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

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

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Let's Get Started

Chapter Overview

- Welcome
- Maurice Systems

Welcome

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

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

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

Maurice Systems

Maurice, Maurice C. 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 cIEF and CE-SDS**. They take cIEF up a notch, and CE-SDS is a breeze. You'll get pI and charge heterogeneity data in less than 10 minutes flat — with the added bonus of same-time absorbance and native fluorescence for sensitivity down to 0.7 µg/mL. Their size applications have the high res and wide molecular weight range you need and they're done in 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.

Chapter 2:

Getting Your Lab Ready

Chapter Overview

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

Introduction

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

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

Space Requirements

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

IMPORTANT

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

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

Recommended space requirements for Maurice.

Physical Specifications

Description	Specification
Maurice's Dimensions (Door Closed)	0.44 m x 0.42 m x 0.61m (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.

Chapter 3:

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.

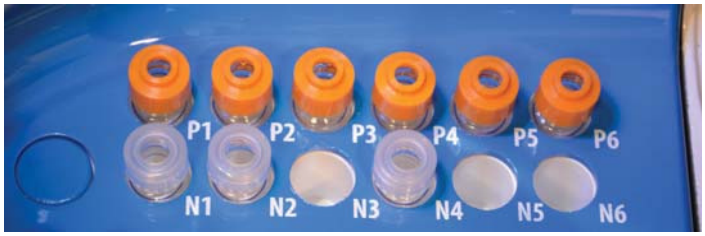
The lights change to **blue** once a cartridge is installed correctly.

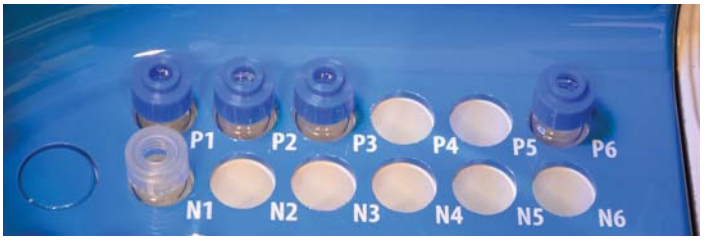
NOTE: You can find cartridge prep, installation and post-run procedures in Chapter 7, "Running cIEF Applications on Maurice and Maurice C." and Chapter 8, "Running CE-SDS Applications on Maurice and Maurice S."

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.

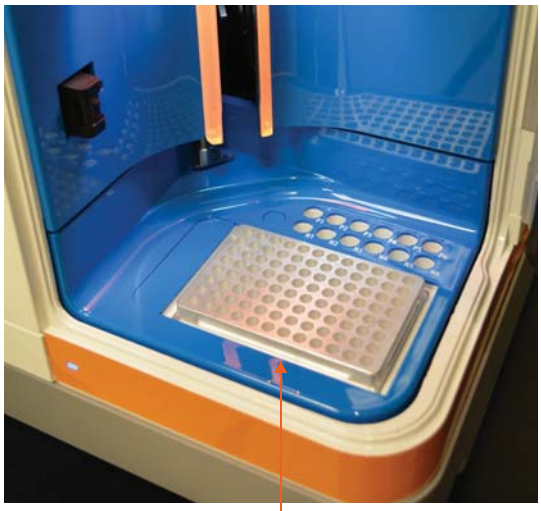




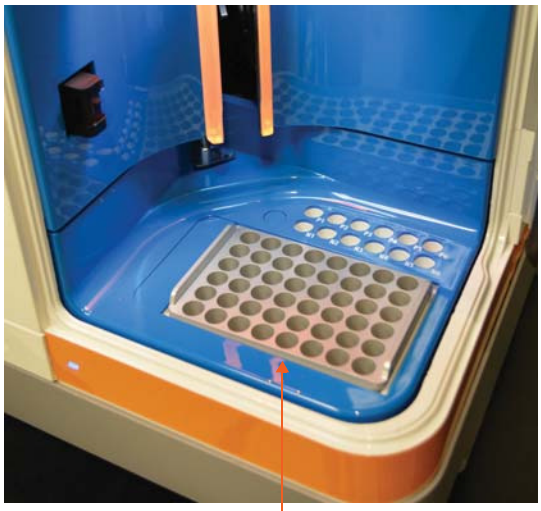
The sample block holds either a 96-well plate or 48-vial metal insert and is temperature-controlled. You can set it to 4 °C, 10 °C, 15 °C or turn the temperature control off in Compass for iCE software.

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.



96-well Plate Insert



48-vial Insert

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

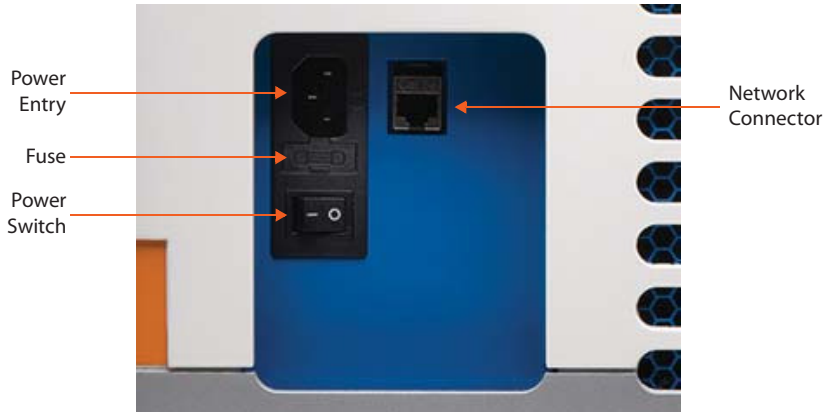
You can only use V-bottom plates with the 96-well plate insert.

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

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!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.

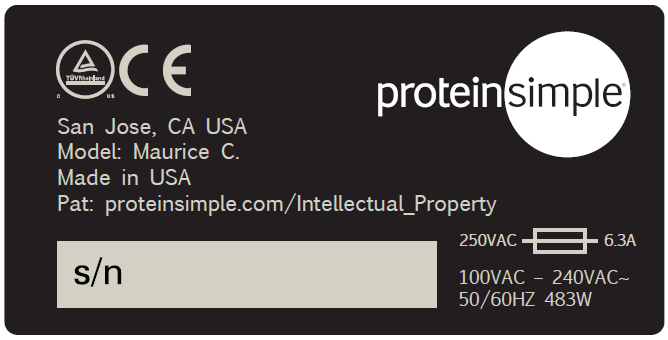
!WARNING! SHOCK HAZARD
Disconnect the power cord from Maurice's power input to disconnect power to the instrument.

- **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

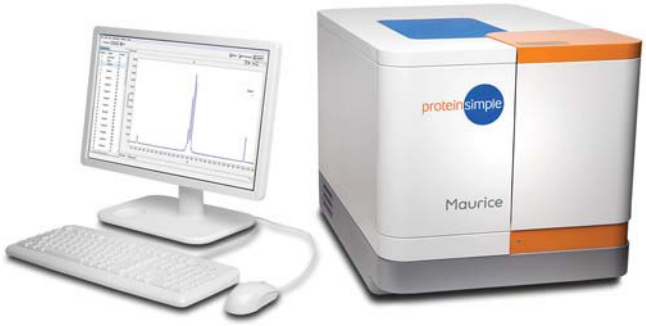
A full system label is located on the rear panel. It includes the ProteinSimple location, system model, power requirements, serial number and certification markings.



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

Launching Compass for iCE

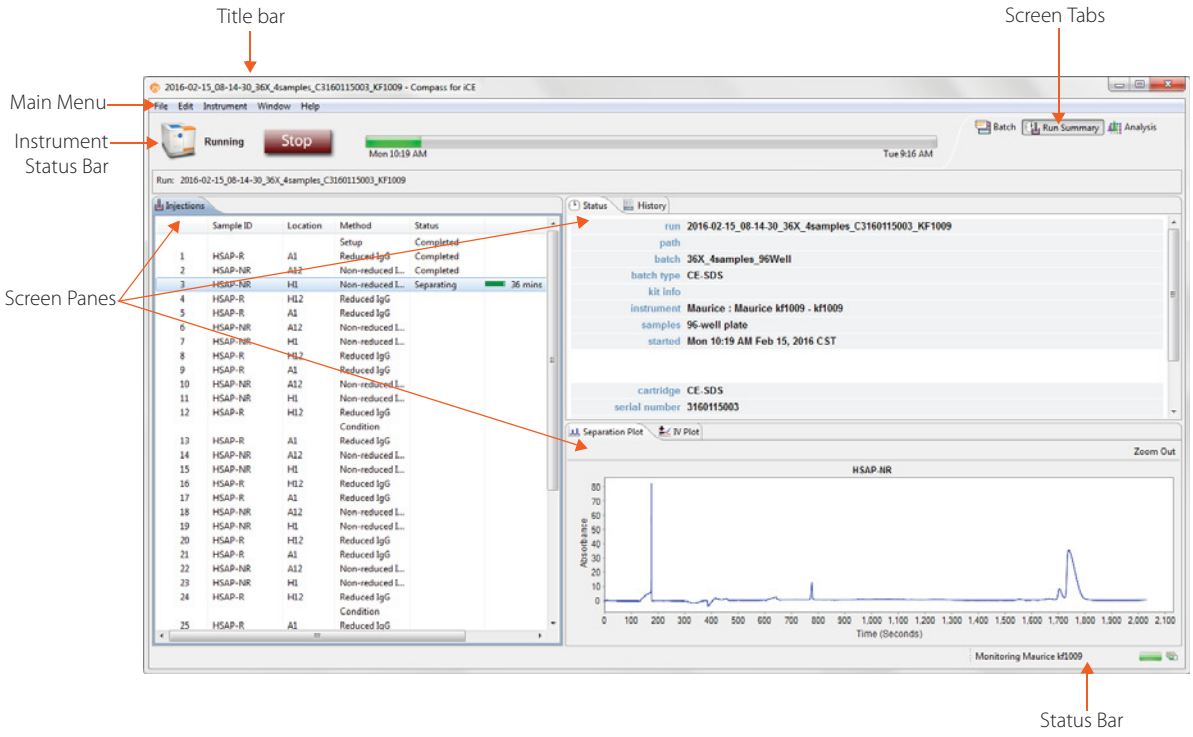
To open Compass for iCE, just double-click the icon on the computer desktop.

Compass for iCE Overview

Compass for iCE has three main screens:

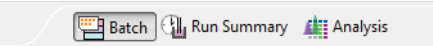
- **Batch** - You'll create and review your batch.
- **Run Summary** - Check out the status of your run.
- **Analysis** - Take a look at the data from your experiment.

Each screen has these components:



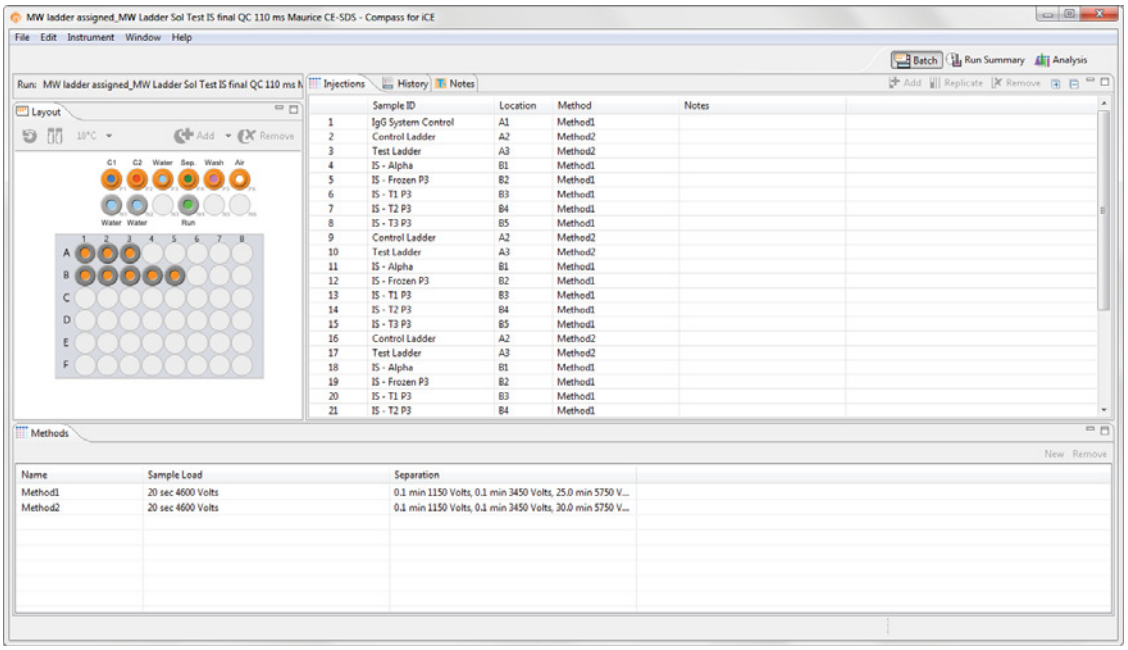
Changing the Screen View

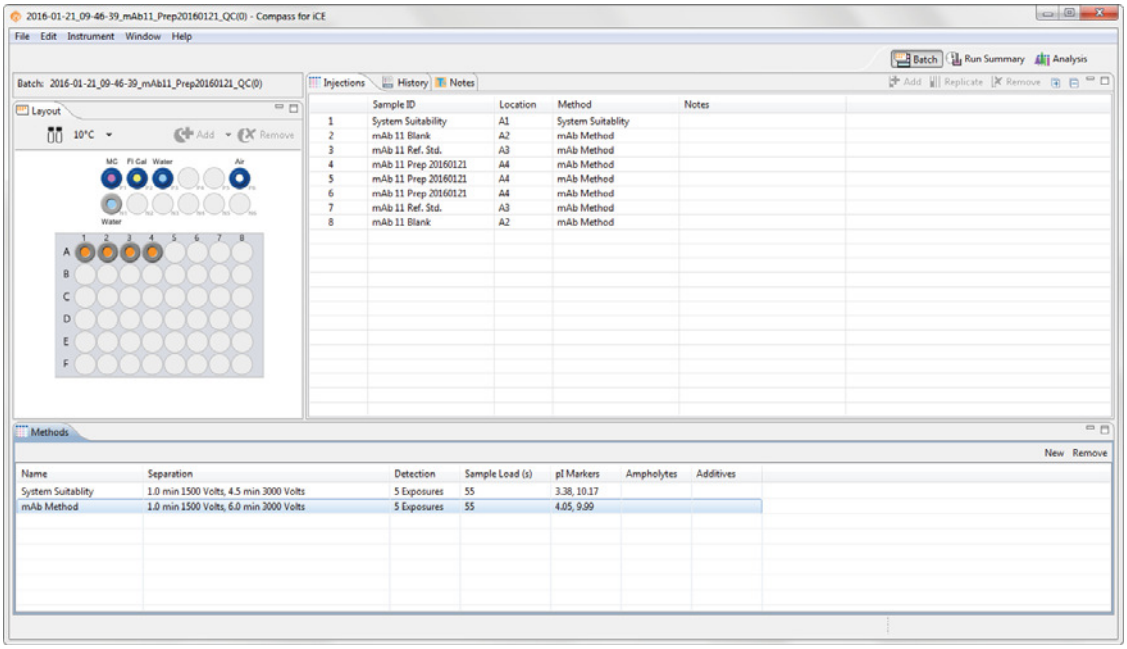
To toggle between the Batch, Run Summary and Analysis screens, just click the button in the screen tab located in the upper right corner of the main window.



Batch Screen

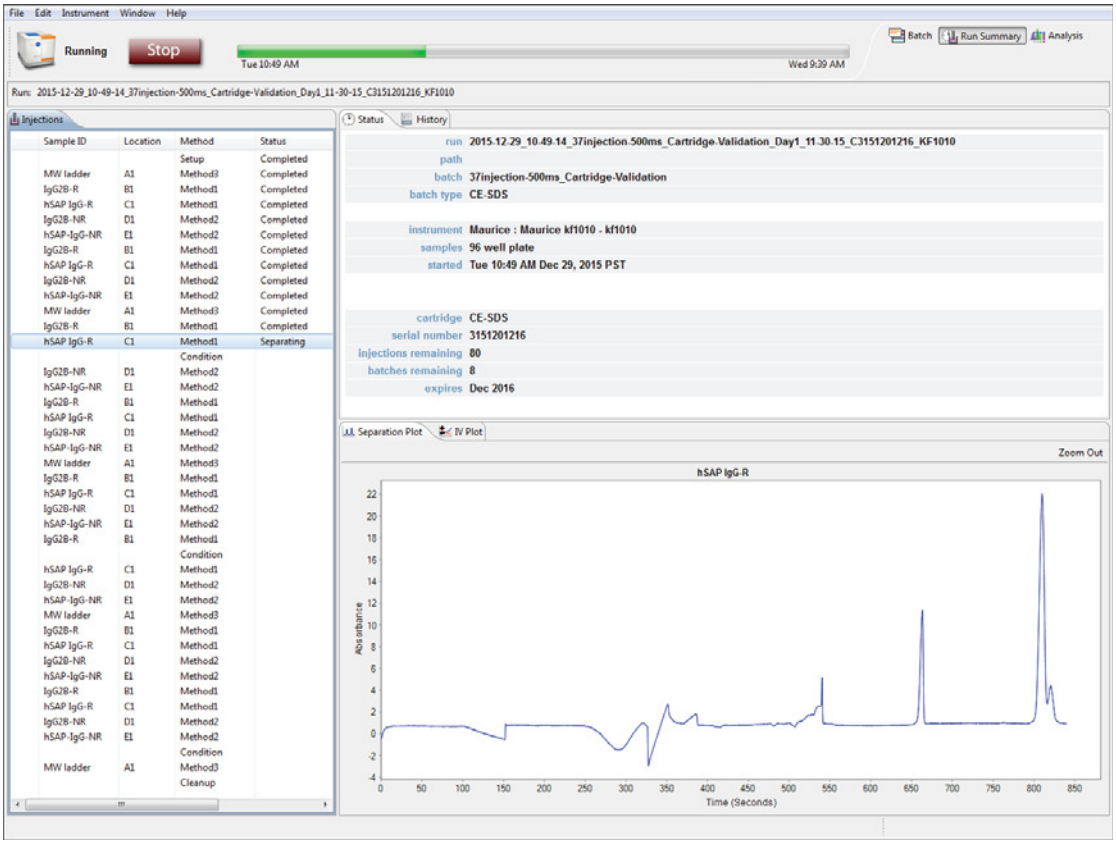
The Batch screen is used to create, view, and edit batches. You can assign samples to 96-well plate wells or vials, create and modify methods, customize your injection list and assign methods to each of your injections.

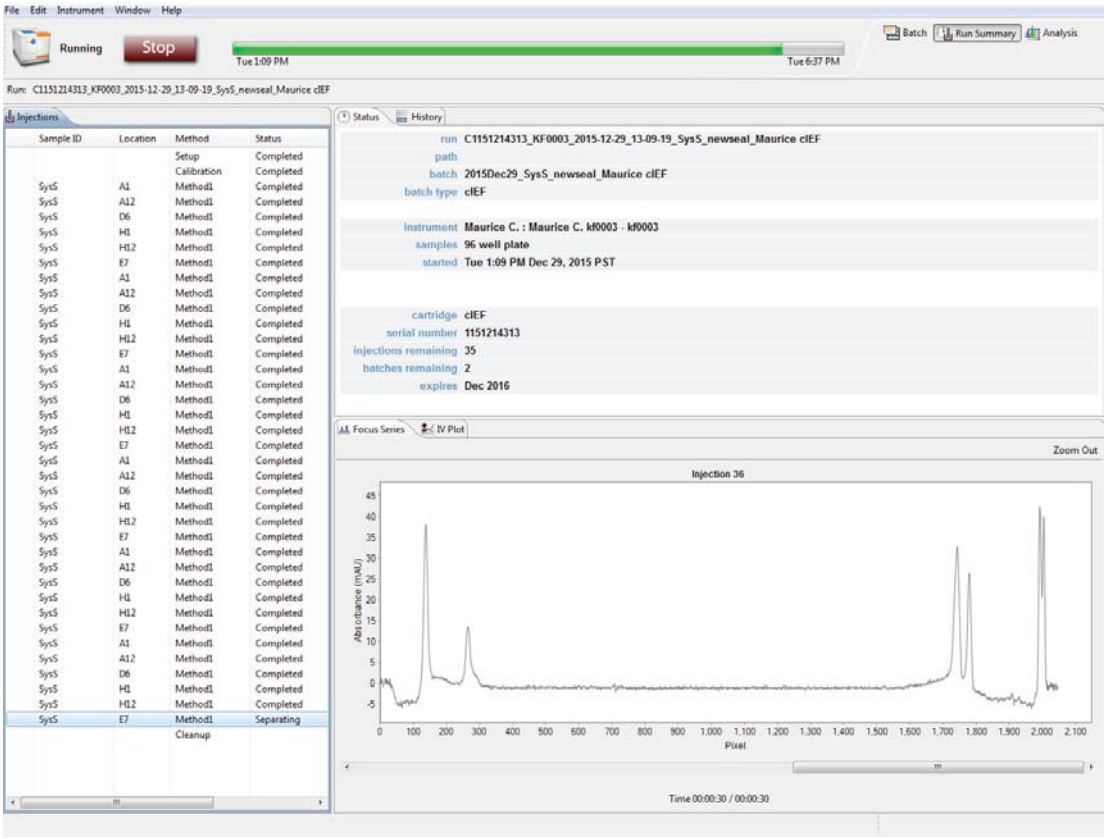




Run Summary Screen

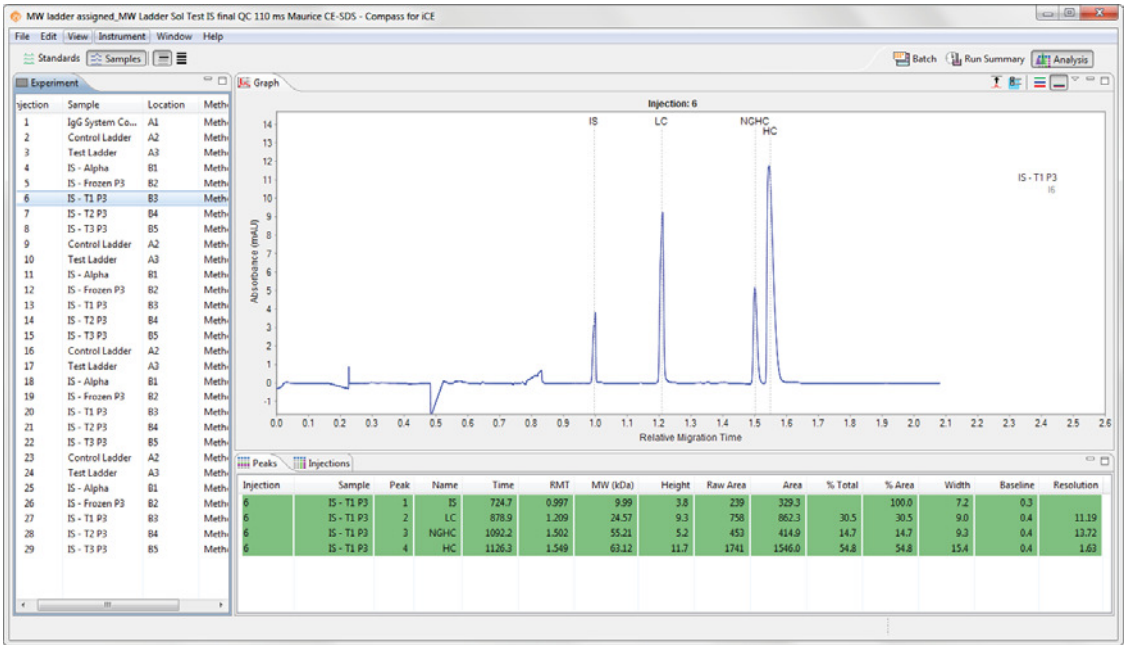
The Run Summary screen is used to monitor status of a batch in progress, the CE-SDS separation or cIEF Focus series for each injection and the current and voltage plots for each injection.

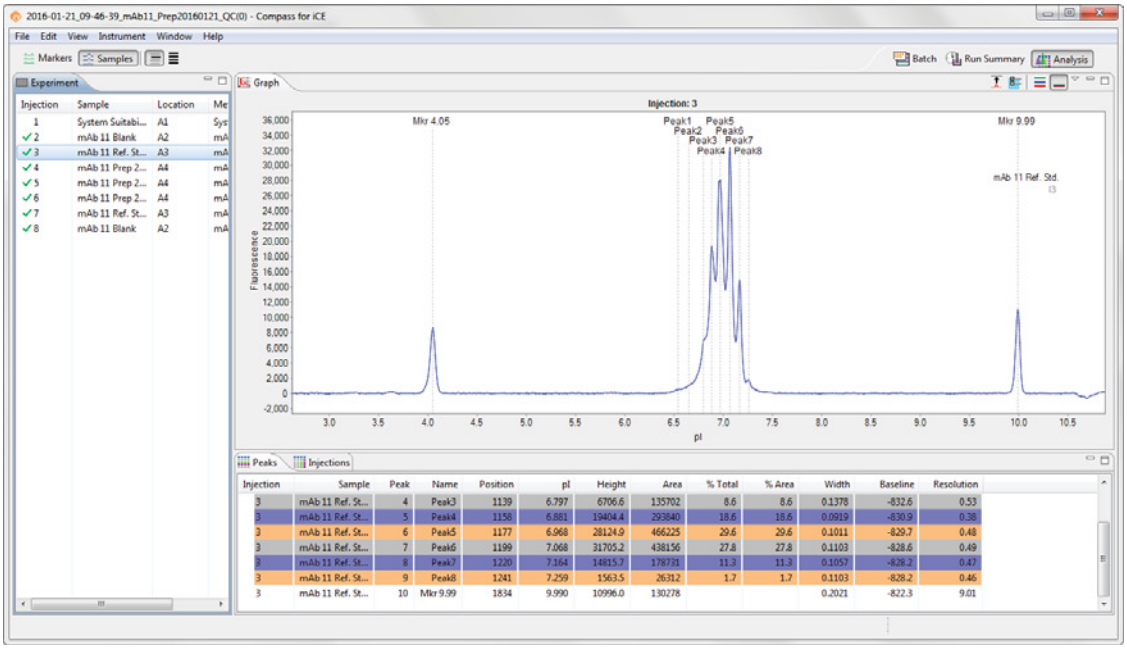

File Edit Instrument Window Help
Running
Stop
Tue 10:49 AM
Wed 9:39 AM
Batch
Run Summary
Analysis
Run: 2015-12-29_10-49-14_37injection-500ms_Cartridge-Validation_Day1_11-30-15_C3151201216_KF1010
Injections
Sample ID Location Method Status
Status
History
run 2015.12.29_10.49.14_37injection.500ms_Cartridge.Validation_Day1_11.30.15_C3151201216_KF1010
path
batch 37injection-500ms_Cartridge-Validation
batch type CE-SDS
instrument Maurice : Maurice kf1010 - kf1010
samples 96 well plate
started Tue 10:49 AM Dec 29, 2015 PST
cartridge CE-SDS
serial number 3151201216
injections remaining 80
batches remaining 8
expires Dec 2016
Separation Plot
IV Plot
Zoom Out
hSAP IgG-R
Absorbance
Time (Seconds)



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.

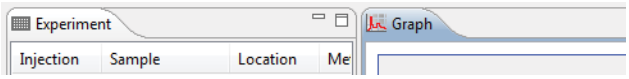

MW ladder assigned_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS - Compass for iCE
File Edit View Instrument Window Help
Standards Samples
Batch Run Summary Analysis
Experiment
Graph
Injection: 6
IS
LC
NGHC
HC
IS - T1 P3
Absorbance (mAU)
Relative Migration Time
Peaks Injections


2016-01-21_09-46-39_mAb11_Prep20160121_QC(0) - Compass for iCE
File Edit View Instrument Window Help
Markers Samples
Batch Run Summary Analysis
Experiment
Graph
Injection: 3
Mkr 4.05
Peak1 Peak5
Peak2 Peak6
Peak3 Peak7
Peak4 Peak8
Mkr 9.99
mAb 11 Ref. Std.
Fluorescence
pI
Peaks Injections

Screen Panes

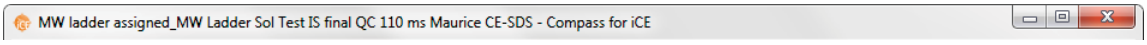
Each of the Batch, Run Summary and Analysis screens have multiple panes that let you view the individual components of a batch, method or data file. Each pane has a labeled tab and a unique icon. We'll describe panes specific to each screen later in the individual screen sections.

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:



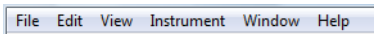
Title Bar

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.



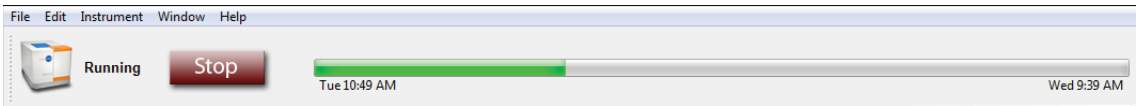
Main Menu

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.



Instrument Status Bar

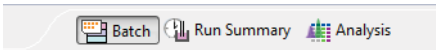
The instrument status bar is used to start batches and cleaning protocols, indicate system status and show run progress. More details on instrument control and status can be found in Chapter 10, *"Controlling Maurice, Maurice C. and Maurice S."*.



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

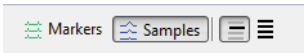
Screen Tab

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



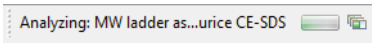
View Bar

The view bar is only displayed in the Analysis screen as part of the main menu, and allows you to switch between viewing standards or sample data, 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.



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.

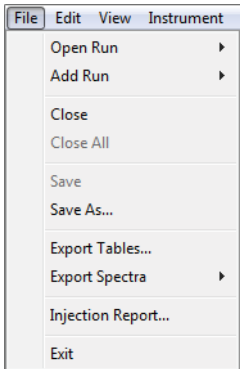


Software Menus

Some of the items in the Compass for iCE main menu are available in specific screens only, and menu commands change depending on which screen is active. You can find menus and commands available for each screen in the Chapter 5, *"cIEF Batches"*, Chapter 6, *"CE-SDS Batches"*, Chapter 9, *"Run Status"*, Chapter 12, *"cIEF Data Analysis"* and Chapter 11, *"CE-SDS Data Analysis"*.

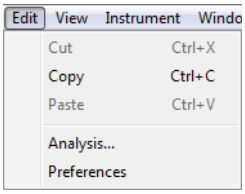
File Menu

The File menu contains basic file commands.



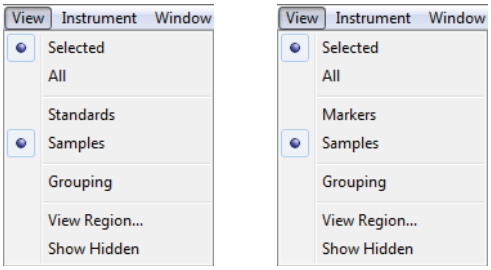
Edit Menu

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



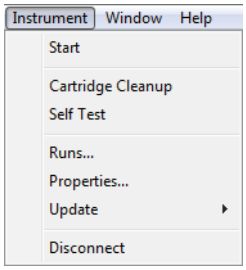
View Menu

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.



