run analysis settings. For more info go to "Manual Peak Integration" on page 547.

1. Right click the peak you want to name in the Graph or Peaks pane.

2. Select Name Peak.

	9.4	24 Zoom Out Remove Peak Hide Name Peak Add Peak		Peak Name	Modi	fy		
	% To	Add Peak Add Baseline Poi Remove Baseline Clear Copy		Ctrl+C	Peak4 New	esolution		
	Injections							
Injection	Injection Nam	e Sample	Pea	ak Name	Position	P	-	
2	Peptide Mix_0			1 Mkr 3.38		3.380		- 1
2	Peptide Mix_0			2 Peak2		3.794		10
2	Peptide Mix_0			3 Peak3		5.269		10
2	Peptide Mix_0			4 Mkr 7.00		7.000		2
2	Peptide Mix_0	-		5 Peak4		9.139		10
2	Peptide Mix_0	2 Peptide Mix			1711 ve Peak	0 / 2/	1067.4	1(
				Name	Peak	>	Peak2	
				Сору		Ctrl+C	Peak3 Peak4	
							New	

3. To use an existing peak name - select a name from the list.

To create a new peak name - select New. Type in a name for the peak. Click All to apply to all injections or Selected to apply only to the injections selected.

ô Add New Peak Name					
Peak Name:	Peak 5]		
Apply Name to:	All	○ Selected			
C	ОК	Cancel			

4. Click **OK**. If you want to add an identifying color or change the injections the new peak name applies to, you can do that in the Analysis Options pane.

Changing Peak Name Information

NOTE: Analysis screen options will let you change an existing peak name, its pI, identifying color for peak tables and what injections it applies to. If you need to remove peak names, add peak name analysis settings groups or set pI ranges, you can do that in the run analysis settings. For more info go to "Manual Peak Integration" on page 547.

1. In the Analysis Options pane, click the down arrow in the Name field and select an existing peak name.

Peak Na	mes 🎗
Name	Peak2 ~
pl	Peak2 Peak3
Color	Peak4 [New]
Injects	Peptide Mix
	Modify

2. Change the name, pI, color and injects as needed then click Modify.

Group Statistics

You can use the Grouping view to have Compass for iCE do a statistical analysis of named proteins in your injections (see "Manual Peak Integration" on page 547. for more info on setting named peaks up). Statistics for each protein are also plotted for easy comparison.

Using Groups

- 1. Groups are automatically created for injections that use the same sample name and method, so to use this feature, you need to make sure you've got sample names entered.
 - a. Go to the **Batch** screen.
 - b. Click the Sample ID cells in the Injection pane and type a name for any samples you want to calculate statistics for.

Injectior	ns 🛛 🔚 History 📑 Note	25			🕂 Add 📕 Replicate	🔀 Remove	Ð	- 8
	Sample ID	Location	Method	Notes				
1	Sample 1	A1	Method1					
2	Sample 2	A2	Method1					
3	Sample 3	A3	Method1					
4	Sample 4	A4	Method1					

2. Go back to the Analysis screen. Click View in the main menu and select Grouping.

View	/ Instrument	Window
•	Selected All	
۲	Markers Samples	
	Grouping	
	View Region Show Hidden	

NOTE: To turn Grouping off, select View in the main menu and deselect Grouping.

Viewing Sample Injection Groups

Compass for iCE automatically groups all injections using the same sample name together in the Injection Groups pane.

💷 In	jection Groups	
Sam	ple	Method
	System Suitability	System Suitablity
⊳	mAb 11 Blank (2)	mAb Method
⊳	mAb 11 Prep 20160121 (3)	mAb Method
\triangleright	mAb 11 Ref. Std. (2)	mAb Method

• To expand a group - Click the arrow next to a group to see the individual injections in the group and reported data for each

🔳 Inj	ection Groups	
Samp	ple	Method
	System Suitability	System Suitablity
\triangleright	mAb 11 Blank (2)	mAb Method
⊿	mAb 11 Prep 20160121 (3)	mAb Method
	🗸 mAb 11 Prep 20160121	mAb Method
	🗸 mAb 11 Prep 20160121	mAb Method
	🗸 mAb 11 Prep 20160121	mAb Method
\triangleright	mAb 11 Ref. Std. (2)	mAb Method

- To expand all groups Click Expand All (+) in the upper right corner of the pane.
- To collapse all groups Click Collapse All (-) in the upper right corner of the pane.

Viewing Statistics

Peak and Method Groups

The Peak Groups pane reports statistics for each named protein in every group. Each group shows the statistics for named proteins which includes average area, standard deviation, %CV and SEM (standard error measurement). The number in parenthesis after the sample name is the number of injections in the group.

Peak Groups Method Group	ps 📊 Group Plot							🕀 📄 % Total 🛛 🗛 🕅 🕞
Sample	Method	Injection	Name	Area	Std.Dev.	% CV	SEM	
> Peptide Mix (2)	Method1		Peak2	10292	42.81	0.4	30.27	1
> Peptide Mix (2)	Method1		Peak3	10496	67.27	0.6	47.56	i
> System Suit (2)	Method1		Peak1	22483	544.8	2.4	385.2	2

- To display results using area Click Area in the upper right corner of the pane.
- To display results using % total Click % Total in the upper right corner of the pane to display the calculated percent area for the named peak compared to the total area measured in the injection. This value results from dividing the individual peak area by the sum of all peak areas for the injection and multiplying by 100.
- To display results using % area Click % Area in the upper right corner of the pane to display the calculated percent area for the named peak compared to all named peaks. This value results from dividing the individual peak area by the sum of all named peak areas for the injection and multiplying by 100 (shown for named peak sample data only).
- To expand a group Click the arrow next to a group to see the individual injections in the group and reported data for each

Peak Groups Method G	roups 📊 Group Plot							🕀 📄 % Total 🛛 🗛 🖓 Area 🖓 🗖
Sample	Method	Injection	Name	Area	Std.Dev.	% CV	SEM	
 Peptide Mix (2) 	Method1		Peak2	10292	42.81	0.4	30.27	
Peptide Mix	Method1	2	Peak2	10322				
Peptide Mix	Method1	5	Peak2	10261				
> Peptide Mix (2)	Method1		Peak3	10496	67.27	0.6	47.56	
> System Suit (2)	Method1		Peak1	22483	544.8	2.4	385.2	

- To expand all groups Click Expand All (+) in the upper right corner of the pane.
- To collapse all groups Click Collapse All (-) in the upper right corner of the pane.

The Method Groups pane pivots the Peak Groups pane results to show statistics for named protein peaks in individual columns.

Sample	Method	Injection	Peak1:Area	Std.Dev.	%CV	SEM	Peak2:Area	Std.Dev.	%CV	SEM	Peak3:Area	Std.Dev.	%CV	SEM
> Peptide Mix (2)	Method1		0	0.0000	0.0	0.0000	10292	42.81	0.4	30.27	10496	67.27	0.6	47.56
> System Suit (2)	Method1		22483	544.8	2.4	385.2	0	0.0000	0.0	0.0000	0	0.0000	0.0	0.0000
> mAb (2)	Method2		0	0.0000	0.0	0.0000	0	0.0000	0.0	0.0000	0	0.0000	0.0	0.0000

Group Plots

The mean values for named peaks using the same method in each injection group are plotted in bar graphs with error bars showing the standard deviation in the Group Plots pane. You'll also get plots that compare samples using the same method in the run.



Hiding or Removing Injections in Group Analysis

Hidden injections are not included in injection groups. But, hiding injections gives you an easy way to reject individual injections from the statistical analysis. See Hiding Injection Data for details on how to do this.

Copying Results Tables and Graphs

You can copy and paste data and results tables into other documents, or save the electropherogram as a graphic file.

Copying Results Tables

- 1. Click in the Peaks or Injections pane.
- 2. Select one or multiple rows.
- 3. Select Edit in the main menu and click Copy, or right click on row(s) you selected and click Copy.
- 4. Open a document (Microsoft[®] Word[®], Excel[®], PowerPoint[®], etc.). Right click in the document and select **Paste**. Data for the rows selected will be pasted into the document.

Copying the Graph

- 1. Select the Graph pane.
- 2. Select Edit in the main menu and click Copy, or right click in the Graph pane and select Copy.
- 3. Select an image option (EMF, PNG or PDF) in the pop-up window, then click Copy.

Copy Graph	x						
Graph title:	11						
Metafile (EMF)							
🔘 Bitmap (P	Bitmap (PNG)						
Portable Document Format (PDF)							
Save	Copy Cancel						

4. Open a document (Microsoft[®] Word[®], Excel[®], PowerPoint[®], etc.). Right click in the document and select **Paste**. A graphic of the copied electropherogram will be pasted into the document.

Saving the Graph as an Image File

- 1. Select the Graph pane.
- 2. Select Edit in the main menu and click Copy, or right click in the Graph pane and select Copy.
- 3. Select an image option (EMF, PNG or PDF) in the pop-up window, then click Save.

Copy Graph		×					
Graph title:	11, 12						
Metafile (Metafile (EMF)						
🔘 Bitmap (P	Bitmap (PNG)						
Portable Document Format (PDF)							
Save	Сору	Cancel					

4. Select a directory to save the file to, enter a file name, then click OK.

Exporting Run Files

Results tables and raw plot data can be exported for use in other applications. Data is organized into these folders when exported:

- Absorbance data: <run file name>Export_ABS
- Fluorescence data:
 - <run file name>Export_FL when the same exposure is selected for all methods
 - <run file name>Export_FL_FL458nm when the FL458 nm filter is selected for all methods
 - <run file name>Export_FL_Various when both the native fluorescence and FL458 nm filter are selected

Exporting Results Tables

To export the information in the Peaks and Injections tables:

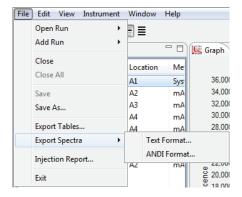
- 1. Click File in the main menu and click Export Tables.
- 2. Select a directory to save the files to and click OK. Data will be exported in .txt format.

NOTE: To exclude export of standards (pI markers) data or export results table data in .csv format, see "Setting Data Export Options" on page 760.

Exporting Raw Sample Electropherogram Data

To export raw sample plot and background data:

1. Click File in the main menu and click Export Spectra.



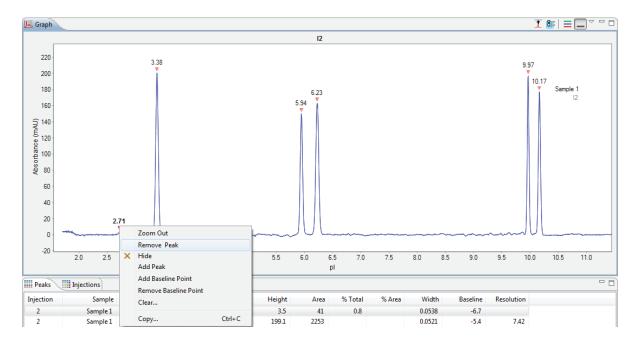
- To export data in .txt format Select Text Format. Data will be exported in one file for all injections.
- To export data in .cdf format Select ANDI Format. Data will be exported in one file per injection.
- 2. Select a directory to save the files to and click OK. Data will be exported in the selected format.

Changing Sample Protein Identification

Compass for iCE lets you customize what sample proteins are reported in the results tables by making manual adjustments in the electropherogram or Peaks table.

Adding or Removing Sample Data

- 1. Click Show Samples in the View bar.
- 2. Click Single View in the View bar.
- 3. Click on the row in the experiment pane that has the injection you want to correct, then click the Graph tab.
 - To remove a peak from the data Right click the peak in the electropherogram or Peaks table and select **Remove** peak. The software will no longer identify it as a sample peak in the electropherogram, and the peak data will be removed in the results tables.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

Experiment 🛛 🗖							
Sample	Location	Method					
Sample 1	A1	Method1					
Sample 1	A1	Method1					
Sample 1	A1	Method1					
Sample 1	A1	Method1					
Sample 1	A1	Method1					
	Sample Sample 1 Sample 1 Sample 1 Sample 1	Sample Location Sample1 A1 Sample1 A1 Sample1 A1 Sample1 A1 Sample1 A1					

• To add an unidentified peak to the data - Right click the peak in the electropherogram or peaks table and select Add Peak. The software will calculate and display the results for the peak in the results tables and identify the peak in the electropherogram.

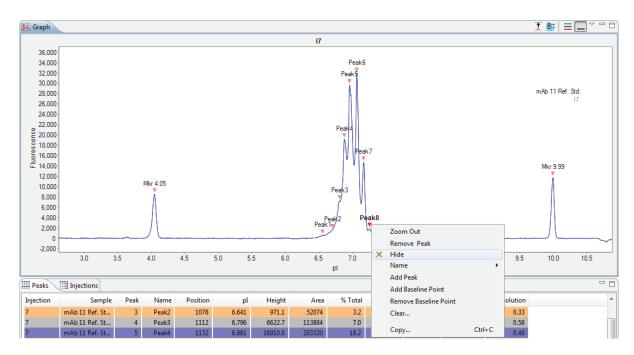
A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

NOTE: To remove sample peak assignments that were made manually and go back to the original peak data, right-click the peak in the electropherogram and select **Clear** for the current injection or **Clear** All for all injections in the batch.

Hiding Sample Data

You can hide the results for a sample protein in the results tables without completely removing it from the reported results.

- 1. Click Show Samples in the View bar.
- 2. Click Single View in the View bar.
- 3. Click on the row in the experiment pane that contains the injection you want to correct, then click the Graph tab.
- 4. Right click the peak in the electropherogram or Peaks table and select Hide. Compass for iCE will hide the peak data in the results tables.



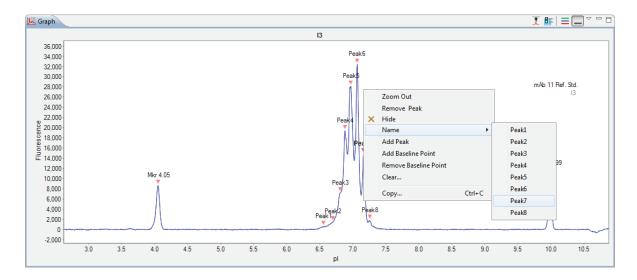
- 🛵 Graph I 🖩 | 🖃 🔲 🗸 🗖 17 36,000 34,000 Peak6 32,000 30.000 mAb 11 Ref. Std 28,000 26,000 24,000 22,000 cence 20,000 18,000 16,000 14,000 Mkr 9.99 12,000 Mkr 4.05 10,000 8 000 6.000 4.000 2,000 0 -2,000 3.0 3.5 4.0 4.5 5.0 5.5 6.0 6.5 7.0 7.5 8.0 8.5 9.0 9.5 10.0 10.5 pl - -Injections Peaks Injection Sample Peak Name Position pI Height Area % Total % Area Width Baseline Resolution nAb 11 Ref. St... 4 Peak3 1112 6.796 6622.7 113884 7.0 7.0 0.0913 -814.3 0.58 nAb 11 Ref. St... Peak4 1132 6.881 18910.8 18.2 18.2 0.0913 811.5 0.49 5 293320 Ab 11 Ref. St Peak5 1151 6 969 28269 513663 31.8 31.8 0 109 -809.3 0.45 mAb 11 Ref. St. 7 Peak6 1173 7.069 31250.3 432320 26.8 26.8 0.1095 -807.6 0.48 mAb 11 Ref. St... Peak7 1195 7.170 14454.9 177032 11.0 11.0 0.1049 806.9 0.49 X mAb 11 Ref. St. 9 Peak8 1216 7.265 1653.1 25742 1.6 1.6 0.1004 -807.2 0.49 10 Mkr 9.99 11786.9 136110 0.2099 -817.4 9.05 mAb 11 Ref. St... 1813 9,990 7
- 5. To view hidden peak data, click **View** in the main menu and click **Show Hidden**. Hidden peak data will display in the results table and be marked with an X.

6. To unhide a peak, right click on the peak in the electropherogram or peaks table and select Unhide.

Changing Peak Names for Sample Data

- If Compass for iCE did not automatically name a sample protein peak, you can do it manually.
- 1. Click **Show Samples** in the View bar.
- 2. Click Single View in the View bar.
- 3. Click on the row in the experiment pane that has the sample you want to correct, then click the Graph pane.

4. Right click the peak in the electropherogram or Peaks table and click **Name**, then select a name from the list. Compass for iCE will change the peak name in the electropherogram and results tables, and adjust peak names for other sample proteins accordingly.



NOTE: For details on how to specify peak name settings, see "Manual Peak Integration" on page 547.

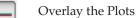
Changing the Electropherogram View

Options in the Graph pane let you zoom and rescale electropherograms, overlay or stack plots and change the peak and plot info displayed.

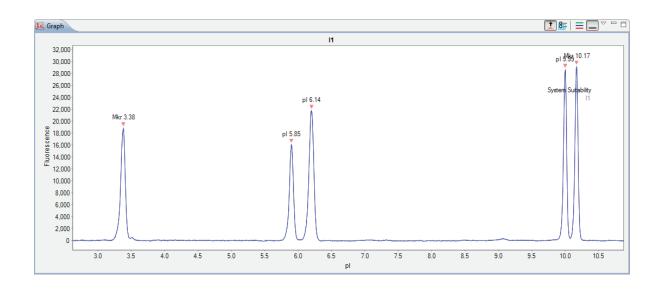
The Graph pane toolbar has these options:





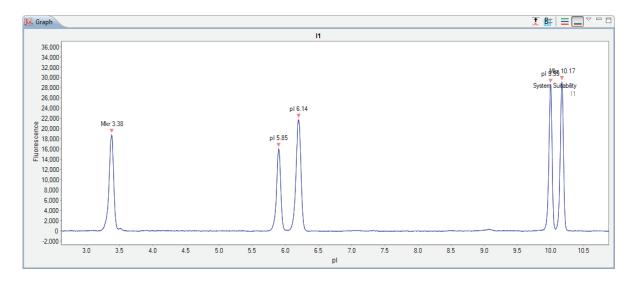


Autoscaling the Electropherogram



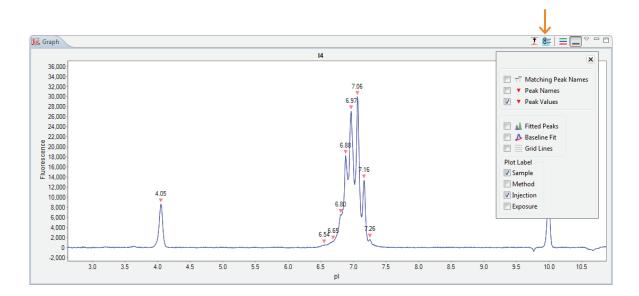
Click the Auto Scale button to scale the y-axis to the largest peak in the electropherogram.

Click the Auto Scale button again to return to default scaling.



Customizing the Data Display

You can customize electropherogram peak labels, plot labels and display options. To do this, just select the **Graph Options** button.

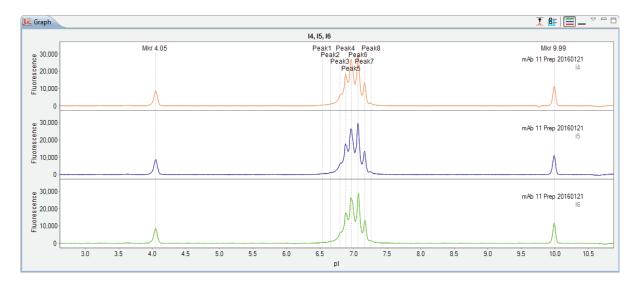


Peak Labels

You can customize the labels used to identify peaks in the electropherogram with these options:

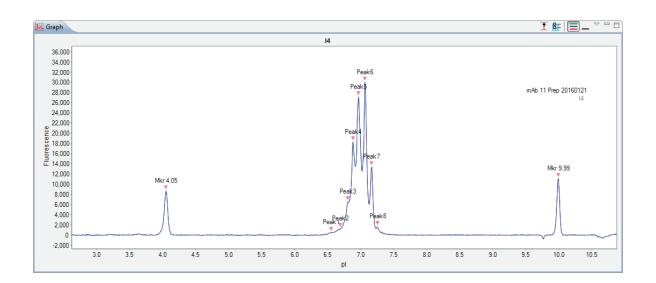


• Matching Peak Names - Checking this box will draw vertical lines through each named peak. Using this option with Stack the Plots or Overlay the Plots features is helpful for visually comparing your named peaks across multiple injections.



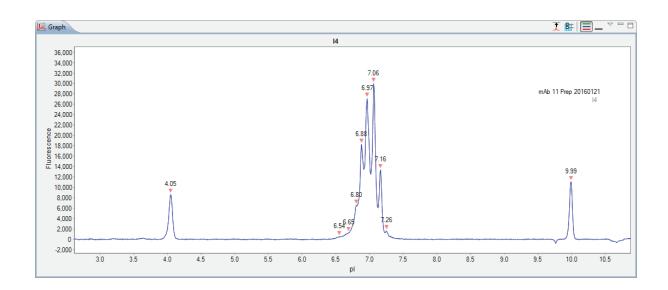
• Peak Names - Checking this box displays peak name labels on all named peaks in the electropherogram.

NOTE: If more than one peak label option is selected, peak name labels will always be used for named peaks.



• Peak Values - Checking this box will display the pI values on all peaks in the electropherogram.

NOTE: If more than one peak label option is selected, peak name labels will always be used for named peaks.



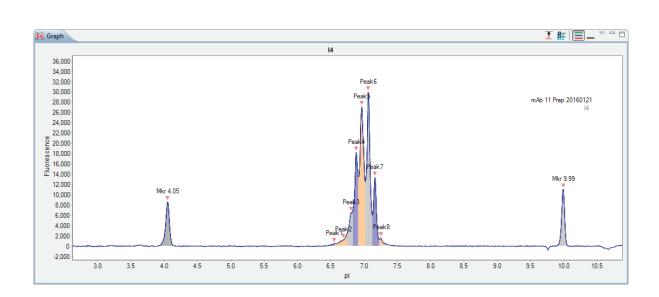
Baseline and Grid Options

You can view the calculated baseline fit, peak integration, show grid lines and overlay fluorescence and absorbance electropherograms with these options.

NOTE: See "Overlaying Fluorescence and Absorbance Electropherograms" on page 437 for information on the detection mode data overlay.

🗌 🔬 Fitted Peaks	🔲 🔬 Fitted Peaks
🔲 📣 Baseline Fit	🗌 📣 Baseline Fit
🗌 🌽 Overlay ABS	🗌 🌈 Overlay FL
Grid Lines	Grid Lines

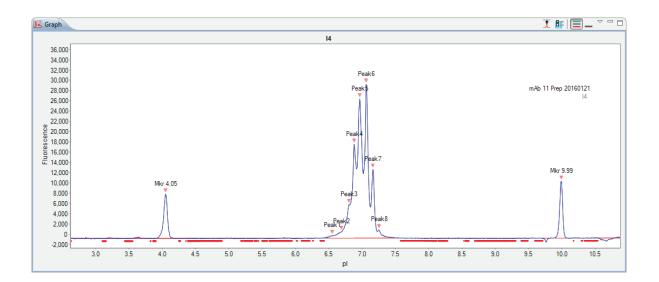
• Fitted peaks - Checking this box displays how the peaks were fit by the software. For cIEF runs, the software uses Gaussian Fit by default. For MauriceFlex cIEF runs, the software uses Dropped Line as the default.



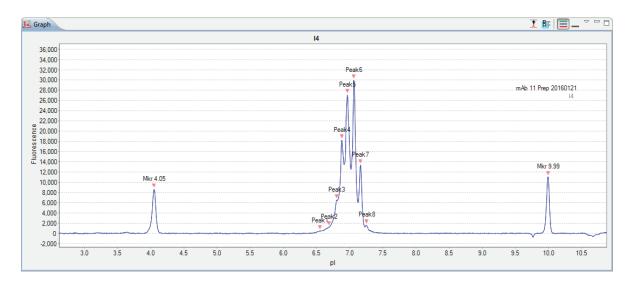
NOTE: This option is only available for sample data.

• **Baseline Fit** - Checking this box displays the calculated baseline for the peaks. Baseline points will also display for regions of the electropherogram considered to be at baseline.

NOTE: This option is only available for sample data.



• Grid Lines - Checking this box adds grid lines in the graph.



Plot Labels

You can customize the plot labels displayed on the electropherogram with these options.



Plot labels are shown in the upper right side of the graph.

- **Sample** Checking this box displays the sample name used for the injection. If sample names were entered with the batch, those names will display here. If not, Sample (default name) displays.
- Method Checking this box displays the method used for the injection.
- Exposure Checking this box display the exposure time(s) used for the data.
- Injection Checking this box displays the injection number. For example, I4 for injection 4 in the run.
- **Injection Name** Checking this box displays the injection name used for the injection. If injection names were entered with the batch, those names will display here. If not, the default name displays.

Chapter 18: cIEF Data Analysis | Changing the Electropherogram View

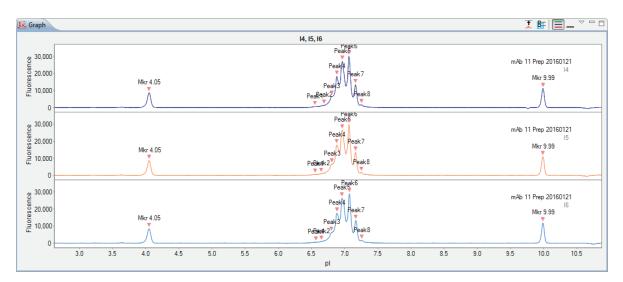
🖳 Graph I 🖭 🖃 🗕 🕴 🗖 🗖 Injection:6 40,000 Peak3k4 35,000 mAb 30,000 Method2 mAb_06 Pez 25,000 Exposure: 20s g Mkr 9.9 20,000 15.000 Mkr 4 05 15,000 10,000 5 000 0 3.5 4.0 4.5 5.0 5.5 6.0 6.5 7.0 7.5 8.0 8.5 9.0 9.5 10.0 10.5 pl

Here's an example of an electropherogram with all plot labels selected:

Stacking Multiple Electropherograms

You can stack electropherograms for multiple injections vertically in the Graph pane for comparison.

- 1. Click Single View.
- 2. Select multiple injection rows in the Experiment pane.
- 3. Click the Stack the Plots button. The individual electropherograms for each injection you selected will stack in the Graph pane.

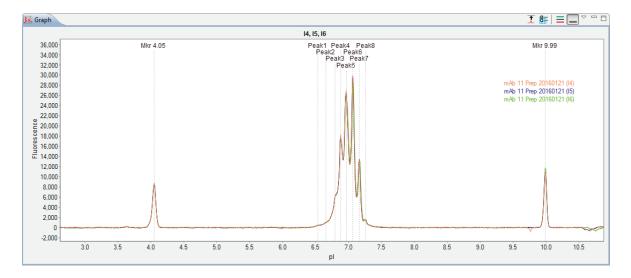


You can also customize the colors used for the stacked plot display. To do that go to "Setting up Automatic Injection Reports" on page 761.

Overlaying Multiple Electropherograms

You can overlay electropherograms for multiple injections on top of each other for comparison in the Graph pane.

- 1. Click Single View.
- 2. Select multiple injection rows in the Experiment pane.
- 3. Click the **Overlay the Plots** button. The individual electropherograms for each injection you selected will overlay in the Graph pane.



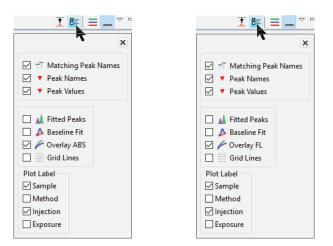
You can also customize the colors used for the overlay plot display. To do that go to "Setting up Automatic Injection Reports" on page 761.

Overlaying Fluorescence and Absorbance Electropherograms (standard cIEF runs only)

You can overlay standard Maurice cIEF fluorescence and absorbance electropherograms for the selected injection in the Graph pane . Due to the different detection methods you'll see slight differences between the two electropherograms when they're overlaid.

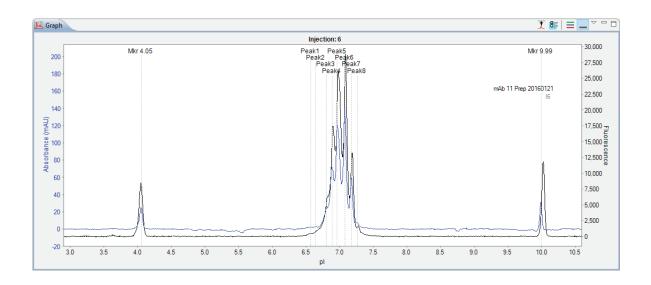
- 1. Click Single View.
- 2. Select an injection row in the Experiment pane.

3. Click Graph Options and select either Overlay Abs or Overlay FL. The option available depends on what detection mode is currently displaying.



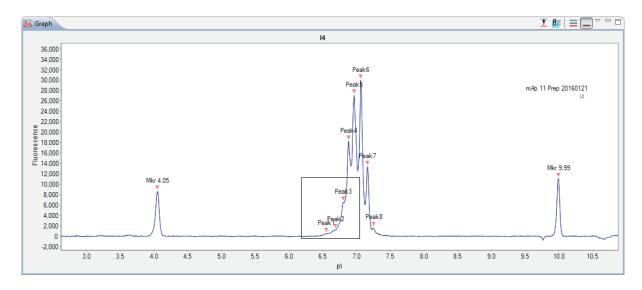
4. The electropherograms for each detection mode will overlay in the Graph pane, and the other detection mode y axis will display on the right.

NOTE: It's helpful to turn on Auto Scale when you're comparing the traces.

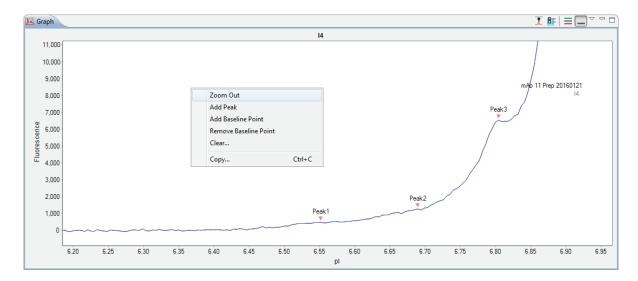


Zooming

To zoom in on a specific area of the electropherogram, hold the mouse button down and draw a box around the area with your mouse:

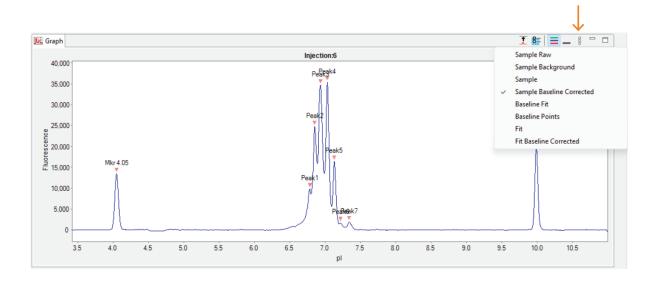


To return to default scaling, right click in the electropherogram and click Zoom Out.



Selecting Data Viewing Options

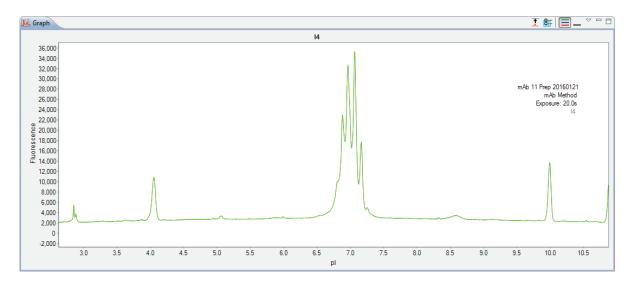
The graph view menu gives you multiple options for changing what type of electropherogram data is displayed. Just click **View Menu** in the graph pane toolbar to view the menu:



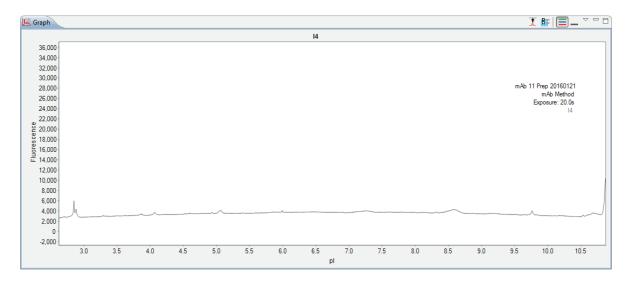
A check mark next to the menu option indicates it's currently selected, and you can select multiple options at once.

NOTE: Unless noted otherwise, graph view menu options are available for sample data only.

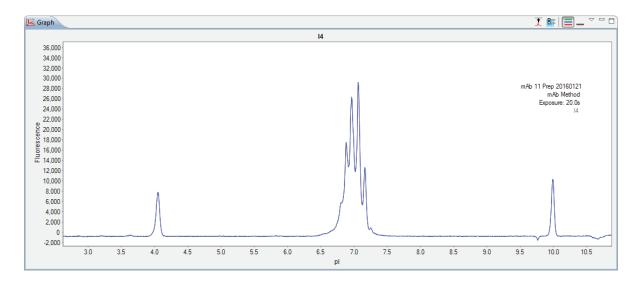
• **Sample Raw** - Clicking this option displays the basic detector values used to calculate peak absorbance or peak fluorescence depending on which mode is being viewed.



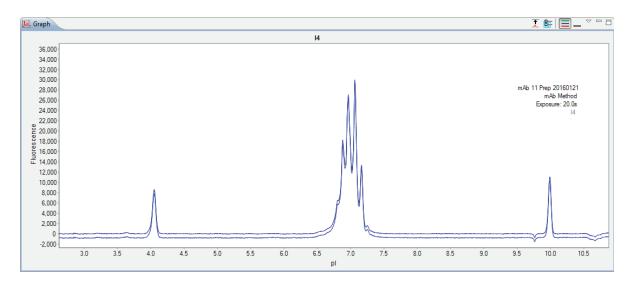
• **Sample Background** - Clicking this option displays the basic detector values used to calculate baseline absorbance or peak fluorescence depending on which mode is being viewed.



• Sample - Clicking this option displays raw, uncorrected sample data.

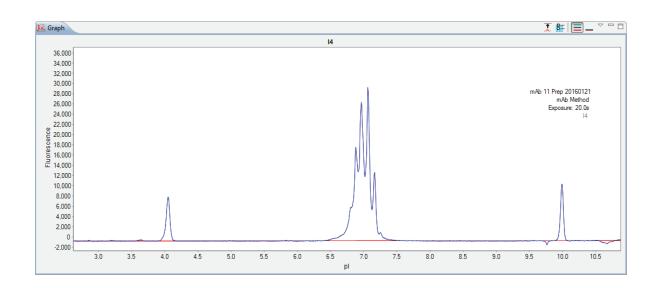


• **Sample Baseline Corrected** - Clicking this option displays sample data with the baseline subtracted (zeroed). This is the default view. In this next example, both Sample and Sample Baseline Corrected are selected.

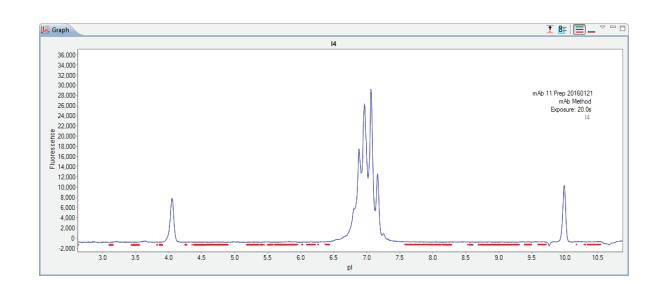


• **Baseline Fit** - Clicking this option displays the calculated baseline for the raw sample data. In this next example, both Baseline Fit and Sample are selected.

NOTE: This option is selected automatically when Baseline Fit is selected in graph options.

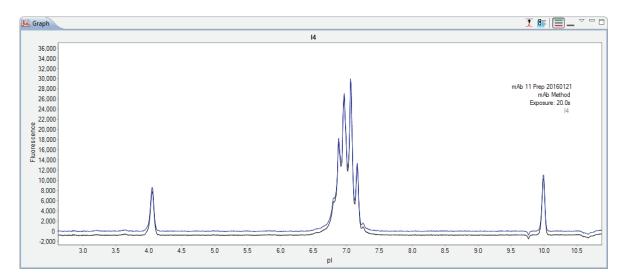


• **Baseline Points** - Clicking this option displays regions of the electropherogram considered to be at baseline. In this example, both Baseline Points and Sample are selected.

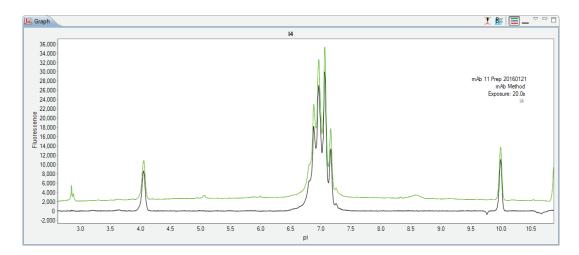


NOTE: This option is selected automatically when Baseline Fit is selected in graph options.

• Fit - Clicking this option displays the bounding envelope of the fitted peaks as calculated by the software for the raw sample data. In this example, both Fit and Sample Baseline Corrected are selected.



• Fit Baseline Corrected - Clicking this option displays the fitted peaks as calculated by the software for the sample baseline corrected data. In this example, both Fit Baseline Corrected and Sample Raw are selected, the fit plot is on the bottom.

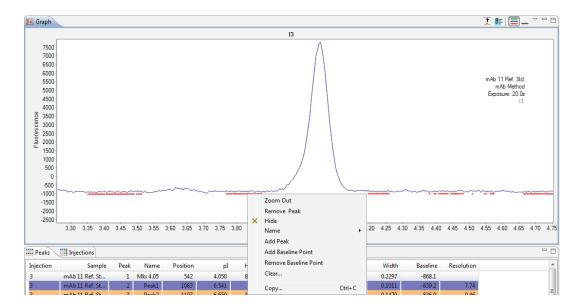


Adjusting the Baseline

Spline Baseline

Points in the baseline can be added or removed as needed.

- 1. Click the **Graph Options** button in the graph pane toolbar and check **Baseline Points**. This will display baseline points for the raw sample data.
- 2. Use the mouse to draw a box around the area you want to correct. This will zoom in on the area.
- 3. Right click a baseline point and select Add Baseline Point or Remove Baseline Point.



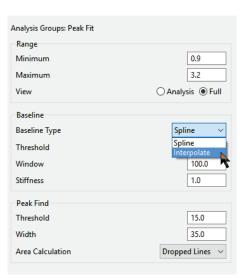
NOTE: To clear the manual addition or removal of baseline points and go back to the original view of the data, right click in the electropherogram and click **Clear All**.

Interpolated Baseline

Compass for iCE lets you interpolate baselines from the base of each peak for named peaks that use Dropped Lines integration.

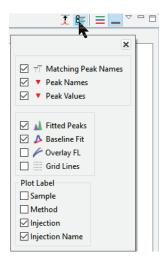
- 1. If you haven't already, name your peaks of interest.
- 2. Select Edit > Analysis, and click Peak Fit in the left sidebar.
- 3. Choose Interpolate as the Baseline Type if it isn't already selected.

NOTE: Baseline Type selection is only available when Dropped Lines is used for the Area Calculation.

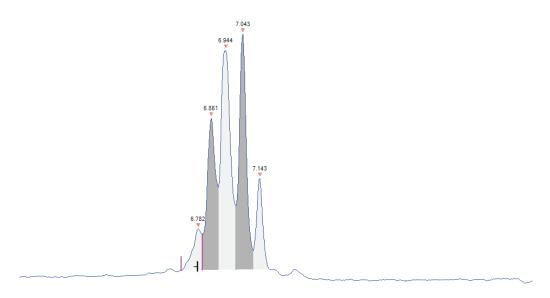


4. Click OK.

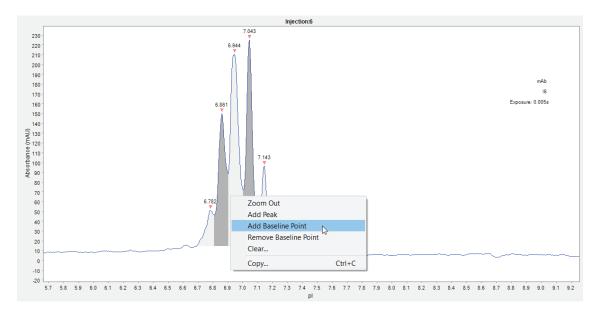
5. In the Analysis window Graph Pane, click Graph Options and select Fitted Peaks and Baseline Fit.



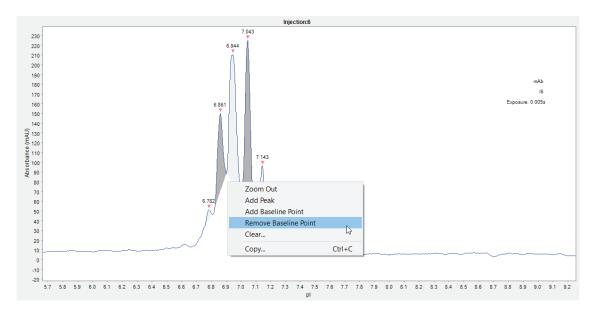
- 6. Select an injection in the Experiment pane.
- 7. Hover the mouse over the peak you want to adjust the baseline on. Two magenta bars will display that show the start and end points of the peak's integration.
- 8. To change the baseline, hover the mouse over one of the magenta bars. Then click the mouse and drag the bar to move it. The cursor changes to indicate which direction you can move the integration point. See "Manual Peak Integration" on page 547 for more info on integrating peaks.



9. Baseline points can also be added between two adjacent peaks for a better fit. Hover the mouse over the peak until the magenta bars appear, then right click and select Add Baseline Point.



10. To remove the baseline point, hover the mouse over the peak until the magenta bars appear, then right click and select **Remove Baseline Point**.

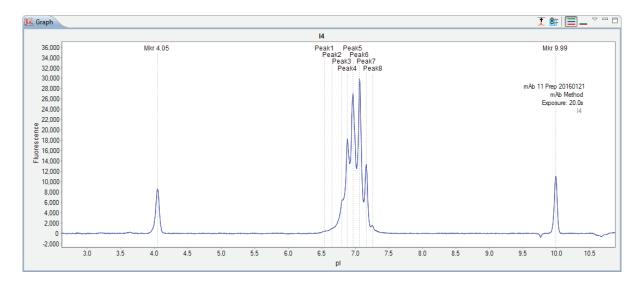


Selecting the Graph X-axis Range

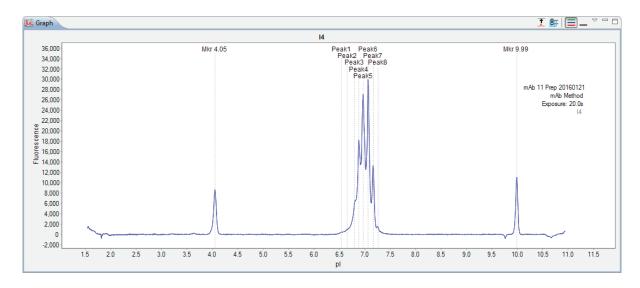
The pI range used for the x-axis can be changed. Just select View in the main menu and click View Region.

🔞 View Region
Range Analysis
Lower: 3,0 Upper: 10.5
OK Cancel

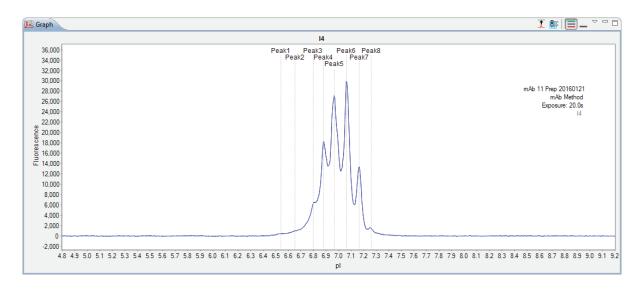
Analysis sets the x-axis range of the electropherogram to what is selected in the Peak Fit range settings. To view or change these analysis settings, go to Edit > Analysis and click Peak Fit in the left sidebar. In this example, the lower and upper range settings are 3.0 and 10.5.



• Full displays the entire separation in the electropherogram. This is the default setting. In this example the lower and upper range settings are 1.5 and 11.4.



• **Custom** lets you manually enter the lower and upper range settings to display in the electropherogram. In this example the lower and upper range settings are 5.0 and 9.0.



NOTE: You can change the default x-axis range that Compass for iCE uses. Go to "Advanced Analysis Settings" on page 551 for more info.

Closing Run Files

If more than one run file is open, you can close just one file or all the open files at the same time.

- To close one run file In the Experiment pane, click on one of the sample rows in the file. Then click File from the main menu and click Close.
- To close all open run files Select File from the main menu and click Close All.

Analysis Settings Overview

Compass for iCE has many analysis features and settings that you can change to enhance your run data.

Select Edit in the main menu and click Analysis. If more than one run file is open, select the run file you want to view settings for from the list:

Edit	View Instrument	Window	Help
	Cut	Ctrl+X	
	Сору	Ctrl+C	
	Paste	Ctrl+V	Graph
	Analysis	•	2016-01-21_09-46-39_mAb11_Prep20160121_QC(0)
	Preferences		2015-12-06_15-13-01_Maurice cIEF_Mab11_TechRep

This opens the Analysis window:

o Analysis: DemoData_Maurice clE			_		×
Detection	Advanced				
Peak Names Peak Fit Advanced pl Markers	Analysis Groups Advanced	Analysis Groups: Advanced pl Markers Peak Width Allowable Drift		15 100	
	Add Remove				
	Apply Override:				
	Apply To Group				
Import Evport		OK Carr		Apph	,
Import Export		OK Canc	el	Apply	/

To move between pages in the window, click on an option in the left sidebar.

- Detection (Standard Maurice cIEF runs only) Lets you choose to view absorbance or native fluorescence data for the run and choose data at different fluorescence exposures.
- **Peak Names** Lets you enter custom naming settings for sample proteins and have Compass for iCE automatically label the peaks in the run data.
- Peak Fit Lets you customize peak fit settings for sample data.
- Advanced Lets you customize analysis settings for the pI markers.
- pI Markers Lets you customize the pI markers and positions Compass for iCE identifies for each method in your run.

On all pages in the Analysis window:

- Click Import to import an analysis settings file. Go to "Importing Analysis Settings" on page 567 to learn how to do
 this.
- Click Export to export the current analysis settings file. Go to "Exporting Analysis Settings" on page 568 to learn how to do this.
- Click Apply to apply changes to the run file and update results in real time.
- Click OK to save changes to the run file and exit.
- Click Cancel to exit without saving changes.

Detection Settings

This page lets you see the absorbance and native fluorescence exposures taken during the run, and select different exposures for data viewing in the Analysis screen. Select **Edit** in the main menu and click **Analysis**, then click **Detection** in the left sidebar.

NOTES:

The FL458 nm fluorescence filter is only available on Maurice, Maurice C. and MauriceFlex systems with the option installed. On MauriceFlex, the filter can only be used with standard Maurice cIEF runs.

Absorbance detection is not available for MauriceFlex cIEF runs.

tection ak Names	Detection						
ak Fit vanced Markers	Method	Absorbance	○ Fluorescence				
Warkers	System	Exposure 1 0.005 seconds	Exposure 1 3 seconds	\sim			
	Method_FI	Exposure 1 0.005 seconds	Exposure 1 3 seconds	\sim			
	Method_M458	Exposure 1 0.005 seconds	Exposure 1 5 seconds FL458nm	\sim			
	PS_FI	Exposure 1 0.005 seconds	Exposure 1 3 seconds	\sim			
	PS_M458	Exposure 1 0.005 seconds	Exposure 1 3 seconds FL458nm	\sim			
nport Export			ОК	Cance	4	Appl	

of Default Analysis: Mauricel	lex clEF		×
Detection Peak Names	Detection		
Peak Fit			
Advanced pl Markers			
	IgG Exposure 1 0.2 seconds ~		
Import Exp	OK Cancel	Apply	

Changing the Detection Method (Standard Maurice cIEF runs only)

You can choose to display either absorbance or fluorescence data for your run in the Analysis screen.

1. Select **Edit** > **Analysis**, and select **Detection** in the left sidebar.

2. Select either the Absorbance or Fluorescence radio button.

Method	Abs	orbance		C	Fluorescend	e	
System	Exposure 1	0.005 seconds	~	Exposure 1	3 seconds		
Method_FI	Exposure 1	0.005 seconds	~	Exposure 1	3 seconds		
Method_M458	Exposure 1	0.005 seconds	~	Exposure 1	5 seconds	FL458nm	
PS_FI	Exposure 1	0.005 seconds	~	Exposure 1	3 seconds		
	and the second second second			-	-	F1 450	
PS_M458	Exposure 1	0.005 seconds	~	Exposure 1	3 seconds	FL458nm	
		0.005 seconds	~		3 seconds		
ection	() Abs		~				
ection Method	Abs Exposure 1	orbance	>) Fluorescent 3 seconds		~
ection Method System	O Abs Exposure 1 Exposure 1	orbance 0.005 seconds	> > >	Exposure 1 Exposure 1) Fluorescent 3 seconds	ce	~

Changing the Detection Exposure

You can change the exposure used for the sample data displayed in the Analysis screen.

NOTES:

You'll only be able to choose exposures for the detection method currently selected.

The number of exposures taken and exposure times shown are specified in the method when you set up your batch. They can't be changed after the run has executed.

The Absorbance exposure at 0.005 seconds is an instrument default exposure setting for Maurice cIEF runs. No other absorbance exposures are available.

1. Select Edit > Analysis, and select Detection in the left sidebar.

2. Click the arrow in the exposure button you want to change and select an exposure setting:

Method	⊖ Abs	orbance		۲) Fluorescence	
System	Exposure 1	0.005 seconds	\sim	Exposure 1	3 seconds	~
Method_FI	Exposure 1	0.005 seconds	\sim	Exposure 1	3 seconds	~
Method_M458	Exposure 1	0.005 seconds	\sim	Exposure 1 Exposure 2	5 seconds	
PS_FI	Exposure 1	0.005 seconds	\sim		10 seconds 20 seconds	
PS_M458	Exposure 1	0.005 seconds	\sim	Exposure 1	3 seconds FL458nm	~

3. Click OK to save changes. Sample data for the exposure selected will display in the Analysis screen.

Peak Names Settings

This page lets you view and change custom naming settings for sample proteins. Select **Edit** in the main menu and click **Analysis**, then click **Peak Names** in the left sidebar.

NOTE: Settings can be changed in the batch default analysis before you start the run, or in run files once they're completed. If you make analysis settings changes to an executing run, they won't be saved to the final run file.

etection	Peak Names					
eak Names						
eak Fit	Analysis Groups					
dvanced	Analysis oroups					
l Markers			Name	pl	Color	Range
	Add	Remove				
	Apply Settings					
	Apply To	Group				
				_		
					Add Rer	nove
	Add	Remove				

Peak Names Analysis Settings Groups

Peak name settings are saved as a group, and you can create multiple settings groups. Specific group settings can be applied to methods, injections, sample names or other attributes in the run data.

NOTE: Analysis settings are run-file specific. But, settings can be imported or exported for use with other run files. For more information see "Importing and Exporting Analysis Settings" on page 567.

Peak name groups are displayed in the analysis settings box:

Analysis Settings
System Suitability
mAb 11
Add Remove

There aren't any Compass for iCE default settings groups, but you can make changes to groups you've created and create new groups. To view settings for a group, click on the group name in the analysis settings box.

Creating a Peak Names Group

- 1. Select Edit > Analysis, and select Peak Names in the left sidebar.
- 2. Click Add under the analysis settings box.



3. Enter a new name for the group.

Analysis Settings	
mAb11	
Add Remove	

4. Click in the first cell in the Name column in the analysis settings peak table and enter a sample protein name.

ame	pI	Color	Range
ak1	6		0.05

5. Click in the first cell in the pI column and enter the expected pI for the sample protein.

lame	pI	Color	Range
eak1	5.55		0.05

6. Click in the first cell in the Color column, then click the button.

nalysis Settin	ıgs: mAb11		
Name	pI	Color	Range
Peak1	6.55	(0,1:	. 0.05

The color selection box displays:



7. The color you pick is used to identify the sample protein peak in the Peaks and Injections panes in the Analysis screen. Click a color or define a custom color and click OK. The color selection will update in the table:

nalysis Settir	ngs: mAb11		
Name	pI	Color	Range
Peak1	6.55		0.05

8. Click in the first cell in the Range column.

ialysis Settii	ngs: mAb11		
Name	pI	Color	Range
eak1	6.55		0.1

- 9. Enter a -/+ range for the pI entered. Compass for iCE will automatically name peaks found within this pI range. For example, if the pI entered is 2 and a 0.1 range is used, all peaks with pIs between 1.9 and 2.1 will be identified with this peak name and color.
- 10. To add another sample protein, click Add under the peak table. Repeat the previous steps for other sample proteins. In this example, eight proteins were entered:

Name	pI	Color	Range
eak1	6.55		0.1
eak2	6.65		0.1
Peak3	6.8		0.1
Peak4	6.9		0.1
Peak5	7		0.1
Рeakб	7.1		0.1
Peak7	7.2		0.1
Peak8	7.3		0.1

To remove a sample protein, select its row and click **Remove**.

11. Click OK to save changes.

Modifying a Peak Names Group

- 1. Select Edit > Analysis, then click Peak Names in the left sidebar.
- 2. Click on the group in the analysis settings box you want to modify.

Analysis Se System Si			
mAb 11			
	Add	Remove	-
	Add	Kemove	

- 3. Change the information in the analysis settings peak table as described in "Creating a Peak Names Group" on page 533.
- 4. Click **OK** to save changes.

Deleting a Peak Names Group

- 1. Select Edit > Analysis, then click Peak Names in the left sidebar.
- 2. Click on the group in the analysis settings box you want to delete and click Remove.

Analysis Settings	
System Suitability	
mAb 11	
Add Remove	

3. Click OK to save changes.

Applying Peak Names Groups to Run Data

1. Select Edit > Analysis, then click Peak Names in the options list.

2. Click on the group in the analysis settings box you want to apply to specific run data.

Analysis Settings	
System Suitability	
mAb11	
Add	Remove

3. Application of peak names groups to specific run data is done in the apply settings box. A default data set automatically gets created whenever you create a new group and it's applied to all injections in the run. You can either modify the default group or click Add under the box to create a new one.

Apply To	Settings
411 411	System Suitability mAb11
Ad	d Remove

4. Click the cell in the Apply To column, then click the down arrow.

Apply To		Settings
All		System Suitability
All	Ŧ	mAb11
System Suitablity mAb Method System Suitabiliti mAb 11 Blank mAb 11 Ref. Std. mAb 11 Prep 201 A1 A2 A3 A4 Custom Settings.	601	21 Remove

- 5. Select an option from the drop down list. This applies the peak names group selected to specific run data as follows:
 - All Selecting this applies peak names group settings to all injections.
 - **Methods** All methods in the run file display in the list. Selecting a method applies the group settings to all injections that used that method.
 - **Sample names** All sample names in the run file display in the list, otherwise the default name of Sample shows. Selecting a sample name applies the group settings to all injections that used that sample name.

- Wells or vials All well or vial numbers used in the run display in the list. Selecting a well/vial number applies the group settings to all injections that used that well/vial.
- **Custom settings** Lets you choose specific injections to apply the group settings to. When you select this in the list, a pop-up box displays to let you enter a specific injection number or range of injections:

Custom Settings	×
Enter injection descriptor	
Examples: 3, 5-10 Injection 3, and injections 5 through 10 6+8+10 Injections 6, 8, and 10	
	OK Cancel

6. If you need to change the peak names group used for a data set, click the cell in the **Settings** column and click the down arrow. Select a group from the drop down list.

Apply To	Settings
All	System Suitability
mAb Method	mAb11 +
	System Suitability
	mAb11
Add	Remove

- 7. Repeat the previous steps to apply other groups to specific run data.
- 8. To remove a data set, click on its cell in the Apply To column, then click Remove.

