

# User Guide for Maurice, Maurice C. and Maurice S.

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# Chapter 1: Let's Get Started

## Chapter Overview

- Welcome
- Maurice Systems

page 1

## 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. and Maurice S. 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 clEF and CE-SDS. They take clEF up a notch, and CE-SDS is a breeze. You'll get pl 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 35 minutes.
- They make it easy. Just pop in a ready-to-go cartridge, drop in your sample vials or a 96-well plate, 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.

# 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 0.61m (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 0.61m (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	0.41 m x 0.66 m x 0.76 m (H x W x D) 1.35' x 2.17' x 2.49' (H x W x D)

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

Table 2-1: Physical Specifications

## **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	18 - 25 °C (64 - 77 °F)
Operating humidity range	20-80% relative, non-condensing

Table 2-2: Environmental requirements.

## Software and Computer Requirements

Maurice brings his own computer to the lab with Compass for iCE software pre-installed. Compass for iCE is used to run cIEF and CE-SDS applications on Maurice 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	Recommended
Operating System	Windows 7
Processor	Core i5
Memory	6 GB
Free Disk Space	100 GB
Ethernet Ports	2 - One is required to connect to Maurice, the other is used for network access
USB Ports	2 - To connect the keyboard and mouse

Table 2-3: Computer requirements.

## 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.

# <sup>Chapter 3:</sup> Maurice

## Chapter Overview

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

## Maurice Systems

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



Maurice with Computer Workstation

cIEF and CE-SDS Cartridges

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

- Maurice: cIEF and CE-SDS applications •
- Maurice C.: cIEF applications only •
- Maurice S.: CE-SDS applications only •

You can run samples in 96-well plates or in up to 48 sample vials with integrated 0.2 mL inserts on all three systems.





Maurice C.

Maurice

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 of the door to open it. Close it by pushing the door until you hear the latch engage.

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.
- Opening Door (long blue flash followed by blue pulses): Maurice's door is opening.
- **Running (pulsing blue)**: Maurice is running a batch.
- 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 and CE-SDS Cartridges
- Maurice C.: cIEF Cartridges only
- **Maurice S.**: CE-SDS Cartridges only

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.

ble

NOTE: You can find cartridge prep, installation and post-run procedures in Chapter 7, "Running cIEF Applications on Maurice and Maurice C." and Chapter 8, "Running CE-SDS Applications on Maurice and Maurice S."

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## Sample and Reagent Platform

Maurice's sample and reagent platform 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.





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.





#### NOTES:

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.

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 90 and for CE-SDS applications in "Step 4: Load Samples and Reagents" on page 124.

## **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 silver 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.



## 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
- Software Help
- Checking for and Installing New Versions of Compass for iCE
- Viewing Release Notes
- Viewing the Software Log
- Compass for iCE Version Information
- Directory and File Information

#### Chapter 4: Compass for iCE Overview

#### page 18

## 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:



Compass for iCE Overview

## 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.

ile Edit Instrument un: MW ladder assigne	Window Help ed_MW Ladder Sol Test IS final QC 110 ms N						
'un: MW ladder assigne	ed_MW Ladder Sol Test IS final QC 110 ms N						
tun: MW ladder assigne	ed_MW Ladder Sol Test IS final QC 110 ms N						💾 Batch 🔃 Run Summary 🕼 Analysis
		Injectio	ns 🔚 History 🔳 Notes	1			🚰 Add 🔛 Replicate 🕼 Remove 🕤 🖻 😁
Laurant			Sample ID	Location	Method	Notes	
T colore		1	IgG System Control	Al	Method1		
5 00 10°C -	C Add - C Remove	2	Control Ladder	A2	Method2		
		3	Test Ladder	A3	Method2		
G1	G2 Water Sep. Wash Air	4	IS - Alpha	81	Method1		
		5	IS - Frozen P3	82	Method1		
-		6	IS - T1 P3	83	Method1		
0		7	15 - T2 P3	84	Method1		
Water	Water Run	8	IS - T3 P3	85	Method1		
1 2	3 4 5 6 7 8	9	Control Ladder	A2	Method2		
A (0) (0)		10	Test Ladder	A3	Method2		
		11	IS - Alpha	81	Method1		
B 🕑 🕗		12	IS - Frozen P3	B2	Method1		
c		13	15 - T1 P3	83	Method1		
		14	IS - T2 P3	84	Method1		
D		15	IS - T3 P3	85	Method1		
F		16	Control Ladder	A2	Method2		
-		17	Test Ladder	A3	Method2		
F ( ) )		18	IS - Alpha	81	Method1		
		19	15 - Frozen P3	82	Method1		
		20	IS - T1 P3	83	Method1		
		21	IS - T2 P3	B4	Method1		
Methods							
							New Rem
Name	Sample Load		Separation				
Method1	20 sec 4600 Volts		0.1 min 1150 Volts,	0.1 min 3450 Vol	ts, 25.0 min 5750 V		
Method2	20 sec 4600 Volts		0.1 min 1150 Volts,	0.1 min 3450 Vol	ts, 30.0 min 5750 V		

ile Edit Instrument								
	Window Help							
								🔚 Batch 🕕 Run Summary 🕼 Analysis
Batch: 2016-01-21_09-4	16-39_mAb11_Prep20160121_QC(0)	III Injectio	ns 🔚 History 🚺 N	lotes				🚰 Add 剻 Replicate 🕼 Remove 🗃 🗎
Through 1			Sample ID	Location	Method		Notes	
		1	System Suitability	A1	System Suitablit	1		
00 10°C -	CH Add - CX Remove	2	mAb 11 Blank	A2	mAb Method			
00	-	3	mAb 11 Ref. Std.	A3	mAb Method			
MC	Fi Gal Water Air	4	mAb 11 Prep 201603	21 A4	mAb Method			
6		5	mAb 11 Prep 201601	21 A4	mAb Method			
		6	mAb 11 Prep 201601	21 A4	mAb Method			
0		7	mAb 11 Ref. Std.	A3	mAb Method			
Wate	N1 - N2 - N1 - N1 - N5 - N5	8	mAb 11 Blank	A2	mAb Method			
B C D E F								
Methods								
Methods								New Ret
Methods	Separation		Detection	Sample Load (s)	pl Markers	Ampholytes	Additives	New Ret
Methods Name System Suitablity	Separation 1.0 min 1500 Volts, 4.5 min 3000 Volt	3	Detection 5 Exposures	Sample Load (s) 55	pl Markers 3.38, 10.17	Ampholytes	Additives	New Re
Methods Name System Suitablity mAb Method	Separation 1.0 min 1500 Volts, 4.5 min 3000 Volt 1.0 min 1500 Volts, 6.0 min 3000 Volt	15	Detection 5 Exposures 5 Exposures	Sample Load (s) 55 55	pl Markers 3.38, 10.17 4.05, 9.99	Ampholytes	Additives	New Ret
Methods Name System Suitablity mAb Method	Separation 1.0 min 1500 Volts, 4.5 min 3000 Volt 1.0 min 1500 Volts, 6.0 min 3000 Volt	5	Detection 5 Exposures 5 Exposures	Sample Load (s) 55 55	pl Markers 3.38, 10.17 4.05, 9.99	Ampholytes	Additives	New Re
Methods Name System Suitability mAb Method	Separation 1.0 min 1500 Volts, 4.5 min 3000 Volt 1.0 min 1500 Volts, 6.0 min 3000 Volt	5	Detection 5 Exposures 5 Exposures	Sample Load (s) 55 55	pI Markers 3.38, 10.17 4.05, 9.99	Ampholytes	Additives	New Re
Methods Name System Suitablity mAb Method	Separation 1.0 min 1500 Volts, 4.5 min 3000 Volt 1.0 min 1500 Volts, 6.0 min 3000 Volt	15	Detection 5 Exposures 5 Exposures	Sample Load (s) 55 55	pl Markers 3.38, 10.17 4.05, 9.99	Ampholytes	Additives	New Re
Methods Name System Suitability mAb Method	Separation 1.0 min 1500 Volts, 4.5 min 3000 Volt 1.0 min 1500 Volts, 6.0 min 3000 Volt	15	Detection 5 Exposures 5 Exposures	Sample Load (s) 55 55	pl Markers 3.38, 10.17 4.05, 9.99	Ampholytes	Additives	New Re
Methods Name System Suitablity mAb Method	Separation 1.0 min 1500 Volts, 4.5 min 3000 Volt 1.0 min 1500 Volts, 6.0 min 3000 Volt	5	Detection 5 Exposures 5 Exposures	Sample Load (s) 55 55	pl Markers 3.38, 10.17 4.05, 9.99	Ampholytes	Additives	New Re
Methods Name System Suitability mAb Method	Separation 1.0 min 1500 Volts, 4.5 min 3000 Volt 1.0 min 1500 Volts, 6.0 min 3000 Volt	15	Detection 5 Exposures 5 Exposures	Sample Load (s) 55 55	pl Markers 3.38, 10.17 4.05, 9.99	Ampholytes	Additives	New Re
Methods Name System Suitability mAb Method	Separation 1.0 min 1500 Volts, 4.5 min 3000 Volt 1.0 min 1500 Volts, 6.0 min 3000 Volt	5	Detection 3 Exposures 5 Exposures	Sample Load (s) 55 55	pl Markers 3.38, 10.17 4.05, 9.99	Ampholytes	Additives	New Re

## Run Summary Screen

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





## Analysis Screen

The Analysis screen is used to view data from your batch, including the graph view (electropherograms) and a table with your results. You can also analyze your data for completed runs.





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## **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 example below shows panes in the Batch screen, and the Graph pane is active:

ĺ	Experime	nt	-	🗖 🗖 🔣 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.

6	MW ladder assigned MW Ladder Sol Test IS final OC 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 25.

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 10, *"Controlling Maurice, Maurice C. and Maurice S."*.