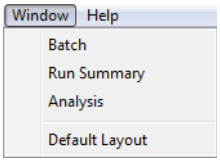
Instrument Menu

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."*



Window Menu

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

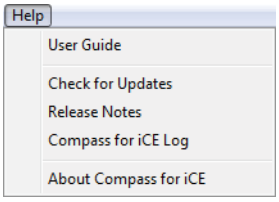


- **Batch** - Displays the Batch screen where you create, view, and edit batches.

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

Help Menu

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



- **User Guide** - Displays the User Guide for Maurice, Maurice C. 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

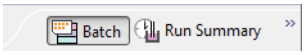
You can easily resize the main window and the individual panes in each screen. Screen panes can also be moved outside of the main window.

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.

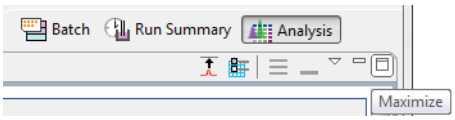
Resizing the Screen Tab

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.

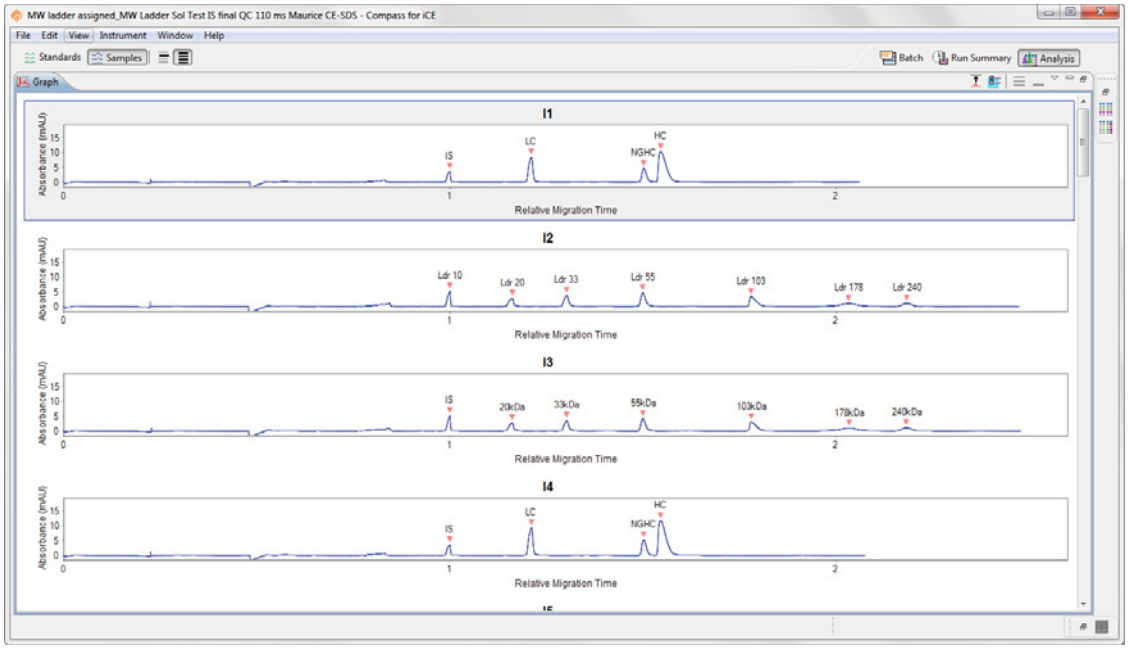


Resizing Screen Panes

- **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.

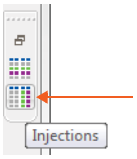


The other panes in the screen will automatically minimize to pane bars in the task area along the window border.

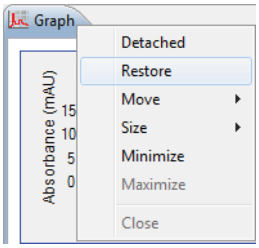


- **To restore all minimized panes** - Click **Restore** on the minimized pane bar.

- **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.

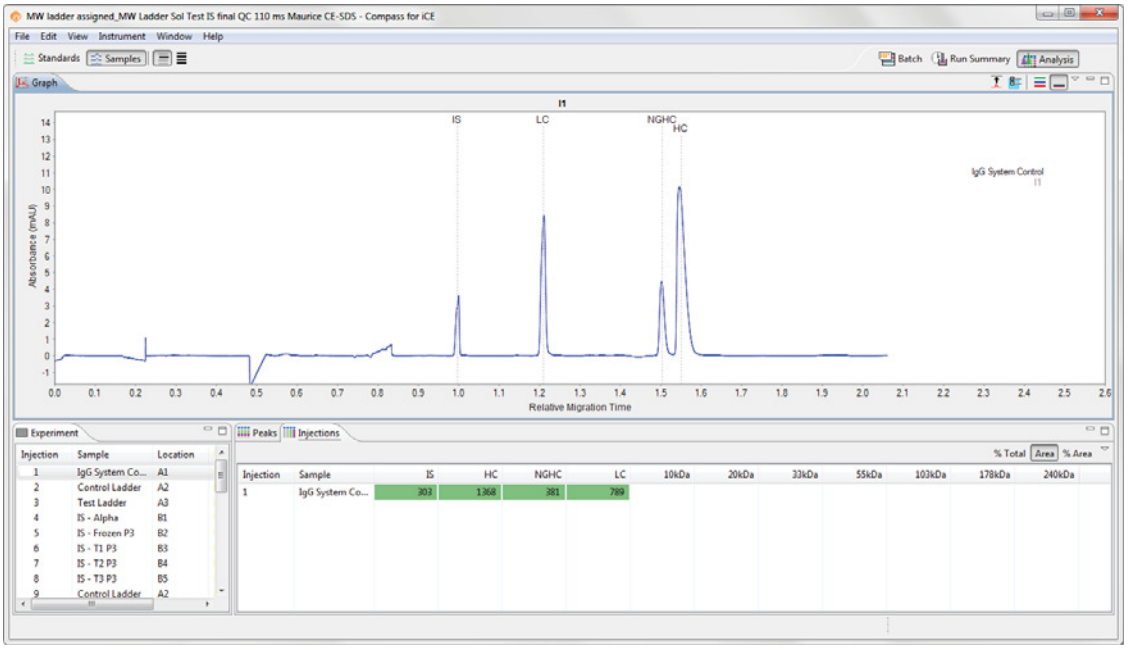
- **To move a pane** - Click on its tab and drag it to the new location. As the pane is moved, area guides will display to assist you in choosing a drop location.

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.

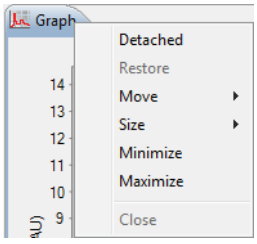
Area guides with a folder let you know that if the pane is dropped at that location, it will be added as a new tab in an area with one or more pane tabs.

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

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



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



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

Restoring the Main Window to the Default Layout

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

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.

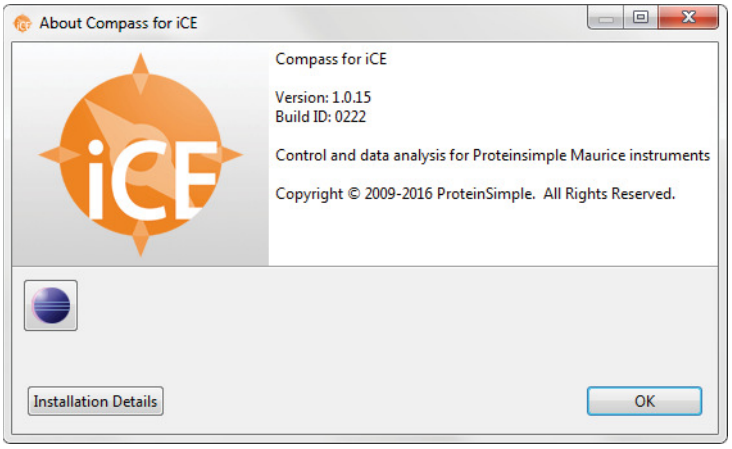
NOTE: You can contact ProteinSimple Technical Support to request the release notes for new versions of Compass for iCE before you install it.

Viewing the Software Log

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

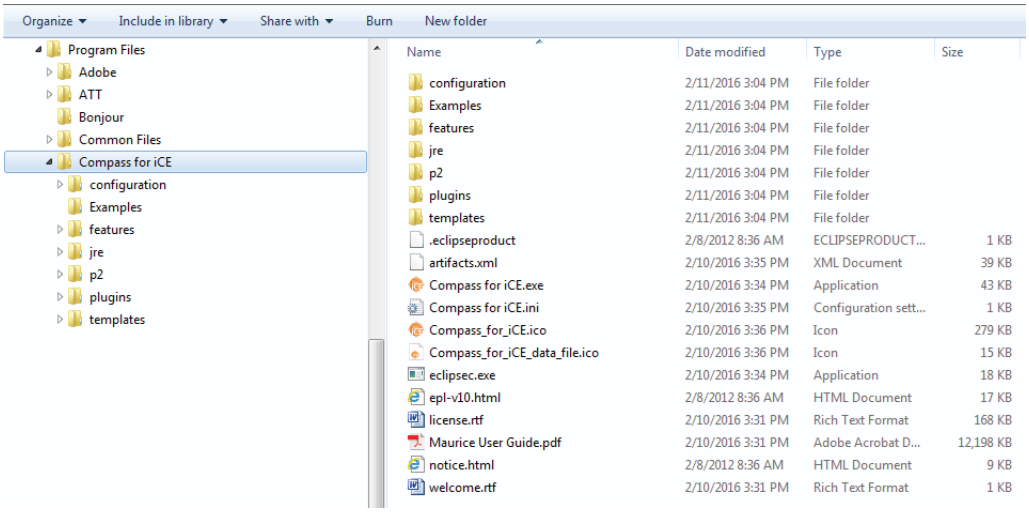
Compass for iCE Version Information

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

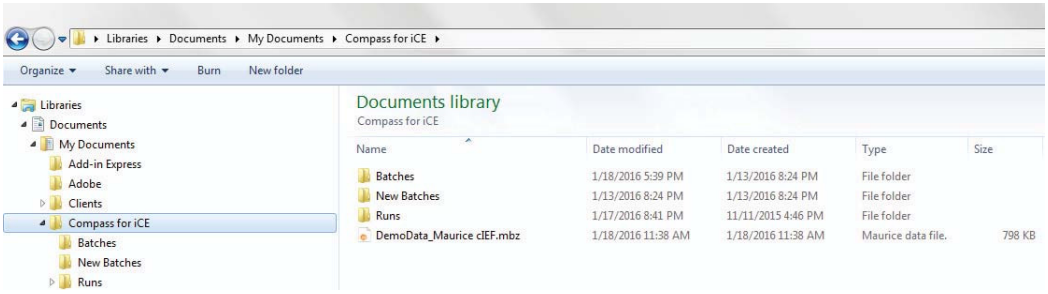


Directory and File Information

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.



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



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

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

File Types

These file types are used by Compass for iCE:

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

Chapter 5:

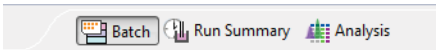
cIEF Batches

Chapter Overview

- 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

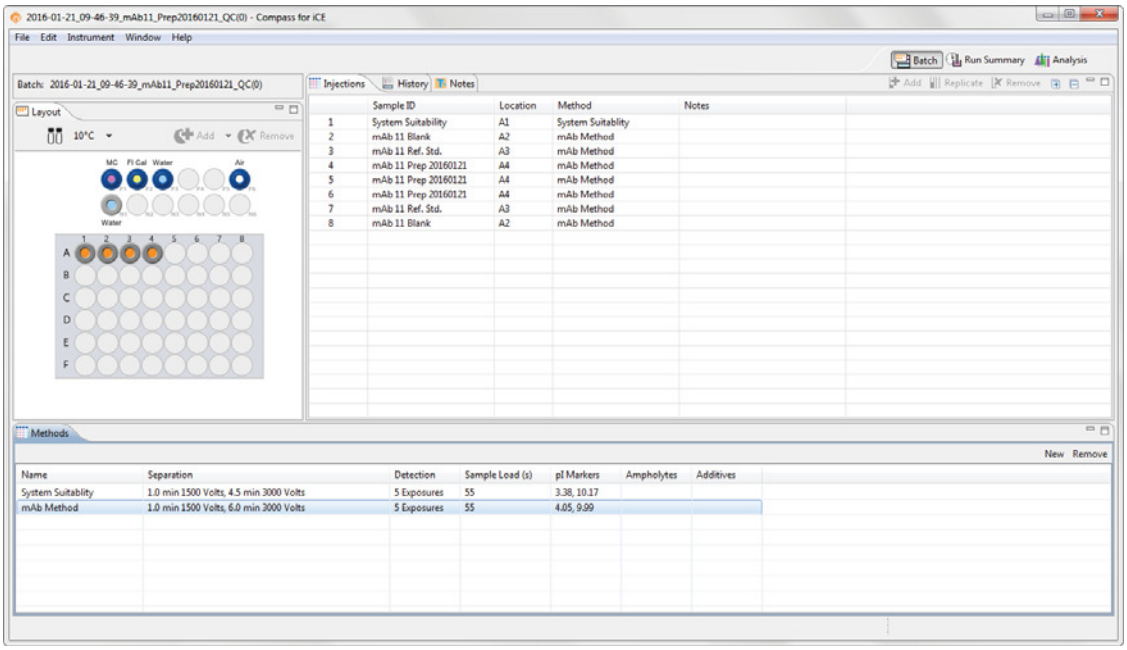
You can use the Batch screen to create, view, and edit batches. To get to this screen, click the **Batch** screen tab:



Batch 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.



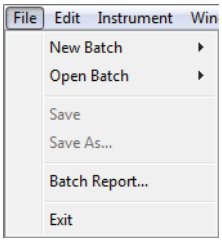
Software Menus Active in the Batch Screen

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

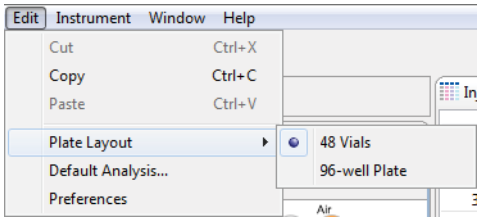
These File menu options are active:



- **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.

Edit Menu

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



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

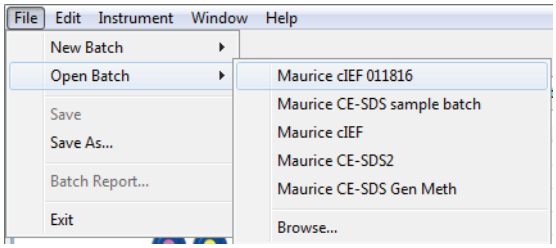
NOTE: Cut, Copy and Paste work differently depending on the pane you're in. How and when you can use them is described throughout the chapter.

- **Plate Layout** - 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**.



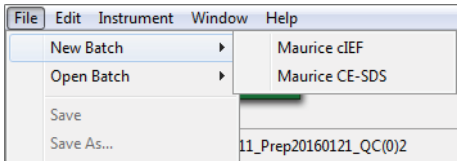
2. A list of the last five batches opened will display. Select one of those or click **Browse** to open the Batches folder and select a different one.
3. To make changes to the batch, see the steps in "Creating a New Batch" on page 42. When you're done, select **File** from the main menu and click **Save**.

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**:



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

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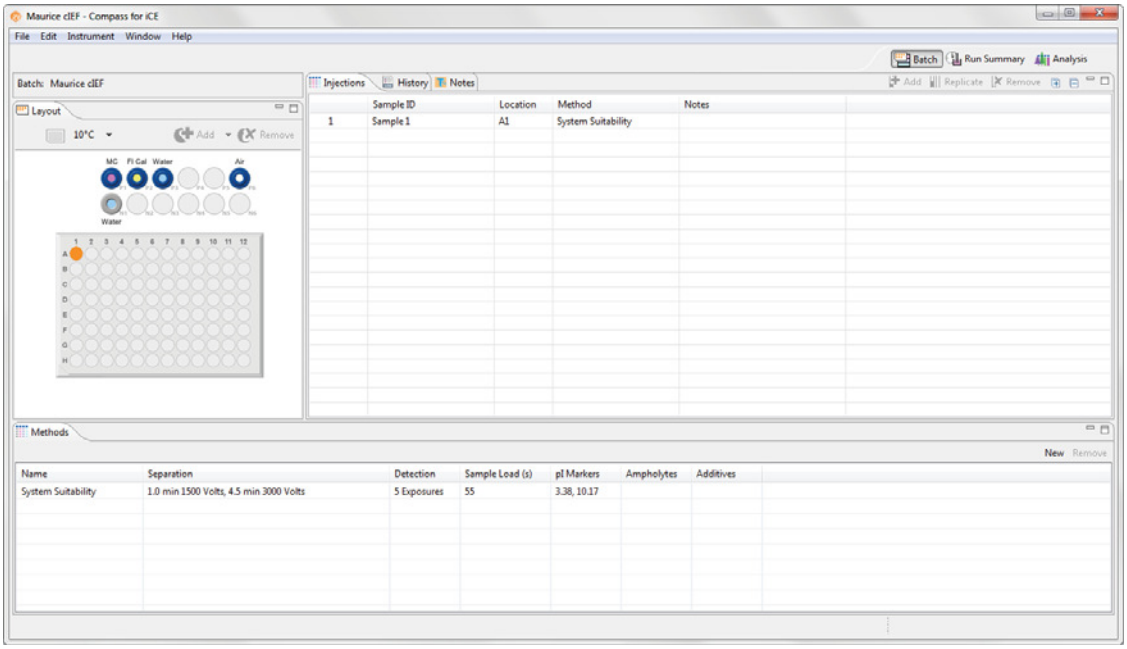
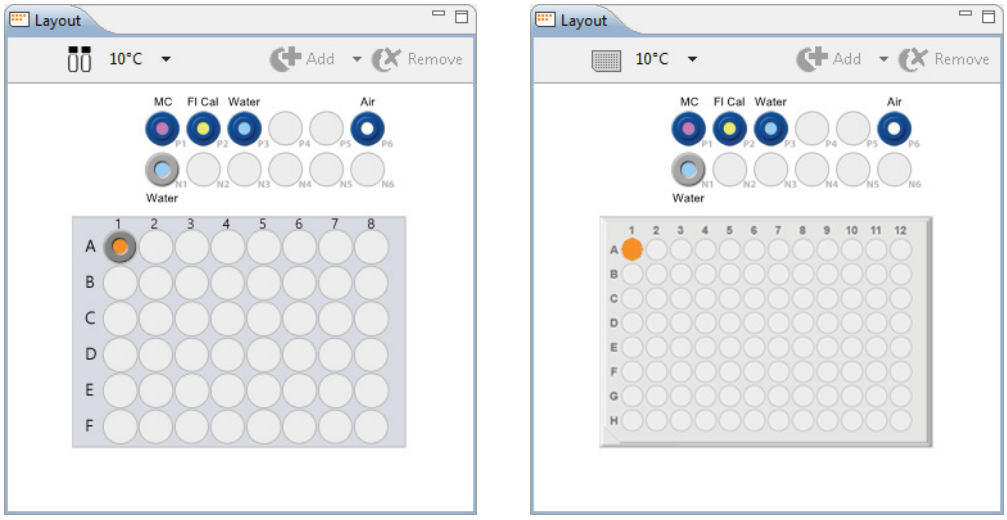
2. Select **Maurice cIEF**. A batch using the default method will display.



Step 2 - Assign Your Samples

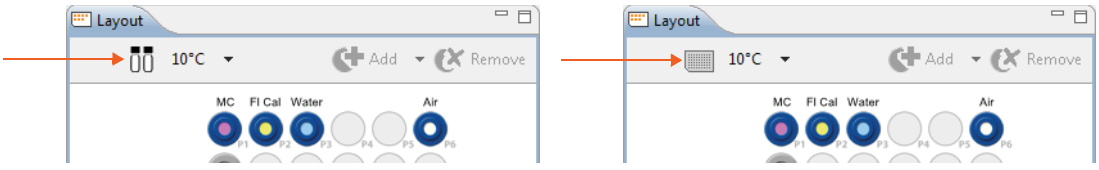
The Layout pane shows the default locations of where batch reagent should be placed in your Maurice system's samples and reagents platform, and a map of either the 96-well plate or the 48-vial tray used for samples.



The same reagent locations are used for every batch:

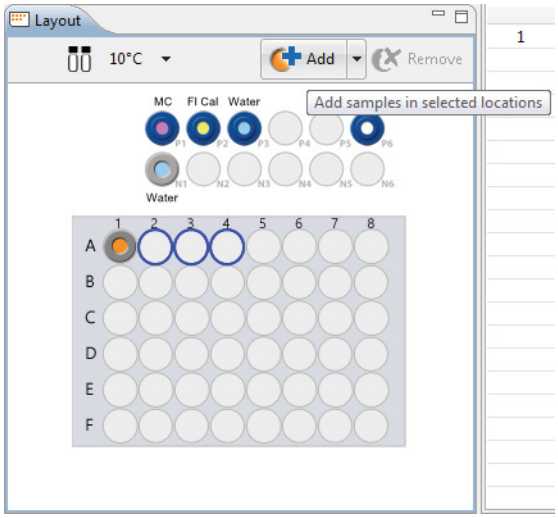
- **P1** - 0.5% Methyl Cellulose with **blue pressure cap**
- **P2** - Fluorescence Calibration Standard with **blue pressure cap**
- **P3** - Water vial with **blue pressure cap**
- **P6** - Empty vial (air) with **blue pressure cap**
- **N1** - Water vial with **clear screw cap**

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.

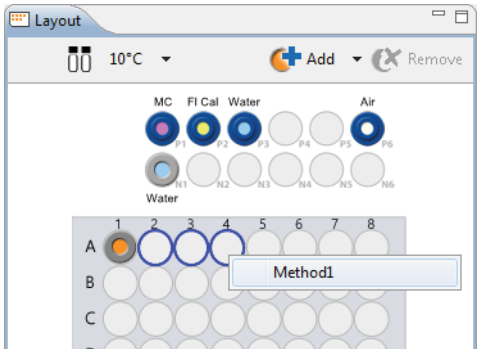


2. To select samples:
   - **Add samples and select methods later:** Use your mouse to highlight the well or vial positions your samples are located in, then click **Add**. For this example we're using vials.

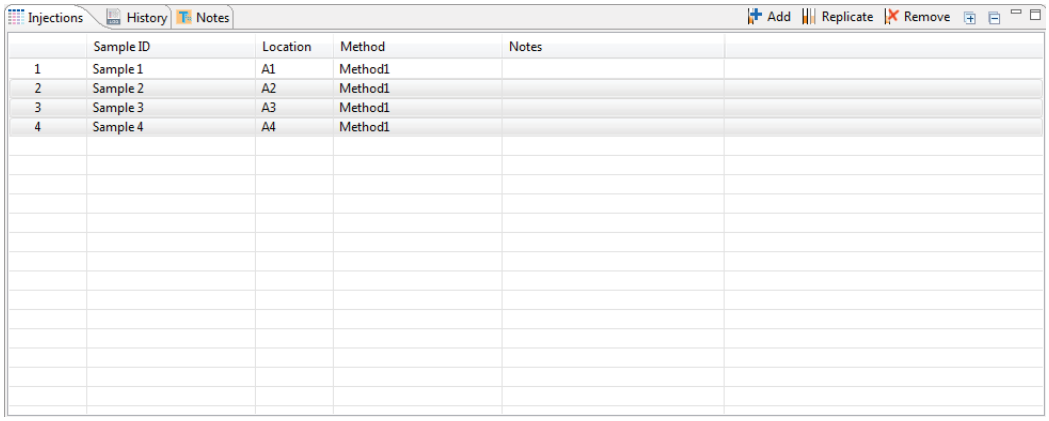
NOTE: The template batch automatically adds a sample in well or vial A1 by default, but if you don't have a sample in this position you can remove it after you've added new positions for your samples.



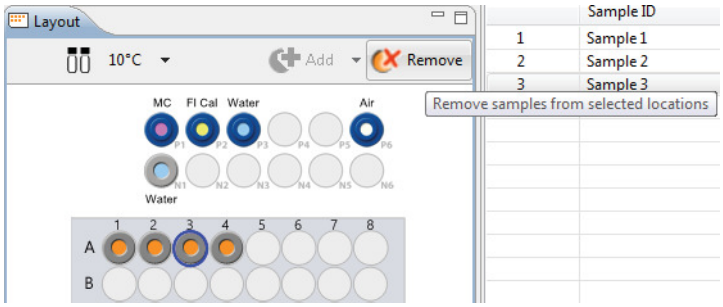
- **Add samples with preassigned methods:** Highlight the well or vial positions your samples are located in, then right-click and select a method.



Either option of adding samples populates the Injections table:

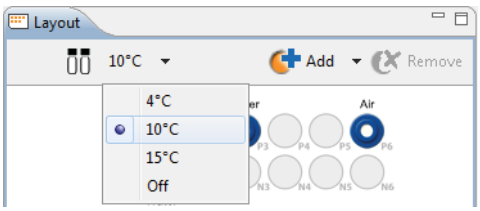


To remove samples, just highlight the ones you want to remove and click **Remove**. They'll also be removed in the Injections table. You can also right-click well(s) or vial(s) in the Layout pane and click **Remove Sample(s).**



3. 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.

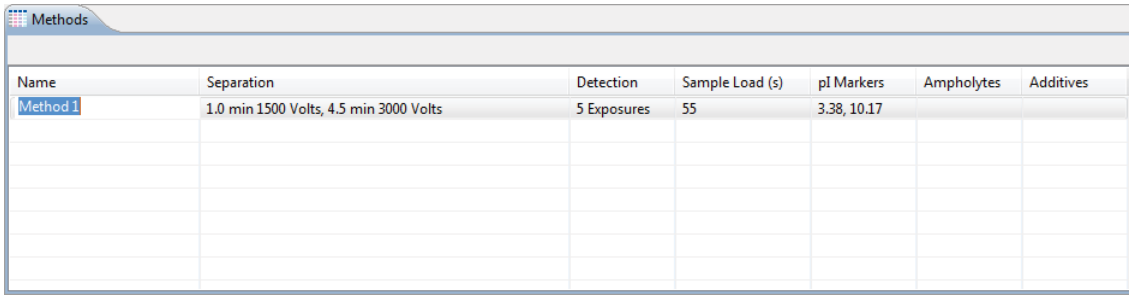


Step 3 - Assign Your Method Parameters

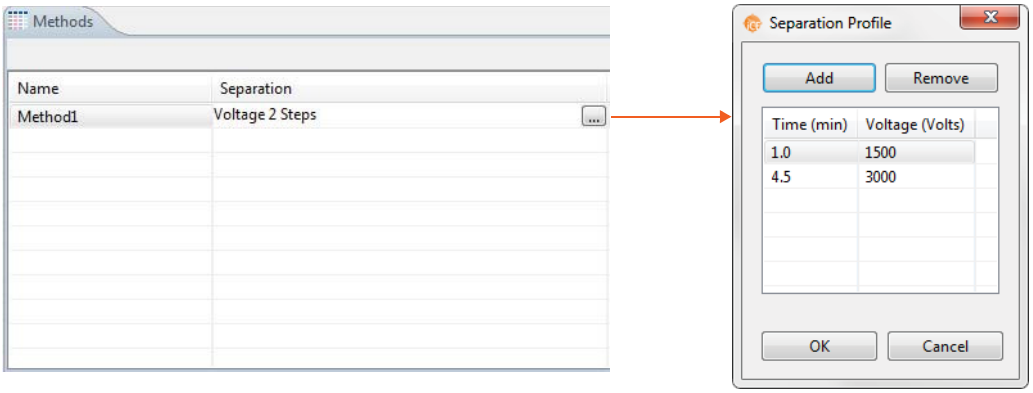
NOTE: We recommend using the default method parameters. Please see the Maurice cIEF Method Development Guide for more information on method optimization.

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.

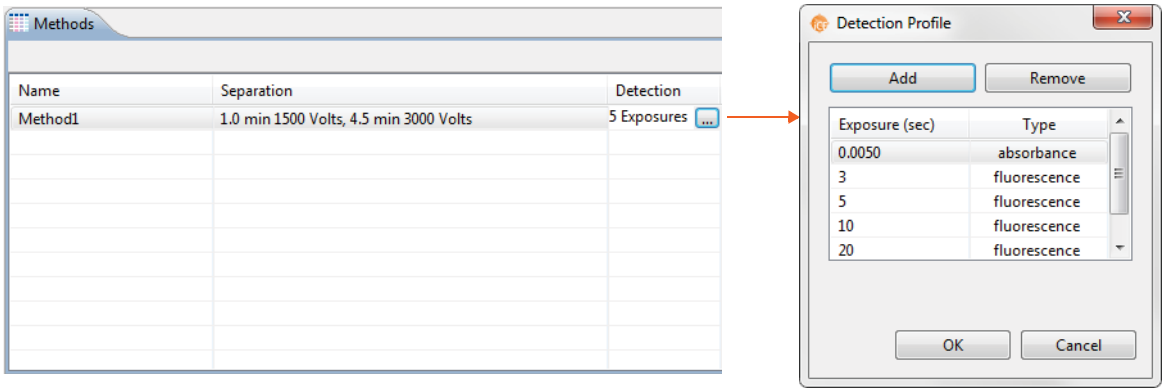


2. Click the first cell in the Separation column, then click the selection button **[...]** to set the pre-focusing and focusing time (in minutes) and voltage (V).



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

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



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

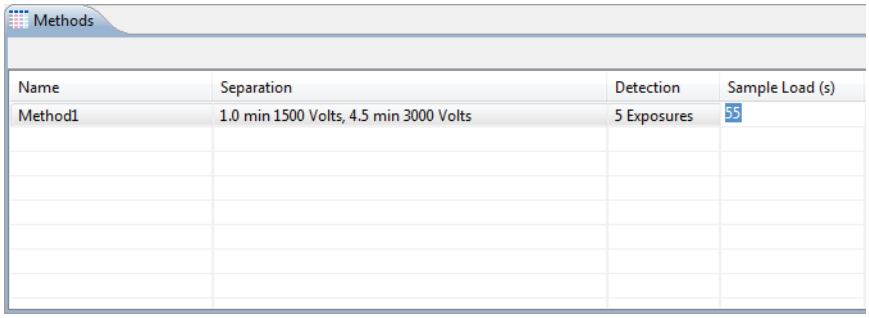
NOTES:
The first exposure is an instrument default setting and can't be changed.

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**.