- 🛵 Graph I 🖩 📃 🗕 ~ - -Injection: 4 Peak1 Peak4 Peak8 Peak2 Peak6 Peak3 Peak7 Peak5 36,000 Mkr 4.05 Mkr 9.99 34,000 32,000 30,000 mAb 11 Prep 20160121 28,000 26,000 24.000 22,000 20,000 18 000 16,000 16,000 12,000 10,000 8,000 6.000 4,000 9.79.83 2,000 0 -2,000 3.0 3.5 4.0 4.5 5.0 5.5 6.0 6.5 7.0 7.5 8.0 8.5 9.0 9.5 10.0 10.5 pl - 0 Peaks III Injections Injection Injection Name Sample Peak Name Position Height Area % Total % Area Width S/N Baseline Resolution ^ pl mAb 11 Prep 2... Peak3 1144 6.805 6518.3 101900 7.2 0.0741 147.6 92.2 0.80 mAb 11 Prep 2... 4 7.2 18239.6 0.64 mAb 11 Prep 2... mAb 11 Prep 2.. Peak4 1163 6.880 17.0 0.0630 413.1 91.4 mAb 11 Prep 2. 451857 31.8 31.8 0.66 mAb 11 Prep 2. Peak5 1182 6.966 0.0889 613.6 90.3 27093.3 Peak6 1203 7.064 29972.8 399366 28.1 28.1 0.0556 678.8 88.9 0.79 mAb 11 Prep 2... mAb 11 Prep 2. mAb 11 Prep 2... mAb 11 Prep 2... 8 Peak7 1225 7.164 13384.4 162878 11.5 11.5 0.0514 303.1 86.9 1.11 mAb 11 Prep 2... mAb 11 Prep 2. Peak8 1262 7.312 328.9 9362 0.7 0. 0.1189 7.4 82.4 1.03 mAb 11 Prep 2... mAb 11 Prep 2. 10 1781 9.713 -28.1 0 0.0000 -0.6 106.2 23.76 ` > <
- 9. Click OK to save changes. Named peaks will be identified with a peak name label in the electropherogram and color-coded in the Peaks and Injections panes:

Peak Fit Analysis Settings

This page lets you view and change peak fit settings for sample data. Select **Edit** in the main menu and click **Analysis**, then click **Peak Fit** in the left sidebar:

NOTE: Settings can be changed in the batch default analysis before you start the run, or in run files once they're completed. If you make analysis settings changes to an executing run, they won't be saved to the final run file.

🐵 Analysis: DemoData_Maurice clE	F			– 🗆 X
Detection	Peak Fit			
Peak Names Peak Fit	Analysis Groups		Analysis Groups: Peak Fit	
Advanced pl Markers	Peak Fit		Range	
pi Markers			Minimum	2.0
			Maximum	11.0
			View	
			View	Analysis O Full
			Baseline	
	Add	Remove	Baseline Type	Spline 🗸
			Threshold	0.5
	Apply Default:		Window	25.0
	Peak Fit	~	Stiffness	
	Apply Override:		Stiffness	1.0
			Peak Find	
	Apply To 0	Group	Threshold	10.0
			Width	5.0
			Area Calculation	Gaussian Fit 🗸
			Area calculation	Guassiantin
	Add	Remove		
Import Export]		ОК С	ancel Apply

Range Settings

- **Minimum** The pI value below which peaks won't be identified. This value is also used as the default lower pI range for data displayed in the electropherogram.
- **Maximum** The pI value above which peaks won't be identified. This value is also used as the default upper pI range for data displayed in the electropherogram.
- View Sets the default range to either Full or Analysis for the electropherogram x-axis range in the View Region window (select View in the main menu and click View Region).

🍖 View Region	×
Range O Analysis	om
Lower: 3.0 Upper:	10.5
OK Car	ncel

• Analysis sets the x-axis range of the electropherogram to the Peak Fit range minimum and maximum settings in the electropherogram. This is the default setting.

• Full displays the entire separation range of the run data in the electropherogram.

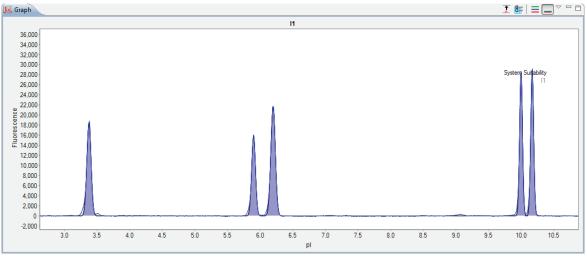
Baseline Settings

These settings apply to spline baselines only.

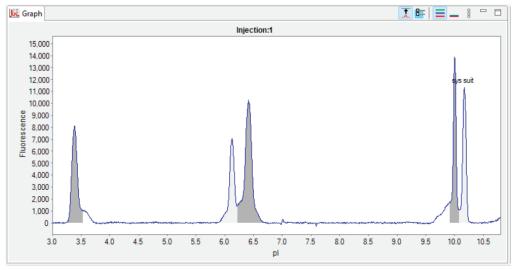
- Threshold The variance, or roughness, in a baseline data segment below which a point is called part of the baseline.
- Window How long baseline data segments are expected to be in pixels. Shorter segments let the baseline follow plateau sections of the signal.
- **Stiffness** The amount the baseline is allowed to vary from a straight line. Settings between 0.1 and 1.0 make the baseline fit closer to a straight line. Settings from 1.0 to 10.0 will make the baseline fit follow the data more closely.

Peak Find Settings

- **Threshold** The minimum signal to noise ratio required for a peak to be identified. A setting of 1.0 will detect many peaks, a setting of 10.0 will detect fewer peaks.
- Width The approximate peak width (at full width half max) in pixels used to detect peaks. The minimum value for this setting is 3.0. Larger widths help eliminate the detection of shoulder and noise peaks.
- Area Calculation Two fits are used, either Gaussian Fit or Dropped Lines. These settings can be changed before or after the run is finished.
 - For Standard cIEF applications, peak area is calculated using Gaussian Fit by default. For MauriceFlex cIEF applications, peak area is calculated using Dropped Line by default.



Standard Maurice cIEF Default Peak Fit



MauriceFlex cIEF Default Peak Fit

• The Dropped Line method type of area calculation is also often called the perpendicular drop method. This is the preferred method when peaks overlap or are close to each other. It draws two vertical lines from the left and right bounds of the peak down to the x-axis and then measures the total area bounded by the signal curve, the x-axis (y=0 line), and the two vertical lines.

Peak Fit Analysis Settings Groups

Peak fit settings are saved as a group, and you can create multiple settings groups. Specific group settings can then be applied to methods, injections, sample names or other attributes in the run data.

NOTES:

We recommend using the Compass for iCE default values for peak fit analysis settings. These settings are included in the default Peak Fit group.

Analysis settings are run-file specific. But, settings can be imported or exported for use with other run files. For more information see "Importing and Exporting Analysis Settings" on page 567.

Peak fit groups are displayed in the analysis settings box:

Analysis Setti	ngs		
Peak Fit			
	Add	Remove	

The Peak Fit group shown contains the Compass for iCE default analysis settings. You can make changes to this group and create new groups. To view settings for a group, click on the group name.

Creating a New Peak Fit Group

- 1. Select Edit > Analysis, and select Peak Fit in the left sidebar.
- 2. Click Add under the analysis settings box. A new group will be created:

Peak Fit		
Peak Fit 2		

3. Click on the new group and enter a new name.

Analysis Settings	
Peak Fit	
Product A	
Add Remove	
Add Remove	

4. Change the settings in the range, baseline or peak find boxes as needed.

Analysis Settings: Product A	
Range	
Minimum	6.3
Maximum	7.4
View	Analysis
Baseline	
Threshold	0.5
Window	25.0
Stiffness	0.1
Peak Find	
Threshold	10.0
Width	10.0
Area Calculation	Dropped Lines 🔻

5. To use the new group as the default peak fit settings for the run file data, click the arrow in the drop down list next to Apply Default, then click the new group from the list. Peak fit settings in the new group will then be applied to the run data.

Apply Default:				
Peak Fit	•			
Peak Fit				
Product A				
Apply To	Settings			
Add	Remove			

6. Click **OK** to save changes.

Changing the Default Peak Fit Group

- 1. Select **Edit** > **Analysis**, and select **Peak Fit** in the left sidebar.
- 2. Click the arrow in the drop down list next to Apply Default, then click a new default group from the list.

Apply Default:				
Peak Fit	•			
Peak Fit				
Product A				
Apply To	Settings			
Add	Remove			

3. Click OK to save changes. Peak fit settings in the group selected will be applied to the run data.

Modifying a Peak Fit Group

- 1. Select Edit > Analysis, and click Peak Fit in the left sidebar.
- 2. Click on the group in the analysis settings box you want to modify.

Analysis Set	tings			
Peak Fit				
Product A				
	Add	Remove	:	

3. Change the settings in the range, baseline or peak find boxes as needed.

Analysis Settings: Product A	
Range	
Minimum	6.3
Maximum	7.4
View	🔘 Analysis 🔘 Full
Baseline	
Threshold	0.5
Window	25.0
Stiffness	0.1
Peak Find	
Threshold	10.0
Width	10.0
Area Calculation	Dropped Lines 🔻

4. Click OK to save changes. The new peak fit settings will be applied to the run data.

Deleting a Peak Fit Group

- 1. Select Edit > Analysis, and select Peak Fit in the left sidebar.
- 2. Click on the group in the analysis settings box you want to delete and click Remove.

Analysis Settings	
Peak Fit	
Product A	
Add Remove	

3. Click **OK** to save changes.

Applying Peak Fit Groups to Specific Run Data

- 1. Select Edit > Analysis, and select Peak Fit in the left sidebar.
- 2. Click on the group in the analysis settings box you want to apply to specific run data.

Analysis	Settings		
Peak F			
Produ	ct A		
	Add	Remove	

3. Application of analysis groups to specific run data is done in the override box. Click Add under the override box. A default override data set will be created from sample information found in the run file.

Apply Override:	
Apply To	Settings
Method1	Product A
Add	Remove

4. Click the cell in the Apply To column, then click the down arrow.

Apply Override:		
Apply To		Settings
Method1	Ŧ	Product A
Method1 mAb11 Sample 1 mAb11 Sample 2 mAb11 Sample 3 mAb11 Sample 4 mAb11 Sample 5 mAb11 Sample 6 mAb11 Sample 7		
A1 A2 A3	Ŧ	Remove

- 5. Select an option from the drop down list. This applies the settings group selected to specific run data as follows:
 - **Methods** All methods in the run file display in the list. Selecting a method applies the group settings to all injections that used that method.
 - **Sample names** All sample names in the run file display in the list, otherwise the default name of Sample shows. Selecting a sample name applies the group settings to all injections that used that sample name.

- Wells or vials All well or vial numbers used in the run display in the list. Selecting a well/vial number applies the group settings to all injections that used that well/vial.
- **Custom settings** Lets you choose specific injections to apply the group settings to. When you select this in the list, a pop-up box displays to let you enter a specific injection number or range of injections:

🄞 Custom Settings	X
Enter injection descriptor	
Examples: 3, 5-10 Injection 3, and injections 5 through 10 6+8+10 Injections 6, 8, and 10	OK Cancel

6. If you need to change the analysis group used for a data set, click the cell in the **Settings** column and click the down arrow. Select a group from the drop down list.

Apply To	Settings
A1	Product A 👻
	Peak Fit
	Product A

- 7. Repeat the previous steps to apply other groups to specific run data.
- 8. To remove a data set, click on its cell in the Apply To column, then click Remove.
- 9. Click **OK** to save changes.

Manual Peak Integration

Compass for iCE lets you manually integrate peaks in individual electropherograms.

1. Select **Edit** > **Analysis**, and select **Peak Fit** in the left sidebar.

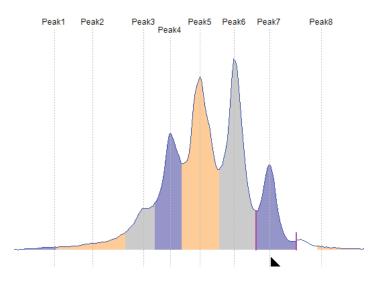
2. Select Dropped lines as the area calculation if it isn't already selected.

Peak Find	
Threshold	15.0
Width	150.0
Area Calculation	Dropped Lines 🗸
	₹

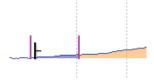
3. Select Fitted Peaks in the Graph Options.



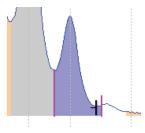
- 4. Select an injection in the Experiment pane.
- 5. Hover the mouse over the peak you want to adjust. Two magenta bars will display that indicate the start and end points of its integration.



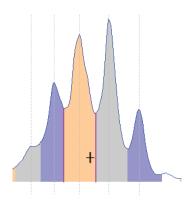
- 6. To change the integration, hover the mouse over either of the magenta bars. Then click the mouse and drag the bar to move it.
 - If the cursor changes to **b** this is the peak start for the peak on the right.



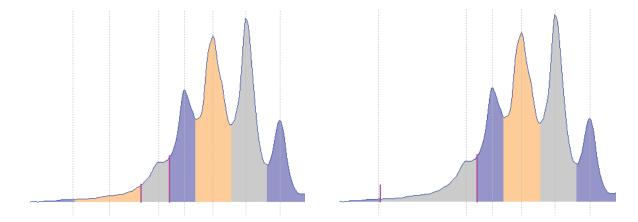
• If the cursor changes to \dashv this is the peak end for the peak on the left.



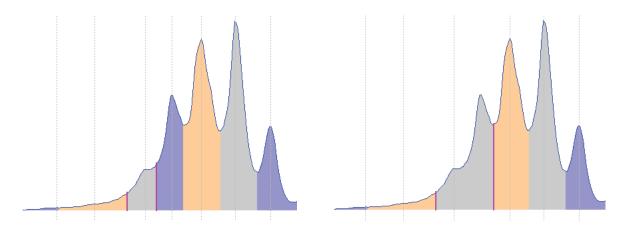
• If the cursor changes to **+** this is a joint boundary for the peaks on the left and right.



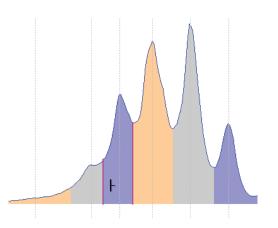
In the example below, we moved the start and end points of the peak to include more area under the peak:



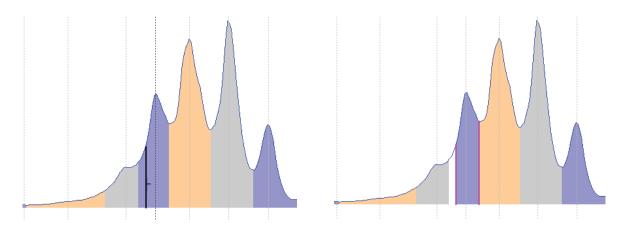
You can also combine peaks by dragging the magenta lines left or right:



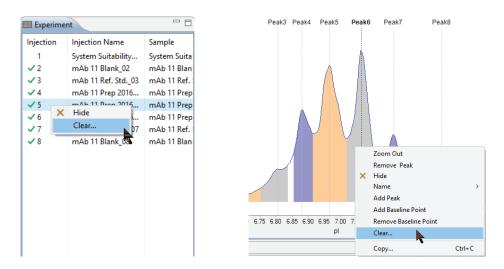
You can also separate areas between peaks. Whenever you have a + cursor between two peaks that aren't baseline resolved, move the mouse slightly to the right or left until you get the | or - cursor.



Click and hold the mouse. A black drop line will display indicating where the current peak start or end point is. While holding the mouse, drag the cursor to the right or left to move the start or end point to where you want it, then release the mouse.



7. To remove the manual integration settings, right click on the graph or on the injection in the Experiment pane and select **Clear**.



Advanced Analysis Settings

This page lets you view and change analysis settings for the pI marker data. Select **Edit** in the main menu and click **Analysis**, then click **Advanced** in the left sidebar:

NOTE: Settings can be changed in batches before you start the run, or in run files once they're completed. If you make analysis settings changes to an executing run, they won't be saved to the final run file.

log Analysis: DemoData_Maurice clE	F			_		Х
Detection	Advanced					
Peak Names Peak Fit Advanced pl Markers	Analysis Groups Advanced Add Apply Default: Advanced Apply Override:	Remove Sroup	Analysis Groups: Advanced pl Markers Peak Width Allowable Drift		15	
Import Export			ОК	Cancel	Apply	

pl Markers Settings

- **Peak Width** The approximate width (at full width half max) used to filter out absorbance and fluorescence artifacts which improves recognition of pI markers.
- Allowable Drift The distance the pI marker(s) are expected to move compared to the position entered on the pI Markers page. This setting helps with recognition of the pI marker.

Advanced Analysis Settings Groups

Advanced analysis settings are saved as a group, and you can create multiple settings groups. Specific group settings can be applied to methods, injections, sample names or other attributes in the run data.

NOTES:

We recommend using the Compass for iCE default values for advanced analysis settings. These settings are included in the default Advanced group.

Analysis settings are run-file specific. But, settings can be imported or exported for use with other run files. See "Importing and Exporting Analysis Settings" on page 567 for more info.

Analysis groups are displayed in the analysis settings box:

Analysis Settings	
Advanced	
Add	Remove

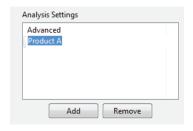
The Advanced group shown contains the Compass for iCE default analysis settings. You can make changes to this group and create new groups. To view settings for a group, click on the group name.

Creating a New Analysis Group

- 1. Select Edit > Analysis, and select Advanced in the left sidebar.
- 2. Click Add under the analysis settings box. A new group will be created:

Analysis Settings	
Advanced	
Advanced 2	
Add Remove	

3. Click on the new group and enter a new name.



4. Change the settings in the Markers box as needed.

Analysis Settings: Product A	
pl Markers	
Peak Width	15
Allowable Drift	100

5. To use the new group as the default analysis settings for the run data, click the arrow in the drop down list next to Apply Default, then click the new group from the list. Analysis settings in the new group will then be applied to the run data.

Apply Default:	
Advanced	•
Advanced	
Product A	
Apply To	Settings
Add	Remove

6. Click **OK** to save changes.

Changing the Default Analysis Group

- 1. Select Edit > Analysis, and select Advanced in the left sidebar.
- 2. Click the arrow in the drop down list next to Apply Default, then click a new default group from the list.

Apply Default:	
Advanced	-
Advanced	
Product A	
Apply To	Settings
Add	Remove

3. Click OK to save changes. Analysis settings in the group selected will be applied to the run data.

Modifying an Analysis Group

- 1. Select **Edit** > **Analysis**, and select **Advanced** in the left sidebar.
- 2. Click on the group in the analysis settings box you want to modify.

Advanced			
Product A			

3. Change the settings in the Markers box as needed.

Analysis Settings: Product A	
pl Markers	
Peak Width	15
Allowable Drift	100

4. Click OK to save changes. The new analysis settings will be applied to the run data.

Deleting an Analysis Group

- 1. Select Edit > Analysis, and select Advanced in the left sidebar.
- 2. Click on the group in the analysis settings box you want to delete and click Remove.

3. Click **OK** to save changes.

Applying Analysis Groups to Specific Run Data

- 1. Select Edit > Analysis, and select Advanced in the left sidebar.
- 2. Click on the group in the analysis settings box you want to apply to specific run data.

Analysis Settings	
Advanced	
Product A	
Add Remove	

3. Application of analysis groups to specific run data is done in the override box. Click **Add** under the override box. A default override data set will be created from sample information found in the run file.

Apply Override:	
Apply To	Settings
System Suitablity	Product A
Add	Remove

4. Click the cell in the Apply To column, then click the down arrow.

Apply Override:	
Apply To	Settings
ystem Suitablity 👻	Product A
System Suitability mAb Method System Suitability mAb 11 Blank mAb 11 Ref. Std. mAb 11 Prep 20160 A1 A2 A3 A4 Custom Settings	121 Remove

- 5. Select an option from the drop down list. This applies the settings group selected to specific run data as follows:
 - **Methods** All methods in the run file display in the list. Selecting a method applies the group settings to all injections that used that method.
 - **Sample names** All sample names in the run file display in the list, otherwise the default name of Sample shows. Selecting a sample name applies the group settings to all injections that used that sample name.

- Wells or vials All well or vial numbers used in the run display in the list. Selecting a well/vial number applies the group settings to all injections that used that well/vial.
- **Custom settings** Lets you choose specific injections to apply the group settings to. When you select this in the list, a pop-up box displays to let you enter a specific injection number or range of injections:

🄞 Custom Settings	X
Enter injection descriptor	
Examples: 3, 5-10 Injection 3, and injections 5 through 10 6+8+10 Injections 6, 8, and 10	OK Cancel

6. If you need to change the analysis group used for a data set, click the cell in the **Settings** column and click the down arrow. Select a group from the drop down list.

Apply To	Settings
mAb 11 Prep 201	Product A 👻
	Advanced
	Product A

- 7. Repeat the previous steps to apply other groups to specific run data.
- 8. To remove a data set, click on its cell in the Apply To column, then click Remove.
- 9. Click **OK** to save changes.

pl Markers Analysis Settings

This page lets you define the pI and position of the pI Markers you're using in your samples. Select **Edit** in the main menu and click **Analysis**, then click **PI Markers** in the left sidebar.

NOTE: Settings can be changed in the batch default analysis before you start the run, or in run files once they're completed. If you make analysis settings changes to an executing run, they won't be saved to the final run file.

💮 Analysis: DemoData_Maurice clE	F		– 🗆 X
Detection	pl Markers		
Peak Names Peak Fit Advanced pl Markers	Analysis Groups Standards	Standards Peaks	
	Method2_Standards Standards 3	pl 4.9 7	Position 200 800
	Add Remove Apply Default: Standards Apply Override:		
	Apply To Group Method2 Method2_Standa Method1 Standards 3		
	Add Remove	Add	Remove
Import Export		ОК	Cancel Apply

pl Markers Analysis Settings Groups

pI marker settings are saved as a group, and you can create multiple settings groups. Specific group settings can be applied to methods, injections, sample names or other attributes in the run data.

NOTES:

We recommend using the Compass for iCE default values. These settings are included in the default Markers group.

When you edit the pI markers in the method for a batch, Compass for iCE automatically creates a Markers group in the pI Markers Analysis settings for you.

Analysis settings are run-file specific. But, settings can be imported or exported for use with other run files. For more information see "Importing and Exporting Analysis Settings" on page 567.

Markers groups are displayed in the analysis settings box:

Analysis Settings	
Method1_Markers	
Add	Remove

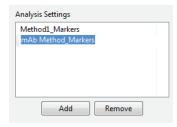
The Markers group shown uses the Compass for iCE default settings. You can make changes to this group and create new groups. To view settings for a group, click on the group name.

Creating a New Markers Group

- 1. Select Edit > Analysis, and select pI Markers in the left sidebar.
- 2. Click Add under the analysis settings box. A new group will be created:

/lethod1_Marker	rs	
lethod1_Marker	rs 2	
Add		Remove

3. Click on the new group and enter a new name.



- 4. The default Maurice and MauriceFlex cIEF pI marker pI and position values are already populated in the pI Marker Peaks table. If you'd like to use these values, skip to the next step. If you're using different markers, here's how to change the values:
 - a. Click in the first cell in the pI column in the table and enter the pI for the marker.

pI Markers		
Peaks		
pI	Position	
4.05	250	
10.17	1,800	
	Add	Remove
	Add	Incinove

b. Click in the first cell in the Position column and enter a value for the marker.

pI	Position	
4.05	500	
10.17	1,800	

NOTE: pI marker peak positions are relative to each other. Only the difference in position is used to help identify them. When entering pI marker peak information for the first time, review the marker data in the Analysis screen to find the correct peak positions.

- c. Repeat the steps above for the remaining markers in the table.
- To add another marker Click Add under the table, then change the information in the new row.
- To remove a marker Select its row and click Remove.

5. To use the new group as the default settings for the run, click the arrow in the drop down list next to Apply Default, then click the new group in the list. The settings in the new group will then be applied to the run data.

Analysis Settings
Method1_Markers
mAb Method_Markers
Add Remove
Apply Default:
Method1_Markers 🗸
Method1_Markers mAb Method_Markers

6. Click **OK** to save changes.

Changing the Default Markers Group

- 1. Select Edit > Analysis, and click pI Markers in the left sidebar.
- 2. Click the arrow in the drop down list next to Apply Default, then select a new default group from the list.

Analysis Settings
Method1_Markers
mAb Method_Markers
Add Remove
Apply Default:
Method1_Markers 🔹
Method1_Markers
mAb Method_Markers

3. Click OK to save changes. Analysis settings in the group selected will be applied to the run data.

Modifying a Markers Group

1. Select Edit > Analysis, and click Markers in the left sidebar.

2. Click on the group in the analysis settings box you want to modify.

Analysis Settings	
Method1_Markers	
mAb Method_Markers	
Add Remove	

- 3. Change the marker info as needed as in Creating a New Markers Group.
- 4. Click OK to save changes. The new analysis settings will be applied to the run data.

Deleting a Markers Group

- 1. Select Edit > Analysis, and click pI Markers in the left sidebar.
- 2. Click on the group in the analysis settings box you want to delete and click Remove.

Analysis Settings	
Method1_Markers	
mAb Method_Markers	
Add Remove	

3. Click **OK** to save changes.

Applying Markers Groups to Specific Run Data

- 1. Select Edit > Analysis, and select pI Markers in the left sidebar.
- 2. Click on the group in the analysis settings box you want to apply to specific run data.

Analysis Settings
Method1_Markers
mAb Method_Markers
Add Remove

3. Application of markers groups to specific run data is done in the override box. Click Add under the override box. A default override data set will be created from sample information found in the run file.

Apply Override:					
Apply To	Settings				
System Suitablity	mAb Method_M				
Add	Remove				

4. Click the cell in the Apply To column, then click the down arrow.

Apply Override:	
Apply To	Settings
ystem Suitablity 👻	mAb Method_M
System Suitablity mAb Method System Suitability mAb 11 Blank mAb 11 Ref. Std. mAb 11 Prep 201601 A1 A2 A3 A4	.21
Custom Settings	Remove

- 5. Select an option from the drop down list. This applies the settings group selected to specific run data as follows:
 - **Methods** All methods in the run file display in the list. Selecting a method applies the group settings to all injections that used that method.
 - **Sample names** All sample names in the run file display in the list, otherwise the default name of Sample shows. Selecting a sample name applies the group settings to all injections that used that sample name.
 - Wells or vials All well or vial numbers used in the run display in the list. Selecting a well/vial number applies the group settings to all injections that used that well/vial.
 - **Custom settings** Lets you choose specific injections to apply the group settings to. When you select this in the list, a pop-up box displays to let you enter a specific injection number or range of injections:

o Custom Settings	×
Enter injection descriptor	
Examples: 3, 5-10 Injection 3, and injections 5 through 10 6+8+10 Injections 6, 8, and 10	
	OK Cancel

6. If you need to change the analysis group used for a data set, click the cell in the **Settings** column and click the down arrow. Select a group from the drop down list.

Apply To	Settings
mAb Method	Method_Markers +
	Method1_Markers mAb Method_Markers

- 7. Repeat the previous steps to apply other groups to specific run data.
- 8. To remove a data set, click on its cell in the Apply To column, then click Remove.
- 9. Click **OK** to save changes.

Injection Reports

You can export PDF files of the raw and analyzed data, IV plot, peaks table, sample and system info for individual or all injections in a run file. You can also export the run history with all analysis events.

NOTES:

You can have Compass for iCE generate reports for you automatically at the end of each run. See ""Setting up Automatic Injection Reports" on page 761 for more information.

Any time a new report is run, it's saved in a separate run folder. Existing reports aren't overwritten.

- 1. Click **File > Open Run** and select a run file.
- 2. If you want reports for all injections, skip to the next step. If you only want reports for certain injections, in the Experiment pane:
 - **To select sequential injections:** Select the first injection, then hold the **Shift** key and select the last injection you want a report for. This selects all rows between the two injections.
 - To select specific injections: Hold the Ctrl key and select just the injections you want reports for.

- 3. Select File from the main menu in either screen and click Injection Report.
 - File
 Edit
 View
 Instrument

 Open Run
 ▶

 Add Run
 ▶

 Close
 Close

 Close All
 >

 Save
 Save

 Save As...
 Export Tables...

 Export Spectra
 ▶

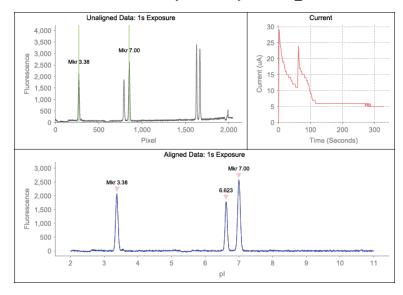
 Injection Report...
 Exit
- 4. In the Injection Reports window:
 - a. Choose either Selected injections or All injections.
 - b. Select Analysis log if you want a run history report with all analysis events.
 - c. Select Batch Report if you want to include the sample and method details for each injection in the batch.
 - d. Select Fitted peaks if you want to show peak fitting in the electropherograms.
 - e. Report PDFs generated by Compass for iCE are secured by default, which means they can be viewed and printed but not modified or renamed. Uncheck **Secure PDF** if you don't want to generate a secure report. To learn more about permissions for secured vs. unsecured reports, see page 800.
 - f. The report name defaults to the run file name. If you want to change it, type in the Report Name box to make updates.
 - g. Click OK.

ô Injections Report		×
Run: DemoData_Maurice	IEF	
◯ Selected injections (1)	Analysis log	
All completed injections	(6) 🗌 Batch report	
	Fitted peaks	
Secure PDF		
Report Name:		Browse
DemoData_Maurice clEF		
Location: C:\Users\Docume	ents\Compass for iCE	
	ОК	Cancel

5. The individual injection report PDF(s) and a combined injection report PDF are exported to the Runs folder in the Compass for iCE directory. They'll be in a folder with the report name used in the prior step. When the reports are done, the folder opens for you automatically.

Desktop	^	Name ^	Date modified	Туре	Size
Documents		DemoData_Maurice clEF_combined_injection_report.pdf	7/20/2020 9:41 PM	Adobe Acrobat D	566 K
Add-in Express		DemoData_Maurice clEF_Injection_1_System Suit.pdf	7/20/2020 9:41 PM	Adobe Acrobat D	95 K
Adobe		DemoData_Maurice clEF_Injection_2_Peptide Mix.pdf	7/20/2020 9:41 PM	Adobe Acrobat D	93 K
CIDFont		DemoData_Maurice clEF_Injection_3_mAb.pdf	7/20/2020 9:41 PM	Adobe Acrobat D	103 K
CMap		DemoData_Maurice clEF_Injection_4_System Suit.pdf	7/20/2020 9:41 PM	Adobe Acrobat D	95 K
Compass for iCE		DemoData_Maurice clEF_Injection_5_Peptide Mix.pdf	7/20/2020 9:41 PM	Adobe Acrobat D	93 K
Batches		DemoData_Maurice clEF_Injection_6_mAb.pdf	7/20/2020 9:41 PM	Adobe Acrobat D	103 K
New Batches					
Runs					

Example Analysis and Injection Report



Uncontrolled Injection 1: System Suit_01

Fluorescence Peaks: 1s Exposure											
Peak	Name	Position	pl	Height	Area	%Total	%Area	Width	S/N	Baseline	Resolution
1	Mkr 3.38	270.1	3.380	2067.9	28502.1			0.0807	112.6	52.7	
2		791.0	6.623	1785.9	22868.7	100.00		0.0750	97.2	41.1	24.56
3	Mkr 7.00	851.9	7.000	2580.0	39590.9			0.0898	140.5	41.0	2.71

Uncontrolled Injection 1: System Suit_01

Sample Information		
Injection Name	System Suit_01	
Sample ID	System Suit	
Location	Plate Well A1	
Batch Name	Aaurice cIEF	
Run Started	Tue 12:11 PM Oct 27, 2015 PDT	
Run Completed	Tue 1:17 PM Oct 27, 2015 PDT	
Date Acquired	Tue 12:17 PM Oct 27, 2015 PDT	
Run Error	None	
Reinjection	No	

Injection Conditions				
Guaranteed Injection	Yes			
On-board Mixing	Off			
Focus Period 1	1500V for 1.0 min			
Focus Period 2	3000V for 4.5 min			
Sample Load Duration	90.0 Seconds			
pl marker 1	3.38			
pl marker 2	7.0			
Tray Temperature	Not Available			

Maurice Settings							
Model	Maurice OBM						
Instrument S/N	kf1004						
Software Version	Compass for iCE 4.0.0, Build ID: 0222						
Firmware Version	2.0.2015.10.20.20.35.52.681a5af						
Tray Type	48 vials						
Cartridge Type							
Cartridge S/N							
Cartridge Expiration							
Injections Remaining							
Batches Remaining							

Importing and Exporting Analysis Settings

The analysis settings in a run file can be exported as a separate file. This allows the same analysis settings to be imported into other batches or run files at a later time, rather than you having to re-enter them manually.

Importing Analysis Settings

NOTE: Importing an analysis settings file populates the settings in all analysis pages.

- 1. Open the run file or batch you want to import analysis settings to.
- 2. Select Edit in the main menu and click Default Analysis (Batch screen) or Analysis (Analysis screen).
- 3. Click **Import** on any page.

4. Select a settings file (*.settings) and click OK. The imported settings will display in all analysis pages.

Exporting Analysis Settings

NOTE: Exporting an analysis settings file exports the settings in all analysis pages.

- 1. Open the run file or batch you want to export analysis settings from.
- 2. Select Edit in the main menu and click Default Analysis (Batch screen) or Analysis (Analysis screen).
- 3. Click Export on any page. The following window displays:

→ JRichards → My Documents →				✓ ✓ Search Run:		
Organize 🔻 New folder					855 -	•
 Favorites Inks My Documents Add-in Express Adobe Clients Clients New Batches New Batches 2016-01-21_09-46-39_mAbil1_Prep201 78664 P3 IS 2015-11-30_16-49-49_MW 	=	Name 1015-12-06_15-13-01_Maurice dEF_Mabl 2016-01-21_09-46-39_mAb11_Prep201601 70664 P3 15 2015-11-30_16-49-49_MW La	1/24/2016 1:04 PM	Type File folder File folder File folder	Size	
File name: mAb11 cIEF.settings Save as type: Analysis Settings (*.settings)						
Save as type: Analysis Settings (*.settings)						

- 4. The default directory is Compass for iCE/Runs. Change the directory if needed.
- 5. Enter a file name and click Save. The settings will be saved as a *.settings file.

Chapter 19: MauriceFlex Fractionation Data Analysis

Chapter Overview

- Analysis Screen Overview
- Opening Run Files
- How Run Data is Displayed
- Viewing Run Data
- Data Notifications and Warnings
- Checking Your Results
- Naming Peaks
- Copying Results Tables and Graphs
- Exporting Run Files
- Changing Sample Protein Identification
- Adding or Removing Fractions Data
- Changing the Electropherogram View
- Closing Run Files
- Analysis Settings Overview
- Detection Settings
- Peak Names Settings
- Peak Fit Analysis Settings
- Manual Peak Integration

- Advanced Analysis Settings
- pI Markers Analysis Settings
- Injection Reports
- Importing and Exporting Analysis Settings

NOTE: To learn more how to analyze data from a cIEF run using the fractions from a MauriceFlex Fractionation batch, check out the MauriceFlex cIEF Fractionation Method Development Guide.

Analysis Screen Overview

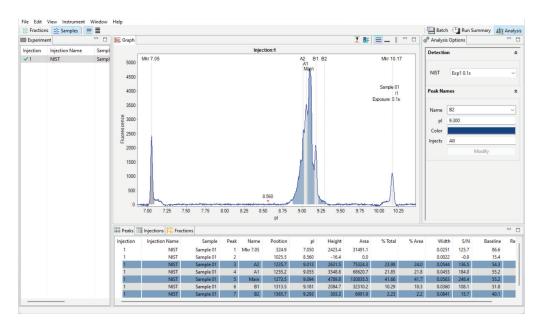
You can use the Analysis screen to view electropherograms and tabulated results for your injections. If any post-run analysis is needed, you can do it here too. To get to this screen, click the **Analysis** screen tab:

Batch 🕒 Run Summary 🚛 Analysis

Analysis Screen Panes

The Analysis screen has four panes:

- **Experiment** Lists the injection number, sample IDs, sample locations and methods for each injection in the run and lets you get a quick view of method parameters.
- Graph Displays the electropherograms for sample proteins or pI markers.
- Peaks Shows the tabulated results for sample proteins and pI markers.
- **Injections** Displays a list of the sample proteins Compass for iCE names automatically using the user-defined peak name analysis parameters.
- Fractions Displays the fractions that each sample peak was collected
- Analysis Options Lets you view absorbance or fluorescence data for the run and view, change and add new custom peak name settings.



Chapter 19: MauriceFlex Fractionation Data Analysis | Analysis Screen Overview

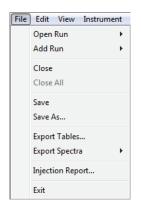
Software Menus Active in the Analysis Screen

These main menu items are active in the Analysis Screen:

- File
- Edit
- View
- Instrument (when Compass for iCE is connected to MauriceFlex.)
- Window
- Help

File Menu

These File menu options are active:



- Open Run Opens a run file.
- Add Run Lets you open and view other run files besides the one that's already open.
- Close Closes the run file currently being viewed.
- Close All Closes all open run files.
- Save/Save As If you made changes in the Analysis screen before you went to the Run Summary screen, this saves your changes to the run file.
- Export Tables Exports the results for all injections in the run in .txt format.
- Export Spectra Exports the raw and analyzed data traces and background for each injection in the run in .txt or .cdf format.
- **Injection Report** Exports the raw and analyzed data, IV plot, peaks table, sample and system info for individual injections as PDF files. You can also export the run history with all analysis events.
- Exit Closes Compass for iCE.

Edit Menu

These Edit menu options are active:

Edit	View	Instrument	Windo
	Cut	Ct	rl+X
	Сору	Cti	l+C
	Paste	Ct	rl+V
	Analysi Prefere		

- **Copy** Lets you copy data shown in the graph, lane, peaks or injections panes. See "Copying Results Tables and Graphs" on page 594 for more information.
- Analysis Displays the analysis settings used to analyze the run data and lets you change them as needed. See "Analysis Settings Overview" on page 620 for more information.
- **Preferences** Lets you set and save your preferences for data export, graph colors, grouped data and Twitter settings. See Chapter 21: "Setting Your Preferences" for more information.

View Menu

These View menu options are active:

View	Instrument	Window
• 5	Selected	
ļ	All	
• F	ractions	
5	Samples	
(Grouping	
N	/iew Region	
5	Show Hidden	

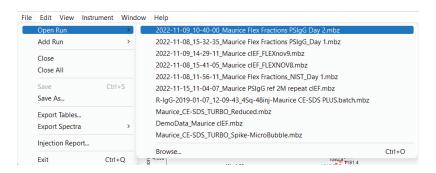
- Selected (Single View) Displays the data for only the injections selected.
- All (Multiple View) Displays data for all injections so you can scroll through them.
- **Fractions** Lets you view and set pI markers for the sample injection and mobilization electropherograms where you can view the protein mobilizing out of the capillary.
- Samples Lets you view and name peaks for the focused sample injection.
- Grouping Displays data for injection groups.
- View Region Lets you change the x-axis range of the data displayed.
- Show Hidden- Shows injections that are hidden from the data view.

Opening Run Files

You can open one run file or multiple files at the same time to compare information between runs.

Opening One Run File

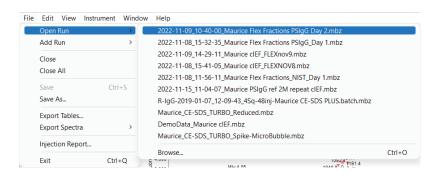
1. Select File in the main menu and click Open Run.



2. A list of the last 10 runs opened will display. Select one of these runs or click **Browse** to open the Runs folder and select a different file.

Opening Multiple Run Files

1. To open the first run file, select File in the main menu and click Open Run.



2. A list of the last 10 runs opened will display. Select one of these runs or click **Browse** to open the Runs folder and select a different file.

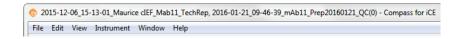
3. To open another run file, select File in the main menu and click Add Run.

e Edit View Instr	ument Windo	w Help
Open Run	>	
Add Run	>	2022-11-08_15-32-35_Maurice Flex Fractions PSIgG_Day 1.mbz
Close		2022-11-09_14-29-11_Maurice cIEF_FLEXnov9.mbz
Close All		2022-11-08_15-41-05_Maurice cIEF_FLEXNOV8.mbz
Close All		2022-11-08_11-56-11_Maurice Flex Fractions_NIST_Day 1.mbz
Save	Ctrl+S	2022-11-15_11-04-07_Maurice PSIgG ref 2M repeat cIEF.mbz
Save As		R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch.mbz
Export Tables		Maurice_CE-SDS_TURBO_Reduced.mbz
Export Spectra	>	DemoData_Maurice cIEF.mbz
Export opectio		Maurice_CE-SDS_TURBO_Spike-MicroBubble.mbz
Injection Report		 Decum
Exit	Ctrl+O	Browse

4. A list of MauriceFlex Fractionation runs will display. Select one of these runs or click **Browse** to open the Runs folder and select a different file. If the run selected is not a MauriceFlex Fractionation run, an alert will appear.



5. When a run is added, its data appends to the open run file and displays as a second set of injections in all screen panes. The second run file name also appears in the title bar:



6. Repeat the last two steps to add additional runs.

How Run Data is Displayed

Data in the run file is organized for easy review.

Experiment Pane: Batch Injection Information

The Experiment pane lists the injection performed followed by the fractions collected in the run. Injection information includes the sample used, the sample location and the method used when the Samples view is selected. Fractionation information includes an image number collected during the mobilization series and the time the mobilization electropherogram image was taken and can be viewed when the Fractions view is selected.

Experime	ent			- E
Injection	Injection N	Sample	Location	Method
1	NIST	Sample 01	A1	NIST
TO	00:00 mins			NIST
T1	01:00 mins			NIST
T2	02:00 mins			NIST
T3	03:00 mins			NIST
🍼 T4	04:00 mins			NIST
T5	05:00 mins			NIST
T6	06:00 mins			NIST
77 💟	07:00 mins			NIST
Т8	08:00 mins			NIST
Т9	09:00 mins			NIST
T10	10:00 mins			NIST
T11	11:00 mins			NIST

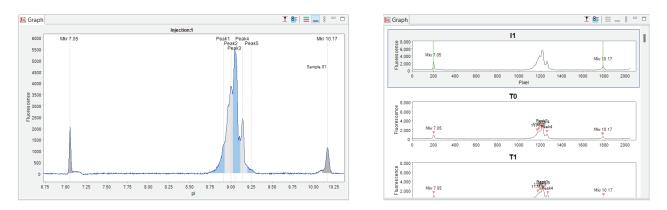
- To view all columns Use the scroll bar or click Maximize in the upper right corner.
- To resize columns Roll the mouse over a column border until the sizing arrow appears, then click and drag to resize.
- To view method parameters Hover the mouse over a method name.

Experim	nent			🗖 🗖 💹 Graph
Injection	Injection Name	Sample	Location	Method 11
1	Sample 01_01	Sample 01	A1	NIST @ 8 000 1
T0	00:00 mins			RIST
T1	01:00 mins			Separation: 10.0 min 500 Volts, 10.0 min 1000 Volts, 25.0 min 1500 Volt
T2	02:00 mins			Detection: 1 Exposure Sample Load (s): 30
T3	03:00 mins			pl Markers: 7.05, 10.17
Т4	04.00 mins			NIST III

NOTE: Data notification icons will display in the Injection column if Compass for iCE detects a potential analysis issue or data was manually modified by the user. For more information see "Data Notifications and Warnings" on page 411.

Graph Pane: Electropherogram Data

The Graph pane displays sample and mobilization electropherograms. When the Fractions view is selected, the sample injection appears first (I1) followed by mobilization electropherograms (T0, T1, T2, etc). The electropherogram viewed depends on the view options you've selected.



You can get more info on graph view options in "Changing the Electropherogram View" on page 601.

Peaks Pane: Calculated Results

The Peaks pane shows the tabulated results for your sample proteins or pI markers. Each row in the table has the individual results for each peak detected in an injection. Results shown will either be for one injection or multiple injections, samples or pI markers depending on the view options you're using. Check out "Analysis Options Pane" on page 580 for more info.

Peaks	Injections	Fractions												-	- 0
Injection	Injection N	Sample	Peak	Name	Position	pl	Height	Area	% Total	% Area	Width	S/N	Baseline	Resoluti	
1	Sample 01	Sample 01	1	Mkr 7	196.8	7.050	2089.8	24085.7			0.0211	96.9	153.2		
1	Sample 01	Sample 01	2	Peak1	1146.5	8.910	1371.7	43234.2	10.19	10.2	0.0446	63.6	60.4	33.32	
1	Sample 01	Sample 01	3	Peak2	1193.3	9.002	3882.5	14723	34.71	34.7	0.0777	180.1	58.6	0.88	
1	Sample 01	Sample 01	4	Peak3	1216.5	9.047	5489.5	17228	40.61	40.6	0.0603	254.6	56.6	0.39	
1	Sample 01	Sample 01	5	Peak4	1263.5	9.139	2435.5	53548.1	12.62	12.6	0.0423	113.0	51.5	1.06	
1	Sample 01	Sample 01	6	Peak5	1322.8	9.255	297.1	7898.0	1.86	1.9	0.0577	13.8	45.0	1.37	

NOTES:

Peaks that Compass for iCE names automatically with user-defined peak name settings are color-coded.

When the Fractions view is selected, the information in the Peaks table includes only injection, injection name, sample, peak, name, position and height. pI markers the software has identified are marked with an M.

- To view all rows Use the scroll bar or click Maximize in the upper right corner.
- To resize columns Roll the mouse over a column border until the sizing arrow appears, then click and drag to resize.

The following results and info are listed in the Peaks table:

- Injection Injection number.
- **Injection name** If injection names were entered in the batch, those names will display here. Otherwise the default 'SampleID_injection number' name will display.
- **Sample** If sample names were entered in the batch, those names will display here. Otherwise, Sample (default name) will display.
- Peak Peaks are numbered in order of detection.
- **Name** Displays peaks Compass for iCE named automatically using the user-defined peak name analysis parameters. These cells are blank if the software wasn't able to name the peak or if you didn't enter naming parameters.
- Position Peak location in pixels.
- pI Displays the calculated peak pI based on the position of the peak relative to to the pI markers.
- Height The calculated peak height.
- Area Displays the count of the pixel values for dropped line fit and the area of the curve fit for gaussian fit.
- % Total Displays the peak area ratio compared to the sum of all peak areas. This value results from dividing the individual peak area by the sum of all peak areas for the injection and multiplying by 100.
- % Area Displays the calculated percent area for the named peak compared to all named peaks. This value results from dividing the individual peak area by the sum of all named peak areas for the injection and multiplying by 100 (shown for named peak sample data only).
- Width Displays the calculated peak width (sample data only).
- **S**/**N** Displays the calculated signal to noise. The signal to noise ratio is reported for each peak based on the noise in the injection and the height of the peak. S/N = 2 x peak height / noise. For the injection noise calculation, the peak to peak noise is calculated by fitting a quadratic to the test region and taking the difference between the max signal above the fit, and the minimum signal below the fit. A fit is used to mitigate the effect of drift in the signal that would give a falsely high noise value. The software looks for the quietest 50 point region in the entire injection excluding 50 points at each end. The test region is approximately 5 times a typical peak width (FWHM).
- Baseline Displays the raw baseline signal of each peak.
- **Resolution** Displays resolution of the peak compared to neighboring peaks. Two peaks that are baseline resolved will have a resolution value of 1.5. Smaller values means the peaks are not completely resolved, larger values mean the peaks are fully resolved.

Injections Pane: User-Specified Peak Names

The Injections pane shows tabulated results for sample proteins Compass for iCE labels automatically using user-defined peak name settings. Each row in the table shows the individual results for the named peaks detected in each injection.

Peaks	Injections	Fractions								
								% Total	Area	% Area
njection	Injection N	Sample	Peak1	Peak2	Peak3	Peak4	Peak5			
1	Sample 01	Sample 01	43234.2	147238.8	172281.2	53548.1	7898.0			

NOTES:

Peaks that Compass for iCE names automatically with user-defined peak name settings are color-coded.

When the Fractions view is selected, the information in the Injections table includes only injection, sample and the positions of the pI marker (Mkr) peaks.

- To view all rows Use the scroll bar or click Maximize in the upper right corner.
- To resize columns Roll the mouse over a column border until the sizing arrow appears, then click and drag to resize.

The following results and info are listed in the Injections table:

- Injection Injection number.
- Injection name If injection names were entered in the batch, those names will display here. Otherwise the default 'SampleID_injection number' name will display.
- **Sample** If sample names were entered in the batch, those names will display here. Otherwise, Sample (default name) will display.
- **Peak Name Columns** An individual column per peak name will display for every peak identified by name or as a pI marker peak in the run data. Cells for injections in these columns will be blank if Compass for iCE didn't find peaks automatically using the user-defined peak name analysis and maker parameters (or none were entered).
 - To view peak area in the peak name columns (default) Select Area in the upper right corner of the pane. This displays calculated peak area for the individual peak only.
 - To view % total in the peak name columns This displays the peak area ratio compared to the sum of all peak areas. This value results from dividing the individual peak area by the sum of all peak areas for the injection and multiplying by 100.

NOTE: The sum of the named peak percentages can be less than 100% if some peaks aren't named.

								% Total	Area	% Area
njection	Injection N	Sample	Peak1	Peak2	Peak3	Peak4	Peak5			
	Sample 01	Sample 01	10.2	34.7	40.6	12.6	1.9			

• To view % area in the peak name columns - This displays the peak area ratio compared to the sum of all named peak areas. This value results from dividing the individual peak area by the sum of all named peak areas for the injection and multiplying by 100.

								% Total A	Area	% Area	
njection	Injection N	Sample	Peak1	Peak2	Peak3	Peak4	Peak5				
1	Sample 01	Sample 01	10.2	34.7	40.6	12.6	1.9				

Fractions Pane: Fraction Peak Predictor

The Fractions Pane appears when the Samples view is selected. It predicts where each sample peak was collected in the 96-well plate. Compass for iCE uses a peak prediction algorithm to model the mobility of sample peaks in the capillary. Results will either be shown for pI markers or named peaks, depending on the view options you're using. Check out the "Analysis Options Pane" on page 580 for more info.

Injection	Injection Name	Location	Mkr 7.05	8.560	A2	A1	Main	B1	B2	Mkr 10.17	
1	NIST	B7							B7		
1	NIST	B8							B8		
1	NIST	B9						B9	B9		
1	NIST	B10					B10	B10	B10		
1	NIST	B11			B11	B11	B11	B11	B11		
1	NIST	B12			B12	B12	B12	B12			
1	NIST	C12			C12	C12	C12				
1	NIST	C11			C11	C11					
1	NIST	C10		C10	C10						
1	NIST	C9		C9							
1	NIST	C8		C8							
1	NIST	C7		C7							
1	NIST	C6		C6							
1	NIST	C5									

NOTES:

Peaks that Compass for iCE names automatically with user-defined peak name settings are color-coded.

Peak pI values will be used if you have not named peaks yet.

Analysis Options Pane

The Analysis Options pane gives you a quick way to view data for different exposures and add peak names without having to open and edit the run's analysis settings.

• Peak names - Lets you view, change and add new custom peak name settings for sample proteins. You can apply peak name settings to all, selected, or specified injections. For details on how to use this option, go to "Naming Peaks" on page 589.

@ [®] Analysi	s Opti	ons	
Detectio	'n		*
Туре		Fluorescence	~
Method	1	Exp1 1s	\sim
Method	2	Exp5 20s	\sim
Peak Na	mes		*
Name			~
pl			
Color			
Injects			
		Modify	

Viewing Run Data

The Analysis screen lets you view one electropherogram, specific electropherograms or all electropherograms in the run. Each run file has data for the sample peaks and pI markers detected. Switching Between Samples and Markers Data Views

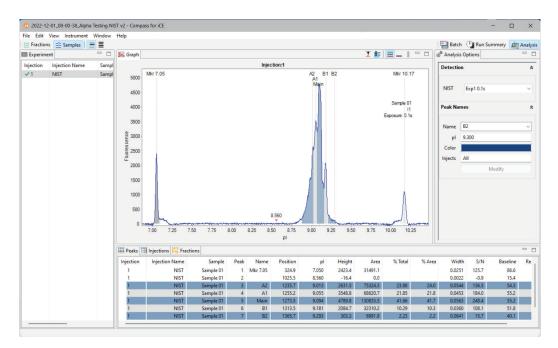
Switching Between Samples and Fractions Data Views

Here's how you switch between viewing data for your sample and pI markers in your final focusing image and viewing mobilization electropherograms:

• To view sample data - Click Samples in the View bar or select View in the main menu and click Samples.



- Data in this view is for the final focusing sample image only.
- The graph displays electropherograms with a y-axis of Fluorescence units and a x-axis of pl.
- Results for each peak are shown in the Peaks and Injections panes. The prediction of which fraction each sample peak was collected in are shown in the Fractions pane.



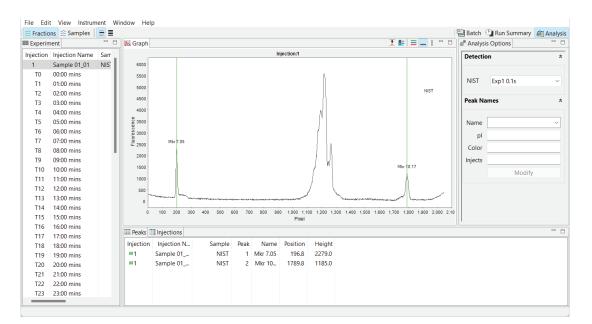
For information on checking and identifying sample peaks, see "Checking Your Data" on page 250.

• To view pI marker data for your sample (I1) - Click Fractions in the View bar or select View in the main menu and click Fractions.

File	Edit	View	Instrument	Window
Ħ	Fracti	ons	🚖 Samples	

Data in this view is for analyzing pI markers for the final focusing sample image. These are the pI markers you add to your sample during prep. pI markers cannot be adjusted in Samples view. pI markers for mobilization electropherograms cannot be adjusted.

- The graph displays electropherograms with a y-axis of Fluorescence units and an x-axis of pixels.
- pI markers are identified in the Peaks pane with an M and as Mkr in the Injections pane.



For information on checking and identifying the pI marker peaks, see "Checking Your Data" on page 250.

• To view Fractions data (T0, T1, T2, etc): Click Fractions in the View bar or select View in the main menu and click Fractions.



Data in the view is for confirming peaks have been correctly identified in the mobilization electropherograms.

- The graph displays electropherograms with a y-axis of Fluorescence units and an x-axis of pixels.
- Incorrectly identified peaks can be removed and missing peaks can be added.
- Peaks will be identified by pixel position by default.
- Compass for iCE will automatically name peaks in the Fractions view using Sample peak names defined by the user in the Samples view. Peak names can be manually adjusted in the Fractions view.

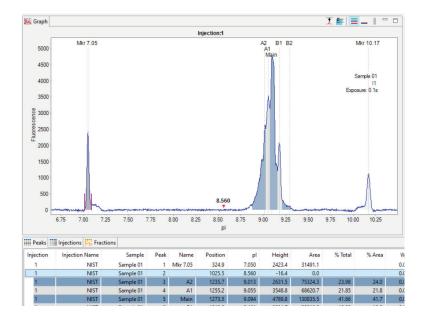
ile Edit	View Instrum	ent Window	Help											
Fractio	ns 🚔 Samples											Batch	Run Summary	Alii An
Experim	ent			- 0	🔍 Graph							1	8= = _	8 - 0
njection	Injection N	Sample	Location	Method	īl –				то					
1	NIST	Sample 01	A1	NIST						м	ain			
TO	00:00 mins	Sample of		NIST	2200 -						32 3			
TI	01:00 mins			NIST	2000					12	\$2.3			
T2	02:00 mins			NIST	1800						ų.		Sample 0	1
T3	03:00 mins			NIST	1600					A1			Exposure: 0.1	s
T4	04:00 mins			NIST	8 1400					p				
T5	05:00 mins			NIST	8 1200					A2				
T6	06:00 mins			NIST	9 1200	Mkr 7.05				1	81			
17	07:00 mins			NIST	1400 1200 1200 1000					1218.7	X			
T8	08:00 mins			NIST	^{tt} 800					1210.7	11		lkr 10.17	
T9	09:00 mins			NIST	600	1				1	Y	P	v	
T10	10:00 mins			NIST	400 -	LI LI							A	
T11	11:00 mins			NIST	200	1				/			A	
T12	12:00 mins			NIST	0	the manufactures and the	**************************************	ang a sub-sub-sub-sub-sub-sub-sub-sub-sub-sub-	ويتحاربني والمتحا والرمير	mont	1 amount		- Lucomann	
T13	13:00 mins			NIST	0	100 200 300 400	500 600 70	0 000 0	00 1000	100 1000	1 200 1 400	1,500 1,600 1,70	1 1 000 1 000	2000 2
T14	14:00 mins			NIST	0	100 200 300 400	500 600 70	10 000 3	1,000	1,100 1,200	1,300 1,400	1,500 1,600 1,70	J 1,000 1,300	2,000 2,
T15	15:00 mins			NIST	Peaks	Injections								
T16	16:00 mins			NIST	Injection	Injection Name Sa	mple Peak	Name	Position	Height				
T17	17:00 mins			NIST	то	00:00	CONT. 200 000000	Mkr 7.05	324.4	947.0				
T18	18:00 mins			NIST	то	00:00	1	IVIKE 7.05	1218.7	415.0				
T19	19:00 mins			NIST	то	00:00	2	A2	1235.5	1177.0				
T20	20:00 mins			NIST	то	00:00	4	A2	1255.5	1540.0				
T21	21:00 mins			NIST	то	00:00	4	Main	1250.1	2116.0				
T22	22:00 mins			NIST	то	00:00	6	Walth	1282.3	2123.0				
T23	23:00 mins			NIST	то	00:00	7	B1	1202.5	903.0				
T24	24:00 mins			NIST	то	00:00	8	Mkr 10.17	1770.5	491.0				
T25	25:00 mins			NIST	10	00.00	•	MM 19417	1110.3	491.0				
T26	26:00 mins			NIST										
T27	27:00 mins			NIST										
T28	28:00 mins			NIST										
	29:00 mins			NIST										
T29				NIST										
T29 T30 T31	30:00 mins 31:00 mins			NIST										

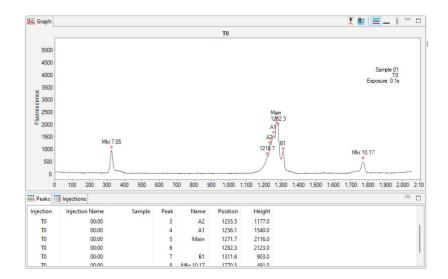
• Information for each peak are shown in the Peaks and Injections panes.