File Edit	Instrument	Window Help		
C	Running	Stop	Tue 10:49 AM	Wed 9:39 AM

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.

💾 Batch 🖫 Run Summary 🏾 🏥 Analysis

## 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, data for a single injection or all injections in the batch, or grouped injection data. View bar options are in "Viewing Run Data" on page 295 for cIEF applications or page 205 for CE-SDS applications.

🚊 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, *"clEF Batches"*, Chapter 6, *"CE-SDS Batches"*, Chapter 9, *"Run Status"*, Chapter 12, *"clEF Data Analysis"* and Chapter 11, *"CE-SDS Data Analysis"*.

Chapter 4: Compass for iCE Overview

## File Menu

The File menu contains basic file commands.



## Edit Menu

The Edit menu contains basic editing commands, analysis and preferences options. Specific details on preferences are described in Chapter 13, *"Setting Your Preferences"*.

Edit	View	Instrument	Windo	
Cut Copy		Ctrl+X		
		Ctrl+C		
	Paste	Ctrl+V		
Analysis				
	Preferences			

page 26
#### 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 "Viewing Run Data" on page 295 for cIEF applications or page 205 for CE-SDS applications, and "Using Groups" on page 306 for cIEF applications or page 216 for CE-SDS applications.



#### Instrument Menu

The Instrument menu is only available when the software is connected directly to your instrument. You can lean more about instrument control options in Chapter 10, *"Controlling Maurice, Maurice C. and Maurice S."* 

Inst	rument Window Help	
	Start	
	Cartridge Cleanup Self Test	
	Runs Properties Update	
	Disconnect	

#### Window Menu

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

Win	dow Help
	Batch
	Run Summary
	Analysis
	Default Layout

• Batch - Displays the Batch screen where you create, view, and edit batches.

#### Chapter 4: Compass for iCE Overview

- **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. and Maurice S.
- 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.
- Compass for iCE Log Displays the software log file.
- 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.

💾 Batch	Run Summary	>3
---------	-------------	----

#### **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.



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



User Guide for Maurice, Maurice C. and Maurice S.

• 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**.



• 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.

User Guide for Maurice, Maurice C. and Maurice S.

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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**.

Graph		
	Detached	
	Restore	
14	Move	•
13	Size	•
12	Minimize	
11	Maximize	
10		
j⊋ <sup>9</sup> L	Close	

- 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.

User Guide for Maurice, Maurice C. and Maurice S.

#### 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**.

## Software Help

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

## 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.
- 2. 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 a PDF with feature updates and bug fixes for new and past versions of Compass for iCE. 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.

## Viewing the Software Log

Select Help and click Compass Log to view the software log file.

## 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. and Maurice S.

Organize ▼ Include in library ▼ Share with ▼	Burn	New folder			
4 🎉 Program Files	*	Name	Date modified	Туре	Size
<ul> <li>► Trigrammes</li> <li>► ATT</li> <li>Bonjour</li> <li>► Common Files</li> <li>▲ Compass for iCE</li> <li>► Configuration</li> <li>Examples</li> </ul>		Configuration Examples features pre p2 plugins templates	2/11/2016 3:04 PM 2/11/2016 3:04 PM 2/11/2016 3:04 PM 2/11/2016 3:04 PM 2/11/2016 3:04 PM 2/11/2016 3:04 PM 2/11/2016 3:04 PM	File folder File folder File folder File folder File folder File folder File folder	5128
<ul> <li>lifeatures</li> <li>jre</li> <li>j2</li> <li>lifeatures</li> <li>lifeatures</li> <li>lifeatures</li> </ul>		colipseproduct     artifacts.xml     Compass for iCE.exe     Compass for iCE.ini     Compass for iCE.ini	2/8/2012 8:36 AM 2/10/2016 3:35 PM 2/10/2016 3:35 PM 2/10/2016 3:35 PM 2/10/2016 3:35 PM	ECLIPSEPRODUCT XML Document Application Configuration sett Icon	1 KB 39 KB 43 KB 1 KB 279 KB
		Compass_for_iCE_data_file.ico     Compass_for_iCE_data_file.ico     elipsec.exe     el-v10.html     iccense.ntf     Maurice User Guide.pdf     fortice.html     @] welcome.ntf	2/10/2016 3:36 PM 2/10/2016 3:34 PM 2/8/2012 8:36 AM 2/10/2016 3:31 PM 2/10/2016 3:31 PM 2/8/2012 8:36 AM 2/10/2016 3:31 PM	Icon Application HTML Document Rich Text Format Adobe Acrobat D HTML Document Rich Text Format	15 KB 18 KB 17 KB 168 KB 12,198 KB 9 KB 1 KB

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

Organize ▼ Share with ▼ Burn N	lew folder				
<ul> <li>Libraries</li> <li>Documents</li> </ul>	Documents library Compass for iCE				
My Documents      Add-in Express	Name	Date modified	Date created	Туре	Size
Adoha	🔒 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	
A Compare for iCE	📕 Runs	1/17/2016 8:41 PM	11/11/2015 4:46 PM	File folder	
Batches  New Batches  Runs	DemoData_Maurice cIEF.mbz	1/18/2016 11:38 AM	1/18/2016 11:38 AM	Maurice data file.	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 4: Compass for iCE Overview

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# clef Batches

## **Chapter 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
- Batch Reports

## **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 C. 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.

									Construction of the local division of the lo
ile Edit Instrument	Window Help								
								Batch 🔂 Run Summ	ary 🕼 Analysis
Batch: 2016-01-21_09-4	6-39_mAb11_Prep20160121_QC(0)	Injection	ns 🔚 History 🔳	Notes				Add 📗 Replicate 🕅 R	emove 💽 🖻 🗖
Through 1			Sample ID	Location	Method		Notes		
		1	System Suitability	Al	System Suitz	iblity			
00 10°C -	Ct Add - CX Remove	2	mAb 11 Blank	A2	mAb Metho	d			
		3	mAb 11 Ref. Std.	A3	mAb Metho	d			
MC	Fi Gal Water Ar	4	mAb 11 Prep 20160	121 A4	mAb Metho	đ			
	$\mathbf{O}$	5	mAb 11 Prep 20160	121 A4	mAb Metho	d			
0		6	mAb 11 Prep 20160	121 A4	mAb Metho	d			
	an had had had had	7	mAb 11 Ref. Std.	A3	mAb Metho	d			
Water		8	mAb 11 Blank	A2	mAb Metho	đ			
1 2	3 4 5 6 7 8								
^ <b>O</b> O									
B									
XX									
c									
D									
E									
F									
and a	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA								
Methods									
									New Remo
Name	Separation		Detection	Sample Load (s)	pl Markers	Ampholytes	Additives		
System Suitablity	1.0 min 1500 Volts, 4.5 min 3000 Volt	3	5 Exposures	55	3.38, 10.17				
mAb Method	1.0 min 1500 Volts, 6.0 min 3000 Volt	3	5 Exposures	55	4.05, 9.99				

**Batch Screen Overview** 

#### 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 or Maurice S.)
- 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.
- **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.

#### page 40

#### 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			lņ
	Plate Layout	•	•	48 Vials	
	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.
- **Preferences** Lets you set and save your preferences for data export, graph colors, grouped data and Twitter settings. See Chapter 13, "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. 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 42. 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**:

File	Edit Instrument	Window	Help
	New Batch	•	Maurice cIEF
	Open Batch	•	Maurice CE-SDS
	Save		
	Save As	11	_Prep20160121_QC(0)2

NOTE: If you're using a Maurice system, both cIEF and CE-SDS template batches are available in the menu.

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

File       Edit Instrument Window Help         Batch: Maurice dIF       Impletions       Impletory       Notes       Impletors       Im	- 0 - X
Detch       Targeton       Intervy       Netes       Production       Methods         1       Sample 1       A1       System Suitability       Image: Suitability       <	
Batch:       Impletions       Impletions       Method       Notes         Impletions       Impletions       Impletions       Impletions       Method         Impletions       Impletions       Impletions       Impletions       Method         Impletions       Impletions       Impletions       Impletions       Impletions         Impletions       Impletions       Impletions       Impletions       Impletions         Impletions       Impletions       Impletions       Impletions       Impletions       Impletions         Impletions       Impletions       Impletions       Impletions       Impletions       Impletions       Impletions         Impletions       Impletions       Impletions       Impletions       Impletions       Impletions       Impletions       Impletions       Impletions       Impletions       Impletions       Impletions       Impletions       Impletions	Analysis
Sample ID       Location       Method       Notes         10°C *       Charles       All       System Subability         10°C *       Charles       Control       All         10°C *       Charles       Control       Control         10°C *       Charles       Control       Control         10°C *       Control       Control       Control         10°C *       Control <th>we 🖲 🖻 🗖</th>	we 🖲 🖻 🗖
1       Sample 1       A1       System Suitability         1       Sample 1       A1       System Suitability         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	
Motions       Motions       Motions         Motions         Motions         Motions         Motions         Motions         Detection         Separation   Detection         Detection         Separation         Detection         Separation         Detection         Separation         Detection         Separation	
II Methods	
"Methods           "Methods           Name         Separation           Detection         Sample Load (s)	
Name Separation Detection Sample Load (s) p1 Markers Ampholytes Additives	New Remo
System Suitability 1.0 min 1500 Volts, 4.5 min 3000 Volts 5 Exposures 55 3.38, 10.17	

User Guide for Maurice, Maurice C. and Maurice S.

Creating a New Batch

#### 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.





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
- 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. To select samples:
  - 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:

Injecti	ons 🛛 🔡 History 🏋 Ne	otes			👫 Add 📊 Replicate 🔀 Remove	
	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			

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)**.