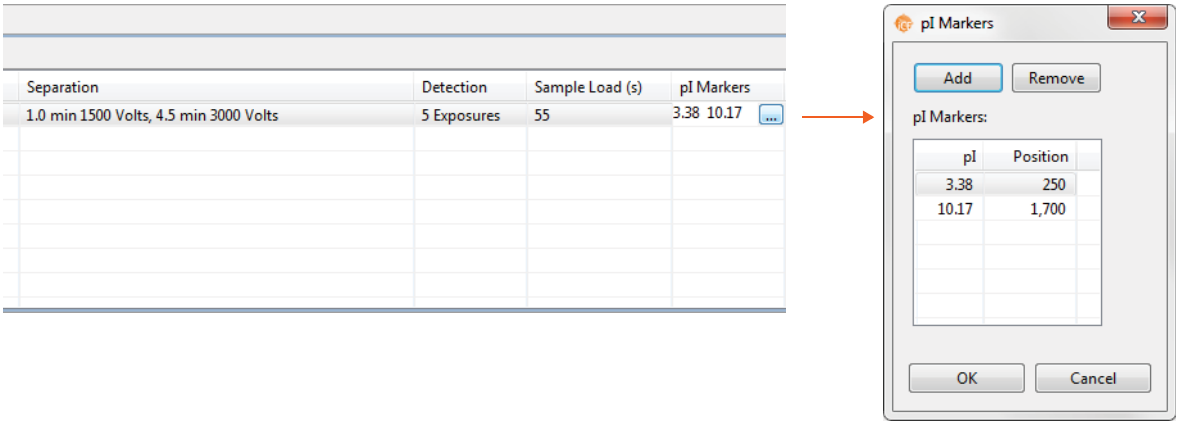
4. Click the first cell in the Sample Load(s) column and set the load time in seconds.

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.



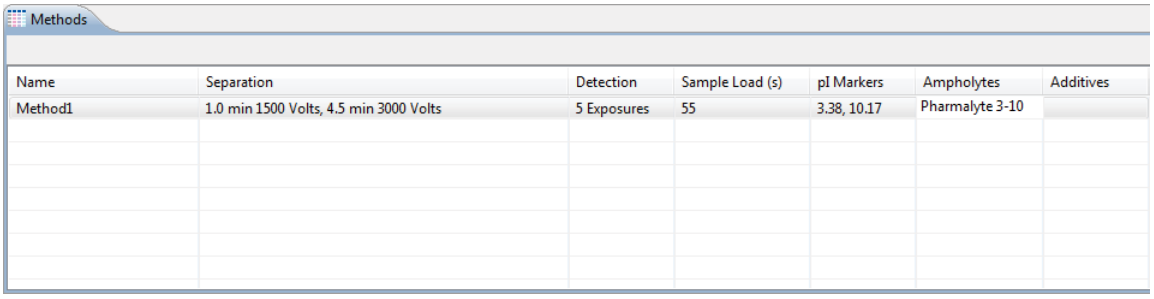
5. Click the first cell in the pI Markers column to select pI markers. Add new markers or remove existing ones then click **OK**.

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

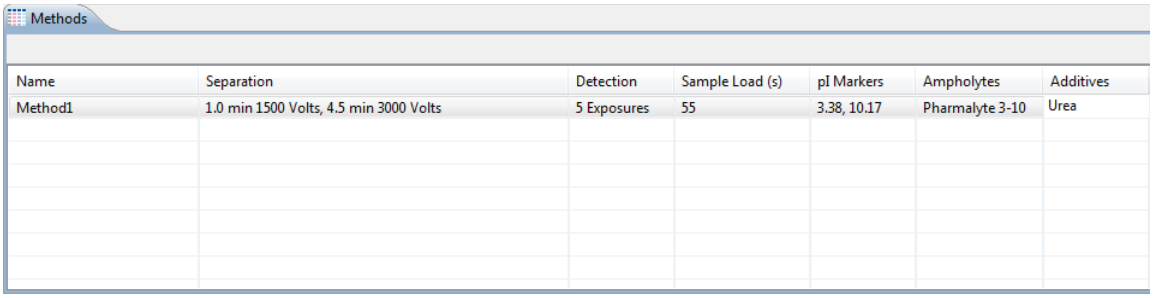


- **To add a pI marker:** Click **Add**. A new row will be added in the table. Then just type in a pI and a position (in pixels).
- **To remove a pI marker:** Select the row you want to remove and click **Remove**.

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



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

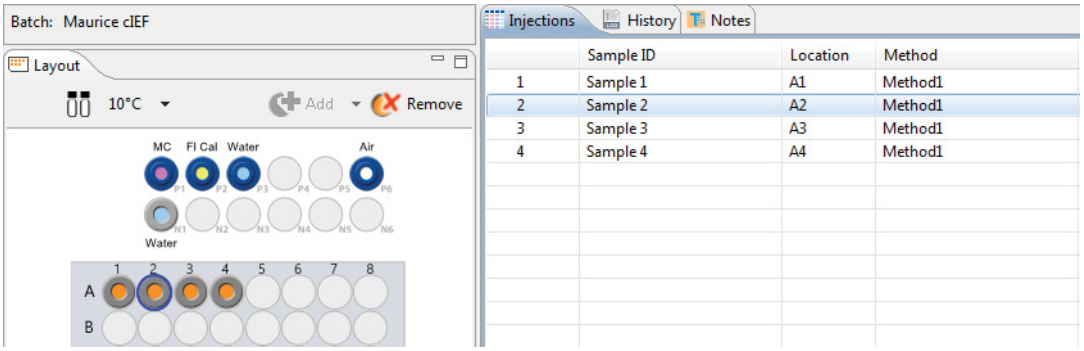


8. You can now:
   - Click **New** in the upper right corner of the Methods pane to add a new one if you want to use different methods for different samples. Then just repeat the steps above for the new method.
   - Make updates to the remaining methods by repeating the prior steps.
   - Select a method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

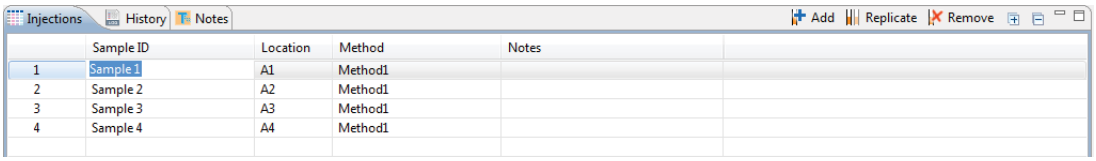
Step 4 - Set Up Your Injections

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.

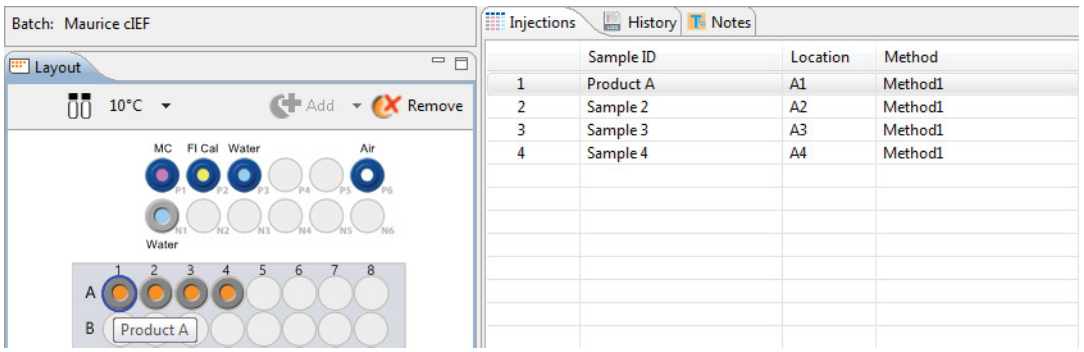
Selecting an injection in the table also selects the sample the injection will be made from in the plate or vial map in the Layout pane and vice-versa.



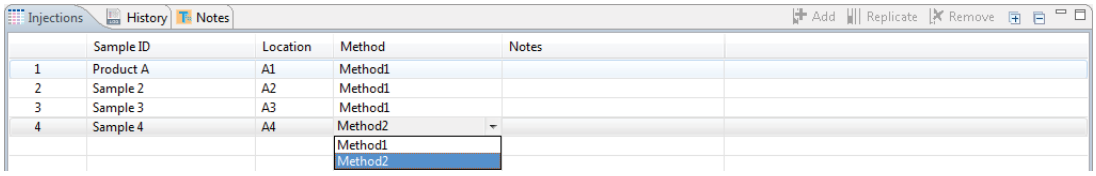
1. To add sample names, click the **Sample ID** cell for the injection and type a name.



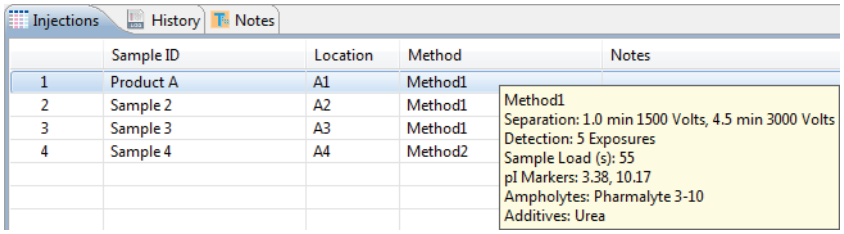
The sample name also displays when you hover the mouse over the sample in the plate or vial map:



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.

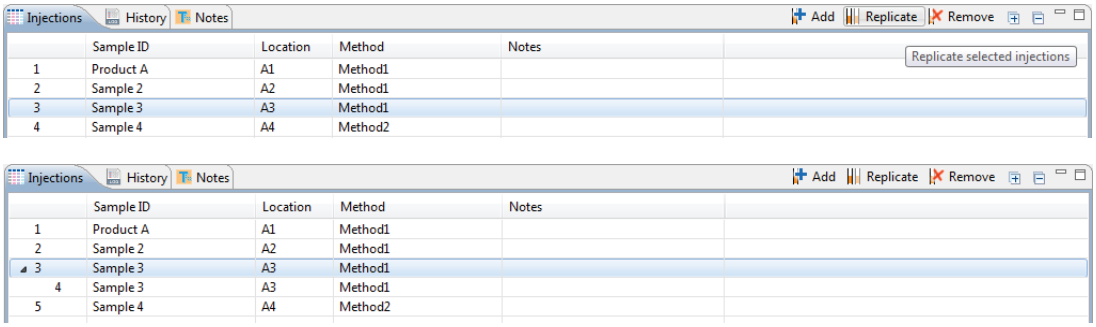


Hovering over a method name displays the method parameters:

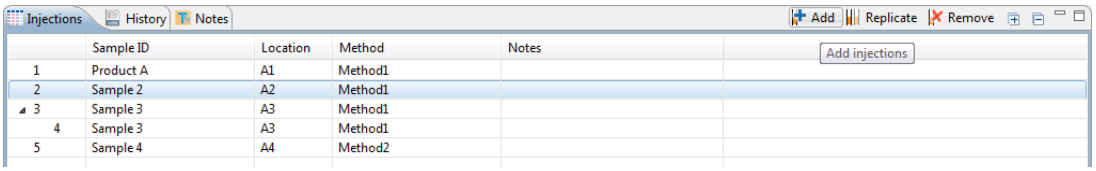


3. You can add or remove injections as needed using a few different options. If you don't need to make any changes here, just skip to the next step.

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



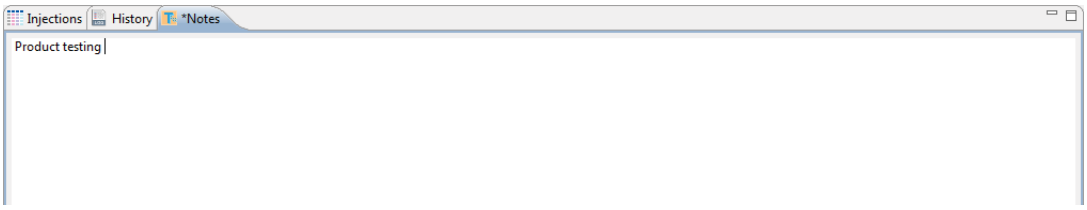
   - **To add injections at the end of the batch:** Click on any sample position in the Layout pane or sample injection in the Injection table and click **Add**. A new injection using the same sample will be added to the end of the table. Assign the method if needed.



   - **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)

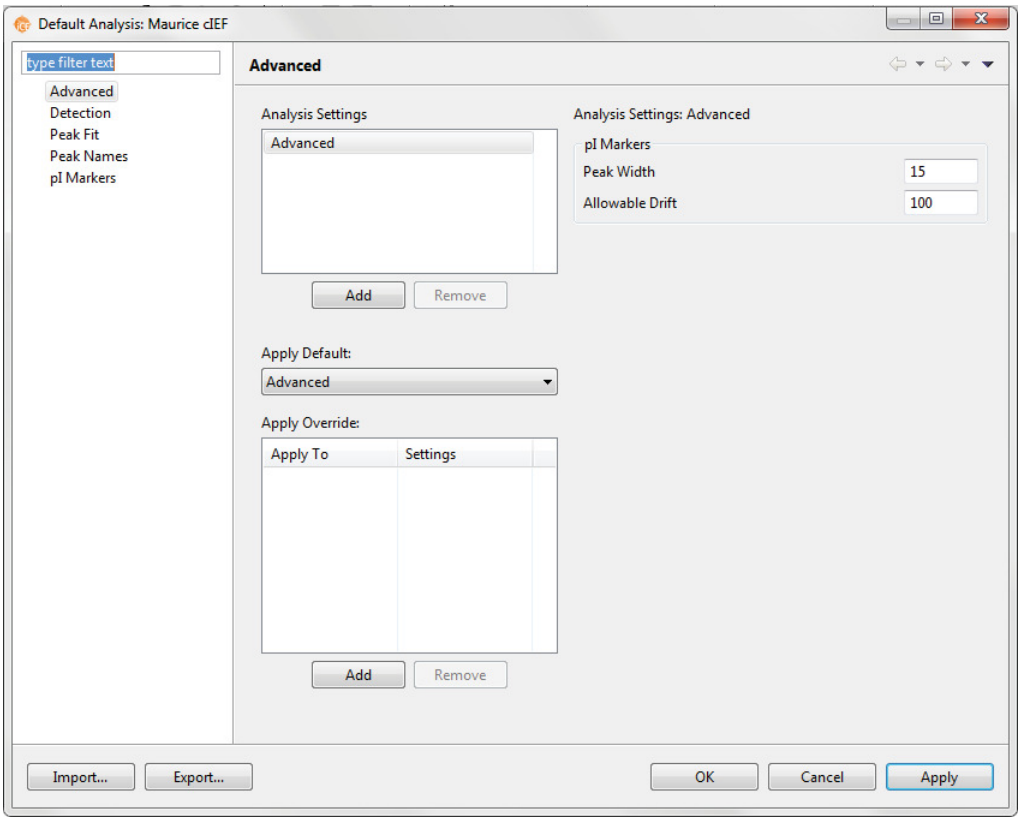
1. Click on the **Notes** pane.
2. Click in the notes area and type any information you want to add about your batch.



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:

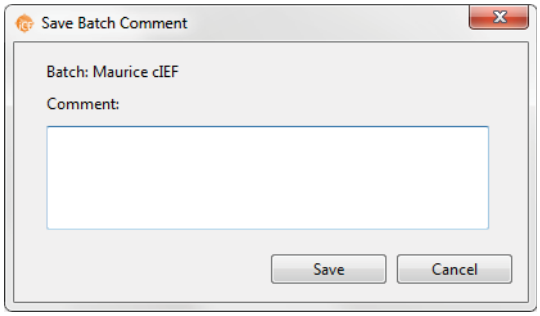
1. Select **Edit** from the main menu and click **Default Analysis**. The following screen will display:



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

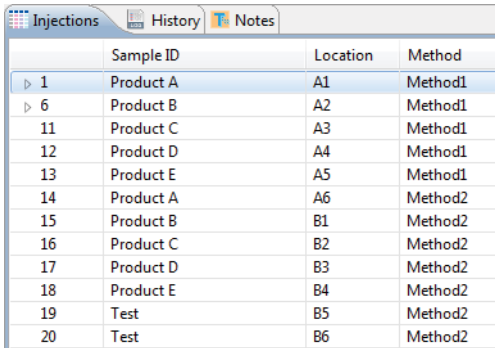
1. Once all of your sample, method and injection info is entered, select **File > Save**. Enter any comments on the batch if you want, then click **Save**.

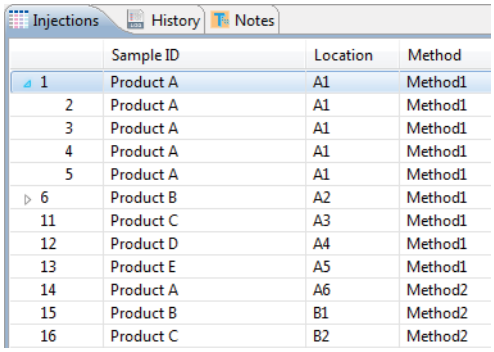


2. Enter a name for your batch then click **Save**.

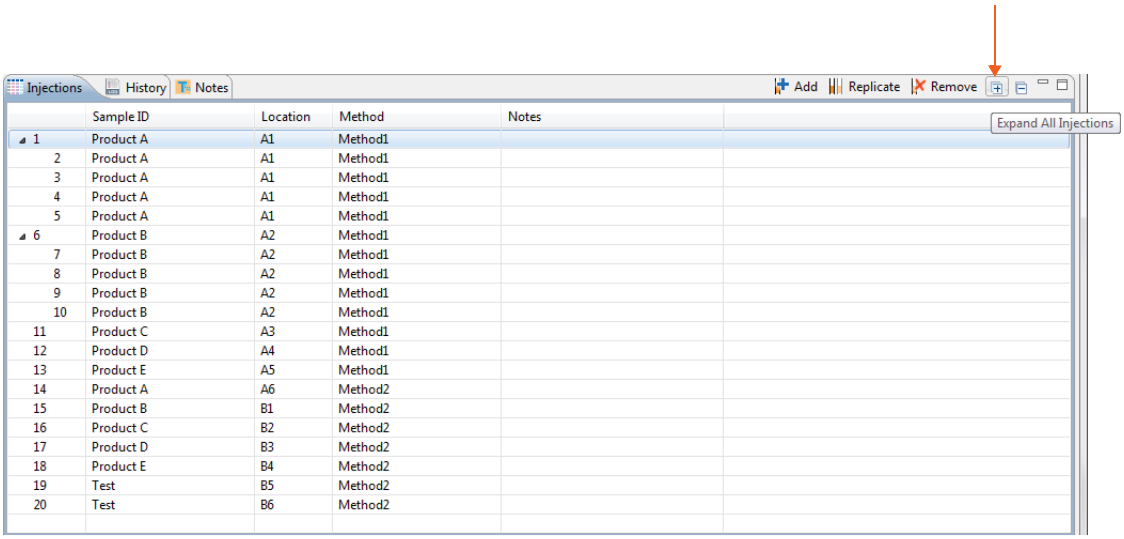
Viewing Replicate Injections

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:

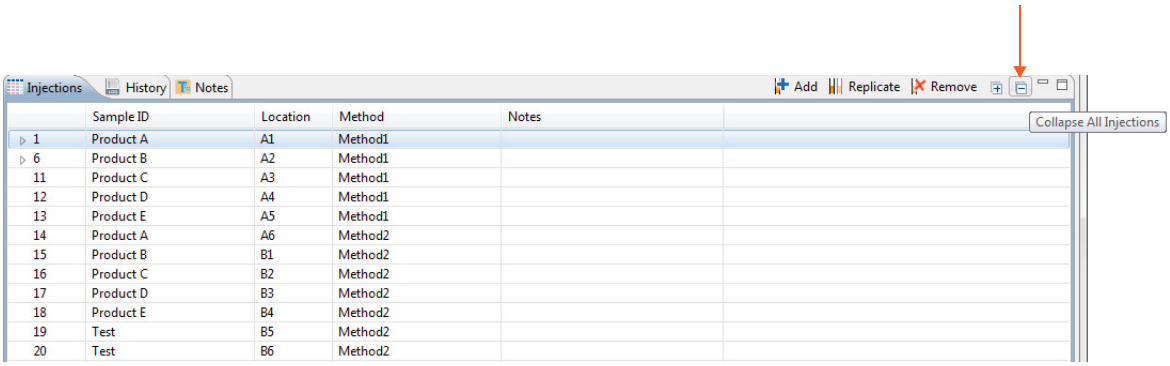




- To show all replicate injections in the batch, click the **Expand All Injections** button.

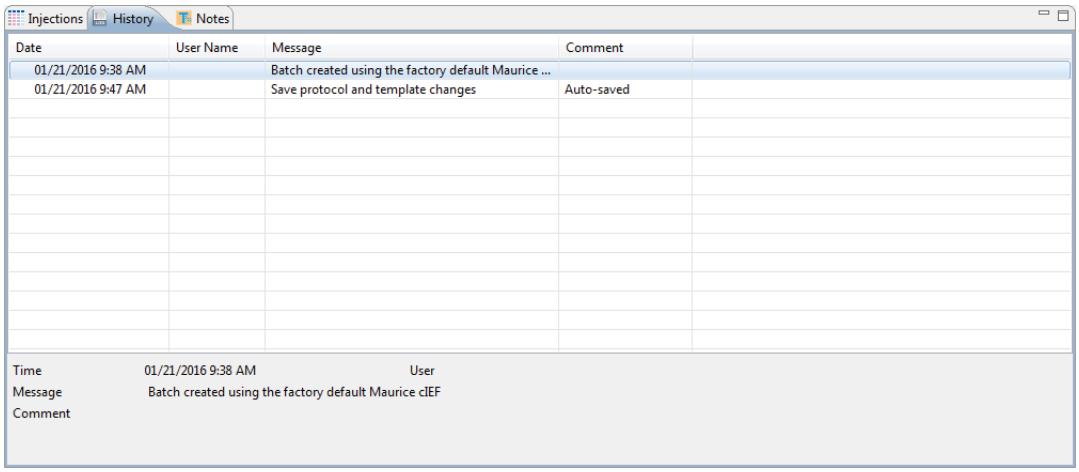


- To hide all replicate injections in the batch, click the **Collapse All Injections** button.



Batch History

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



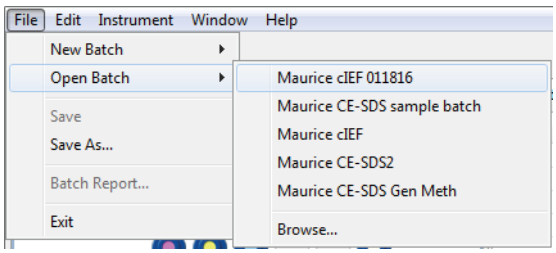
- **Date:** Date and time of the batch event.
- **User Name:** User that initiated the event. User names only display if you're using the Access Control feature to help satisfy the 21CFR Part 11 data security requirements. Go to "Enabling Access Control" on page 391 to learn how to set it up.
- **Message:** 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:

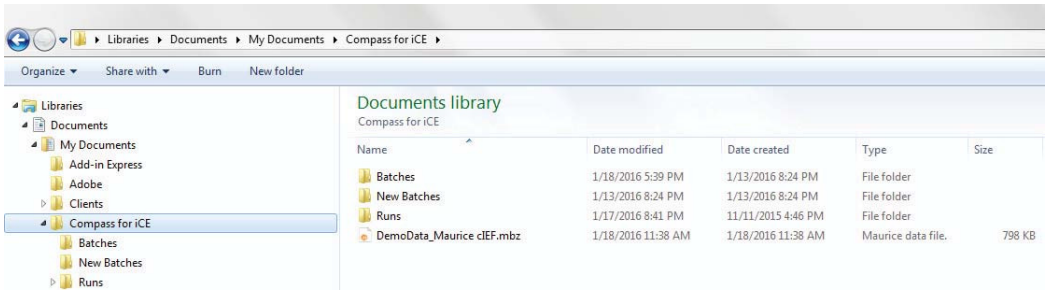
1. Click the **History** pane to make sure it's active.
2. Click **Edit** in the main menu and select **Copy**.
3. Open a document and click **Paste**.

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.

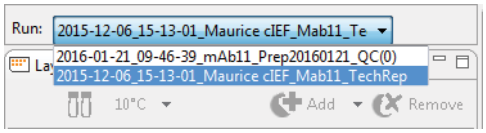


3. To make changes to the batch, see the steps in "Creating a New Batch" on page 42. Then select **File** from the main menu and click **Save** or **Save As.**

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.

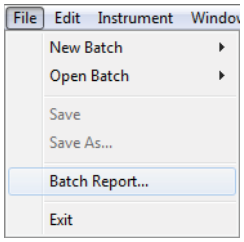


3. In completed run files, you can only make edits to the **sample** and **method** names in a batch, and these changes are saved to the run file only. Update sample and method names as needed.
4. Click the **Analysis** screen. Then select **File** from the main menu and click **Save** or **Save As**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

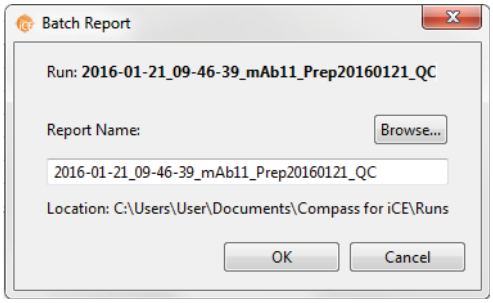
Batch Reports

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

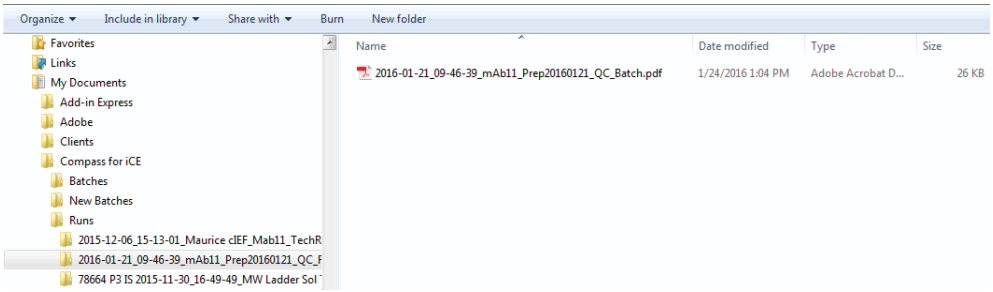
1. Go to the **Analysis** or **Run Summary** screen, then click **File** > **Open Run** and select a run file (if you don't have one open already).
2. After the run opens, go to the **Batch** screen.
3. Select **File** from the main menu and click **Batch Report**.



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.



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:

cIEF Batch: Maurice cIEF

Injection	Sample ID	Location	Method	Separation	Sample Load (s)	Standards (pI)	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		

Created: Thu 1:51 PM Feb 25, 2016 Created By: User
C:\Users\User\Documents\Compass for iCE\Runs\2016-01-21_09-46-39_mAb11_Prep20160121_QC(0).mbz
Computer: JRichards

Chapter 6:

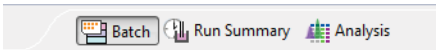
CE-SDS Batches

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

Batch Screen Overview

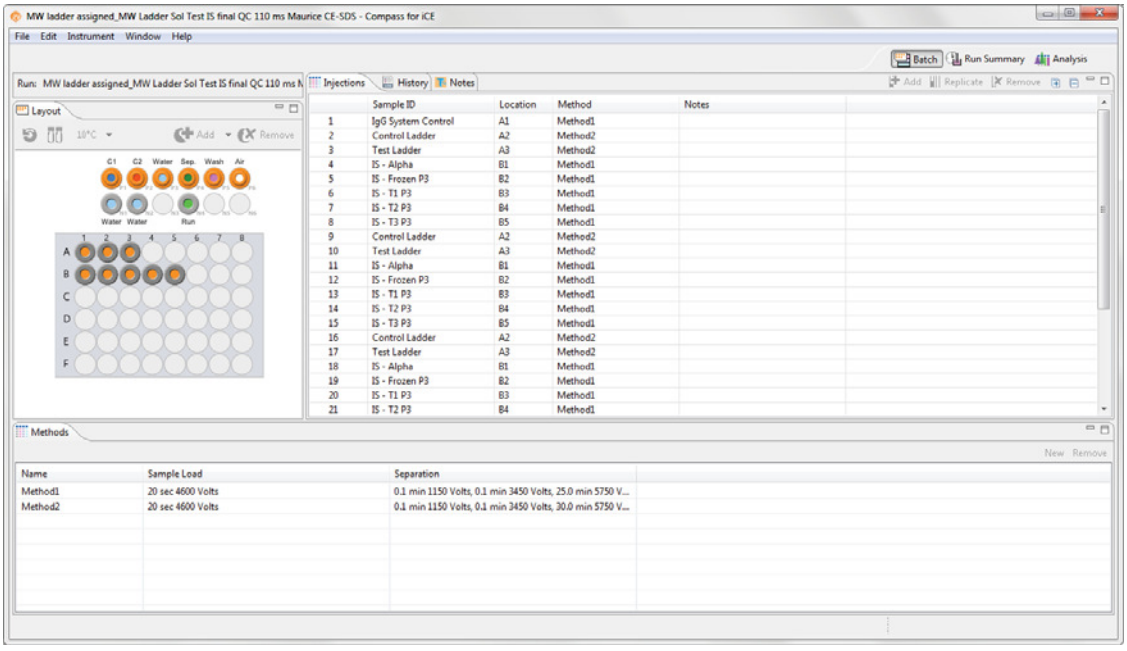
You can use the Batch screen to create, view, and edit batches. To get to this screen, click the **Batch** screen tab:



Batch 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.



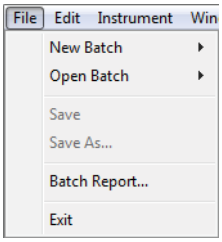
Software Menus Active in the Batch Screen

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

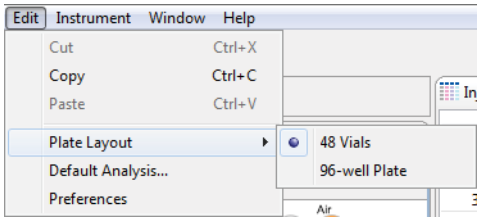
These File menu options are active:



- **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.

Edit Menu

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



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

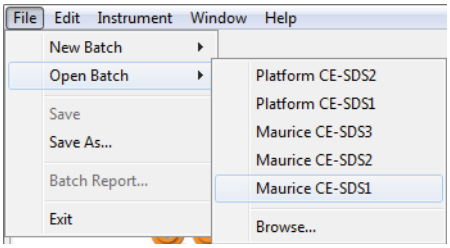
NOTE: Cut, Copy and Paste work differently depending on the pane you're in. How and when you can use them is described throughout the chapter.

- **Plate Layout** - 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**.



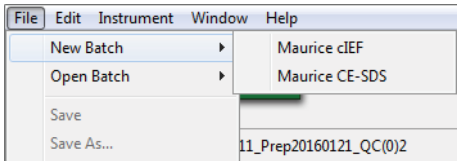
2. A list of the last five batches opened will display. Select one of those or click **Browse** to open the Batches folder and select a different one.
3. To make changes to the batch, see the steps in "Creating a New Batch" on page 64. When you're done, select **File** from the main menu and click **Save**.