Selecting and Displaying Injection Data

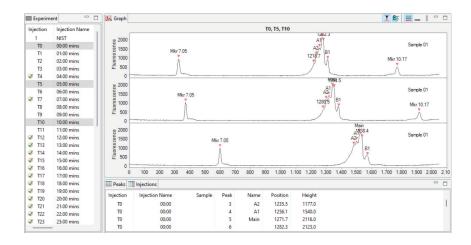
You can view the sample injection and name peaks in the Samples View. You can view the pI markers, injection and mobilization data for the sample and collected fractions in the Fractions View.

• **To look at data for one electropherogram** - Select the injection or mobilization electropherogram in the Experiment pane. Data for just that electropherogram displays in the graph and tables.

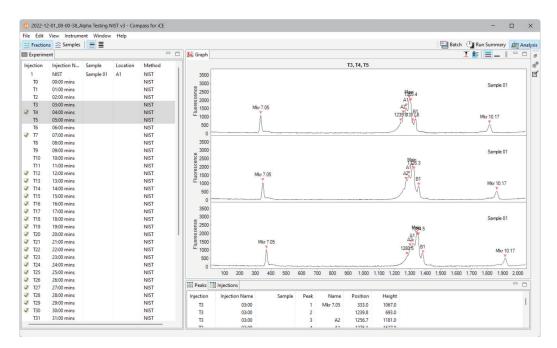




• To look at data for specific mobilization electropherograms - In the Fractions view, hold the Ctrl key and select just the rows you want to view in the Experiment pane. Data for only the rows selected display in the graph and tables.



• To look at data for sequential mobilization electropherograms - In the Fractions view, select the first row in the Experiment pane that you want to view, then hold the Shift key and select the last. This selects all rows between the two rows. Data for only the rows selected display in the graph and tables.



• To look at data for all mobilization electropherograms - Just click View All in the View bar. Data for all rows displays in the graph and tables.



Switching Between Selected and All Electropherogram Views (Fractions View)

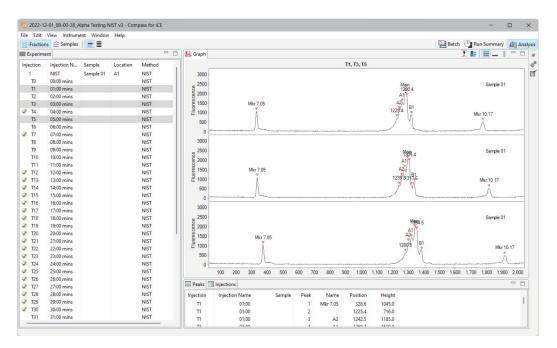
You can switch between displaying run data in a single electropherogram format or a multi-electropherogram format.

• To view data in a selected electropherogram format - Click Selected View in the View bar or select View in the main menu and click Selected.



Data for the electropherograms selected in the Experiment pane:

- Displays with electropherograms either overlaid or stacked in the Graph pane depending on the option you've got chosen.
- Shows only results for the selected row(s) in the Peaks and Injections panes.

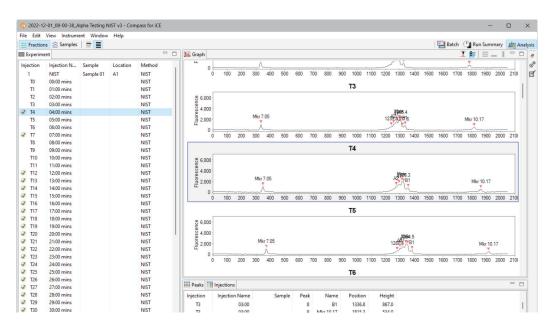


• To view all electropherograms in a multi-electropherogram format - Click View All in the View bar or select View in the main menu and click All:



Data for the electropherogram:

- Displays with the electropherograms in the Graph pane in stacked view.
- Graph pane will scroll to the electropherogram when selected in the Experiment pane.
- Shows the results for electropherograms in the Peaks and Injections panes.



Data Notifications and Warnings

If Compass for iCE detects a potential data issue, a notification or warning icon will display next to the injection row in the Experiment pane.

Manual correction of sample data notification - This means the sample data was manually changed by a user, for example to add or remove a sample peak. Roll your mouse over the icon to display the type of modification that was made.

Injection	Injection Name	S
V 1	Sample 01_01	S
TO	00:00 mins	
T1	01:00 mins	

Markers warning - This means one or more of the pI markers may not be identified properly. You can fix this by manually identifying the pI marker using the steps in ""Step 1: Check the pI Markers for the Injected Sample" on page 251. Roll your mouse over the icon to display warning details.

🚊 Fractions	🚖 Samples 📃			
Experime	nt	- 0		
Injection	Injection Injection Name			
Q 1	Sample 01_01	Sample 0 [*]		
Markers E	rror: Not Found			

Manual correction of markers data notification - This means a user changed the pI marker data manually. Roll your mouse over the icon to display the type of modification that was made.

📰 Experime	Experiment								
Injection	Injection N	Sample	Location						
V 1	NIST	Sample 01	A1						
T0 Markers N	00:00 mins <mark>Aanual</mark> mins								
T2	02:00 mins								

Manual correction of peak notification - This means a user added or removed a peak in a mobilization electropherogram.

Experime	ent		
Injection	Injection N	Sample	L
T8	08:00 mins		
Т9	09:00 mins		
T10	10:00 mins		
🧭 T11	11:00 mins		
🧭 T12	12:00 mins		
CN T12	12.00 mine		

Peak fit warning - Means that a peak can't be fit properly. This can sometimes be caused when a broad peak is fitted as multiple narrow peaks. Changing the peak width can help in this case. The warning is also caused by very small peaks around main peaks, or small peaks that are close to the end of the separation range. You can often fix this by removing the peak(s) using the steps in "Step 2: Checking Sample Peaks" on page 254. Roll your mouse over the icon to display warning details.

-	11010-200							
Δ 6	mAb 25	A3						
Peak Fit Warning: Too many iterations								
9	mAB 250	A2						

Checking Your Results

If you see a data warning in the Experiment pane, these steps will also help you identify and correct any issues. Compass for iCE detects your sample protein and pI marker peaks and reports results automatically. But, we always recommend you review your data using the steps in this section as a good general practice to make sure your results are accurate. Please see the step by step procedure in "Checking Your Data" on page 250 to do this. If you see a data warning in the Experiment pane, these steps will also help you identify and correct any issues.

Naming Peaks

NOTE: Analysis screen options will let you add a new peak name, its pI, identifying color for peak tables and what injections it applies to. If you need to remove peak names, add peak name analysis settings groups or set pI ranges, you can do that in the run analysis settings. For more info go to "Peak Names Settings" on page 622.

Adding New Peak Names in the Analysis Options Pane

1. Click the down arrow in the Name field and select New.

Peak Names *				
Name				
pl	Peak1 Peak2			
Color	Peak3 Peak4			
Injects	Peak5			
	[New]			

2. Type a name.

Peak Names *				
Name	mAB1			
pl	6.0			
Color				
Injects	All			
	Create			

3. Click in the pI field and enter the pI value of your sample protein.

Peak Na	mes	2
Name	mAB1	~
pl	6.78	
Color		
Injects	All	
	Creat	e

4. Click on the Color field to display the color selection box.

Peak Na	imes 🎗	Color
Name pl Color Injects	mAB1 ~ 6.78	Basic colors:
	Create	Custom colors: Define Custom Colors >> OK Cancel

5. The color you pick is used to identify the sample protein peak in the Peaks and Injections panes in the Analysis screen. Click a color or define a custom color and click OK. The color selection will update in the field:

Peak Na	mes	*
Name	mAB1	~
pl	6.78	
Color		
Injects	All	
	Create	

6. Click in the Injects field:

To apply the new peak name to all injections - leave the default setting of All.

To apply the new peak name to specific injections - enter individual injections separated by commas (for example 2, 5, 8), a range of injections (for example 3-15) or a combination of both (for example 8, 10, 12-15). You can also click the tool tip for more examples.

Peak Na	mes	*
Name	mAB1	~
Inj	ection descriptor r example, 3, 5-10	
Injects	All	
	Create	

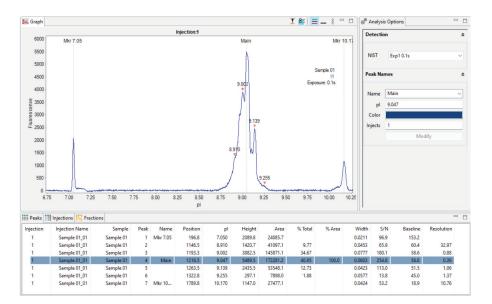
To apply the new peak name to specific run data - type the first letter of a method, sample name, well or vial location. Compass for iCE will search the run data and display a list of matching options for you to choose from. Alternatively you can highlight the text in the Injects cell, hit **Delete**, then select an option from the drop down list.

Detection	*	Detectio	n
VIST Exp1 0.1s	~	NIST	Exp1 0.1s
Names	*	Peak Nan	nes
lame Main	~	Name	Main
pl 9.105		pl	9.105
olor		Color	
njects NI		Injects	
NIST			1
			All
			NIST
			Sample 01 A1

- Injection Applies the peak name to the injection number
- All Applies the peak name to all injections.
- **Methods** All methods in the run file display in the list. Selecting a method applies the peak name to all injections that used that method.
- **Sample names** All sample names in the run file display in the list, otherwise the default name of Sample shows. Selecting a sample name applies the peak name to all injections that used that sample name.
- Wells or vials The well or vial numbers currently selected will display in the list. Selecting a well or vial number applies the peak name to all injections that used that well or vial.
- 7. Click Create to save changes.

NOTE: To clear the new peak name information you've entered without saving changes, just delete the peak name in the Name field.

The named peak will be identified with a peak name label in the electropherogram and color-coded in the Peaks and Injections panes:



Adding Peak Names from the Graph or Peaks Table

NOTE: Analysis screen options will let you change an existing peak name, its pI, identifying color in peak tables and what injections it applies to. If you need to remove peak names, add peak name analysis settings groups or set pI ranges, you can do that in the run analysis settings. For more info go to "Manual Peak Integration" on page 637.

1. Right click the peak you want to name in the Graph or Peaks pane.

2. Select Name Peak.

Peaks	Injections	E Fr	actions						Mkr 10.17	
Injection	Injection N.		Sample	Peak	Nam	e Position	pl	Height	Zoom Out Remove Peak	Exp1
1	Sample 01		Comple 01		Males 7.	. 196.8	7.050	2089.8	Hide	
1	Sample 01		Remove Pea	ak	aki	I 1146.5	8.910	1420.7	Name Peak >	Main
1	Sample 01	×	Hide		alc	1175 5	8 967	3017.4	Add Peak	B1
1	Sample 01		Name Peak		>	Peak1	02	3882.5	Add Baseline Point	A1
1	Sample 01		Сору			Peak2	47	5489.5	Remove Baseline Point	A2
_	_	_	copy	_	_	Peak3	_		Clear	B2
						Peak4			Copy Ctrl+C	New
						Peak5				<u> </u>
						Peak6				
						Peak7			Å	
						New				

3. To use an existing peak name - select a name from the list.

To create a new peak name - select New. Type in a name for the peak. Click All to apply to all injections or Selected to apply only to the injections selected.

🔯 Add New Peak Name			Х
Peak Name:	Peak 5		7
Apply Name to:	IIA (◯ Selected	
C	ОК	Cancel	

4. Click **OK**. If you want to add an identifying color or change the injections the new peak name applies to, you can do that in the Analysis Options pane.

Changing Peak Name Information

NOTE: Analysis screen options will let you change an existing peak name, its pI, identifying color for peak tables and what injections it applies to. If you need to remove peak names, add peak name analysis settings groups or set pI ranges, you can do that in the run analysis settings. For more info go to "Manual Peak Integration" on page 637.

1. In the Analysis Options pane, click the down arrow in the Name field and select an existing peak name.

Peak Na	mes :
Name	Peak2 ~
pl	Peak2 Peak3
Color	Peak4 [New]
Injects	Peptide Mix
	Modify

2. Change the name, pI, color and injects as needed then click Modify.

Copying Results Tables and Graphs

You can copy and paste data and results tables into other documents, or save the electropherogram as a graphic file.

Copying Results Tables

- 1. Click in the Peaks or Injections pane.
- 2. Select one or multiple rows.
- 3. Select Edit in the main menu and click Copy, or right click on row(s) you selected and click Copy.
- 4. Open a document (Microsoft[®] Word[®], Excel[®], PowerPoint[®], etc.). Right click in the document and select **Paste**. Data for the rows selected will be pasted into the document.

Copying the Graph

- 1. Select the Graph pane.
- 2. Select Edit in the main menu and click Copy, or right click in the Graph pane and select Copy.
- 3. Select an image option (EMF, PNG or PDF) in the pop-up window, then click Copy.

Copy Graph	×			
Graph title:	11			
Metafile ((EMF)			
🔘 Bitmap (PNG)				
O Portable	Document Format (PDF)			
Save	Copy Cancel			

4. Open a document (Microsoft[®] Word[®], Excel[®], PowerPoint[®], etc.). Right click in the document and select **Paste**. A graphic of the copied electropherogram will be pasted into the document.

Saving the Graph as an Image File

- 1. Select the Graph pane.
- 2. Select Edit in the main menu and click Copy, or right click in the Graph pane and select Copy.
- 3. Select an image option (EMF, PNG or PDF) in the pop-up window, then click Save.

Copy Graph	×		
Graph title:	n		
Metafile	(EMF)		
💿 Bitmap (PNG)			
Portable	Document Format (PDF)		
Save	Copy Cancel		

4. Select a directory to save the file to, enter a file name, then click OK.

Exporting Run Files

Results tables and raw plot data can be exported for use in other applications. Data is organized into these folders when exported:

• <run file name>Export_FL when the same exposure is selected for all methods

Exporting Results Tables

To export the information in the Peaks and Injections tables:

- 1. Click File in the main menu and click Export Tables.
- 2. Select a directory to save the files to and click OK. Data will be exported in .txt format.

NOTE: To exclude export of standards (pI markers) data or export results table data in .csv format, see "Setting Data Export Options" on page 760.

Chapter 19: MauriceFlex Fractionation Data Analysis | Changing Sample Protein Identification

Exporting Raw Sample Electropherogram Data

To export raw sample plot and background data:

1. Click File in the main menu and click Export Spectra.

File	Edit View	Instrument	Win	dow	Help			
	Open Run	+						
	Add Run	+				🔣 Graph		
	Close		Location		Me	Jos Graph		
	Close All		A1		Sys	36,000		
	Save		A2		mA	34,00		
	Save As		A3 A4		mA mA	32,000 30,000		
	Export Tables.		A4			28,00		
	Export Spectra	a 🕨 🕨		Text	Format.			
	Injection Repo	ort		AND	I Format	t		
	Exit		AZ		mA	22,001		

- To export data in .txt format Select Text Format. Data will be exported in one file for the sample injection and all fractions.
- To export data in .cdf format Select ANDI Format. Data will be exported in one file per injection/fraction.
- 2. Select a directory to save the files to and click OK. Data will be exported in the selected format.

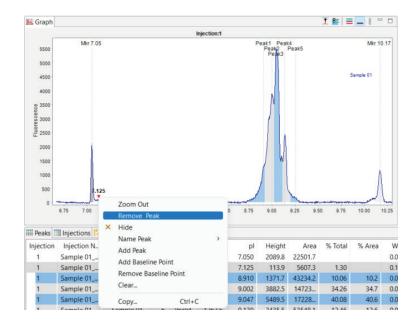
Changing Sample Protein Identification

Compass for iCE lets you customize what sample proteins are reported in the results tables by making manual adjustments in the electropherogram or Peaks table.

Adding or Removing Sample Data

- 1. Click Show Samples in the View bar.
- 2. Click Single View in the View bar.

- 3. Click on the row in the experiment pane that has the injection you want to correct, then click the Graph tab.
 - To remove a peak from the data Right click the peak in the electropherogram or Peaks table and select **Remove peak**. The software will no longer identify it as a sample peak in the electropherogram, and the peak data will be removed in the results tables.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

Injection	Injection Name	Samp
√ 1	Sample 01_01	Samp

• To add an unidentified peak to the data - Right click the peak in the electropherogram or peaks table and select Add Peak. The software will calculate and display the results for the peak in the results tables and identify the peak in the electropherogram.

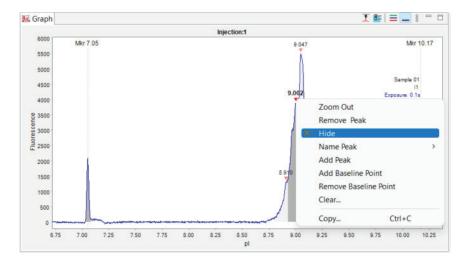
A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

NOTE: To remove sample peak assignments that were made manually and go back to the original peak data, right-click the peak in the electropherogram and select **Clear** for the current injection or **Clear** All for all injections in the batch.

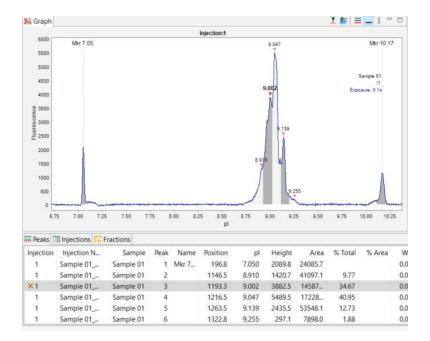
Hiding Sample Data

You can hide the results for a sample protein in the results tables without completely removing it from the reported results.

- 1. Click Show Samples in the View bar.
- 2. Click Single View in the View bar.
- 3. Click on the row in the experiment pane that contains the injection you want to correct, then click the Graph tab.
- 4. Right click the peak in the electropherogram or Peaks table and select Hide. Compass for iCE will hide the peak data in the results tables.



5. To view hidden peak data, click View in the main menu and click Show Hidden. Hidden peak data will display in the results table and be marked with an X.

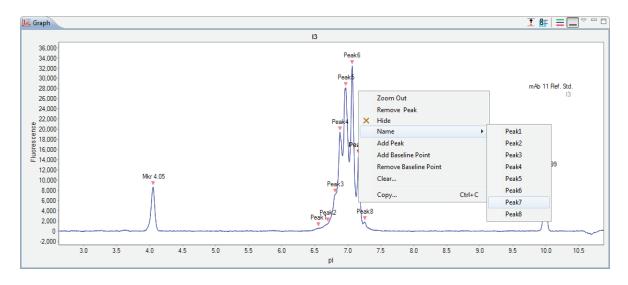


6. To unhide a peak, right click on the peak in the electropherogram or peaks table and select Unhide.

Changing Peak Names for Sample Data

If Compass for iCE did not automatically name a sample protein peak, you can do it manually.

- 1. Click Show Samples in the View bar.
- 2. Click Single View in the View bar.
- 3. Click on the row in the experiment pane that has the sample you want to correct, then click the Graph pane.
- 4. Right click the peak in the electropherogram or Peaks table and click **Name**, then select a name from the list. Compass for iCE will change the peak name in the electropherogram and results tables, and adjust peak names for other sample proteins accordingly.

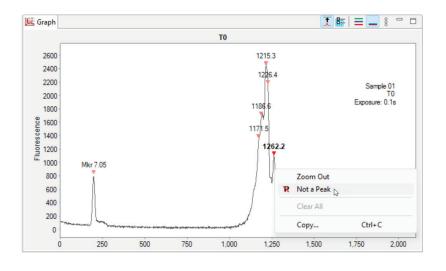


NOTE: For details on how to specify peak name settings, see "Manual Peak Integration" on page 637.

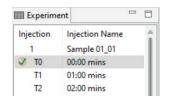
Adding or Removing Fractions Data

- 1. Click **Fractions** in the View bar.
- 2. Click Single View in the View bar.

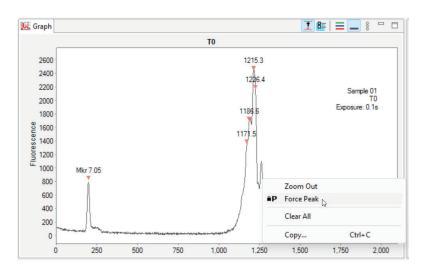
- 3. Click the Graph tab.
 - To remove a peak Right click the peak in the electropherogram or Peaks table and select Not a Peak. The software will not longer identify it as a sample peak in the electropherogram, and the peak data will be removed from the results table.



A checkmark will appear next to electropherogram in the Experiment pane to indicate a manual correction was made.



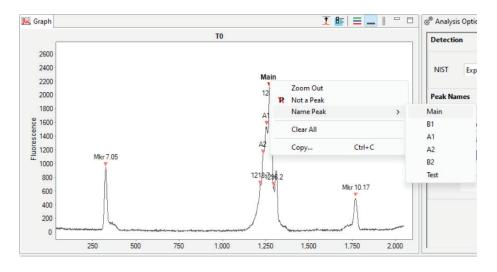
• **To add an unidentifed peak**: Right click the peak in the electropherogram and select **Force Peak**. The software will calculate and display the results for the peak in the results table and identify the peak in the electropherogram.



A checkmark will appear next to the electropherogram in the Experiment pane to indicate a manual correct was made.

NOTE: To remove sample peak assignments that were made manually and go back to the original peak data, right-click the peak in the electropherogram and select Clear for the current injection or Clear All for all injections in the batch.

• To name a peak: Right check the peak in the electropherogram or peaks table and select Name Peak. Select the name to assign to the peak. The software will update the peak name in the results table.



IMPORTANT: The sample peaks in the final focusing sample injection image must first be named in the Samples view before peaks can be named in the Fractions view.

Changing the Electropherogram View

Options in the Graph pane let you zoom and rescale electropherograms, overlay or stack plots and change the peak and plot info displayed.

The Graph pane toolbar has these options:

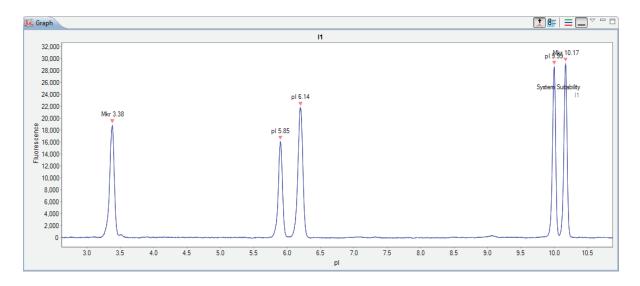




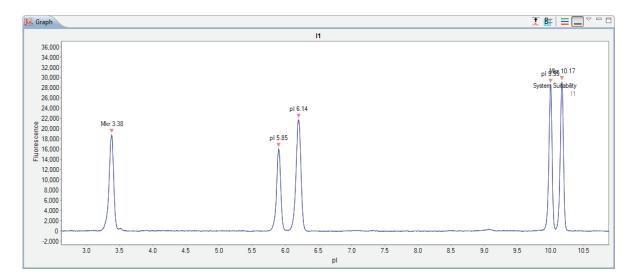
Chapter 19: MauriceFlex Fractionation Data Analysis | Changing the Electropherogram View

Autoscaling the Electropherogram

Click the Auto Scale button to scale the y-axis to the largest peak in the electropherogram.

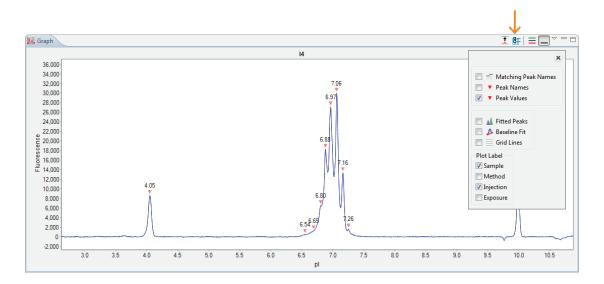


Click the Auto Scale button again to return to default scaling.



Customizing the Data Display

You can customize electropherogram peak labels, plot labels and display options. To do this, just select the **Graph Options** button.

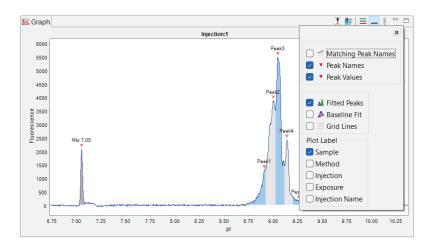


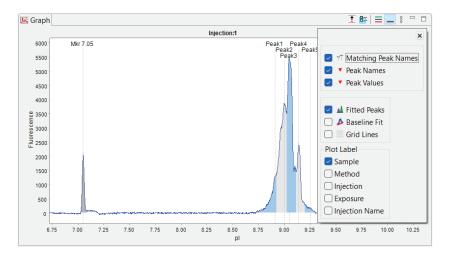
Peak Labels

You can customize the labels used to identify peaks in the electropherogram with these options:



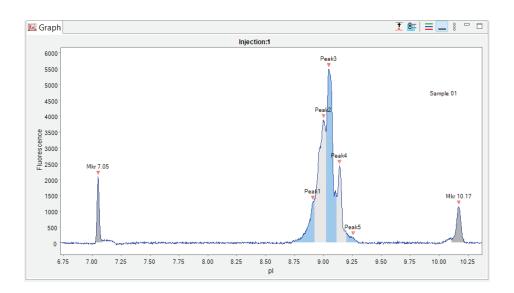
• Matching Peak Names - Checking this box will draw vertical lines through each named peak. Using this option with Stack the Plots or Overlay the Plots features is helpful for visually comparing your named peaks across multiple injections.





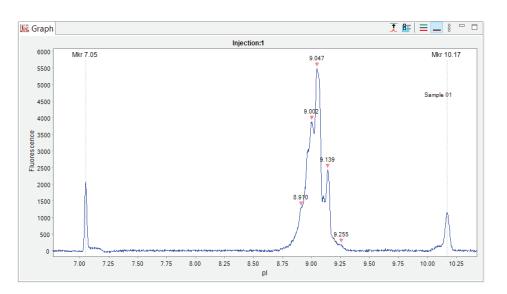
• Peak Names - Checking this box displays peak name labels on all named peaks in the electropherogram.

NOTE: If more than one peak label option is selected, peak name labels will always be used for named peaks.



• Peak Values - Checking this box will display the pI values on all peaks in the electropherogram.

NOTE: If more than one peak label option is selected, peak name labels will always be used for named peaks.

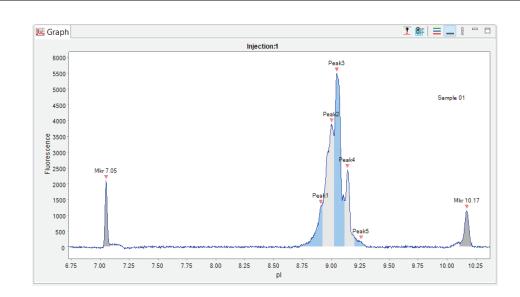


Baseline and Grid Options

You can view the calculated baseline fit, peak integration, show grid lines and overlay fluorescence electropherograms with these options.



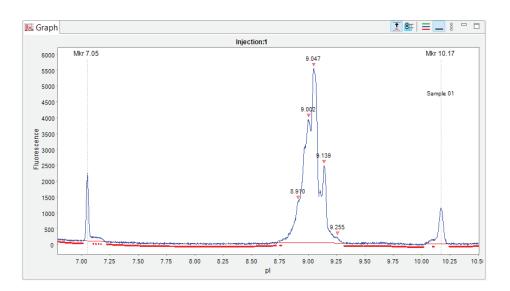
• Fitted peaks - Checking this box displays how the peaks were fit by the software. For MauriceFlex Fractionation runs, the software uses Dropped Line as the default.



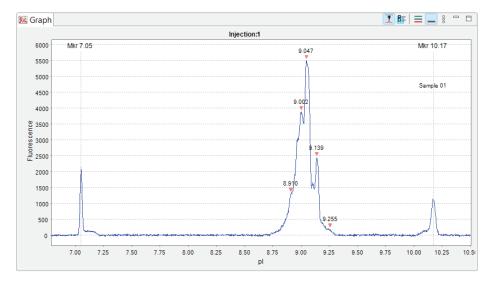
NOTE: This option is only available for sample data.

• **Baseline Fit** - Checking this box displays the calculated baseline for the peaks. Baseline points will also display for regions of the electropherogram considered to be at baseline.

NOTE: This option is only available for sample data.



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• Grid Lines - Checking this box adds grid lines in the graph.

Plot Labels

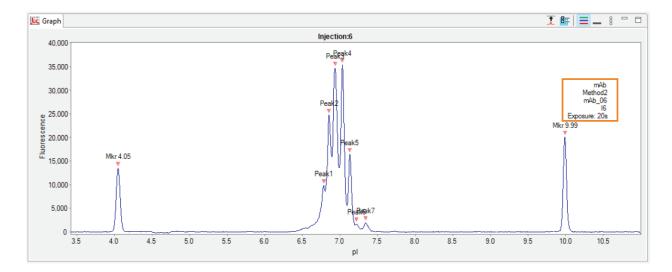
You can customize the plot labels displayed on the electropherogram with these options.



Plot labels are shown in the upper right side of the graph.

- **Sample** Checking this box displays the sample name used for the injection. If sample names were entered with the batch, those names will display here. If not, Sample (default name) displays.
- Method Checking this box displays the method used for the injection.
- Injection Checking this box displays the injection number. For example, I1 for injection 1 in the run.
- Exposure Checking this box display the exposure time(s) used for the data.
- Injection Name Checking this box displays the name used for the injection.
- Injection Name Checking this box displays the injection name used for the injection.

Chapter 19: MauriceFlex Fractionation Data Analysis | Changing the Electropherogram View

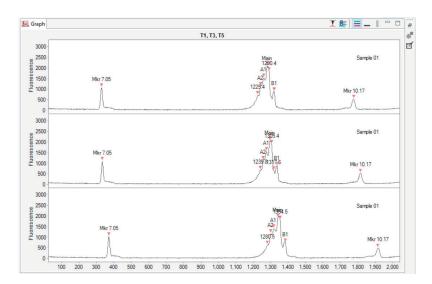


Here's an example of an electropherogram with all plot labels selected:

Stacking Multiple Electropherograms

You can stack electropherograms in the Fractions View for multiple injections or mobilization electropherograms vertically in the Graph pane for comparison. lick **Single View**.

- 4. Select multiple rows in the Experiment pane.
- 5. Click the **Stack the Plots** button. The individual electropherograms for each row you selected will stack in the Graph pane.

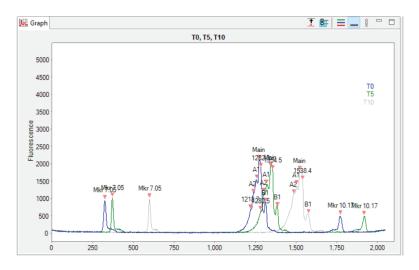


You can also customize the colors used for the stacked plot display. To do that go to "Setting up Automatic Injection Reports" on page 761.

Overlaying Multiple Electropherograms

You can overlay electropherograms in the Fractions View for multiple $iv\phi \epsilon \chi tiov\sigma$ or $\mu o \beta i \lambda i \zeta \alpha tiov$ electropherograms on top of each other for comparison in the Graph pane.

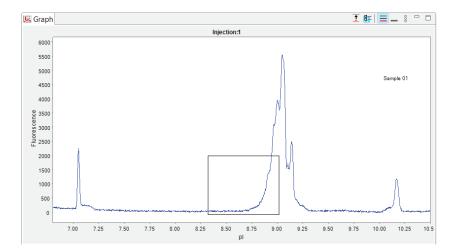
- 1. Click Single View.
- 2. Select multiple rows in the Experiment pane.
- 3. Click the **Overlay the Plots** button. The individual electropherograms for each row you selected will overlay in the Graph pane.



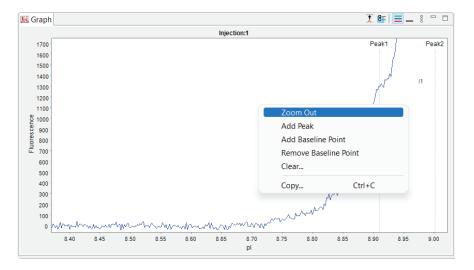
You can also customize the colors used for the overlay plot display. To do that go to "Setting up Automatic Injection Reports" on page 761.

Zooming

To zoom in on a specific area of the electropherogram, hold the mouse button down and draw a box around the area with your mouse:



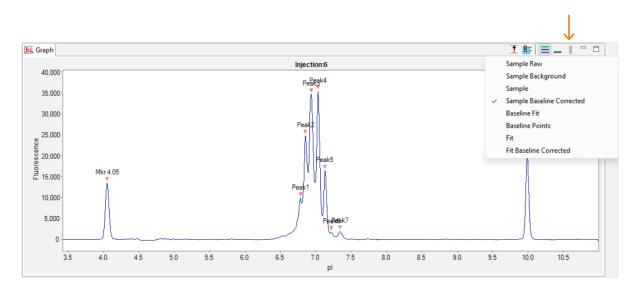
Chapter 19: MauriceFlex Fractionation Data Analysis | Changing the Electropherogram View



To return to default scaling, right click in the electropherogram and click **Zoom Out**.

Selecting Data Viewing Options

The graph view menu gives you multiple options for changing what type of electropherogram data is displayed. Just click **View More** in the graph pane toolbar to view the menu:



A check mark next to the menu option indicates it's currently selected, and you can select multiple options at once.

NOTE: Unless noted otherwise, graph view menu options are available for sample data only.

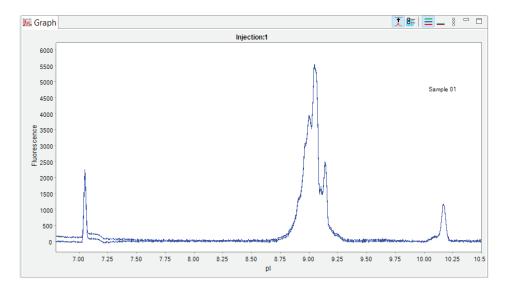
- 1 🖩 📃 🗕 🕴 🗖 🗖 😹 Graph Injection:1 7000 6500 6000 Sample 01 5500 5000 2 4500 4000 84000 8100 11 3500 3000 2500 2000 1500 1000 7.00 7.25 7.50 7.75 8.00 8.25 9.00 9.25 9.50 10.25 8.50 8.75 9.75 10.00 10.5 pl
- Sample Raw Clicking this option displays the basic detector values used to calculate peak fluorescence.

• Sample Background - Clicking this option displays the basic detector values used to calculate baseline fluorescence.

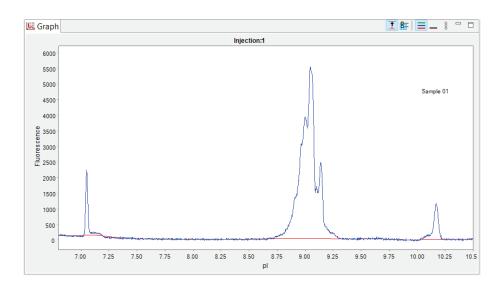
😹 Graph												1		- 8 1	
							Injection:	1							
6000 -															
5500															
5000													S	mple 01	
4500													Sal	mple 01	
4000															
월 3500 ·															
8 3000 ·															
8 3500 - 3000 - 2500 -															
2000															
1500		يلور - يەسىرە ئورۇر يەرىپ	مى ئەرىمىيە تەرىپىيە مەرىپىيە مەرىپىيە مەرىپىيە مەرىپىيە مەرىپىيە مەرىپىدە مەرىپىدە مەرىپىدە مەرىپىدە مەرىپىدە	يو، در ور	القاديرور فقر رستر وروور	late	agenation of the state of the			M _e m _e m _e tan gangkodo p	ىلىدىر، مورد رومەن	engaan serangkan ara dar	4°47	^{Const} ations, and the same	
1000	Water of a contract of the														
500															
0 -															
	7.00	7.25	7.50	7.75	8.00	8.25	8.50	8.75	9.00	9.25	9.50	9.75	10.00	10.25	10.5
								pl							

- 属 Graph 1 🖩 😑 🗕 🕴 🗖 Injection:1 6000 5500 5000 Sample 01 4500 4000 월 3500 3000 01 2500 2000 1500 1000 500 0 9.25 7.00 7.25 7.50 7.75 8.00 8.25 9.00 9.50 9.75 10.00 10.25 8.50 8.75 10.5 pl
- Sample Clicking this option displays raw, uncorrected sample data.

• **Sample Baseline Corrected** - Clicking this option displays sample data with the baseline subtracted (zeroed). This is the default view. In this next example, both Sample and Sample Baseline Corrected are selected.

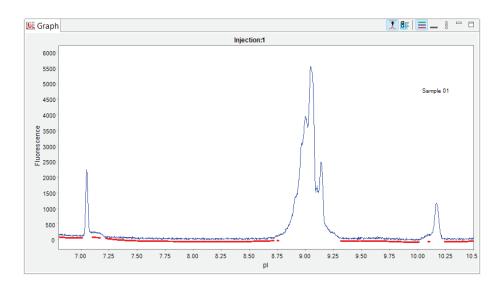


- **Baseline Fit** Clicking this option displays the calculated baseline for the raw sample data. In this next example, both Baseline Fit and Sample are selected.
 - NOTE: This option is selected automatically when Baseline Fit is selected in graph options.

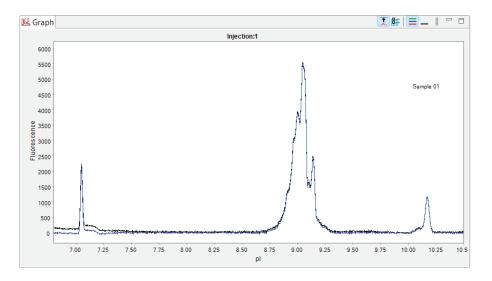


• **Baseline Points** - Clicking this option displays regions of the electropherogram considered to be at baseline. In this example, both Baseline Points and Sample are selected.

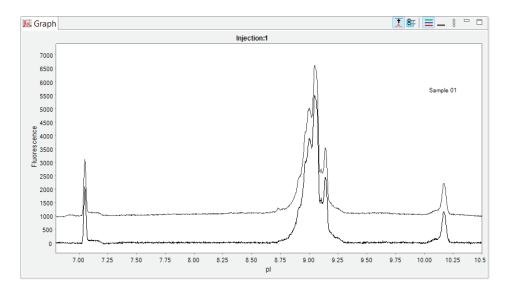
NOTE: This option is selected automatically when Baseline Fit is selected in graph options.



• Fit - Clicking this option displays the bounding envelope of the fitted peaks as calculated by the software for the raw sample data. In this example, both Fit and Sample Baseline Corrected are selected.



• Fit Baseline Corrected - Clicking this option displays the fitted peaks as calculated by the software for the sample baseline corrected data. In this example, both Fit Baseline Corrected and Sample Raw are selected, the fit plot is on the bottom.

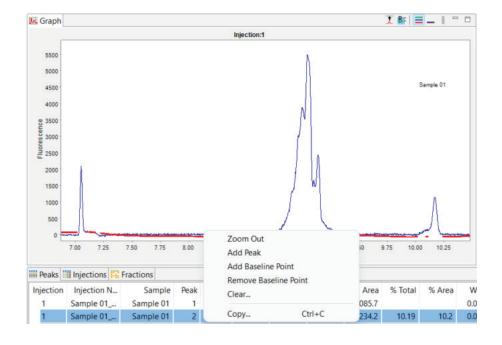


Adjusting the Baseline

Spline Baseline

Points in the baseline can be added or removed as needed.

- 1. Click the **Graph Options** button in the graph pane toolbar and check **Baseline Points**. This will display baseline points for the raw sample data.
- 2. Use the mouse to draw a box around the area you want to correct. This will zoom in on the area.
- 3. Right click a baseline point and select Add Baseline Point or Remove Baseline Point.



NOTE: To clear the manual addition or removal of baseline points and go back to the original view of the data, right click in the electropherogram and click **Clear All**.

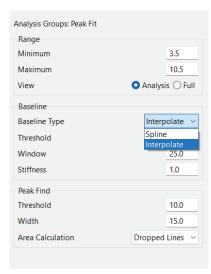
Interpolated Baseline

Compass for iCE lets you interpolate baselines from the base of each peak for named peaks that use Dropped Lines integration.

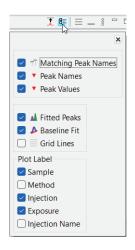
- 1. If you haven't already, name your peaks of interest.
- 2. Select Edit > Analysis, and click Peak Fit in the left sidebar.

3. Choose Interpolate as the Baseline Type if it isn't already selected.

NOTE: Baseline Type selection is only available when Dropped Lines is used for the Area Calculation.

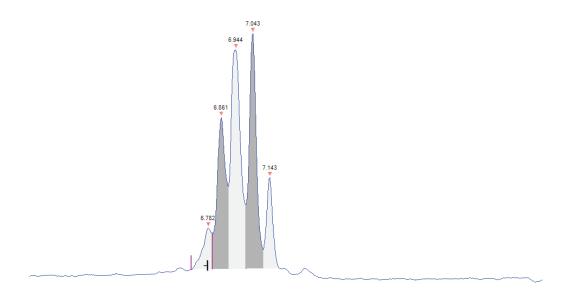


- 4. Click OK.
- 5. In the Analysis window Graph Pane, click Graph Options and select Fitted Peaks and Baseline Fit.

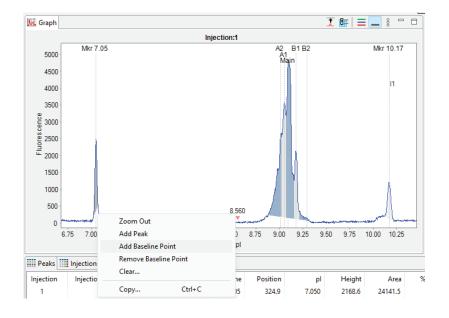


- 6. Select an injection in the Experiment pane.
- 7. Hover the mouse over the peak you want to adjust the baseline on. Two magenta bars will display that show the start and end points of the peak's integration.

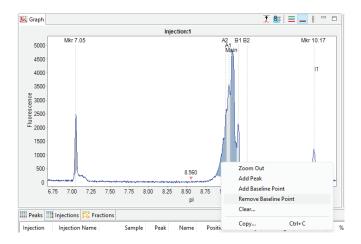
8. To change the baseline, hover the mouse over one of the magenta bars. Then click the mouse and drag the bar to move it. The cursor changes to indicate which direction you can move the integration point. See "Manual Peak Integration" on page 637 for more info on integrating peaks.



9. Baseline points can also be added between two adjacent peaks for a better fit. Hover the mouse over the peak until the magenta bars appear, then right click and select Add Baseline Point.



10. To remove the baseline point, hover the mouse over the peak until the magenta bars appear, then right click and select **Remove Baseline Point**.

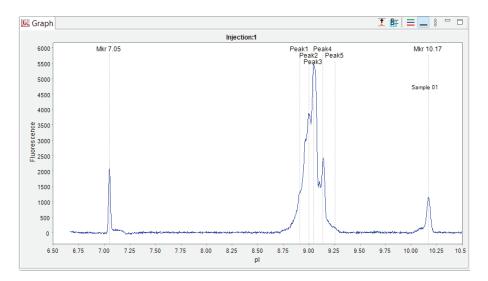


Selecting the Graph X-axis Range

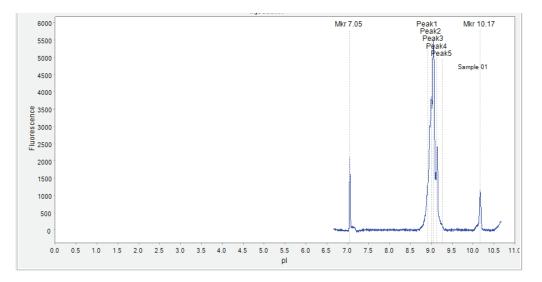
The pI range used for the x-axis can be changed. Just select View in the main menu and click View Region.

ô View Region	×
Range Analysis Fu	II 🔘 Custom
Lower: 3,0	Upper: 10.5
ок	Cancel

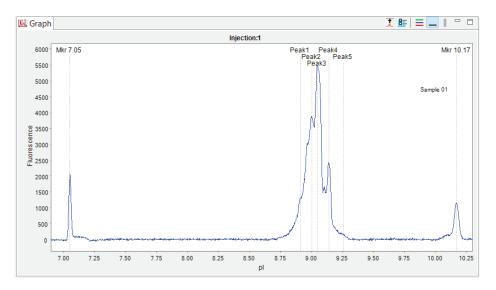
• Analysis sets the x-axis range of the electropherogram to what is selected in the Peak Fit range settings. To view or change these analysis settings, go to Edit > Analysis and click Peak Fit in the left sidebar. In this example, the lower and upper range settings are 6.5 and 10.5.



• Full displays the entire separation in the electropherogram. This is the default setting. In this example the lower and upper range settings are 0 and 11.



• **Custom** lets you manually enter the lower and upper range settings to display in the electropherogram. In this example the lower and upper range settings are 6.8 and 10.3.



NOTE: You can change the default x-axis range that Compass for iCE uses. Go to "Advanced Analysis Settings" on page 642 for more info.

Closing Run Files

If more than one run file is open, you can close just one file or all the open files at the same time.

- To close one run file In the Experiment pane, click on one of the sample rows in the file. Then click File from the main menu and click Close.
- To close all open run files Select File from the main menu and click Close All.

Analysis Settings Overview

Compass for iCE has many analysis features and settings that you can change to enhance your run data.

Select Edit in the main menu and click Analysis. If more than one run file is open, select the run file you want to view settings for from the list:

Edit	View Instrument	Window	Help
	Cut	Ctrl+X	
	Сору	Ctrl+C	
	Paste	Ctrl+V	Graph
	Analysis	•	2016-01-21_09-46-39_mAb11_Prep20160121_QC(0)
	Preferences		2015-12-06_15-13-01_Maurice cIEF_Mab11_TechRep

This opens the Analysis window:

Detection Peak Names	Advanced			
leak Fit Idvanced	Analysis Groups	Analysis Groups: Advanced		
l Markers	Advanced	pl Markers Peak Width	15	
		Allowable Drift	100	_
	Add Remove			
	Apply Default: Advanced	~		
	Apply Override:			
	Apply To Group			
	Add Remove			

To move between pages in the window, click on an option in the left sidebar.

- Detection Lets you view data at different fluorescence exposures.
- **Peak Names** Lets you enter custom naming settings for sample proteins and have Compass for iCE automatically label the peaks in the run data.
- Peak Fit Lets you customize peak fit settings for sample data.
- Advanced Lets you customize analysis settings for the pI markers.
- pI Markers Lets you customize the pI markers and positions Compass for iCE identifies for each method in your run.

On all pages in the Analysis window:

- Click **Import** to import an analysis settings file. Go to "Importing Analysis Settings" on page 657 to learn how to do this.
- Click Export to export the current analysis settings file. Go to "Exporting Analysis Settings" on page 657 to learn how to do this.
- Click Apply to apply changes to the run file and update results in real time.
- Click OK to save changes to the run file and exit.
- Click **Cancel** to exit without saving changes.

Detection Settings

This page lets you see the native fluorescence exposures taken during the run, and select different exposures for data viewing in the Analysis screen. Select **Edit** in the main menu and click **Analysis**, then click **Detection** in the left sidebar.

💮 Analysis: 2022-11-08_11-5	6-11_Maurice Flex Fractions_NIST_Day 1_AT			×
Detection Peak Names Peak Fit Advanced pl Markers	Detection			
	NIST Exposure 1 0.1 seconds v			
Import Exp	OK Cance	<u>ا</u>	Apply	

Peak Names Settings

This page lets you view and change custom naming settings for sample proteins. Select **Edit** in the main menu and click **Analysis**, then click **Peak Names** in the left sidebar.

NOTE: Settings can be changed in the batch default analysis before you start the run, or in run files once they're completed. If you make analysis settings changes to an executing run, they won't be saved to the final run file.

Peak Names					
Analysis Groups		Analysis Gro	oups: Peak G	roup 1	
Peak Group 1		Name Peak1 Peak2	pl 8.91 9.002	Color	Range 0.05 0.05
		Peak3 Peak4	9.047 9.139		0.05
Add	Remove	Peak5	9.255		0.05
Apply Settings	Constant	_			
[1]	Peak Group 1				
Add	Remove		[Add	Remove
	Peak Group 1 Add Apply Settings Apply To [1]	Add Remove Apply Settings Apply To Group [1] Peak Group 1	Peak Group 1 Name Peak1 Peak1 Peak2 Peak3 Peak4 Peak3 Peak4 Peak5 Apply Settings Image: Comp 1 [1] Peak Group 1	Peak Group 1 Name pl Peak Group 1 Peak1 8.91 Peak2 9.002 Peak3 9.047 Peak3 9.047 Peak4 9.139 Peak5 9.255 9.255 Apply Settings Peak6 9.255 [1] Peak Group 1 Peak1 Peak2	Peak Group 1 Name pl Color Peak Group 1 Peak1 8.91 Peak2 9.002 Peak3 9.047 Peak3 9.047 Peak3 9.047 Add Remove Peak3 9.047 Peak4 9.139 Peak4 9.139 Peak4 9.139 Peak5 9.255 Peak5 9.255 Peak5 9.255 Peak5 Peak5 9.255 Peak5 <

Peak Names Analysis Settings Groups

Peak name settings are saved as a group, and you can create multiple settings groups. Specific group settings can be applied to methods, injections, sample names or other attributes in the run data.

NOTE: Analysis settings are run-file specific. But, settings can be imported or exported for use with other run files. For more information see "Importing and Exporting Analysis Settings" on page 657.

Peak name groups are displayed in the analysis settings box:

Analysis Settings	
System Suitability	
mAb 11	
Add Remove	

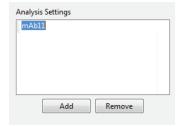
There aren't any Compass for iCE default settings groups, but you can make changes to groups you've created and create new groups. To view settings for a group, click on the group name in the analysis settings box.

Creating a Peak Names Group

- 1. Select Edit > Analysis, and select Peak Names in the left sidebar.
- 2. Click Add under the analysis settings box.

Analysis Settings	
Peak Names 1	
Add Remove	

3. Enter a new name for the group.



4. Click in the first cell in the Name column in the analysis settings peak table and enter a sample protein name.

ame	pI	Color	Range
k1	6		0.05

5. Click in the first cell in the pI column and enter the expected pI for the sample protein.

lame	pI	Color	Range
eak1	5.55		0.05

6. Click in the first cell in the Color column, then click the button.

nalysis Settin	ıgs: mAb11		
Name	pI	Color Ra	nge
Peak1	6.55	(0,1 0.0)5

The color selection box displays:



7. The color you pick is used to identify the sample protein peak in the Peaks and Injections panes in the Analysis screen. Click a color or define a custom color and click OK. The color selection will update in the table:

Analysis Settir	ngs: mAb11			
Name	pI	Color	Range	
Peak1	6.55		0.05	

8. Click in the first cell in the Range column.

ialysis Settii	ngs: mAb11		
Name	pI	Color	Range
eak1	6.55		0.1

- 9. Enter a -/+ range for the pI entered. Compass for iCE will automatically name peaks found within this pI range. For example, if the pI entered is 2 and a 0.1 range is used, all peaks with pIs between 1.9 and 2.1 will be identified with this peak name and color.
- 10. To add another sample protein, click Add under the peak table. Repeat the previous steps for other sample proteins. In this example, eight proteins were entered:

Name	pI	Color	Range
eak1	6.55		0.1
eak2	6.65		0.1
Peak3	6.8		0.1
Peak4	6.9		0.1
Peak5	7		0.1
Peak6	7.1		0.1
Peak7	7.2		0.1
Peak8	7.3		0.1

- 11. To remove a sample protein, select its row and click Remove.
- 12. Click OK to save changes.

Modifying a Peak Names Group

- 1. Select Edit > Analysis, then click Peak Names in the left sidebar.
- 2. Click on the group in the analysis settings box you want to modify.

Analysis Groups	
NIST	
Add Remove	

- 3. Change the information in the analysis settings peak table as described in "Creating a Peak Names Group" on page 623.
- 4. Click **OK** to save changes.

Deleting a Peak Names Group

- 1. Select Edit > Analysis, then click Peak Names in the left sidebar.
- 2. Click on the group in the analysis settings box you want to delete and click Remove.

Analysis	Groups		
<u> </u>			
	Add	Remove	

3. Click OK to save changes.

Applying Peak Names Groups to Run Data

1. Select Edit > Analysis, then click Peak Names in the options list.

2. Click on the group in the analysis settings box you want to apply to specific run data.

Analysis Se	ttings			
System S	uitability			
mAb11				
	Add	Rem	ove	

3. Application of peak names groups to specific run data is done in the apply settings box. A default data set automatically gets created whenever you create a new group and it's applied to all injections in the run. You can either modify the default group or click Add under the box to create a new one.

Apply To	Settings
All	System Suitability mAb11
Ad	d Remove

4. Click the cell in the Apply To column, then click the down arrow.

Apply Settings	
Apply To	Group
[1]	Peak Group 1
All NIST Sample 01 A1	
[1] Custom Settings	
Add	Remove

- 5. Select an option from the drop down list. This applies the peak names group selected to specific run data as follows:
 - All Selecting this applies peak names group settings to all injections.
 - **Methods** All methods in the run file display in the list. Selecting a method applies the group settings to all injections that used that method.
 - **Sample names** All sample names in the run file display in the list, otherwise the default name of Sample shows. Selecting a sample name applies the group settings to all injections that used that sample name.
 - Wells or vials All well or vial numbers used in the run display in the list. Selecting a well/vial number applies the group settings to all injections that used that well/vial.

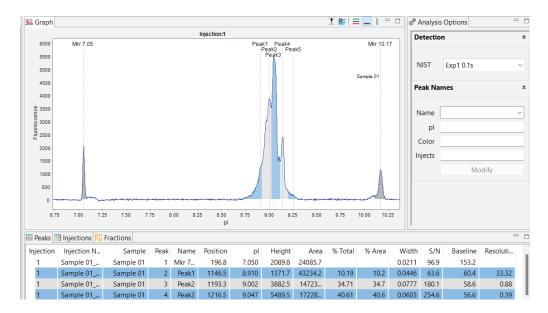
• **Custom settings** - Lets you choose specific injections to apply the group settings to. When you select this in the list, a pop-up box displays to let you enter a specific injection number or range of injections:

Custom Settings	
Enter injection descriptor	
Examples: 3, 5-10 Injection 3, and injections 5 through 10 6+8-10 Injections 6, 8, and 10	OK Cancel

6. If you need to change the peak names group used for a data set, click the cell in the Settings column and click the down arrow. Select a group from the drop down list.

Apply To	Settings
All	System Suitability
mAb Method	mAb11 +
	System Suitability
	mAb11

- 7. Repeat the previous steps to apply other groups to specific run data.
- 8. To remove a data set, click on its cell in the Apply To column, then click Remove.
- 9. Click OK to save changes. Named peaks will be identified with a peak name label in the electropherogram and colorcoded in the Peaks and Injections panes:



Peak Fit Analysis Settings

This page lets you view and change peak fit settings for sample data. Select **Edit** in the main menu and click **Analysis**, then click **Peak Fit** in the left sidebar:

IMPORTANT:

There are two default Peak Fit analysis settings for MauriceFlex Fractionation runs. One set is applied to the final sample injection focusing image and the other set is applied to Fractions data to account for peak shape changes during mobilization.

Only Peak Find settings (threshold and width) can be adjusted when defining analysis settings for Fractions.

NOTE: Settings can be changed in the batch default analysis before you start the run, or in run files once they're completed. If you make analysis settings changes to an executing run, they won't be saved to the final run file.

nalysis Groups Peak Fit Peak Fit Fractions		Analysis Groups: Peak Fit Range Minimum Maximum	<u>3.5</u> 10.5
		Minimum	
		Minimum	
		Maximum	10.5
		View	🔾 Analysis 🔵 Full
		Baseline	
Add	Remove	Baseline Type	Spline
			0.5
oply Default:			
eak Fit	~	/	25.0
		Stiffness	1.0
ply Override:		Peak Find	
	Group		10.0
ractionation	Peak Fit Fractions		15.0
		Area Calculation	Dropped Lines
	Add pply Default: eeak Fit pply Override: Apply To Fractionation	pply Default: leak Fit pply Override: Apply To Group	Add Remove Baseline Type Threshold Window stiffness pply Override: Peak Find Apply To Group Threshold

Default Peak Fit settings for sample injection data.