			- 8)		Sample ID
				1	Sample 1
00 10°C <del>-</del>	CH Ac	id 👻 💓 R	emove	2	Sample 2
				3	Sample 3
MC FI Ca	4 Water P2 0 P3 0 P4 N2 N3 N4	Air P5 P6 N5 N6	Remove	samples f	rom selected locations
A 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 5 6	7 8			

3. 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.

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

Methods							
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		🎯 Separation Profile	×
Name	Separation	Add Remo	ove
Method1	Voltage 2 Steps	Time (min) Voltage (Vol	ts)
		1.0 1500	
		4.5 3000	
		ОК Сап	cel

- 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.

#### Creating a New Batch

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

Methods			© Detection Profile	
Name	Separation	Detection	Add	Remove
Method1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures 🛄	Exposure (sec)	Туре
			0.0050	absorbance
			3	fluorescence
			5	fluorescence
			10	fluorescence
			20	fluorescence

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

NOTES:

The first exposure is an instrument default setting and can't be changed.

Fluorescence is the default detection for the remaining exposures and can't be changed.

- 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 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 pl Markers column to select pl markers. Add new markers or remove existing ones then click **OK**.

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

Separation	Detection	Sample Load (s)	pI Markers	Add	Kemove
1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures	55	3.38 10.17	pI Markers:	
				pI	Position
				3.38	250
				10.17	1,700

- To add a pl marker: Click Add. A new row will be added in the table. Then just type in a pl and a position (in pixels).
- To remove a pl 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.

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

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 cIEF		Injectio	ons 🔚 History 👖 N	lotes		
			Sample ID	Location	Method	
		1	Sample 1	A1	Method1	
00 10°C <del>-</del>	📢 Add 👻 💓 Remove	2	Sample 2	A2	Method1	
55		3	Sample 3	A3	Method1	
MC FI Cal	Water Air 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4	Sample 4	Α4	Method1	
A 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 5 6 7 8					

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

Injections	📙 History 🚹 Notes				👫 Add 🚻 Replicate 🔀 Remove 🗉 🖻 🖱
	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		

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

Batch: Maurice cIEF		Injectio	ons 🔚 History 🎵 N	lotes		
	- 8		Sample ID	Location	Method	
			Product A	A1	Method1	
00 10°C -	📢 Add 👻 🚺 Remove	2	Sample 2	A2	Method1	
		3	Sample 3	A3	Method1	
MC FI Cal	Water Air 2 0 p3 p4 p5 0 p6 12 H3 N4 N5 N6	4	Sample 4	Δ4	Method1	
A O O O O O O O O O O O O O O O O O O O	4 5 6 7 8					

2. 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.

Injecti	ons 🛛 🔚 History 👖 N	lotes					🖁 Add	📗 Replicate	🔀 Remove	Ŧ	
	Sample ID	Location	Method		Notes						
1	Product A	A1	Method1								
2	Sample 2	A2	Method1								
3	Sample 3	A3	Method1								
4	Sample 4	A4	Method2	-							
			Method1		]						
			Method2								

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Hovering over a method name displays the method parameters:

📗 Injecti	ons 🛛 🔚 History 🔣 No	otes		
	Sample ID	Location	Method	Notes
1	Product A	A1	Method1	
2	Sample 2	A2	Method1	Method1
3	Sample 3	A3	Method1	Separation: 1.0 min 1500 Volts, 4.5 min 3000 Volts
4	Sample 4	A4	Method2	Sample Load (s): 55
				pI Markers: 3.38, 10.17
				Ampholytes: Pharmalyte 3-10
				Additives: Urea

- 3. 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	ns 🛛 🔚 History 👖 Note	es			👫 Add 📗 Replicate 🔀 Remove 🕤 🖻 🗖 🗖
	Sample ID	Location	Method	Notes	Penlicate relected injections
1	Product A	A1	Method1		Replicate selected injections
2	Sample 2	A2	Method1		
3	Sample 3	A3	Method1		
4	Sample 4	A4	Method2		

Injections	🔚 History 🎵 Notes				<b>#</b>	Add	Replicate	🔀 Remove	Ŧ	8 - 8
	Sample ID	Location	Method	Notes						
1	Product A	A1	Method1							
2	Sample 2	A2	Method1							
<b>⊿</b> 3	Sample 3	A3	Method1							
4	Sample 3	A3	Method1							
5	Sample 4	A4	Method2							

• 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				🚰 Add 🔛 Replicate 🔀 Remove 🕞 📄 🗖 🗖
	Sample ID	Location	Method	Notes	Add injections
1	Product A	A1	Method1		
2	Sample 2	A2	Method1		
a 3	Sample 3	A3	Method1		
4	Sample 3	A3	Method1		
5	Sample 4	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 - 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.

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III Injections 🔚 History 🎹 *Notes	- 0
Product testing	

#### Step 6 - 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:

Default Analysis: Maurice	dEF		
pe filter text	Advanced		⇔ • ⇔ •
Advanced Detection Peak Fit Peak Names pl Markers	Analysis Settings Advanced	Analysis Settings: Advanced pI Markers Peak Width Allowable Drift	15 100
	Add Remove Apply Default: Advanced	•	
	Apply Override: Apply To Settings		
	Add Remove		
Import Expo	ort	ОК Са	ncel 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 334.

#### Step 7 - 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**.

or 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:

Injectio	ns 🔚 History 👖 Notes			Injection:	s 🛛 🔚 History 🔣 No	otes	
	Sample ID	Location	Method		Sample ID	Location	
⊳ <b>1</b>	Product A	A1	Method1	⊿ 1	Product A	A1	
⊳ 6	Product B	A2	Method1	2	Product A	A1	
11	Product C	A3	Method1	3	Product A	A1	
12	Product D	A4	Method1	4	Product A	A1	
13	Product E	A5	Method1	5	Product A	A1	
14	Product A	A6	Method2	⊳ 6	Product B	A2	
15	Product B	B1	Method2	11	Product C	A3	
16	Product C	B2	Method2	12	Product D	A4	
17	Product D	B3	Method2	13	Product E	A5	
18	Product E	B4	Method2	14	Product A	A6	
19	Test	B5	Method2	15	Product B	B1	
20	Test	B6	Method2	16	Product C	B2	

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

Injection	s 🛛 🔚 History 🚺 Not	es			🚰 Add 📗 Replicate 💢 Remove 🕞 🖻 🗖
	Sample ID	Location	Method	Notes	Expand All Inie
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 👖 Notes			🚰 Add 🔛 Replicate 🔀 Remove 🕀 📄 🖓 🗖				
	Sample ID Lo	ocation Method	Notes	Collapse All Inject				
⊳ 1	Product A At	1 Method1						
6	Product B A2	2 Method1						
11	Product C A3	3 Method1						
12	Product D A4	4 Method1						
13	Product E A	5 Method1						
14	Product A Ad	6 Method2						
15	Product B B1	1 Method2						
16	Product C B2	2 Method2						
17	Product D B3	3 Method2						
18	Product E B4	4 Method2						
19	Test B5	5 Method2						
20	Test B6	5 Method2						

## **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.

e	User Name	Message	Comment	
01/21/2016 9:38 AM		Batch created using the factory default Maurice		
01/21/2016 9:47 AM		Save protocol and template changes	Auto-saved	
me 01.	/21/2016 9:38 AM	1 User		
essage Ba	tch created usin	g the factory default Maurice cIEF		
mment		······		

- 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 391 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**.



- 2. A list of the last five batches opened will display.
  - 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.



3. To make changes to the batch, see the steps in "Creating a New Batch" on page 42. 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	-13-0	1_Maurice cIEF_Mab11_Te ╺
😇 Laj	2016-01 2015-12	2-06_15	<b>46-3</b> 9	9_mAb11_Prep20160121_QC(0)
	00	10°C	Ŧ	🗲 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.

**Batch Reports** 

#### **Batch Reports**

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

- 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.

File	Edit Instrument	Window
	New Batch	•
	Open Batch	•
	Save	
	Save As	
	Batch Report	
	Exit	

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: 2016-01-21_09-46-39_mAb11_Pre	p20160121_QC
Report Name:	Browse
2016-01-21_09-46-39_mAb11_Prep201601	21_QC
Location: C:\Users\User\Documents\Com	pass for iCE\Runs
ОК	Cancel

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   B	Burn	New folder			
Favorites	*	Name	Date modified	Туре	Size
👔 Links		2016 01 21 00 46 20 mAb11 Bran 20160121 OC Batch adf	1/24/2016 1-04 DM	Adaba Assobat D	26 V P
My Documents		2010-01-21_09-40-39_mAD11_Prep20100121_QC_Batch.pdf	1/24/2010 1:04 PIVI	Adobe Acrobat D	20 Kt
퉬 Add-in Express					
🌗 Adobe					
🌗 Clients					
퉬 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					
퉬 78664 P3 IS 2015-11-30_16-49-49_MW Ladder Sol					

Here's an example Batch Report:

Injection	Sample ID	Location	Method	Separation	Sample Load (s)	Standards (pl)	Ampholytes	Additives
1	System Suitability	A1	System Suitablity	1.0 min, 1500 Volts 4.5 min, 3000 Volts	90	3.38 10.17		
2	mAb 11 Blank	A2	mAb Method	1.0 min, 1500 Volts 6.0 min, 3000 Volts	90	4.05 9.99		
3	mAb 11 Ref. Std.	A3	mAb Method	1.0 min, 1500 Volts 6.0 min, 3000 Volts	90	4.05 9.99		
4	mAb 11 Prep 20160121	A4	mAb Method	1.0 min, 1500 Volts 6.0 min, 3000 Volts	90	4.05 9.99		
5	mAb 11 Prep 20160121	A4	mAb Method	1.0 min, 1500 Volts 6.0 min, 3000 Volts	90	4.05 9.99		
6	mAb 11 Prep 20160121	A4	mAb Method	1.0 min, 1500 Volts 6.0 min, 3000 Volts	90	4.05 9.99		
7	mAb 11 Ref. Std.	A3	mAb Method	1.0 min, 1500 Volts 6.0 min, 3000 Volts	90	4.05 9.99		
8	mAb 11 Blank	A2	mAb Method	1.0 min, 1500 Volts 6.0 min, 3000 Volts	90	4.05 9.99		

#### cIEF Batch: Maurice cIEF

Created: Thu 1.51 PM Feb 25, 2016 Created By: User C:\UserSiJsenUcocuments/Compass for ICE\Runsi2016-01-21\_09-46-39\_mAb11\_Prep20160121\_QC(0).mbz Computer: JRichards



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# Chapter 6: CE-SDS Batches

## **Chapter 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
- Batch Reports

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#### **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.