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**:



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

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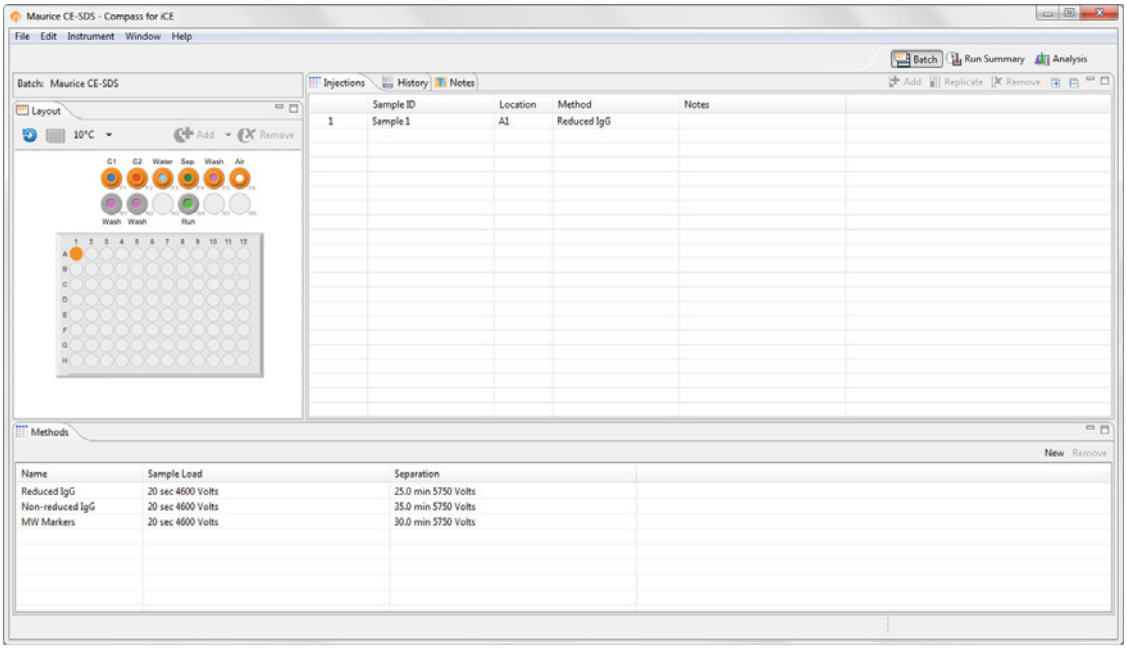
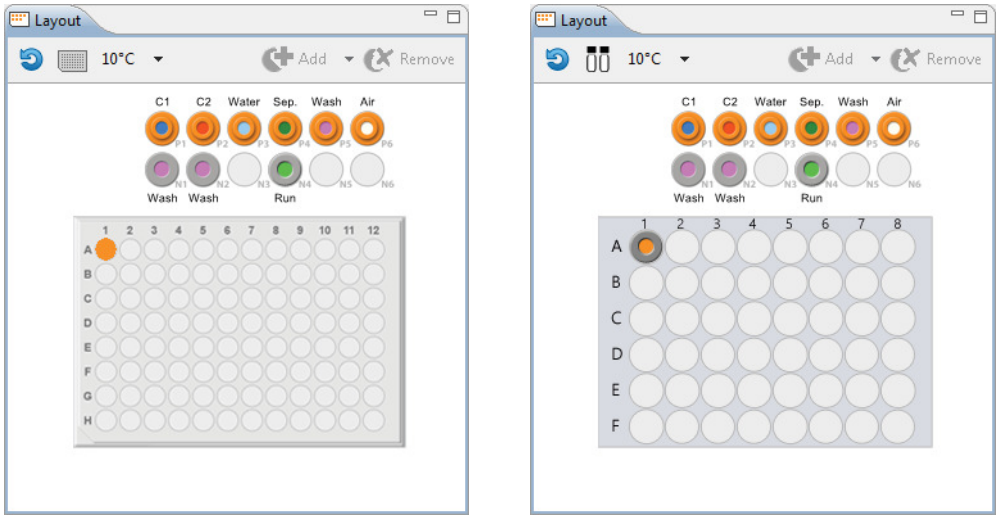
2. Select **Maurice CE-SDS**. A batch using the default method will display.



Step 2 - Assign Your Samples

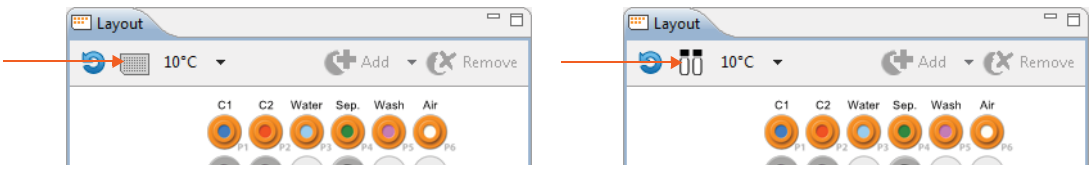
The Layout pane shows the default locations of where batch reagent should be placed in your Maurice system's samples and reagents platform, and a map of either the 96-well plate or the 48-vial tray used for samples.



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**

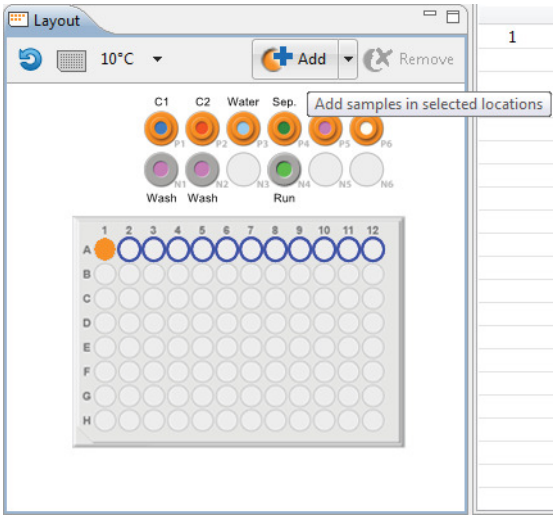
1. To assign samples, select a 96-well plate or 48 vials depending on what you're running. Clicking on the vial/plate icon toggles between formats.



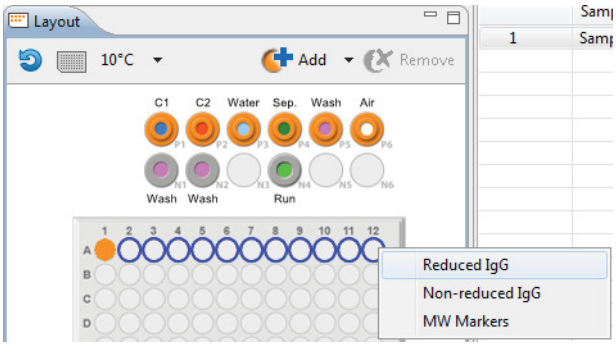
2. To select samples:

   - **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.

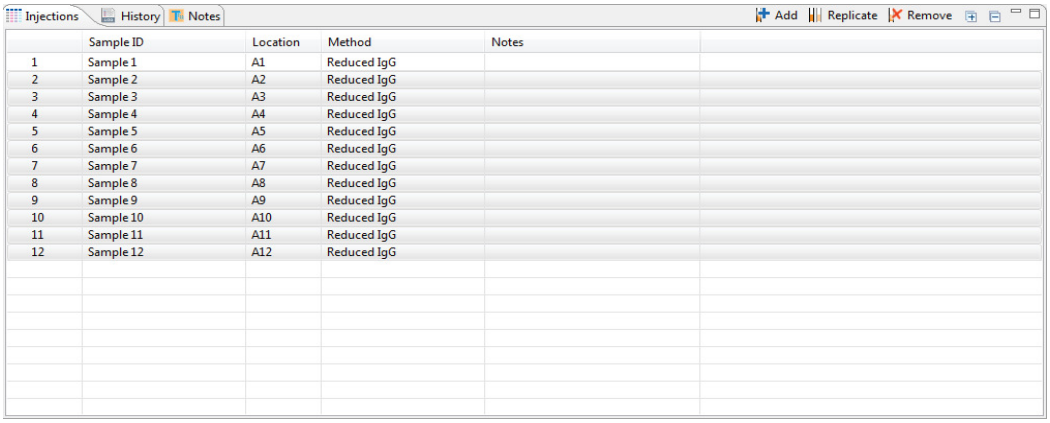
NOTE: The template batch automatically adds a sample in well or vial A1 by default, but if you don't have a sample in this position you can remove it after you've added new positions for your samples.



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

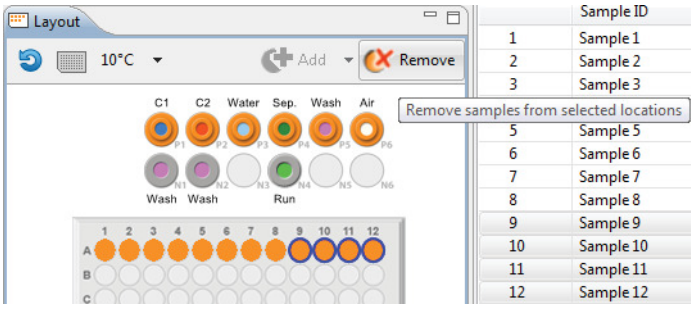


Either option of adding samples populates the Injections table:



	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).**

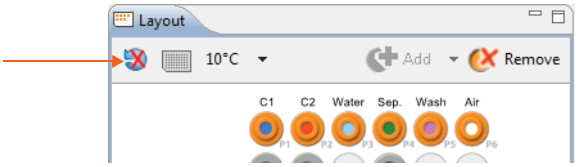


3. Compass for iCE can monitor the current during a separation for you, stop it if the current drops below the minimum value and reinject the sample for you automatically. Reinjections are enabled by default, but if you don't want to use this feature just click the reinject icon to toggle it off.

NOTES:

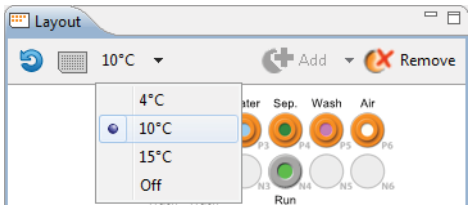
If a sample was reinjected, the injection row will be flagged in the Injections pane in the Run Summary screen. See "Injection Flags" on page 158 for more info.

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.

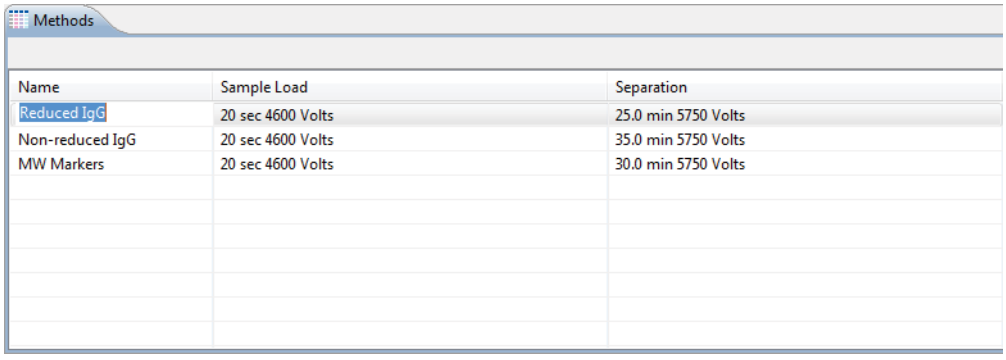


Step 3 - Assign Your Method Parameters

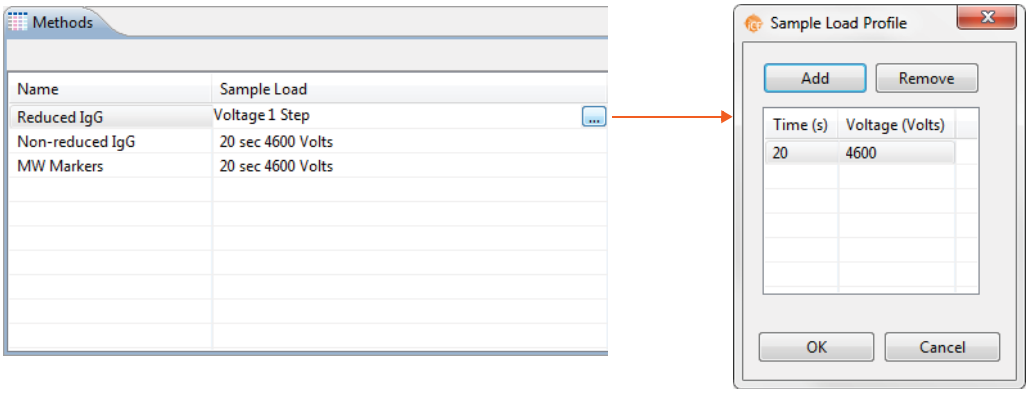
NOTE: There are three default methods. We recommend using the default method parameters for the listed sample types. Please see the Maurice CE-SDS Application Guide for more information on method optimization.

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.



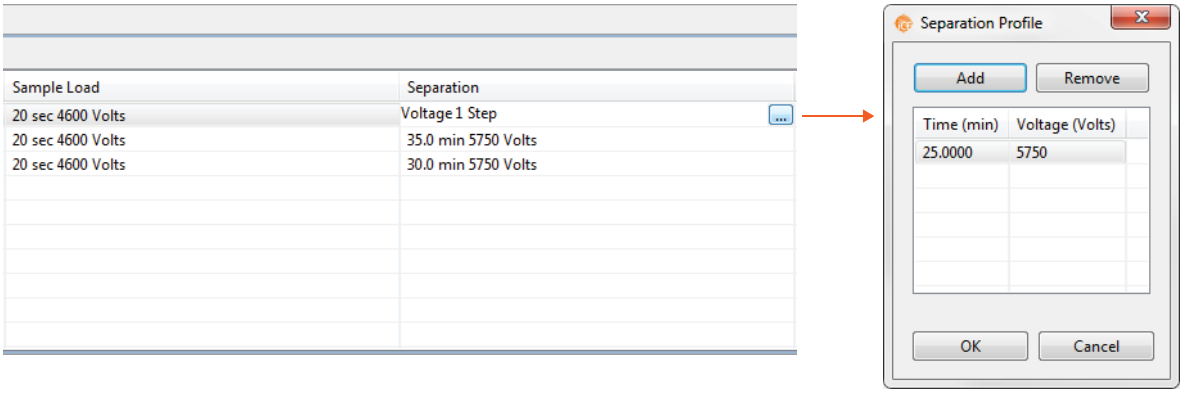
2. Click the first cell in the Sample Load column, then click the selection button **[...]** to set your sample load profile time (in seconds) and voltage.



- **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.



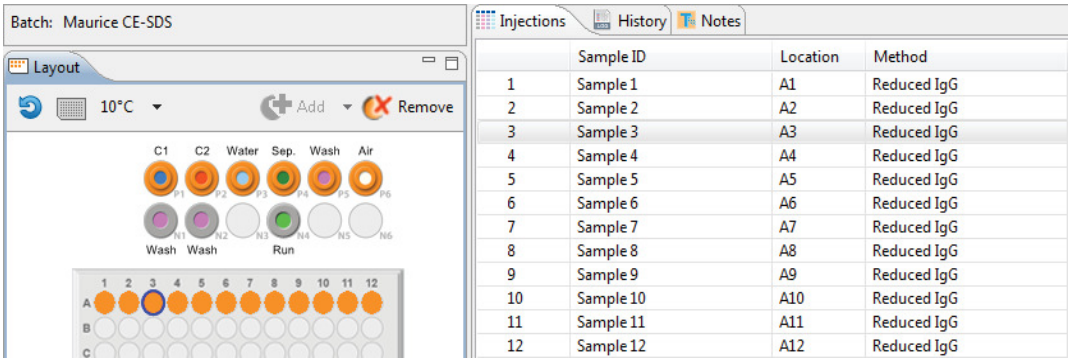
- **To change time and voltage parameters:** Just click in a cell under **Time** or **Voltage** and type the new value(s).
- **To add a profile step:** Click **Add**. A new row will be added in the table. Then just type in a load time (in seconds) and voltage value.
- **To remove a profile step:** Select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

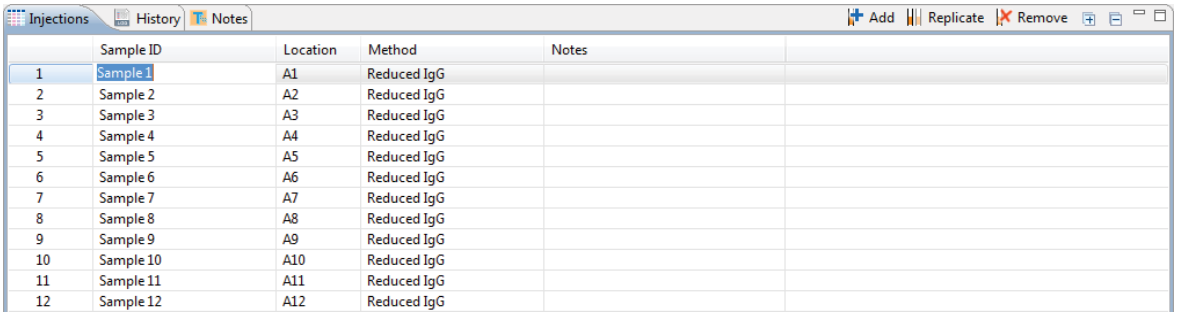
Step 4 - Set Up Your Injections

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.

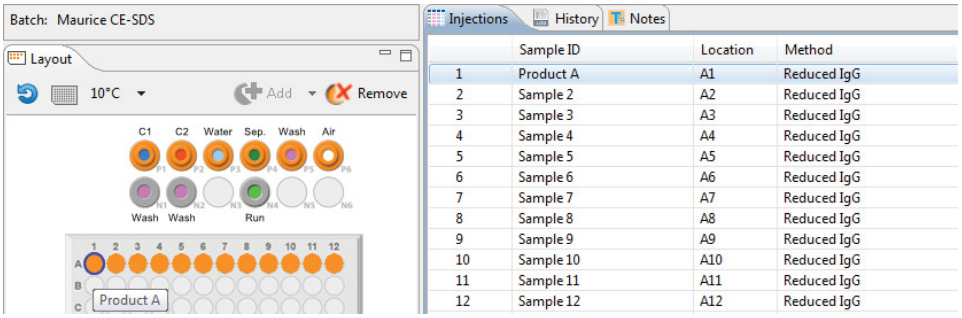
Selecting an injection in the table also selects the sample the injection will be made from in the plate or vial map in the Layout pane and vice-versa.



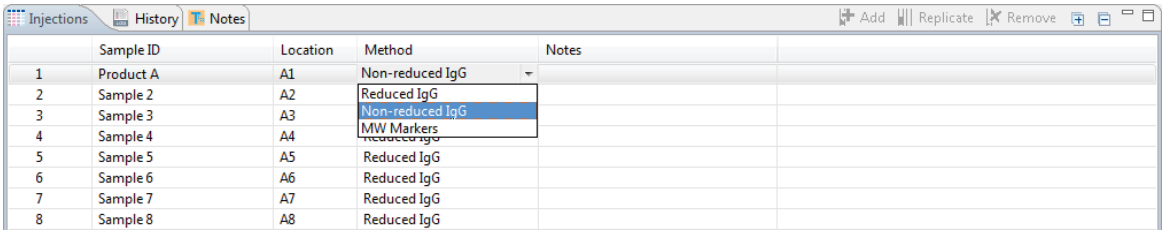
1. To add sample names, click the **Sample ID** cell for the injection and type a name.



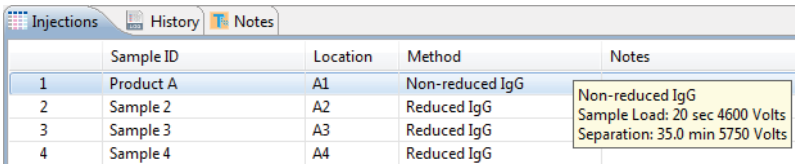
The sample name also displays when you hover the mouse over the sample in the plate or vial map:



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.

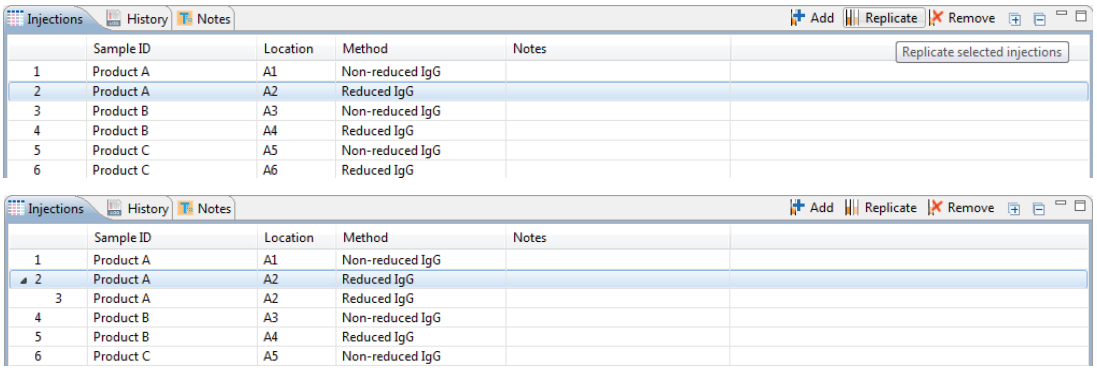


Hovering over a method name displays the method parameters:

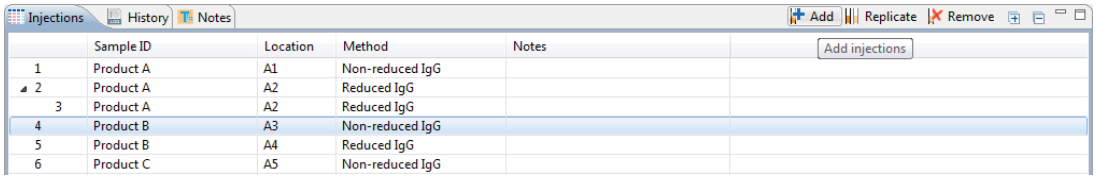


3. You can add or remove injections as needed using a few different options. If you don't need to make any changes here, just skip to the next step.

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



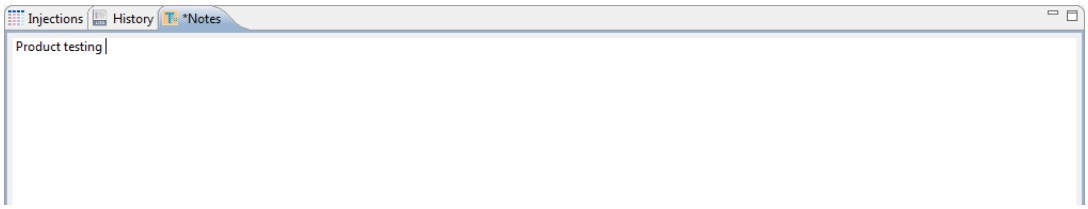
   - **To add injections at the end of the batch:** Click on any sample position in the Layout pane or sample injection in the Injection table and click **Add**. A new injection using the same sample will be added to the end of the table. Assign the method if needed.



- **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)

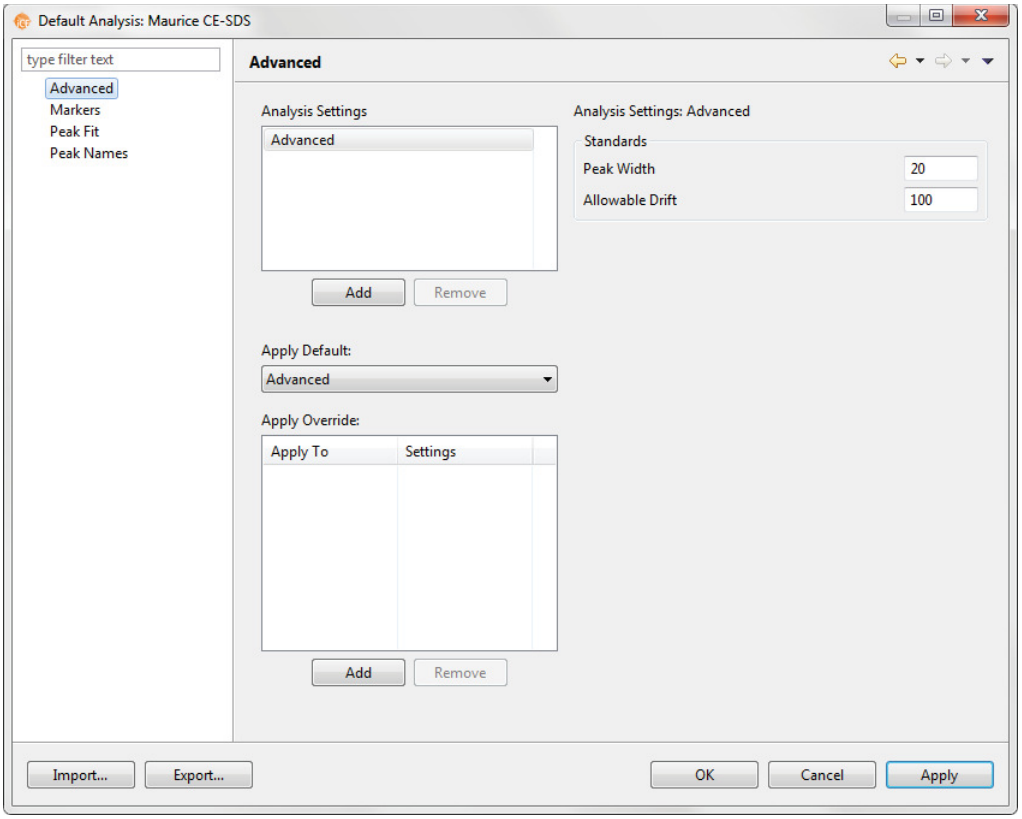
1. Click on the **Notes** pane.
2. Click in the notes area and type any information you want to add about your batch.



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:

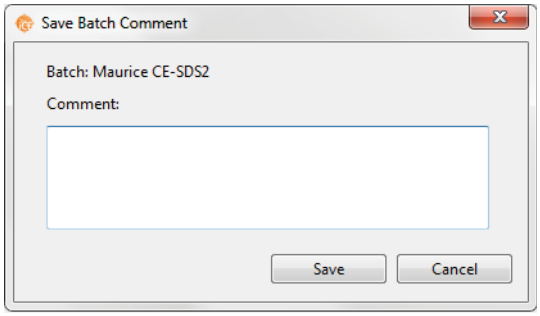
1. Select **Edit** from the main menu and click **Default Analysis**. The following screen will display:



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

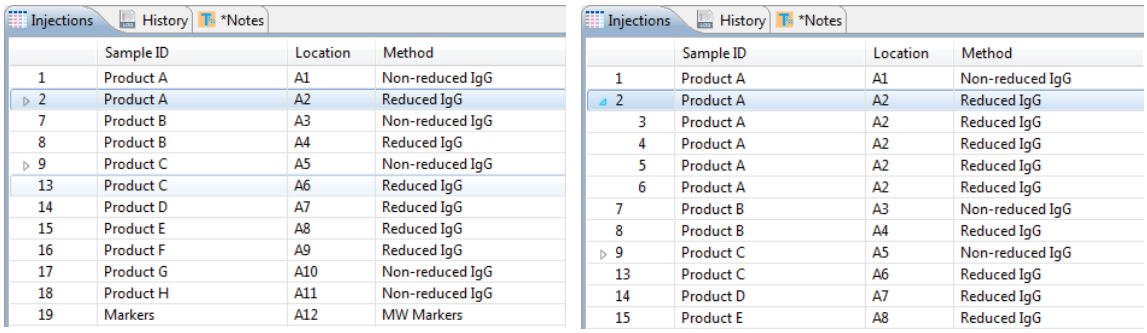
1. Once all of your sample, method and injection info is entered, select **File** > **Save**. Enter any comments on the batch if you want, then click **Save**.



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:



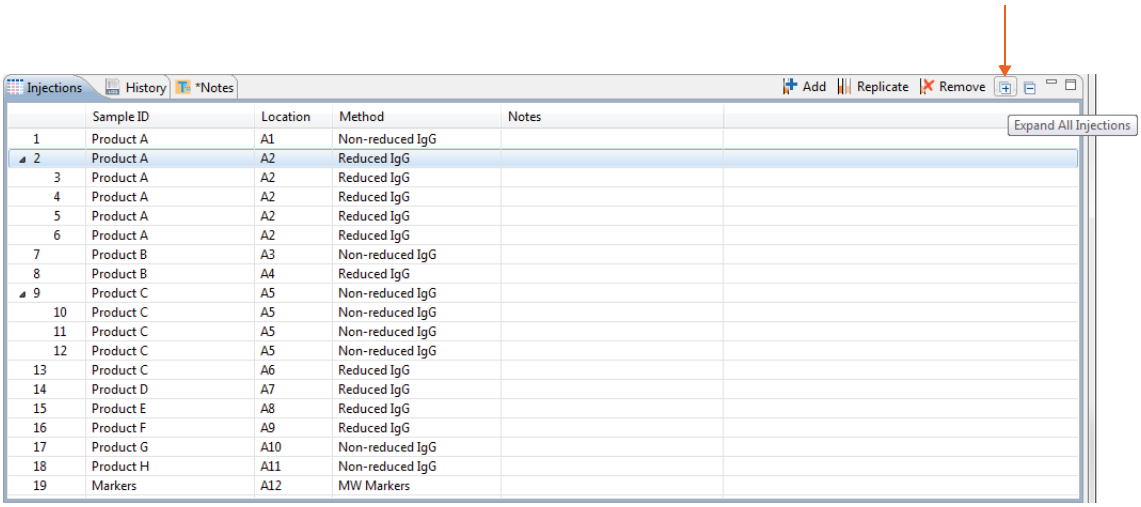
Injections | History | *Notes

	Sample ID	Location	Method
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

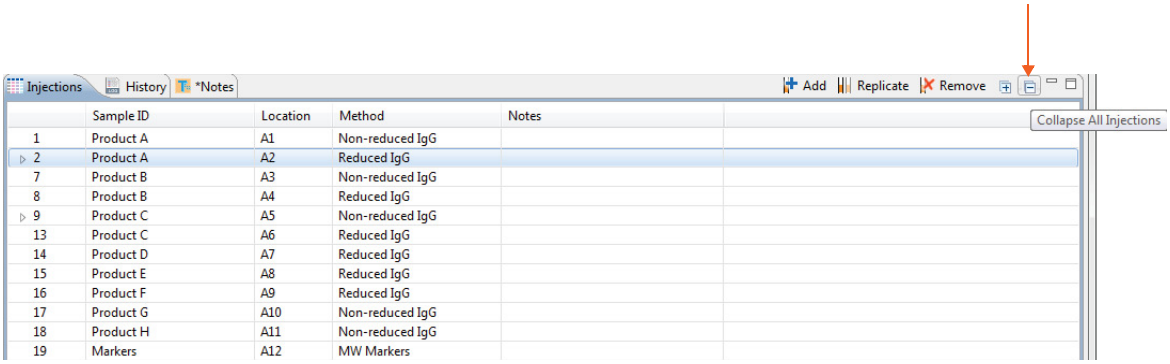
Injections | History | *Notes

	Sample ID	Location	Method
1	Product A	A1	Non-reduced IgG
◢ 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
▷ 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

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

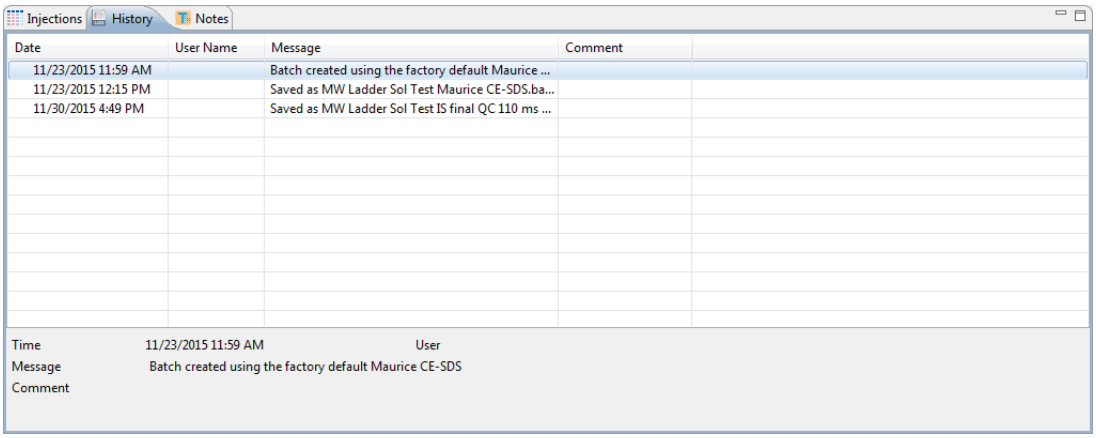


- To hide all replicate injections in the batch, click the **Collapse All Injections** button.