Detection Peak Names	Peak Fit		
Peak Fit Advanced pl Markers	Analysis Groups Peak Fit	Analysis Groups: Peak Fit Fractions Range	
•	Peak Fit Fractions	Minimum	
		Maximum	
		View	O Analysis O Full
	Add Remove	Baseline Baseline Type	Spline 🗸
	Apply Default:	Threshold	Spine
	Peak Fit	Vindow Stiffness	
	Apply Override:	Peak Find	
	Apply To Group Fractionation Peak Fit Fractions	Threshold	10.0
		Width	20.0
		Area Calculation Droppe	d Lines 🗸 🗸
	Add Remove		
Import Expo	ort	OK Cancel	I Apply

Default Peak Fit settings for Fractions data.

Range Settings

- **Minimum** The pI value below which peaks won't be identified. This value is also used as the default lower pI range for data displayed in the electropherogram.
- **Maximum** The pI value above which peaks won't be identified. This value is also used as the default upper pI range for data displayed in the electropherogram.
- View Sets the default range to either Full or Analysis for the electropherogram x-axis range in the View Region window (select View in the main menu and click View Region).

🎯 View Region
Range Analysis
Lower: 3.0 Upper: 10.5
OK Cancel

- Analysis sets the x-axis range of the electropherogram to the Peak Fit range minimum and maximum settings in the electropherogram. This is the default setting.
- Full displays the entire separation range of the run data in the electropherogram.

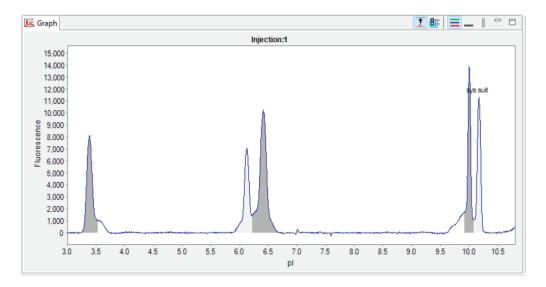
Baseline Settings

These settings apply to spline baselines only.

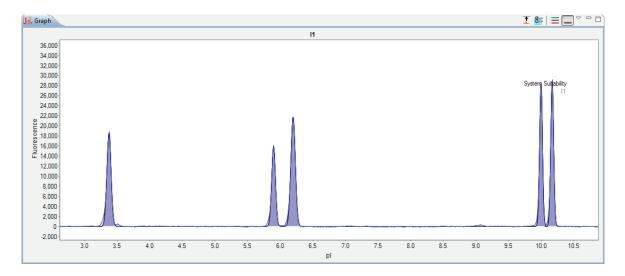
- Threshold The variance, or roughness, in a baseline data segment below which a point is called part of the baseline.
- Window How long baseline data segments are expected to be in pixels. Shorter segments let the baseline follow plateau sections of the signal.
- **Stiffness** The amount the baseline is allowed to vary from a straight line. Settings between 0.1 and 1.0 make the baseline fit closer to a straight line. Settings from 1.0 to 10.0 will make the baseline fit follow the data more closely.

Peak Find Settings

- **Threshold** The minimum signal to noise ratio required for a peak to be identified. A setting of 1.0 will detect many peaks, a setting of 10.0 will detect fewer peaks.
- Width The approximate peak width (at full width half max) in pixels used to detect peaks. The minimum value for this setting is 3.0. Larger widths help eliminate the detection of shoulder and noise peaks.
- Area Calculation Two fits are used, either Gaussian Fit or Dropped Lines. These settings can be changed before or after the run is finished.
 - For MauriceFlex Fractionation applications, peak area is calculated using Dropped Line by default.



• The Dropped Line method type of area calculation is also often called the perpendicular drop method. This is the preferred method when peaks overlap or are close to each other. It draws two vertical lines from the left and right bounds of the peak down to the x-axis and then measures the total area bounded by the signal curve, the x-axis (y=0 line), and the two vertical lines.



• The next view is of the similar data using the Gausiann peak fit method instead.

Peak Fit Analysis Settings Groups

Peak fit settings are saved as a group, and you can create multiple settings groups. Specific group settings can then be applied to methods, injections, sample names or other attributes in the run data.

NOTES:

We recommend using the Compass for iCE default values for peak fit analysis settings. These settings are included in the default Peak Fit group.

Analysis settings are run-file specific. But, settings can be imported or exported for use with other run files. For more information see "Importing and Exporting Analysis Settings" on page 657.

Peak fit groups are displayed in the analysis settings box:

Peak Fi	Groups t	
Peak Fi	t Fractions	

The Peak Fit group shown contains the Compass for iCE default analysis settings. You can make changes to this group and create new groups. To view settings for a group, click on the group name.

Creating a New Peak Fit Group

- 1. Select **Edit** > **Analysis**, and select **Peak Fit** in the left sidebar.
- 2. Click Add under the analysis settings box. A new group will be created:

Peak Fit Fractions	
Peak Fit 3	

3. Click on the new group and enter a new name.

Peak Fit	
Peak Fit Fractions	
Molecule X	
Add	Remove

4. Change the settings in the range, baseline or peak find boxes as needed.

Range			
Minimum	3.5	i	
Maximum	10.	.5	
View O An		nalysis 🔿 Full	
Baseline			
Baseline Type	Spline	~	
Threshold	0.5	i	
Window	25	.0	
Stiffness	1.0)	
Peak Find			
Threshold	10.	.0	
Width	15	.0	
Area Calculation	Dropped Lines	~	

5. To use the new group as the default peak fit settings for the run file data, click the arrow in the drop down list next to Apply Default, then click the new group from the list. Peak fit settings in the new group will then be applied to the run data.

Apply Default:	
Peak Fit	~
Peak Fit Peak Fit Fractions	
Molecule X	

6. Click OK to save changes.

Changing the Default Peak Fit Group

- 1. Select Edit > Analysis, and select Peak Fit in the left sidebar.
- 2. Click the arrow in the drop down list next to Apply Default, then click a new default group from the list.

Apply Default:	
Peak Fit	~
Peak Fit	
Peak Fit Fractions	
Molecule X	

3. Click OK to save changes. Peak fit settings in the group selected will be applied to the run data.

Modifying a Peak Fit Group

- 1. Select Edit > Analysis, and click Peak Fit in the left sidebar.
- 2. Click on the group in the analysis settings box you want to modify.

Peak Fit	
eak Fit Fractions	
Aolecule X	

Range	
Minimum	3.5
Maximum	10.5
View	🔾 Analysis 🔾 Full
Baseline	
Baseline Type	Spline ~
Threshold	0.5
Window	25.0
Stiffness	1.0
Peak Find	
Threshold	10.0
Width	15.0
Area Calculation	Dropped Lines V

3. Change the settings in the range, baseline or peak find boxes as needed.

4. Click OK to save changes. The new peak fit settings will be applied to the run data.

Deleting a Peak Fit Group

- 1. Select **Edit** > **Analysis**, and select **Peak Fit** in the left sidebar.
- 2. Click on the group in the analysis settings box you want to delete and click Remove.

eak Fit Fractio	ons		
Molecule X			

3. Click **OK** to save changes.

Applying Peak Fit Groups to Specific Run Data

1. Select Edit > Analysis, and select Peak Fit in the left sidebar.

Chapter 19: MauriceFlex Fractionation Data Analysis | Peak Fit Analysis Settings

2. Click on the group in the analysis settings box you want to apply to specific run data.

Peak Fit		
Peak Fit	Fractions	
Molecul	еX	

3. Application of analysis groups to specific run data is done in the override box. Click **Add** under the override box. A default override data set will be created from sample information found in the run file.

Apply To	Group
Fractionation	Peak Fit Fractions
lgG	Molecule X
Add	Remove

4. Click the cell in the Apply To column, then click the down arrow.

Apply Override:	
Apply To	Group
Fractionation	Peak Fit Fractions
lgG	Molecule X
Fractionation	
lgG	
Custom Settings	
Add	Remove

- 5. Select an option from the drop down list. This applies the settings group selected to specific run data as follows:
 - Fractionation All mobilization electropherograms in the run file. Selecting Fractionation applies group settings to all Fractions data.

NOTE: Only the Peak Find Threshold and Width can be adjusted when an Analysis Group is applied to a Fractionation settings group.

- **Methods** All methods in the run file display in the list. Selecting a method applies the group settings to all injections that used that method.
- **Custom settings** Lets you choose specific electropherograms to apply the group settings to. When you select this in the list, a pop-up box displays to let you enter a specific injection number or range of injections:

log Custom Settings	X
Enter injection descriptor	
Examples: 3, 5-10 Injection 3, and injections 5 through 10 6+8+10 Injections 6, 8, and 10	OK Cancel

6. If you need to change the analysis group used for a data set, click the cell in the **Settings** column and click the down arrow. Select a group from the drop down list.

Peak Fit Fractions Molecule X
Malacula V
MOIECULE X
Peak Fit
Peak Fit Fractions
Molecule X

- 7. Repeat the previous steps to apply other groups to specific run data.
- 8. To remove a data set, click on its cell in the Apply To column, then click Remove.
- 9. Click **OK** to save changes.

Manual Peak Integration

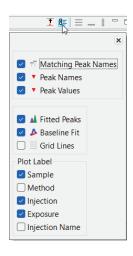
Compass for iCE lets you manually integrate peaks in individual electropherograms when in the Samples view.

1. Select Edit > Analysis, and select Peak Fit in the left sidebar.

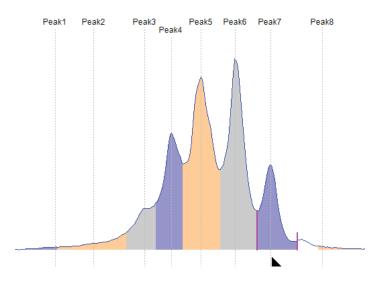
2. Select Dropped lines as the area calculation if it isn't already selected.

Peak Find	
Threshold	15.0
Width	150.0
Area Calculation	Dropped Lines 🗸

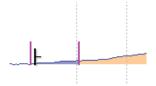
3. Select Fitted Peaks in the Graph Options.



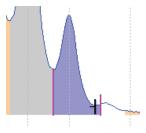
- 4. Select an injection in the Experiment pane.
- 5. Hover the mouse over the peak you want to adjust. Two magenta bars will display that indicate the start and end points of its integration.



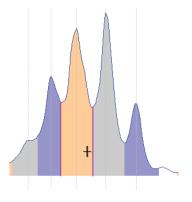
- 6. To change the integration, hover the mouse over either of the magenta bars. Then click the mouse and drag the bar to move it.
 - If the cursor changes to **b** this is the peak start for the peak on the right.

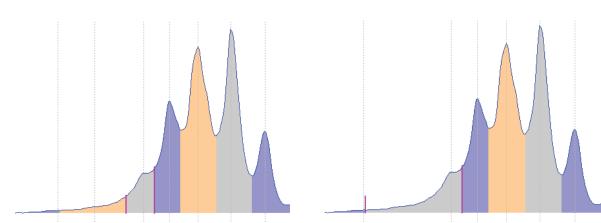


• If the cursor changes to \dashv this is the peak end for the peak on the left.



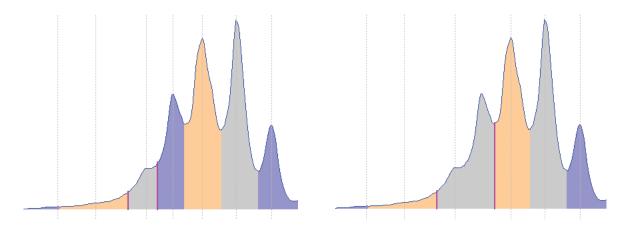
• If the cursor changes to **+** this is a joint boundary for the peaks on the left and right.



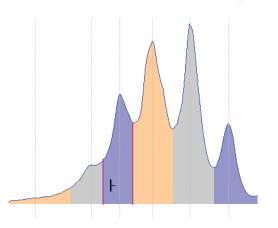


In the example below, we moved the start and end points of the peak to include more area under the peak:

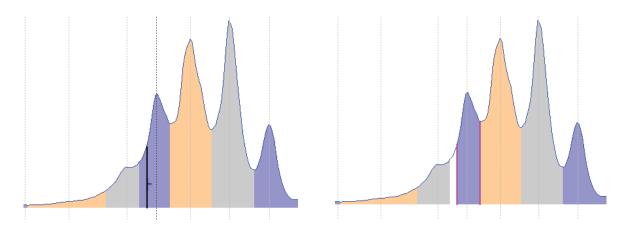
You can also combine peaks by dragging the magenta lines left or right:



You can also separate areas between peaks. Whenever you have a + cursor between two peaks that aren't baseline resolved, move the mouse slightly to the right or left until you get the + or - cursor.

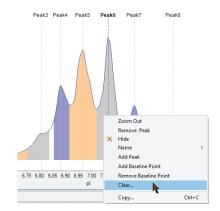


Click and hold the mouse. A black drop line will display indicating where the current peak start or end point is. While holding the mouse, drag the cursor to the right or left to move the start or end point to where you want it, then release the mouse.



7. To remove the manual integration settings, right click on the graph or on the injection in the Experiment pane and select Clear.

Injection	Injection N	Sample	Location	Method
√ 1	NIST	Sample 01	A1	NIST
	3	K Hide		
		Clear		



Advanced Analysis Settings

This page lets you view and change analysis settings for the pI marker data. Select **Edit** in the main menu and click **Analysis**, then click **Advanced** in the left sidebar:

NOTE: Settings can be changed in batches before you start the run, or in run files once they're completed. If you make analysis settings changes to an executing run, they won't be saved to the final run file.

6 Analysis: 2022-12-01_08-00-38_	Alpha Testing NIST v3		- 0	×	
Detection Peak Names	Advanced				
Peak Names Peak Fit Advanced pl Markers	Analysis Groups Advanced	Analysis Groups: Advanced pl Markers Peak Width	15		
	Add Remove Apply Default: Advanced	Allowable Drift	100		
	Apply Override:				
	Apply To Group				
Import Export	Add Remove	OK Cancel	Appl	у	

pl Markers Settings

- **Peak Width** The approximate width (at full width half max) used to filter out fluorescence artifacts which improves recognition of pI markers.
- Allowable Drift The distance the pI marker(s) are expected to move compared to the position entered on the pI Markers page. This setting helps with recognition of the pI marker.

Advanced Analysis Settings Groups

Advanced analysis settings are saved as a group, and you can create multiple settings groups. Specific group settings can be applied to methods, injections, sample names or other attributes in the run data.

NOTES:

We recommend using the Compass for iCE default values for advanced analysis settings. These settings are included in the default Advanced group.

Analysis settings are run-file specific. But, settings can be imported or exported for use with other run files. See "Importing and Exporting Analysis Settings" on page 657 for more info.

Analysis groups are displayed in the analysis settings box:

Adva	nced	

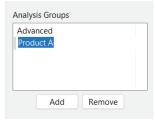
The Advanced group shown contains the Compass for iCE default analysis settings. You can make changes to this group and create new groups. To view settings for a group, click on the group name.

Creating a New Analysis Group

- 1. Select Edit > Analysis, and select Advanced in the left sidebar.
- 2. Click Add under the analysis settings box. A new group will be created:

Analysis Groups	
Advanced	
Advanced 2	
Add Remove	

3. Click on the new group and enter a new name.



4. Change the settings in the Markers box as needed.

Analysis Settings: Product A	
pl Markers	
Peak Width	15
Allowable Drift	100

5. To use the new group as the default analysis settings for the run data, click the arrow in the drop down list next to Apply Default, then click the new group from the list. Analysis settings in the new group will then be applied to the run data.

Apply Default: Advanced Advanced Product A	•
Apply To	Settings
Add	Remove

6. Click **OK** to save changes.

Changing the Default Analysis Group

- 1. Select **Edit** > **Analysis**, and select **Advanced** in the left sidebar.
- 2. Click the arrow in the drop down list next to Apply Default, then click a new default group from the list.

Apply Default:	
Advanced	-
Advanced	
Product A	
Apply To	Settings
Add	Remove

3. Click OK to save changes. Analysis settings in the group selected will be applied to the run data.

Modifying an Analysis Group

- 1. Select Edit > Analysis, and select Advanced in the left sidebar.
- 2. Click on the group in the analysis settings box you want to modify.

ove

3. Change the settings in the Markers box as needed.

Analysis Settings: Product A	
pl Markers	
Peak Width	15
Allowable Drift	100

4. Click OK to save changes. The new analysis settings will be applied to the run data.

Deleting an Analysis Group

- 1. Select Edit > Analysis, and select Advanced in the left sidebar.
- 2. Click on the group in the analysis settings box you want to delete and click Remove.

Analys	is Groups		
Adva			
Produ	ict A		
	Add	Remove	

3. Click **OK** to save changes.

Applying Analysis Groups to Specific Run Data

1. Select Edit > Analysis, and select Advanced in the left sidebar.

Chapter 19: MauriceFlex Fractionation Data Analysis | Advanced Analysis Settings

2. Click on the group in the analysis settings box you want to apply to specific run data.

Analys	is Groups		
Adva			
Prod	uct A		
	Add	Remove	

3. Application of analysis groups to specific run data is done in the override box. Click Add under the override box. A default override data set will be created from sample information found in the run file.

Apply To	Group
gG	Advanced

4. Click the cell in the Apply To column, then click the down arrow.

Apply To	Group
gG	Advanced
gG Custom Setting	gs

- 5. Select an option from the drop down list. This applies the settings group selected to specific run data as follows:
 - **Methods** All methods in the run file display in the list. Selecting a method applies the group settings to all injections that used that method.

• **Custom settings** - Lets you choose specific injections to apply the group settings to. When you select this in the list, a pop-up box displays to let you enter a specific injection number or range of injections:

😨 Custom Settings	X
Enter injection descriptor	
Examples: 3, 5-10 Injection 3, and injections 5 through 10 6+8+10 Injections 6, 8, and 10	OK Cancel

6. If you need to change the analysis group used for a data set, click the cell in the **Settings** column and click the down arrow. Select a group from the drop down list.

Apply To	Group	
gG	Advanced	
	Advanced Product A	

- 7. Repeat the previous steps to apply other groups to specific run data.
- 8. To remove a data set, click on its cell in the Apply To column, then click Remove.
- 9. Click OK to save changes.

pl Markers Analysis Settings

This page lets you define the pI and position of the pI Markers you're using in your samples. Select **Edit** in the main menu and click **Analysis**, then click **pI Markers** in the left sidebar.

NOTE: Settings can be changed in the batch default analysis before you start the run, or in run files once they're completed. If you make analysis settings changes to an executing run, they won't be saved to the final run file.

Detection Deak Names	pl Markers		
eak Fit dvanced	Analysis Groups	lgG_Markers	
Markers	IgG_Markers	Peaks	
		pl	Position
		7.05	300 1,900
	Add Remove		
	Apply Default:		
	IgG_Markers Apply Override:	<u>~</u>	
	Apply To Group IgG IgG_Markers		
	Add Remove	Add Remov	/e
	Add Remove	Add Kemov	re

pl Markers Analysis Settings Groups

pI marker settings are saved as a group, and you can create multiple settings groups. Specific group settings can be applied to methods, injections, sample names or other attributes in the run data.

NOTES:

We recommend using the Compass for iCE default values. These settings are included in the default Markers group.

When you edit the pI markers in the method for a batch, Compass for iCE automatically creates a Markers group in the pI Markers Analysis settings for you.

Analysis settings are run-file specific. But, settings can be imported or exported for use with other run files. For more information see "Importing and Exporting Analysis Settings" on page 657.

Chapter 19: MauriceFlex Fractionation Data Analysis | pl Markers Analysis Settings

Markers groups are displayed in the analysis settings box:

lgG_Markers		

The Markers group shown uses the Compass for iCE default settings. You can make changes to this group and create new groups. To view settings for a group, click on the group name.

Creating a New Markers Group

- 1. Select Edit > Analysis, and select pI Markers in the left sidebar.
- 2. Click Add under the analysis settings box. A new group will be created:

gG_Markers	
gG_Markers 2	

3. Click on the new group and enter a new name.

lgG_Mar	kers	
mAb Me	thod Marke	rs

4. The default Maurice cIEF pI marker pI and position values are already populated in the pI Marker Peaks table. If you'd like to use these values, skip to the next step. If you're using different markers, here's how to change the values:

a. Click in the first cell in the pI column in the table and enter the pI for the marker.

	l Markers – Peaks		
ſ	pI	Position	
	4.05	250	
	10.17	1,800	
		Ad	d Remove

b. Click in the first cell in the Position column and enter a value for the marker.

pI Markers		
Peaks		
pI	Position	
4.05	500	
10.17	1,800	
	Ad	d Remove

NOTE: pI marker peak positions are relative to each other. Only the difference in position is used to help identify them. When entering pI marker peak information for the first time, review the marker data in the Analysis screen to find the correct peak positions.

- c. Repeat the steps above for the remaining markers in the table.
- To add another marker Click Add under the table, then change the information in the new row.
- To remove a marker Select its row and click Remove.
- 5. To use the new group as the default settings for the run, click the arrow in the drop down list next to Apply Default, then click the new group in the list. The settings in the new group will then be applied to the run data.

Apply Default:	
mAb Method Markers	~
lgG_Markers	
mAb Method Markers	

6. Click **OK** to save changes.

Changing the Default Markers Group

- 1. Select Edit > Analysis, and click pI Markers in the left sidebar.
- 2. Click the arrow in the drop down list next to Apply Default, then select a new default group from the list.

Apply Default:	
mAb Method Markers	~
lgG_Markers	
mAb Method Markers	

3. Click OK to save changes. Analysis settings in the group selected will be applied to the run data.

Modifying a Markers Group

- 1. Select Edit > Analysis, and click Markers in the left sidebar.
- 2. Click on the group in the analysis settings box you want to modify.

lgG_Markers	
mAb Method Mark	(ers

- 3. Change the marker info as needed as in Creating a New Markers Group.
- 4. Click OK to save changes. The new analysis settings will be applied to the run data.

Deleting a Markers Group

- 1. Select Edit > Analysis, and click pI Markers in the left sidebar.
- 2. Click on the group in the analysis settings box you want to delete and click Remove.

lgG_Markers	
mAb Method Mark	ers

3. Click OK to save changes.

Chapter 19: MauriceFlex Fractionation Data Analysis | pl Markers Analysis Settings

Applying Markers Groups to Specific Run Data

- 1. Select Edit > Analysis, and select pI Markers in the left sidebar.
- 2. Click on the group in the analysis settings box you want to apply to specific run data.

IgG_Markers	
mAb Method Marker	rs
Add	Remove

3. Application of markers groups to specific run data is done in the override box. Click Add under the override box. A default override data set will be created from sample information found in the run file.

Apply To	Group
lgG	lgG_Markers

4. Click the cell in the Apply To column, then click the down arrow.

Apply To	Group
lgG	IgG_Markers
lgG Custom Settings	

- 5. Select an option from the drop down list. This applies the settings group selected to specific run data as follows:
 - **Methods** All methods in the run file display in the list. Selecting a method applies the group settings to all injections that used that method.

• **Custom settings** - Lets you choose specific injections to apply the group settings to. When you select this in the list, a pop-up box displays to let you enter a specific injection number or range of injections:

log Custom Settings	×
Enter injection descriptor	
Examples: 3, 5-10 Injection 3, and injections 5 through 10 6+8+10 Injections 6, 8, and 10	
	OK Cancel

6. If you need to change the analysis group used for a data set, click the cell in the **Settings** column and click the down arrow. Select a group from the drop down list.

IgG_Markers IgG_Markers mAb Method Markers
IgG_Markers mAb Method Markers

- 7. Repeat the previous steps to apply other groups to specific run data.
- 8. To remove a data set, click on its cell in the Apply To column, then click Remove.
- 9. Click OK to save changes.

Injection Reports

You can export PDF files of the raw and analyzed data, IV plot, peaks table, sample and system info for individual or all injections and mobilization electropherograms in a run file. You can also export the run history with all analysis events.

NOTES:

You can have Compass for iCE generate reports for you automatically at the end of each run. See "Setting up Automatic Injection Reports" on page 761 for more information.

Any time a new report is run, it's saved in a separate run folder. Existing reports aren't overwritten.

- 1. Select File from the main menu in either screen and click Injection Report.
 - File
 Edit
 View
 Instrument

 Open Run
 ▶

 Add Run
 ▶

 Close
 Close

 Close All
 >

 Save
 Save

 Save As...
 Export Tables...

 Export Spectra
 ▶

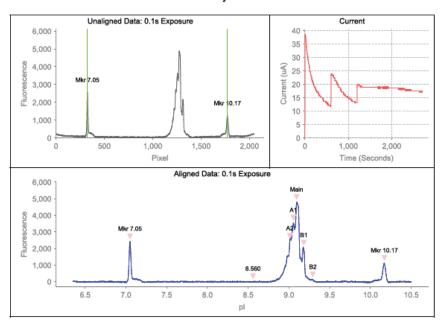
 Injection Report...
 Exit
- 2. In the Injection Reports window:
 - a. Choose either **Selected injections** or **All injections**. Either option will give you the same report since there is only one sample injection in a MauriceFlex Fractionation run.
 - b. Select Analysis log if you want a run history report with all analysis events.
 - c. Select Batch Report if you want to include the sample and method details for each injection in the batch.
 - d. Select Fitted peaks if you want to show peak fitting in the electropherograms.
 - e. Report PDFs generated by Compass for iCE are secured by default, which means they can be viewed and printed but not modified or renamed. Uncheck **Secure PDF** if you don't want to generate a secure report. To learn more about permissions for secured vs. unsecured reports, see page 800.
 - f. The report name defaults to the run file name. If you want to change it, type in the Report Name box to make updates.
 - g. Click OK.

😨 Injections Report		×
Run: 2022-11-08_11-56-11_Maur	ice Flex Fractions_N	NIST_Day 1
Selected injections (1)	Analysis log	
○ All completed injections (1)	Batch report	
	Fitted peaks	
Secure PDF		
Report Name:		Browse
2022-11-08_11-56-11_Maurice Fle	x Fractions_NIST_Da	y 1
Location: C:\Users\Andrea\Docume	ents\Compass for iCE	E\Runs
	ОК	Cancel

3. The individual injection report PDF(s) and a combined injection report PDF are exported to the Runs folder in the Compass for iCE directory. They'll be in a folder with the report name used in the prior step. When the reports are done, the folder opens for you automatically.

$ ightarrow$ \checkmark \uparrow $ ightarrow$ Reports $ ightarrow$	2022-11-08_11-56-11_Maurice Flex Fractions_NIS	T_Day 1_Report_FL(2)	∽ C Sear	rch 2022-11-08_1
Creative Cloud Files	Name	Date modified	Туре	Size
 OneDrive 	🛃 2022-11-08_11-56-11_Maurice Flex Fracti	3/19/2023 12:47 AM	Adobe Acrobat D	130 KB
Andrea	🛃 2022-11-08_11-56-11_Maurice Flex Fracti	3/19/2023 12:47 AM	Adobe Acrobat D	130 KB
E Desktop				
Documents				
Let in the				

Example Analysis and Injection Report



Uncontrolled Injection 1: NIST

Peak	Name	Position	pl	Height	Area	%Total	%Area	Width	S/N	Baseline	Resolution
1	Mkr 7.05	324.9	7.050	2423.4	31491.1			0.0251	125.7	86.6	
2		1025.5	8.560	-16.4	0.0			0.0022	-0.9	15.4	65.29
3	A2	1235.7	9.013	2631.5	75324.3	24.29	24.3	0.0544	136.5	54.3	9.44
4	A1	1255.2	9.055	3548.8	68620.7	22.13	22.1	0.0453	184.0	55.2	0.49
5	Main	1273.5	9.094	4789.8	121793.8	39.28	39.3	0.0563	248.4	55.2	0.46
6	B1	1313.5	9.181	2084.7	37366.5	12.05	12.0	0.0425	108.1	51.8	1.03
7	B2	1365.7	9.293	303.3	6991.9	2.25	2.3	0.0841	15.7	40.1	1.05
8	Mkr 10.17	1772.5	10.170	1119.3	22427.8			0.0398	58.0	102.3	8.34

Fluorescence Peaks: 0.1s Exposure

Uncontrolled Injection 1: NIST

Peak Predictions

Peak	Name	Predicted Wells		
1	Mkr 7.05			
2	8.560	C10, C9, C8, C7, C6		
3	A2	B11, B12, C12, C11, C10		
4	A1	B11, B12, C12, C11		
5	Main	B10, B11, B12, C12		
6	B1	B9, B10, B11, B12		
7	B2	B7, B8, B9, B10, B11		
8	Mkr 10.17	B1, B2		

Sample Information

Injection Name	NIST	
Sample ID	Sample 01	
Location	Plate Well A1	
Batch Name	Alpha Testing NIST	
Run Started	hu 8:01 AM Dec 1, 2022 PST	
Run Completed	Thu 9:50 AM Dec 1, 2022 PST	
Date Acquired	Thu 8:13 AM Dec 1, 2022 PST	
Run Error	None	
Reinjection	No	

Injection Conditions

Guaranteed Injection	Yes
On-board Mixing	Off
Focus Period 1	500V for 10.0 min
Focus Period 2	1000V for 10.0 min
Focus Period 3	1500V for 25.0 min
Detection Exposure	0.1 sec
Detection Interval	5.0 min
Sample Load Duration	30.0 Seconds
pl marker 1	7.05
pl marker 2	10.17
Tray Temperature	11.0°C

Fractionation Conditions

Mobilization	000 Volts for 25.0 min	
Refocus	1500 Volts for 0.0 min	
Fractions	1000 Volts for 45.0 sec	
Detection Exposure	0.1 sec	
Detection Interval	1.0 min	

Maurice Settings

Model	MauriceFlex	
Instrument S/N	mm0008	
Software Version	Compass for iCE 4.0.0, Build ID: 0222	
Firmware Version	.2022.11.03.21.24.04.b15d551f6	
Tray Type	96-well plate	
Cartridge Type	MauriceFlex	
Cartridge S/N	5221128022	
Cartridge Expiration	Nov 2023	
Injections Remaining	16 (16 guaranteed)	
Batches Remaining	16	

Importing and Exporting Analysis Settings

The analysis settings in a run file can be exported as a separate file. This allows the same analysis settings to be imported into other batches or run files at a later time, rather than you having to re-enter them manually.

Importing Analysis Settings

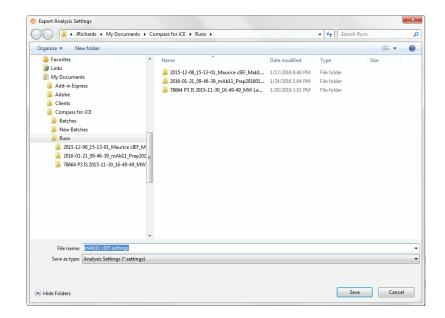
NOTE: Importing an analysis settings file populates the settings in all analysis pages.

- 1. Open the run file or batch you want to import analysis settings to.
- 2. Select Edit in the main menu and click Default Analysis (Batch screen) or Analysis (Analysis screen).
- 3. Click Import on any page.
- 4. Select a settings file (*.settings) and click OK. The imported settings will display in all analysis pages.

Exporting Analysis Settings

NOTE: Exporting an analysis settings file exports the settings in all analysis pages.

- 1. Open the run file or batch you want to export analysis settings from.
- 2. Select Edit in the main menu and click Default Analysis (Batch screen) or Analysis (Analysis screen).
- 3. Click Export on any page. The following window displays:



Chapter 19: MauriceFlex Fractionation Data Analysis | Importing and Exporting Analysis Settings

- 4. The default directory is Compass for iCE/Runs. Change the directory if needed.
- 5. Enter a file name and click **Save**. The settings will be saved as a *.settings file.

Chapter 20: CE-SDS Data Analysis

Chapter Overview

- Analysis Screen Overview
- Opening Run Files
- How Run Data is Displayed
- Viewing Run Data
- Data Notifications and Warnings
- Checking Your Results
- Naming Peaks
- Group Statistics
- Copying Data Views and Results Tables
- Exporting Run Files
- Changing Sample Protein Identification
- Changing the Electropherogram View
- Changing the Virtual Gel View
- Closing Run Files
- Analysis Settings Overview
- Markers Analysis Settings
- Peak Names Settings
- Peak Fit Analysis Settings

- Manual Peak Integration
- Advanced Analysis Settings
- Signal Processing Settings
- Injection Reports
- Importing and Exporting Analysis Settings

Analysis Screen Overview

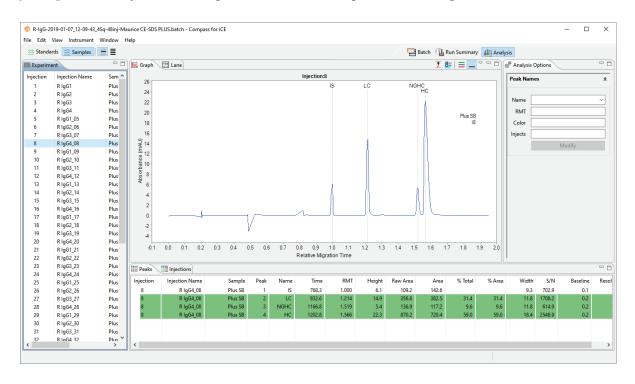
You can use the Analysis screen to view electropherograms, lane view data and tabulated results for your injections. If any post-run analysis is needed, you can do it here too. To get to this screen, click the **Analysis** screen tab:

Batch 🔮 Run Summary 🚛 Analysis

Analysis Screen Panes

The Analysis screen has four panes:

- **Experiment** Lists the injection number, sample IDs, sample locations and methods for each injection in the run and lets you get a quick view of method parameters.
- Graph Displays the electropherograms for sample proteins or standards.
- Lane Displays data for sample proteins as bands in individual lanes. This virtual gel-like image is similar to traditional gel results.
- Peaks Shows the tabulated results for sample proteins, internal standards and CE-SDS MW Markers.
- Injections Displays a list of the sample proteins Compass for iCE names automatically using the user-defined peak name analysis parameters.
- Analysis Options Lets you view, change and add new custom peak name settings.



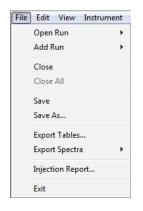
Software Menus Active in the Analysis Screen

These main menu items are active in the Analysis Screen:

- File
- Edit
- View
- Instrument (when Compass for iCE is connected to Maurice, Maurice C., Maurice S. or MauriceFlex)
- Window
- Help

File Menu

These File menu options are active:



- Open Run Opens a run file.
- Add Run Lets you open and view other run files besides the one that's already open.
- **Close** Closes the run file currently being viewed.
- Close All Closes all open run files.
- Save/Save As If you made changes in the Analysis screen before you went to the Run Summary screen, this saves your changes to the run file.
- Export Tables Exports the results for all injections in the run in .txt format.
- Export Spectra Exports the raw and analyzed data traces and background for each injection in the run in .txt or .cdf format.
- **Injection Report** Exports the raw and analyzed data, IV plot, peaks table, sample and system info for individual injections as PDF files. You can also export the run history with all analysis events.
- Exit Closes Compass for iCE.

Edit Menu

These Edit menu options are active:

Edit	View	Instrument	Windo
	Cut	Ct	rl+X
	Сору	Ctr	·l+C
	Paste	Ct	rl+V
	Analysi Preferer		

- **Copy** Lets you copy data shown in the graph, lane, peaks or injections panes. See "Copying Data Views and Results Tables" on page 688 for more information.
- Analysis Displays the analysis settings used to analyze the run data and lets you change them as needed. See "Analysis Settings Overview" on page 713 for more information.
- **Preferences** Lets you set and save your preferences for data export, graph colors, grouped data and Twitter settings. See "Setting Your Preferences" on page 758 for more information.

View Menu

These View menu options are active:



- Selected Displays the data for only the injections selected.
- All Displays data for all injections so you can scroll through them.
- Standards Lets you view data just for the internal standards in your injections.
- Samples Lets you view data just for sample proteins in your injections.
- Grouping Displays data for injection groups.
- View Region Lets you change the x-axis range of the data displayed.
- Show Hidden- Shows injections that are hidden from the data view.

Opening Run Files

You can open one run file or multiple files at the same time to compare information between runs.

Opening One Run File

1. Select File in the main menu and click **Open Run**.

Edit View Instrument	Window Help				
Open Run 🕨	MW ladder assigned_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS				
Add Run 🕨	2016-01-14_09-53-54_Maurice cIEF Ab dilution				
Close	3160106286 KF1011 DG 2016-01-15_15-25-52_Maurice CE-SDS				
Close All	3160106284 KF1011 DG 2016-01-15_12-42-55_Maurice CE-SDS				
CIOSCIAI	3160106283 KF1011 DG 2016-01-14_18-50-33_Maurice CE-SDS				
Save	1151120281-KF1007-BP-2015-12-04_10-17-58_2015Dec3_QC_plateA1_Maurice cIEF				
Save As	1151120284-KF1007-BP-RERUN-2015-12-04_12-48-18_2015Dec3_QC_plateA1_Maurice cIEF				
Export Tables	1151120284-KF1007-BP-2015-12-04_11-21-51_2015Dec3_QC_plateA1_Maurice cIEF				
Export Spectra	1151120284-KF1007-BP-2015-12-04_12-16-51_2015Dec3_QC_plateA1_Maurice cIEF				
Injection Report	KF1007_C1151214314_1X 2015-12-29_14-15-45_cIEF_ViaIA1_Maurice cIEF				
Exit	Browse				

2. A list of the last 10 runs opened will display. Select one of these runs or click **Browse** to open the Runs folder and select a different file.

Opening Multiple Run Files

1. To open the first run file, select File in the main menu and click Open Run.

Open Run	•	MW ladder assigned_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS
Add Run	•	2016-01-14_09-53-54_Maurice cIEF Ab dilution
Close		3160106286 KF1011 DG 2016-01-15_15-25-52_Maurice CE-SDS
Close All		3160106284 KF1011 DG 2016-01-15_12-42-55_Maurice CE-SDS
close rai		3160106283 KF1011 DG 2016-01-14_18-50-33_Maurice CE-SDS
Save		1151120281-KF1007-BP-2015-12-04_10-17-58_2015Dec3_QC_plateA1_Maurice cIEF
Save As		1151120284-KF1007-BP-RERUN-2015-12-04_12-48-18_2015Dec3_QC_plateA1_Maurice cIEF
Export Tables		1151120284-KF1007-BP-2015-12-04_11-21-51_2015Dec3_QC_plateA1_Maurice cIEF
Export Spectra	•	1151120284-KF1007-BP-2015-12-04_12-16-51_2015Dec3_QC_plateA1_Maurice cIEF
		KF1007_C1151214314_1X 2015-12-29_14-15-45_cIEF_VialA1_Maurice cIEF
Injection Report		

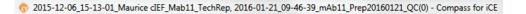
2. A list of the last 10 runs opened will display. Select one of these runs or click **Browse** to open the Runs folder and select a different file. If the run selected is not a CE-SDS PLUS or Turbo CE-SDS batch, an alert will appear.



3. To open another run file, select File in the main menu and click Add Run.

File	Edit View Instrument	Window	v Help	
	Open Run 🕨		1	
	Add Run 🕨	316	60106286 KF1011 DG 2016-01-15_15-25-52_Maurice CE-SDS	
	Close	316	60106284 KF1011 DG 2016-01-15_12-42-55_Maurice CE-SDS	
	Close All	316	60106283 KF1011 DG 2016-01-14_18-50-33_Maurice CE-SDS	
	Save	Bro	owse	
	Save As	A3 B1	Me 20 10 Me 20 5 Me 5	
	Export Tables	B2	Me 50	_
	Export Spectra	B3	Me d 0	
	Injection Report	B4 B5	Me Me	
	Exit	A2		

- 4. A list of CE-SDS runs will display. Select one of these runs or click **Browse** to open the Runs folder and select a different file.
- 5. When a run is added, its data appends to the open run file and displays as a second set of injections in all screen panes. The second run file name also appears in the title bar:



6. Repeat the last two steps to add additional runs.

How Run Data is Displayed

Data in the run file is organized for easy review.

Experiment Pane: Batch Injection Information

The Experiment pane lists all the injections performed in the run, which samples were used for each, the sample location in the 96-well plate or 48-vial tray and the method used.

Experime	ent			- E
Injection	Injection Name	Sample	Location	Method
1	IgG System Contr	IgG System Co	A1	Method1
2	Control Ladder_02	Control Ladder	A2	Method2
3	Test Ladder_03	Test Ladder	A3	Method2
4	IS - Alpha_04	IS - Alpha	B1	Method1
5	IS - Frozen P3_05	IS - Frozen P3	B2	Method1
6	IS - T1 P3_06	IS - T1 P3	B3	Method1
7	IS - T2 P3_07	IS - T2 P3	B4	Method1
8	IS - T3 P3_08	IS - T3 P3	B5	Method1
9	Control Ladder_09	Control Ladder	A2	Method2

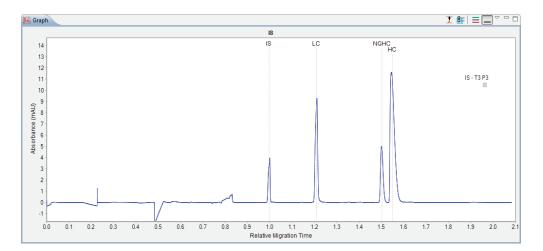
- To view all columns Use the scroll bar or click Maximize in the upper right corner.
- To resize columns Roll the mouse over a column border until the sizing arrow appears, then click and drag to resize.
- To view method parameters Hover the mouse over a method name.

Experime	ent			🗖 🗖 🞼 Graph
Injection	Injection Name	Sample	Location	Method
1	IgG System Contr	IgG System Co	A1	Me Method 1
2	Control Ladder_02	Control Ladder	A2	Me Sample Load: 20 sec 4600 Volts
3	Test Ladder_03	Test Ladder	A3	Me Separation: 0.1 min 1150 Volts, 0.1 min 3450 Volts, 25.0 min 5750 Volts
4	IS - Alpha_04	IS - Alpha	B1	Method1
5	IS - Frozen P3_05	IS - Frozen P3	B2	Method1 11-

NOTE: Data notification icons will display in the Injection column if Compass for iCE detects a potential analysis issue or data was manually modified by the user. For more information see "Data Notifications and Warnings" on page 678.

Graph Pane: Electropherogram Data

The Graph pane displays the electropherogram(s) for sample proteins or internal standards depending on the view options you've selected.



You can get more info on graph view options in "Changing the Electropherogram View" on page 694.

Lane Pane: Virtual Gel-Like Image Data

Click the **Lane** tab to view data for sample proteins as bands in individual lanes. This virtual gel-like image is similar to traditional gel results.



To view information for a band, roll the mouse over a band until the info box appears.

Lane data displayed in the virtual gel is automatically aligned by Compass for iCE. You can get more info on virtual gel view options, see "Changing the Virtual Gel View" on page 711.

Peaks Pane: Calculated Results

The Peaks pane shows the tabulated results for your sample proteins or internal standards. Each row in the table has the individual results for each peak detected in an injection. Results shown will either be for one injection or multiple injections, samples or standards depending on the view options you're using. Check out "Analysis Options Pane: Peak Names" on page 671 for more info.

njection	Injection Name	Sample	Peak	Name	Time	RMT	MW (kDa)	Height	Raw Area	Area	% Total	% Area	Width	S/N
4	IS - Alpha 04	IS - Alpha	1	IS	729.0	1.000	10	3.5	217	298.4		100.0	7.2	250.3
4	IS - Alpha_04	IS - Alpha	2	LC	883.1	1.211	25	9.2	762	864.5	30.7	30.7	9.1	665.6
4	IS - Alpha_04	IS - Alpha	3	NGHC	1095.0	1.502	55	5.2	459	418.6	14.8	14.8	9.3	372.1
4	IS - Alpha_04	IS - Alpha	4	HC	1126.9	1.546	63	11.6	1739	1536.6	54.5	54.5	15.6	832.7
5	IS - Frozen P3	IS - Frozen P3	1	IS	727.3	1.000	10	3.7	230	317.8		100.0	7.2	233.1
5	IS - Frozen P3	IS - Frozen P3	2	LC	880.8	1.211	25	9.4	773	878.3	30.7	30.7	9.1	592.3
5	IS - Frozen P3	IS - Frozen P3	3	NGHC	1092.0	1.502	55	5.2	462	422.2	14.8	14.8	9.3	328.5

NOTES:

Peaks that Compass for iCE names automatically with user-defined peak name settings are color-coded.

When the Standards view is selected, the information in the Peaks table includes only injection, sample, peak, time and height. Internal standards the software has identified are marked with an **S**.

- To view all rows Use the scroll bar or click Maximize in the upper right corner.
- To resize columns Roll the mouse over a column border until the sizing arrow appears, then click and drag to resize.

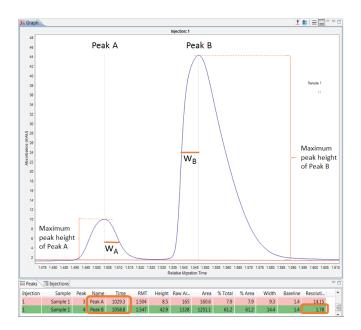
The following results and info are listed in the Peaks table:

- Injection Injection number.
- **Injection name** If injection names were entered in the batch, those names will display here. Otherwise the default 'SampleID_injection number' name will display.
- **Sample** If sample names were entered in the batch, those names will display here. Otherwise, Sample (default name) will display.
- Peak Peaks are numbered in order of detection.
- **Name** Displays peaks Compass for iCE named automatically using the user-defined peak name analysis parameters. These cells are blank if the software wasn't able to name the peak or if you didn't enter naming parameters.
- **Time** Peak detection time (seconds). This is the elapsed time between the start of the separation and when the peak is detected.
- RMT Relative migration time of the peak to the Internal Standard which has an RMT of 1.0.
- **MW** (**kDa**) Displays the relative molecular weight in kDa for sample peaks. MW only displays if you've run the CE-SDS MW Markers as one of the injections in the run and identified that injection in your analysis parameters.

- Height The calculated peak height.
- Raw Area Displays the uncorrected peak area.
- Area Displays the time-corrected peak area. This includes corrections for big and/or slow moving peaks which can be artificially large when uncorrected.
- % Total Displays the peak area ratio compared to the sum of all peak areas (excluding the Internal Standard peak). This value results from dividing the individual peak area by the sum of all peak areas for the injection and multiplying by 100.
- % Area Displays the calculated percent area for the named peak compared to all named peaks. This value results from dividing the individual peak area by the sum of all named peak areas for the injection and multiplying by 100 (shown for named peak sample data only).
- Width Displays the calculated peak width (sample data only).
- **S**/**N** Displays the calculated signal to noise. The signal to noise ratio is reported for each peak based on the noise in the injection and the height of the peak. S/N = 2 x peak height / noise. For the injection noise calculation, the peak to peak noise is calculated by fitting a quadratic to the test region and taking the difference between the max signal above the fit, and the minimum signal below the fit. A fit is used to mitigate the effect of drift in the signal that would give a falsely high noise value. The software looks for the quietest 50 sec region in the first 10 to 600 sec of the injection. The test region is approximately 5 times a typical peak width (FWHM).
- Baseline Displays the raw baseline signal of each peak.
- **Resolution** Displays resolution of the peak compared to neighboring peaks. Two peaks that are baseline resolved will have a resolution value of 1.5. Smaller values mean the peaks are not baseline resolved. Resolution is calculated using this formula:

R=
$$1.18*\frac{t_{B}-t_{A}}{(2w_{B}+2w_{A})}$$

- R Resolution between Peak A and Peak B in Peaks Table.
- \mathbf{w}_{A} Right half peak width at half maximum peak height of Peak A in seconds.
- \mathbf{w}_{B} Left half peak width at half maximum peak height of Peak B in seconds.
- \mathbf{t}_{A} Migration time of Peak A in seconds in Peaks Table.
- $t_{_{\rm B}}$ Migration time of Peak B in seconds in Peaks Table.



Injections Pane: User-Specified Peak Names

The Injections pane shows tabulated results for sample proteins Compass for iCE labels automatically using user-defined peak name settings. Each row in the table shows the individual results for the named peaks detected in each injection.

									% Total	Area	% Area
Injection	Injection Name	Sample	IS	HC	NGHC	LC	10kDa	20kDa	33k	Da	55
1	IgG System Co	IgG System Co	303	1376	381	789					
3	Test Ladder_03	Test Ladder							3	75	
4	IS - Alpha_04	IS - Alpha	298	1537	419	865					
5	IS - Frozen P3	IS - Frozen P3	318	1560	422	878					
6	IS - T1 P3 06	IS - T1 P3	329	1551	415	863					

NOTES:

Peaks that Compass for iCE names automatically with user-defined peak name settings are color-coded.

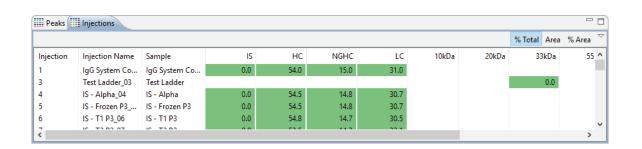
When the Standards view is selected, the information in the Injections table includes only injection, sample and std 1 (the migration time of the standard peak).

- To view all rows Use the scroll bar or click Maximize in the upper right corner.
- To resize columns Roll the mouse over a column border until the sizing arrow appears, then click and drag to resize.

The following results and info are listed in the Injections table:

- Injection Injection number.
- **Injection name** If injection names were entered in the batch, those names will display here. Otherwise the default 'SampleID_injection number' name will display.
- **Sample** If sample names were entered in the batch, those names will display here. Otherwise, Sample (default name) will display.
- **Peak Name Columns** An individual column per peak name will display for every peak identified by name or as a MW Marker peak in the run data. Cells for injections in these columns will be blank if Compass for iCE didn't find peaks automatically using the user-defined peak name analysis and maker parameters (or none were entered).
 - To view peak area in the peak name columns (default) Select Area in the upper right corner of the pane. This displays calculated peak area for the individual peak only.
 - To view % total in the peak name columns This displays the peak area ratio compared to the sum of all peak areas (excluding the Internal Standard peak). This value results from dividing the individual peak area by the sum of all peak areas for the injection and multiplying by 100.

NOTE: The sum of the named peak percentages can be less than 100% if some peaks aren't named.



• To view % area in the peak name columns - This displays the peak area ratio compared to the sum of all named peak areas. This value results from dividing the individual peak area by the sum of all named peak areas for the injection and multiplying by 100.

Peaks	Injections									
									% Total Area	% Area
Injection	Injection Name	Sample	IS	HC	NGHC	LC	10kDa	20kDa	33kDa	55
1	IgG System Co	IgG System Co	100.0	54.0	15.0	31.0				
3	Test Ladder_03	Test Ladder							51.7	
4	IS - Alpha_04	IS - Alpha	100.0	54.5	14.8	30.7				
5	IS - Frozen P3	IS - Frozen P3	100.0	54.5	14.8	30.7				
6	IS - T1 P3_06	IS - T1 P3	100.0	54.8	14.7	30.5				
	TO CO CT 21	IC TO DO	100.0	52.6	14.2	22.1				>

Analysis Options Pane: Peak Names

The Analysis Options pane gives you a quick way to view, change and add new custom peak name settings for sample proteins without having to open and edit the run's analysis settings. You can apply peak name settings to all, selected, or specified injections. For details on how to use this option, go to "Naming Peaks" on page 679.

Name RMT Color Injects Modify	*	5		Peak P
Color]	~	me	Name
Injects]		MT	RMT
]		olor	Colo
Modify]		ects	Inject
1				

Viewing Run Data

The Analysis screen lets you view data for just one injection, specific injections or all injections in the run. Each run file has data for the sample peaks and the Internal Standard detected in each injection.

Switching Between Samples and Standards Data Views

Here's how you switch between viewing data for your samples and standards:

• To view sample data - Click Samples in the View bar or select View in the main menu and click Samples.

File	Edit	View	Instrument	Window
Ħ	Stand	ards [Samples	≣≡

- Data in this view is for sample proteins only.
- The graph displays electropherograms with a y-axis of Absorbance units (mAU) and an x-axis of RMT (relative migration time).
- Lane view data displays sample proteins only.

	19-01-07_12-09-43_ /iew Instrument			PLUS.batch - Compas	s for iCE												- 0	×
	ds 🚖 Samples		icip									Batch 🕼	Run Summar	Anal	ysis			
Experime		- 0	Je Graph	🖽 Lane								I			analysis C	ptions		- 0
Injection	Injection Name	Sam ^	1					Injection:	в						Peak Name	-	-	*
1	R lgG1	Plus	26						IS	LC	NGH	IC .			reak Name			~
2	R lgG2	Plus	24 -									HC						
3	R lgG3	Plus	22												Name			~
4	R laG4	Plus	20												BMT			_
5	R lgG1_05	Plus											Plus SB					_
6	R lgG2_06	Plus	18										18		Color			
7	R lgG3_07	Plus	16												Injects			
8	R lgG4_08	Plus	€ 14							1							Modify	
9	R lgG1_09	Plus	(NWU) 12 10 800 ctpance (MWU)							- 1							widdily	
10	R lgG2_10	Plus	2 2															
11	R lgG3_11	Plus	2 10 ·															
12	R lgG4_12	Plus	8 8									11						
13	R lgG1_13	Plus	₹ 6.									11						
14	R lgG2_14	Plus	4						1		A.	11						
15	R lgG3_15	Plus																
16	R lgG4_16	Plus	2 -							- 14	1							
17	R lgG1_17	Plus	0		~ ~ ~	1/		/										
18	R lgG2_18	Plus	-2			V												
19	R lgG3_19	Plus	-4 -			·												
20	R lgG4_20	Plus	· · _															
21	R lgG1_21	Plus	-0.1	0.0 0.1 0.2	0.3 0.4	0.5 0.6			1.0 1.1	1.2 1.3	1.4 1.5	1.6 1.	7 1.8	1.9 2.0				
22	R lgG2_22	Plus						Relative Mig	ration Time									
23	R lgG3_23	Plus	III Peaks	Injections														- 0
24	R lgG4_24	Plus		~ • •												_		_
25	R lgG1_25	Plus	Injection	Injection Name	Sampl		Name	Time	RMT	Height	Raw Area	Area	% Total	% Area	Width	S/N	Baseline	Resol
26	R lgG2_26	Plus	8	R lgG4_08	Plus St		IS	768.3	1.000	6.1	109.2	142.6			9.3	702.9	0.1	
27	R lgG3_27	Plus	8	R lgG4_08	Plus St		LC	932.6	1.214	14.9	356.6	382.5	31.4	31.4	11.8	1708.2	0.2	
28	R lgG4_28	Plus	8	R lgG4_08	Plus St		NGHC	1166.8	1.519	5.4	136.9	117.2	9.6	9.6	11.8	614.9	0.2	
29	R IgG1_29	Plus	8	R lgG4_08	Plus St	4	HC	1202.8	1.566	22.3	870.2	720.4	59.0	59.0	18.4	2548.9	0.2	
30	R lgG2_30	Plus																
31	R lgG3_31	Plus																
30 K	R InG4 32	Plus Y	<															>
L .		>																,

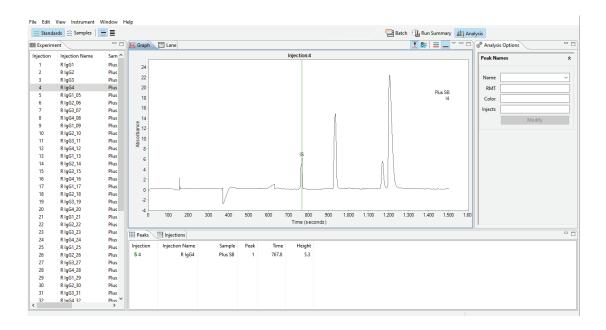
• Results for each protein are shown in the Peaks and Injections panes.

For information on checking and identifying sample peaks, see "Checking Your Data" on page 319 for CE-SDS PLUS runs and page 388 for Turbo CE-SDS runs.

• To view Internal Standard data - Click Standards in the View bar or select View in the main menu and click Standards.



- Data in this view is for analyzing standards only. This is the Internal Standard you add to your samples during prep.
- The graph displays electropherograms with a y-axis of Absorbance units (mAU) and an x-axis of time in seconds.
- Lane view data displays standards only.
- The Internal Standard is identified in the Peaks pane with an S and as IS in the Injections pane.

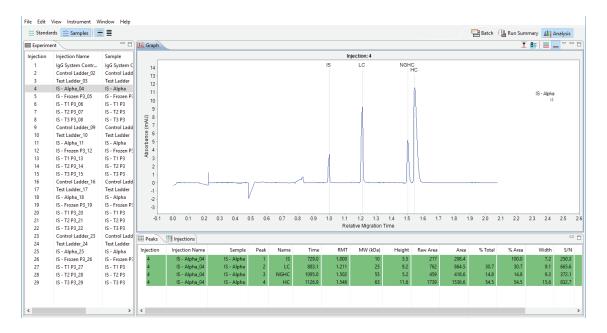


For information on checking and identifying the Internal Standard peak, see "Checking Your Data" on page 319 for CE-SDS PLUS runs and page 388 for Turbo CE-SDS runs.