MW ladder assigned	ed_MW Ladder Sol Test IS final QC 110 ms Mau	arice CE-SDS	- Compass for iCE				
le Edit Instrume	nt Window Help						
							📴 Batch 📵 Run Summary 🕼 Analysis
Run: MW ladder ass	igned_MW Ladder Sol Test IS final QC 110 ms N	III Injectio	ns 🔚 History 🔳 Notes	1			🚰 Add 📓 Replicate 🕼 Remove 🗃 🖻 🖱
Lavout	= 0		Sample ID	Location	Method	Notes	
		1	IgG System Control	A1	Method1		
5 00 10°C	<ul> <li>Ct Add</li> <li>CX Remove</li> </ul>	2	Control Ladder	A2	Method2		
		3	Test Ladder	A3	Method2		
	G1 G2 Water Sep. Wash Air	4	IS - Alpha	81	Method1		
		5	15 - Frozen P3	82	Method1		
		6	IS - T1 P3	83	Method1		
		7	15 - T2 P3	B4	Method1		
v	Vater Water Run	8	IS - T3 P3	85	Method1		
1	2 3 4 5 6 7 8	9	Control Ladder	A2	Method2		
A (0)		10	Test Ladder	A3	Method2		
		11	15 - Alpha	81	Method1		
в 🜔 🕻		12	IS - Frozen P3	82	Method1		
c ()		13	15 - T1 P3	83	Method1		
-		14	IS - T2 P3	84	Method1		
D		15	IS - T3 P3	85	Method1		
		16	Control Ladder	A2	Method2		
-		17	Test Ladder	A3	Method2		
F		18	IS - Alpha	81	Method1		
and a	AAAAAA	19	IS - Frozen P3	82	Method1		
		20	IS-TIP3	83	Methodl		
		21	IS - T2 P3	R4	Method1		
Mathada			10-10-12		11001004		
mennos							New Ren
Name	Sample Load		Separation				
Method1	20 sec 4600 Volts		0.1 min 1150 Volte	0.1 min 3450 Vol	ts. 25.0 min 5750 V		
Mathod2	20 rac 4500 Valta		0.1 min 1150 Volte	0.1 min 3450 Vol	te 30.0 min 5750 V		
WIELING AL	20 Sec 1000 TOILS		Via mini 22.00 Yorks,	0.4 mm 3430 YO	5, 2010 min 27.20 Y		

**Batch Screen Overview** 

#### 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 or Maurice S.)
- 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.
- **Batch Report** Exports a table of sample and method details for each injection in the batch as a PDF file. This menu item is only active for batches in completed runs.
- Exit Closes Compass for iCE.

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#### Edit Menu

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

Edit	] Instrument Wi	ndow Help		
	Cut	Ctrl+X		
	Сору	Ctrl+C		
	Paste	Ctrl+V		Ini
	Plate Layout	•	۲	48 Vials
	Default Analysis			96-well Plate
	Preferences	L		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.
- **Preferences** Lets you set and save your preferences for data export, graph colors, grouped data and Twitter settings. See Chapter 13, "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. 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 64. 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**:

File	) Edit Instrument	Window	Help
	New Batch	۱.	Maurice cIEF
	Open Batch	۱.	Maurice CE-SDS
	Save		
	Save As		_Prep20160121_QC(0)2

NOTE: If you're using a Maurice system, both cIEF and CE-SDS template batches are available in the menu.

2. Select Maurice CE-SDS. A batch using the default method will display.

Maurice CE-SDS - Corr	npass for iCE						
ile Edit Instrument	Window Help						
							Batch 🕒 Run Summary 🎄 Analysis
Batch: Maurice CE-SDS		III Injectio	ns 🔚 History 🔳 Notes				🚰 Add 📓 Replicate 🕼 Remove 🗃 🖻 🖬
Lavout	- 0		Sample ID	Location	Method	Notes	
🗐 🥅 10°C 👻	CH Add - CX Remove	1	Sample 1	A1	Reduced IgG		
	C2 Water Sep. Wash Ar C3 C C C C C C C C C C C C C C C C C C						
	4 5 6 7 8 5 10 11 12						
D E							
a0000							
Methods							- (
							New Remov
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 4000 Volts		30.0 min 5/50 Volts				

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Creating a New Batch

# 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.





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.

🛄 Layout		🛄 Layout	
<b>€</b> 10°C	- CH Add - CK Remove	<b>10°</b> C	- CH Add - CX Remove
	C1 C2 Water Sep. Wash Air		C1 C2 Water Sep. Wash Air

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- 2. To select samples:
  - 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:

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Creating a New Batch

Injectio	ons 🛛 🔚 History 🚺 N	lotes			🚰 Add 📊 Replicate 🔀 Remove 🕞	₽ - 0
	Sample ID	Location	Method	Notes		
1	Sample 1	A1	Reduced IgG			
2	Sample 2	A2	Reduced IgG			
3	Sample 3	A3	Reduced IgG			
4	Sample 4	A4	Reduced IgG			
5	Sample 5	A5	Reduced IgG			
6	Sample 6	A6	Reduced IgG			
7	Sample 7	A7	Reduced IgG			
8	Sample 8	A8	Reduced IgG			
9	Sample 9	A9	Reduced IgG			
10	Sample 10	A10	Reduced IgG			
11	Sample 11	A11	Reduced IgG			
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)**.

		Sample ID
	1	Sample 1
🕘 📖 10°C 🔻 🛛 🚺 🕂 🚺 🚽 🚺 🛃	2	Sample 2
	3	Sample 3
C1 C2 Water Sep. Wash Air Remove si	amples fror	n selected location
	5	Sample 5
	6	Sample 6
	7	Sample 7
Wash Wash Run	8	Sample 8
1 2 3 4 5 6 7 8 9 10 11 12	9	Sample 9
	10	Sample 10
BOOOOOOOOOOOO	11	Sample 11
c0000000000000000000000000000000000000	12	Sample 12

3. Compass for iCE can monitor the current during a separation for you, stop it if the current drops below the minimum value 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 158 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.

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
educed 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	
Non-reduced IgG	20 sec 4600 Volts	
MW Markers	20 sec 4600 Volts	20 4600
		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 30 minutes. Run your non-reduced IgG samples and IgG Standard for 35 minutes. The default separation voltage for all sample types is 5750 volts.

		for Separation Profile
Sample Load	Separation	Add Remove
20 sec 4600 Volts	Voltage 1 Step	 Time (min) Voltage (Volts)
20 sec 4600 Volts	35.0 min 5750 Volts	25.0000 5750
20 sec 4600 Volts	30.0 min 5750 Volts	23.0000 3730
		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.
- 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.

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	Injectio	ns 🛛 🔚 History 🚺 No	ites	
		Sample ID	Location	Method
	1	Sample 1	A1	Reduced IgG
🗐 🥅 10°C 👻 🚺 🕂 🚺 🐨 🚺 🐨 🚺	2	Sample 2	A2	Reduced IgG
	3	Sample 3	A3	Reduced IgG
C1 C2 Water Sep. Wash Air	4	Sample 4	A4	Reduced IgG
		Sample 5	A5	Reduced IgG
		Sample 6	A6	Reduced IgG
		Sample 7	A7	Reduced IgG
Wash Wash Run	8	Sample 8	A8	Reduced IgG
	9	Sample 9	A9	Reduced IgG
<b>^ÓÓÓÓÓÓÓÓŐŐŐ</b>		Sample 10	A10	Reduced IgG
		Sample 11	A11	Reduced IgG
	12	Sample 12	A12	Reduced IgG

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

Injectio	ns 🛛 🔚 History 👖 N	lotes			👫 Add 📗 Replicate 🔀 Remove 🕀 🖻 🗖
	Sample ID	Location	Method	Notes	
1	Sample 1	A1	Reduced IgG		
2	Sample 2	A2	Reduced IgG		
3	Sample 3	A3	Reduced IgG		
4	Sample 4	A4	Reduced IgG		
5	Sample 5	A5	Reduced IgG		
6	Sample 6	A6	Reduced IgG		
7	Sample 7	A7	Reduced IgG		
8	Sample 8	A8	Reduced IgG		
9	Sample 9	A9	Reduced IgG		
10	Sample 10	A10	Reduced IgG		
11	Sample 11	A11	Reduced IgG		
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:

atch: Maurice CE-SDS	Injectio	ns 🔚 History 🎵 Note	s	
		Sample ID	Location	Method
	1	Product A	A1	Reduced IgG
🔄 📖 10°C 🔻 🛛 🧲 Add 👻 🚺 Remove 📗	2	Sample 2	A2	Reduced IgG
	3	Sample 3	A3	Reduced IgG
C1 C2 Water Sep. Wash Air	4	Sample 4	A4	Reduced IgG
	5	Sample 5	A5	Reduced IgG
P1 P2 P3 P4 P5 P6		Sample 6	A6	Reduced IgG
	7	Sample 7	A7	Reduced IgG
Wash Wash Run	8	Sample 8	A8	Reduced IgG
1 2 3 4 5 6 7 8 9 10 11 12	9	Sample 9	A9	Reduced IgG
	10	Sample 10	A10	Reduced IgG
BOOODOOOOOOOO	11	Sample 11	A11	Reduced IgG
Product A	12	Sample 12	A12	Reduced IgG

2. 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.