Batch History

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



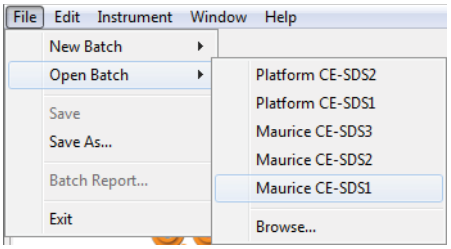
- **Date:** Date and time of the batch event.
- **User Name:** User that initiated the event. User names only display if you're using the Access Control feature to help satisfy the 21CFR Part 11 data security requirements. Go to "Enabling Access Control" on page 391 to learn how to set it up.
- **Message:** 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:

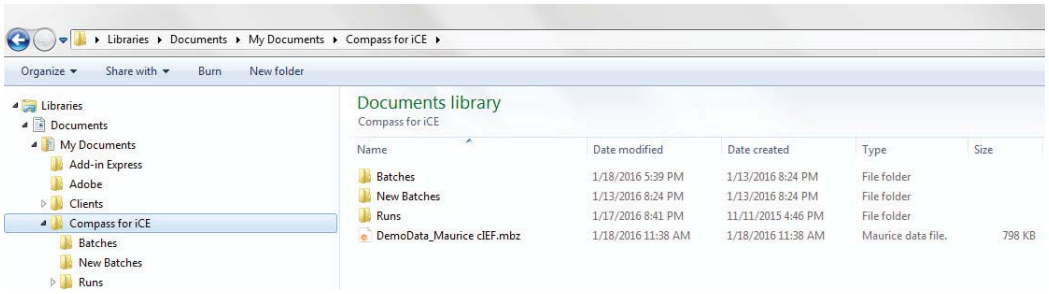
1. Click the **History** pane to make sure it's active.
2. Click **Edit** in the main menu and select **Copy**.
3. Open a document and click **Paste**.

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.

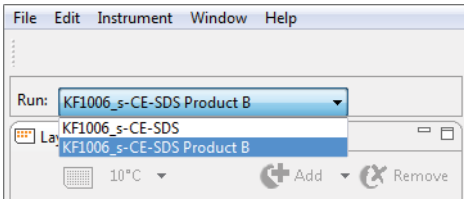


3. To make changes to the batch, see the steps in "Creating a New Batch" on page 64. Then select **File** from the main menu and click **Save** or **Save As.**

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.

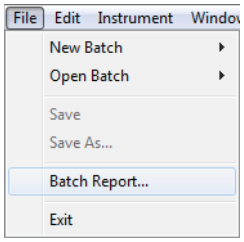


3. In completed run files, you can only make edits to the **sample** and **method** names in a batch, and these changes are saved to the run file only. Update sample and method names as needed.
4. Click the **Analysis** screen. Then select **File** from the main menu and click **Save** or **Save As**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

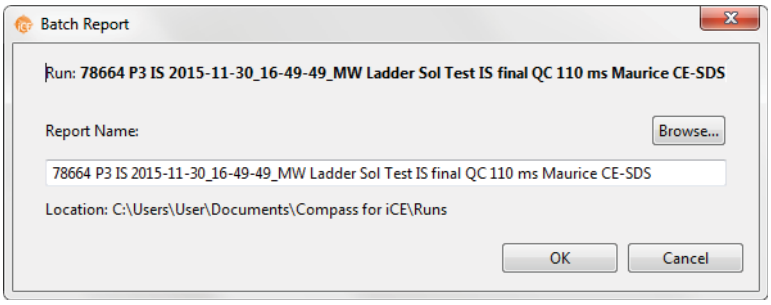
Batch Reports

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

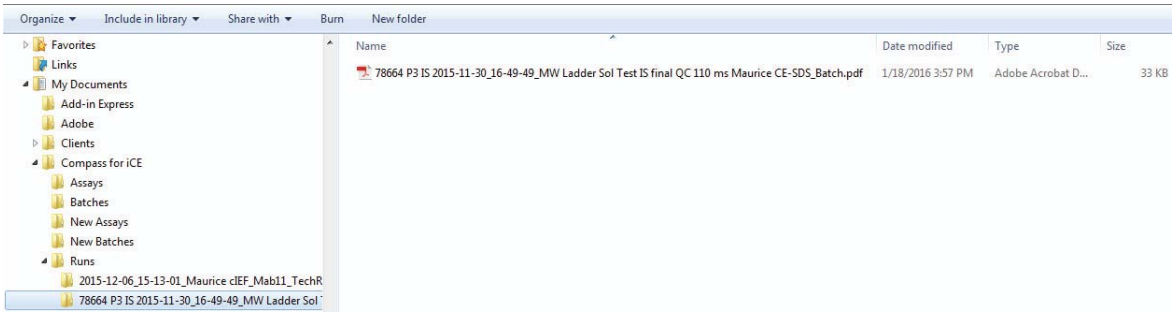
1. Go to the **Analysis** or **Run Summary** screen, then click **File** > **Open Run** and select a run file (if you don't have one open already).
2. After the run opens, go to the **Batch** screen.
3. Select **File** from the main menu and click **Batch Report**.



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.



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:

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

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	Method1	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	Method1	20 sec 4600 Volts	0.1 min, 1150 Volts 0.1 min, 3450 Volts 25.0 min, 5750 Volts

Created: Thu 1:54 PM Feb 25, 2016 Created By: User
C:\Users\User\Documents\Compass for iCE\Runs\MW ladder assigned_MW Ladder Sol Test IS final QC 110 ms Maurice CE-SDS.mbz
Computer: JRichards

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 cIEF pI 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

- 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.

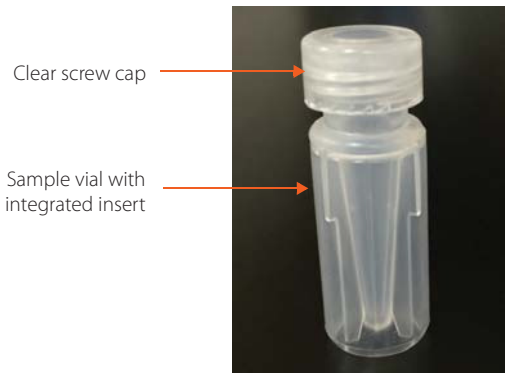
1. Using scissors, carefully cut the top the package off leaving the sealing strip intact.
2. Take out the strip of tubes and cut one clear tube of lyophilized System Suitability Peptide Panel from the strip. Return the remaining tubes to the original package, reseal tightly and store at 2-8°C.
3. Pierce the foil on the tube with a clean pipette tip.
4. Add 40 µL of DI water to the tube. Gently resuspend by pipetting up and down to mix.
5. Add 160 µL of the System Suitability Test Mix to the freshly reconstituted Peptide Panel. Gently mix by pipetting up and down. Transfer this solution to a 1.5 mL microcentrifuge tube.
6. Vortex the tube 3 times, 5 seconds each.
7. Centrifuge the tube at 10,000 xg for 3 minutes to sediment any particulates.

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 µL in DI water.
2. In a separate tube, prepare IEF Separation Mix containing your chosen pI marker(s).

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

---

3. Add 160 µL of IEF Separation Mix to the 40 µL 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.

pI Markers

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

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

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

---

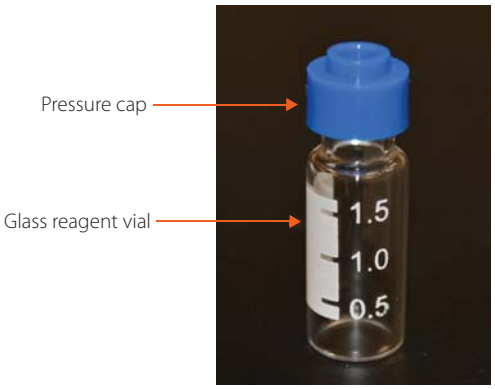
5. Use 2 µL of each pI marker for every 200 µL of sample.

Reagents

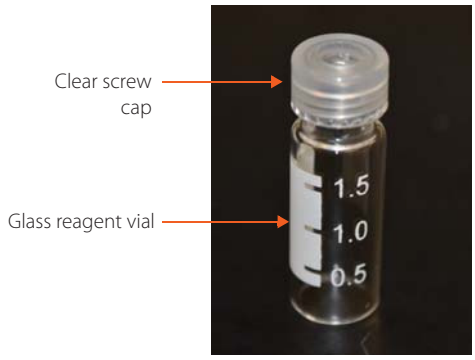
NOTE: Don't reuse reagents, vials or the clear screw caps. Always keep the blue pressure caps paired with their respective reagents. If you want to reuse pressure caps, first wash them thoroughly with DI water, soak overnight in DI water, rinse caps thoroughly with DI water again and air dry them before 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**.
5. Pipette 2 mL of DI water into a glass reagent vial, label and close with a **clear screw cap**.

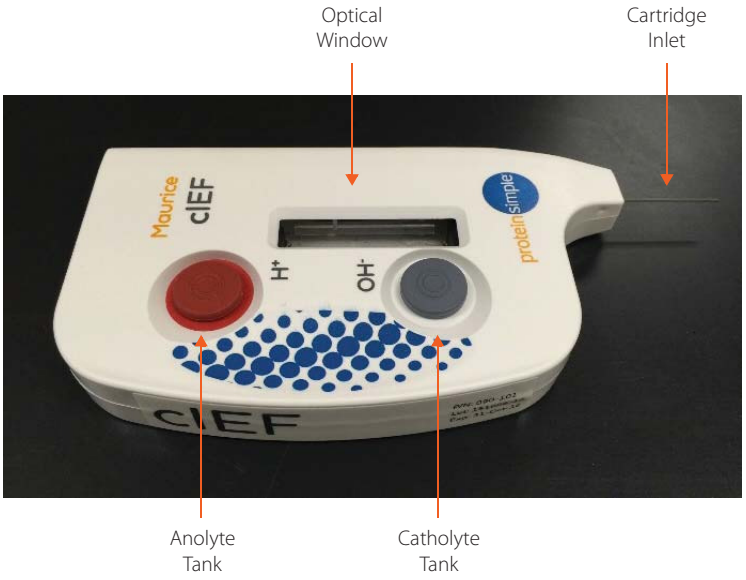


Step 2: Prep the Cartridge

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^- electrolyte tank (white port).
5. Add 2 mL Anolyte solution to the H^+ electrolyte tank (red port).

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

---

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

Step 3: Install the Cartridge

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

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

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

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

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

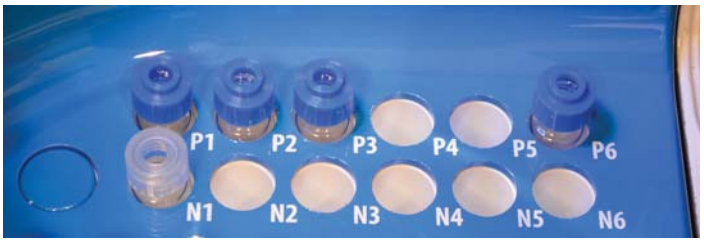
Step 4: Load Samples and Reagents

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

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

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

- **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.

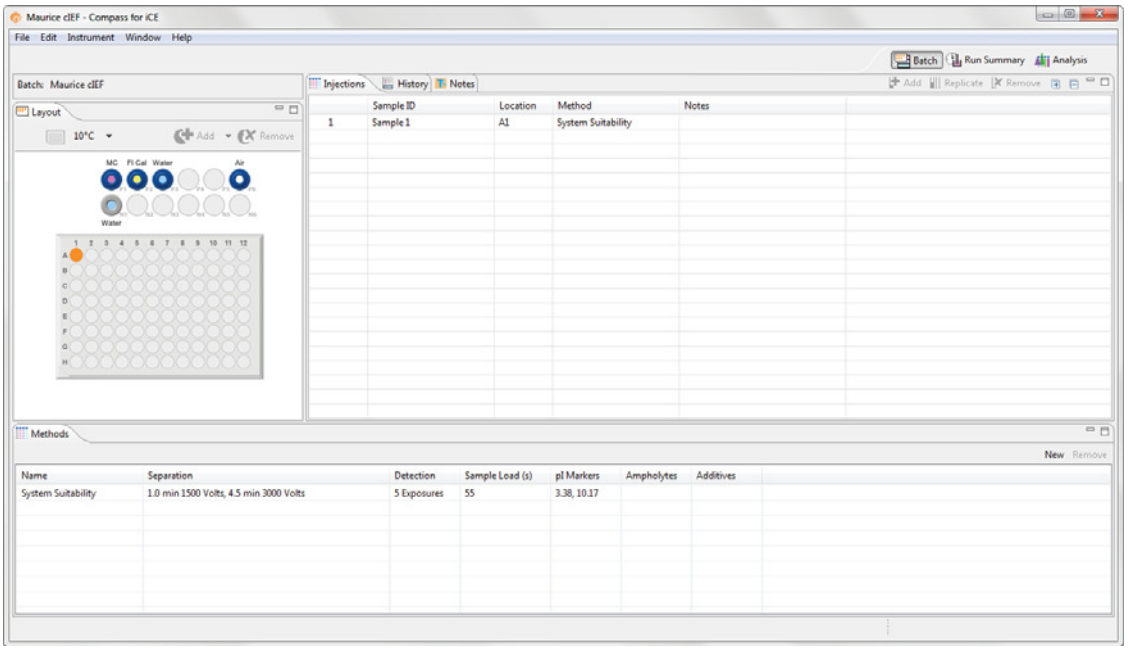
Well A1 on the 96-well plate should be in the top left corner of the insert.

---

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.



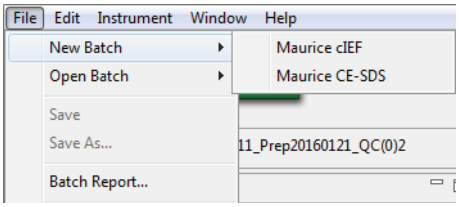
3. To create a batch, make sure Maurice is connected to Compass for iCE. If he isn't, select **Instrument** and click **Connect**. Then select your Maurice system and click **Connect**.

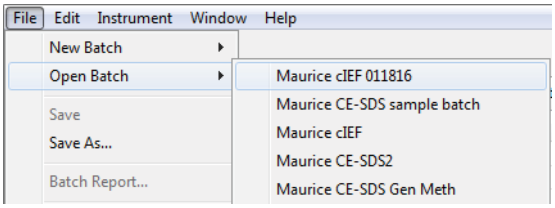
   To create a new batch:

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

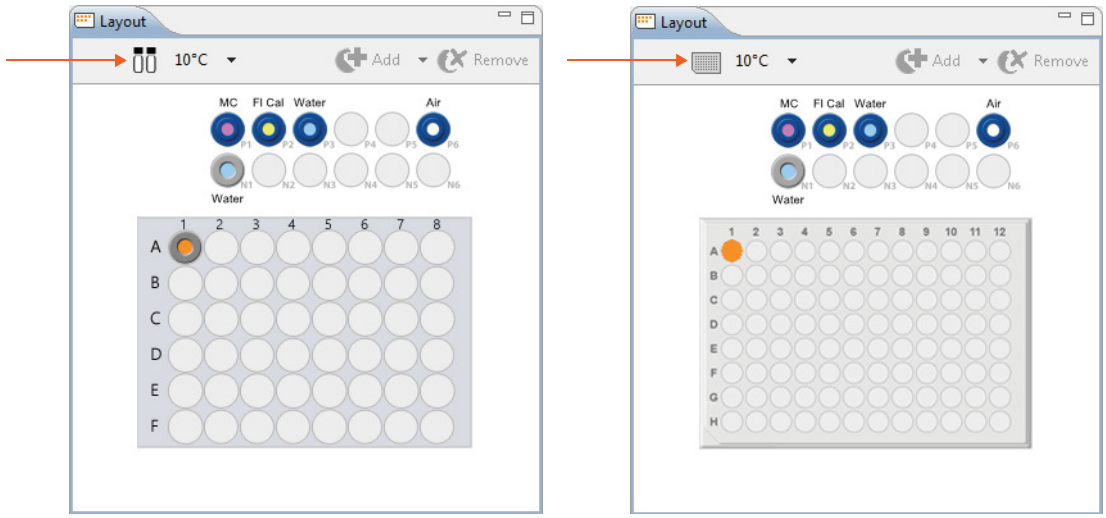
   To use an existing batch: In the main menu, select **File > Open Batch.**

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.

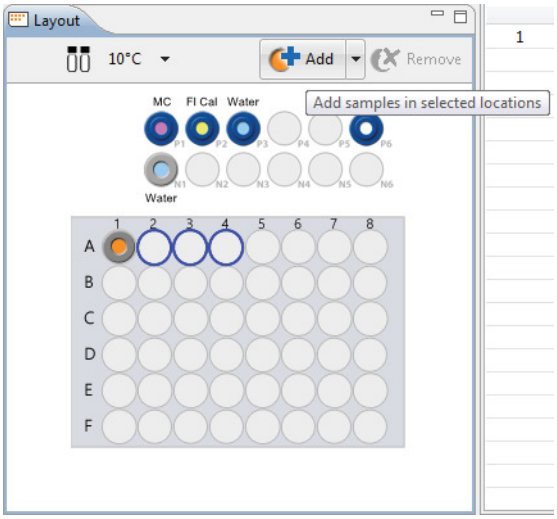




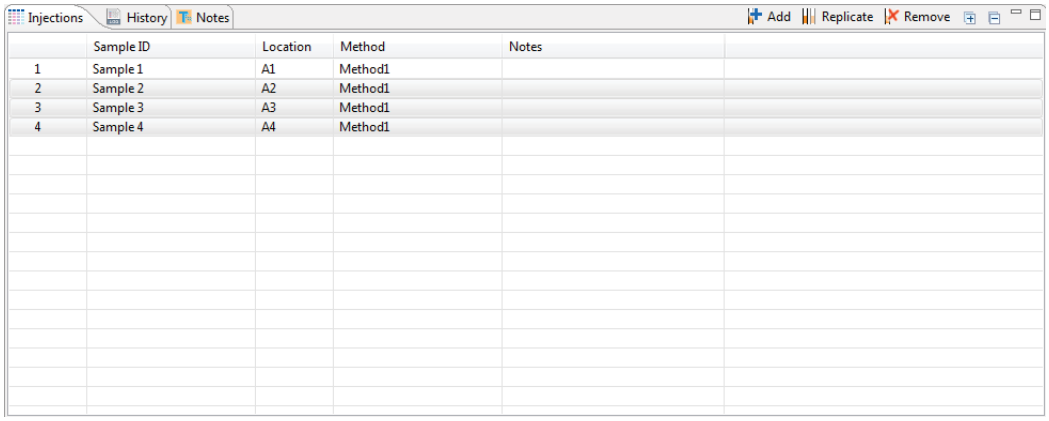
4. In the Layout pane, clicking on the vial/plate icon toggles between formats. Select 48 vials or a 96-well plate depending on what you're running.



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



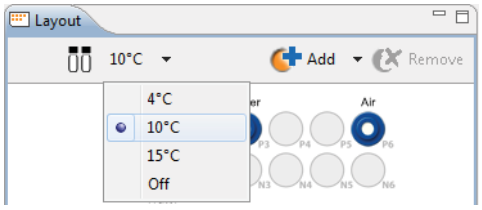
This populates the Injections table:



	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.

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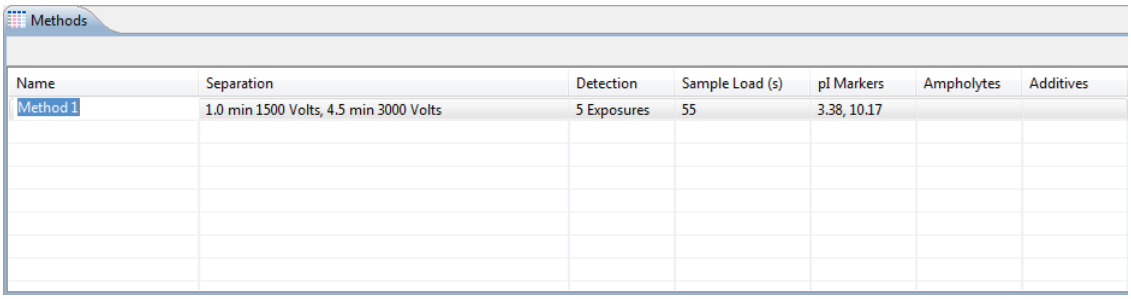
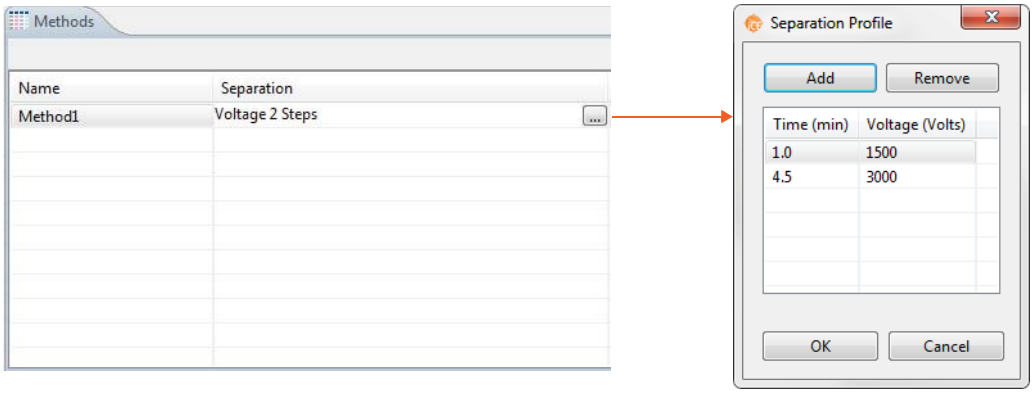
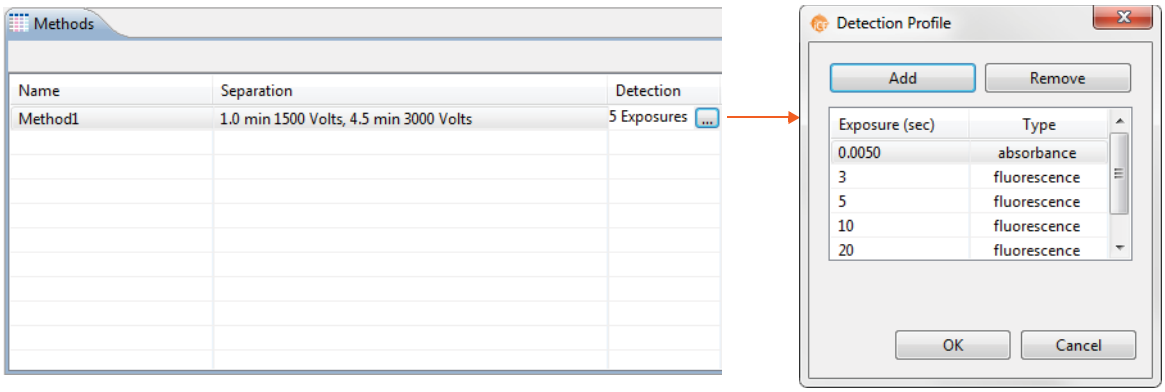
a. Click the first cell in the Name column and enter a method name.



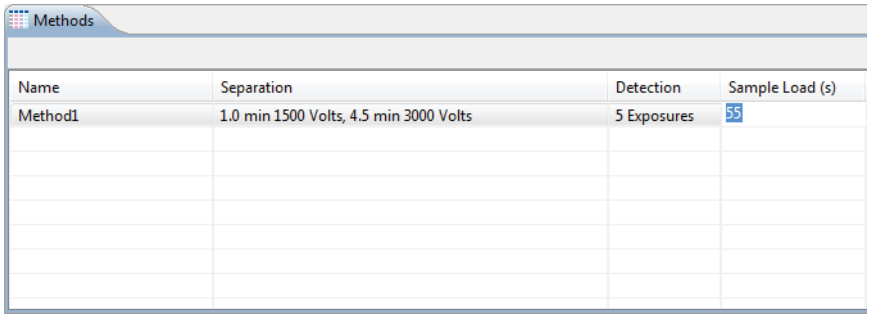
b. Click the first cell in the Separation column, then click the selection button **[...]** to set the pre-focusing and focusing time (in minutes) and voltage.



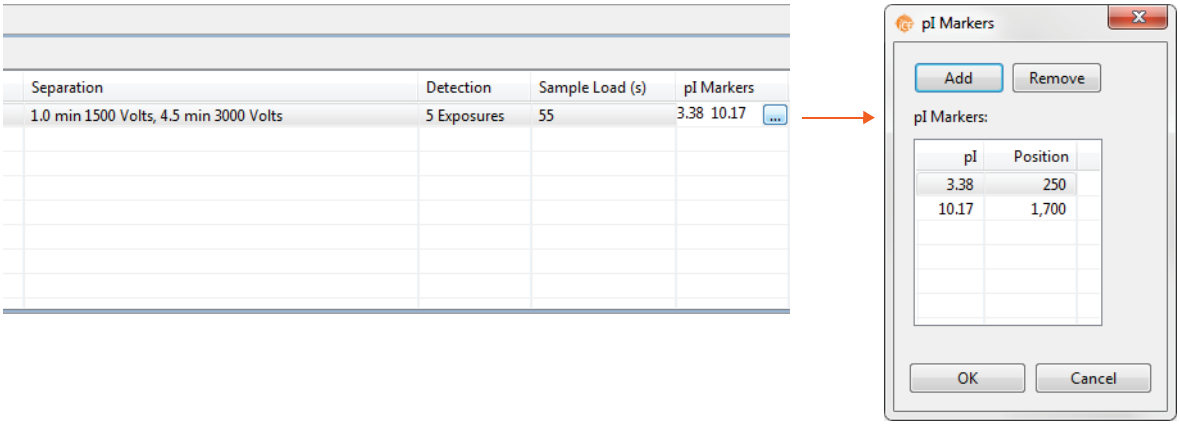
c. Click the first cell in the Detection column then click the selection button **[...]** to set your exposure times for absorption and fluorescence detection modes.



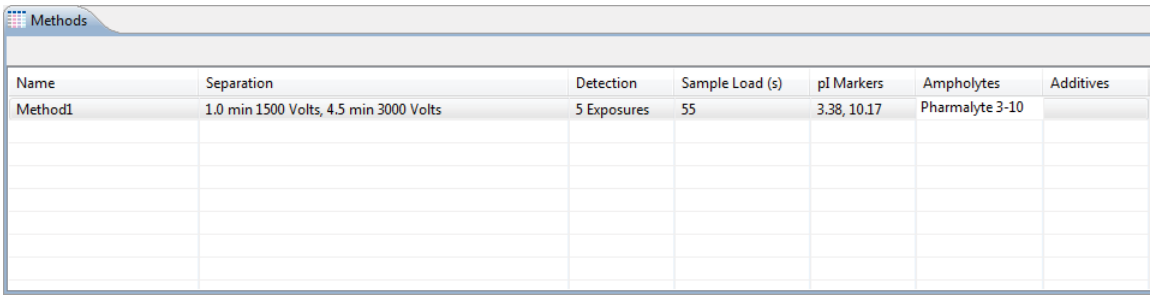
d. Click the first cell in the Sample Load(s) column and set the load time in seconds.



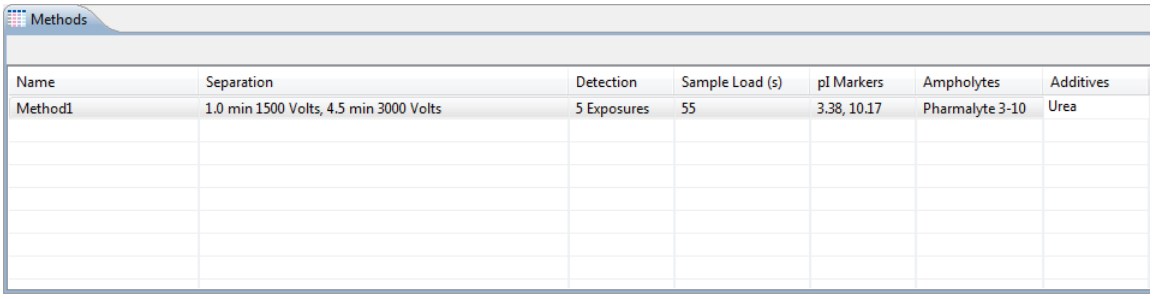
e. Click the first cell in the pI Markers column to select pI markers. Add new markers or remove existing ones then click **OK**.



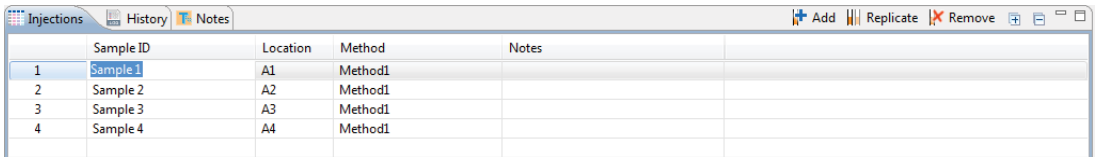
f. Optional: Click the first cell in the Ampholytes column and enter the ampholytes you're using.



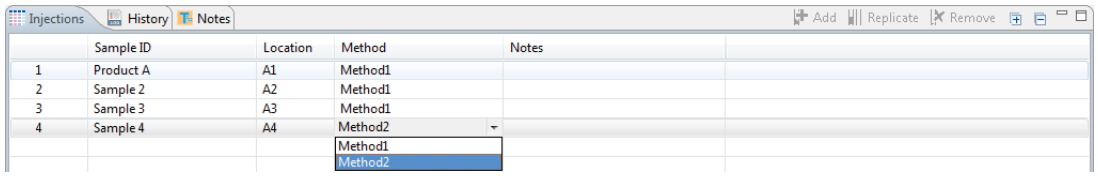
g. Optional: Click the first cell in the Additives column and enter any additives you're using.