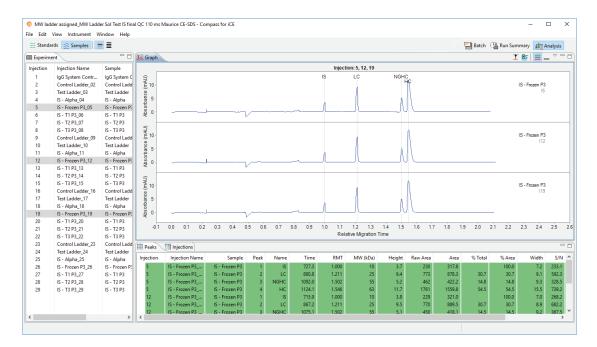
Selecting and Displaying Injection Data

You can view data from one, multiple, or all injections at once.

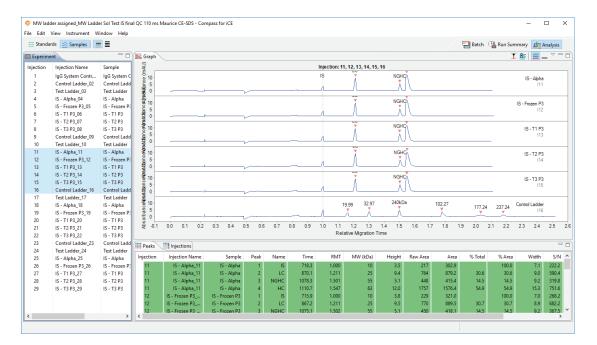
• **To look at data for one injection** - Click an injection row in the Experiment pane. Data for just that injection displays in the data views and tables.



• **To look at data for specific injections** - Hold the **Ctrl** key and select just the injection rows you want to view in the Experiment pane. Data for only the injections selected display in the data views and tables.



• To look at data for sequential injections - Select the first injection row in the Experiment pane that you want to view, then hold the Shift key and select the last. This selects all rows between the two injections. Data for only the injections selected display in the data views and tables.



• To look at data for all injections - Just click View All in the View bar. Data for all injections displays in the graph and tables.

\uparrow

Switching Between Single and Multiple Views of Injections

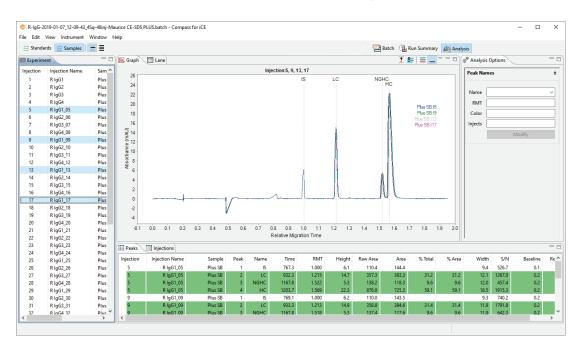
You can switch between displaying run data in a single, per-injection format or a multi-injection format.

• To view data in a per-injection format - Click View Selected in the View bar or select View in the main menu and click Selected.

Window	Instrument	/iew	Edit	File
≣≣	Samples	ds [Stand	Ħ
\uparrow				

Data for the injection row(s) selected in the Experiment pane:

- Displays with electropherograms either overlaid or stacked in the Graph pane depending on the option you've got chosen.
- Lanes for only the selected row(s) are displayed in the lane pane.
- Shows only results for the selected row(s) in the Peaks and Injections panes.

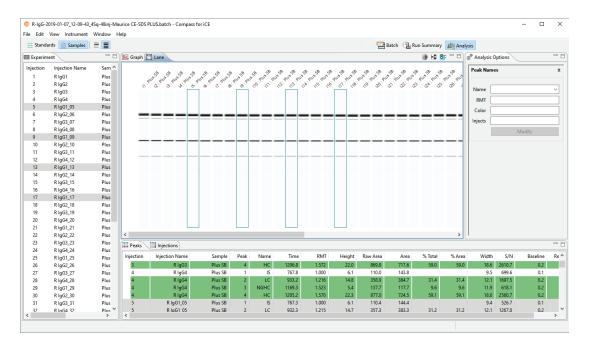


• To view data in a multi-injection format - Click View All in the View bar or select View in the main menu and click View All:

File Edit View Instrument	Window
🚊 Standards 🚊 Samples	≣∎
	\uparrow

Data for the injection row(s) selected in the Experiment pane:

- Displays with the electropherograms of the selected injections highlighted in the Graph pane.
- Displays all lanes in the lane pane, and lanes corresponding to the selected row(s) are highlighted.
- Shows the results for the selected injections highlighted in the Peaks and Injections panes.



Hiding Injection Data

You can hide injection data from the view if needed.

• To hide injections - Select the injection rows you want to hide in the Experiment pane, then right click one and select Hide.

Experime	ent	- 8
Injection	Injection Name	Sample
1	IgG System Contr	IgG System C
2	Control Ladder_02	Control Ladd
3	Test Ladder_03	Test Ladder
4	IS - Alpha_04	IS - Alpha
5	IS - Frozen P3_05	IS - Frozen PS
6	IS - T1 P3_06	IS - T1 P3
7	IS - T2 P3_07	IS - T2 P3
8	IS - T3 P3_08	IS - T3 P3
9	Control Ladder_09	Control Ladd
10	T	Test Ladder
11 🗡	Hide	IS - Alpha
12	Clear	IS - Frozen PS
13	IS - T1 P3 13	IS - T1 P3

Data for the injections will be hidden in all data views and results tables.

• To view hidden injections - Select View in the main menu and click Show Hidden. Hidden rows will become visible again in all panes, and are marked with an X in the Experiment pane.

Experime	ent	
Injection	Injection Name	Sample
1	IgG System Contr	IgG System C
2	Control Ladder_02	Control Ladd
X 3	Test Ladder_03	Test Ladder
4	IS - Alpha_04	IS - Alpha
5	IS - Frozen P3_05	IS - Frozen PS
6	IS - T1 P3_06	IS - T1 P3
7	IS - T2 P3_07	IS - T2 P3
8	IS - T3 P3_08	IS - T3 P3
9	Control Ladder_09	Control Ladd
× 10	Test Ladder_10	Test Ladder
11	IS - Alpha_11	IS - Alpha
12	IS - Erozen P3, 12	IS - Frozen PS

• To unhide injections - Select the hidden row(s). Right click on one and click Unhide.

Data Notifications and Warnings

If Compass for iCE detects a potential data issue, a notification or warning icon will display next to the injection row in the Experiment pane.

 \checkmark

Manual correction of sample data notification - This means the sample data was manually changed by a user, for example to add or remove a sample peak. Roll your mouse over the icon to display the type of modification that was made.

-			
3	Test Ladder	A3	Me
√ 4	IS - Alpha	B1	Me
5	IS - Frozen P3	B2	Me
6	Peak Fit Manual	B3	Me

Standards warning - This means the Internal Standard may not be identified properly. You can fix this by manually identifying the standard using the steps in "Step 1: Check Your Internal Standard" on page 319 for a CE-SDS PLUS run or page 388 for a Turbo CE-SDS run. Roll your mouse over the icon to display warning details.

11	IgG2B-R	B1	Method1
12	hSAP IgG-R	C1	Method1
🚯 13	IgG2B-NR	D1	Method2
6 14	hSAP-IaG-NR	E1	Method2
15	Standards Warning: L	ow Confidence	vethod1

Manual correction of standards data notification - This means a user changed the standards data manually. Roll your mouse over the icon to display the type of modification that was made.

I	8	IS - T3 P3	B5	Me
	9	Control Ladder	A2	Me
	Ø 10	Test Ladder	A3	Me
	11	IS - Alpha	B1	Me
	12	IS - Frozen PE Star	idards Manua	Me
	13	IS - T1 P3	B3	Me

Peak fit warning - Means that a peak can't be fit properly. This can sometimes be caused when a broad peak is fitted as multiple narrow peaks. Changing the peak width can help in this case. The warning is also caused by very small peaks around main peaks, or small peaks that are close to the end of the separation range. You can often fix this by removing the peak(s) using the steps in "Step 3: Checking Sample Peaks" on page 325 for CE-SDS PLUS runs or page 394 for Turbo CE-SDS runs. Roll your mouse over the icon to display warning details.

Δ 6	mAb 25	A3	
<u>A 7</u>	m A P 250	A2	
Peak Fit	Warning: Too ma	ny iterations	
9	mAB 250	A2	
10	mAb 25	A3	

Checking Your Results

Compass for iCE detects your sample protein, CE-SDS MW Markers and Internal Standard peaks and reports results automatically. But, we always recommend you review and check your data as a good general practice to make sure your results are accurate. Please see the step by step procedure in "Checking Your Data" on page 319 for CE-SDS PLUS runs or page 388 for Turbo CE-SDS runs to do this. If you see a data warning in the Experiment pane, these steps will also help you identify and correct any issues.

Naming Peaks

NOTE: Analysis screen options will let you add a new peak name, its RMT, identifying color for peak tables and what injections it applies to. If you need to remove peak names, add peak name analysis settings groups or set RMT ranges, you can do that in the run analysis settings. For more info go to "Peak Names Settings" on page 723.

Adding New Peak Names in the Analysis Options Pane

1. Click the down arrow in the Name field and select New.

@ [®] Analysi	🖗 Analysis Options 🛛 🗖 🗄	
Peak Names		*
Name	I	~
RMT	LC NGHC	
Color	HC [New]	
Injects		
	Modify	

2. Type a name.

@ [®] Analys	is Options 📃 🗖
Peak Na	mes 🎗
Name	Peak 1 🗸
RMT	2
Color	
Injects	All
	Create

3. Click in the **RMT** field and enter the relative migration time of your sample protein.

⊜ [®] Analysi	Analysis Options 🛛 🗖 🗖	
Peak Na	mes 🎗	
Name	Peak 1 V	
RMT	1.25	
Color		
Injects	All	
	Create	

4. Click on the Color field to display the color selection box.

Name	Peak 1	~
RMT	1.25	
Color		
Injects	All	
	Create	



5. The color you pick is used to identify the sample protein peak in the Peaks and Injections panes in the Analysis screen. Click a color or define a custom color and click OK. The color selection will update in the field:

@ [®] Analysi	Analysis Options	
Peak Na	mes 🎗	
Name	Peak 1 v	
RMT	1.25	
Color		
Injects	All	
	Create	

6. Click in the Injects field:

To apply the new peak name to all injections - leave the default setting of All.

To apply the new peak name to specific injections - enter individual injections separated by commas (for example 2, 5, 8), a range of injections (for example 3-15) or a combination of both (for example 8, 10, 12-15). You can also click the tool tip for more examples.

🖗 Analysis Options 🛛 🗖 🗖				
Peak Na	mes 🎗			
Name	Peak 1 v			
RMT Inje ColeFor	ection descriptor example, 3, 5-10			
Injects	All			
	Create			

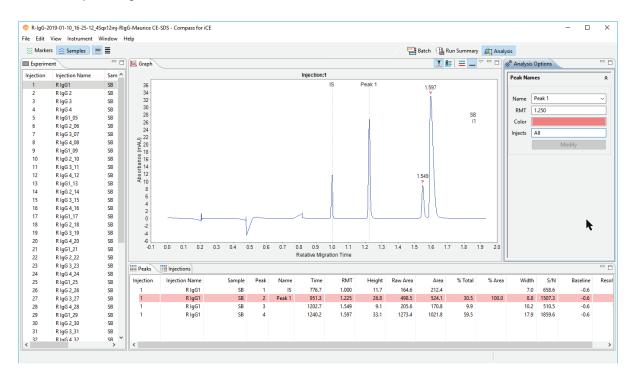
To apply the new peak name to specific run data - type the first letter of a method, sample name, well or vial location. Compass for iCE will search the run data and display a list of matching options for you to choose from. Alternatively you can highlight the text in the Injects cell, hit **Delete**, then select an option from the drop down list.

Peak Na	mes	*	Peak Nar	mes	:
Name	Peak 1	~	Name	Peak 1	~
RMT	1.25		RMT	1.25	
Color			Color		
Injects₽	r T		Injects		
	Reduced IgG			All	
				Reduced IgG	
				Non-reduced IgG	
				MW Markers	
				SB	
				B2	
				B3	
				1	

- All Applies the peak name to all injections.
- **Methods** All methods in the run file display in the list. Selecting a method applies the peak name to all injections that used that method.
- **Sample names** All sample names in the run file display in the list, otherwise the default name of Sample shows. Selecting a sample name applies the peak name to all injections that used that sample name.
- Wells or vials The well or vial numbers currently selected will display in the list. Selecting a well or vial number applies the peak name to all injections that used that well or vial.
- 7. Click Create to save changes.

NOTE: To clear the new peak name information you've entered without saving changes, just delete the peak name in the Name field.

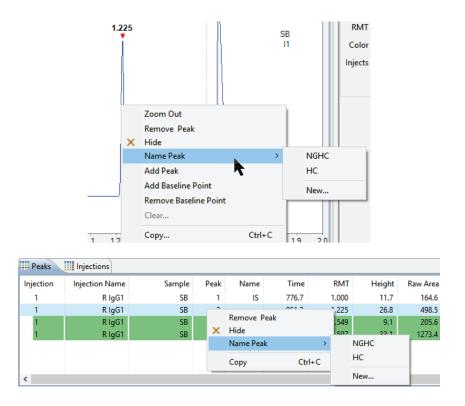
The named peak will be identified with a peak name label in the electropherogram and lane view, and color-coded in the Peaks and Injections panes:



Adding Peak Names from the Graph or Peaks Table

NOTE: Analysis screen options will let you change an existing peak name, its RMT, identifying color in peak tables and what injections it applies to. If you need to remove peak names, add peak name analysis settings groups or set RMT ranges, you can do that in the run analysis settings. For more info go to "Peak Names Settings" on page 723.

- 1. Right click the peak you want to name in the Graph or Peaks pane.
- 2. Select Name Peak.



3. To use an existing peak name - select a name from the list.

To create a new peak name - select New. Type in a name for the peak. Click All to apply to all injections or Selected to apply only to the injections selected.

😚 Add New Peak I	Name		\times
Peak Name:	LC]
Apply Name to:	All	○ Selected	
	ОК	Cancel	

4. Click **OK**. If you want to add an identifying color or change the injections the new peak name applies to, you can do that in the Analysis Options pane.

Changing Peak Name Information

NOTE: Analysis screen options will let you change an existing peak name, its RMT, identifying color for peak tables and what injections it applies to. If you need to remove peak names, add peak name analysis settings groups or set RMT ranges, you can do that in the run analysis settings. For more info go to "Peak Names Settings" on page 723.

1. In the Analysis Options pane, click the down arrow in the Name field and select an existing peak name.

Analysis Options				
Peak Na	*			
Name	LC	~		
RMT	LC NGHC	k		
Color	HC [New]	•		
Injects	All			
	Mod	dify		

2. Change the name, RMT, color and injects as needed then click Modify.

Group Statistics

You can use the Grouping view to have Compass for iCE do a statistical analysis of named proteins in your injections (see "Peak Names Settings" on page 723 for more info on setting named peaks up). Statistics for each protein are also plotted for easy comparison.

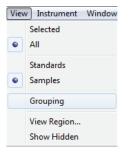
Using Groups

- 1. Groups are automatically created for injections that use the same sample name and method, so to use this feature, you need to make sure you've got sample names entered.
 - a. Go to the **Batch** screen.

	Injection Name	Sample ID	Location	Method	Notes			
1	Sample 1_01	Product A	A1	Reduced IgG				
2	Sample 02_02	Sample 02	A2	Reduced IgG				
3	Sample 03_03	Sample 03	A3	Reduced IgG				
4	Sample 04_04	Sample 04	A4	Reduced IgG				
5	Sample 05_05	Sample 05	A5	Reduced IgG				
6	Sample 06_06	Sample 06	A6	Reduced IgG				
7	Sample 07_07	Sample 07	A7	Reduced IgG				
8	Sample 08_08	Sample 08	A8	Reduced IgG				
9	Sample 09_09	Sample 09	A9	Reduced IgG				
10	Sample 10_10	Sample 10	A10	Reduced IgG				
11	Sample 11_11	Sample 11	A11	Reduced IgG				
12	Sample 12_12	Sample 12	A12	Reduced IgG				

b. Click the **Sample ID** cells in the Injection pane and type a name for any samples you want to calculate statistics for.

2. Go back to the Analysis screen. Click View in the main menu and select Grouping.



NOTE: To turn Grouping off, select View in the main menu and deselect Grouping.

Viewing Sample Injection Groups

Compass for iCE automatically groups all injections using the same sample name together in the Injection Groups pane.

🛛 Inj	jection Groups	
Sam	ple	Method
⊳	Control Ladder (3)	Method2
\triangleright	IS - Alpha (4)	Method1
\triangleright	IS - Frozen P3 (4)	Method1
\triangleright	IS - T1 P3 (4)	Method1
\triangleright	IS - T2 P3 (4)	Method1
\triangleright	IS - T3 P3 (4)	Method1
	IgG System Control	Method1
\triangleright	Test Ladder (4)	Method2

• To expand a group - Click the arrow next to a group to see the individual injections in the group and reported data for each

In In	jection Groups	
Sam	ple	Method
\triangleright	Control Ladder (3)	Method2
\triangleright	IS - Alpha (4)	Method1
\triangleright	IS - Frozen P3 (4)	Method1
\triangleright	IS - T1 P3 (4)	Method1
4	IS - T2 P3 (4)	Method1
	IS - T2 P3	Method1
	IS - T2 P3	Method1
	IS - T2 P3	Method1
	IS - T2 P3	Method1
\triangleright	IS - T3 P3 (4)	Method1
	IgG System Control	Method1
\triangleright	Test Ladder (4)	Method2

- To expand all groups Click Expand All (+) in the upper right corner of the pane.
- To collapse all groups Click Collapse All (-) in the upper right corner of the pane.

Viewing Statistics

Peak and Method Groups

The Peak Groups pane reports statistics for each named protein in every group. Each group shows the statistics for named proteins which includes average area, standard deviation, %CV and SEM (standard error measurement). The number in parenthesis after the sample name is the number of injections in the group.

Peak Groups Method G	roups 📊 Group Plot							🕀 📄 % Total 🛛 🗛 🗮
Sample	Method	Injection	Name	Area	Std.Dev.	% CV	SEM	
> SB (48)	Reduced IgG		LC	450	54.73	12.2	7.899	
> SB (48)	Reduced IgG		NGHC	181	24.26	13.4	3.502	
> SB (48)	Reduced IgG		HC	1134	143.7	12.7	20.74	

- To display results using area Click Area in the upper right corner of the pane.
- To display results using % total Click % Total in the upper right corner of the pane to display the calculated percent area for the named peak compared to the total area measured in the injection. This value results from dividing the individual peak area by the sum of all peak areas for the injection and multiplying by 100.
- To display results using % area Click % Area in the upper right corner of the pane to display the calculated percent area for the named peak compared to all named peaks. This value results from dividing the individual peak area by the sum of all named peak areas for the injection and multiplying by 100 (shown for named peak sample data only).

• To expand a group - Click the arrow next to a group to see the individual injections in the group and reported data for each

III Peak Groups III Method Groups III Group Plot						🕀 📄 % Total 🛛 🗛 🖓 Area 🖓 🗖		
Sample	Method	Injection	Name	Area	Std.Dev.	% CV	SEM	^
✓ SB (48)	Reduced IgG		LC	450	54.73	12.2	7.899	
SB	Reduced IgG	1	LC	499				
SB	Reduced IgG	2	LC	584				
SB	Reduced IgG	3	LC	495				
SB	Reduced IgG	4	LC	487				
SB	Reduced IgG	5	LC	488				
SB	Reduced IgG	6	LC	568				
SB	Reduced IgG	7	LC	472				v

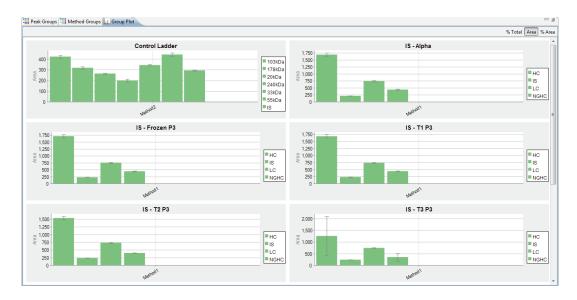
- To expand all groups Click Expand All (+) in the upper right corner of the pane.
- To collapse all groups Click Collapse All (-) in the upper right corner of the pane.

The Method Groups pane pivots the Peak Groups pane results to show statistics for named protein peaks in individual columns.

🖽 Peak Groups 🖽 Method Groups 📊 Group Plot 🕞 🕆 Total Area 🛠 Are								Area % Area			
Sample	Method	Injection	IntSt:Area	Std.Dev.	%CV	SEM	BSA:Area	Std.Dev.	%CV	SEM	^
> 0 (3)	Reduced IgG		0	0.0000	0.0	0.0000	0	0.05963	87.7	0.03443	
> 0 PLUS (3)	IS		0	0.06329	21.6	0.03654	0	0.0000	0.0	0.0000	
> 0.13 PLUS (3)	IS		1	0.2110	41.7	0.1218	0	0.0000	0.0	0.0000	
> 0.41 (3)	Reduced IgG		0	0.0000	0.0	0.0000	1	0.3290	51.1	0.1899	
> 0.41 PLUS (3)	IS		1	0.1279	17.2	0.07382	0	0.0000	0.0	0.0000	
> 1.23 (3)	Reduced IgG		0	0.0000	0.0	0.0000	1	0.2445	17.3	0.1412	
> 1.23 PLUS (3)	IS		2	0.09553	3.9	0.05515	0	0.0000	0.0	0.0000	
> 100 PLUS (3)	IS		148	4.119	2.8	2.378	0	0.0000	0.0	0.0000	~

Group Plots

The mean values for named peaks using the same method in each injection group are plotted in bar graphs with error bars showing the standard deviation in the Group Plots pane. You'll also get plots that compare samples using the same method in the run.



Hiding or Removing Injections in Group Analysis

Hidden injections are not included in injection groups. But, hiding injections gives you an easy way to reject individual injections from the statistical analysis. See Hiding Injection Data for details on how to do this.

Copying Data Views and Results Tables

You can copy and paste data and results tables into other documents, or save a data view as a graphic file.

Copying Results Tables

- 1. Click in the Peaks or Injections pane.
- 2. Select one or multiple rows.
- 3. Select Edit in the main menu and click Copy, or right click on row(s) you selected and click Copy.
- 4. Open a document (Microsoft[®] Word[®], Excel[®], PowerPoint[®], etc.). Right click in the document and select **Paste**. Data for the rows selected will be pasted into the document.

Copying Data Views

- 1. Click in the Graph or Lane pane.
- 2. Select Edit in the main menu and click Copy, or right click and select Copy.
- 3. Select an image option in the pop-up window, then click Copy.

Copy Graph	×	Copy Gel X
 Metafile (El Bitmap (PN) 	-	PNG Format JPG Format BMP Format Save Copy Cancel

4. Open a document (Microsoft[®] Word[®], Excel[®], PowerPoint[®], etc.). Right click in the document and select **Paste**. A graphic of the copied electropherogram will be pasted into the document.

Saving the Data Views as an Image File

- 1. Click in the Graph or Lane pane.
- 2. Select Edit in the main menu and click Copy, or right click and select Copy.

3. Select an image option in the pop-up window, then click Save.

Copy Graph X	Copy Gel X
Graph title: Injection:8 Metafile (EMF) Bitmap (PNG) Portable Document Format (PDF) Save Copy Cancel	PNG Format JPG Format BMP Format Save Copy Cancel

4. Select a directory to save the file to, enter a file name, then click OK.

Exporting Run Files

Results tables and raw plot data can be exported for use in other applications.

Exporting Results Tables

To export the information in the Peaks and Injections tables:

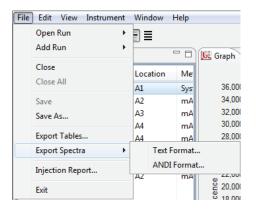
- 1. Click File in the main menu and click Export Tables.
- 2. Select a directory to save the files to and click OK. Data will be exported in .txt format.

NOTE: To exclude export of standards data or export results table data in .csv format, see "Setting Data Export Options" on page 760.

Exporting Raw Sample Electropherogram Data

To export raw sample plot and background data:

1. Click File in the main menu and click Export Spectra.



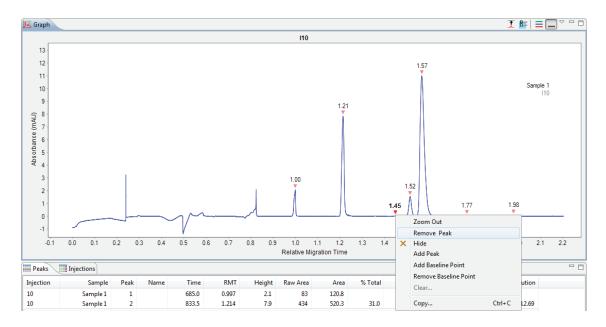
- To export data in .txt format Select Text Format. Data will be exported in one file for all injections.
- To export data in .cdf format Select ANDI Format. Data will be exported in one file per injection.
- 2. Select a directory to save the files to and click OK. Data will be exported in the selected format.

Changing Sample Protein Identification

Compass for iCE lets you customize what sample proteins are reported in the results tables by making manual adjustments in the electropherogram or Peaks table.

Adding or Removing Sample Data

- 1. Click Show Samples in the View bar.
- 2. Click Single View in the View bar.
- 3. Click on the row in the experiment pane that has the injection you want to correct, then click the Graph tab.
 - To remove a peak from the data Right click the peak in the electropherogram or Peaks table and select **Remove peak**. The software will no longer identify it as a sample peak in the electropherogram, and the peak data will be removed in the results tables.



A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

Experime	nt		- 0
Injection	Sample	Location	Method
1	Sample 1	A1	Method1
2	Sample 1	A1	Method1
3	Sample 1	A1	Method1
4	Sample 1	A1	Method1
5	Sample 1	A1	Method1
6	Sample 1	A1	Method1
7	Sample 1	A1	Method1
8	Sample 1	A1	Method1
9	Sample 1	A1	Method1
✓10	Sample 1	A1	Method1
11	Sample 1	A1	Method1
12	Sample 1	A1	Method1

• To add an unidentified peak to the data - Right click the peak in the electropherogram or peaks table and select Add Peak. The software will calculate and display the results for the peak in the results tables and identify the peak in the electropherogram.

A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.

NOTES:

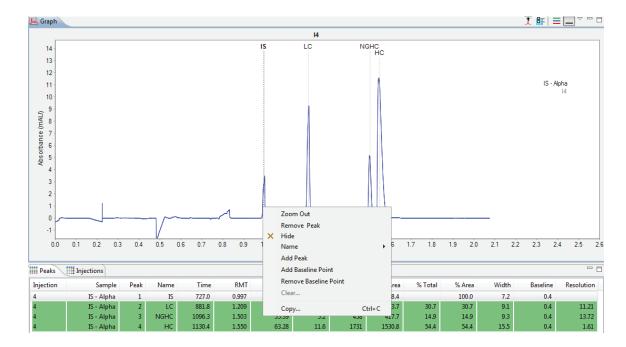
To remove sample peak assignments that were made manually and go back to the original peak data, right-click the peak in the electropherogram and select **Clear** for the current injection or **Clear All** for all injections in the batch.

Virtual gel data in the lane pane will also update to reflect changes made in the graph pane.

Hiding Sample Data

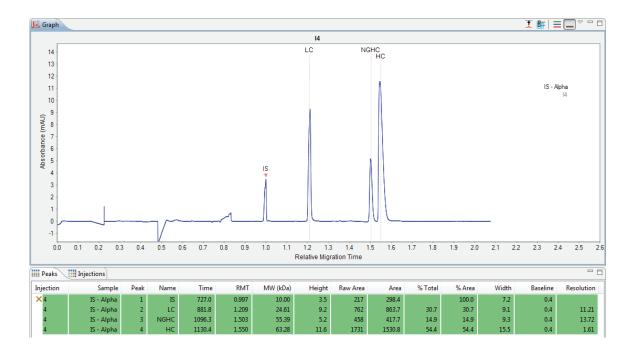
You can hide the results for a sample protein in the results tables without completely removing it from the reported results.

- 1. Click Show Samples in the View bar.
- 2. Click Single View in the View bar.
- 3. Click on the row in the experiment pane that contains the injection you want to correct, then click the Graph tab.



4. Right click the peak in the electropherogram or Peaks table and select Hide. Compass for iCE will hide the peak data in the results tables.

5. To view hidden peak data, click View in the main menu and click Show Hidden. Hidden peak data will display in the results table and be marked with an X.

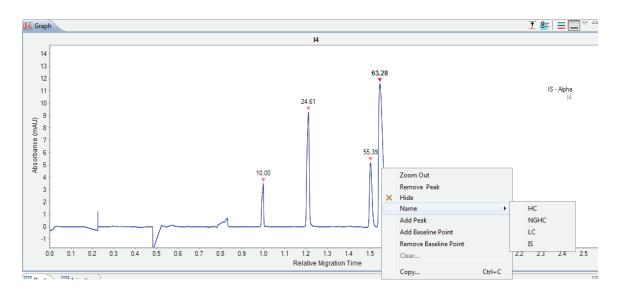


6. To unhide a peak, right click on the peak in the electropherogram or peaks table and select Unhide.

Changing Peak Names for Sample Data

If Compass for iCE did not automatically name a sample protein peak, you can do it manually.

- 1. Click Show Samples in the View bar.
- 2. Click Single View in the View bar.
- 3. Click on the row in the experiment pane that has the sample you want to correct, then click the Graph pane.
- 4. Right click the peak in the electropherogram or Peaks table and click **Name**, then select a name from the list. Compass for iCE will change the peak name in the electropherogram and results tables, and adjust peak names for other sample proteins accordingly.



NOTES:

For details on how to specify peak name settings, see "Peak Names Settings" on page 723.

Virtual gel data in the lane pane will also update to reflect changes made in the graph pane.

Changing the Electropherogram View

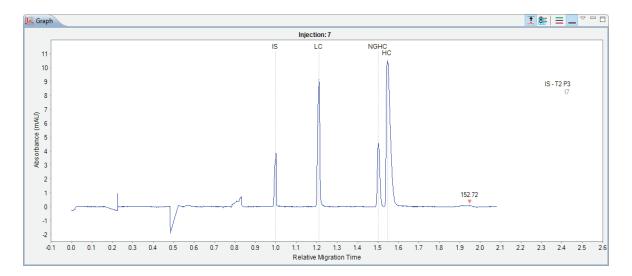
Options in the Graph pane let you zoom and rescale electropherograms, overlay or stack plots and change the peak and plot info displayed.

The Graph pane toolbar has these options:



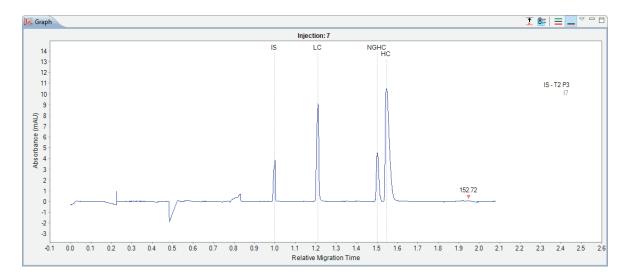
Autoscaling the Electropherogram

Click the Auto Scale button to scale the y-axis to the largest peak in the electropherogram.



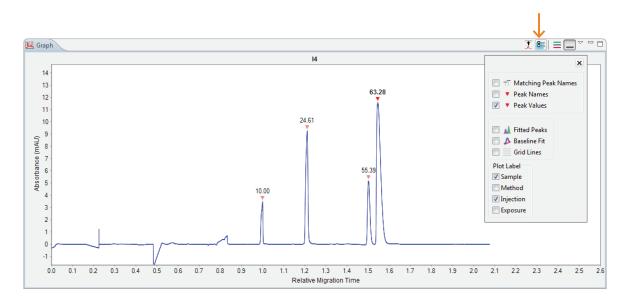
Chapter 20: CE-SDS Data Analysis | Changing the Electropherogram View

Click the Auto Scale button again to return to default scaling.



Customizing the Data Display

You can customize electropherogram peak labels, plot labels and display options. To do this, just select the **Graph Options** button.

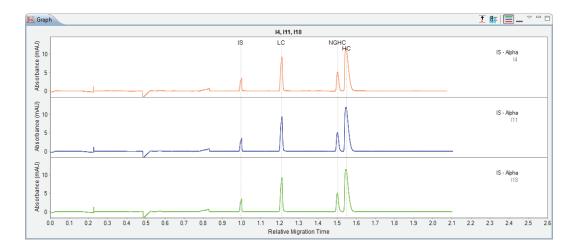


Peak Labels

You can customize the labels used to identify peaks in the electropherogram with these options:

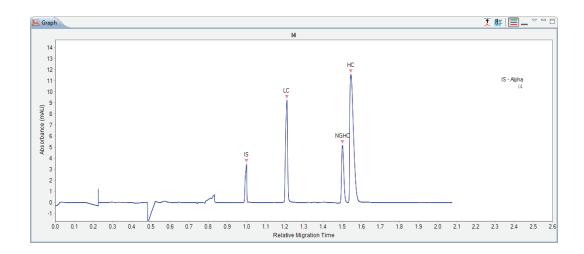


• Matching Peak Names - Checking this box will draw vertical lines through each named peak. Using this option with Stack the Plots or Overlay the Plots features is helpful for visually comparing your named peaks across multiple injections.



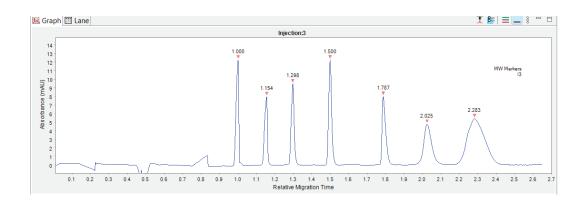
• Peak Names - Checking this box displays peak name labels on all named peaks in the electropherogram.

NOTE: If more than one peak label option is selected, peak name labels will always be used for named peaks.



• **Peak Values** - Checking this box will display the molecular weight labels on all peaks in the electropherogram. If a MW Marker wasn't run, RMT values are displayed.

NOTE: If more than one peak label option is selected, peak name labels will always be used for named peaks.



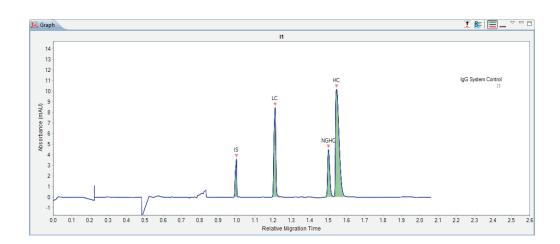
Baseline and Grid Options

You can view the calculated baseline fit, peak integration and show grid lines with these options.

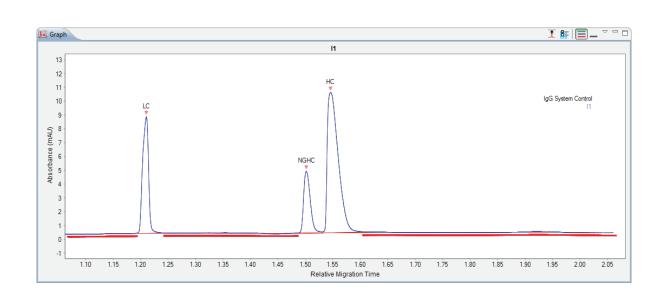


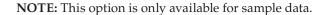
• Fitted peaks - Checking this box displays how the peaks were fit by the software. For CE-SDS runs, the software uses Dropped Lines by default.

NOTE: This option is only available for sample data.

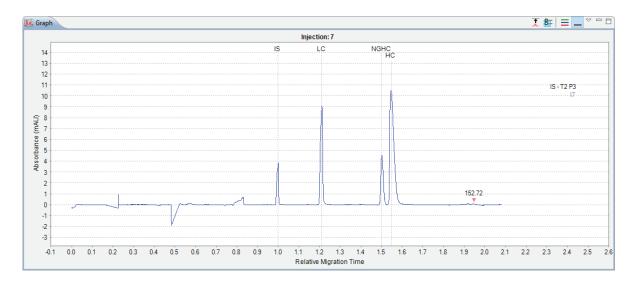


• **Baseline Fit** - Checking this box displays the calculated baseline for the peaks. Depending on your baseline type setting (baseline points or interpolated baseline) baseline points will also display for regions of the electropherogram considered to be at baseline.





• Grid Lines - Checking this box adds grid lines in the graph.



Plot Labels

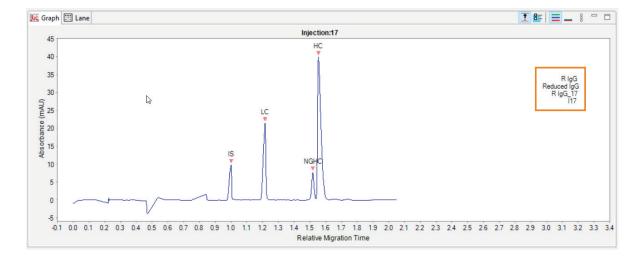
You can customize the plot labels displayed on the electropherogram with these options.

Plot Label
Sample
Method
Injection
Injection Name

Plot labels are shown in the upper right side of the graph.

- **Sample** Checking this box displays the sample name used for the injection. If sample names were entered with the batch, those names will display here. If not, Sample (default name) displays.
- Method Checking this box displays the method used for the injection.
- Injection Checking this box displays the injection number. For example, I4 for injection 4 in the run.
- **Injection Name** Checking this box displays the injection name used for the injection. If injection names were entered with the batch, those names will display here. If not, the default name displays.

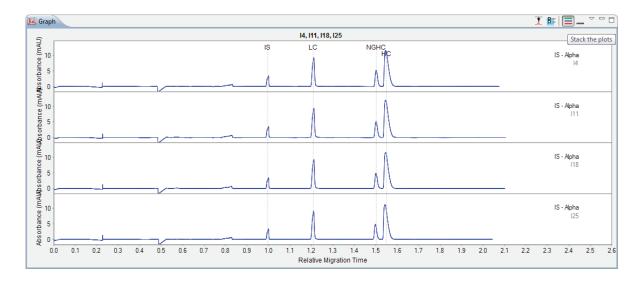
Here's an example of an electropherogram with all plot labels selected:



Stacking Multiple Electropherograms

You can stack electropherograms for multiple injections vertically in the Graph pane for comparison.

- 1. Click Single View.
- 2. Select multiple injection rows in the Experiment pane.



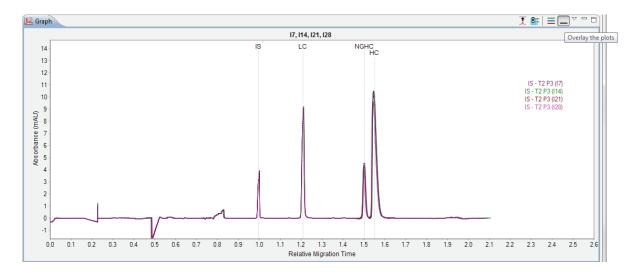
3. Click the **Stack the Plots** button. The individual electropherograms for each injection you selected will stack in the Graph pane.

You can also customize the colors used for the stacked plot display. To do that go to "Setting up Automatic Injection Reports" on page 761.

Overlaying Multiple Electropherograms

You can overlay electropherograms for multiple injections on top of each other for comparison in the Graph pane.

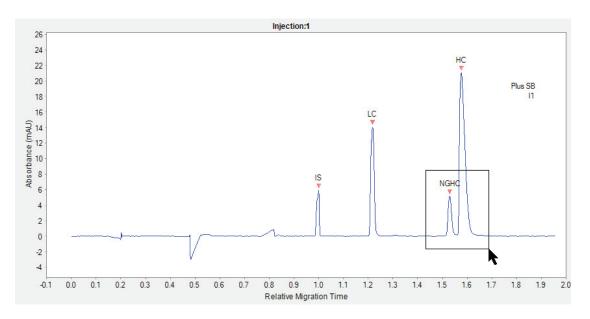
- 1. Click Single View.
- 2. Select multiple injection rows in the Experiment pane.
- 3. Click the **Overlay the Plots** button. The individual electropherograms for each injection you selected will overlay in the Graph pane.



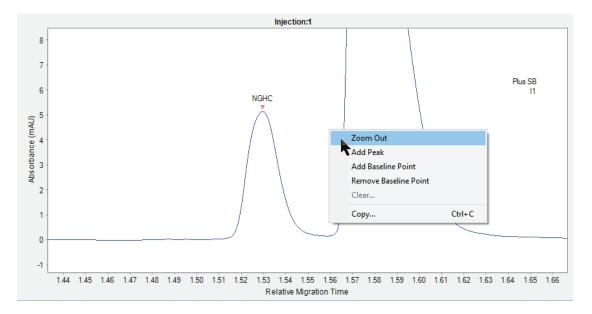
You can also customize the colors used for the overlay plot display. To do that go to "Setting up Automatic Injection Reports" on page 761.

Zooming

To zoom in on a specific area of the electropherogram, hold the mouse button down and draw a box around the area with your mouse:

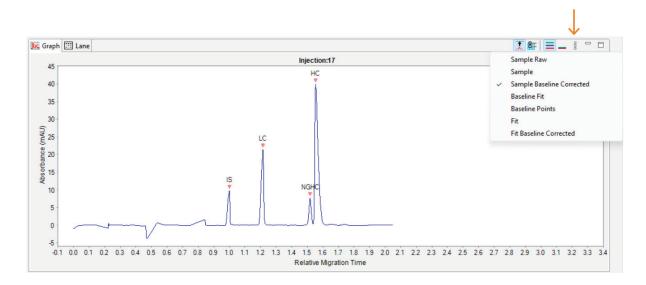


To return to default scaling, right click in the electropherogram and click Zoom Out.



Selecting Data Viewing Options

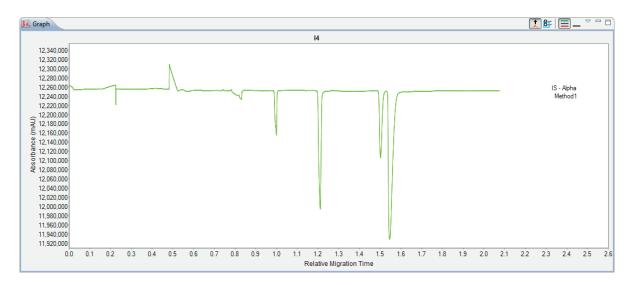
The graph view menu gives you multiple options for changing what type of electropherogram data is displayed. Just click **View More** in the graph pane toolbar to view the menu:



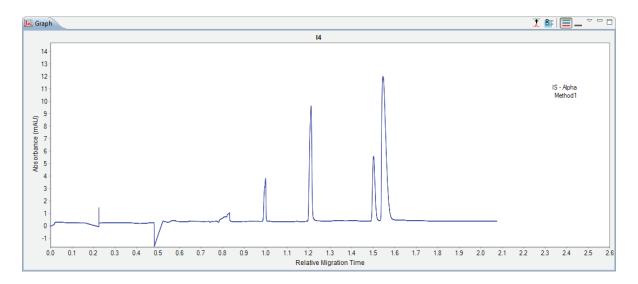
A check mark next to the menu option indicates it's currently selected, and you can select multiple options at once.

NOTE: Unless noted otherwise, graph view menu options are available for sample data only.

• **Sample Raw** - Clicking this option displays the basic detector values used to calculate peak absorbance. To view this you'll need to select **Auto Scale** in the Graph pane tool bar.

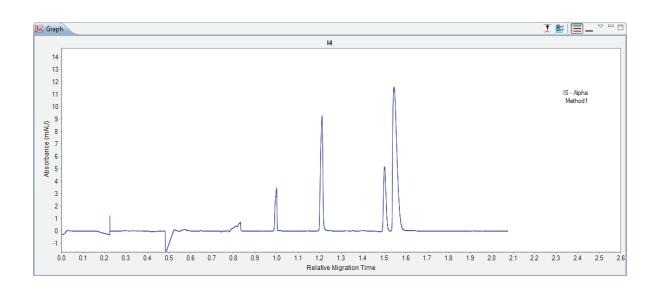


• **Sample** - Clicking this option displays raw, uncorrected sample data.

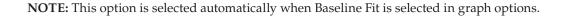


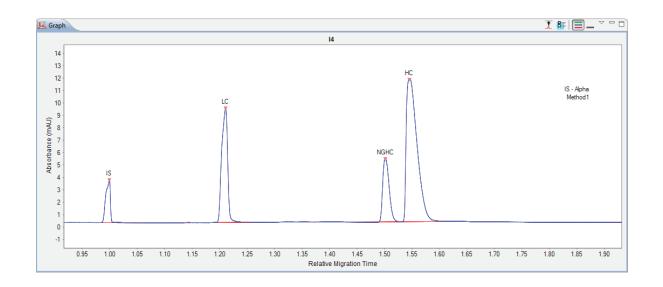
• **Sample Baseline Corrected** - Clicking this option displays sample data with the baseline subtracted (zeroed). This is the default view.

NOTE: The Sample Baseline Corrected data line will not be displayed if Baseline Type is set to Interpolate in the analysis menu option.



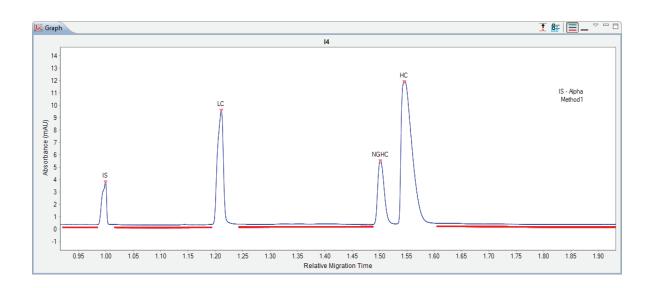
• **Baseline Fit** - Clicking this option displays the calculated baseline for the raw sample data. In this next example, both Baseline Fit and Sample are selected.



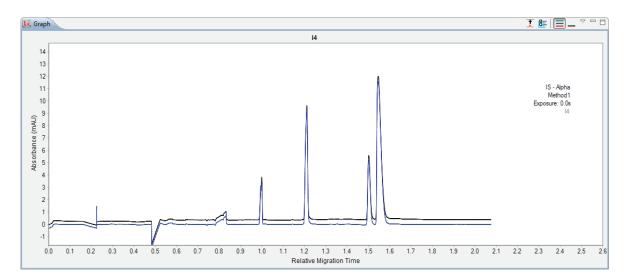


• **Baseline Points** - Clicking this option displays regions of the electropherogram considered to be at baseline. In this example, both Baseline Points and Sample are selected.

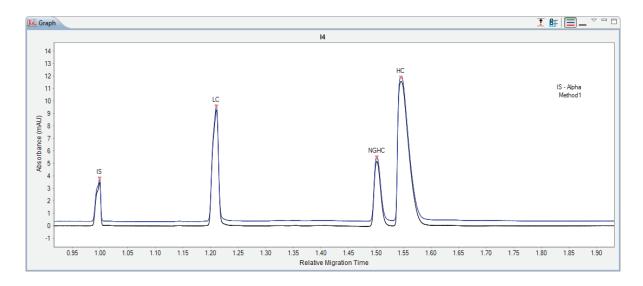
NOTE: This option is selected automatically when Baseline Fit is selected in graph options.



• Fit - Clicking this option displays the bounding envelope of the fitted peaks as calculated by the software for the raw sample data. In this example, both Fit and Sample Baseline Corrected are selected.



• Fit Baseline Corrected - Clicking this option displays the fitted peaks as calculated by the software for the sample baseline corrected data. In this example, both Fit Baseline Corrected and Sample are selected, the fit plot is on the bottom.

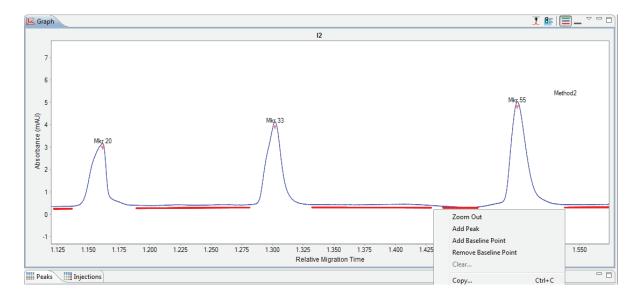


Adjusting the Baseline

Spline Baseline

Points in the baseline can be added or removed as needed.

- 1. Click the **Graph Options** button in the graph pane toolbar and check **Baseline Points**. This will display baseline points for the raw sample data.
- 2. Use the mouse to draw a box around the area you want to correct. This will zoom in on the area.
- 3. Right click a baseline point and select Add Baseline Point or Remove Baseline Point.



NOTE: To clear the manual addition or removal of baseline points and go back to the original view of the data, right click in the electropherogram and click **Clear All**.

Interpolated Baseline

Compass for iCE lets you interpolate baselines from the base of each peak for named peaks that use Dropped Lines integration.

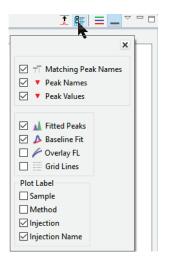
- 1. If you haven't already, name your peaks of interest.
- 2. Select Edit > Analysis, and click Peak Fit in the left sidebar.

3. Choose Interpolate as the Baseline Type if it isn't already selected.

NOTE: Baseline Type selection is only available when Dropped Lines is used for the Area Calculation.

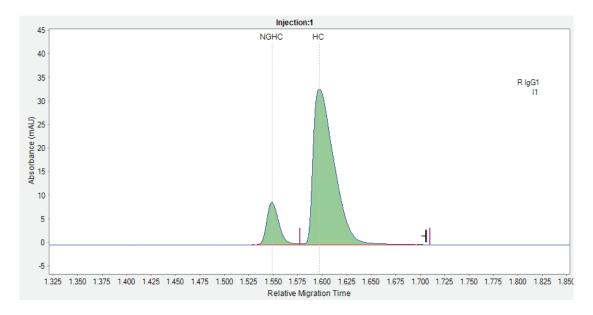
Analysis Groups: Peak Fit	
Range	
Minimum	0.9
Maximum	3.2
View	🔾 Analysis 💿 Full
Baseline	
Baseline Type	Spline 🗸
Threshold	Spline Interpolate
Window	100.0
Stiffness	1.0
Peak Find	
Threshold	15.0
Width	35.0
Area Calculation	Dropped Lines $\ \lor$

- 4. Click OK.
- 5. In the Analysis window Graph Pane, click Graph Options and select Fitted Peaks and Baseline Fit.

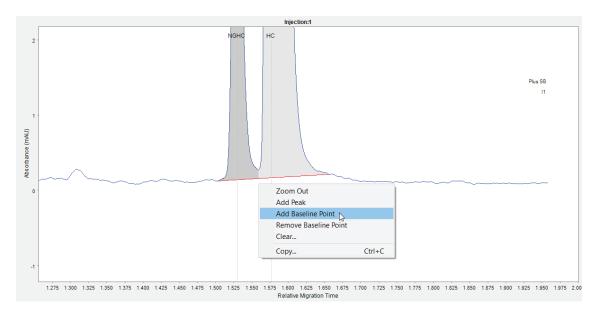


- 6. Select an injection in the Experiment pane.
- 7. Hover the mouse over the peak you want to adjust the baseline on. Two magenta bars will display that show the start and end points of the peak's integration.

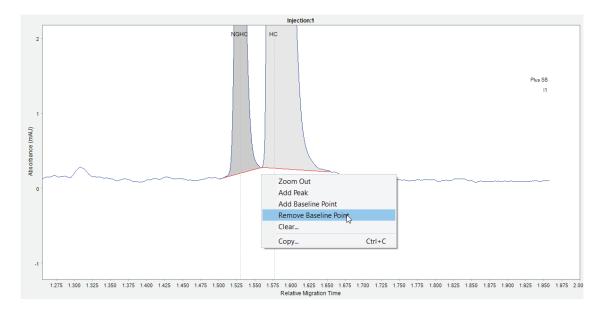
8. To change the baseline, hover the mouse over one of the magenta bars. Then click the mouse and drag the bar to move it. The cursor changes to indicate which direction you can move the integration point. See "Manual Peak Integration" on page 739 for more info on integrating peaks.



9. Baseline points can also be added between two adjacent peaks for a better fit. Hover the mouse over the peak until the magenta bars appear, then right click and select Add Baseline Point.



10. To remove the baseline point, hover the mouse over the peak until the magenta bars appear, then right click and select **Remove Baseline Point**.

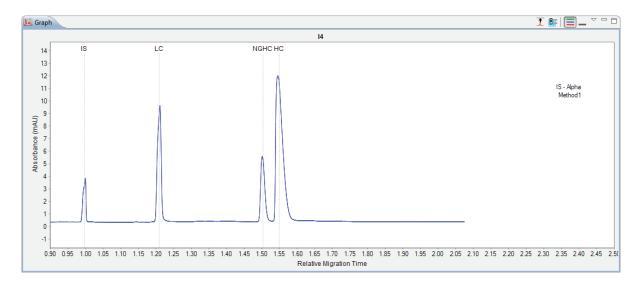


Selecting the Graph X-axis Range

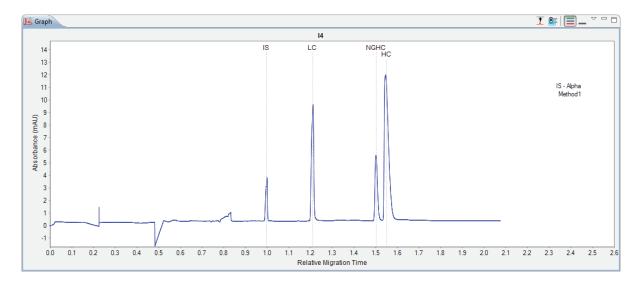
The RMT (relative migration time) range used for the x-axis can be changed. Just select **View** in the main menu and click **View Region**.

🎯 View Region	×
Range O Analysis I Full O Custom	
Lower: 0.0 Upper: 2.6	
OK Cancel	

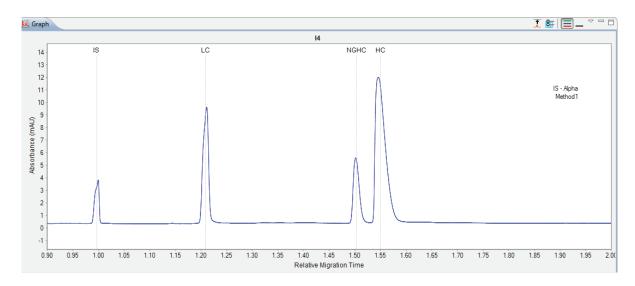
• Analysis sets the x-axis range of the electropherogram to what is selected in the Peak Fit range settings. To view or change these analysis settings, go to Edit > Analysis and click Peak Fit in the left sidebar. In this example, the lower and upper range settings are 0.9 and 2.5.



• **Full** displays the entire separation in the electropherogram. This is the default setting. In this example the lower and upper range settings are 0 and 2.6.



• **Custom** lets you manually enter the lower and upper range settings to display in the electropherogram. In this example the lower and upper range settings are 0.9 and 2.0.



NOTE: You can change the default x-axis range that Compass for iCE uses. Go to "Advanced Analysis Settings" on page 743 for more info.

Changing the Virtual Gel View

Options in the lane pane let you change the contrast or invert the virtual gel or change lane labels.

The Lane pane toolbar has the following options:



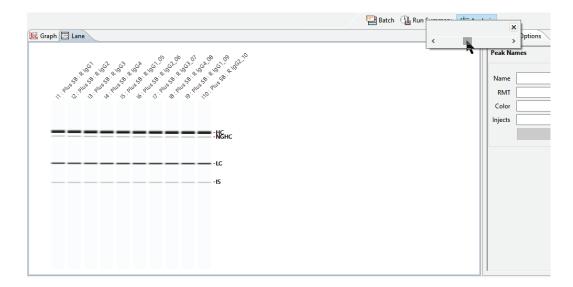
Contrast Adjustment



Lane Options

Adjusting the Contrast

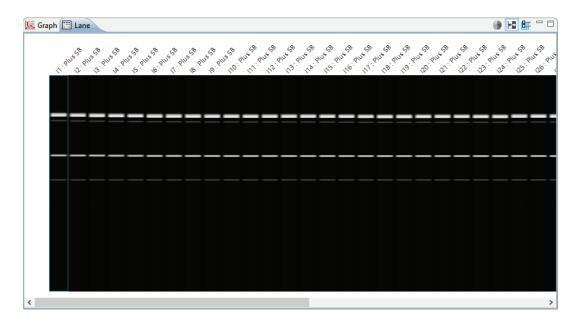
1. Click the Contrast Adjustment button. The contrast tool will display:



2. Use the mouse to move the slider left or right until the desired contrast is reached.

Inverting the Virtual Gel

1. Click the **Invert** button. The virtual gel image will invert:



2. Click the Invert button again to return to the default view.

Selecting Lane Labels

The labels shown above the lanes in the virtual gel can be customized. To do this:

1. Click the Lane Options button. The label box will display:

🔀 Graph 🖽 Lane	۴ 🖲	🗖 🗋 👳 Analysis Opt
1. 10-5 10-5 10-5 10-5 10-5 10-5 10-5 10-5	Lane Label Sample Injection Named Peaks	x ☑ Injection Name

- 2. The following lane display options are available:
 - Sample Displays the sample IDs entered in the batch above each lane.
 - Injection Displays the batch injection number above each lane.
 - Named peaks Displays peak names (if entered) next to the individual bands in the lane view.
 - Injection name Displays the injection name entered in the batch above each lane.