000	~	72
pay	c	12

Injections	🔚 History <u> N</u> otes				Add	📗 Replicate	🔀 Remove	Ŧ	• -	8
	Sample ID	Location	Method	Notes						
1	Product A	A1	Non-reduced IgG 🛛 👻							
2	Sample 2	A2	Reduced IgG							
3	Sample 3	A3	Non-reduced IgG							
4	Sample 4	A4	MW Markers							
5	Sample 5	A5	Reduced IgG							_
6	Sample 6	A6	Reduced IgG							
7	Sample 7	A7	Reduced IgG							
8	Sample 8	A8	Reduced IgG							

Hovering over a method name displays the method parameters:

Injections 🔚 History 🚹 Notes									
	Sample ID	Location	Method		Notes				
1	Product A	A1	Non-reduced IgG	Ne	n and used InC				
2	Sample 2	A2	Reduced IgG	Sar	n-reduced 190 mple Load: 20 sec 4600 Volts				
3	Sample 3	A3	Reduced IgG	Sep	Separation: 35.0 min 5750 Volts				
4	Sample 4	A4	Reduced IgG						

- 3. 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	s 🔛 History 🌃 Notes				🕂 Add 📗 Replicate 🔀 Remove 🕞 📄 🗆 🗖
	Sample ID	Location	Method	Notes	Replicate selected injections
1	Product A	A1	Non-reduced IgG		
2	Product A	A2	Reduced IgG		
3	Product B	A3	Non-reduced IgG		
4	Product B	A4	Reduced IgG		
5	Product C	A5	Non-reduced IgG		
6	Product C	A6	Reduced IgG		
Injection	s 🔚 History 👖 Notes				👫 Add 📊 Replicate 🔀 Remove 🕀 🖻 🗖
	Sample ID	Location	Method	Notes	
1	Product A	A1	Non-reduced IgG		
a 2	Product A	A2	Reduced IgG		
3	Product A	A2	Reduced IgG		
4	Product B	A3	Non-reduced IgG		
5	Product B	A4	Reduced IgG		
6	Draduct C	A5	Non-reduced InG		

• **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	ıs 🔚 History 👖 Notes				🎼 Add 🚻 Replicate 🔀 Remove 👍 📄 🗆 🗋
	Sample ID	Location	Method	Notes	Add injections
1	Product A	A1	Non-reduced IgG		
<b>⊿</b> 2	Product A	A2	Reduced IgG		
3	Product A	A2	Reduced IgG		
4	Product B	A3	Non-reduced IgG		
5	Product B	A4	Reduced IgG		
6	Product C	A5	Non-reduced IgG		

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• **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 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	- 8
Product testing	

### Step 6 - 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 applications, but if you need to modify parameters:

Analysis Settings		
Advanced	Analysis Settings: Advanced Standards Peak Width Allowable Drift	20 100
Add Remove Apply Default: Advanced	•	
Apply Override:           Apply To         Settings		
Add Remove		
	Advanced Apply Default: Advanced Apply Override: Apply To Settings Advanced Apply To Settings Add Remove	Advanced Standards Peak Width Allowable Drift Add Remove Apply Default: Advanced • Apply Override: Apply To Settings Add Remove

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

2. Change the parameters you want to, then click **OK**. For detailed information on analysis parameters, please refer to "Analysis Settings Overview" on page 244.

### Step 7 - 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**.

Viewing Replicate Injections

📀 Save Batch Comment	×
Batch: Maurice CE-SDS2 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:

Injectio	Injections 🔚 History 👖 *Notes				Injections 🔚 History 🌃 *Notes				
	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	<u>⊿</u> 2	Product A	A2	Reduced IgG		
7	Product B	A3	Non-reduced IgG	3	Product A	A2	Reduced IgG		
8	Product B	A4	Reduced IgG	4	Product A	A2	Reduced IgG		
⊳ 9	Product C	A5	Non-reduced IgG	5	Product A	A2	Reduced IgG		
13	Product C	A6	Reduced IgG	6	Product A	A2	Reduced IgG		
14	Product D	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	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	Evpand All Ini
1	Product A	A1	Non-reduced IgG		Lepting An Al
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.

( <b></b> ,	· ···· · · · · · · · · · · · · · · · ·				
# Injections	History III "Notes				H Add III replicate K remove H -
	Sample ID	Location	Method	Notes	Collapse All Injections
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.

ate	User Name	Message	Comment	
11/23/2015 11:59 AM		Batch created using the factory default Maurice		
11/23/2015 12:15 PM		Saved as MW Ladder Sol Test Maurice CE-SDS.ba		
11/30/2015 4:49 PM		Saved as MW Ladder Sol Test IS final QC 110 ms		
ne 11	/23/2015 11:59 A	M User		
essage B	atch created usir	g the factory default Maurice CE-SDS		

- 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 391 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**.



- 2. A list of the last five batches opened will display.
  - 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.



3. To make changes to the batch, see the steps in "Creating a New Batch" on page 64. 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	Window	Help		
1							
1							
Run:	KF1	006_s-CE	-SDS F	Product B		-	
(m)		06_s-CE	-SDS				
	KF10	06_s-CE	-SDS P	roduct B			
		] 10°C	*		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.

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**Batch Reports** 

# **Batch Reports**

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

- 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: 78664 P3 IS 2015-11-30_16-49-49_MW Ladde	er Sol Test IS final QC 110 ms Maurice CE-SDS
Report Name:	Browse
78664 P3 IS 2015-11-30_16-49-49_MW Ladder Sol Tes	t IS final QC 110 ms Maurice CE-SDS
Location: C:\Users\User\Documents\Compass for iCE	\Runs
	OK Cancel

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.



Here's an example Batch Report:

Injection	Sample ID	Location	Method	Sample Load	Separation
1	IgG System Control	A1	Method1	20 sec 4600 Volts	0.1 min, 1150 Volts 0.1 min, 3450 Volts 25.0 min, 5750 Volts
2	Control Ladder	A2	Method2	20 sec 4600 Volts	0.1 min, 1150 Volts 0.1 min, 3450 Volts 30.0 min, 5750 Volts
3	Test Ladder	A3	Method2	20 sec 4600 Volts	0.1 min, 1150 Volts 0.1 min, 3450 Volts 30.0 min, 5750 Volts
4	IS - Alpha	B1	Method1	20 sec 4600 Volts	0.1 min, 1150 Volts 0.1 min, 3450 Volts 25.0 min, 5750 Volts
5	IS - Frozen P3	B2	Method1	20 sec 4600 Volts	0.1 min, 1150 Volts 0.1 min, 3450 Volts 25.0 min, 5750 Volts
6	IS - T1 P3	B3	Method 1	20 sec 4600 Volts	0.1 min, 1150 Volts 0.1 min, 3450 Volts 25.0 min, 5750 Volts
7	IS - T2 P3	B4	Method1	20 sec 4600 Volts	0.1 min, 1150 Volts 0.1 min, 3450 Volts 25.0 min, 5750 Volts
8	IS - T3 P3	B5	Method1	20 sec 4600 Volts	0.1 min, 1150 Volts 0.1 min, 3450 Volts 25.0 min, 5750 Volts
9	Control Ladder	A2	Method2	20 sec 4600 Volts	0.1 min, 1150 Volts 0.1 min, 3450 Volts 30.0 min, 5750 Volts
10	Test Ladder	A3	Method2	20 sec 4600 Volts	0.1 min, 1150 Volts 0.1 min, 3450 Volts 30.0 min, 5750 Volts
11	IS - Alpha	B1	Method 1	20 sec 4600 Volts	0.1 min, 1150 Volts 0.1 min, 3450 Volts 25.0 min, 5750 Volts

#### CE-SDS Batch: MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS

Created: Thu 1.54 PM Feb 25, 2016 Created By: User C:VLstere/User/Documents/Compass for iCE/Runs/MW ladder assigned\_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS mbz Computer: JRichards



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# Chapter 7: Running cIEF Applications on Maurice and Maurice C.

# **Chapter Overview**

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

# 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 clEF pl Markers (3.38, 4.05, 5.85, 6.14, 7.05, 8.4, 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
- 96-well plate or vials with integrated inserts for samples
- Clear screw caps for vials

User Guide for Maurice, Maurice C. and Maurice S.

#### **Running cIEF Applications**

- 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)

### 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 4titude Pierceable Film (PN 4ti-0566, 4titude). 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 for 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  $\mu$ L 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.

#### **Running cIEF Applications**

8. 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  $\mu L$  in DI water.
- 2. In a separate tube, prepare IEF Separation Mix containing your chosen pl marker(s).

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

- 3. Add 160  $\mu$ L of IEF Separation Mix to the 40  $\mu$ 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
- 6. 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.

#### pl Markers

- 1. Open the vial of lyophilized pl 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 pl markers you're using.
- 4. Aliquot 20 µL of each reconstituted pl marker into separate tubes for storage.

#### NOTES:

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

If you'll use the pl 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  $\mu$ L of each pl marker for every 200  $\mu$ L of sample.

#### 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**.

Pressure cap

Glass reagent vial

5. Pipette 2 mL of DI water into a glass reagent vial, label and close with a **clear screw cap**.



# Step 2: Prep the Cartridge

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<sup>-</sup> electrolyte tank (white port).
- 5. Add 2 mL Anolyte solution to the H<sup>+</sup> electrolyte tank (red port).

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

#### **Running cIEF Applications**

6. Seal each tank with the rubber stoppers. Use the grey stopper for the OH<sup>-</sup> tank and the red one for the H<sup>+</sup> 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.