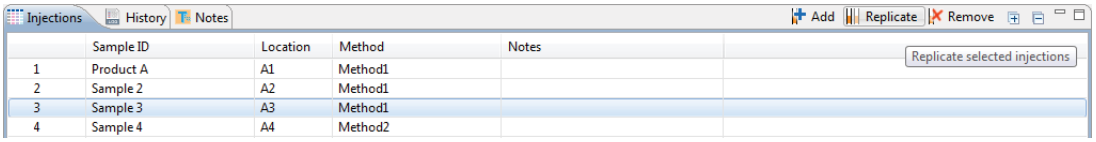
8. You can now:
   - Make updates to the remaining methods by repeating the prior steps.
   - Select a method and click **Remove** in the upper right corner of the Methods pane to delete it.
   - Click **New** in the upper right corner of the Methods pane to add a new one if you want to use different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

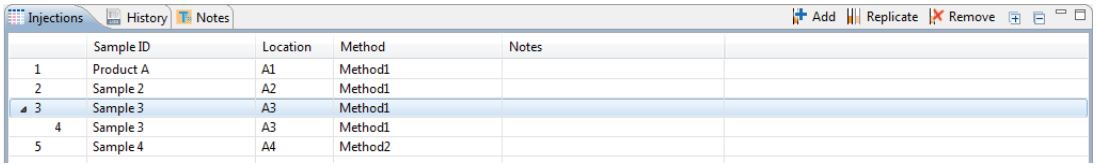


   - **To assign methods for each injection:** Click the **Method** cell for the injection and select a method from the drop down menu.

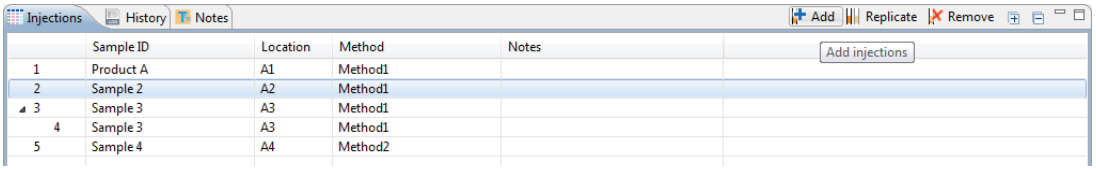


   - **To add sequential replicate injections:** Highlight an injection and click **Replicate**. A new injection will be added under the row you selected



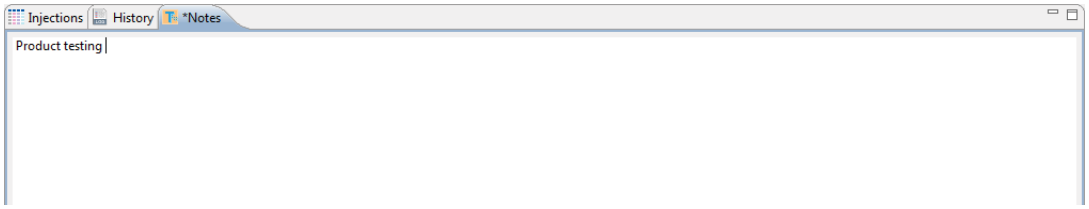


- **To add injections at the end of the batch:** Click on any sample position in the Layout pane or sample injection in the Injection table and click **Add**. A new injection using the same sample will be added to the end of the table. Assign the method if needed.

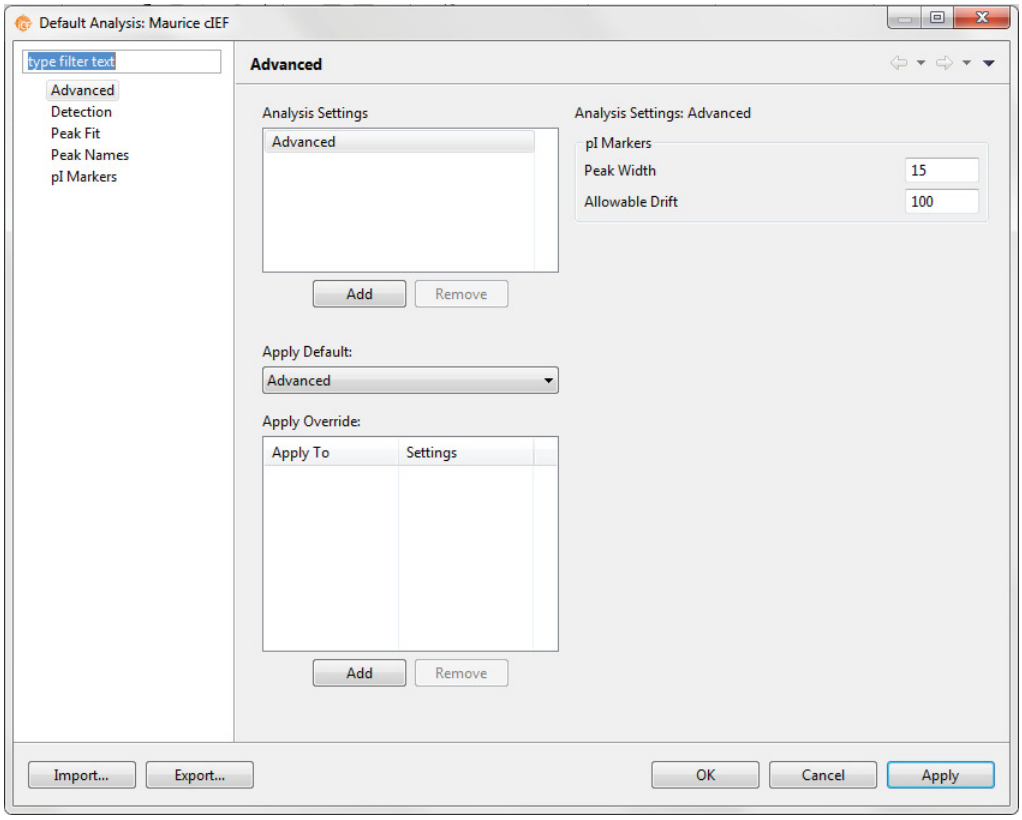


- **To copy and paste injections:** Right-click on an injection in the Injection table and select **Copy**. Click on the injection number above where you want to insert the copied injection, right click and select **Paste**. The copied injection will be inserted under the row you selected.

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

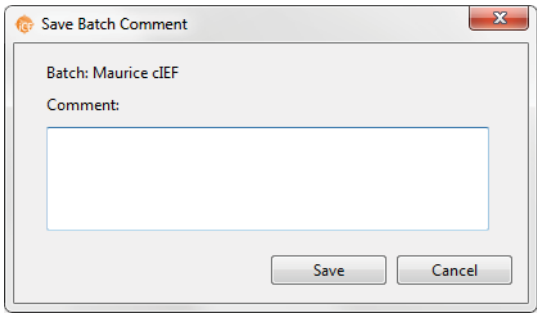


11. You can preset the parameters used to analyze data generated with the batch (optional). We recommend using the default parameters for cIEF applications, but if you want to modify parameters:
    a. Select **Edit** from the main menu and click **Default Analysis**. The following screen will display:



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

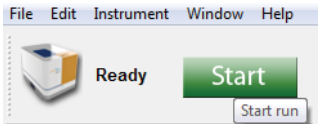
12. Once all of your sample, method and injection info is entered, select **File > Save**. Enter any comments on the batch if you want, then click **Save**.



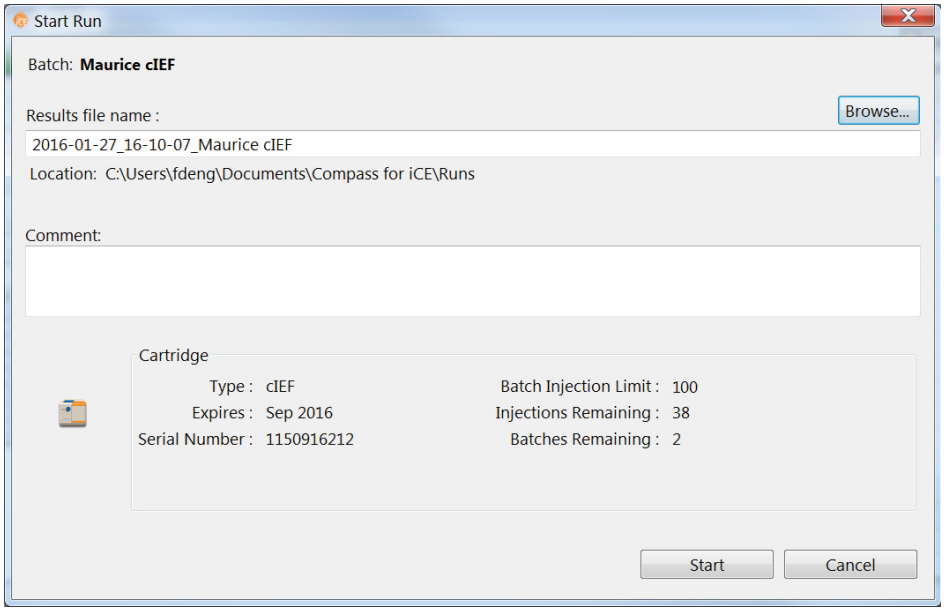
13. Enter a name for your batch then click **Save**.

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.



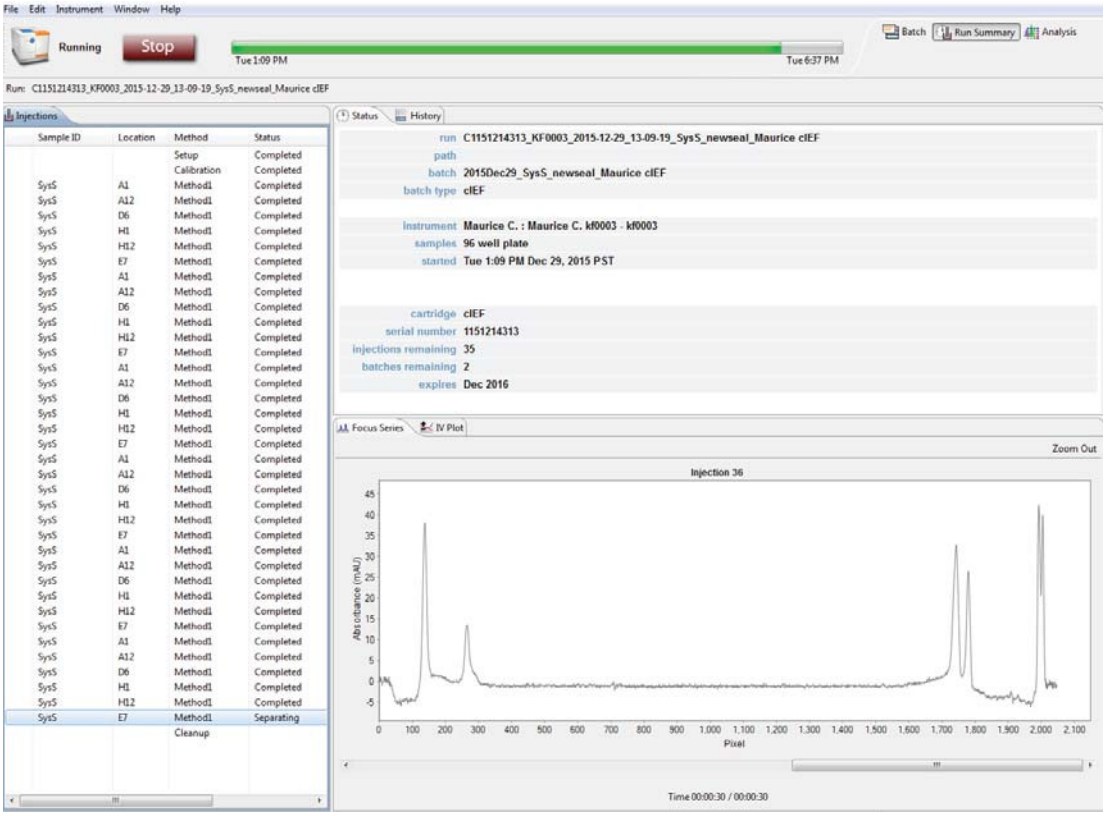
3. The Start Run box shows you the number of injections and batches remaining on your cartridge. Make sure you still have enough injections left before you start the run. If not, prep a new cartridge.
4. Click in the **Results File name** box if you want to change the default run file name. Otherwise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



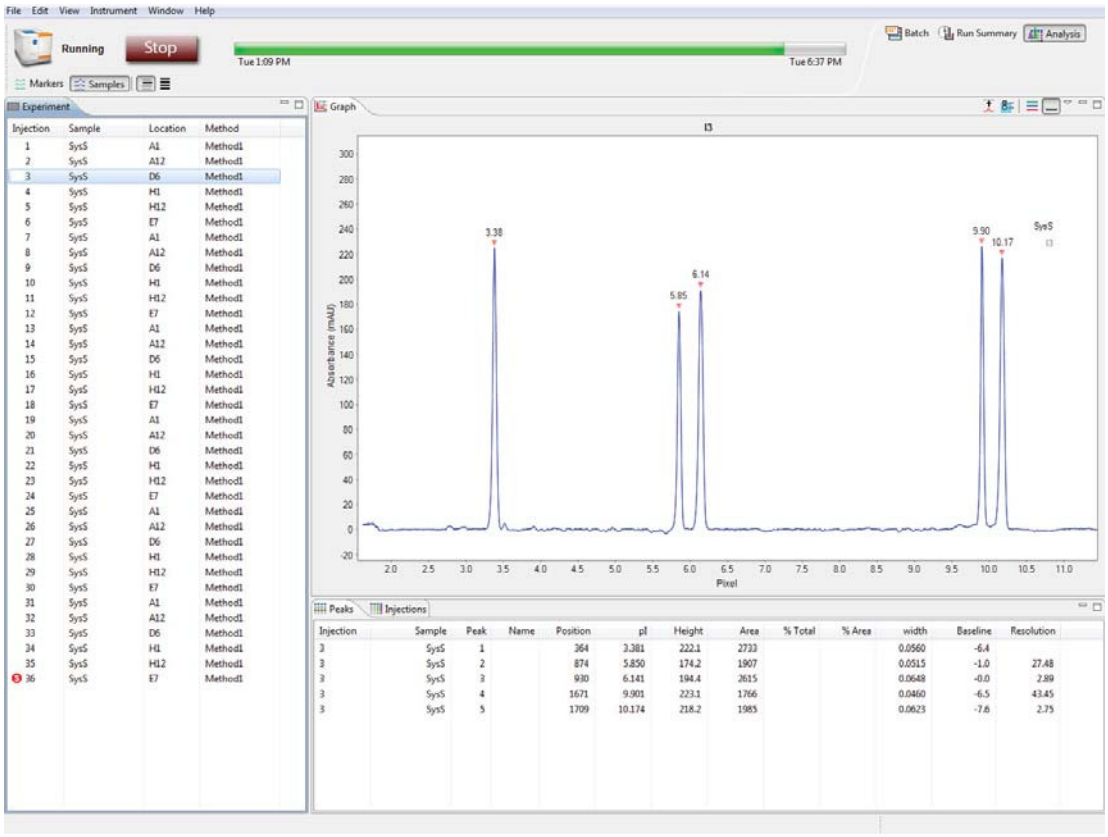
5. If you don't want to save the file to the default Runs folder, click **Browse** to select a different location.
6. Enter any run details you'd like in the Comments box (optional).
7. Click **Start** to start the run.

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.

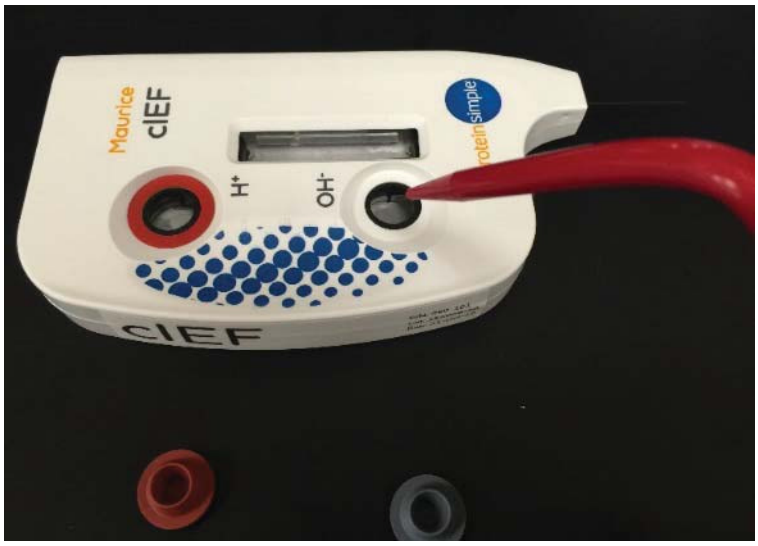
NOTE: Disposal of cartridges, sample plates and vials depends on the samples you ran. If you aren't sure what your sample origins are, we recommend you dispose of everything in biohazard waste.

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 lab-

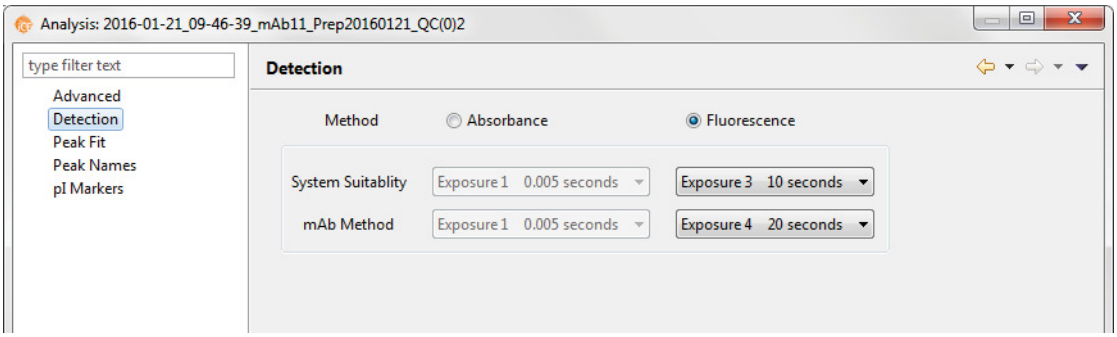
oratory practices and local, state/provincial, or national environmental and health regulations. Read and understand the Safety Data Sheets (SDSs) provided by the manufacturers of the chemicals in the waste content before you store, handle, or dispose of chemical waste.

Checking Your Data

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

Step 1: Select Your Detection Mode

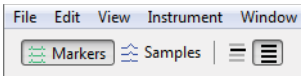
1. Go to the **Analysis** screen and open your run (if it isn't already open).
2. The data displays in absorbance mode by default. If you want to look at fluorescence data instead, select **Edit** from the main menu and click **Analysis**. In the Analysis window, select **Detection** in the left side-bar,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



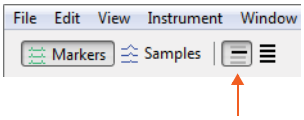
Step 2: Check Your pI Markers

To make sure your pI markers are identified correctly:

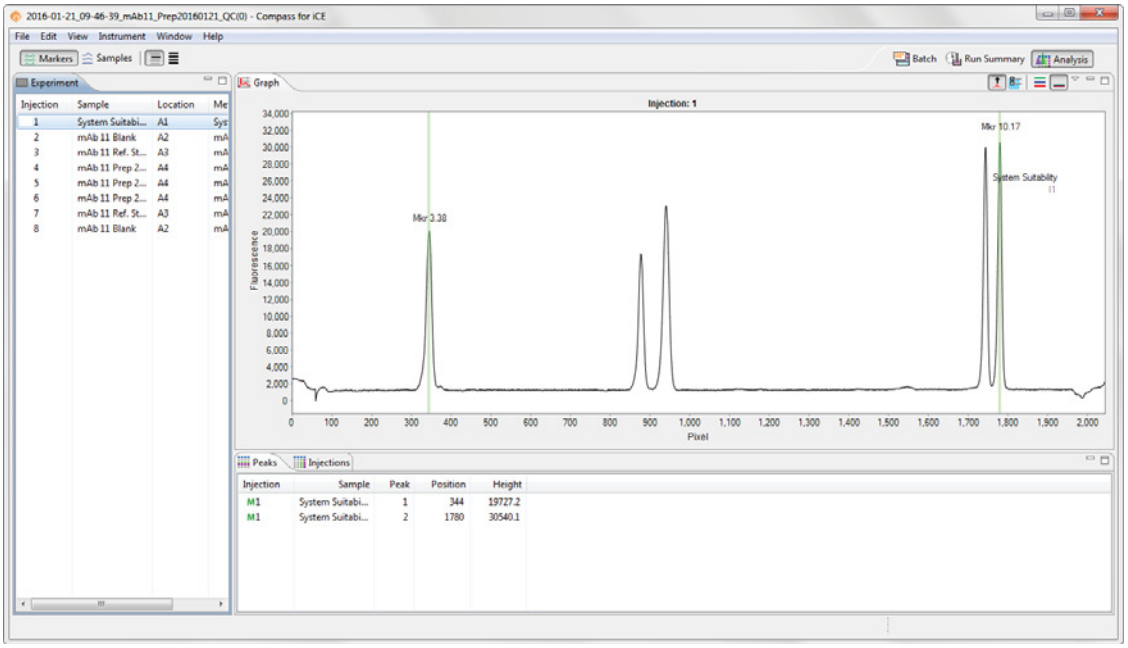
1. Go to the **Analysis** screen.
2. Click **Markers** in the View bar.



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

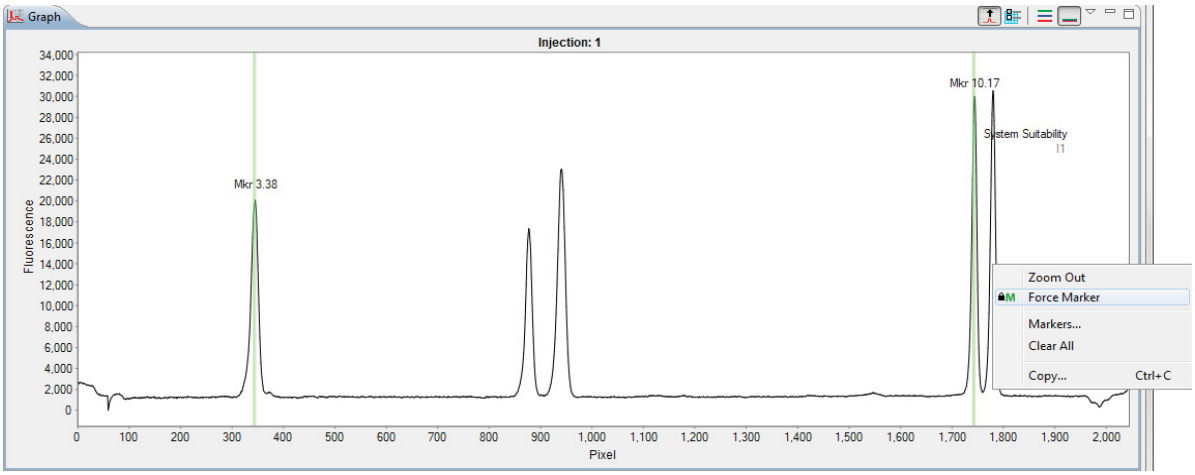


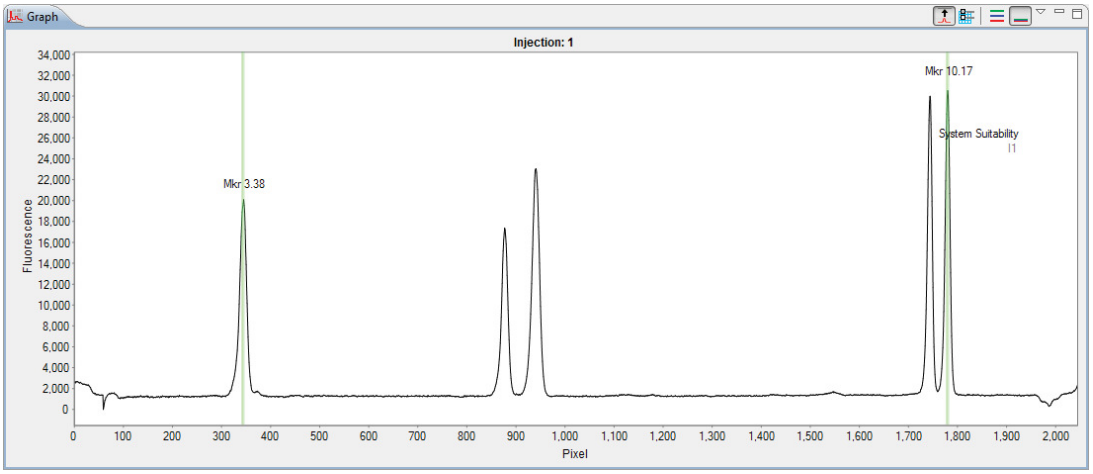
4. Click **Injection 1** in the Experiment pane.
5. Check that your pI markers in the electropherogram have been correctly identified. Each marker peak will have a green vertical line running through it and be labeled Mkr. They're also identified with an **M** in the Peaks table.



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

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





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

Peaks | Injections

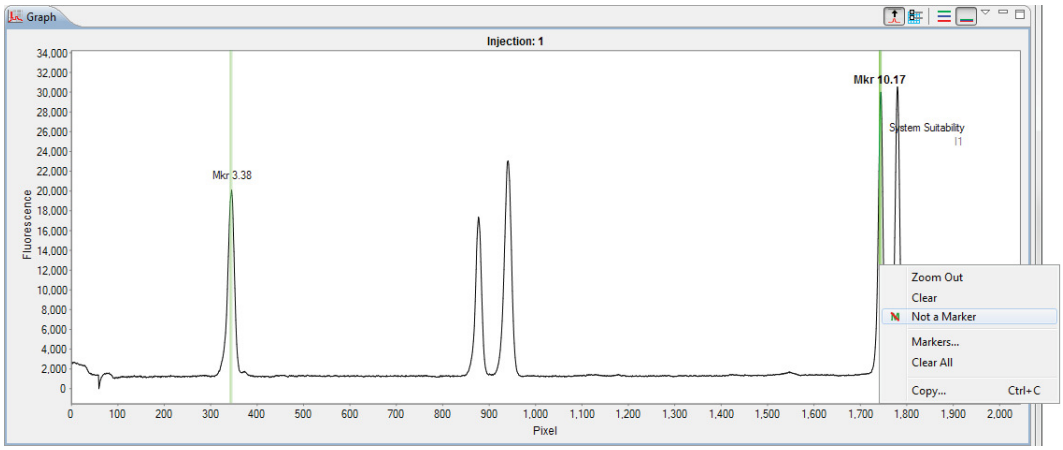
Injection	Sample	Peak	Position	Height
1	System Suitabi...	14	1315	1315.8
1	System Suitabi...	15	1422	1433.6
1	System Suitabi...	16	1549	1627.6
M1	System Suitabi...	17	1743	29396.8
1	System Suitabi...	18	1780	30540.1
1	System Suitabi...	19	1959	1399.5
1	System Suitabi...	20	2018	1470.4

Experiment

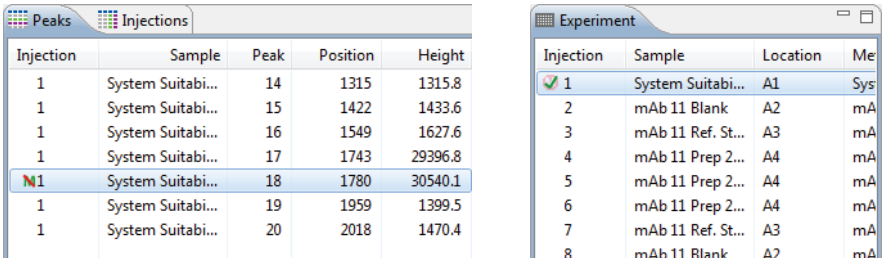
Injection	Sample	Location	Me
1	System Suitabi...	A1	Sys
2	mAb 11 Blank	A2	mA
3	mAb 11 Ref. St...	A3	mA
4	mAb 11 Prep 2...	A4	mA
5	mAb 11 Prep 2...	A4	mA
6	mAb 11 Prep 2...	A4	mA
7	mAb 11 Ref. St...	A3	mA

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

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



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
M1	System Suitabi...	18	1780	30540.1
1	System Suitabi...	19	1959	1399.5
1	System Suitabi...	20	2018	1470.4

Experiment

Injection	Sample	Location	Me
✓ 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
8	mAb 11 Blank	A2	mA

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

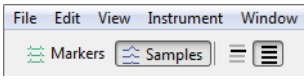
Step 3: Checking Sample Peaks

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

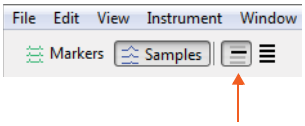
NOTE: The reported protein pI in Compass may vary slightly from predicted pIs based on sample, buffer, and method conditions.

To make sure your sample proteins are identified correctly:

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

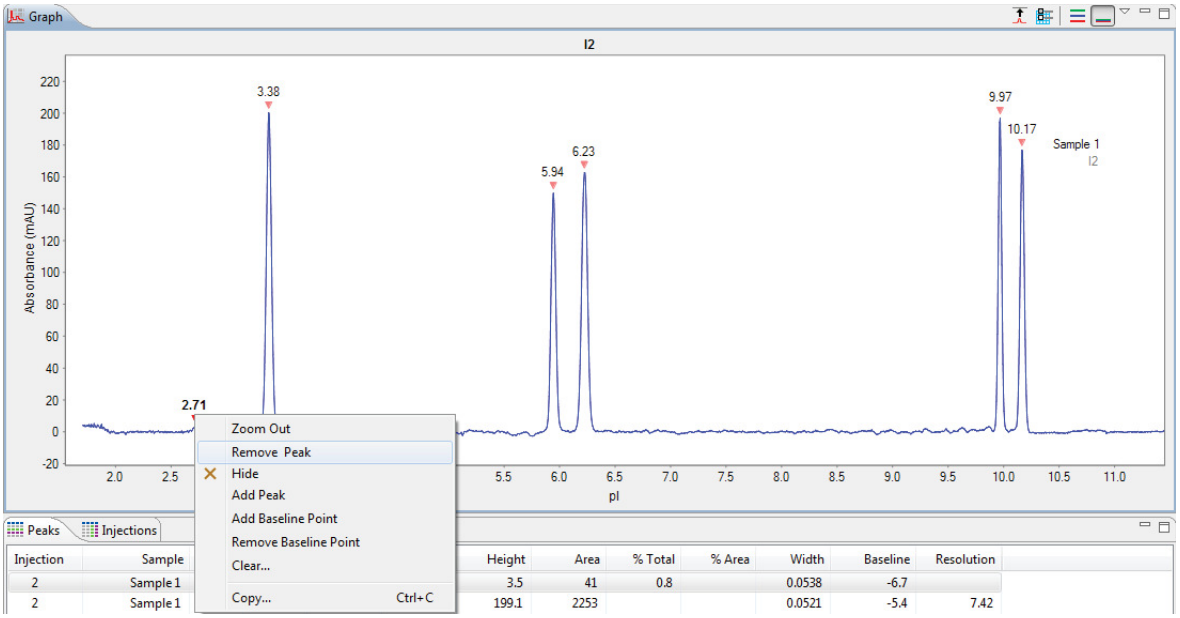


2. Click the **Single View** icon in the View bar.

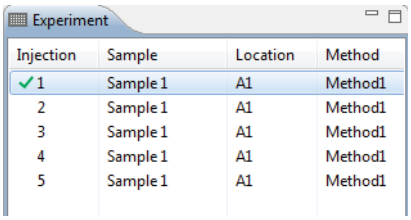


3. Click **Injection 1** in the Experiment pane.
4. If your sample peaks aren't identified correctly, here's how to manually correct them:

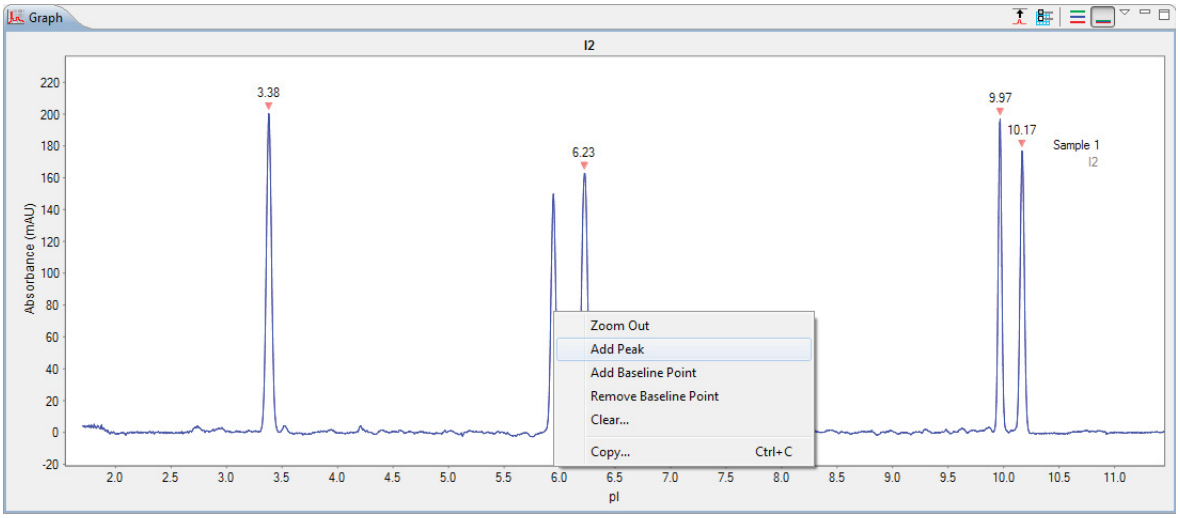
   If a peak is incorrectly identified as a sample peak: Right-click the peak in the electropherogram or Peaks table and select **Remove Peak**. Compass will no longer identify it as a sample peak in the electropherogram and the peak data will be removed in the results table.