Closing Run Files

If more than one run file is open, you can close just one file or all the open files at the same time.

- To close one run file In the Experiment pane, click on one of the sample rows in the file. Then click File from the main menu and click Close.
- To close all open run files Select File from the main menu and click Close All.

Analysis Settings Overview

Compass for iCE has many analysis features and settings that you can change to enhance your run data.

Select **Edit** in the main menu and click **Analysis**. If more than one run file is open, select the run file you want to view settings for from the list:

Edit	View Instrum	ent Windo	w Help
	Cut	Ctrl+X	
	Copy Paste	Ctrl+C Ctrl+V	Graph
	Analysis	•	MW ladder assigned_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS
	Preferences		3160106283 KF1011 DG 2016-01-14_18-50-33_Maurice CE-SDS

This opens the Analysis window:

Markers Peak Names	Markers						
Peak Fit	Analysis Groups		Markers				
Advanced	Standards		Internal Standard Time 750	Internal Standard Time 750 Seconds			
Signal Processing	Standards		Markers Injection no markers				
			MW (kDa)	RMT			
			10	1			
	Add	Remove	20	1.15			
			33	1.3			
	Apply Default:		55	1.5			
	Standards	\ \	✓ 103 178	1.8			
	Apply Override:		270	2.4			
	Apply To	Group					
	Sample	Standards					
			Add	Remove			
	Add	Remove					

To move between pages in the window, click on an option in the left sidebar.

- Markers Lets you customize the Internal Standard migration time, and the molecular weight and RMT Compass for iCE uses to identify your CE-SDS MW Markers.
- **Peak Names** Lets you enter custom naming settings for sample proteins and have Compass for iCE automatically label the peaks in the run data.
- **Peak Fit** Lets you customize peak fit settings for sample data.
- Advanced Lets you customize analysis settings for the Internal Standard.
- Signal Processing Lets you apply reference signal corrections and baseline smoothing options to your data.

On all pages in the Analysis window:

- Click **Import** to import an analysis settings file. Go to "Importing Analysis Settings" on page 756 to learn how to do this.
- Click **Export** to export the current analysis settings file. Go to "Exporting Analysis Settings" on page 757 to learn how to do this.
- Click Apply to apply changes to the run file and update results in real time.
- Click **OK** to save changes to the run file and exit.
- Click Cancel to exit without saving changes.

Markers Analysis Settings

This page lets you select the injection for your CE-SDS MW Markers, enter a list of molecular weights and RMTs for each marker peak, and set the expected migration time of the Internal Standard for all injections. Select **Edit** in the main menu and click **Analysis**, then click **Markers** in the left sidebar.

NOTE: Settings can be changed in the batch default analysis before you start the run, or in run files once they're completed. If you make analysis settings changes to an executing run, they won't be saved to the final run file.

1arkers eak Names	Markers		
eak Fit	Analysis Groups	Markers	
dvanced	Standards	Internal Standard Time 750	Seconds
ignal Processing	Statuarus	Markers Injection no markers	
		MW (kDa)	RMT
		10	1
	Add Rem	10Ve 20	1.15
		33	1.3
	Apply Default:	55	1.5
	Standards	103	1.8
		178	2.05
	Apply Override:	270	2.4
	Apply To Group		
	Sample Standard	ls	
		Add	Remove
	Add Rem	nove	

Markers Settings

• Internal Standard Time - The approximate migration time (in seconds) of the Internal Standard. This is applied to all injections.

Changing the Injection Used for the CE-SDS MW Markers

You can use known markers to calculate molecular weights of your unknown sample proteins. You can select the injection you ran your CE-SDS MW Markers in, or opt to not use one.

NOTE: When the markers injection is set to no markers, the molecular weight for sample proteins in the run isn't displayed.

To change the markers injection:

- 1. Select Edit > Analysis, and select Markers in the left sidebar.
- 2. Click the arrow in the drop down list next to Markers Injection, then select an injection number or no markers from the list.

Markers Injection	2	-		
	no markers			
	1		RMT	
	3	=	1	
	4	-	1.15	
	5 6		1.3	
	7	_	1.5	
	8		1.8	
	9 10		2.05	
	10		2.2	
	12			
	13			
	14	_		
	15		1	

Compass for iCE will use the data in the selected injection to calculate molecular weights for sample proteins in the run data using the information in the table. If no markers is selected, Compass for iCE doesn't display molecular weight for sample proteins.

Standards Analysis Settings Groups

Standards settings are saved as a group, and you can create multiple settings groups. Specific group settings can be applied to methods, injections, sample names or other attributes in the run data.

NOTES:

We recommend using the Compass for iCE default values. These settings are included in the default Standards group.

Analysis settings are run-file specific. But, settings can be imported or exported for use with other run files. For more information see "Importing and Exporting Analysis Settings" on page 756.

Standards groups are displayed in the analysis settings box:

Analysis Settings		
Standards		
Add	Remove	

The Standards group shown uses the Compass for iCE default settings. You can make changes to this group and create new groups. To view settings for a group, click on the group name.

Creating a New Standards Group

- 1. Select Edit > Analysis, and select Markers in the left sidebar.
- 2. Click Add under the analysis settings box. A new group will be created:

Standards		
Standards 2		

3. Click on the new group and enter a new name.

Analysis Settings
Standards
New Standards
Add Remove

4. Change the Internal Standard time as needed.

Markers		
Internal Standard Time	750	Seconds

5. Click the arrow in the drop down list next to Markers Injection, then click an injection number or no markers from the list.

larkers Injection	2	-	
	no markers	*	1
	1 2		RMT
	3	E	1
	4 5		1.15
	6		1.3
	7		1.5
	8 9		1.8
	10		2.05
	11		2.2
	12		
	13 14		
	15	Ŧ	

Compass for iCE will use the data in the selected injection to recalculate molecular weights for sample proteins in the run data using the information in the table. If no markers is selected, Compass for iCE doesn't display molecular weight for sample proteins.

- 6. If a markers injection was selected, the default Maurice CE-SDS MW Markers molecular weights and relative migration time (RMT) values are already populated in the table. If you'd like to use these values, skip to the next step. If you're using different markers, here's how to change the values:
 - a. Click in the first cell in the MW column in the table and enter the molecular weight (in kDa) for the marker.

Markers Injection 2	\sim
MW (kDa)	RMT
15	1
20	1.15
33	1.3
55	1.5
103	1.8
178	2.05
270	2.4
Add	Remove

b. Click in the first cell in the RMT column and enter a value for the marker.

Markers Injection 2	\checkmark
MW (kDa)	RMT
10	0.9
20	1.15
33	1.3
55	1.5
103	1.8
178	2.05
270	2.4
Add	Remove

NOTE: Marker peak positions are relative to each other. Only the difference in RMT is used to help identify them. When entering marker peak information for the first time, review the marker data in the Analysis screen to find the correct peak RMT.

- c. Repeat the steps above for the remaining markers in the table.
- To add another marker Click Add under the table, then change the information in the new row.
- To remove a marker Select its row and click Remove.
- 7. To use the new group as the default settings for the run, click the arrow in the drop down list next to Apply Default, then click the new group in the list. The settings in the new group will then be applied to the run data.

Analysis Settings
Standards
New Standards
Add Remove
Apply Default:
Standards 🗸
Standards
New Standards

8. Click **OK** to save changes.

Changing the Default Standards Group

- 1. Select Edit > Analysis, and click Markers in the left sidebar.
- 2. Click the arrow in the drop down list next to Apply Default, then select a new default group from the list.

Analysis Settings
Standards
New Standards
Add Remove
Apply Default:
Standards 🔹
Standards New Standards
New Standards

3. Click OK to save changes. Analysis settings in the group selected will be applied to the run data.

Modifying a Standards Group

- 1. Select Edit > Analysis, and click Markers in the left sidebar.
- 2. Click on the group in the analysis settings box you want to modify.

anda	rds					
ew St	andaro	ds				
(A	dd	ר	Rem	ove	

- 3. Change the marker info as needed as in Creating a New Standards Group.
- 4. Click OK to save changes. The new analysis settings will be applied to the run data.

Deleting a Standards Group

1. Select Edit > Analysis, and click Markers in the left sidebar.

2. Click on the group in the analysis settings box you want to delete and click Remove.

Analysis Settings	
Standards	
New Standards	
Add Remove	

3. Click **OK** to save changes.

Applying Standards Groups to Specific Run Data

- 1. Select Edit > Analysis, and select Markers in the left sidebar.
- 2. Click on the group in the analysis settings box you want to apply to specific run data.

Analysis Settings	
Standards	
New Standards	
Add Remove	

3. Application of standards groups to specific run data is done in the override box. Click Add under the override box. A default override data set will be created from sample information found in the run file.

Apply Override:	
Apply To	Settings
Method1	New Standards
Add	Remove

4. Click the cell in the Apply To column, then click the down arrow.

Apply Override:		
Apply To		Settings
Method1	Ŧ	New Standards
Method1 Method2 IgG System Control Ladder Test Ladder IS - Alpha IS - Frozen P3 IS - T1 P3 IS - T2 P3 IS - T3 P3 A1 A2	rol	Remove

- 5. Select an option from the drop down list. This applies the settings group selected to specific run data as follows:
 - **Methods** All methods in the run file display in the list. Selecting a method applies the group settings to all injections that used that method.
 - **Sample names** All sample names in the run file display in the list, otherwise the default name of Sample shows. Selecting a sample name applies the group settings to all injections that used that sample name.
 - Wells or vials All well or vial numbers used in the run display in the list. Selecting a well/vial number applies the group settings to all injections that used that well/vial.
 - **Custom settings** Lets you choose specific injections to apply the group settings to. When you select this in the list, a pop-up box displays to let you enter a specific injection number or range of injections:

or Custom Settings	×
Enter injection descriptor	
Examples: 3, 5-10 Injection 3, and injections 5 through 10 6+8+10 Injections 6, 8, and 10	OK Cancel

6. If you need to change the analysis group used for a data set, click the cell in the Settings column and click the down arrow. Select a group from the drop down list.

Apply To	Settings	
A2	New Standards 👻	
	Standards	
	New Standards	

- 7. Repeat the previous steps to apply other groups to specific run data.
- 8. To remove a data set, click on its cell in the Apply To column, then click Remove.
- 9. Click OK to save changes.

Peak Names Settings

This page lets you view and change custom naming settings for sample proteins. Select **Edit** in the main menu and click **Analysis**, then click **Peak Names** in the left sidebar.

NOTE: Settings can be changed in the batch default analysis before you start the run, or in run files once they're completed. If you make analysis settings changes to an executing run, they won't be saved to the final run file.

Names					
: Fit anced	Analysis Groups	Analysis Grou	ps: IS		
al Processing	IS BSA Add Remove	Name IntSt	RMT 1.2	Color	Range
	Apply Settings Apply To Group IS IS Reduced IgG BSA				
	Add Remove			Add	Remove

Peak Names Analysis Settings Groups

Peak name settings are saved as a group, and you can create multiple settings groups. Specific group settings can be applied to methods, injections, sample names or other attributes in the run data.

NOTE: Analysis settings are run-file specific. But, settings can be imported or exported for use with other run files. For more information see "Importing and Exporting Analysis Settings" on page 756.

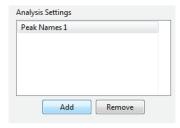
Peak name groups are displayed in the analysis settings box:

Remove

There aren't any Compass for iCE default settings groups, but you can make changes to groups you've created and create new groups. To view settings for a group, click on the group name in the analysis settings box.

Creating a Peak Names Group

- 1. Select Edit > Analysis, and select Peak Names in the left sidebar.
- 2. Click Add under the analysis settings box.



3. Enter a new name for the group.

Analysis Settings
IgG
Add Remove

4. Click in the first cell in the Name column in the analysis settings peak table and enter a sample protein name.

Vame	RMT	Color	Range
łC	2		0.1

5. Click in the first cell in the RMT column and enter the relative migration time for the sample protein.

Analysis Settings: IgG				
Name	RMT	Color	Range	
HC	1.55		0.1	

6. Click in the first cell in the Color column, then click the button.

Analysis Settin	igs: IgG				
Name	RMT	Color	Range		
HC	1.55	(0,1)	0.1		
			Line:		

The color selection box displays:



7. The color you pick is used to identify the sample protein peak in the Peaks and Injections panes in the Analysis screen. Click a color or define a custom color and click OK. The color selection will update in the table:

Analysis Settings: IgG				
Name	RMT	Color	Range	
HC	1.55		0.1	

8. Click in the first cell in the Range column.

Color	Range
	0.1
	Color

- 9. Enter a -/+ range for the RMT entered. Compass for iCE will automatically name peaks found within this RMT range. For example, if the RMT entered is 2 and a 0.1 range is used, all peaks with RMTs between 1.9 and 2.1 will be identified with this peak name and color.
- 10. To add another sample protein, click Add under the peak table. Repeat the previous steps for other sample proteins. In this example, three proteins were entered:

Analysis Gro	oups: IgG			
Name	RMT	Color	Range	
HC	1.55		0.1	
NGHC	1.5		0.1	
LC	1.2		0.1	

To remove a sample protein, select its row and click Remove.

11. Click **OK** to save changes.

Modifying a Peak Names Group

- 1. Select Edit > Analysis, then click Peak Names in the left sidebar.
- 2. Click on the group in the analysis settings box you want to modify.

Analysis Settings	
Internal Standard	
IgG-NR	
IgG-Red	
MW ladder	
Add Remove	

- 3. Change the information in the analysis settings peak table as described in Creating a Peak Names Group.
- 4. Click **OK** to save changes.

Deleting a Peak Names Group

- 1. Select Edit > Analysis, then click Peak Names in the left sidebar.
- 2. Click on the group in the analysis settings box you want to delete and click Remove.

Analysis Settings	
Internal Standard	
IgG-Red	
MW ladder	
Add Remove	

3. Click **OK** to save changes.

Applying Peak Names Groups to Run Data

- 1. Select Edit > Analysis, then click Peak Names in the options list.
- 2. Click on the group in the analysis settings box you want to apply to specific run data.

Analysis	s Settings		
IgG			
IgG 2			
	Add	Remove	

3. Application of peak names groups to specific run data is done in the apply settings box. A default data set automatically gets created whenever you create a new group and it's applied to all injections in the run. You can either modify the default group or click Add under the box to create a new one.

Apply Settings	
Apply To	Settings
All	IgG
All	IgG 2
Add	Remove

4. Click the cell in the Apply To column, then click the down arrow.

Apply To		Se	ettings
Method1	Ŧ	Ig	G
All		*	G 2
Method1			
Method2			
IgG System Contr	rol	_	
Control Ladder		Ε	
Test Ladder			
IS - Alpha			
IS - Frozen P3			
IS - T1 P3			
IS - T2 P3			
IS - T3 P3			Remove
A1		÷	

- 5. Select an option from the drop down list. This applies the peak names group selected to specific run data as follows:
 - All Selecting this applies peak names group settings to all injections.
 - **Methods** All methods in the run file display in the list. Selecting a method applies the group settings to all injections that used that method.
 - **Sample names** All sample names in the run file display in the list, otherwise the default name of Sample shows. Selecting a sample name applies the group settings to all injections that used that sample name.
 - Wells or vials All well or vial numbers used in the run display in the list. Selecting a well/vial number applies the group settings to all injections that used that well/vial.

• **Custom settings** - Lets you choose specific injections to apply the group settings to. When you select this in the list, a pop-up box displays to let you enter a specific injection number or range of injections:

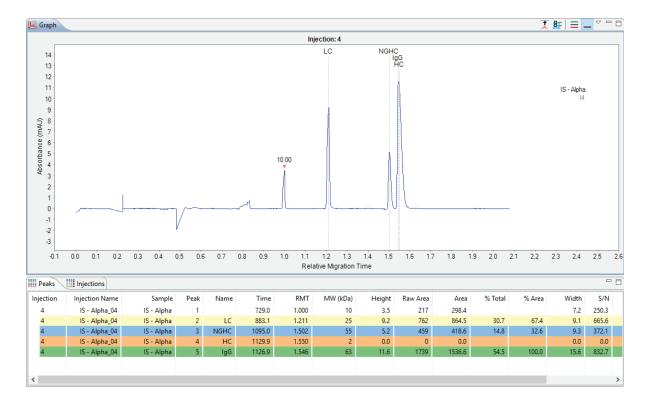
🕼 Custom Settings	×
Enter injection descriptor	
Examples: 3, 5-10 Injection 3, and injections 5 through 10 6+8+10 Injections 6, 8, and 10	OK Cancel

6. If you need to change the peak names group used for a data set, click the cell in the Settings column and click the down arrow. Select a group from the drop down list.

Apply To	Settings	
Method1	IgG	Ŧ
All	IgG IgG 2	

- 7. Repeat the previous steps to apply other groups to specific run data.
- 8. To remove a data set, click on its cell in the Apply To column, then click Remove.

9. Click OK to save changes. Named peaks will be identified with a peak name label in the electropherogram and color-coded in the Peaks and Injections panes:



Peak Fit Analysis Settings

This page lets you view and change peak fit settings for sample data. Select **Edit** in the main menu and click **Analysis**, then click **Peak Fit** in the left sidebar:

NOTE: Settings can be changed in the batch default analysis before you start the run, or in run files once they're completed. If you make analysis settings changes to an executing run, they won't be saved to the final run file.

Markers	Peak Fit		
Peak Names Peak Fit	Analysis Groups	Analysis Groups: Peak Fit	
Advanced	Peak Fit		
Signal Processing	Peak Fit	Range	
		Minimum	0.9
		Maximum	3.2
		View	🔾 Analysis 💿 F
		Baseline	
	Add Remove	Baseline Type	Spline
		Threshold	2.0
	Apply Default:	Window	100.0
	Peak Fit	~	
	Apply Override:	Stiffness	1.0
	Apply To Group	Peak Find	
		Threshold	15.0
		Width	10.0
		Area Calculation	Dropped Lines
	Add Remove		

Range Settings

- **Minimum** The RMT value below which peaks won't be identified. This value is also used as the default lower RMT range for data displayed in the electropherogram.
- **Maximum** The RMT value above which peaks won't be identified. This value is also used as the default upper RMT range for data displayed in the electropherogram.

• View - Sets the default range to either Full or Analysis for the electropherogram x-axis range in the View Region window (select View in the main menu and click View Region).

🎯 View Region	x
Range O Analysis I Full O Custom	
Lower: 0.0 Upper: 2.6	
OK Cancel	

- Analysis sets the x-axis range of the electropherogram to the Peak Fit range minimum and maximum settings in the electropherogram.
- Full displays the entire separation range of the run data in the electropherogram. This is the default setting.

Baseline Settings

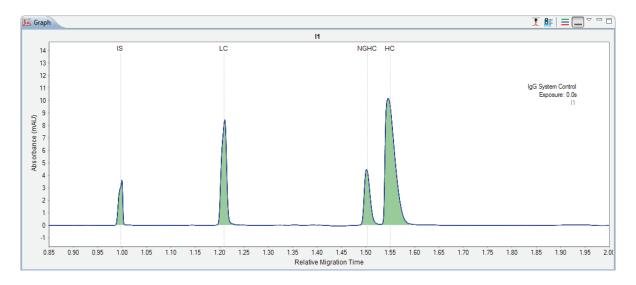
These settings apply to spline baselines only.

- Threshold The variance, or roughness, in a baseline data segment below which a point is called part of the baseline.
- Window How long baseline data segments are expected to be in pixels. Shorter segments let the baseline follow plateau sections of the signal.
- **Stiffness** The amount the baseline is allowed to vary from a straight line. Settings between 0.1 and 1.0 make the baseline fit closer to a straight line. Settings from 1.0 to 10.0 will make the baseline fit follow the data more closely.

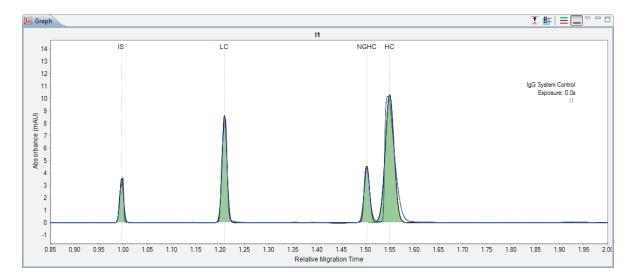
Peak Find Settings

- **Threshold** The minimum signal to noise ratio required for a peak to be identified. A setting of 1.0 will detect many peaks, a setting of 10.0 will detect fewer peaks.
- Width The approximate peak width (at full width half max) in pixels used to detect peaks. The minimum value for this setting is 3.0. Larger widths help eliminate the detection of shoulder and noise peaks.
- Area Calculation Two fits are used, either Gaussian Fit or Dropped Lines. These settings can be changed before or after the run is finished.

• For CE-SDS applications, peak area is calculated using Dropped Lines by default. This type of area calculation is also often called the perpendicular drop method. This is the preferred method when peaks overlap or are close to each other. It draws two vertical lines from the left and right bounds of the peak down to the x-axis and then measures the total area bounded by the signal curve, the x-axis (y=0 line), and the two vertical lines.



• This next view is of the same data using Gaussian fit instead:



Peak Fit Analysis Settings Groups

Peak fit settings are saved as a group, and you can create multiple settings groups. Specific group settings can then be applied to methods, injections, sample names or other attributes in the run data.

NOTES:

We recommend using the Compass for iCE default values for peak fit analysis settings. These settings are included in the default Peak Fit group.

Analysis settings are run-file specific. But, settings can be imported or exported for use with other run files. For more information see "Importing and Exporting Analysis Settings" on page 756.

Peak fit groups are displayed in the analysis settings box:

Peak Fit		

The Peak Fit group shown contains the Compass for iCE default analysis settings. You can make changes to this group and create new groups. To view settings for a group, click on the group name.

Creating a New Peak Fit Group

- 1. Select Edit > Analysis, and select Peak Fit in the left sidebar.
- 2. Click Add under the analysis settings box. A new group will be created:

Analysis Settings	
Peak Fit	
Peak Fit 2	
Add Remove	

3. Click on the new group and enter a new name.

Analysis Se Peak Fit Product	-			
e.				
	Add) 🛛 🛛 🛛	emove	

4. Change the settings in the range, baseline or peak find boxes as needed.

Analysis Settings: Product A	
Range	
Minimum	0.9
Maximum	2.5
View	🔘 Analysis 🔘 Full
Baseline	
Threshold	2.0
Window	100.0
Stiffness	0.7
Peak Find	
Threshold	15.0
Width	150.0
Area Calculation	Dropped Lines 💌

5. To use the new group as the default peak fit settings for the run file data, click the arrow in the drop down list next to Apply Default, then click the new group from the list. Peak fit settings in the new group will then be applied to the run data.

Apply Default:	
Peak Fit	•
Peak Fit Product A	
Apply To	Settings
Add	Remove

6. Click **OK** to save changes.

Changing the Default Peak Fit Group

- 1. Select Edit > Analysis, and select Peak Fit in the left sidebar.
- 2. Click the arrow in the drop down list next to Apply Default, then click a new default group from the list.

Apply Default:	
Peak Fit	•
Peak Fit	
Product A	
Apply To	Settings
Add	Remove

3. Click OK to save changes. Peak fit settings in the group selected will be applied to the run data.

Modifying a Peak Fit Group

- 1. Select **Edit** > **Analysis**, and click **Peak Fit** in the left sidebar.
- 2. Click on the group in the analysis settings box you want to modify.

Analysis Settings	
Peak Fit	
Product A	
Add Remove	

Analysis Settings: Product A		
Range		
Minimum Maximum	0.9	
	2.5	
View	🔘 Analysis 🔘 Full	
Baseline		
Threshold	2.0	
Window	100.0	
Stiffness	0.7	
Peak Find		
Threshold	15.0	
Width	150.0	
Area Calculation	Dropped Lines 💌	

3. Change the settings in the range, baseline or peak find boxes as needed.

4. Click OK to save changes. The new peak fit settings will be applied to the run data.

Deleting a Peak Fit Group

- 1. Select **Edit** > **Analysis**, and select **Peak Fit** in the left sidebar.
- 2. Click on the group in the analysis settings box you want to delete and click Remove.

Analysis Settings	
Peak Fit	
Product A	
Add Remove	

3. Click **OK** to save changes.

Applying Peak Fit Groups to Specific Run Data

1. Select Edit > Analysis, and select Peak Fit in the left sidebar.

2. Click on the group in the analysis settings box you want to apply to specific run data.

Analysis Settings	
Peak Fit	
Product A	
Add Remove	

3. Application of analysis groups to specific run data is done in the override box. Click Add under the override box. A default override data set will be created from sample information found in the run file.

Apply To	Settings
Method1	Product A

4. Click the cell in the Apply To column, then click the down arrow.

Apply To		Settings
Method1	Ŧ	Product A
Method1		*
Method2		
IgG System Cont	rol	
Control Ladder		-
Test Ladder		=
IS - Alpha		
IS - Frozen P3		
IS - T1 P3		
IS - T2 P3		
IS - T3 P3		
A1		Remove
Δ2		*

- 5. Select an option from the drop down list. This applies the settings group selected to specific run data as follows:
 - **Methods** All methods in the run file display in the list. Selecting a method applies the group settings to all injections that used that method.
 - **Sample names** All sample names in the run file display in the list, otherwise the default name of Sample shows. Selecting a sample name applies the group settings to all injections that used that sample name.
 - Wells or vials All well or vial numbers used in the run display in the list. Selecting a well/vial number applies the group settings to all injections that used that well/vial.

• **Custom settings** - Lets you choose specific injections to apply the group settings to. When you select this in the list, a pop-up box displays to let you enter a specific injection number or range of injections:

💮 Custom Settings	×
Enter injection descriptor	
Examples: 3, 5-10 Injection 3, and injections 5 through 10 6+8+10 Injections 6, 8, and 10	OK Cancel

6. If you need to change the analysis group used for a data set, click the cell in the **Settings** column and click the down arrow. Select a group from the drop down list.

Apply To	Settings	
S - T1 P3	Product A	-
	Peak Fit Product A	

- 7. Repeat the previous steps to apply other groups to specific run data.
- 8. To remove a data set, click on its cell in the Apply To column, then click Remove.
- 9. Click OK to save changes.

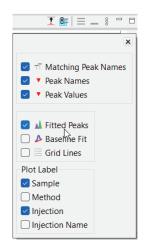
Manual Peak Integration

Compass for iCE lets you manually integrate peaks in individual electropherograms.

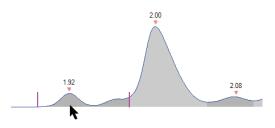
- 1. Select **Edit** > **Analysis**, and select **Peak Fit** in the left sidebar.
- 2. Select Dropped lines as the area calculation if it isn't already selected.

Peak Find	
Threshold	15.0
Width	150.0
Area Calculation	Dropped Lines 🗸
	T

3. Select Fitted Peaks in the Graph Options.



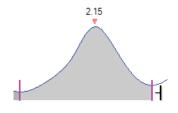
- 4. Select an injection in the Experiment pane.
- 5. Hover the mouse over the peak you want to adjust. Two magenta bars will display that indicate the start and end points of its integration.



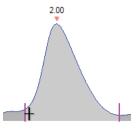
- 6. To change the integration, hover the mouse over either of the magenta bars. Then click the mouse and drag the bar to move it. The cursor changes to indicate which direction you can move the integration point:
 - If the cursor changes to **b** this is the peak start for the peak on the right.



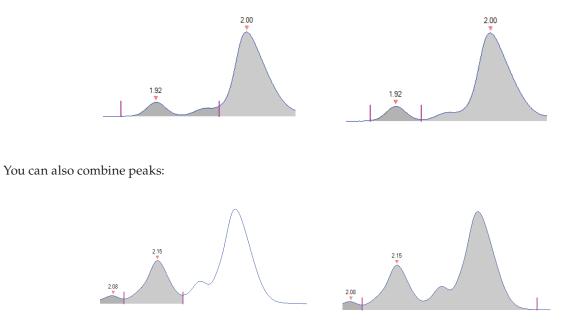
If the cursor changes to \mathbf{H} this is the peak end for the peak on the left.



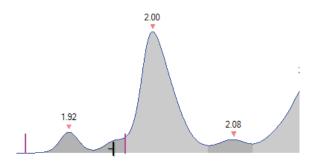
• If the cursor changes to + this is a joint boundary for the peaks on the left and right.



In the example below, we moved the start and end points of the peak at 1.92 RMT to just include the area under the peak:



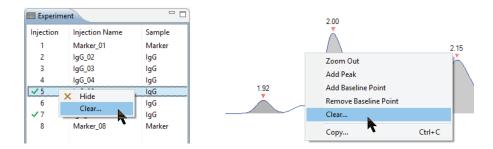
You can also separate areas between peaks. Whenever you have a + cursor between two peaks tha aren't baseline resolved, move the mouse slightly to the right or left until you get the |- or -| cursor.



Click and hold the mouse. A black drop line will display indicating where the current peak start or end point is. While holding the mouse, drag the cursor to the right or left to move the start or end point to where you want it, then release the mouse.



7. To remove the manual integration settings, right click on the graph or on the injection in the Experiment pane and select Clear.



Advanced Analysis Settings

This page lets you view and change analysis settings for the Internal Standard data. Select **Edit** in the main menu and click **Analysis**, then click **Advanced** in the left sidebar:

NOTE: Settings can be changed in batches before you start the run, or in run files once they're completed. If you make analysis settings changes to an executing run, they won't be saved to the final run file.

log Analysis: IS-BSA-TITR-2018-12-2	_10-59-20_3x16inj-Mauri	ice CE-SDS PLUS		_		×
Markers	Advanced					
Peak Names Peak Fit Advanced Signal Processing	Analysis Groups Advanced		Analysis Groups: Advanced Standards Peak Width Allowable Drift		20	
	Add Apply Default: Advanced	Remove]			
	Apply Override:					
	Apply To	Group				
Import Export			OK	Cancel	Apply	

Internal Standard Settings

- **Peak Width** The approximate width (at full width half max) used to filter out absorbance artifacts which improves recognition of standards.
- Allowable Drift The distance the Internal Standard is expected to move compared to the entered number of seconds on the Markers page. This setting helps with recognition of the Internal Standard.

Advanced Analysis Settings Groups

Advanced analysis settings are saved as a group, and you can create multiple settings groups. Specific group settings can be applied to methods, injections, sample names or other attributes in the run data.

NOTES:

We recommend using the Compass for iCE default values for advanced analysis settings. These settings are included in the default Advanced group.

Analysis settings are run-file specific. But, settings can be imported or exported for use with other run files. See "Importing and Exporting Analysis Settings" on page 756.

Analysis groups are displayed in the analysis settings box:

Analysis Settings	
Advanced	
Add	Remove

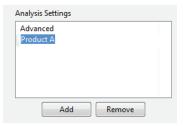
The Advanced group shown contains the Compass for iCE default analysis settings. You can make changes to this group and create new groups. To view settings for a group, click on the group name.

Creating a New Analysis Group

- 1. Select Edit > Analysis, and select Advanced in the left sidebar.
- 2. Click Add under the analysis settings box. A new group will be created:

Analysis Settings	
Advanced	
Advanced 2	
Add Rem	ove

3. Click on the new group and enter a new name.



4. Change the settings in the Standards box as needed.

Analysis Settings: Product A	
Standards	
Peak Width	10
Allowable Drift	50

5. To use the new group as the default analysis settings for the run data, click the arrow in the drop down list next to Apply Default, then click the new group from the list. Analysis settings in the new group will then be applied to the run data.

Apply Default:	
Advanced	•
Advanced	
Product A	
Apply To	Settings
Add	Remove

6. Click **OK** to save changes.

Changing the Default Analysis Group

- 1. Select Edit > Analysis, and select Advanced in the left sidebar.
- 2. Click the arrow in the drop down list next to Apply Default, then click a new default group from the list.

Apply Default:	
Advanced	•
Advanced	
Product A	
Apply To	Settings
Add	Remove

3. Click OK to save changes. Analysis settings in the group selected will be applied to the run data.

Modifying an Analysis Group

- 1. Select Edit > Analysis, and select Advanced in the left sidebar.
- 2. Click on the group in the analysis settings box you want to modify.

	Ren	Remove	Remove

3. Change the settings in the Standards box as needed.

Analysis Settings: Product A	
Standards	
Peak Width	10
Allowable Drift	50

4. Click OK to save changes. The new analysis settings will be applied to the run data.

Deleting an Analysis Group

- 1. Select Edit > Analysis, and select Advanced in the left sidebar.
- 2. Click on the group in the analysis settings box you want to delete and click Remove.

Advanced Product A	
Product A	- 1
	_
Add Remove	

3. Click **OK** to save changes.

Applying Analysis Groups to Specific Run Data

- 1. Select Edit > Analysis, and select Advanced in the left sidebar.
- 2. Click on the group in the analysis settings box you want to apply to specific run data.

Analysis Settings
Advanced
Product A
Add Remove

3. Application of analysis groups to specific run data is done in the override box. Click Add under the override box. A default override data set will be created from sample information found in the run file.

Apply To	Settings	
Method1	Product A	
Ad	Remove	

4. Click the cell in the Apply To column, then click the down arrow.

Apply Override:	
Apply To	Settings
ystem Suitablity 👻	Product A
System Suitablity mAb Method System Suitability mAb 11 Blank mAb 11 Ref. Std. mAb 11 Prep 201601 A1 A2 A3 A4 Custom Settings	.21 Remove

- 5. Select an option from the drop down list. This applies the settings group selected to specific run data as follows:
 - **Methods** All methods in the run file display in the list. Selecting a method applies the group settings to all injections that used that method.
 - **Sample names** All sample names in the run file display in the list, otherwise the default name of Sample shows. Selecting a sample name applies the group settings to all injections that used that sample name.
 - Wells or vials All well or vial numbers used in the run display in the list. Selecting a well/vial number applies the group settings to all injections that used that well/vial.
 - **Custom settings** Lets you choose specific injections to apply the group settings to. When you select this in the list, a pop-up box displays to let you enter a specific injection number or range of injections:

© Custom Settings	×
Enter injection descriptor	
Examples: 3, 5-10 Injection 3, and injections 5 through 10 6+8+10 Injections 6, 8, and 10	OK Cancel

6. If you need to change the analysis group used for a data set, click the cell in the **Settings** column and click the down arrow. Select a group from the drop down list.

pply Override:	
Apply To	Settings
IS - Alpha	Product A 👻
	Advanced
	Product A
Add	d Remove

- 7. Repeat the previous steps to apply other groups to specific run data.
- 8. To remove a data set, click on its cell in the Apply To column, then click Remove.
- 9. Click OK to save changes.

Signal Processing Settings

This page lets you apply reference signal corrections and baseline smoothing options to your data. Select **Edit** in the main menu and click **Analysis**, then click **Signal Processing** in the left sidebar:

NOTE: Settings can be changed in batches before you start the run, or in run files once they're completed. If you make analysis settings changes to an executing run, they won't be saved to the final run file.

@ Analysis: IS-new-titr-2019-01-15	12-00-27_Maurice CE-SDS PLUS	_		Х
Markers	Signal Processing			
Peak Names				
Peak Fit	Processing			
Advanced	Reference Channel Correction			
Signal Processing				
	Smooth Data			
Import Export	OK Cancel		Apply	

Reference Channel Correction

The Reference Channel Correction improves CE-SDS data quality by automatically removing any signal within a certain range that can be attributed to lamp variability. It's on by default for new CE-SDS PLUS and Turbo CE-SDS batches and runs in Compass for iCE 2.1 or higher, and off when opening runs collected in previous versions of the software. It can be turned on when analyzing older runs if preferred.

NOTE: We recommend keeping the Reference Channel Correction on for the highest data quality. For more information, contact Protein Simple Technical Support.

To turn reference channel correction on or off:

- 1. From the Batch screen, select Edit > Default Analysis. From the Analysis screen, select Edit > Analysis.
- 2. Click Signal Processing in the left sidebar.

3. Select or deselect the Reference Channel Correction checkbox.

ô Analysis: IS-new-titr-2019-01-15	_12-00-27_Maurice CE-SDS PLUS	_		×
Markers	Signal Processing			
Peak Names				
Peak Fit	Processing			
Advanced Signal Processing	Reference Channel Correction			
Signal Processing	Smooth Data			
Import Export	ОК С	ancel	Apply	

4. Click Apply.

Baseline Smoothing

Compass for iCE can apply baseline smoothing to CE-SDS data to decrease noise and improve signal-to-noise ratios. Smoothing is on by default but can be turned off in the Default Analysis Settings before you start a batch or during analysis after a batch is completed.

To turn baseline smoothing on or off:

- 1. From the Batch screen, select Edit > Default Analysis. From the Analysis screen, select Edit > Analysis.
- 2. Click Signal Processing in the left sidebar.

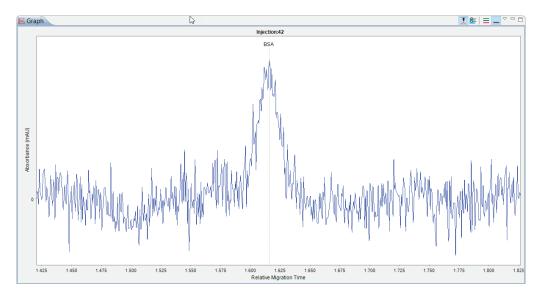
3. Select or deselect the **Smooth Data** checkbox.

📀 Analysis: IS-new-titr-2019-01-15	j_12-00-27_Maurice CE-SDS PLUS		×
Markers	Signal Processing		
Peak Names Peak Fit Advanced Signal Processing	Processing		
Import Export	OK Cance	Apply	

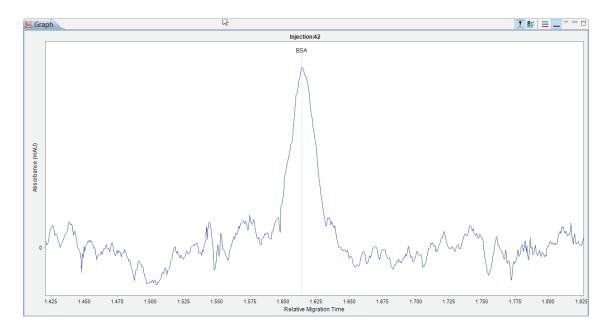
4. Click Apply.

The examples below show data with and without the Smooth Data option:

• Smooth Data off



Smooth Data on



Injection Reports

You can export PDF files of the raw and analyzed data, IV plot, peaks table, sample and system info for individual or all injections in a run file. You can also export the run history with all analysis events.

NOTES:

You can have Compass for iCE generate reports for you automatically at the end of each run. See "Setting up Automatic Injection Reports" on page 761 for more information.

Any time a new report is run, it's saved in a separate run folder. Existing reports aren't overwritten.

- 1. Click **File > Open Run** and select a run file.
- 2. If you want reports for all injections, skip to the next step. If you only want reports for certain injections, in the Experiment pane:
 - To select sequential injections: Select the first injection, then hold the Shift key and select the last injection you want a report for. This selects all rows between the two injections.
 - To select specific injections: Hold the Ctrl key and select just the injections you want reports for.

- 3. Select File from the main menu in either screen and click Injection Report.
 - File
 Edit
 View
 Instrument

 Open Run
 ▶

 Add Run
 ▶

 Close
 Close

 Close All
 >

 Save
 Save

 Save As...
 Export Tables...

 Export Spectra
 ▶

 Injection Report...
 Exit
- 4. In the Injection Reports window:
 - a. Choose either Selected injections or All injections.
 - b. Select Analysis log if you want a run history report with all analysis events.
 - c. Select **Batch Report** if you want to include the sample and method details for each injection in the batch.
 - d. Select Fitted peaks if you want to show peak fitting in the electropherograms.
 - e. Select Lanes if you want to show lane view data.
 - f. Report PDFs generated by Compass for iCE are secured by default, which means they can be viewed and printed but not modified or renamed. Uncheck **Secure PDF** if you don't want to generate a secure report. To learn more about permissions for secured vs. unsecured reports, see page 800.
 - g. The report name defaults to the run file name. If you want to change it, type in the Report Name box to make updates.
 - h. Click OK.

Run: R-lgG-2019-01-07_12-09-43	_4Sq-48inj-Maurice CE-SDS	PLUS.batch
 Selected injections (1) 	🗌 Analysis log	
 All completed injections (48) 	Batch report	
	Fitted peaks	
	Lanes	
Secure PDF		
Report Name:		Browse
R-IgG-2019-01-07_12-09-43_4Sq-48	Binj-Maurice CE-SDS PLUS.ba	atch
Location: C:\Users\Andrea\Docume	nts\Compass for iCE\Runs	

5. The individual injection report PDF(s) and a combined injection report PDF are exported to the Runs folder in the Compass for iCE directory. They'll be in a folder with the report name used in the prior step. When the reports are done, the folder opens for you automatically.

😻 Dropbox	^	Name	Date modified	Туре	Size
OneDrive		R-lgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_combined_injection_report.pdf	7/20/2020 9:11 PM	Adobe Acrobat D	5,032
OneDrive		R-lgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_1_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108
This PC		R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_2_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	105
🗊 3D Objects		R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_3_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108
Desktop		R-lgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_4_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108
Documents		R-lgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_5_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108
		R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_6_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	106
Add-in Express		R-lgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_7_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108
Adobe		R-lgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_8_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108
CIDFont		R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_9_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	109
СМар		R-IgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_10_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	109
Compass for iCE		R-lgG-2019-01-07_12-09-43_4Sq-48inj-Maurice CE-SDS PLUS.batch_Injection_11_Plus SB.pdf	7/20/2020 9:10 PM	Adobe Acrobat D	108

Example Analysis and Injection Report

Run File R-IgG-2019-01-10_16-25-12_4Sqx12inj-RIgG-Maurice CE-SDS

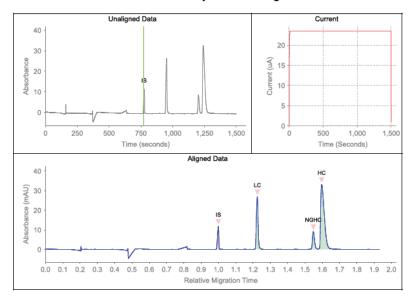
Analysis Log

Date	User Name	Message	Comment
2019-01-10 17:25:27		Started run: R-IgG-2019-01-10_16-25-12_4Sqx12inj-RIgG-Maurice CE-SDS Batch: 4Sqx12inj- RIgG-Maurice CE-SDS.batch	3180910338
2019-01-14 10:39:07		Saved analysis and methods changes from Compass for iCE v2.1.0-1219	
		Added Peak Names Apply Settings "apply IgG to all"	
		Added Peak Names Group IgG	
		Protein name: LC RMT: 1.21 Color: 32512 Range: 0.1	
		Protein name: NGHC RMT: 1.54 Color: 32512 Range: 0.05	
		Protein name: HC RMT: 1.58 Color: 32512 Range: 0.1	

Created By: Jacquelyn Sat 4.17 PM Feb 2, 2019 CST Software Version: 2.1.0, Build ID: 0130 C:UbersLbacquelymDocuments/CliensProtenSimple/Maurice/User Guide Rev 12 edis/Data from Andrea - no edis/R-IgO-2019-01-10_16-26-12_4Sqx12nj-RigO-Maurice CE-SDS Inte Computer: DESKTOP-C1FPQ0B



Page 1 of 2



Uncontrolled Injection 1: R IgG1

P	ea	ks	5

Peak	Name	Time	RMT	Height	Raw Area	Area	%Total	%Area	Width	S/N	Baseline	Resolution
1	IS	776.7	1.000	11.7	164.6	212.4			7.0	658.6	-0.6	
2	LC	951.3	1.225	26.8	498.5	524.1	30.5	30.5	8.8	1507.3	-0.6	15.02
3	NGHC	1202.7	1.549	9.1	205.6	170.8	9.9	9.9	10.2	510.5	-0.6	17.58
4	HC	1240.2	1.597	33.1	1273.4	1021.8	59.5	59.5	17.9	1859.6	-0.6	1.98

Created By: Jacquelyn Sat 4:47 PM Feb 2, 2019 CST	Software Version: 2.1.0, Build ID: 0130	
C:(Users/Jacquelyn/Documents/Clients/ProteinSimple/Maurice/User G	ulde/Rev 12 edits/Data from Andrea - no edits/R-IgG-2019-01-10_16-25-12_48qx12inj-RigG-Maurice CE-	
SDS.mbz		proteinsimple
Computer: DESKTOP-C7FPQGB		classes tori
	Page 1 of 2	

Uncontrolled Injection 1: R IgG1

Sample Information

Injection Name	R lgG1
Sample ID	SB
Location	Plate Well B2
Batch Name	4Sqx12inj-RlgG-Maurice CE-SDS
Run Started	Thu 5:25 PM Jan 10, 2019 CST
Run Completed	Fri 8:07 PM Jan 11, 2019 CST
Date Acquired	Thu 6:08 PM Jan 10, 2019 CST
Run Error	None
Reinjection	No

jection	

Yes
5750V for 25.0 min
20 sec 4600 Volts
9.1°C

Maurice Settings			
Model	Maurice OBM		
Instrument S/N	kf1077		
Software Version	2.1.0, Build ID: 0130		
Firmware Version	3.1.2019.01.04.20.16.20.5eb707f		
Tray Type	96-well plate		
Cartridge Type	CE-SDS		
Cartridge S/N	3180910338		
Cartridge Expiration	Sep 2019		
Injections Remaining	152 (52 guaranteed)		
Batches Remaining	24		



Importing and Exporting Analysis Settings

The analysis settings in a run file can be exported as a separate file. This allows the same analysis settings to be imported into other batches or run files at a later time, rather than you having to re-enter them manually.

Importing Analysis Settings

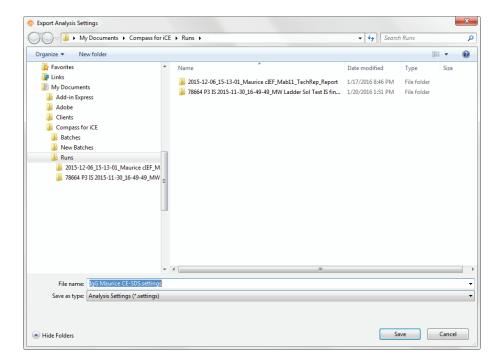
NOTE: Importing an analysis settings file populates the settings in all analysis pages.

- 1. Open the run file or batch you want to import analysis settings to.
- 2. Select Edit in the main menu and click Default Analysis (Batch screen) or Analysis (Analysis screen).
- 3. Click Import on any page.
- 4. Select a settings file (*.settings) and click OK. The imported settings will display in all analysis pages.

Exporting Analysis Settings

NOTE: Exporting an analysis settings file exports the settings in all analysis pages.

- 1. Open the run file or batch you want to export analysis settings from.
- 2. Select Edit in the main menu and click Default Analysis (Batch screen) or Analysis (Analysis screen).
- 3. Click Export on any page. The following window displays:



- 4. The default directory is Compass for iCE/Runs. Change the directory if needed.
- 5. Enter a file name and click Save. The settings will be saved as a *.settings file.

Chapter 21: Setting Your Preferences

Chapter Overview

- Customize Your Preferences
- Enabling Access Control
- Setting Data Export Options
- Setting up Automatic Injection Reports
- Selecting Custom Plot Colors for Graph Overlay
- Grouping Options
- Setting Up Maurice Systems to Send Tweets

Customize Your Preferences

You can set and save several custom preferences in Compass for iCE. To view and change these settings, select **Edit** in the main menu and click **Preferences**.

😯 Preferences				×
Access Control	Access Control			
Analysis Export Auto Reports Graph Grouping Twitter	Enable Server 127.0.1 Auto Lock Insctivity (min) 20 These settings apply to all uses	re Defaults	Δppl	ły
		ок	Cance	el l

To move between preferences pages, click on an option in the left sidebar. Here's what you can customize:

- Access Control Lets you log on to Compass for iCE through an Authorization Server.
- Analysis Export Lets you customize data export options.
- Auto Reports Lets you set reports to generate automatically at the end of a run.
- Graph Lets you customize graph color displays.
- **Grouping** Groups samples with the same name together across runs, so you can get statistics for the same sample in multiple runs.
- Twitter Lets you configure Compass for iCE to tweet Maurice, Maurice C., Maurice S. and MauriceFlex. run status.

In all preferences windows:

- Click Apply to apply changes to any open run files in Compass for iCE.
- Click Restore Defaults to restore the values on the page to default settings.
- Click **OK** to save changes and exit.
- Click Cancel to exit without saving changes.

Enabling Access Control

You can use the Access Control feature to help satisfy 21CFR Part 11 data security requirements when using Maurice instruments. Please go to "Enabling Access Control" on page 781 to get more info.

Setting Data Export Options

Select Analysis Export in the sidebar.

- Text:
 - **Export Standards** This option exports data for the standards in each injection when run data is exported. It's selected by default. If it's not selected, only sample injection data is exported.
 - **Export using a comma as the column deliminator** This option exports run data with a comma separator in .csv format. When it's not selected, data is exported in .txt format with a tab separator (this is the default setting).
- ANDI Export Compatibility:
 - **Empower** This option exports run data in a format that is compatible for further analysis in Empower and other analysis programs that use standard formats.
 - Chromeleon This option exports run data in a format that is compatible for further analysis in Chromeleon.
 - **ChromPerfect (cIEF only)** This option exports standard cIEF, MauriceFlex cIEF and MauriceFlex Fractionation run data in a format that is compatible for further analysis in ChromPerfect.
- ANDI cIEF Export Type:
 - pI Exports the pI of identified peaks in the cIEF run data.
 - Relative Pixel Units (RPU) Exports the RPU of identified peaks in the cIEF run data.
 - Uncalibrated Exports uncalibrated cIEF run data.

NOTE: ANDI spectra data for standard cIEF, MauriceFlex cIEF and MauriceFlex Fractionation can be exported. For MauriceFlex Fractionation, only sample injection data can be exported. Mobilization electropherograms can not be exported.

- ANDI CE-SDS Export Type:
 - Time Exports the peak detection time
 - Relative Migration Time (RMT) Exports the RMT of identified peaks in the CE-SDS run data.
- ANDI Export Units:
 - Milli Absorbance Units- Exports peak height in milli absorbance units (mAU).
 - Absorbance Units Exports peak height in absorbance units (AU).

- Auto Export Spectra:
 - When Text or ANDI options are selected, spectra will automatically export at the end of every run. Data is saved in \Documents\Compass for iCE\Runs by default. To save the files in another folder, click Browse and select a different location.
 - Text Exports spectra in text format.
 - ANDI Exports spectra in ANDI format.

cess Control alysis Export	Analysis Export		
to Reports sph puping litter	Text Export Standards Export scing a comma as the column deliminator ANDI Export Compatibility Finder		
	Chromeleon ChromPerfect (cEF only)		
	ANDI cIEF Export Type o pi Relative Pixel Units (RPU) Ourcalibrated		
	"Note: Exporting in pl is only supported when two pl markers are defined in Analysis Settings ANDI CE-SOS Export Type ● Time ● Relative Migration Time (RMT)		
	AND/Export Units Milli Absorbance Units (mAU) () Absorbance Units (AU)		
	Auto Export Spectra Export Format Format Auto Auto		
	Export Directory: C\Users\Andrea\Documents\Compass for iCE\Runs		Brows
		Restore <u>D</u> efaults	Appl
		ОК	Cance

Setting up Automatic Injection Reports

- 1. Select Auto Reports in the sidebar.
- 2. Check the Auto Injection Reports checkbox.
- 3. Check any additional reports you'd like to have automatically generated at the end of each run
- 4. Check Secure PDF to have the software automatically generate secure report PDFs that can be viewed and printed but not modified or renamed.

Reports include all injections in the batch, and are saved in \Documents\Compass for iCE\Runs by default. To save reports in another folder, click Browse and select a different location.

🗇 Preferences				×
Access Control	Auto Reports			
Analysis Export Autor Reports Graph Grouping Twitter	Auto injection reports Opions Analysis log Batch report Show fitted peaks in injection reports Secure PDF files	(Brows	
	ОК		Cance	

Selecting Custom Plot Colors for Graph Overlay

Select Graph in the sidebar.

• Apply colors to stacked plots - This option applies the color scheme shown to individual plots when Stack the plots is selected in the Analysis screen's Graph pane. When this option isn't selected, all plots use the same color (this is the default setting).

NOTE: If **Apply colors to stacked plots** isn't selected, the colors shown are only applied to plots when Overlay the plots is selected in the Graph pane.

o Preferences		-		×
Access Control Analysis Export	Graph			
Auto Reports	Apply colors to stacked plots			
Graph Grouping	Plot color 1			
Twitter	Plot color 2			
	Plot color 3			
	Plot color 4			
	Plot color 5			
	Plot color 6			
	Plot color 2 Plot color 3 Plot color 4 Plot color 5 Plot color 6 Plot color 7 Plot color 8 Plot color 9 Plot color 10 Plot color 12			
	Plot color 8			
	Plot color 9			
	Plot color 10			
	Plot color 11			
	Plot color 12			
	Plot color 13			
	Red	ore <u>D</u> efaults	Appl	v
		Terrard	- PP	
		ок	Cance	

Changing Plot Colors

1. Click the button next to a Plot color number. You'll get a color selection box:

Color					x	Γ
Basic colors:						
						h
		Ξ		Ξ	Ξ.	
	Ξ.	Ξ	Ξ.	Ξ.		
	Ξ.	Ξ.	Ξ.	Ξ.	Ξ.	
	_	_	_	-		
Custom colors:						
Define Custom Colors >>						
ОК	Car	ncel				
	_	_	_	_		J

- 2. Select a color or define a custom color and click OK. The color button will update to the new color selected.
- 3. Repeat the steps above for any other plot colors.

- 4. Check Apply Colors to Stacked Plots if you also want the new color settings to be used for the Stack the plots option in the Graph pane.
- 5. Click **Apply** to apply the new color settings to the plots currently displayed. This lets you see the changes without having to close the Graph window.
- 6. Click OK to save changes and exit.
- 7. Select Overlay the plots in the Graph pane. The new color scheme will be used.

Grouping Options

Select Grouping in the sidebar.

Selecting the **Group Across Runs** box groups samples with the same name together even if they're in different runs, so you can get statistics for the same samples across multiple runs. When the box isn't selected, only samples with the same name within the same run are grouped for statistics (this is the default setting).

NOTE: To activate grouping and get statistics for runs you have open in the Analysis Screen, select **View** in the main menu and click **Grouping**.

			-	
Preferences Access Control		—		×
	Grouping			
Access Control Analysis Export Auto Reports Graph Grouping Twitter	GroupIng Group Across Runs			
	3	lestore <u>D</u> efaults	Аррђ	(
	C	ОК	Cancel	

Setting Up Maurice Systems to Send Tweets

Select Twitter in the sidebar.

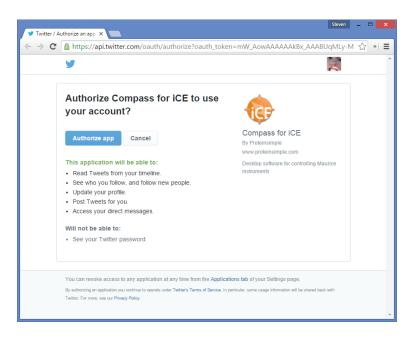
NOTES:

To set your Maurice system up to tweet, the computer you're using needs to be connected to the internet through a network connection or the local lab computer.

We recommend setting up separate Twitter accounts for each system. This lets multiple people in the lab follow run progress.