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#### **Running cIEF Applications**

- proteinsimple
- 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.

- 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







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.

#### NOTES:

If you need to seal the 96-well plate during your run, we recommend the 4titude Pierceable Film (PN 4ti-0566, 4titude). 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.

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

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

### Step 5: 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 clEF - Compa	ss for iCE							
ile Edit Instrument	Window Help							
								🔚 Batch 🔃 Run Summary 🕼 Analysis
Batch: Maurice cIEF		Injectio	ns 🔚 History 🔳 I	Votes				🛃 Add 📓 Replicate 🔀 Remove 📵 🖻 🖱
- Levout	- 0		Sample ID	Location	Method		Notes	
10°C -	Ct Add - CK Remove	1	Sample 1	Al	System Suita	bility		
A 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 5 6 7 8 9 10 11 12							
°0000								
10000	000000000							
° Contra								
Methods					-			- c
								New Remov
Name	Separation		Detection	Sample Load (s)	pl Markers	Ampholytes	Additives	
System Suitability	1.0 min 1500 Volts, 4.5 min 3000 Volt	5	5 Exposures	55	3.38, 10.17			

3. To create a batch, 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**.

#### To create a new batch:

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

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 6: Start the Batch" on page 100.

File Edit	Instrument Windo	w Help	File	Edit Instrument	Window	v Help
New	Batch 🕨	Maurice cIEF		New Batch	•	
Ope	n Batch 🕨 🕨	Maurice CE-SDS		Open Batch		Maurice cIEF 011816
Save	:			Save		Maurice CE-SDS sample batch Maurice cIEF
Save	e As	11_Prep20160121_QC(0)2		Save As		Maurice CE-SDS2
Batc	h Report	[		Batch Report		Maurice CE-SDS Gen Meth



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.

5. Use your mouse to highlight the well positions for each of your samples, then click Add.



This populates the Injections table:

Injectio	ns 🛛 🔚 History 🚺 N	otes			👉 Add 📊 Replicate	Remove 🕀 🖻 🗖
	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			

6. 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.



#### 7. 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.

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.

Methods		👴 Separation Profile
Name	Separation	Add Remove
Method1	Voltage 2 Steps	Time (min) Voltage (Volts)
		1.0 1500
		4.5 3000
		OK Cancel

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.

Methods			© Detection Profile	
Name	Separation	Detection	Add	Remove
Method1	1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures 🛄	Exposure (sec)	Туре
			0.0050	absorbance
			3	fluorescence
			5	fluorescence
			10	fluorescence
			20	fluorescence

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 pl Markers column to select pl markers. Add new markers or remove existing ones then click **OK**.

Separation	Detection	Sample Load (s)	pI Markers	
1.0 min 1500 Volts, 4.5 min 3000 Volts	5 Exposures	55	3.38 10.17 🛄	 pI Ma
				3
				10



f. 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	

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

Methods						
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:

- 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 add sample names: click the Sample ID cell for the injection and type a name.

Injections	History 📑 Notes				📌 Add	Replicate	🔀 Remove	Ð Ð	- 0
	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						

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

Injec	📰 Injections 🔚 History 🏗 Notes 🕅 🖶 🖶 🗖 🗖										
	Sample ID	Location	Method		Notes						
1	Product A	A1	Method1								
2	Sample 2	A2	Method1								
3	Sample 3	A3	Method1								
4	Sample 4	A4	Method2	-							
			Method1		]						
			Method2								

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

Sample 4

۸4

Method2

Injectio	ons 🔚 History 👖 Notes				🕂 Add 📕 Replicate 🔀 Remove 🗉 🖻 🗖
	Sample ID	Location	Method	Notes	Paplicate calested injections
1	Product A	A1	Method1		Replicate selected injections
2	Sample 2	A2	Method1		
3	Sample 3	A3	Method1		
4	Sample 4	A4	Method2		
Injectio	ons 🔚 History 👖 Notes				📑 Add 📗 Replicate 🔀 Remove 🗉 🖻 🗖
	Sample ID	Location	Method	Notes	
1	Product A	A1	Method1		
2	Sample 2	A2	Method1		
a 3	Sample 3	A3	Method1		
4	Sample 3	A3	Method1		

• **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				👫 Add 🔛 Replicate 🔀 Remove 🕞 😑 🗆 🗆
	Sample ID	Location	Method	Notes	Add injections
1	Product A	A1	Method1		
2	Sample 2	A2	Method1		
a 3	Sample 3	A3	Method1		
4	Sample 3	A3	Method1		
5	Sample 4	A4	Method2		
	bampie i	~~~	memora		

- **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.
- 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 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:
| Analysis Settings                             | Analysis Settings: Advanced  |  |
|---|--|--|
| Advanced                                      | pI Markers   |  |
|   | Peak Width   | 15   |
|   | Allowable Drift  | 100  |
| Apply Default:<br>Advanced<br>Apply Override: | <b>v</b>   |  |
| Apply To Settings                             |  |  |
| Add Remove                                    |  |  |
|   | Analysis Settings Advanced Advanced Apply Default: Advanced Apply Override: Apply To Settings Advanced Apply To Remove | Analysis Settings Analysis Settings: Advanced  PI Markers Peak Width Allowable Drift  Add Remove  Apply Default:  Advanced  Apply Override:  Apply To Settings  Add Remove  Add Remove |

- b. Change the parameters you want to, then click **OK**. For detailed information on analysis parameters, please refer to "Analysis Settings Overview" on page 244
- 12. 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**.

or Save Batch Comment	x
Batch: Maurice cIEF Comment:	
	Save Cancel

13. Enter a name for your batch then click **Save**.

### Step 6: 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.



- 3. 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.
- 4. 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			X
Batch: Maur	ice cIEF		
Results file n	ame :		Browse
2016-01-27	_16-10-07_Maurice cIEF		
Location: C:	\Users\fdeng\Documents\Compass for it	CE\Runs	
Comment:			
	Cartridge		
	Type : cIEF	Batch Injection Limit : 100	
	Expires : Sep 2016	Injections Remaining: 38	
	Serial Number: 1150916212	Batches Remaining: 2	
		Start	Cancel

- 5. If you don't want to save the file to the default Runs folder, click **Browse** to select a different location.
- 6. Enter any run details you'd like in the Comments box (optional).
- 7. 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 9, *"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 12, *"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 383 for more info.

# **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 reagent vials and samples and discard.
- 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, the cartridge is at its limit. Put it back 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 you've still got injections left and the cartridge will be used again within 24 hours. You don't need to do anything. Just leave the cartridge in Maurice.

If you've still got injections left and the cartridge won't be used within 24 hours. Clean and store the cartridge. Maurice has already cleaned the capillary for you, so here's all you need to do:

- 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.
- f. Put the stoppers back on the tanks.
- g. 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 protein and pl 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.

dvanced etection Method © Absorbance © Fluorescence eak Fit			Detection	
	Fluorescence	O Absorbance	Method	dvanced etection eak Fit
sak Names     Markers     System Suitablity     Exposure 1 0.005 seconds v     Exposure 3 10 seconds v	Exposure 3 10 seconds 🔹	Exposure 1 0.005 seconds	System Suitablity	ak Names Markers
mAb Method Exposure 1 0.005 seconds V Exposure 4 20 seconds V	Exposure 4 20 seconds 🔻	Exposure 1 0.005 seconds	mAb Method	

# Step 2: Check Your pl Markers

To make sure your pl markers are identified correctly:

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

File	Edit	View	Instrume	nt	Window
E	Mark	ers 🚔	Samples		≣∎

3. Click the **Single View** icon in the View bar.



- 4. Click Injection 1 in the Experiment pane.
- 5. Check that your pl 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 pl markers aren't identified correctly, here's how to manually correct them:

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



A lock icon indicating the pl 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

Experime	ent		
Injection	Sample	Location	Me
<b>V</b> 1	System Suitabi	A1	Sys
2	mAb 11 Blank	A2	mA
3	mAb 11 Ref. St	A3	mA
4	mAb 11 Prep 2	A4	mA
5	mAb 11 Prep 2	A4	mA
6	mAb 11 Prep 2	A4	mA
7	mAb 11 Ref. St	A3	mA

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NOTE: To remove pl 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 pl marker:** Right-click the peak in the electropherogram or Peaks table and select **Not a Marker**. Compass should correctly reassign the remaining peaks as pl markers and update the Peaks table.



An **M** with a red slash through it will appear next to the incorrectly assigned 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
1	System Suitabi	17	1743	29396.8
<b>N</b> 1	System Suitabi	18	1780	30540.1
1	System Suitabi	19	1959	1399.5
1	System Suitabi	20	2018	1470.4

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

# Step 3: Checking Sample Peaks

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

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NOTE: The reported protein pl in Compass may vary slightly from predicted pls 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 Single View 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.

Experime	ent		- 8
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.

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		

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 "Peak Names Settings" on page 354.

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# Chapter 8: Running CE-SDS Applications on Maurice and Maurice S.

# **Chapter Overview**

- Before You Throw the Switch
- Power Up
- Running CE-SDS Applications
- Post-batch Procedures
- Checking Your Data

# 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 Applications**

### What You'll Need

- Maurice CE-SDS Size Application Kit which includes:
  - Maurice CE-SDS Cartridges
  - Cartridge Cleaning Vials
  - Separation Matrix
  - Running Buffer (Top and Bottom)
  - 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)

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- Maurice CE-SDS MW Markers (optional)
- $\beta$ -mercaptoethanol ( $\beta$ ME,  $\geq$ 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 -80 °C for long term storage. For short-term storage (< 1 week), the solution can be stored at 2-8 °C

- 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.
- 2. 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

### Reduced IgG Sample

1. In a microcentrifuge tube, dilute your IgG sample with 1X Sample Buffer to a concentration of 1mg/mL in a final volume of 50 μL.