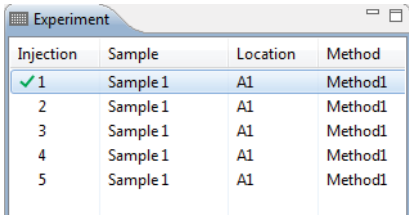
A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.



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.



---

*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.

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)

- Maurice CE-SDS MW Markers (optional)
- β-mercaptoethanol (βME, ≥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 µL of 14.2 M β-mercaptoethanol to 50 µL 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 µL of 14.2 M β-mercaptoethanol.
7. Mix thoroughly by vortex.

8. Centrifuge the tube and heat mixture in a water bath or thermocycler at 70 °C for 10 minutes.
9. Put the tube on ice for 5 minutes.
10. Vortex briefly and spin down.

CE-SDS Molecular Weight (MW) Markers (Optional)

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 µL of 14.2 M β-mercaptoethanol.
7. Mix thoroughly.
8. Centrifuge the tube and heat the mixture in a water bath or thermocycler at 70 °C for 10 minutes.
9. Put the tube on ice for 5 minutes.
10. Vortex briefly and spin down.

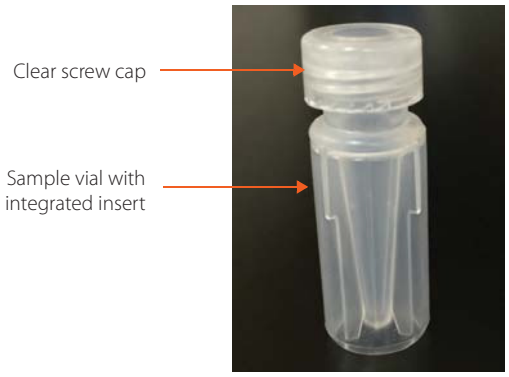
Spin Samples, Standards and CE-SDS MW Markers

If you're using a 96-well plate:

1. Transfer 50 µL of each of your samples, IgG Standard and CE-SDS MW Markers to their designated wells in a 96-well plate.
2. Cover the plate with a lid and spin for 10 minutes at 1000 xg in a centrifuge with a plate adapter.
3. Pop any bubbles in the samples with a clean pipette tip.

If you're using vials:

1. Transfer 50 µL of each of your samples, IgG Standard and CE-SDS MW Markers to their designated sample vials with 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.



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 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 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.

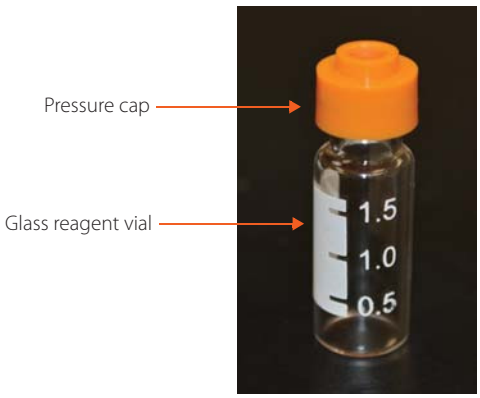
3. Place the vials in a centrifuge using vial adapter (12 mm, 2 mL vials) and spin for 10 minutes at 1000 xg.

Reagents

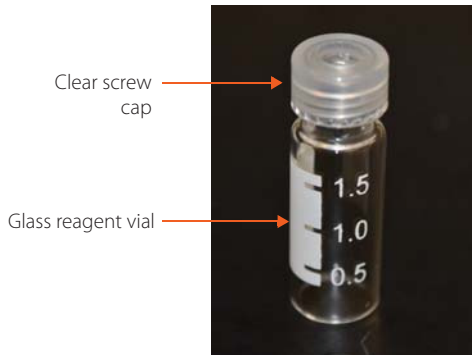
NOTE: Don't reuse reagents, vials or the clear screw caps. Always keep the orange pressure caps paired with their respective reagents. If you want to reuse pressure caps, first wash them thoroughly with DI water, soak overnight in DI water, rinse caps thoroughly with DI water again and air dry them before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

---

1. Pipette 1.5 mL of Conditioning Solution 1 into a glass reagent vial, label and close with an **orange pressure cap**.



2. Pipette 1.5 mL of Conditioning Solution 2 into a glass reagent vial, label and close with an **orange pressure cap**.
3. Pipette 1.0 mL of Wash Solution into a glass reagent vial, label each and close with an **orange pressure cap**.
4. Pipette 1.5 mL of Wash Solution into two glass reagent vials. Label each and close both with **clear screw caps**.



5. Pipette 1 mL of Separation Matrix into a glass reagent vial, label and close with an **orange pressure cap**.
6. Pipette 1 mL of Running Buffer - Bottom into 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

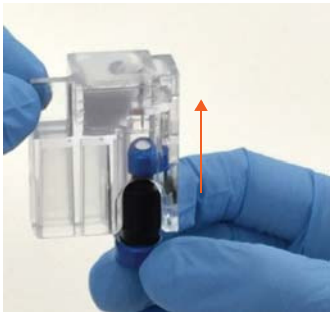
1. Take the CE-SDS Cartridge out of its packaging. Save the packaging, you'll need it later to store the cartridge.

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

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.

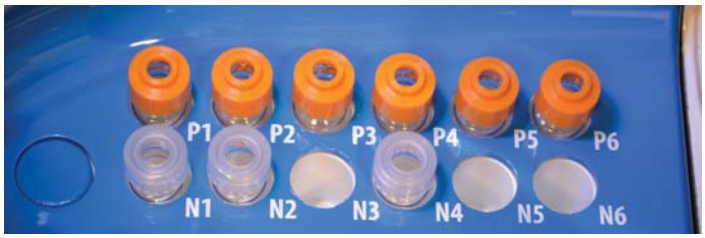
Step 4: Load Samples and Reagents

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.

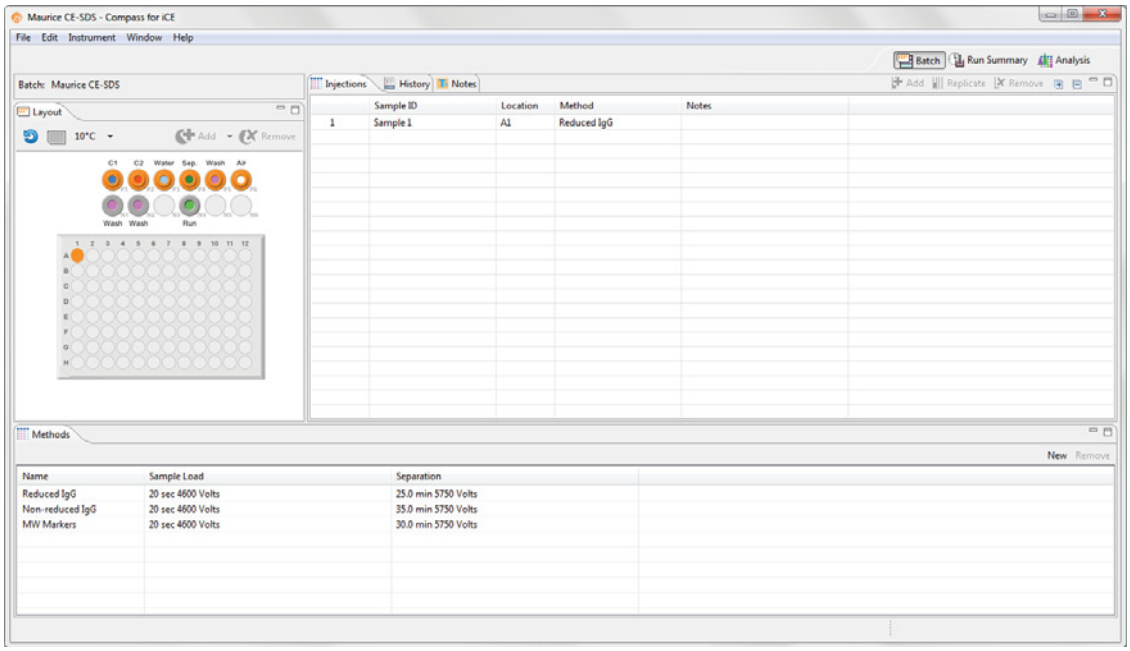
NOTE: Well A1 on the 96-well plate should be in the top left corner of the insert.

---

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.



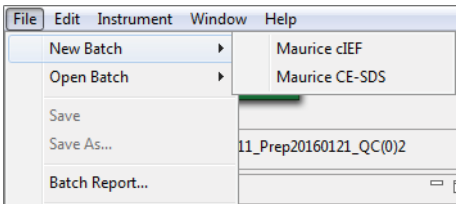
3. To create a batch, make sure Maurice is connected to Compass for iCE. If he isn't, select **Instrument** and click **Connect**. Then select your Maurice system and click **Connect**.

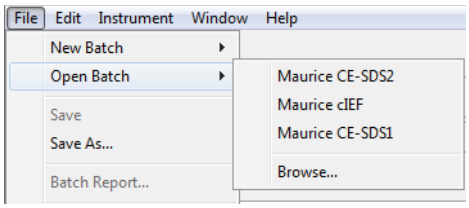
   To create a new batch:

   - 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.**

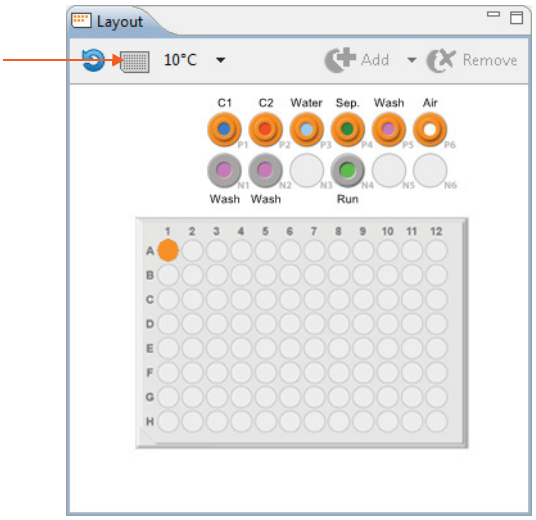
   To use an existing batch: In the main menu, select **File > Open Batch.**

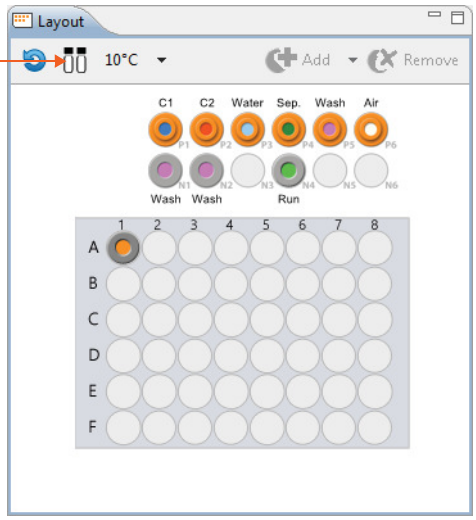
NOTE: If you're making changes to an existing batch, follow the steps in this section. Otherwise skip to "Step 6: Start the Batch" on page 133.



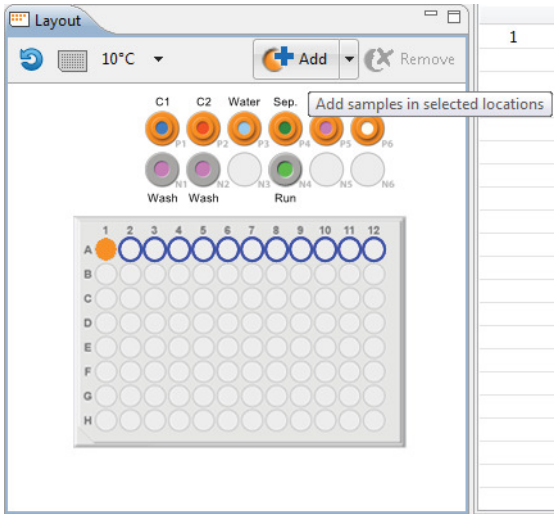


4. In the Layout pane, clicking on the vial/plate icon toggles between formats. Select a 96-well plate or 48 vials depending on what you're running.

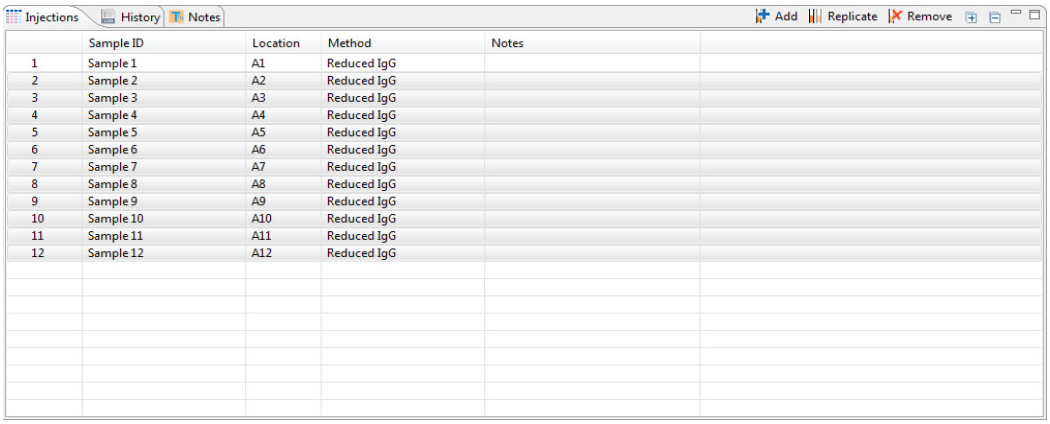




5. Use your mouse to highlight the well positions for each of your samples, then click **Add**.



This populates the Injections table:



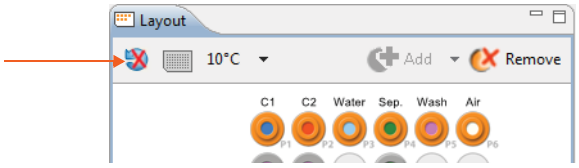
	Sample ID	Location	Method	Notes
1	Sample 1	A1	Reduced IgG	
2	Sample 2	A2	Reduced IgG	
3	Sample 3	A3	Reduced IgG	
4	Sample 4	A4	Reduced IgG	
5	Sample 5	A5	Reduced IgG	
6	Sample 6	A6	Reduced IgG	
7	Sample 7	A7	Reduced IgG	
8	Sample 8	A8	Reduced IgG	
9	Sample 9	A9	Reduced IgG	
10	Sample 10	A10	Reduced IgG	
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:

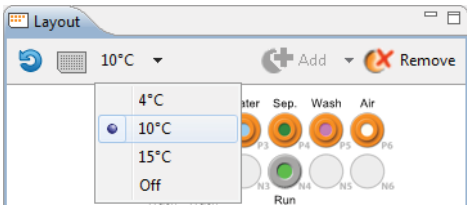
If a sample was reinjected, the injection row will be flagged in the Injections pane in the Run Summary screen. See "Injection Flags" on page 158 for more info.

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.

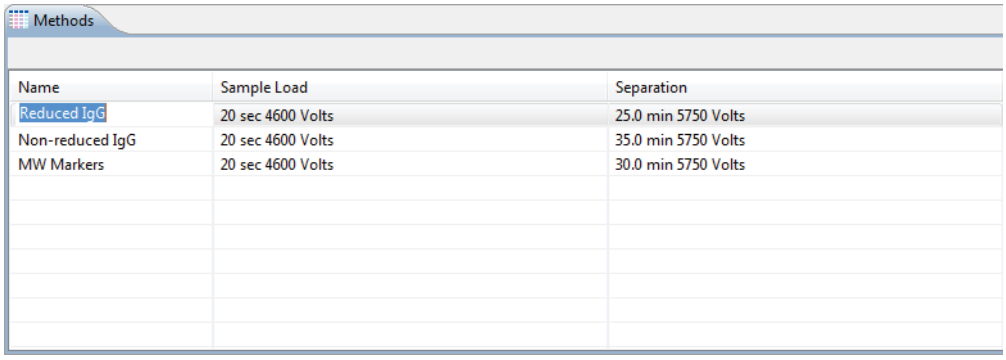


8. In the Methods pane:

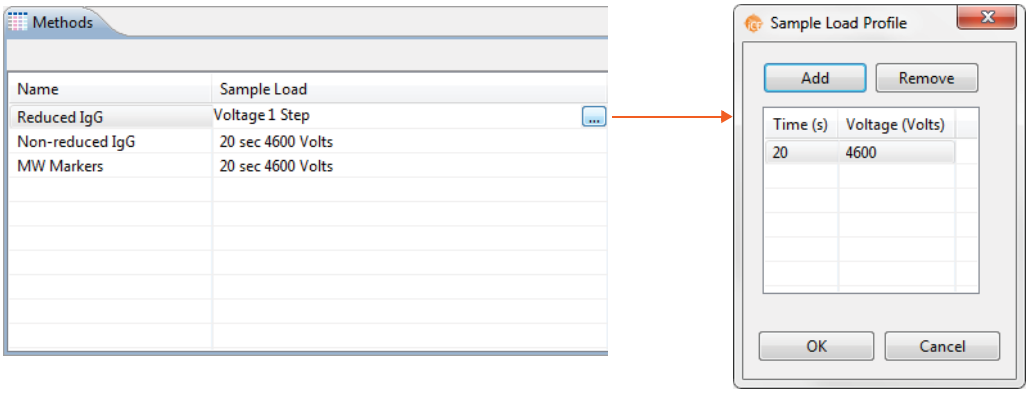
NOTE: There are three default methods. We recommend using the default method parameters for the listed samples. Please see the Maurice CE-SDS Application Guide for more information on method optimization.

---

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

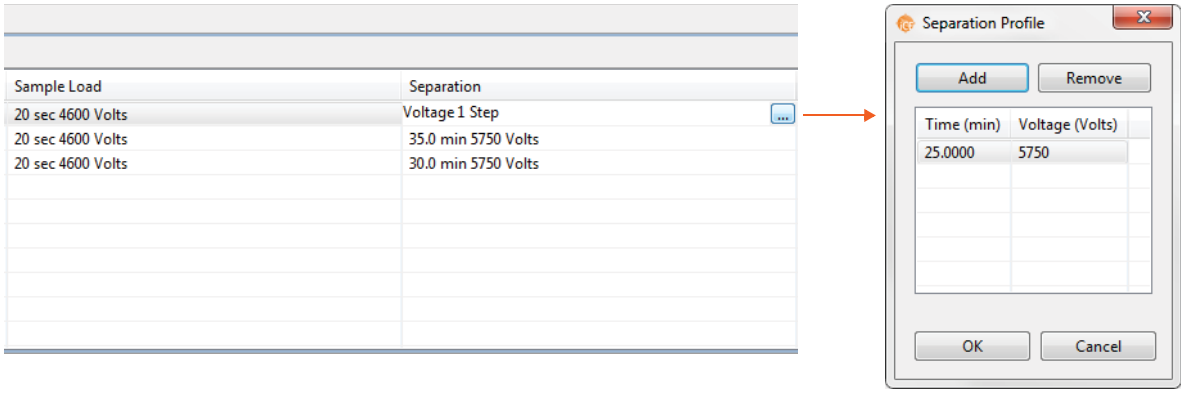


b. Click the first cell in the Sample Load column, then click then click the selection button **[...]** to set your load profile time (in seconds) and voltage.

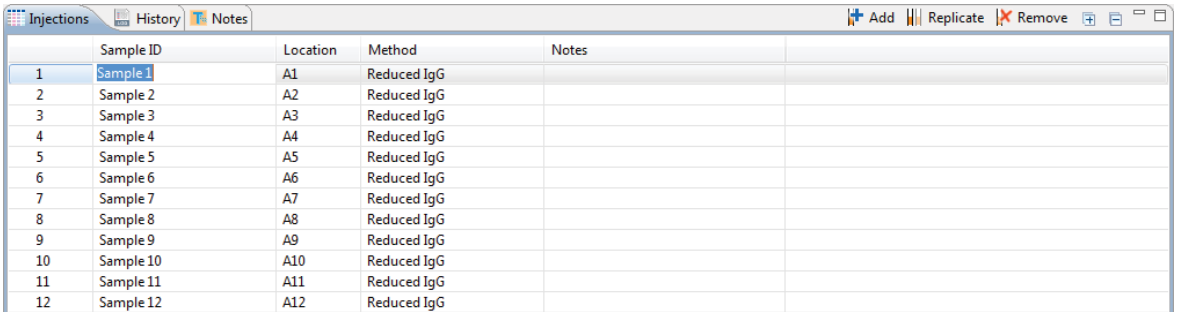


c. Click the first cell in the Separation column then click the selection button **[...]** to set your separation time (in minutes) and voltage.

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.

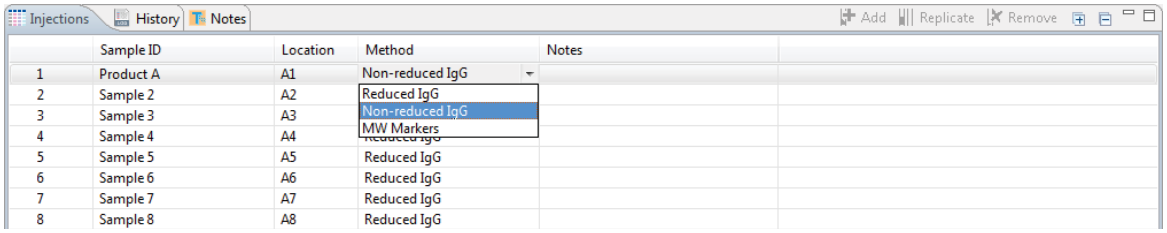


9. You can now:
   - Make updates to the remaining methods by repeating the prior steps.
   - Select a method and click **Remove** in the upper right corner of the Methods pane to delete it.
   - Click **New** in the upper right corner of the Methods pane to add a new one if you want to use different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



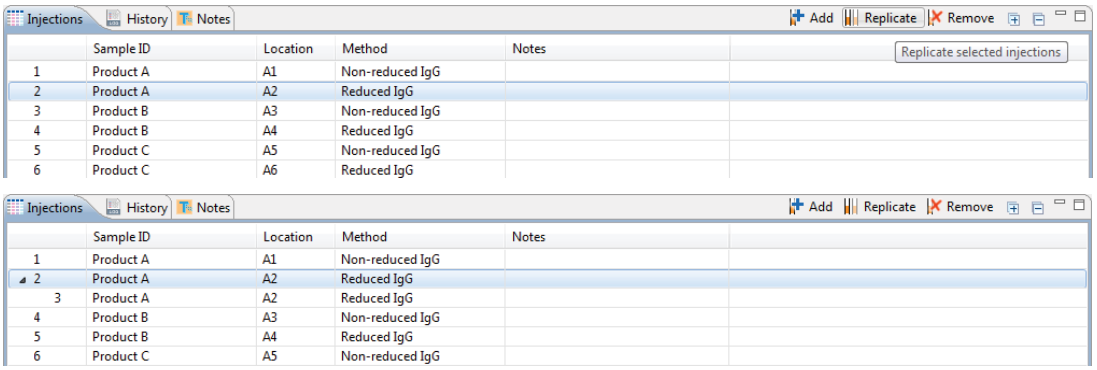
	Sample ID	Location	Method	Notes
1	Sample 1	A1	Reduced IgG	
2	Sample 2	A2	Reduced IgG	
3	Sample 3	A3	Reduced IgG	
4	Sample 4	A4	Reduced IgG	
5	Sample 5	A5	Reduced IgG	
6	Sample 6	A6	Reduced IgG	
7	Sample 7	A7	Reduced IgG	
8	Sample 8	A8	Reduced IgG	
9	Sample 9	A9	Reduced IgG	
10	Sample 10	A10	Reduced IgG	
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.



	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		
5	Sample 5	A5	Reduced IgG	
6	Sample 6	A6	Reduced IgG	
7	Sample 7	A7	Reduced IgG	
8	Sample 8	A8	Reduced IgG	

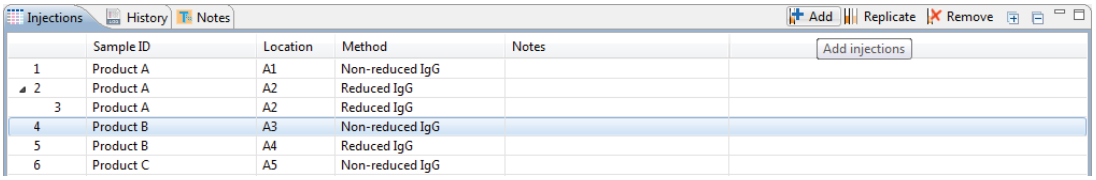
- **To add sequential replicate injections:** Highlight an injection and click **Replicate**. A new injection will be added under the row you selected



	Sample ID	Location	Method	Notes
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	

	Sample ID	Location	Method	Notes
1	Product A	A1	Non-reduced IgG	
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	

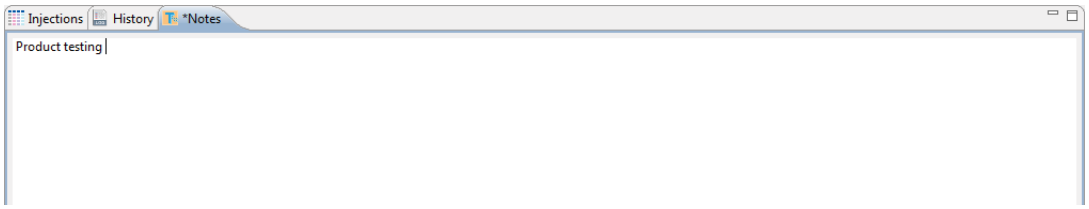
- **To add injections at the end of the batch:** Click on any sample position in the Layout pane or sample injection in the Injection table and click **Add**. A new injection using the same sample will be added to the end of the table. Assign the method if needed.



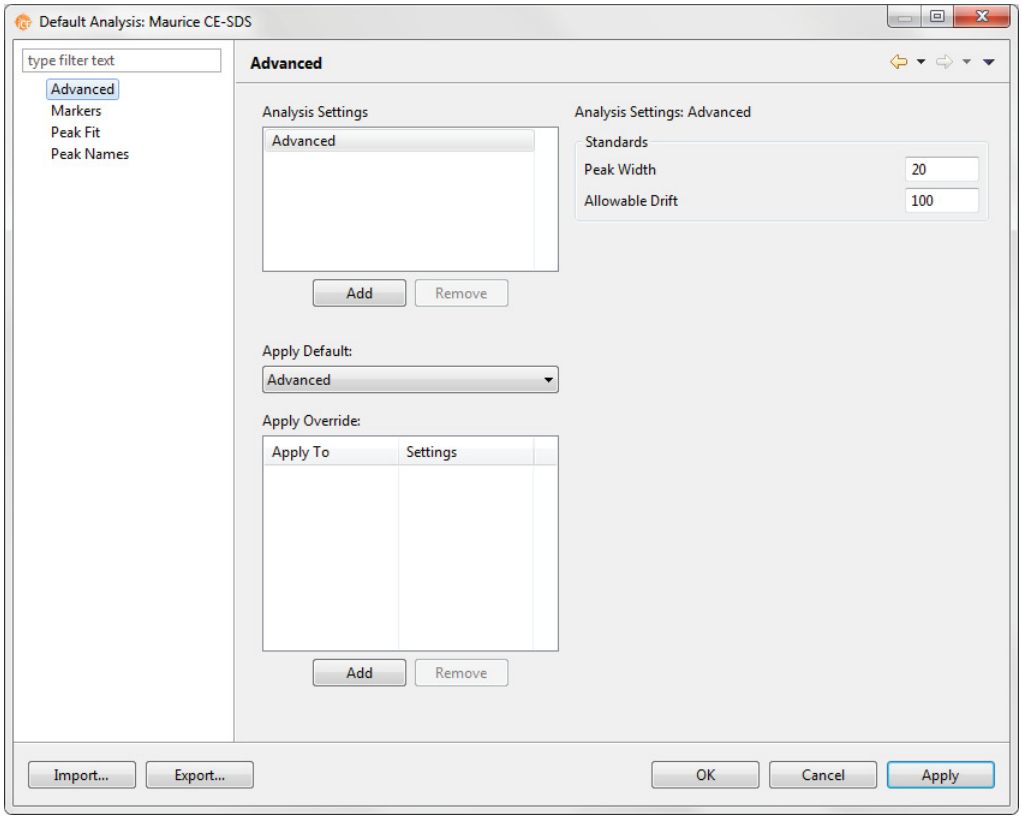
	Sample ID	Location	Method	Notes
1	Product A	A1	Non-reduced IgG	
2	Product A	A2	Reduced IgG	
3	Product A	A2	Reduced IgG	
4	Product B	A3	Non-reduced IgG	
5	Product B	A4	Reduced IgG	
6	Product C	A5	Non-reduced IgG	

- **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).