Preferences					×
Access Control Analysis Export	Twitter				
Auto Reports	Twitter User Name:				
Access Control Twitter Analysis Export		Set Account			
		Clear			
	Run is started Run is completed Run is paused Errors				
		Restore De	aults	Арр	ly
		ОК		Cance	8

1. Click Set Account. A set account window will display in Compass for iCE and a browser window will open:



- 2. Enter a user name or email and password, then click **Authorize app**. A new page will display in the browser with a PIN number.
- 3. Enter the PIN number in the Compass for iCE set account window and click OK:

🕼 Set Account	×
Enter PIN given by Twitter Web Sit	e
	OK Cancel

4. The user name will now appear in the Twitter User Name box. Select your Tweet When options and click Apply.

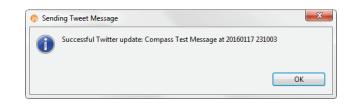
Preferences		– 🗆 X			
type filter text	Twitter 🔶 🗸				
type filter text Access Control Analysis Export Auto Reports Graph Grouping Twitter	Twitter Twitter User Name: Tweet When : Run is started Run is completed Run is paused Frrors Send Test Tweet	← ← ← ← ← ←			
		Restore Defaults Apply OK Cancel			

5. To confirm the Twitter account is receiving messages, click Tweet Message. Enter a test message and click OK.

freest Message	×
Message to send to Twitter	
Compass Test Message at 20160117 231003	
	OK Cancel

Chapter 21: Setting Your Preferences | Setting Up Maurice Systems to Send Tweets

6. If the test Tweet was successful, you'll get this message:



7. Click OK to save changes and exit. Maurice, Maurice C., Maurice S. and MauriceFlex will automatically tweet as the selected options occur:

Home Home	Moments	Notifications	Messages	y	Search Twitt	er Q	Tweet
protein							
	•	_	TWEETS FOLLOWING	FOLLOWERS 3		2	Following
Mauric @kifer2016 忆		e Kifer	C3160121012_F		_Maurice CE-SDS		
				16 · Feb 1 ment Maurice kf1010: Completed faurice cIEF_vialA1_5x_Time-red			
				16 · Feb 1 ment Maurice kf1010: Completed faurice cIEF_vialA1_5x_Time-red			

Changing the Twitter Account

To change the Twitter account your system uses:

- 1. Select **Edit > Preferences**, then select **Twitter** in the left sidebar.
- 2. Click Clear.
- 3. Follow the same steps to set up the account as in "Setting Up Maurice Systems to Send Tweets".

Chapter 22: Compass Access Control and 21 CFR Part 11 Compliance

Chapter Overview

- Overview
- Compass Authorization Server for iCE
- Enabling Access Control
- Changing the Software Inactivity Auto Lock
- Logging In to Compass for iCE
- Saving Changes
- Signing Files
- Exporting Uncontrolled Files
- Instrument Command Log
- Run File History
- Troubleshooting Problems and Suggested Solutions



Overview

The Compass Access Control feature can be used to help satisfy the 21CFR Part 11 data security requirements when using Maurice instruments. When Access Control is enabled and the Compass Authorization Server for iCE has been installed:

- Users are required to log in to Compass for iCE when the software is launched
- A history of all actions is maintained
- Data files are signed and encrypted to prevent unauthorized changes (e.g., all files are controlled)
- · Each instrument maintains a history of user commands
- Each batch and data file includes a history of signed changes to the file

Compass for iCE can be run with or without Access Control enabled. When Access Control is disabled, no user log in is required and files are not encrypted or signed. The instrument history and file history are still maintained but the entries are not signed.

Compass Authorization Server for iCE

The Compass Authorization Server for iCE controls the log in access to Compass for iCE. In the simplest configuration, the server is run on the same computer as Compass for iCE and only that copy of Compass for iCE is controlled. A single server can also be used to control access to multiple copies of Compass for iCE running on different computers, so long as they have network access to the server. Multiple copies of the server may be run on the same network, and each server will have its own user database.

To enable Compass for iCE to use a particular Authorization Server for iCE, click **Edit**, then **Preferences** and **Access Control** and enter the server IP address using format X.X.X.X.

NOTES:

Always use the default port setting of 8443, this should not be changed.

If the server is installed on the same computer as Compass for iCE (e.g., the local machine), enter localhost:8443 instead of the IP address. Contact your local IT Administrator to assist with installing the Compass Authorization Server for iCE in your preferred format.

Server Administration

The Authorization Server for iCE is configured through a web interface at the IP address of the server on port 8443. To access the Server home page, open any browser and type the IP address on port 8443 in a X.X.X.X8443 or http:// X.X.X.X8443 format. Use localhost:8443 instead of the IP address if the Server is installed on the local machine.

NOTE: If you have upgraded your system from a previous version of Compass Authorization Service, the localhost login page will have changed from http://localhost:8000/admin/login/?next=/ to http://localhost:8443/admin/login/?next=/

The default server administrator is:

- User: admin
- Password: admin

NOTE: The user account "admin" is not an active Compass for iCE login account. In order to log into Compass for iCE in the 21 CFR Part 11 compliant mode, at least one user account must be created in the Authorization Server for iCE application.

After installing the Compass Authorization Server for iCE, the administrator user name and password can be changed.

NOTE: Sites are responsible for maintaining their own admin and user account credentials. Record these and keep them safe. ProteinSimple can't provide access once the admin account has been edited.

S Log in Compass Authorization S	+		\sim	-	×
\leftarrow \rightarrow C \bullet https://local.hos	st:8443/admin/login/?next=/	Ê	☆	*	÷
	Compass Authorization Server				
	Username:				
	Password:				
	•••••				
	Log in				

Adding Non-admin Users

Add a user to the server to allow that user to log in to Compass for iCE. To do this:

1. Select **Users** from the Site Administration home page:

Site administration Compass Au × +								
← → C https://localhost:8443/admin/					Ē	☆	*	
Compass Authorization Server				Welco	me, admi	n. Chai	nge pa	issword
Site administration								
Authentication and Authorization			Recent Actions					
Groups	Add 🖶	🧷 Change	My Actions					
Users	🖨 Add	🥜 Change	/ johndoe					
Compass Authorization Server			♣ johndoe					
Blocked Users		🧷 Change	User / ismith					
LDAP settings		🧷 Change	User					
LDAF Settings			🧷 jsmith					
Password policy settings		🥜 Change						
		🧷 Change	User • jsmith					
Password policy settings		🥜 Change	User					

2. From the Users page, select Add User:

Select user to chang	e Compass 🛛 🗙	+								×
\rightarrow C h	ttps://localhost:8	8443/admin/auth/user/				Ê	☆			:
ompass Autho	rization Se	rver			Welcome	, admin . Change	a passi	word /	Log out	ł
me > Authentication an	d Authorization > I	Users								
Select user to	o change							Add us	er +	~
Select user to ૧	o change	Search				Filter		Add us	er +	
Select user to Q Username	change	Search Email address	First name	Last name	Staff status	By sta			er +)	
۹.	-		First name	Last name	Staff status				er +)	
Q Username admin	-		First name User	Last name		By sta All			er +)	
Q Username	-			Last name	0	By sta All Yes	ff sta	tus		

3. Fill in the fields to create a new user:

Add user Compass Authori	atio × +		\sim	-		;
← → C â https://k	calhost:8443/admin/auth/user/add/		È	☆		•
Compass Authorizat	on Server	Welco	me, <mark>admin</mark> . Cha	nge pa	ssword /	/ Log
me > Authentication and Autho	ization > Users > Add user					
Add user irst, enter a username and p	assword. Then, you'll be able to edit more user options.					
Username:	Required. 30 characters or fewer. Letters, digits and @///+/-/_ only.					
First name:						
Last name:						
LDAP User						
Password:						
Password confirmation:						
Staff Users may log in and view a	udit trail					
		Save and add another	Save and conti	nue ed	liting	Save

After adding a new user more information can be added:

S Change user C	Compass Authoriz 🗙	+					\sim	-	E	1	X
← → C (https://localhost:8	8443/admin/auth	user/2/				Ê	☆			:
Compass Aut	thorization Se	rver				Welcome, adm	in. Chan	je passv	word /		
ome > Authenticatio	n and Authorization > I	Users > user1									
Change use	er								H	istory	
Username:	user1										
	Required, 30 character	rs or fewer. Letters, d	gits and @/./+/-/_ only.								
Password:	Click here to change										
Personal info											i.
First name:											
Last name:											
Email address:											
Permissions											í.
Active Designates whethe	r this user should be trea	ited as active. Unsele	t this instead of deleting a	ccounts.							
Staff status Designates whethe	r the user can log into th	is server and change	their password.								
Superuser sta Designates whethe	atus r the user can manage u	ser accounts.									
Groups:	Available groups	0			Chosen groups 📀			•			
	Q Filter				Administrator		*				
	Operator			*							

NOTE: Users are blocked after the number of login failures defined in the Password policy setting.

Permissions

All users can log in to Compass for iCE, but the commands available within Compass for iCE are controlled by Permission settings. Commands a user does not have permission to use will be disabled. After user permissions have been changed on the server the user must close and re-open Compass for iCE to use the new permissions.

Users can belong to groups that have multiple permissions such as Operator or Scientist:

Change user Compass Authoriz: × +						\sim	-	C	כ
\rightarrow C https://localhost:8443/admin/auth/user/5/				G	Ŀ	☆	*		-
Available groups ⊛ Q Filter	· ·	00	Chosen groups Administrator Operator Reviewer Scientist				÷		
Choose all O The groupe this user belongs to. A user will get all per more than one.	rmissi	ions <u>c</u>	Remove all granted to each of their groups. Hold down "Control", of the control of the contro	er "Comr	mand"	on a M	ac, to s	elect	
ermissions:									
Available user permissions			Chocon upor parmissions						
Available user permissions Pilter Constraint in the second sec	*	00	Chosen user permissions ⊘				*		

Use the Groups page to change the permissions in a group or create new groups:

									1
← → C ♠ https://localhost:8443/admin/					Ŀ		*		
Compass Authorization Server				Welo	ome, admi	n. Chai	nge pa	issword	d
Site administration									
Authentication and Authorization			Recent Actions						
Groups	Add 🗣	🥒 Change	My Actions						
Users	🖨 Add	🥜 Change	/ johndoe						
Compass Authorization Server			johndoe						
Blocked Users		🥒 Change	User / jsmith						
LDAP settings		🤌 Change	User						
Password policy settings		🤌 Change	Jsmith User						
Audit Trail			jsmith User						
View Audit Trail			user2						

To change permissions for a group click **Change**, then select a group:

Select group to change Compa: × +	✓ - □ ×
← → C ▲ https://localhost:8443/admin/auth/group/	e 🛧 🗖 😩 :
Compass Authorization Server	Welcome, admin. Change password / Log ou
ome > Authentication and Authorization > Groups	
Select group to change	Add group +
Q Search	
Action: Go 0 of 4 selected	
Action: G_0 0 of 4 selected	
Group Administrator	
Group Administrator	

Move individual group permissions in or out of the Available Permissions and Chosen Permissions boxes by selecting a permission in either box. Click the **left** or **right** arrow button to move the permission into the other box.

Change group	Compass Authori × +						\sim	-		×
← → C (https://localhost:8443/admin/auth/group/3/						Ê	☆		1 I
Compass Aut	horization Server				Welcome	, admin	ı. Char	nge pa	assword /	Log out
Home > Authenticatio	n and Authorization > Groups > Operator									
Change gro	oup								Hi	istory
Name:	Operator									
Permissions:	Available permissions @			Chosen permissions () access proteinsimplepermission	Allow copy, export of da	ta	*			
	• Filter	•	0	access proteinsimplepermission access proteinsimplepermission access proteinsimplepermission access proteinsimplepermission access proteinsimplepermission access proteinsimplepermission access proteinsimplepermission	Allow instrument contro Allow plate/injection ed Allow analysis editing Allow instrument admin Allow protocol/method Allow report printing	il iting istration	*			
	Choose all 🕥			Rem	nove all					
	Hold down "Control", or "Command" on a Mac, to select more than one.									
# Delete				Sa	ave and add another	Save and	conti	nue ec	liting s	ave

Here are the current user and group permissions:

- Allow analysis editing lets users change analysis settings
- Allow copy, export of data lets users copy and export data
- Allow instrument control gives users permission to connect to an instrument
- Allow plate editing lets users update the plate layout and edit injections
- Allow protocol/method editing gives users permission to edit methods
- Allow report printing lets users print the Batch and Injection reports
- Allow sign off of data gives users permission to sign off on changes using e-signatures

• Allow instrument administration - lets users update the Maurice embedded software, delete run dates, update the Compass for iCE software and turn Access Control on or off

Adding Admin Users

To create a user with administrator permissions:

- 1. Follow the steps described in "Adding Non-admin Users" on page 771" to create the admin user.
- 2. Under permissions, select Staff status and Superuser status:

Permissions
Active Designates whether this user should be treated as active. Unselect this instead of deleting accounts.
Staff status Designates whether the user can log into this admin site.
Superuser status Designates that this user has all permissions without explicitly assigning them.

3. Assign the admin user to a group.

NOTE: Selecting Superuser status enables server permissions only. Admin users must be also be assigned to a group to in order to have Compass for iCE permissions.

Resetting User Passwords

NOTE: Users are blocked after the number of login failures defined in the Password policy setting.

To reset a user password:

1. Select Users from the Site Administration home page, then select the user to change. The following screen displays:

S Change user	Compass Authoriz × +	✓ - □ ×
← → C	https://localhost:8443/admin/auth/user/2/	🖻 🏚 🖬 😩 🗄
Compass Au	ithorization Server	Welcome, admin. Change password / Log out
ome > Authenticati	ion and Authorization > Users > user1	
Change us	er	History
Username:	user1	
	Required. 30 characters or fewer. Letters, digits and $\oplus /./+/-/_$ only.	
Password:	Click here to change	
Personal info		
First name:		
Last name:		
Email address:		
Permissions		
Active Designates whether	er this user should be treated as active. Unselect this instead of deleting accounts.	
Staff status		
Designates wheth	er the user can log into this server and change their password.	
Superuser st		
Designates wheth	er the user can manage user accounts.	

2. Click the text link to access the password change form:

Change password: user1 Comp: × +	\vee	-		×
← → C ≜ https://localhost:8443/admin/auth/user/2/password/	e t	r 🔲		:
Compass Authorization Server	Welcome, admin . Chang	a passwo	rd / Lo	og out
Home > Authentication and Authorization > Users > user1 > Change password				
Change password: user1 Enter a new password for the user user1.				
New password:				
New password				
	Ch	ange pa	isswor	rd

3. Enter the new password, then click Change password.

Audit Trail

Admin users with Staff Status can view, print and download the Audit Trail. Select **View Audit Trail** from the Site Administration home page to access it.

	4	> C	https://localh	nost-8443/adm	in/				8 \$	- 1	1 1	:		
					117									
	Cor	npass Aut	horization	Server				Welcome, a	dmin. Cha	nge passv	rord / Log	out		
		e admini												
		hentication an	d Authorizatio	n			ent Actions							
	Us	oups					Actions							
		npass Authoriz	ration Server			Us	ser ohndoe							
		cked Users	atton server			Change Ut	ser							
	LD	AP settings				🧷 Change 🛛 🗤	smith Iser							
	Pa	ssword policy	settings			Change Us	smith Iser							
		lit Trail					smith							
	· · · · · · · · · · · · · · · · · · ·	w Audit Trail					iser2							
	70	dit Trail Setti	iga			2 u	iser1							
ompass A	uthorization S							**	elconie,	aunnin.	change	passwu	rd / Log o	ľ
me > Audit Trail Audit Trai current server v	 version 3.0.0.189)													
udit Trai	version 3.0.0.189)	user 🋆	first	last	action △	description 🛆		comment						
udit Trai urrent server v ownload as P age: 1	Persion 3.0.0.189) DF machine Compass Authorization	user 🗢 –	first name △ -	last name △ -	action	description ≏ Version 3.0.0.189		comment						
age: 1 latetime \triangle 1022-05-05 1022-05-05 1022-05-05	Persion 3.0.0.189) DF machine Compass			name 🛆					4					
udit Trai urrent server v ownload as P age: 1 latetime △ 022-05-05 .4:56 -0700 022-05-05 .5:47 -0700 022-05-05	ersion 3.0.0.189) DF machine △ Compass Authorization Server Compass Authorization	-		name 🛆	install	Version 3.0.0.189	1		<u> </u>					
uurrent server v ownload as P age: 1 latetime △ 1022-05-05 .4:56 -0700 1022-05-05 .5:48 -0700 1022-05-05	Persion 3.0.0.189) DF machine △ Compass Authorization Server Compass Authorization Server Compass Authorization	 admin		name 🛆	install login User	Version 3.0.0.189			4					
udit Trai urrent server v ownload as P age: 1 latetime 1022-05-05 5:47 -0700 1022-05-05 5:48 -0700 1022-05-05 5:49 -0700 1022-05-05	machine machine machine machine machine compass Authorization Server Compass Authorization Server Compass Authorization Server Compass Authorization	admin admin		name 🛆	install login User Created User	Version 3.0.0.189 success Tu, Andrea as user Removed group Op	perator from user	-						
Audit Trai uurent server v ownload as P age: 1 latetime △ 1022-05-05 4:56 -0700 1022-05-05 5:49 -0700 1022-05-05 5:49 -0700 1022-05-05 5:49 -0700 1022-05-05 1022-05-05 5:49 -0700 1022-05-05 1022-05-05	machine	admin admin admin		name 🛆	install login User Created User Modified User	Version 3.0.0.189 success Tu, Andrea as user Removed group Op user1 Added group Admin	nistrator from user	-						
utilt Trai uurent server v ownload as P age: 1 latetime 022-05-05 14:56-0700 022-05-05 5:48-0700 022-05-05 5:49-0700 022-05-05 5:49-0700 022-05-05 5:49-0700 022-05-05 5:49-0700 022-05-05 5:49-0700 022-05-05 5:49-0700 022-05-05 022-05-05 022-05-05 022-05-05 022-05-05 022-05-05	machine	- admin admin admin admin admin		name 🛆	install login User Created User Modified User	Version 3.0.0.189 success Tu, Andrea as user Removed group Op user1 Added group Admin user1	nistrator from user nistrator to user Allow analysis r1 Allow copy,	-						
audit Trai aurrent server v ownload as P age: 1 latetime a 2022-05-05	revision 3.0.0.189) DF machine machine machine machine compass authorization Server Compass Compas	- admin admin admin admin admin admin		name 🛆	install login User Created User Modified User Modified User	Version 3.0.0.189 success Tu, Andrea as user Removed group Op user1 Added group Admin user1 Added permission / Added permission /	nistrator from user nistrator to user Allow analysis r1 Allow copy, iser user1 Allow instrument	-						

Here are the actions currently logged in the Audit Trail:

- Login. User logged into CAS or Compass.
- Logout. User logged out of CAS or Compass.
- Start run. User started a run in Compass.
- **Stop run.** User stopped a run in Compass.
- Delete run. Run file was deleted.
- Cartridge Cleanup. User initiated a cartridge cleanup routine from Compass.

- Self test. User initiated a self-test on an instrument.
- **Open runfile.** User opened a run file (*.mbz) in Compass.
- Save runfile. User saved a run file (*.mbz) in Compass to the file location shown.
- **Open batchfile.** User opened a batch file (*.batch) in Compass.
- Save batchfile. User saved a batch file (*.batch) in Compass to the file location shown.
- Instrument upgrade. User initiated an update of instrument software from Compass.
- Change Control Settings. User disabled Access Control from Compass.
- Generate Batch Report. User generated Batch Report from open batch in Compass.
- Generate Injection Report. User generated Injection Report from run in Compass.
- Export spectra and i format. User exported the raw and analyzed data traces and background for each injection in the run in .cdf format from Compass.
- Export spectra text format. User exported the raw and analyzed data traces and background for each injection in the run in .txt format from Compass.
- Export tables. User exported the results for all injections in the run in .txt format from Compass.
- User created. A new user was created on CAS.
- User modified. A user was modified on CAS.
- User deleted. A user was deleted on CAS.
- Group created. A group was created on CAS.
- Group modified. A group was modified on CAS.
- Group deleted. A group was deleted on CAS.
- Change password. A user's password was changed.
- Sign off. A user signed off on changes to the file location shown utilizing e-signatures in Compass.
- Edit LDAP settings. LDAP settings in CAS were modified.
- Edit password policy. Password policy settings were modified in CAS.
- Install. CAS software was installed.
- Upgrade. CAS software was upgraded to new version.
- Blocked. A user has been blocked from logging in.

- Unblock. A user has been unblocked, allowed to log in.
- Emergency Stop. User initiated the Emergency Stop command to instrument from Compass.
- Pause. User added a Pause operation to the running batch on the instrument from Compass.
- Continue. User initiated the Continue command to the instrument from Compass.
- Stop events. User initiated a stop to the instrument from Compass.

Audit Trail Settings

←

Co

The Secure Audit Trail PDF setting (selected by default), allows users to download audit trail PDFs securely. Secure audit trial PDFs can be viewed and printed, but content cannot be copied or modified.

	Site administration Compass Au × +					~	-		×					
	\leftarrow \rightarrow C \triangleq https://localhost:8443/ac	lmin/			Ŀ.	☆	* 0		:					
	Compass Authorization Server			Welcome	e, admin.	Change	e passi	word / Lo	og out					
	Site administration													
	Authentication and Authorization		Recent Actions											
	Groups	🖶 Add 🛛 🥒 Change	My Actions											
	Users	🖶 Add 🛛 🥜 Change	/ johndoe											
	Compass Authorization Server		- johndoe											
	Blocked Users	🥒 Change	User <i>ismith</i>											
	LDAP settings	🥒 Change	User											
	Password policy settings	🧷 Change	Jsmith User											
	Audit Trail		∲ jsmith											
	View Audit Trail		User user2											
	Audit Trail Settings	🧷 Change	User											
\leftrightarrow \rightarrow \mathfrak{C} Δ \textcircled{h} loc	alhost:8443/admin/proteinsimple/audittrail	settings/								Ê	☆ 1	• 0	1 4	:
Compass Authorizat								We	elcome,	admin.	Change	passv	vord / L	.og out
Iome > Compass Authorization S	Server > Audit Trail Settings > AuditTrailSettings o	bject												
Change Audit Tra	il Settings												His	tory
Secure Audit Trail PDF														

Save and continue editing Save

Password Policy Settings

These settings let administrators set password policies. Select **Password policy settings** from the Site Administration home page to make changes.

Select password policy setting to x +	✓ - □ X
← → C ▲ https://localhost.8443/admin/proteinsimple/passwordpolicysetting/	i∂ ☆ 🛯 💄 :
Compass Authorization Server	Welcome, admin. Change password / Log out
Home > Compass Authorization Server > Password policy settings	
Select password policy setting to change	
Display name	Value
Number of previous passwords to compare to	3
Minimum number of uppercase characters	1
Minimum amount of symbol characters	0
Minimum amount of number characters	1
Minimum number of lowercase characters	1
Minimum password length	8
Number of login attempts permitted	3
Days password is valid	180
8 password policy settings	Save

LDAP Settings

LDAP settings allow you to connect the Compass Authorization Server for iCE to your own network's domain controller, so users can log on with their existing network password. With LDAP, passwords are not maintained by the Compass Authorization Server for iCE they are administered by the network admin.

First select LDAP settings from the Site Administration page and set your LDAP settings.

Change LDAP setting Compass × +	∨ - □ X
← → C	🖻 🖈 🔲 😩 :
Compass Authorization Server	Welcome, admin. Change password / Log out
Home > Compass Authorization Server > LDAP settings > LDAPSetting object	
Change LDAP setting	
Enabled	
Address:	
Domain:	
SSL Port:	
Sync Information	
	Save and continue editing Save

Next, add users as described in "Adding Non-admin Users" on page 771 and select the LDAP User checkbox. Passwords aren't required for LDAP users.

Encryption Details

Compass for iCE uses the SHA1 hash algorithm to generate a 160 bit hash code that is unique for all files. All files saved by Compass for iCE are encrypted with a digital key. This key along with the hash codes guarantees the file history is correct and no other edits were made. All changes saved to a file have the electronic signature of the user who saved the file. The **e-Signature** command allows a user to sign off on a state such as approved or verified.

There is no individual ownership of files, all users who log into Compass for iCE can open any file.

Enabling Access Control

Access Control is enabled in Preferences. Select Edit in the main menu, click Preferences, then select Access Control.

📀 Preferences		—		\times
Access Control	Access Control			
Analysis Export Auto Reports Graph Grouping Twitter	Enable Server 127.0.0.1	efaults	Apply	
	ОК		Cancel	

To enable Access Control:

- 1. Check the Enable box.
- 2. Enter the IP address of the Authorization Server for iCE. Use format X.X.X.X:8443 or localhost:8443 if installing the server on the local machine.
- 3. Close Compass for iCE. The next time the software is launched, a user log in will be required.

NOTE: Access Control can only be disabled by logging into Compass for iCE and deselecting the **Enable** box in the Access Control page of Preferences.

Chapter 22: Compass Access Control and 21 CFR Part 11 Compliance | Changing the Software Inactivity Auto Lock

Changing the Software Inactivity Auto Lock

Compass for iCE software automatically locks to prevent user access after a period of inactivity. Once the software is locked, users must login again. Only users with instrument administrator permission can set the auto lock inactivity time.

- 1. Select Edit > Preferences > Access Control.
- 2. Enter an Auto Lock Inactivity time in minutes. The default setting is 20 minutes.

Access Control						
Enable	 Image: A set of the set of the					
Server	127.0.0.1					
Auto Lo	ck Inactivity (min)	20	•		-	
These se	ettings apply to all	users				

Logging In to Compass for iCE

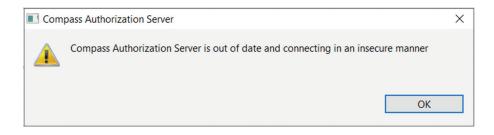
With Access Control enabled, all users must log in to Compass for iCE whenever the software is launched.

or Compass fo	r iCE Login
User:	
Password:	
	Login Cancel

Enter your user name and password previously setup by your Compass for iCE Administrator.

NOTE: Your account will be blocked after a certain number of login failures. If this happens, contact your administrator to unblock the account.

A window will appear if Compass for iCE is connecting to a previous version of the Compass Authorization Server that does not support a secure connection.



A successful log in will display the Compass for iCE main window with the user information in the lower status bar. The full user name is displayed with the unique user ID in parenthesis:

📀 Compass for iCE				- • ×
File Edit View Instrument Window H	lp			
🚊 Standards 🚉 Samples 📄 🚍				🔤 Batch 🔮 Run Summary 🚛 Analysis
Experiment 🔍 🗆	🔣 Graph		፲ 🖭 📃 🕴 🗆 🗉	🛛 🐠 Analysis Options 👘 🗖
Injection Injection Name Sample				
	Peaks III Injections			
	Injection Injection Name Sample	Peak Name Position pl	Height Area % Total % Area	Viidth S/N Baseline Resolution
	Lock			

Locking and Unlocking the Application

You can click the **Lock** button to lock Compass for iCE and prevent access by other users. To unlock the application, users must re-enter their password.



If there is no activity in Compass for iCE for 20 minutes, the application automatically locks. Users must re-enter their passwords to perform any controlled actions:

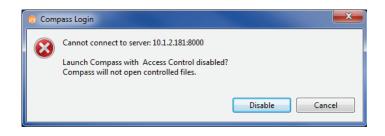
Compass for ICE (Locked)		_ O X
Compass for iCE	Locked	
	Congass for ICE Login Pesse re-enter password. User: film Password: Login Login Login Login	
		proteinsimple

Resolving Log In Issues

Log in failures may occur when:

- The server is temporarily unavailable
- Compass for iCE is using the wrong IP address

When this happens, the following message displays:



Click **Disable** to restart Compass for iCE with Access Control disabled. Verify or correct the server IP address then close and restart the software to log in with Access Control enabled.

Saving Changes

When **Save** is selected from the **File** menu, a dialog box will display to allow you to enter a comment before saving the signed file:

👸 Save Comment		×
File: cIEF1151219320_KF1004_on board mixing - stress t Comment:	test_2016-01-20_15-11-14_Ma	aurice cIEF
Change Baseline from 0.5 to 1.0		
	Save	Cancel

The comment is added to the signature entry in the file History:

🕑 Status 🔛 H	History				E E
Date		User Name	Message	Comment	
01/20/2016	3:11 PM	Ipriya	Started run: cIEF1151219320_KF1004_on board mi		
> 02/19/2016	10:39 AM	lzhu	Saved analysis changes	Change Baseline fro	
Time	02/19/20	16 10:39 AM	User Lujun Zhu (Izhu)		
Message	Saved a	nalysis changes			
Comment	Change	Baseline from 0.5	i to 1.0		

Signing Files

Select e-Signature from the File menu to add an electronic signature to a file.

6	e-Signature
	Add your e-signature to File: cIEF1151219320_KF1004_on board mixing - stress test_2016-01-20_15-11-14_Maurice cIEF Comment:
	Approved
	e-Sign Cancel

The signed entry will be added to the file History with the meaning of the signature entered in the comment, such as *Approved* or *Verified*.

Date	User Name	Message	Comment	
01/20/2016 3:11 PM	Ipriya	Started run: cIEF1151219320_KF1004_on board mi		
> 02/19/2016 10:39 AM	1 Izhu	Saved analysis changes	Change Baseline fro	
02/19/2016 10:50 AN	1 Izhu	e-Signature applied	Approved	
Time 02/19	/2016 10:50 AM	User Lujun Zhu (Izhu)		
Message e-Sid	nature applied			
Comment App				

Exporting Uncontrolled Files

You can export an uncontrolled file by selecting **File** > **Export Uncontrolled**.... The export will also be logged in the Audit Trail and the History log for the exported file.

File	Edit V	iew	Instrument	Win
	Open Ru	in		
	Add Run			
	Close			
	Close All			
	Save			
	Save As.			
	e-Signat	ure		
	Export U	ncon	trolled	
	Export Ta	ables		
	Export S	pectr	a	•
	Injection	Rep	ort	
	Exit			

Instrument Command Log

The Instrument Command Log can be viewed at any time by selecting the **Instrument** menu and clicking **Properties**, and then clicking the **Command Log** button:

2016-02-19	9_09-50-2	5_116010734	4_KF1004_RT-SG-Cartri	dge QC_Maurice cIE	F - Compass for iCE	×
Name :	Kifer kf10	004				
Location :						
		Type: Maur	ice	Network Name :	kf1004.local.	
	Serial Number : kf1004				10.1.3.214	
Instru	iment Soft	tware : 2.0.20	16.02.16.19.48.42.2e5ct	29		
Instrument	Date and	Time: 2016-	02-19 10:52:57 -08:00		Set to PC time	
		er k1004 Type: Maurice Network Name: k1004.local. al Number: k1004 Network Address: 10.13.214 tt Software: 20.2016.02.16.19.48.42.26.56729 e and Time: 2016-02.19 10.52.57 -08.00 Set to PC time lock: vials Sample Chiller: 9.8°C Time: 807 hours CEF Batch Injection Limit: 25 : Jan 2017 Injections Remaining: 95 : 116010734 Batches Remaining: 9				
Adap	ter Block :	vials		Sample Chiller : 9.8°	c	
				Sumple entiter : 5.0	0	
Cartridge						
	ype: cIEl					
Schurredin	10011 110			-		
		1	12 Jan 2016		5	
			\checkmark			
Error Lo	g	Test Log	Command Log		OK Cance	

The Command Log lists all the commands sent to the instrument that were signed by the user who sent the command. If you want to copy the Command Log at any time, right click in the table and select **Copy**, then paste into another document.

Date		User Name	Message	Comment
01/19/2016 2:	12 PM	Service	performUpgrade	
01/19/2016 4:	38 PM	rd	Started run: 2016-01-19_16-38-36_Maurice CE-SD	
01/20/2016 8:	58 AM	rd	Started cleanup	
01/20/2016 10	0:43 AM	rd	Started run: cIEF1151219320_KF1004_seal test_co	
01/20/2016 3:	11 PM	Ipriya	Started run: cIEF1151219320_KF1004_on board mi	
01/21/2016 10	0:14 AM	hxu	Started run: 2016-01-21_10-14-17_Maurice CE-SD	
01/22/2016 12	2:57 PM	atu	Started run: 2016-01-22_12-57-57_Maurice CE-SD	
01/25/2016 8:	34 AM	bpurandare	Started cleanup	
01/26/2016 7:	44 AM	bpurandare	Started run: 2016-01-26_07-44-10_6X_test-cartrid	
01/26/2016 12	2:22 PM	bpurandare	Started cleanup	
01/26/2016 1:	07 PM	ikazakova	Started run: C3151201218-NewCondVial-PIN_201	
01/27/2016 9:	35 AM	ikazakova	Started cleanup	
01/27/2016 10	0:19 AM	ikazakova	Started run: C3151218250-NewCondVial-PIN-201	
01/27/2016 5:09 PM ikazakova		ikazakova	Stopped run	
01/27/2016 5:	13 PM	ikazakova	Started run: C3151218250-OLDVial-NO_PIN-2016	
01/28/2016 9:	32 AM	ikazakova	Started cleanup	
lime 01	1/27/2016	5:13 PM	User ikazakova	11
Message S	tarted run	: C3151218250-0	DLDVial-NO_PIN-2016-01-27_17-12-51_24inj-A5A6-Ma	urice CE-SDS Assay:
Comment				

Run File History

Select the **Run Summary** screen tab and then the **History** tab to see the file History. To copy the file History, right click in the table and select **Copy**, then paste into another document.

									latch 🔠 Run Summary	Analysis
un: cIEF	1151219320_KF1004_c	n board mixi	ng - stress test_2	016-01-20_15-11-14_M	aurice cIEF					
Injectio	ns					🕐 Status 📗 History				Ŧ
	Sample ID	Location	Method	Status	-	Date	User Name	Message	Comment	
			Setup	Completed		01/20/2016 3:11 PM	Ipriya	Started run: cIEF1151219320_KF1004_on board mi		
			Calibration	Completed		> 02/19/2016 10:39 AM	Izhu	Saved analysis changes	Change Baseline fro	
	blank	A12	Method1	Completed		02/19/2016 10:50 AM	lzhu	e-Signature applied	Approved	
	blank	B12	Method1	Completed						
	SS Control - Ie	Cl	Method1	Completed						
	Blank - contro	C2	Method1	Completed						
	Mater Mix A1	H1	Method1	Completed						
	Master Mix B1	H2	Method1	Completed						
	Wash 1 @ plat	H3	Method1	Completed						
	Master mix @	H9	Method1	Completed	-	Time 02/19/201	L6 10:50 AM	User Lujun Zhu (Izhu)		
	Wash 1 @ plat	H11	Method1	Completed	-	Message e-Signat	ure applied	· · · ·		
.0	Wash 2 @ plat	H12	Method1	Completed		Comment Approve				
1	blank	A12	Method1	Completed						
2	blank	B12	Method1	Completed		🔔 Focus Series 🛛 🔛 IV P	lot			
3	SS Control - le	C1	Method1	Completed						Zoon
.4	Blank - contro	C2	Method1	Completed						
5	Mater Mix A1	H1	Method1	Completed		20		Injection 1		
.6	Master Mix B1	H2	Method1	Completed		e 20		man provide the second		
.7	Wash 1 @ plat	H3	Method1	Completed		E 15	- mon		many	144
8	 Master mix @	H9	Method1	Completed		9 15 40 10 89 5		1	. A marken have a	mandMaple
9	Wash 1 @ plat	H11	Method1	Completed		°q₽ 5				
0	Wash 2 @ plat	H12	Method1	Completed		0				
1	blank	A12	Method1	Completed		0 250	500	750 1,000 1,250	1,500 1,750	2,000
2	blank	B12	Method1	Completed				Pixel		
3	SS Control - le	Cl	Method1	Completed						
4	Blank - contro	C2	Method1	Completed						
5	Mator Miy A1	ш	Mathadi	Completed	-			Time 00:05:20 / 00:05:20		
					•			Third constant (constant		

Troubleshooting Problems and Suggested Solutions

If any of the following error messages are encountered, follow the recommended steps below to resolve the issue.

- Unknown user name or password.
 - Check if the Caps Lock is on, user name and password are case sensitive.
 - Ask a Compass for iCE administrator to confirm your user name. If your password is unknown then the administrator can reset your password (see Resetting User Passwords for more information).
- Server not available.
 - From the Edit menu, click Preferences and then Access Control to confirm the server address is set to the correct Authorization Server for iCE address. Compass for iCE must be able to reach the server on the network.
- Controlled file cannot be opened without log in. To open a controlled Run file, enable Access Control by clicking Edit, then Preferences and Access Control. Select Enable, close Compass for iCE, then re-launch the software with a valid log in.
- Uncontrolled file cannot be opened when logged in. To open an uncontrolled Run file, disable Access Control by clicking Edit, then Preferences and Access Control. Deselect Enable, close Compass for iCE then re-launch the software.

NOTES:

Only users with Instrument Administrator permission can turn Access Control on or off. This event will also be logged in the Audit Trail.

Uncontrolled files cannot be opened when Compass Access Control is enabled (controlled mode).

- **Command disabled.** Certain commands are only available when a user with the correct permissions is logged in. To change user permissions, use a web browser to log in to the Authorization Server for iCE web interface at the address shown on the **Access Control** page in **Preferences**, such as: 10.1.3.231:8443.
- **Compass for iCE does not prompt for log in.** Compass for iCE will only prompt for a log in on launch when Access Control is enabled in Preferences. Enable Access Control by clicking **Edit**, then **Preferences** and **Access Control**. Select **Enable**, close Compass for iCE, then re-launch the software. You should now be prompted for a log in.

Chapter 23: Maintenance and Troubleshooting

Chapter Overview

- Cartridge Handling and Care
- Installing or Replacing the System Filter
- Maintenance
- Spare Parts
- Software Updates
- Instrument Software (Embedded) Updates
- Frequently Asked Questions: General
- Frequently Asked Questions: cIEF Applications
- Frequently Asked Questions: cIEF Fractionation Applications
- Frequently Asked Questions: CE-SDS Applications
- Best Practices
- Troubleshooting

Cartridge Handling and Care

The cIEF, cIEF Fractionation, CE-SDS PLUS and Turbo CE-SDS Cartridges were developed for use with Maurice systems. Each cartridge is individually tested and shipped with a Certificate of Analysis, are also online at https://www.bio-techne.com/resources/cofa-finder-tool. The cartridges are shipped dry and should be stored free of liquid.

- **Cartridges need to be used, cleaned and stored properly to reach their maximum lifetime**. Additional cleaning vials (PN 046-125) and cartridge inserts (PN 046-124) for CE-SDS PLUS cartridges may be purchase separately.
- Store cartridges in their original packaging at room temperature when you receive them.
- Hold cartridges using the blue or orange finger holds on either side of the cartridge.
- Don't touch the recessed optical windows of the cartridge.



• Whenever you handle the cartridge or remove it from its packaging, make sure the cartridge inlet doesn't come in contact with any surfaces. A damaged inlet may compromise the cartridge and cause a failed injection.



- cIEF Cartridges are guaranteed for 100 injections and an absolute maximum of 200 injections.
- CE-SDS PLUS Cartridges are guaranteed for 100 injections and an absolute maximum of 500 injections.

- Turbo CE-SDS Cartridges are guaranteed for 100 injections.
- cIEF Fractionation Cartridges support 15 injections.
- Maurice reads the cartridge's RFID and keeps track of how many injections are left for you automatically.
- Always clean the cartridge before storing. See page 120 for cIEF Cartridge cleaning steps, page 182 or page 248 for cIEF Fractionation Cartridge cleaning steps, page 316 for CE-SDS PLUS Cartridge cleaning steps and page 385 for Turbo CE-SDS Cartridge cleaning steps.
- Always store the cartridge in its original packaging at room temperature when not in use.

cIEF Cartridge

A cIEF Cartridge is guaranteed for 100 injections with an absolute maximum of 200 injections and a maximum of 20 batches. Its RFID will keep track of how many are left for you.

- The cartridge is designed for use with common cIEF reagents like methyl cellulose, ampholytes, urea and other protein solubilizing agents, anolyte and catholyte, but over exposure or high concentrations of certain components can harm it. The cartridge is optimized for 0.35% methyl cellulose in the sample mixture.
- Make sure to not get any liquid on the cartridge's optical window.
- Always clean the electrolyte tank and run the cartridge post-run cleanup at the end of a run. See page 120 for cIEF Cartridge post-run cleaning steps.

Compatibility with Sample Components

- Methyl Cellulose (MC): The sample mix must contain 0.35% methyl cellulose. The cartridge must be flushed with 0.5% methyl cellulose between runs.
- **Solvents:** The cartridge is not compatible with organic solvents. Do not rinse with untested solvents and minimize the amount of solvent in the sample mix.
- Salt and surfactants: High current can harm the internal coating in the cartridge capillary. High concentrations of salt and surfactants in the sample mix can generate high currents above 40 microamps. This high current will compress the pH gradient and also damage the cartridge. Please take care to minimize the concentration of salts in the final sample mix to below 15 mM. To keep current at a minimum, we suggested using only non-ionic or zwitterionic surfactants. Don't use aromatic surfactants as they can interfere with sample detection.

Cleaning the Outside of the Cartridge

If you see spikes in your data, the outside of the cartridge should be cleaned with canned air. You'll need to use residueand moisture-free canned air to prevent fouling of the optical path through the separation capillary.

- 1. Place the can's nozzle or tube opening 10–12 inches from the cartridge surface. Then depress the aerosol actuator down about halfway so you get a gentle flow of air.
- 2. Sweep the air stream across the entire length of the optical window.
- 3. Flip the cartridge over and repeat the prior steps.

4. Flip the cartridge over again and gently clean the top surface one last time before reinstalling in Maurice.

cIEF Fractionation Cartridge

A cIEF Fractionation Cartridge supports up to 15 injections and a maximum of four injections per MauriceFlex cIEF batch and one injection per MauriceFlex Fractionation batch. Its RFID will keep track of how many are left for you.

- The cartridge is designed for use with common cIEF reagents like methyl cellulose, ampholytes, urea and other protein solubilizing agents, anolyte and catholyte, but over exposure or high concentrations of certain components can harm it. The cartridge also requires 0.35% methyl cellulose in the sample mixture. We do not recommend using more than 0.8% methyl cellulose in the sample mixture.
- Make sure to not get any liquid on the cartridge's optical window.
- Always clean the electrolyte tanks and run the cartridge post-run cleanup at the end of a run. See page 182 or page 248 for cIEF Fractionation Cartridge post-run cleanup steps.

Compatibility with Sample Components

- Methyl Cellulose (MC): The sample mix must contain 0.35% methyl cellulose. The cartridge must be flushed with 0.5% methyl cellulose between runs.
- **Solvents:** The cartridge is not compatible with organic solvents. Do not rinse with solvents and minimize the amount of solvent in the sample mix.
- Salt and surfactants: High current can harm the internal coating in the cartridge capillary. High concentrations of salt and surfactants in the sample mix can generate high currents above 90 microamps. This high current will compress the pH gradient and also damage the cartridge. Please take care to minimize the concentration of salts in the final sample mix to below 10 mM. To keep current at a minimum, we suggested using only non-ionic or zwitterionic surfactants. Don't use aromatic surfactants as they can interfere with sample detection.

Cleaning the Outside of the Cartridge

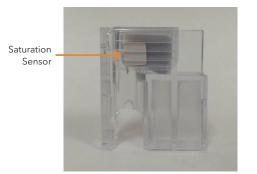
If you see spikes in your data, the outside of the cartridge should be cleaned with canned air. You'll need to use residueand moisture-free canned air to prevent fouling of the optical path through the separation capillary.

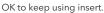
- 1. Place the can's nozzle or tube opening 10-12 inches from the cartridge surface. Then depress the aerosol actuator down about halfway so you get a gentle flow of air.
- 2. Sweep the air stream across the entire length of the optical window.
- 3. Flip the cartridge over and repeat the prior steps.
- 4. Flip the cartridge over again and gently clean the top surface one last time before reinstalling in MauriceFlex.

CE-SDS PLUS Cartridges

A CE-SDS PLUS Cartridge is guaranteed for 100 injections with an absolute maximum of 500 injections, a maximum of 48 injections per batch and a maximum of 25 batches. Its RFID will keep track of how many are left for you.

- Once you've inserted the Top Running Buffer vial in the cartridge insert, the CE-SDS PLUS Cartridge **must** be kept in an upright position at all times.
- If you see any separation matrix sticking to the cartridge inlet, soak the inlet in DI water for 5 minutes. Then wipe it using a lint-free laboratory wipe that's been moistened with DI water. Other than this, no external cleaning of the cartridge is required.
- Check the saturation sensor on the back of the CE-SDS PLUS Cartridge insert after every run. If it's red, you'll need to use a new cartridge insert for your next batch. If the saturation sensor isn't red, you can keep using the current cartridge insert.







Replace cartridge insert.

- We highly recommend running a Cartridge Purge if the cartridge has not been used in more than 3 months. See "Cartridge Purge" on page 439 for instructions.
- Always run the post-run cleanup at the end of a run. See page 316 for CE-SDS PLUS Cartridge post-run steps.

Compatibility with Sample Components

• Salt: The salt concentration in your sample should be <50 mM. Higher concentrations will adversely affect electrokinetic injections. Dilute your sample with CE-SDS Sample Buffer to reach the recommended salt concentration. If the protein concentration in your samples is low, we recommend desalting the sample.

Turbo CE-SDS Cartridges

A Turbo CE-SDS Cartridge is guaranteed for 100 injections with a maximum of 96 injections per batch and a maximum of 25 batches. Its RFID will keep track of how many are left for you.

- Prepare your samples and reagents before preparing the cartridge. Allowing the Separation Matrix to sit in the cartridge for longer than 15 minutes may result in cartridge clogs.
- If you see any separation matrix sticking to the cartridge inlet, soak the inlet in DI water for 5 minutes. Then wipe it using a lint-free laboratory wipe that's been moistened with DI water. Other than this, no external cleaning of the cartridge is required.
- We highly recommend running a Cartridge Purge if the cartridge has not been used in more than 3 months. See "Cartridge Purge" on page 439 for instructions.

• Always clean the Running Buffer and Waste Tanks and run the post-run cleanup at the end of a run. See page 385 for Turbo CE-SDS Cartridge post-run cleanup steps.

Compatibility with Sample Components

• Salt: The salt concentration in your sample should be <50 mM. Higher concentrations will adversely affect electrokinetic injections. Dilute your sample with CE-SDS Sample Buffer to reach the recommended salt concentration. If the protein concentration in your samples is low, we recommend desalting the sample.

Installing or Replacing the System Filter

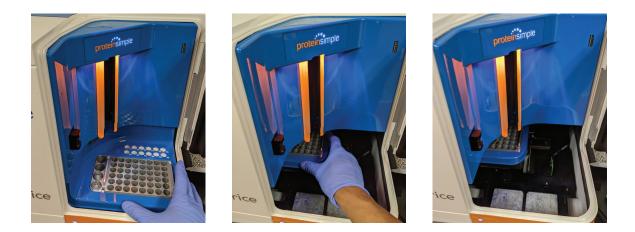
If the optional Maurice System Filter Upgrade is installed on your Maurice, Maurice S. or MauriceFlex system, we recommend changing the filter every 3 months.

- 1. Make sure Maurice isn't running a batch (light should be steady blue).
- 2. Open Maurice's door by touching the metal plate on top of the door. If a cartridge is installed, remove it. For more info on removing and storing cartridges, see "Post-batch Procedures" on page 316 for a CE-SDS PLUS Cartridge and "Post-batch Procedures" on page 385 for a Turbo CE-SDS Catridge.

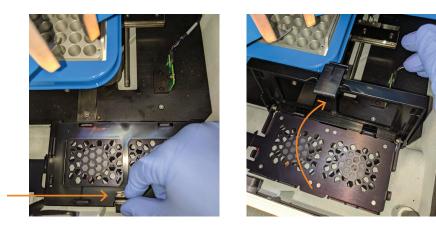


NOTE: The indicator light on Maurice's front panel will blink rapidly as the door disengages.

- 3. Swing the door open to access the reagents and samples platform.
- 4. Gently apply pressure to the front right corner of the reagents and samples platform and push the platform to the left and then back until the front corner is below the cartridge slot (orange lights). The filter holder will now be accessible.



5. Open the filter holder by squeezing the front tab inward (orange arrow) and lifting the hinged holder door up and open. The images below show the filter holder without a filter installed.



- 6. Remove the old filter (if present) and discard.
- 7. Remove the new filter from the plastic wrapping.

NOTE: Use scissors to cut open the filter packaging, taking care not to cut the filter itself. Tearing open the package may bend or damage the filter. We recommend handling the filter with gloves to prevent contamination.

8. Place the new filter in the holder, it doesn't matter which side is up or down. It should lie flat and within the raised edges on the sides of the holder.

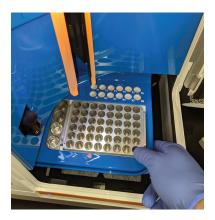


9. Close the holder lid until the latch clicks into place. Gently tug on the latch to make sure the filter holder is fully closed.



10. Gently move the reagents and sample platform back into position by pulling on the corner of the platform until the reagent and sample locations are visible.

NOTE: The exact positioning of the platform isn't critical. Maurice will automatically home the platform to the correct position once the door has been closed.



11. Close Maurice's door. A steady blue light will indicate that the system is ready to use.

Maintenance

Daily

- Empty out any condensation in the sample plate or sample tray inserts. Wipe out the sample block too if needed.
- Dispose of your samples and reagent vials after each run. Compass for iCE will let you know when a cartridge is at the end of its useful life and should be discarded.

Yearly

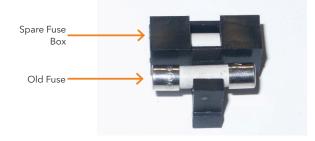
We recommend Maurice systems have annual preventive maintenance performed by an authorized ProteinSimple engineer. Please contact Technical Support to schedule a visit.

Changing the Fuse

- 1. Power down Maurice and unplug his power cord.
- 2. Locate the fuse holder on his rear panel.



3. Use a flat-head screwdriver to gently pry the fuse holder open and remove the fuse holder.



- 4. Remove the old fuse.
- 5. There's a spare fuse in the small box. Pull the box out, pull the new fuse out and use it to replace defective fuse.



- 6. Reinsert the fuse holder.
- 7. Plug Maurice's power cord back in and turn his power on.

Spare Parts

Maurice, Maurice C., Maurice S. and MauriceFlex don't have any user replaceable parts except for the filter and power fuse. Please contact ProteinSimple Technical Support if they get sick and need repair. • Maurice Filter Kit - PN 046-576, includes 4 filters and 8 plate lids.

!WARNING! You can't replace or service any parts on Maurice systems except for the filter and power entry fuse.

Software Updates

To check for software updates, first make sure the computer you're using has an active internet connection. Then go to Compass for iCE software, select **Help** in the main menu and click **Check for Updates**. If you don't have internet access, call your FAS for assistance on getting the latest update.

Instrument Software (Embedded) Updates

To check for embedded updates, go to Compass for iCE software, select **Instrument** in the main menu, then **Update** and select **Network**. If you're not on the network, contact Technical Support for assistance on getting the latest update.

Frequently Asked Questions: General

Should I download a secured or non-secured batch or injection report?

See the table below for what you can do with a secured PDF (Compass default) vs. a non-secured PDF.

Parameter	Secured PDF	Non-Secured PDF
Security Method	Random password security	No security
Printing	Allowed	Allowed
Document Assembly	Not allowed	Allowed
Content Copying	Not allowed	Allowed
Content Copying for Accessibility	Not allowed	Allowed
Page Extraction	Not allowed	Allowed
Commenting	Not allowed	Allowed
Filling of Form Fields	Not allowed	Allowed
Signing	Not allowed	Allowed
Creation of Template Pages	Not allowed	Allowed
Encryption Level	128-bit RC4	N/A

Frequently Asked Questions: cIEF Applications

NOTE: Please refer to the Maurice cIEF Method Development Guide for info on initial application conditions and method optimization.

I have a new protein sample to analyze. What starting conditions should I use?

Begin with the following initial sample conditions:

- Carrier ampholytes: pH 3-10 Pharmalytes (4%)
- Additive: 0.35% methyl cellulose
- Sample analyte: 0.1 mg/mL concentration in final solution. The balance of the solution should be HPLC-grade deionized water.
- 10 mM arginine
- 1X pI 4.05 and 9.99 markers

NOTES:

If you want to use pI markers below pI 4.05, we suggest adding iminodiacetic acid 10 mM IDA to the sample solution

ProteinSimple provides a 1% methyl cellulose solution (PN 101876).

Another way to start is to simply use the same sample conditions used if you were successful in running this sample on slab gel IEF. Use the same carrier ampholytes and additives for analysis on Maurice systems.

What carrier ampholytes are commercially available, and which one is best for my sample?

At present, carrier ampholytes are commercially available from four different manufacturers under the following brand names:

- Pharmalytes (Cytiva formerly GE)
- Servalyts (Serva)

Other carrier ampholytes exist, however, they are all repackaged and resold using one of the products listed above.

Each brand may give slightly different separation resolution due to slight differences in ampholytic compositions. Identification of the optimal carrier ampholytes for a given protein sample is best determined experimentally.

Along with native fluorescence, Maurice systems use UV absorption detection at 280 nm. All carrier ampholytes exhibit some degree of absorption at this wavelength, which causes some baseline noise. Pharmalytes have low and uniform UV absorption and produce no background signal in native fluorescence along the entire pH range. Because of the low background noise of Pharmalytes, these ampholytes are recommended for initial sample conditions.

Does my sample matrix affect my results?

Yes. However, the sample is diluted 20X in carrier ampholytes, methyl cellulose and HPLC-grade deionized water, which minimizes matrix effects. For example, if the concentration of your sample stock solution is 2 mg/ μ L, 10 μ L of the sample can be directly diluted by adding 112 μ L of HPLC-grade deionized water, 8 μ L of pH 3–10 Pharmalytes and 70 μ L of 1% methyl cellulose. The final solution is 200 μ L with a sample concentration of 0.1 mg/ μ L. In this example, the original sample matrix will not affect analysis.

If the original stock sample concentration is >2 mg/mL and contains high salt concentrations, then diluting further and using native fluorescence to boost signal is recommended. If detection in both absorbance and fluorescence is required, desalting may be necessary.

I cannot get reproducible peaks due to sample precipitation, what should I do?

- 1. Dilute the sample.
- 2. The native fluorescence detection mode provides higher sensitivity and can be used for low concentration samples.

Doing either or both of the above reduces the potential for aggregation or precipitation. If the issue is still observed, several additives can be tested to increase protein solubility. The following additives have been successfully tested with Maurice systems and should help stabilize proteins during analysis:

- Up to 40% SimpleSol
- Up to 4 M urea
- Up to 20% formamide
- Up to 25% sorbitol
- Up to 25% sucrose
- Up to 25% glycerol
- Denaturing conditions, such as 8 M urea

In rare cases, sample precipitation may be caused by the carrier ampholytes. To avoid this problem, try using a different brand of carrier ampholytes. If additive conditions for stable sample runs have been established for gel IEF, then these additive conditions can often be successfully used for cIEF analysis on Maurice systems.

NOTE: All additives may change the pI value of the protein slightly, especially if the method uses pI markers in the acidic range of the pH gradient.

How do I prepare sample solutions in 8 M Urea?

For a 200 µL final sample solution:

- Weigh 96 mg of urea powder in a 1.5 mL centrifuge tube.
- Add 32 µL HPLC-grade deionized water, 70 µL of 1% methyl cellulose, 8 µL of carrier ampholytes and 10 µL of sample to the urea powder in the centrifuge tube.

This will make a final volume of 200 μ L (96 mg urea powder and 120 μ L liquid). If more than 10 μ L or less than 10 μ L of sample is added, the volume of water should be adjusted to ensure a final volume of 120 μ L.

NOTE: Urea must always be prepared fresh before use. Do not heat to dissolve urea in solution.

When running samples in 8 M urea, the focusing time should be increased 1-2 minutes compared to normal conditions. This is due to the higher viscosity of the urea-containing solution.

How do I choose a protein solubilizer?

Protein precipitation or aggregation may occur during the isoelectric focusing step as proteins concentrate close to their pIs, leading to non-reproducible peak profiles. One of the strategies to address this issue is the addition of protein solubilizers to the protein-ampholyte mixture. Urea, a chaotropic agent, is a popularly used protein solubilizer that disrupts non-covalent bonds to reduce protein precipitation and aggregation. However, a number of known issues exist for urea, including potential induction of carbamylation, anodic gradient drift causing shift of apparent pI values, and protein

denaturation above 4 M. In addition, urea needs to be prepared fresh daily which creates an additional step in sample analysis.

SimpleSol can effectively solubilize proteins for icIEF but is a significantly more stable agent than urea, eliminating the need for analysts to prepare urea fresh every day. SimpleSol is also stable when pre-mixed with methyl cellulose as opposed to urea, and is compatible with absorbance and native fluorescence detection on Maurice icIEF. In addition, SimpleSol has less of an impact on the acidic portion of the pH gradient formed during icIEF compared to urea, resulting in more stable pI values of protein peaks relative to using urea. Consider SimpleSol if you are concerned about solution stability, pH gradient formation, or ease-of-use for your protein solubilizer.

How can I identify peaks in different runs and different samples?

A reliable way to identify peaks in electropherograms is to use internal pI Markers. First run the sample without internal pI Markers. The pI values of sample peaks can be estimated from their peak positions relative to the full pI range of the carrier ampholytes.

In Compass for iCE graphs, the left side of the electropherogram is the anodic end of the capillary (acidic) and the right side is the cathodic end (basic). For example, if pH 3-10 Pharmalytes are used as the carrier ampholytes, the x-axis of the electropherogram represents pI 3 to pI 10 from left to right. The pI value of a peak at the middle of the trace should be about 6.5.

Two pI Markers are mixed into the sample solution. Ideally, the peaks of the two markers should bracket the sample peaks and the two marker peaks should be as close as possible in order to achieve good precision in peak identification.

The electropherograms of the sample mixed with pI Markers are processed using Compass for iCE for pI determination. The software uses the method settings to automatically identify the pI markers to convert from pixel position in the Markers View to pI in the Samples View.