NOTE: Dilute at least 1:1 with 1X Sample Buffer.

- 2. Add 2 µL of reconstituted 25X Internal Standard for every 50 µL of sample volume.
- 3. Add 2.5  $\mu$ L of 14.2 M  $\beta$ -mercaptoethanol to 50  $\mu$ L of sample.
- 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)

NOTE: The IgG Standard is lyophilized. Always reseal the foil bag containing the unopened tubes with desiccant to prevent moisture absorption.

- 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  $\mu$ L of 14.2 M  $\beta$ -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)

NOTE: The CE-SDS MW Markers are lyophilized. Always reseal the foil bag containing the unopened tubes with desiccant to prevent moisture absorption.

- 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  $\mu$ L of 14.2 M  $\beta$ -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 integrated inserts.
- 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.

#### User Guide for Maurice, Maurice C. and Maurice S.

**Running CE-SDS Applications** 



# 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

1. In a microcentrifuge tube, dilute your IgG sample with 1X Sample Buffer to a concentration of 1 mg/mL in a final volume of 50  $\mu$ L.

NOTE: Dilute at least 1:1 with 1X Sample Buffer.

- 2. Add 2  $\mu$ L of reconstituted 25X Internal Standard for every 50  $\mu$ L of sample volume.
- 3. Add 2.5 µL of 250 mM IAM.
- 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)

NOTE: The IgG Standard is lyophilized. Always reseal the foil bag containing the unopened tubes with desiccant to prevent moisture absorption.

- 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 integrated inserts.
- 2. Close the vials with a clear screw cap.

**Running CE-SDS Applications** 

3. Place the vials in a centrifuge using vial adapter (12 mm, 2 mL vials) and spin for 10 minutes at 1000 xg.

#### 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 pres**sure cap.



- 2. Pipette 1.5 mL of Conditioning Solution 2 into a glass reagent vial, label and close with an **orange pres**sure 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 both with **clear screw caps**.

#### **Running CE-SDS Applications**



- 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 a 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

1. Take the 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.



User Guide for Maurice, Maurice C. and Maurice S.

2. Pull the cartridge insert out of the cartridge.



3. Slide the Top Running Buffer vial 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.

NOTE: The Top Running Buffer vial has metal pins on either side, so no specific orientation is necessary.



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 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 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



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.

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

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

# Step 5: 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 - Cor	mpass for iCE						- 0 <del>- X</del>
File Edit Instrument	Window Help						
							🔛 Batch 🕒 Run Summary 🕼 Analysis
Batch: Maurice CE-SDS	5	Injectio	ns 🔛 History 🏋 No	otes			🖟 Add 剻 Replicate 🕅 Remove 💽 🖻 🗖 🕻
(m) ( and			Sample ID	Location	Method	Notes	
Cayour		1	Sample 1	Al	Reduced IgG		
D 10.C -	GT Add • C Remove						
61	C2 Water Sep. Wash Air						
0	<b>), (), (), (), (), (), (), (), (), (), (</b>						
Was	h Wash Run						
A 000	4 5 6 7 8 9 10 11 12						
#0000	0000000000						
° 000							
10000	0000000000						
*000							
H C C C							
Methods							
Mama	Sample Load		Securities				New Remov
Reduced IgG	20 sec 4600 Volts		25.0 min 5750 V	olts			
Non-reduced IgG	20 sec 4600 Volts		35.0 min 5750 V	olts			
MW Markers	20 sec 4600 Volts		30.0 min 5750 V	olts			
							* :

User Guide for Maurice, Maurice C. and Maurice S.

3. To create a batch, 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**.

#### To create a new batch:

- On Maurice systems in the main menu, select File > New Batch > Maurice CE-SDS.
- On Maurice S. systems in the main menu, select **File > New Batch**.

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 6: Start the Batch" on page 133.

File	Edit Instrument Windo	w Help	Fi	ile Edit	Instrument	Window	Help
	New Batch	Maurice cIEF		New	Batch	۱.	
	Open Batch 🕨	Maurice CE-SDS		Oper	n Batch	•	Maurice CE-SDS2
	Save Save As	11 Prep20160121 QC(0)2	-	Save Save	As		Maurice cIEF Maurice CE-SDS1
	Batch Report		t	Batc	h Report		Browse

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

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This populates the Injections table:

Injectio	ns 🛛 🔚 History 👖 N	lotes			🚰 Add 📊 Replicate 🔀 Remove 🕀 🖻 🗖
	Sample ID	Location	Method	Notes	
1	Sample 1	A1	Reduced IgG		
2	Sample 2	A2	Reduced IgG		
3	Sample 3	A3	Reduced IgG		
4	Sample 4	A4	Reduced IgG		
5	Sample 5	A5	Reduced IgG		
6	Sample 6	A6	Reduced IgG		
7	Sample 7	A7	Reduced IgG		
8	Sample 8	A8	Reduced IgG		
9	Sample 9	A9	Reduced IgG		
10	Sample 10	A10	Reduced IgG		
11	Sample 11	A11	Reduced IgG		
12	Sample 12	A12	Reduced IgG		

6. Compass for iCE can monitor the current during a separation for you, stop it if the current drops below the minimum value 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 158 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. In the Methods 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.

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

Methods						
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.

Name	Sample Load	Ad	d 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	4000

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 30 minutes. Run your non-reduced IgG samples and IgG Standard for 35 minutes. The default separation voltage for all sample types is 5750 volts.

		© Separation Profile
Sample Load	Separation	Add Remove
20 sec 4600 Volts	Voltage 1 Step	Time (min) Voltage (Volta)
20 sec 4600 Volts	35.0 min 5750 Volts	
20 sec 4600 Volts	30.0 min 5750 Volts	25.0000 5750
		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:
  - a. To add sample names: Click the Sample ID cell for the injection and type a name.

Injectio	ns 🛛 🔚 History 🔣 N	lotes			👉 Add 📊 Replicate 🧩 Remove 🕞 📄 🗖
	Sample ID	Location	Method	Notes	
1	Sample 1	A1	Reduced IgG		
2	Sample 2	A2	Reduced IgG		
3	Sample 3	A3	Reduced IgG		
4	Sample 4	A4	Reduced IgG		
5	Sample 5	A5	Reduced IgG		
6	Sample 6	A6	Reduced IgG		
7	Sample 7	A7	Reduced IgG		
8	Sample 8	A8	Reduced IgG		
9	Sample 9	A9	Reduced IgG		
10	Sample 10	A10	Reduced IgG		
11	Sample 11	A11	Reduced IgG		
12	Sample 12	A12	Reduced IgG		

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

Injections	📰 Injections 🔚 History 🎦 Notes 🕅 🖶 🖶 🗖 🗖									
	Sample ID	Location	Method	Notes						
1	Product A	A1	Non-reduced IgG 🛛 👻							
2	Sample 2	A2	Reduced IgG							
3	Sample 3	A3	Non-reduced IgG							
4	Sample 4	A4	MW Markers							
5	Sample 5	A5	Reduced IgG							
6	Sample 6	A6	Reduced IgG							
7	Sample 7	A7	Reduced IgG							
8	Sample 8	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				👫 Add 📗 Replicate 🔀 Remove 🕞 🖻 🗖
	Sample ID	Location	Method	Notes	Replicate selected injections
1	Product A	A1	Non-reduced IgG		
2	Product A	A2	Reduced IgG		
3	Product B	A3	Non-reduced IgG		
4	Product B	A4	Reduced IgG		
5	Product C	A5	Non-reduced IgG		
6	Product C	A6	Reduced IgG		
Injections	🔛 History 🌃 Notes				🚰 Add 📗 Replicate 🔀 Remove 📑 🖻 🗖 🗖
	Sample ID	Location	Method	Notes	
1	Product A	A1	Non-reduced IgG		
a 2	Product A	A2	Reduced IgG		
3	Product A	A2	Reduced IgG		
4	Product B	A3	Non-reduced IgG		
5	Product B	A4	Reduced IgG		
6	Product C	Δ5	Non-reduced InG		

• 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				📌 Add 📊 Replicate	🔀 Remove	
	Sample ID	Location	Method	Notes	Add injections		
1	Product A	A1	Non-reduced IgG				
a 2	Product A	A2	Reduced IgG				
3	Product A	A2	Reduced IgG				
4	Product B	A3	Non-reduced IgG				
5	Product B	A4	Reduced IgG				
6	Product C	A5	Non-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. Click on the **Notes** pane, then click in the notes area and type any information you want to add about your batch (optional).



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

er text	Advanced		⇔ ◄ ⇔
kers	Analysis Settings	Analysis Settings: Advanced	
k Fit k Names	Advanced	Standards	
		Peak Width	20
		Allowable Drift	100
	Add Remove		
	Advanced	•	
	Apply Override:		
	Apply To Settings		
	Add Remove		

- b. Change the parameters you want to, then click **OK**. For detailed information on analysis parameters, please refer to "Analysis Settings Overview" on page 244
- 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**.

or Save Batch Comment	×
Batch: Maurice CE-SDS2 Comment:	
	Save Cancel

14. Enter a name for your batch then click **Save**.

### Step 6: 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.



- 3. 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.
- 4. 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				×
Batch: Mauric	e CE-SDS			
5 1 5				Browse
Results file han				
2013-12-10_13	-21-49_Iviaurice CE-SDS	6 100 D 114 1		
Location: C:\I	Jsers\Administrator\Documents\Cor	npass for ICE\Runs\Mark		
Comment:				
	Cartridge			
	Turner CE CDC			
-	Type: CE-SDS	Batch Injection Limit :	48	
	Serial Number : 3151022198	Injections Remaining :	80	
	Schartfamber - SISISEEDS			
			Start	Cancel

- 5. If you don't want to save the file to the default Runs folder, click **Browse** to select a different location.
- 6. Enter any run details you'd like in the Comments box (optional).
- 7. 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 9, *"Run Status"* for more details.