In this way, the sample peaks are identified by their measured pI values. The precision of peak identification by measuring the pI values using Maurice systems is less than +0.03 pH units.

Since the measured pI value of a protein is affected by many factors such as sample matrix and the type of carrier ampholytes used, to correctly identify peaks in different samples or different runs, all runs should be done under the exact same conditions.

What kind of pI markers can I use?

ProteinSimple recommends using low molecular weight amphoteric compounds with well defined isoelectric points and strong UV absorbance when using Maurice systems. Conversely, we do not recommend using protein pI markers since they often produce multiple isoelectric points and, on occasion, may interact with the sample analyte.

ProteinSimple offers a selection of absorbance- and fluorescence-compatible pI markers at pI 3.38, 4.05, 5.85, 6.14, 7.05, 8.40, 9.50, 9.99 and 10.17.

The distance between the two pI Markers in my sample electropherograms is different from run to run even though I use the same pI Markers and carrier ampholytes. What is the reason for this?

Usually this is caused by different salt concentrations in the sample solutions. Salt can compress the pH gradient created by the carrier ampholytes. So, the higher the salt concentration, the shorter the distance between the two pI Markers.

However, since the whole pH gradient is compressed by the salt, this will not affect peak identification results as long as two pI Markers are used and their peaks bracket the sample peaks.

Can I use narrow pH range carrier ampholytes to improve the resolution for my sample?

Yes. The most efficient way to do this is to use a mixture of narrow pH range carrier ampholytes and wide pH range carrier ampholytes. The proportion of carrier ampholytes can be from 1:1 (narrow range: wide range) up to 5:1 depending on the resolution requirement. Focusing time should be increased with the increasing proportion of the narrow pH range carrier ampholytes, from 6 to 12 minutes.

The measured pI value of my sample peak is slightly different when I use different pI Markers or different carrier ampholytes with the same pI markers. What is the reason for this?

When using different pI Markers, the small difference in the measured pI value is due to the slight non-linearity of the pH gradient established by the carrier ampholytes along the separation capillary. Compass for iCE pI calibration assumes that the pH gradient is perfectly linear between the two pI Markers. In reality, carrier ampholytes are not perfectly linear throughout their pH gradient.

When different carrier ampholytes are used, their pH gradients may be slightly different causing a small difference in measured pI value. This effect is most obvious when using a carrier ampholyte mixture (i.e. narrow and wide pH range carrier ampholytes). Under these conditions, the pH gradient will not be linear at the edges of the overlapping pH regions of the different carrier ampholytes. Changing the ratio of the different carrier ampholytes in the mixture will affect the measured pI values of a protein.

In conclusion, only measured pI values obtained using the same carrier ampholytes and the same pI markers can be compared. Also, as long as the run conditions are the same, the measured pI values can be used to identify protein peaks.

Frequently Asked Questions: cIEF Fractionation Applications

NOTE: Please refer to the MauriceFlex cIEF Fractionation Method Development Guide for info on initial application conditions and method optimization. Refer to the Maurice cIEF Method Development Guide and "Frequently Asked Questions: cIEF Applications" on page 801 for initial sample and method optimization of Maurice cIEF prior to running cIEF fractionation.

How do I optimize a cIEF fractionation batch?

Method development starts with a previously developed Maurice cIEF method, and you'll typically only need to optimize a few parameters from there. For many molecules, adding an additional 20 mM arginine to the final sample with the separation mix used for Maurice cIEF methods provides sufficient fractionation performance and don't need further development.

For more challenging molecules that do not fractionate well and/or have limited solubility refer to the MauriceFlex cIEF Fractionation Method Development Guide. In summary, the first step is to start with a generic method and evaluate the

separation current and focused peak profile. Once you have the desired peak profile, fractionation can be optimized for the desired peak purity and concentration.

What is the recommended sample concentration for cIEF fractionation?

cIEF fractionation typically uses higher sample concentrations than used for Maurice cIEF. ProteinSimple recommends initial sample concentrations of 1 mg/mL. Increasing the sample concentration can improve concentrations of the fractions, but may also result in aggregation. Addition of protein solubilizers, such as 2 M urea, will eliminate sample aggregation most of the time.

How are sample peaks mobilized and collected during cIEF fractionation?

Samples migrate out of the cartridge capillary and into the fraction wells using chemical mobilization with 5 mM ammonium acetate (Mobilizer Solution). During the chemical mobilization, acetate ions from the Mobilizer Solution enter the capillary to displace the hydroxy ions when a voltage is applied. This results in the change of the local pH and charged molecules in the capillary, including protein charge variants, become positively charged. The positively charged protein moves toward the cathodic end of the capillary, eventually into the fraction wells with Mobilizer Solution. Other charged molecules in the sample, like ampholytes, will also be mobilized and collected in fractions.

How do I prepare sample solutions in 4 M urea?

The total sample volume should be 200 μ L. You'll need the following amount of components per 160 μ L of master mix prepared with 48 mg urea powder:

- 70 µL of 1% Methyl Cellulose
- 8 µL of carrier ampholytes (total)
- 1.5 µL of each pI marker
- 8 µL of 500 mM Arginine
- Add DI water to reach 160 µL total volume

NOTE: Urea must always be prepared fresh before use. Do not heat to dissolve urea in solution.

How do I check the purity and identity of the sample in the fractions?

To verify the presence and identity of charge variants in specific fractions, we recommend performing a Maurice cIEF batch with the fractions and a sample of the unfractionated molecule as a reference. Peaks detected in the fractions can be aligned based on pI with peaks in the unfractionated reference sample to verify identify. Peak purity can be assessed in the fractions by measuring percent peak area for each peak detected in a fraction. We recommend using fluorescence detection in a Maurice cIEF batch for calculating peak purity and estimating concentration of charge variants within a fraction.

Can I use the cIEF Fractionation Cartridge for standard Maurice cIEF analysis/batches?

No, the cIEF Fractionation Cartridge cannot be used with a Maurice cIEF batch. In addition, the cIEF Fractionation Cartridge is not designed for quantitative cIEF analysis of proteins – use the Maurice cIEF Cartridge for this purpose. Focused images on a cIEF Fractionation Cartridge are provided for qualitative purposes only.

Frequently Asked Questions: CE-SDS Applications

NOTE: Please refer to the Maurice CE-SDS Application Guide for info on initial application conditions and method optimization.

What is the molecular weight size range?

The CE-SDS application lets you size proteins between sizing between 10 and 270 kDa.

What wavelength is used for detection?

Proteins are detected via absorbance at 220 nm.

How good is the resolution?

The CE-SDS application was optimized to achieve baseline resolution (>1.5) between the glycosylated and nonglycosylated heavy chain.

Can I run non-reduced samples?

You can run both reduced and non-reduced IgG samples on Maurice. See the instructions in Chapter 12: "Running CE-SDS PLUS Applications" or Chapter 14: "Running Turbo CE-SDS Applications" for sample preparation. Compass for iCE also has default methods for running reduced and non-reduced samples, so you can select the appropriate method for your sample.

Best Practices

Maurice cIEF

Follow the setup and cleanup instructions in the Maurice cIEF Cartridge Product Insert (PN 046-298).

Important Tips:

- Immediately empty and rinse the electrolyte tanks on the cartridges after opening the Maurice door at the end of a run. After clean-up, leave the stoppers off the cartridge for storage. Store the stoppers and the cartridge together in its original packaging.
- Confirm you are using the correct glass reagents for the application you are running. cIEF batch reagents should be prepared usign 2 mL glass reagent vials (PN 046-017).
- Use only ProteinSimple-recommended plate seals (https://biochromato.com/slit-seal/). Use plate seals for standard Maurice cIEF ONLY, DO NOT use plate seals for MauriceFlex cIEF, MauriceFlex Fractionation or CE-SDS applications.

MauriceFlex cIEF and MauriceFlex Fractionation

Follow the setup and cleanup instructions in the MauriceFlex cIEF Fractionation Cartridge Product Insert (PN PL3-0058).

Important Tips:

- Immediately empty and rinse the electrolyte tank on the cartridge after opening the MauriceFlex door at the end of a run. After clean-up, leave the stopper off the cartridge for storage. Store the stopper and the cartridge together in its original packaging.
- When installing the fractionation adapter, confirm the adapter is seated and sitting flat in MauriceFlex.
- Remove batch reagent vials from the reagent platform prior to placing the fractionation adapter in MauriceFlex if a Maurice cIEF or CE-SDS application was previously performed.
- Confirm you are using the correct glass reagent vials for the application you are running. MauriceFlex cIEF and MauriceFlex Fractionation batch reagents should be prepared using glass reagent vials, 0.3 mL (PN 110-0018) for the Fluorescence Calibration Standard and 2 mL crimp top glass vials (PN 110-0019) for all other reagents.
- DO NOT use plate seals for MauriceFlex cIEF or MauriceFlex Fractionation applications.

Maurice CE-SDS

Follow the setup and cleanup instructions in the Maurice CE-SDS PLUS Cartridge Product Insert (PN PL3-0013) of the Maurice Turbo CE-SDS Product Insert (PN PL3-055) depending on the cartridge you are using.

Important Tips:

- Clean the cartridge according to the procedure outlined in the Product Insert immediately after opening the Maurice door at the end of a run.
- The Top Running Buffer (TRB) vial should be inserted into the CE-SDS PLUS cartridge only once. Do not remove and re-insert the vial.
- Once a TRB vial is inserted into a cartridge, keep the cartridge upright.
- CE-SDS PLUS Cleaning vials may only be used up to 5 times.
- Immediately empty and rinse the Top Chamber on the Turbo CE-SDS cartridge after opening the Maurice door at the end of a run. After clean-up, leave the stopper off the cartridge for storage. Store the stopper and the cartridge together in its original packaging.
- DO NOT use plate seals for CE-SDS applications.

General Tips

- Use only the recommended sample vials, sample plates and reagent vials from ProteinSimple.
- Avoid touching the cartridge capillary tip to any surfaces.
- Store all cartridges in their original packaging when not in use.
- Use only compressed air to clean dust off the Maurice system. Do not clean with alcohol.
- Verify batch reagents are prepared using the appropriate glass vial.
- If a run is stopped midway, always perform a cleanup or purge.
- DO NOT use plate seals for CE-SDS applications.
- For Maurice cIEF, CE-SDS PLUS and Turbo CE-SDS batches only:
 - Verify that pressure caps have O-rings installed prior to use.
 - Verify that vials and caps are sitting flush and level in the sample tray. Check that caps are on correctly and vials are seated correctly.
 - Verify that the correct vial caps are being used in the correct positions according to the Assay map.
- For batches run on a MauriceFlex system:
 - Verify batch reagents are locked in the reagent platform or fractionation adapter before starting a batch.

Troubleshooting

Compass for iCE lets you run a self test on Maurice, Maurice C., Maurice S. and MauriceFlex systems. These diagnostic tests check many internal components and can help you determine if you have an instrument issue or not. Go to "Instrument Self Test" on page 446 for details on how to get started.

For more Maurice and application troubleshooting information, please contact ProteinSimple Technical Support at (888) 607-9692 (option 3), support@proteinsimple.com or visit https://www.bio-techne.com/support/instrument-support. You can also contact your local Field Application Specialist for help.

Maurice System Troubleshooting

Problem	Solution
Maurice does not initialize The status light on Maurice's front panel does not turn blue.	Restart the instrument. If Maurice still does not initialize, contact Technical Support at support@proteinsimple.com.
Maurice's door won't open Maurice's door is unresponsive and won't open when you touch the Touch Plate at the top of the door.	Turn off Maurice and engage the emergency door release on the lower, left-hand side of the machine. Remove the cap and press up on the bar inside to pop the door open. Return the cap to its original position and try to power on Maurice. If the door is unresponsive contact Technical Support at support@proteinsimple.com.

cIEF Application Troubleshooting

Problem	Solution
Error message: Calibration standard not detected The Fluorescence Calibration Standard was not stored at the proper temperature, the reagent vial is in the wrong position, or the reagent vial doesn't contain the right volume of solution. The cartridge may be clogged or the tip may be damaged.	• The Fluorescence Calibration Standard should always be stored at 4 °C. If it's been stored at another temperature, replace the bottle with a new one then prepare a fresh reagent vial with the new solution.
The callinge may be clogged of the up may be damaged.	 Make sure reagent vials are placed in the right positions in the sample and reagent platform.
	 Confirm that there is 500 μL of Fluorescence Calibration Standard in the reagent vial.
	• Ensure the cap on the reagent vial for the Fluorescent Calibration Standard is properly aligned and tightened.
	 Ensure that you are using the newer pressure caps: clEF blue pressure caps (PN 046-573) or CE-SDS orange pressure caps (PN 046-572).
	• Examine the tip of the cartridge. If damaged, discard the cartridge and replace with a new one.
	If the cartridge tip is undamaged, soak the tip in warm DI water overnight, with the cartridge positioned vertically (prop against a wall or stable object). Perform a Cartridge Purge after the overnight soaking.

Abnormal Focusing

Problem	Solution
clEF Cartridge tank level low If the anolyte or catholyte tank fluid level is not high enough to make good contact with the electrodes, the current will drop to < 2μ A.	2 mL of electrolyte is needed in each tank. Aspirate out all the electrolyte solution and add 2 mL of anolyte and catholyte into their designated tanks.
Electrolyte contamination	Replace the anolyte and catholyte solutions in the electrolyte tanks.
Current keeps increasing beyond 80 µA	Either the electrolytes are in the wrong tanks or the cartridge is defective.
	 Immediately stop the system and run the Maurice Cartridge Purge in Compass for iCE.
	2. When the purge is done, remove the cartridge, wash out the tanks and transfer new electrolyte solutions into the proper tanks.
	3. Rerun the System Suitability test to confirm the internal coating is intact.
	 Replace the cartridge if the System Suitability run fails to meet resolution specifications or the current still remains high at >80 μA.

Artificial Peaks

Problem	Solution
Dust or particulates on the optical window	Remove the cartridge. Use compressed air or nitrogen to gently clean the optical window, then reinstall the cartridge.
	NOTE: Don't wash or submerge the cartridge's optical window in water or solvent.
Particles or precipitate in sample	Use an aqueous additive to stabilize the sample solution.
Air bubble in capillary	• Always spin samples for 5 minutes at 1000 xg before adding them to sample vials or wells of a 96-well plate.
	• Dispense the solution at the bottom of the vial/well to avoid trapping any air bubbles.

cIEF Fractionation Application Troubleshooting

Problem	Solution
Error message: Calibration standard not detected The Fluorescence Calibration Standard was not stored at the proper temperature, the reagent vial is in the wrong position, or the reagent vial doesn't contain the right volume of solution. The cartridge may be clogged or the tip may be damaged.	 The Fluorescence Calibration Standard should always be stored at 4 °C. If it's been stored at another temperature, replace the bottle with a new one then prepare a fresh reagent vial with the new solution. Make sure reagent vials are placed in the right positions in the fractionation adapter. Confirm that there is 350 µL of Fluorescence Calibration Standard in the reagent vial. Confirm the Fluorescence Calibration Standard is prepared in the glass reagent vial with insert, 0.3 mL (PN 110-0018) Examine the tip of the cartridge. If damaged, discard the cartridge and replace with a new one.

Abnormal Focusing

Problem	Solution
Unstable current: cIEF Fractionation Cartridge tank level low. If the anolyte tank fluid level is not high enough to make good contact with the electrodes, the current will drop to $< 2 \mu$ A.	2 mL of anolyte is needed in the tank. Aspirate out all the anolyte solution and add 2 mL of fresh to the tank.
Unstable current, large peak shift or poor resolution: Electrolyte contamination. If the electrolytes are contaminated or aged, the separation current could be unstable, peak position could shift significantly, or the peak resolution could be poor.	Replace the anolyte and catholyte solutions in the anolyte tank in the cartridge and catholyte vial. Do not reuse electrolytes between batches.
Current keeps increasing beyond 80 µA. Either the electrolytes are in the wrong locations or the cartridge is defective.	 Immediately stop the system and run the Maurice Cartridge Purge in Compass for iCE. When the purge is done, remove the cartridge, wash out the tank and transfer new anolyte solution into the tank. Add new catholyte solution to a new reagent vial. Inspect the cartridge to ensure there is no anolyte leaking out of the tank. Replace the cartridge if the current still remains high at >80 μA.

Artificial Peaks

Problem	Solution
Dust or particulates on the optical window	Remove the cartridge. Use compressed air or nitrogen to gently clean the optical window, then reinstall the cartridge.
	NOTE: Don't wash or submerge the cartridge's optical window in water or solvent.
Particles or precipitate in sample	Use an aqueous additive to stabilize the sample solution.
Air bubble in capillary	• Always spin samples for 5 minutes at 1000 xg before adding them to sample vials or wells of a 96-well plate.
	• Dispense the solution at the bottom of the vial/well to avoid trapping any air bubbles

CE-SDS Application Troubleshooting

Error Message: Detected current below minimum threshold

Problem	Solution
Run stops before the first injection Capillary is likely clogged.	Run the Cartridge Purge then start the batch again. If the error reoccurs, replace the cartridge with a new one.

Spikes, Poor Resolution

Problem	Solution
Air bubble in capillary	Always spin samples for 10 min at 1000 xg and use fresh reagents to minimize bubble occurrence.

Late Peak Arrival, Poor Resolution

Problem	Solution
Top Running Buffer vial leak	Use a new Top Running Buffer vial.
Insufficient conditioning	Use fresh Conditioning Buffers with each run.
Partial capillary clog	Run the Cartridge Purge.

Current Drifts to 0, No Signal, Saturation Sensor is Red

Problem	Solution
Non-viscous liquid in Separation Buffer vial	Make sure reagent vials are placed in the right positions in the sample and reagent platform.
Top Running Buffer vial is overloaded	Use a new cartridge insert and new Top Running Buffer vial.
Top Running Buffer vial leak	Use a new cartridge insert and new Top Running Buffer vial.

Low Signal

Problem	Solution
Sample composition is affecting the electrokinetic injection	Make sure the salt and protein concentrations of your sample are within the recommended ranges.

Rising Baseline

Problem	Solution
UV lamp is approaching the life time limit	Replace the lamp. Call ProteinSimple Technical Support for assistance.

Chapter 24: General Information

Chapter Overview

- Compliance
- Safety Guidelines
- Consumables and Reagents
- Customer Service and Technical Support
- Legal Notices

Compliance

Maurice complies with:

- UL 61010-1:2001: Safety requirements for electrical equipment for measurement, control, and laboratory use Part 1: General requirements (US)
- EN 61010-1:2010: Safety requirements for electrical equipment for measurement, control, and laboratory use Part 1: General requirements (EU)
- CAN/CSA 22.2 No. 61010-1-04: Safety requirements for electrical equipment for measurement, control, and laboratory use Part 1: General requirements (CA)
- EN 61326-1:2013: Electrical equipment for measurement, control and laboratory use. EMC Requirements. General requirements (EU)



This device complies with Part 15 of the FCC Rules. Operation is subject to the following two conditions:

- 1. This device may not cause harmful interference.
- 2. This device must accept any interference received, including interference that may cause undesired operation.

Note: This equipment has been tested and found to comply with the limits for a Class B digital device, pursuant to Part 15 of the FCC Rules. These limits are designed to provide reasonable protection against harmful interference in a residential installation. This equipment generates, uses and can radiate radio frequency energy and, if not installed and used in accordance with the instructions, may cause harmful interference to radio communications. However, there is no guarantee that interference will not occur in a particular installation. If this equipment does cause harmful interference to radio or television reception, which can be determined by turning the equipment off and on, the user is encouraged to try to correct the interference by one or more of the following measures:

- Reorient or relocate the receiving antenna.
- Increase the separation between the equipment and receiver.
- Connect the equipment into an outlet on a circuit different from that to which the receiver is connected.
- Consult the dealer or an experienced radio/television technician for help.

Modifications: Any modifications made to this device that are not approved by ProteinSimple, Inc. may void the authority granted to the user by the FCC to operate this equipment.

FCC ID: 2AHGG-MAURICE

Safety Guidelines

!WARNING!

If Maurice is not used as specified by ProteinSimple, overall safety will be impaired.

!WARNING!

If Maurice is damaged and doesn't function properly, stop him safely and contact ProteinSimple Technical Support right away.

!WARNING!

You can't replace or service any parts on Maurice except for the power entry fuse.

!WARNING! SHARPS HAZARD

The capillary inlet of the cartridge may present a potential sharps hazard. Dispose of used cartridges according to your organizations health and safety regulations.

CAUTION

Avoid using Maurice ways not specified by ProteinSimple. Although Maurice has been designed to protect you, this protection may not be effective if he isn't used properly.

Chemical Hazards

!WARNING! CHEMICAL HAZARD

Some chemicals used can be potentially hazardous, and can cause injury or illness.

- Read and understand the Product Inserts and Safety Data Sheets (SDSs) provided by the chemical manufacturer before you store, handle, or work with any chemicals or hazardous materials.
- Minimize contact with and inhalation of chemicals. Wear appropriate personal protective equipment when handling chemicals (e.g., safety glasses, gloves, or clothing). For additional safety guidelines, consult the SDS.
- Do not leave chemical containers open.
- Check regularly for chemical leaks or spills. If a leak or spill occurs, follow the manufacturer's cleanup procedures as recommended on the SDS.
- Comply with all local, state/provincial, or national laws and regulations related to chemical storage, handling, and disposal.

Chemical Waste Hazards



!WARNING! BIOHAZARD

Cartridges, sample plates and vials should be handled by procedures recommended in the CDC/NIH manual: Biosafety in Microbiological and Biomedical Laboratories (BMBL). The manual is available from the U.S. Government Printing Office or online at http://www.cdc.gov/biosafety/publications/bmbl5/.

Depending on the samples used, the cartridges, plates and vials may constitute a chemical or a biohazard. Dispose of the cartridges, plates and vials in accordance with good laboratory practices and local, state/ provincial, or national environmental and health regulations. Read and understand the Safety Data Sheets (SDSs) provided by the manufacturers of the chemicals in the waste content before you store, handle, or dispose of chemical waste.

- Read and understand the Safety Data Sheets (SDSs) provided by the manufacturers of the chemicals in the waste container before you store, handle, or dispose of chemical waste.
- Minimize contact with chemical waste. Wear appropriate personal protective equipment when handling chemicals (e.g., safety glasses, gloves, or clothing).
- Use precaution when emptying waste.
- Dispose of waste in accordance with good laboratory practices and local, state/provincial, or national environmental and health regulations.

Waste Production and Disposal

cIEF Application on Maurice, Maurice C. and MauriceFlex

Maurice produces approximately 0.75 mL of waste per 100 injections run on a single cIEF cartridge and will contain the following:

- Samples
- Methyl cellulose (~0.5%)
- Carrier ampholytes
- Fluorescence calibration standard
- pI markers
- Sample additives

Additionally, the Anolyte and Catholyte used in the cIEF cartridge will also need to be discarded and replaced after each batch and during cartridge cleanup prior to storage.

- Catholyte: 100 mM sodium hydroxide in 0.1% methyl cellulose, 1.5 mL
- Anolyte: 80 mM phosphoric acid in 0.1% methyl cellulose, 1.5 mL

MauriceFlex cIEF and MauriceFlex Fractionation Application on MauriceFlex

MauriceFlex produces approximately 0.35 mL of waste per injection run on a single cIEF Fractionation Cartridge and will contain the following:

- Water
- Samples
- Methyl cellulose (~0.5%)
- Carrier ampholytes
- Fluorescence calibration standard
- pI markers
- Sample additives

Additionally, the Anolyte used in the cIEF Fractionation Cartridge will also need to be discarded and replaced after each batch and during cartridge cleanup prior to storage.

• Anolyte: 80 mM phosphoric acid in 0.1% methyl cellulose, 2.0 mL

CE-SDS Application on Maurice, Maurice S. and MauriceFlex

Maurice produces approximately 0.75 mL of waste per 48 injections that is contained within the Top Running Buffer vial or Waste Tank. It contains the following:

- Samples
- Conditioning Solution 1 and 2
- Separation Matrix
- Running Buffer
- Wash Solution
- Additives such as β-mercaptoethanol or iodoacetamide.

Waste should be disposed of in accordance with good laboratory practices and local, state/provincial, or national environmental and health regulations.

Safety Data Sheets

Some chemicals used with Maurice may be listed as hazardous. Warnings are displayed on the labels of all chemicals when hazards exist.

SDSs provide users with safety information needed to store, handle, transport and dispose of the chemicals safely. We recommend updating laboratory SDS records periodically.

Safety Data Sheets for ProteinSimple reagents are available online at https://www.bio-techne.com/ on the reagent product page or by calling (888) 607-9692. Otherwise, call the chemical manufacturer directly or visit their web site.

Instrument Safety Labels

The following safety labels are located on Maurice. Each label will display a safety alert symbol indicating a potential safety hazard.

Symbol	Description
4	Risk of Electric Shock.
	Refer to Maurice User Guide before proceeding.
	Danger of hazardous waste. Use caution in these areas. This warning only applies if using hazardous material. Maurice reagents are not considered hazardous waste. If you are using hazardous materials, please contact your field service representative to place labels in the appropriate locations.

Consumables and Reagents

Maurice CE-SDS Consumabes, Kits and Reagents

ltem	PN	Description
Maurice CE-SDS PLUS Cartridges (2-pack)	PS-MC02-SP	Cartridges to run CE-SDS PLUS batches, 2 cartridges/pk. For use with Maurice, Maurice S. and MauriceFlex systems only.
Maurice Turbo CE-SDS Cartridges (2-pack)	PS-MC02-TS	Cartridges to run Turbo CE-SDS batches, 2 cartridges/pk. For use with Maurice. Maurice S. and MauriceFlex systems only.
Maurice Turbo CE-SDS Cartridges (1-pack)	PS-MC01-TS	Cartridges to run Turbo CE-SDS batches, 1 cartridge/pk. For use with Maurice, Maurice S. and MauriceFlex systems only.
Maurice glass reagent vials, 2 mL	046-017	Screw-top glass vials, 2 mL. 100/pk. Suitable for use with Maurice, Maurice S. and Maurice C. systems only.
Maurice sample vials with integrated inserts	046-083	Vials with integrated inserts for samples, accommodate 200 µL sample volume. 100/pk. Suitable for use with Maurice, Maurice S., Maurice C. and MauriceFlex systems only.
Maurice CE-SDS Orange Pressure Caps	046-572	Pressure screw tops with o-ring for glass reagent vials (PN 046-017), 12/pk. Suitable for use with Maurice and Maurice S. systems only.

ltem	PN	Description
Maurice clear screw caps	046-138	Clear screw caps with round opening, 100/pk. Suitable for use with Maurice, Maurice S., Maurice C systems only.
96-well plates	046-021	96-well plate for high-throughput analysis, 10/pk. Suitable for use with Maurice, Maurice S., Maurice C. and MauriceFlex systems only.
Maurice CE-SDS PLUS Application Kit	PS-MAK03-S	The CE-SDS PLUS Application Kit contains all components required to run CE-SDS PLUS batches. The kit includes 2 CE-SDS PLUS Cartridges, Separation Matrix, Running Buffer, CE-SDS PLUS Sample Buffer, Wash Solution, Conditioning Solutions, Internal Standard, Reagent Vials, Pressure Caps and 96-Well Plates. 200 samples/kit. Molecular weight markers can be ordered separately.
Maurice CE-SDS PLUS Reagent Kit	PS-MRK01-S	The CE-SDS PLUS Reagent Kit contains reagents for running CE-SDS PLUS batches. The kit includes Separation Matrix, Running Buffer, CE-SDS PLUS Sample Buffer, Wash Solution, Conditioning Solutions, and Internal Standard. 200 samples/kit. Molecular weight markers can be ordered separately.
Maurice Turbo CE-SDS Application Kit	PS-MAK01- TS	The Turbo CE-SDS Application Kit contains all components required to run a Turbo CE-SDS batch. The kit includes one (1) Turbo CE-SDS Cartridge, Separation Matrix, Running Buffer, CE-SDS 1X Sample Buffer, CE-SDS PLUS 1X Sample Buffer, Wash Solution, Conditioning Solutions, Internal Standard, Reagent Vials, Pressure Caps and 96-Well Plates. 200 samples/kit. Molecular weight markers can be ordered separately.
Maurice Turbo CE-SDS Reagent Kit	PS-MRK01- TS	The Turbo CE-SDS Reagent Kit contains reagents for running Turbo CE-SDS batches. The kit includes Separation Matrix, Running Buffer, CE-SDS Sample Buffer, CE-SDS PLUS Sample Buffer, Wash Solution, Conditioning Solutions, and Internal Standard. 200 samples/kit. Molecular weight markers can be ordered separately.
Maurice CE-SDS IgG Standard	046-039	Lyophilized antibody standard for 8 runs.
Maurice CE-SDS Molecular Weight Markers	046-432	Lyophilized molecular weight markers (10, 20, 33, 55, 103, 178 and 270 kDa) for 8 runs.
Maurice CE-SDS Separation Matrix	046-386	Separation Matrix for CE-SDS application, 15 mL. For use with CE-SDS PLUS cartridge (PS-MC02-SP) or Turbo CE-SDS cartridge (PS-MC02-TS, PS-MC01-TS) on Maurice, Maurice S. and MauriceFlex systems only.
Maurice CE-SDS Running Buffer - Top	046-384	Pre-assembled vial insert containing Top Running Buffer for CE-SDS application. For use with the cartridge insert (046-124) of CE-SDS PLUS cartridge (PS-MC02-SP) on Maurice, Maurice S. and MauriceFlex systems only. 12 vials. Top Running Buffer should be stored at 2-8 °C when not in use.
Maurice CE-SDS Running Buffer - Bottom	046-385	Running Buffer for CE-SDS application, 15 mL. For use with CE-SDS PLUS cartridge (PS-MC02-SP) on Maurice, Maurice S. and MauriceFlex systems only.
Maurice Turbo CE-SDS Running Buffer - Bottom	046-579	Buffer for sample preparation for CE-SDS application, 25 mL. For use with Turbo CE-SDS cartridge (PS-MC02-TS, PS-MC01-TS) on Maurice, Maurice S. and MauriceFlex systems only.

ltem	PN	Description
Maurice CE-SDS 1X Sample Buffer	046-012	Buffer for sample preparation for CE-SDS application, 25 mL. For use with CE-SDS PLUS cartridge (PS-MC02-SP) or Turbo CE-SDS cartridge (PS-MC02-TS, PS-MC01-TS) on Maurice and Maurice S. systems only.
Maurice CE-SDS PLUS 1X Sample Buffer	046-567	Buffer for sample preparation for CE-SDS application, 25 mL. For use with CE-SDS PLUS cartridge (PS-MC02-SP), or Turbo CE-SDS cartridge (PS-MC02- TS, PS-MC01-TS) on Maurice, Maurice S. and MauriceFlex systems only.
Maurice CE-SDS Wash Solution	046-013	Wash Solution for CE-SDS application, 20 mL. For use with CE-SDS PLUS cartridge (PS-MC02-SP) or Turbo CE-SDS cartridge (PS-MC02-TS, PS-MC01-TS) on Maurice, Maurice S. and MauriceFlex systems only.
Maurice CE-SDS Conditioning Solution 1	046-014	Conditioning Solution 1 CE-SDS application, 20 mL. For use with CE-SDS PLUS cartridge (PS-MC02-SP) or Turbo CE-SDS cartridge (PS-MC02-TS, PS-MC01-TS) on Maurice, Maurice S. and MauriceFlex systems only.
Maurice CE-SDS Conditioning Solution 2	046-015	Conditioning Solution 2 CE-SDS application, 20 mL. For use with CE-SDS PLUS cartridge (PS-MC02-SP) or Turbo CE-SDS cartridge (PS-MC02- TS, PS-MC01-TS) on Maurice, Maurice S. and MauriceFlex systems only.
Maurice CE-SDS Internal Standard	046-144	Internal Standard for addition to each sample for CE-SDS application. 2 vials/pk. For use with CE-SDS PLUS cartridge (PS-MC02-SP) or Turbo CE-SDS cartridge (PS-MC02-TS, PS-MC01-TS) on Maurice, Maurice S. and MauriceFlex systems only.
Maurice CE-SDS Cartridge inserts	046-124	Cartridge Inserts for holding the Top Running Buffer vial assembly (046-010) in the CE-SDS PLUS cartridge (PS-MC02-SP). 2 inserts/pk. For use with Maurice, Maurice S. and MauriceFlex systems only.
Maurice CE-SDS Cartridge Cleaning Vial	046-125	Clear cleaning vial for use with the Maurice CE-SDS Cartridge insert (046-124). 2 vials/pk.

Maurice cIEF Consumables, Kits and Reagents

ltem	PN	Description
Maurice cIEF Cartridges	PS-MC02-C	Cartridges for cIEF application, 2 cartridges/pk. For use with Maurice, Maurice C. and MauriceFlex systems only.
Maurice glass reagent vials, 2 mL	046-017	Screw-top glass vials, 2 mL. 100/pk. Suitable for use with Maurice, Maurice S. and Maurice C. systems only.

Chapter 24: General Information | Consumables and Reagents

ltem	PN	Description
Maurice sample vials with integrated inserts	046-083	Vials with integrated inserts for samples, accommodate 200 µL sample volume. 100/pk. Suitable for use with Maurice, Maurice S., Maurice C. and MauriceFlex systems only.
Maurice cIEF Blue Pressure Caps	046-573	Pressure screw tops with o-ring for glass reagent vials (P/N 046-017), 12/pk. Suitable for use with Maurice, Maurice C. and MauriceFlex systems only.
Maurice clear screw caps	046-138	Clear screw caps with round opening, 100/pk. Suitable for use with Maurice, Maurice S., Maurice C systems only.
96-well plates	046-021	96-well plate for high-throughput analysis, 10/pk. Suitable for use with Maurice, Maurice S., Maurice C. and MauriceFlex systems only.
Maurice clEF Method Development Kit	PS-MDK01-C	The cIEF Method Development Kit provides all the reagents and instructions to help you develop fast and robust cIEF methods on Maurice, Maurice C. and MauriceFlex systems. The kit includes a Method Development Guide as well as a selection of reagents required for cIEF method development on the system. This kit includes a Fluorescence Calibration Standard, System Suitability Kit, Anolyte, Catholyte, Methyl Cellulose, five types of Ampholytes (Pharmalyte pH ranges 3-10, 2.5-5, 5-8 and 8 to 10.5 and Servalyte pH range 2-9), nine pl Markers (3.38, 4.05, 5.85, 6.14, 7.05, 8.40, 9.50, 9.99 and 10.17) and additives (SimpleSol Protein Solubilizer, PN 046-574, lyophilized urea and arginine). 30 samples/kit. The expiration date for this kit is 12 months from date of manufacture. For use with the cIEF cartridge (PS-MC02-C) on Maurice, Maurice C. and MauriceFlex systems only.
Maurice clEF Chemical Test Kit	046-036	The cIEF Chemical Test Kit is designed to confirm the overall performance of the Maurice, Maurice C. and MauriceFlex. systems with the cIEF cartridge (PS-MC02-C) on 8 separate occasions. The kit contains Anolyte, Catholyte, Methyl Cellulose, Fluorescence Calibration Standard and a System Suitability kit. Each time, the performance can be checked up to 24 hours. The expiration date for this kit is 12 months from date of manufacture. 8 runs/kit. For use with the cIEF cartridge (PS-MC02-C) on Maurice, Maurice C. and MauriceFlex systems only.
Maurice clEF System Suitability Kit	046-044	The cIEF System Suitability Kit is used to run a control test for cIEF application on Maurice, Maurice C. and MauriceFlex systems on 8 separate occasions. Each time, the performance can be checked up to 24 hours.The kit contains a vial of lyophilized Peptide Panel and a vial of System Suitability Test mix. 8 runs/kit. The expiration date for this kit is 12 months from date of manufacture. For use with the cIEF cartridge (PS-MC02-C) on Maurice, Maurice C. and MauriceFlex systems only.
Maurice cIEF Fluorescence Calibration Standard	046-025	Fluorescence Calibration Standard for cIEF application, 5.5 mL. For use with Maurice, Maurice C. and MauriceFlex systems only.
SimpleSol Protein Solubilizer	046-575	SimpleSol is a protein solubilizer, 200 mL. This reagent is more stable than urea, eliminating the need to prepare urea fresh every day. For use with Maurice, Maurice C., MauriceFlex and iCE3 systems.

ltem	PN	Description
0.5% Methyl Cellulose Solution	102505	0.5% Methyl Cellulose Solution, 100 mL. Use this concentration for the wash cycle between injections. The solution is filtered to ensure consistent viscosity to coat the capillary lumen to minimize electroosmotic flow (EOF). Conveniently packaged in 2 x 100 mL bottles. The expiration date for this kit is 12 months from date of manufacture. Suitable for use with Maurice, Maurice C., MauriceFlex, iCE3 and iCE280.
1% Methyl Cellulose Solution	101876	1% Methyl Cellulose Solution, 100 mL. This solution is used to prepare samples for cIEF applications. The expiration date for this kit is 12 months from date of manufacture. Suitable for use with Maurice, Maurice C., MauriceFlex, iCE3 and iCE280.
iCE Electrolyte Kit	102506	These 100 mL Anolyte and Catholyte solutions in 0.1% MC are used to fill the electrolyte tanks on Maurice cIEF cartridge as well as FC and HT cartridges. The labels and bottles are color coded to improve safety. The kit contains 2 x 100 mL bottles. The expiration date for this kit is 12 months from date of manufacture. Suitable for use with Maurice, Maurice C., MauriceFlex, iCE3 and iCE280.
Maurice cIEF pl Marker - 3.38	046-028	Maurice cIEF pl Marker - 3.38, 210 µL, lyophilized.
Maurice cIEF pl Marker - 4.05	046-029	Maurice cIEF pl Marker - 4.05, 210 µL, lyophilized.
Maurice cIEF pl Marker - 5.85	046-030	Maurice cIEF pl Marker - 5.85, 210 µL, lyophilized.
Maurice cIEF pl Marker - 6.14	046-031	Maurice clEF pl Marker - 6.14, 210 µL, lyophilized.
Maurice cIEF pl Marker - 7.05	046-032	Maurice clEF pl Marker - 7.05, 210 µL, lyophilized.
Maurice cIEF pl Marker - 8.40	046-033	Maurice clEF pl Marker - 8.4, 210 µL, lyophilized.
Maurice cIEF pl Marker - 9.50	046-047	Maurice clEF pl Marker - 9.50, 210 µL, lyophilized.
Maurice cIEF pl Marker - 9.99	046-034	Maurice clEF pl Marker - 9.99, 210 µL, lyophilized.
Maurice cIEF pl Marker - 10.17	046-035	Maurice clEF pl Marker - 10.17, 210 µL, lyophilized.
Maurice cIEF electrolyte tank caps	046-123	Electrolyte tank caps, 20 mm. Red is used for the Anolyte tank and the grey cap is used for the Catholyte tank. 5 pairs/pk.
Electrolyte Pipette	101788	Pipettes with soft tips for adding Anolyte and Catholyte into the electrolyte tanks in the clEF cartridge. 10/pk.

MauriceFlex cIEF Fractionation Consumables, Kits and Reagents

ltem	PN	Description
MauriceFlex clEF Fractionation Cartridge	PS-MC02-F	The MauriceFlex cIEF Fractionation Cartridge is designed for icIEF-based fractionation on the MauriceFlex system. Each pack contains 2 Cartridges, and each Cartridge supports up to 15 fractionation runs. Suitable for use with MauriceFlex systems only. Not for analytical icIEF analysis.
MauriceFlex crimp top glass reagent vials, 2 mL, 100/pkg	110-0019	Glass vial, crimp top, 2mL, 100/pkg. Reagent vials for MauriceFlex cIEF fractionation use. Suitable for use with MauriceFlex systems only.
MauriceFlex glass vials with insert, 0.3 mL, 15/pkg	110-0018	Glass vials, 2mL, with 0.3 mL insert, 15/pkg. For MauriceFlex cIEF fractionation use. Suitable for use with MauriceFlex systems only.
96-well plates	046-021	96-well plate for high-throughput analysis, 10/pk. Suitable for use with Maurice, Maurice S., Maurice C. and MauriceFlex systems only.
MauriceFlex clEF Fractionation Method Development Kit	PS- MDK01-F	The MauriceFlex clEF Fractionation Method Development Kit provides all the reagents and instructions to help you develop both analytical iclEF method as well as the iclEF fractionation method. The kit includes a Maurice clEF Method Development Kit (PS-MDK01-C) and additional reagents and consumables for clEF fractionation method development. A single MauriceFlex clEF Fractionation Cartridge is also included to support up to 15 iclEF fractionation runs. The expiration date for this kit is 12 months from date of manufacture. For use with the clEF cartridge (PS-MC02-C) for analytical iclEF analysis. The kit is to be ordered with a new MauriceFlex system.
MauriceFlex cIEF Fractionation Reagent Kit	PS- MRK01-F	The MauriceFlex clEF Fractionation Reagent Kit contains Fluorescence Calibration Standard, Anolyte, Catholyte, Methyl Cellulose, arginine and ammonium acetate to support up to 15 clEF fractionation runs on the MauriceFlex system with a MauriceFlex clEF Fractionation Cartridge.
MauriceFlex clEF Fractionation Application Kit	PS- MAK01-F	The MauriceFlex clEF Fractionation Application Kit contains one MauriceFlex clEF Fractionation Reagent Kit (PS-MRK01-F), one clEF Fractionation Cartridge, Reagent Vials, and 96-well Plates to support up to 15 iclEF fractionation runs. For initial iclEF fractionation method development on a new MauriceFlex system, order MauriceFlex clEF Fractionation Method Development Kit (PS-MDK-01) instead.
2 M Ammonium Acetate, 350 μL	046-580	Ammonium acetate aqueous solution, 2 M, 350 μL . Stock for preparing chemical mobilizer for MauriceFlex clEF fractionation use.

Customer Service and Technical Support

Need pricing information or want to know who your sales rep is? Our Customer Service team can help.

Email: orders@proteinsimple.com Telephone: 1-408-510-5500, option 1

Toll-free (US and Canada): 1-888-607-9692, option 1

Fax: 1-408-520-4831

Have product-related questions? Ping our Tech Support group, they'll be happy to help!

Use our online technical support request Email: support@proteinsimple.com Telephone: 1-408-510-5500 Toll-free (US and Canada): 1-888-607-9692, option 3

Web

www.bio-techne.com

Address

ProteinSimple 3001 Orchard Parkway San Jose, CA 95134 USA

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1. Definitions

- 1.1. "Authorized Use Parameters" means the following usage restrictions, which restrict the operation of the Licensed Software to a particular set of conditions: Customer shall (a) limit simultaneous use of the Licensed Software to a maximum of ten (10) Authorized Users; and (b) use the Licensed Software only in connection with the accompanying System purchased by Customer pursuant to the System Quotation and located at the Site.
- 1.2. "Authorized User" means one (1) User who initiates the execution of the Licensed Software and/or interacts with or directs the Licensed Software in the performance of its functions. Multiple Authorized Users may work simultaneously with one installation of the Licensed Software, as on a server, or they may each have their own installation on single-user machines, or a mix of these, provided that in all cases the total number of simultaneous Users does not exceed the applicable Authorized Use Parameters.
- 1.3. "Company" means ProteinSimple.
- 1.4. "Documentation" means Company's then-current manuals, guides, and on-line help pages, if any, applicable to the Licensed Software and made generally available by Company to its customers.
- 1.5. "Enterprise" means those organizations that have Internet addresses located at top level and second-level domain names set forth in the System Quotation.
- 1.6. "Error" means a reproducible error in the Licensed Software that prevents such Licensed Software from operating substantially in accordance with its Documentation.
- 1.7. **"Executable Code"** means the fully compiled binary version of Licensed Software that can be executed by a computer and used by an end user without further compilation.
- 1.8. "Intellectual Property Rights" means all copyrights, trade secrets, patents, patent applications, moral rights, contract rights, and other proprietary rights, but specifically excluding any trademarks or service marks.

- 1.9. "Licensed Software" means the Compass software program in Executable Code form, and any Updates that Company makes available to Customer in accordance with this Agreement.
- 1.10. "Site" means the facility or campus set forth in the System Quotation.
- 1.11. **"System"** means the proprietary NP1000, NP100, Simon, Sally, Peggy, Wes, Sally Sue, Peggy Sue and Maurice protein analysis system or any future model or successor thereto that is provided to Customer by Company pursuant to a separate agreement between the parties (the "System Quotation").
- 1.12. **"Update"** means those releases of the Licensed Software that Company provides to customers to correct Errors, fix bugs, or create minor improvements, incremental features, or enhancements of existing features which Company designates by a change in the number to the right of the first or second decimal point. Updates do not include those releases of the Licensed Software that provide substantial new features or additional functionality which Company designates by a change in the number to the left of the first decimal point.
- 1.13. "User" means any individual that has an e-mail address within the Enterprise.

2. License and Restrictions

- 2.1. License Grant. Subject to the terms and conditions of this Agreement and the payment of the required fees set forth in the System Quotation, Company grants to Customer a nontransferable, nonexclusive, royalty-free, revocable, worldwide license (without the right to sublicense) to (a) install the Licensed Software on any computer located at any Site; (b) use, execute, and display the Licensed Software, in Executable Code form only; and (c) copy the Licensed Software and Documentation, solely as necessary to support Authorized Users; in each of the foregoing, solely in accordance with the Documentation and the Authorized Use Parameters. Customer agrees that it will comply with the Authorized Use Parameters.
- 2.2. License Restrictions. Customer acknowledges that the Licensed Software and its structure and organization constitute valuable trade secrets of Company. Accordingly, the license granted in this Agreement is subject to the following restrictions: Customer and its Authorized Users (a) may not reverse engineer, disassemble, decompile, or otherwise attempt to derive the source code of Licensed Software; (b) may not modify, adapt, alter, translate, or create derivative works from the Licensed Software; (c) may not merge the Licensed Software with other software; (d) may not use the Licensed Software in any service bureau or time-sharing arrangement, license, sell, rent, lease, transfer, assign, distribute, host, outsource, disclose, or otherwise commercially exploit or make the Licensed Software or Documentation available to any third party; (e) shall only make that number of exact copies of the Licensed Software and Documentation as delivered by Company that are necessary to support Customer's use of the Licensed Software in accordance with this Agreement; (f) shall include any titles, trademarks, and copyright and restricted rights notices that are included on or in the Licensed Software as delivered by Company on and in any copies of the Licensed Software that it makes; and (g) shall ensure that Customer's use of the Licensed pursuant to this Agreement.
- 2.3. **Open Source Software.** Certain items of independent, third-party code may be included in the Licensed Software that are subject to open source licenses ("Open Source Software"). Such Open Source Software is licensed under the terms of the license that accompanies such Open Source Software. Nothing in this Agreement limits Customer's rights under, or grants Customer rights that supersede, the terms and conditions of any applicable end user license for such Open Source Software. In particular, nothing in this Agreement restricts Customer's right to copy, modify, and distribute such Open Source Software that is subject to the terms of such open source licenses.
- 2.4. **Ownership.** Company reserves all rights not expressly granted to Customer in this Agreement. Without limiting the generality of the foregoing, Customer acknowledges and agrees that, except as expressly set forth in this Agreement, Company and its suppliers retain all Intellectual Property Rights, title and interest in and to the Licensed Software and Documentation.

3. Support and Maintenance Services

3.1. Services. Subject to Customer's payment of the Services fees, as set forth in the System Quotation, and to the terms and conditions herein, Company will use commercially reasonable efforts to provide to Customer the following support and maintenance services (the "Services") for the Licensed Software: (a) Company will answer technical questions concerning functions and features of the Licensed Software; (b) Company will provide Error verification, analysis and corrective efforts for the Licensed Software; and (c) Company will provide, without charge, Updates of the software released during the term of this Agreement. Customer will be responsible for providing, in a manner consistent with good industry practice, all Services to Users. Customer acknowledges that Company may not be able to correct all reported Errors. Any Update of the Licensed Software will be deemed part of the Licensed Software and Customer will use such Updates in accordance with the requirements and obligations in this Agreement.

- 3.2. Service Conditions. Company's obligation to provide the Services is conditioned on Customer: (a) notifying Company of any Error within a reasonable period of time; (b) providing Company all information relating to the Error; (c) providing access to the Licensed Software and Customer's facility where the Licensed Software is located and informing Company of any potential hazards which may be encountered while servicing the Licensed Software. Customer may contact Company via telephone at 1-888-607-9692 or e-mail at support@proteinsimple.com during the hours of 8 a.m. (Pacific Time) and 5 p.m. (Pacific Time) Monday through Friday, excluding holidays, to report any Error. A list of standard holidays will be provided to Customer upon request. Company shall have the right to determine in its sole discretion what corrective action Company will perform to support the Licensed Software. Company may subcontract the Services to a third party contractor provided that Company will be responsible for the third party contractor's compliance with this Agreement.
- 3.3. Service Exclusions. Company will not be obligated to provide the Services if (a) Company determines that an Error is caused by malfunction of any hardware (other than malfunction of the System) or third party software used with the Licensed Software; or (b) Customer has failed to incorporate the latest Update previously released to Customer.
- 4. Warranty
 - 4.1. Licensed Software Warranty. Company warrants that the Licensed Software, as properly installed, and under normal use, will perform substantially in accordance with its Documentation during the Warranty Period. The "Warranty Period" for the Licensed Software begins on date Customer downloads the Licensed Software and ends twelve (12) months thereafter.
 - 4.2. Remedy. If Customer notifies Company in writing during the Warranty Period of an Error, Company will, at its expense and as its sole obligation for any breach of the foregoing warranty, use commercially reasonable efforts to correct the Error or replace the Licensed Software. Any Error correction or replacement of the Licensed Software will not extend the original Warranty Period. The warranty and the remedies provided above will not apply to the Licensed Software if (a) Company determines that an Error is caused by accident, abuse, misuse, negligence, fire, earthquake, flood, other force majeure event, failure of electrical power, the use of unauthorized products, or unauthorized repairs or modifications; (b) Company determines that an Error is caused during or as a result of delivery; (c) a problem arises from or is based on Company's compliance with Customer's specifications; or (d) Company determines that an Error is caused by malfunction of any hardware (other than malfunction of the System) or third party software used with the Licensed Software.
 - 4.3. **Disclaimer.** THE WARRANTIES ABOVE ARE EXCLUSIVE AND IN LIEU OF ALL OTHER WARRANTIES, WHETHER EXPRESS, IMPLIED OR STATUTORY, INCLUDING WITHOUT LIMITATION THE IMPLIED WARRANTIES OF MERCHANTABILITY, FITNESS FOR A PARTICULAR PURPOSE, TITLE, AND NONINFRINGEMENT.
- 5. Limitation of Liability. NEITHER COMPANY NOR ITS SUPPLIERS SHALL BE RESPONSIBLE OR LIABLE WITH RESPECT TO ANY SUBJECT MATTER OF THIS AGREEMENT OR TERMS OR CONDITIONS RELATED THERETO UNDER ANY CONTRACT, NEGLIGENCE, STRICT LIABILITY OR OTHER THEORY (A) FOR LOSS OR INACCURACY OF DATA, LOSS OF PROFITS OR COST OF PROCUREMENT OF SUBSTITUTE GOODS, SERVICES OR TECHNOLOGY, OR (B) FOR ANY INDIRECT, INCIDENTAL OR CONSEQUENTIAL DAMAGES INCLUDING, BUT NOT LIMITED TO LOSS OF REVENUES AND LOSS OF PROFITS. COMPANY'S AGGREGATE CUMULATIVE LIABILITY HEREUNDER SHALL NOT EXCEED THE GREATER OF FIVE HUNDRED DOLLARS (\$500.00).

6. Term and Termination

- 6.1. **Term of Agreement.** The Agreement is effective on the date Customer downloads the Licensed Software and shall remain in effect until terminated by either party as provided in this section.
- 6.2. **Termination For Material Breach.** Either party may terminate this Agreement upon written notice if the other party materially breaches this Agreement and fails to cure such breach within thirty (30) calendar days following receipt of written notice from the other party specifying the breach in detail. Notwithstanding the foregoing, Company may immediately terminate this Agreement and all licenses granted hereunder if Customer breaches Section 2 (License and Restrictions) hereof or upon termination of the System Quotation. The foregoing rights of termination are in addition to any other rights and remedies provided in this Agreement or by law.
- 6.3. Effect of Termination. Upon termination of this Agreement (or termination or expiration of any license granted hereunder), all rights of Customer to use the Licensed Software and Documentation will cease and (a) all license rights granted under this Agreement will immediately terminate and Customer shall promptly stop all use of the Licensed Software and Documentation; (b) all Services will terminate immediately; (c) Customer shall promptly erase all copies of the Licensed Software from Customer's computers, and destroy all copies of the Licensed Software and Documentation on tangible media in Customer's possession or control or return such copies to Company; and (d) upon request by Company, Customer shall certify in writing to Company that it has returned or destroyed such Licensed Software and Documentation. The parties' rights and obligations under Sections 1 (Definitions), 2.4 (Ownership), 4.3 (Disclaimer), 5 (Limitation of Liability), 6 (Term and Termination), and 7 (General) shall survive termination of this Agreement.

7. General

- 7.1. Assignment. This Agreement and Customer's rights hereunder may not be assigned to any third party by Customer except with the prior written approval of Company. Any attempted assignment of this Agreement or any rights or obligations hereunder will be null and void.
- 7.2. **Governing Law.** This Agreement is made in, governed by, and shall be construed in accordance with the laws of the State of California, without regard to any conflicts of law principles that would result in application of laws of any other jurisdiction. The United Nations Convention on Contracts for the International Sale of Goods does not apply to this contract. Any legal action or other legal proceeding relating to this contract or the enforcement of any provision of this contract must be brought in any state or federal court located in Santa Clara County, California. Customer and Company expressly and irrevocably consents and submits to the jurisdiction of such courts.
- 7.3. **Injunctive Relief.** Customer acknowledges that the Licensed Software contains valuable trade secrets and proprietary information of Company, that any actual or threatened breach of this Agreement will cause harm to Company for which monetary damages would be an inadequate remedy, and that injunctive relief is an appropriate remedy for such breach.
- 7.4. **Modifications.** Company reserves the right to change the terms and conditions of this Agreement or its policies relating to the Licensed Software at any time. Company will notify Customer of any material changes to this Agreement by sending Customer an e-mail to the last e-mail address Customer provided to Company or by prominently posting notice of the changes on Company's website. Any material changes to this Agreement will be effective upon the earlier of thirty (30) calendar days following Company's dispatch of an e-mail notice to Customer or thirty (30) calendar days following Company's posting of notice of the changes on Company's website. These changes will be effective immediately for new users of our Licensed Software. Please note that at all times Customer is responsible for providing Company with its most current e-mail address. In the event that the last e-mail address that Customer has provided Company is not valid, or for any reason Company is not capable of delivering to Customer the notice described above, Company's dispatch of the e-mail containing such notice will nonetheless constitute effective notice of the changes described in the notice. If Customer does not agree with the changes to this Agreement, Customer must notify Company prior to the effective date of the changes that Customer wishes to terminate its license to the Licensed Software. Continued use of the Licensed Software, following notice of such changes, shall indicate Customer's acknowledgement of such changes and agreement to be bound by the terms and conditions of such changes.
- 7.5. Severability. In the event any provision of this Agreement is held to be invalid or unenforceable, the remaining provisions of this Agreement will remain in full force.
- 7.6. **Waiver.** The waiver by either party of any default or breach of this Agreement shall not constitute a waiver of any other or subsequent default or breach.
- 7.7. **Export.** Customer agrees not to export, reexport, or transfer, directly or indirectly, any U.S. technical data acquired from Company, or any products utilizing such data, in violation of the United States export laws or regulations.
- 7.8. Force Majeure. Company shall not be liable, directly or indirectly, for any delay or failure in performance of any obligation under this Agreement, including any delivery obligation, where such delay or failure arises or results from a cause beyond Company's reasonable control, or beyond the reasonable control of Company's suppliers or contractors, including, but not limited to strike, boycott or other labor disputes, embargo, governmental regulation, inability or delay in obtaining materials, acts of God, war, earthquake, fire, or flood. In the event of such force majeure, the time for delivery or other performance will be extended for a period equal to the duration of the delay caused thereby, provided that Company notifies Customer of the nature and duration of such force majeure event.
- 7.9. Entire Agreement; Notice. This Agreement constitutes the complete agreement between the parties and supersedes all prior or contemporaneous agreements or representations, written or oral, concerning the subject matter of this Agreement. Except as otherwise expressly provided in this Agreement, any modifications of this Agreement must be in writing and agreed to by both parties. Company may provide any notice to Customer by e-mail. Customer may provide notice to Company by sending an e-mail to info@proteinsimple.com or a letter by United States mail to ProteinSimple, 3040 Oakmead Village Drive, Santa Clara, CA 95051, or to such other address as Company may specify in writing by posting the new address on the Company website.
- 7.10. **Relationship of the Parties.** The parties are acting hereunder as independent contractors and not as partners, agents, fiduciaries, or joint venturers. Neither party has the power or authority represent, act for, bind, or otherwise create or assume any obligation on behalf of the other party.

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