Running	Sto	p	Tue 10:49 AM	Wed 9:39 AM	💾 Batch [ 🕌 Run Summary) 🐗 Analys
015-12-29_10-49-	14_37injectio	n-500ms_Cartric	ge-Validation_Day1	11-30-15_C3151201216_KF1010	
tions				🕑 Status 🔚 History	
Sample ID	Location	Method	Status	run 2015-12-29 10-49-14 37injection-500ms Cartridge-Validation Day1 11-30-15	C3151201216 KF1010
		Setun	Completed	nath	
MW ladder	AL	Method3	Completed	hatch 27injection 500ms Castridae Validation	
laG2B-R	81	Methodl	Completed	batch shinjection-soons_carthdge-vandation	
hSAP JoG-R	C1	Method1	Completed	batch type CE-SUS	
InG2B-NR	D1	Method2	Completed		
hSAP-loG-NR	E1	Method2	Completed	instrument Maurice : Maurice kf1010 - kf1010	
InG2R-R	81	Methodl	Completed	samples 96 well plate	
hSAP InG-R	CI	Method1	Completed	started Tue 10:49 AM Dec 29, 2015 PST	
InG2B-NR	D1	Method2	Completed		
hSAP-loG-NR	El	Method2	Completed		
MW ladder	A1	Mathoda	Completed		
laG2B-R	R1	Methodl	Completed	cartridge CE-SDS	
hSAD InG.R	(1	Method	Senaration	serial number 3151201216	
inger ide u		Condition	schengund	injections remaining 80	
InG2R-NR	DI	Method2		batches remaining 8	
hSAP-loG-NR	F1	Method2		evolves Dec 2016	
aG2R-R	R1	Methodl		expires Dec 2016	
ISAR InG.R	(1	Methodl			
LaC2D_NID	01	Mathod?		I Senaration Plot	
SAP-IoG-NP	E1	Method2		and the second	
MW ladder	41	Method3			Zoc
laG2R-R	RI	Method		hSAP IgG-R	
hSAP InG-R	CI	Methodl		22.	
InG2R-NR	01	Method2		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	
hSAP-InG-NR	FI	Method2		20	
laG2P.P	P1	Method		18	
gozo-n	0.4	Condition			
INSAR ING.R	(1	Methodi		16	
aG2R-NR	DI	Method2		14 -	
hSAP-loG-NR	EI	Method2		. 17	
MW ladder	Al	Method3		0.14	
laG2B-R	BI	Methodl		2 10	
hSAP InG-R	CI	Methodl			
InG2R+NR	DI	Method2		٢.	
hSAP-laG-NP	EL	Method2		6	
laG2B-R	BI	Methodl		4	
hSAP InG-R	CI	Method			
InG2R+NR	DI	Method2			
SAP.InG.NR	EL	Method2			
name igo nas		Condition			
MW ladder	41	Method2		2	
	-41	Hethods			
10000		Cleanup			

To view results, analyze results or change analysis parameters on completed injections while the batch is still running, click the **Analysis** tab. See Chapter 11, *"CE-SDS Data Analysis"* for more details.
Ru	unning	Stop	Tue 10:	49 AM		-							Wed 9:39	АМ	P Batch	ျို့ Run Su	mmary 🕼 A	nalysis
dards	Samples			- 0	Les Graph												8≓   ≡ [⊒	)
	ample	Location	Mathod	100								6					C. Contraction of the local data	
	NW Inddar	At	Method 2								-	~						_
T.	aG2R-R	P1	Method		35													
h	SAP InG-R	CI	Methodl		80									1.31				
E.	aG2R-NR	01	Method2		50									1				
h	CAD.InG.NP	61	Mathod2		1.1													
h	wG2R-R	RI	Methodl		40													
	SAD LIG.P	(1	Methodi		1												IgG28-R	
T.	AC2D-ND	01	Method?		40												16	
1	SAD LIG MP	E1	Methoda		221													
	Sale ago nen	41	Mathadi		35													
1	and souder	D1	Mathed															
1	gozo-n	01	Methodi		5 30													
	ISAP IGU-R	01	Methodi		Ne l													
19	GOZB-NR	01	Methodz		e 25							1						
n	SAP-Igu-NK	11	Methodz		en en													
1	guze-k	81	Methodi		8 20													
h	hanP lgts-K	C	Methodi		Abs									- 11				
I	g62B-NR	01	Method2		15									- 11				
h	hSAP-IgG-NR	EL	Method2		<u> </u>													
	MW ladder	AI	Method3		10.													
ł	gG2B-R	81	Methodl		10													
h	hSAP IgG-R	C	Method1		1.00													
ł	gG2B-NR	D1	Method2		5									11				
h	hSAP-IgG-NR	EI	Method2				٨		1			11						
1	gG2B-R	81	Method1		0		1/~											
h	hSAP IgG-R	CI	MethodI		122	$\sim$	V											
ł	gG2B-NR	D1	Method2		-5													
h	sap-lgG-NR	E	Method2		2001													
1	MW ladder	AI	Method3		-10													
h	IgG2B-R	61	MethodI		0.2	0.3	0.4	0.5	0.6 0.7	0.8	0.9	1.0	1.1 1.4	1.1	1.4	1.5	1.6 1.	e
h	hSAP IgG-R	CI	Methodl								Relative	e Migration I	ime					
Ig	gG2B-NR	D1	Method2		Peaks I	Injections												- 1
h	SAP-IgG-NR	El	Method2		111111111111111111111111111111111111111	• • • • • • • • • • • • • • • • • • • •												
I	igG2B-R	81	Methodl		Injection	Sample	Peak	Name	e Time	RMT	Height	Raw Area	Area	% Total	% Area	width	Baseline	Resolut
h	SAP IgG-R	CI	Methodl		6	lgG2B-R	1		1061.8	1.307	49.2	1385	1304.3	100.0		10.5	0.8	
le	igG2B-NR	D1	Method2															
h	hSAP-lgG-NR	El	Method2															
N	MW ladder	AI	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 383 for more info.

# **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 reagent vials and samples and discard.
- 3. 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.



- 4. Pull the cartridge insert out.
- 5. Remove the Top Running Buffer vial and dispose of it according to your institution's safety and waste disposal guidelines.
- 6. 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, the cartridge is at its limit. 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 you've still got injections left and the cartridge will be used again within 2 hours. You can leave the cartridge in Maurice. When you're ready to run the next batch, just replace the Top Running Buffer vial with a fresh one.

If you've still got injections left and the cartridge won't be used within 2 hours. Clean and store the cartridge:

- a. Pipette 1.5 mL of DI water in a new glass reagent vial and close it with an **orange pressure cap**. Place this vial in P3.
- 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. In the Compass main menu, select Instrument and click Cartridge Cleanup.



f. You'll get the following message. Click OK. It'll only take six minutes.



- g. Once the cleanup procedure is done, 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 three 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.

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#### 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.



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

File	Edit	View	Instrument	Window
Ħ	Stand	ards	🚊 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 Std 1 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	Injections				Experime	ent		
Injection	Sample	Peak	Time	Height	Injection	Sample	Location	Method
1	Sample 1	11	548.2	115.1	<b>Ø</b> 1	Sample 1	A1	Method1
1	Sample 1	12	557.7	115.2	2	Sample 1	A1	Method1
1	Sample 1	13	572.0	134.0	3	Sample 1	A1	Method1
1	Sample 1	14	583.5	149.7	4	Sample 1	A1	Method1
<b>≜S</b> 1	Sample 1	15	590.6	190.0	5	Sample 1	A1	Method1
1	Sample 1	16	710.8	230.3	6	Sample 1	A1	Method1
1	Sample 1	17	714.6	278.5	7	Sample 1	A1	Method1

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.



An **S** with a red slash through it will appear next to the incorrectly assigned 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				Experime	ent		
ijection	Sample	Peak	Time	Height	Injection	Sample	Location	
1	Sample 1	11	548.2	115.1	<b>V</b> 1	Sample 1	A1	
1	Sample 1	12	557.7	115.2	2	Sample 1	A1	
1	Sample 1	13	572.0	134.0	3	Sample 1	A1	
1	Sample 1	14	583.5	149.7	4	Sample 1	A1	
<b>S</b> 1	Sample 1	15	590.6	190.0	5	Sample 1	A1	
1	Sample 1	16	710.8	230.3	6	Sample 1	A1	
<b>S</b> 1	Sample 1	17	714.6	278.5	7	Sample 1	A1	
1	Sample 1	18	869.0	737.9				

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 240 kDa.

To get MW data:

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



 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.

e filter text	Markers						🔶 🔹 🔿
Advanced	A 1 1 6 10		Markers				
Deals Eit	Analysis Settings		_				
Peak Names	Standards		Interna	al Standard	Time 750	Seconds	
			Marke				
			IVIarke	rs injection	no markers		
			MW	RMT	1		
			10	1	3		
	Add	Remove	20	1.15	4		
			33	1.3	5		
			55	1.5	7		
	Apply Default:		103	1.8	8		
	Standards		• 178	2.15	9	-	
	Apply Override:		240	2.2	10		
	Apply To	Settings			12		
	Sample	Standards			14		
					16		
					17		
					18		
					20	emove	
					21		_
			· · · · · ·		22		
	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.

MW	RMT	
15	1	
20	1.15	
33	1.3	
55	1.5	
103	1.8	
178	2.15	
240	2.2	

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.

Experime	ent		- 0
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	ent		
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 **Single View** 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.

ĺ	Experime	int		- 8		
	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		
	<b>√</b> 10	Sample 1	A1	Method1		
	11	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.

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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			
<b>√</b> 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 "Peak Names Settings" on page 354.

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