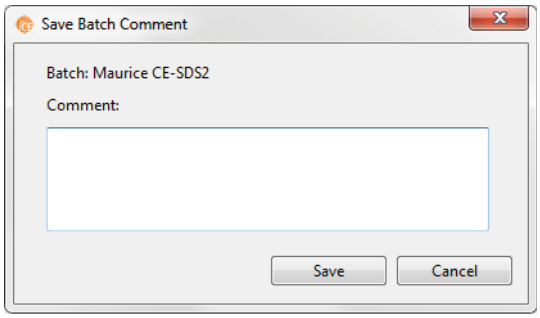


12. You can preset the parameters used to analyze data generated with the batch (optional). We recommend using the default parameters for CE-SDS applications, but if you want to modify parameters:
    a. Select **Edit** from the main menu and click **Default Analysis**. The following screen will display:



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

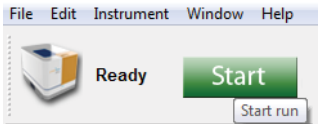
13. Once all of your sample, method and injection info is entered, select **File > Save**. Enter any comments on the batch if you want, then click **Save**.



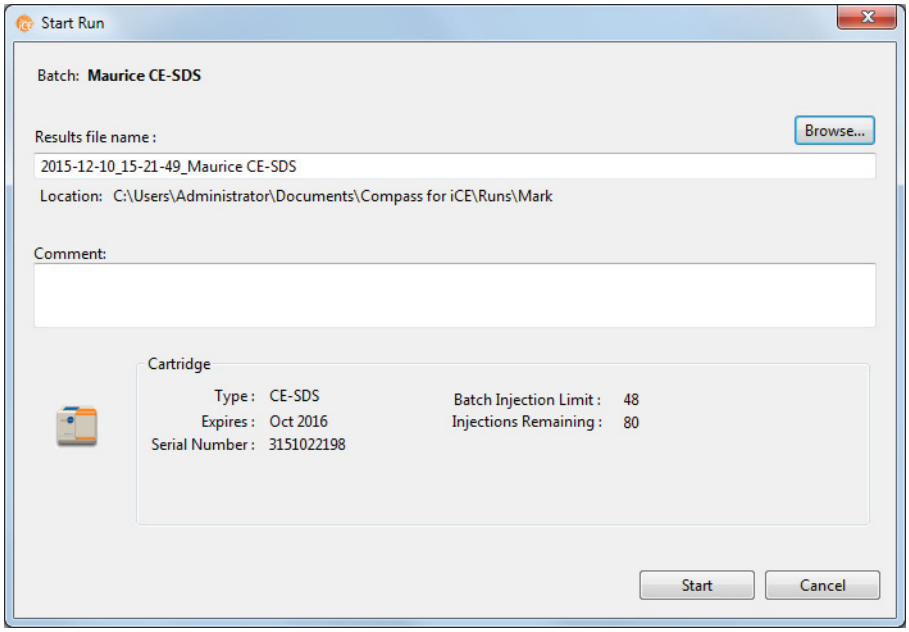
14. Enter a name for your batch then click **Save**.

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.



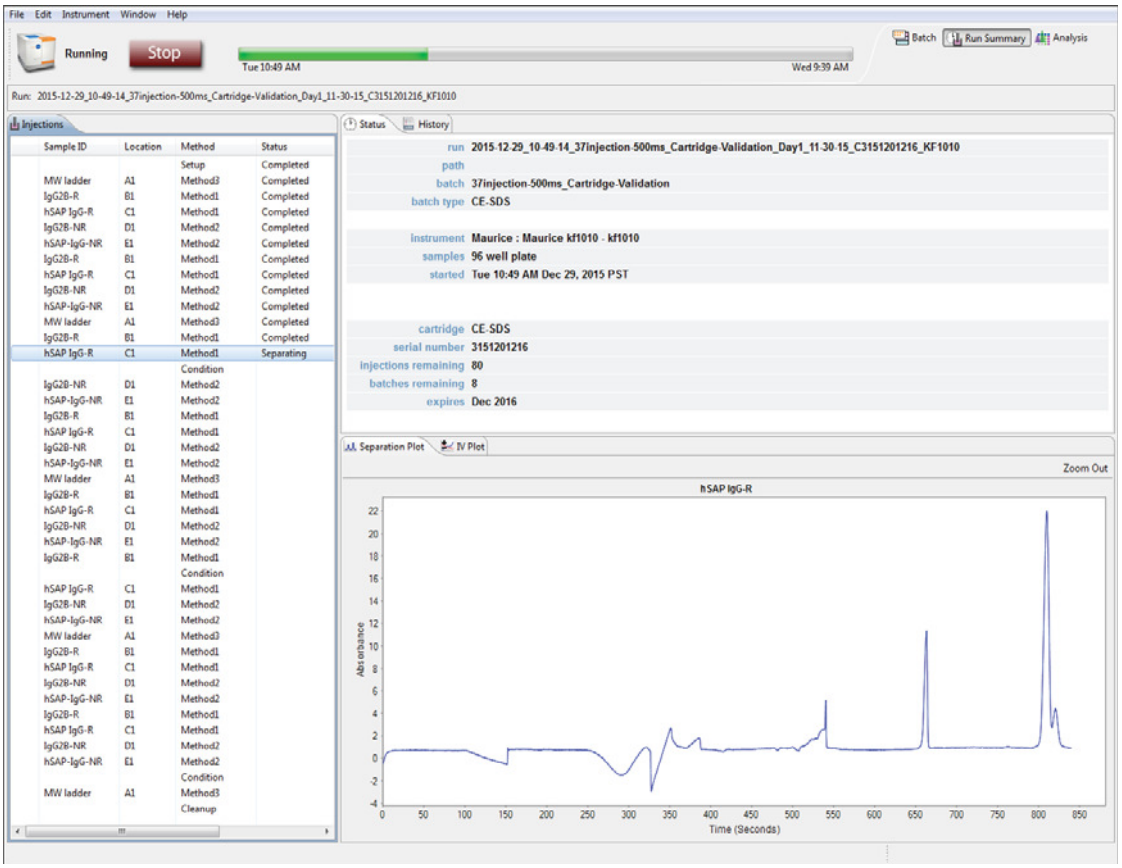
3. The Start Run box shows you the number of injections and batches remaining on your cartridge. Make sure you still have enough injections left before you start the run. If not, prep a new cartridge.
4. Click in the **Results File name** box if you want to change the default run file name. Otherwise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



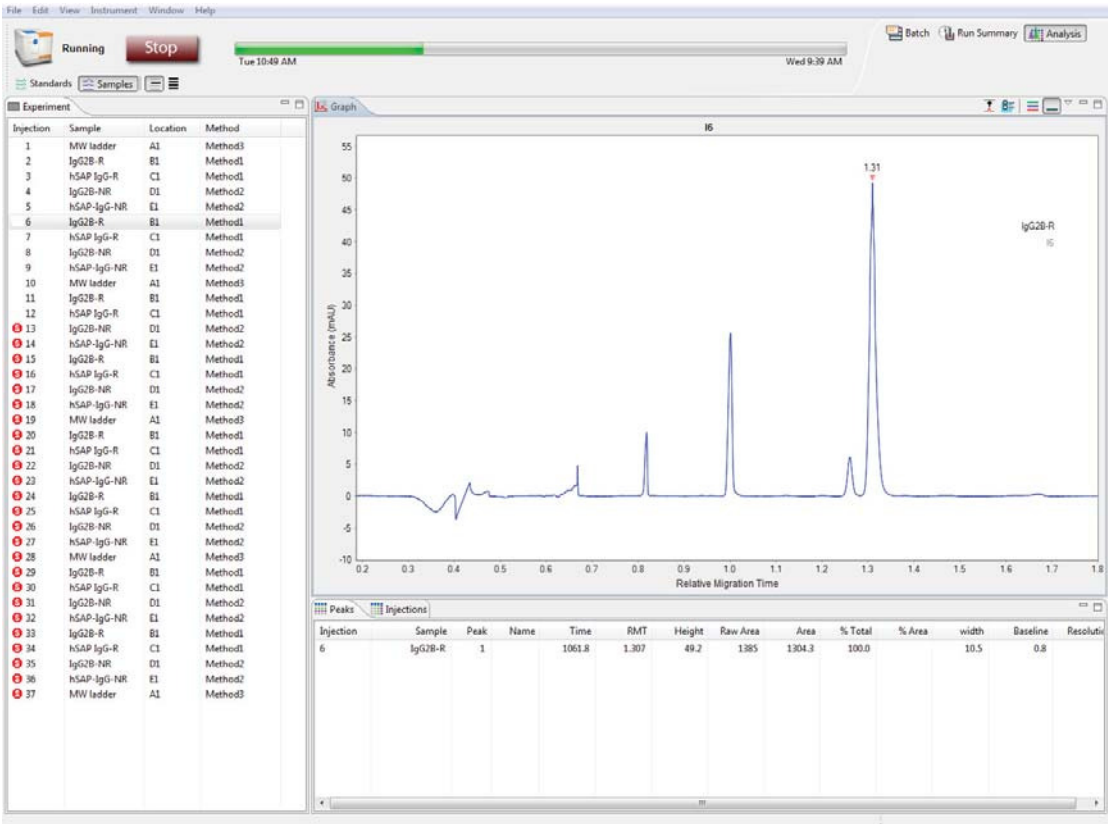
5. If you don't want to save the file to the default Runs folder, click **Browse** to select a different location.
6. Enter any run details you'd like in the Comments box (optional).
7. Click **Start** to start the run.

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 11, *"CE-SDS Data Analysis"* for more details.



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

NOTE: If you'd like Maurice to let you know when your run is done, you can set him up to tweet you. Go to "Setting Up Maurice Systems to Send Tweets" on page 383 for more info.

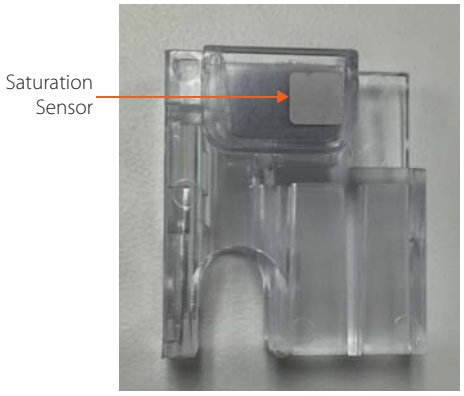
Post-batch Procedures

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:

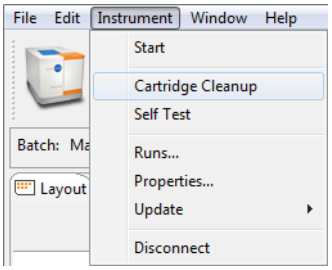
a. Pipette 1.5 mL of DI water in a new glass reagent vial and close it with an **orange pressure cap**. Place this vial in P3.

b. Insert a Cleaning Vial into the cartridge insert.

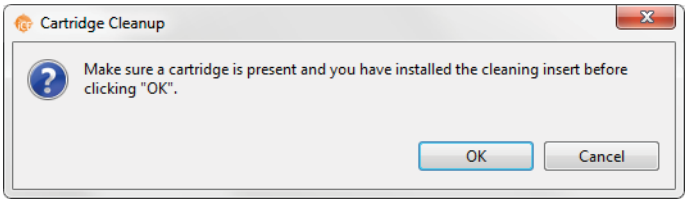
c. Slide the cartridge insert back into the cartridge.

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.

!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.

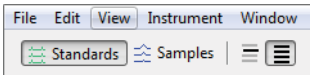
Checking Your Data

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.

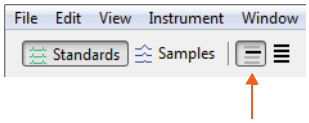
Step 1: Check Your Internal Standard

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.

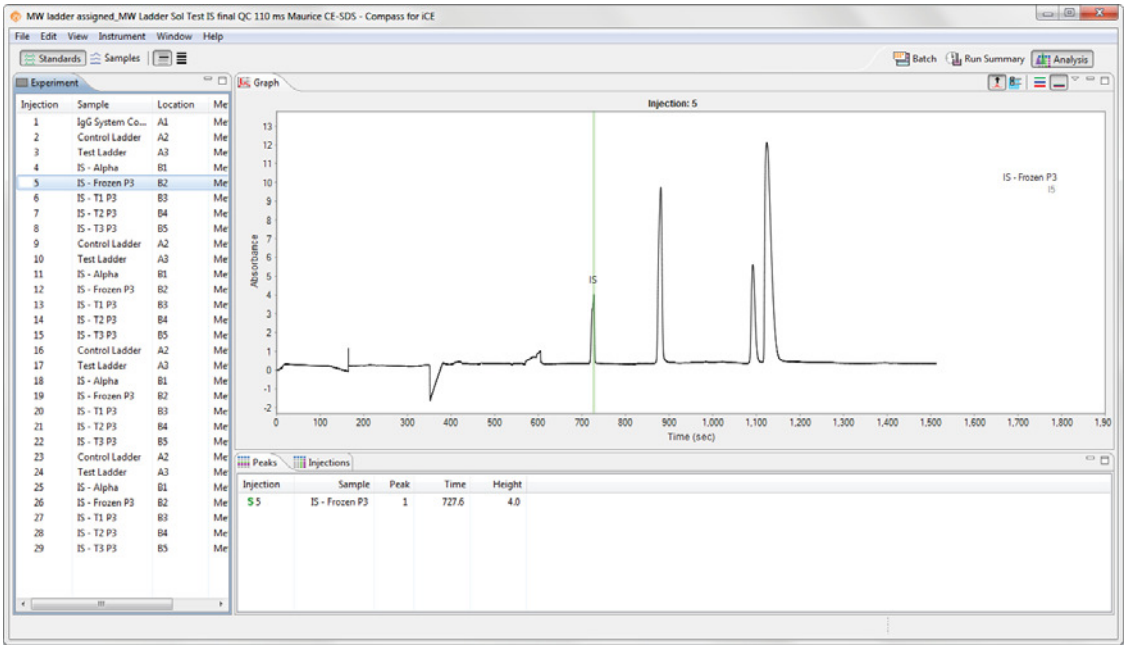


3. Click the **Single View** icon in the View bar.



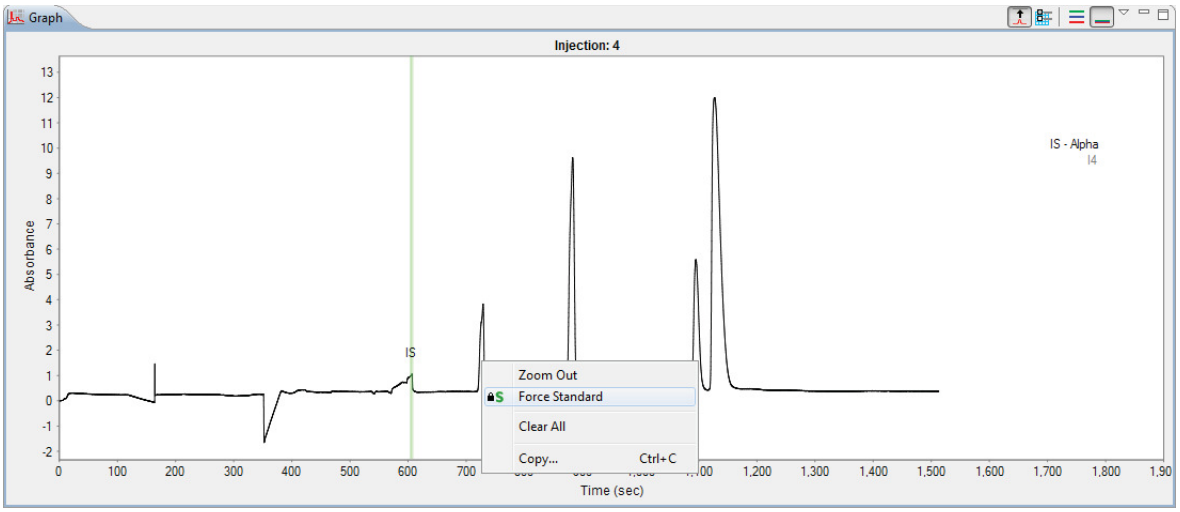
4. Click **Injection 1** in the Experiment pane.

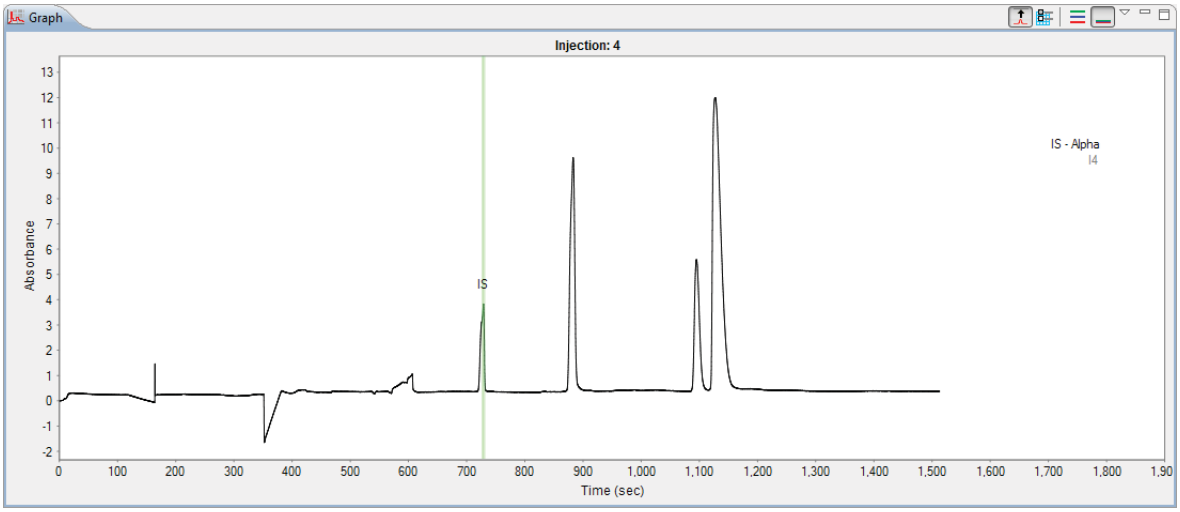
5. Check that your Internal Standard in the electropherogram has been correctly identified. It'll be labeled Std 1 and will have a green vertical line running through it. The Internal Standard is also identified with an **S** in the Peaks table.



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

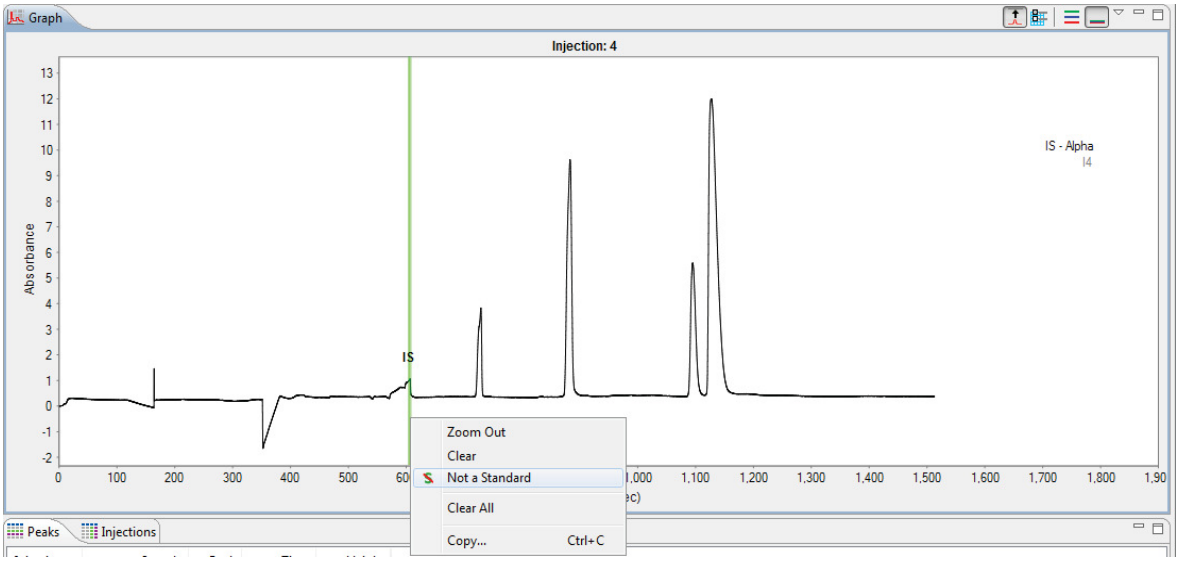
Injection	Sample	Peak	Time	Height
1	Sample 1	11	548.2	115.1
1	Sample 1	12	557.7	115.2
1	Sample 1	13	572.0	134.0
1	Sample 1	14	583.5	149.7
S 1	Sample 1	15	590.6	190.0
1	Sample 1	16	710.8	230.3
1	Sample 1	17	714.6	278.5

Experiment

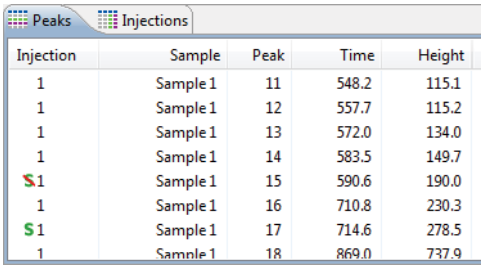
Injection	Sample	Location	Method
1	Sample 1	A1	Method1
2	Sample 1	A1	Method1
3	Sample 1	A1	Method1
4	Sample 1	A1	Method1
5	Sample 1	A1	Method1
6	Sample 1	A1	Method1
7	Sample 1	A1	Method1

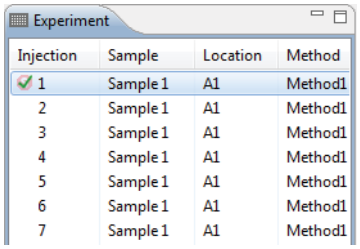
*NOTE: To remove an Internal Standard peak assignment that was made manually, right click on the peak in the electropherogram or Peaks table and click **Clear**. To clear all the manual settings for the injection, click **Clear All**.*

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.





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

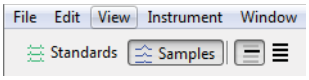
NOTE: You'll only need to do this if you ran the CE-SDS MW Markers. If you didn't, you can skip to the next section.

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.

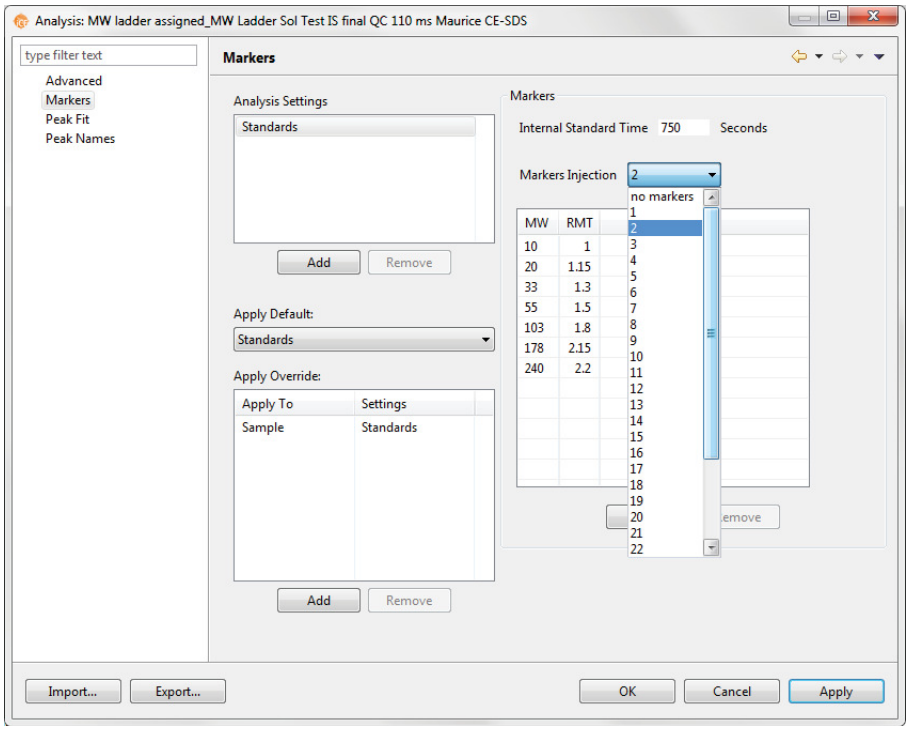
You'll see these sizing markers when you run the CE-SDS MW Markers: 10, 20, 33, 55, 103, 178, and 240 kDa.

To get MW data:

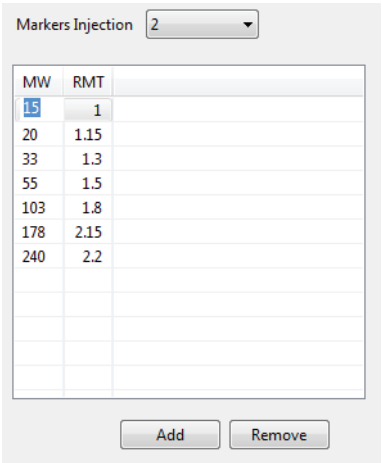
1. Click **Samples** in the View bar.



2. Select **Edit** from the main menu and click **Analysis**. In the Analysis window, select **Markers** in the left sidebar. Then click the **Markers Injection** drop down menu to select the injection you ran your CE-SDS MW Markers in.

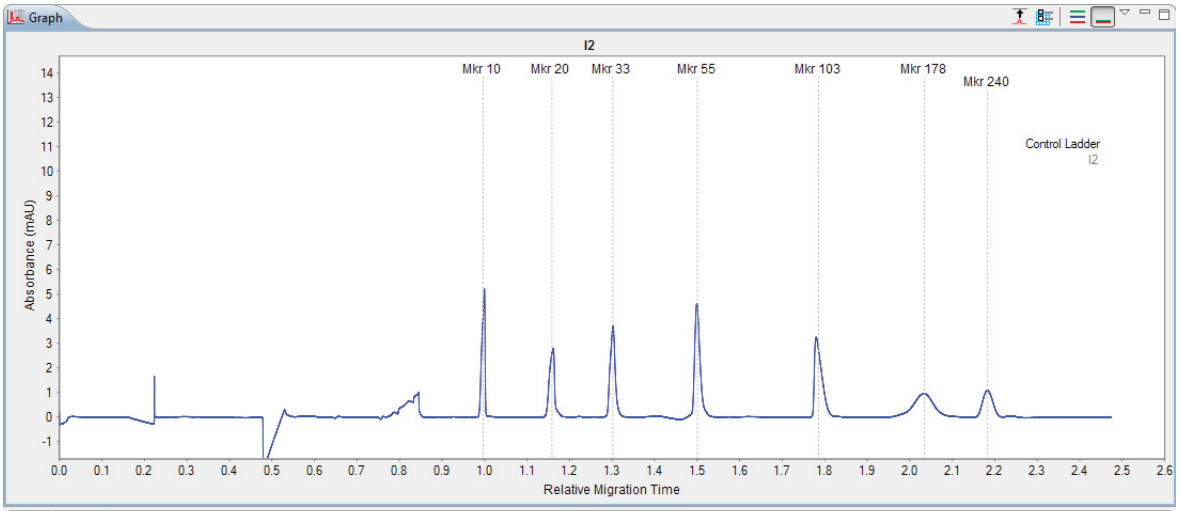


3. The default Maurice CE-SDS MW Markers molecular weights and relative migration time (RMT) values are already populated in the table. If you'd like to use these values, skip to the next step. If you're using different markers, click in the MW and RMT cells to type new values, click a row and select **Remove** to delete, or click **Add** to add a new one.



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.

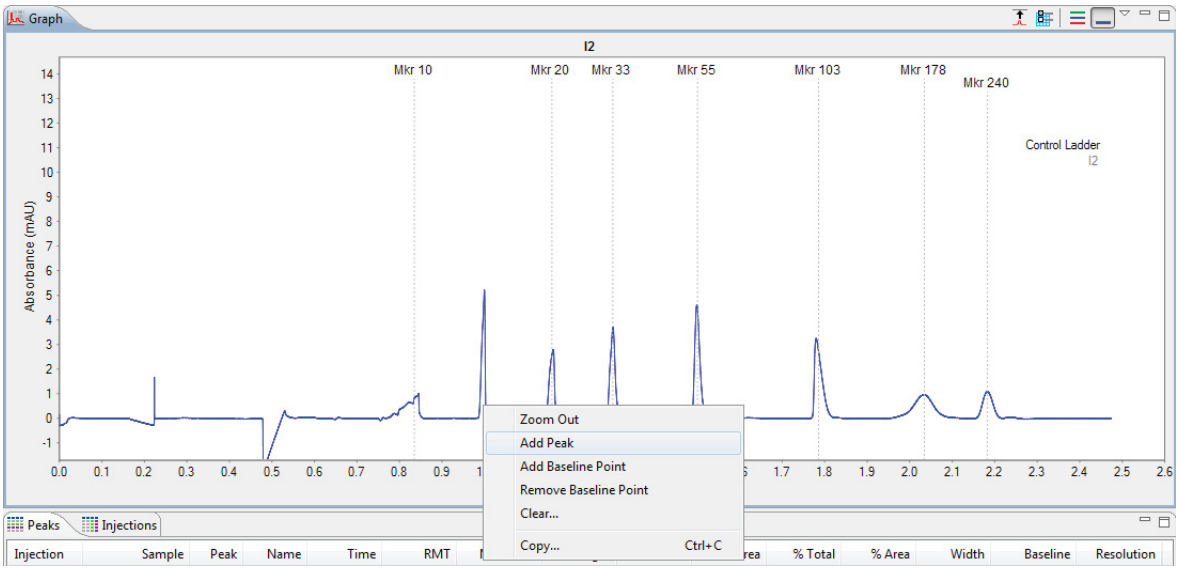


Peaks | Injections

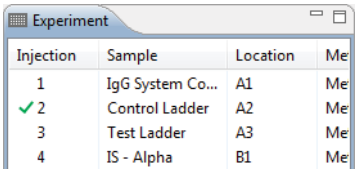
Injection	Sample	Peak	Name	Time	RMT	MW (kDa)	Height	Raw Area	Area	% Total	% Area	Width	Baseline	Resolution
2	Control Ladder	1	Mkr 10	730.6	0.997	10.00	5.2	297	407.2			6.4	0.3	
2	Control Ladder	2	Mkr 20	849.1	1.158	20.00	2.8	268	315.8	17.9		9.9	0.4	8.54
2	Control Ladder	3	Mkr 33	954.0	1.302	33.00	3.7	346	362.9	20.5		9.8	0.4	6.27
2	Control Ladder	4	Mkr 55	1100.0	1.501	55.00	4.6	454	413.0	23.4		9.8	0.4	8.81
2	Control Ladder	5	Mkr 103	1308.7	1.786	103.00	3.2	434	331.7	18.8		13.9	0.4	10.39
2	Control Ladder	6	Mkr 178	1491.0	2.034	178.00	1.0	329	220.8	12.5		36.2	0.5	4.29
2	Control Ladder	7	Mkr 240	1600.0	2.183	240.00	1.1	199	124.2	7.0		19.6	0.5	2.30

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.



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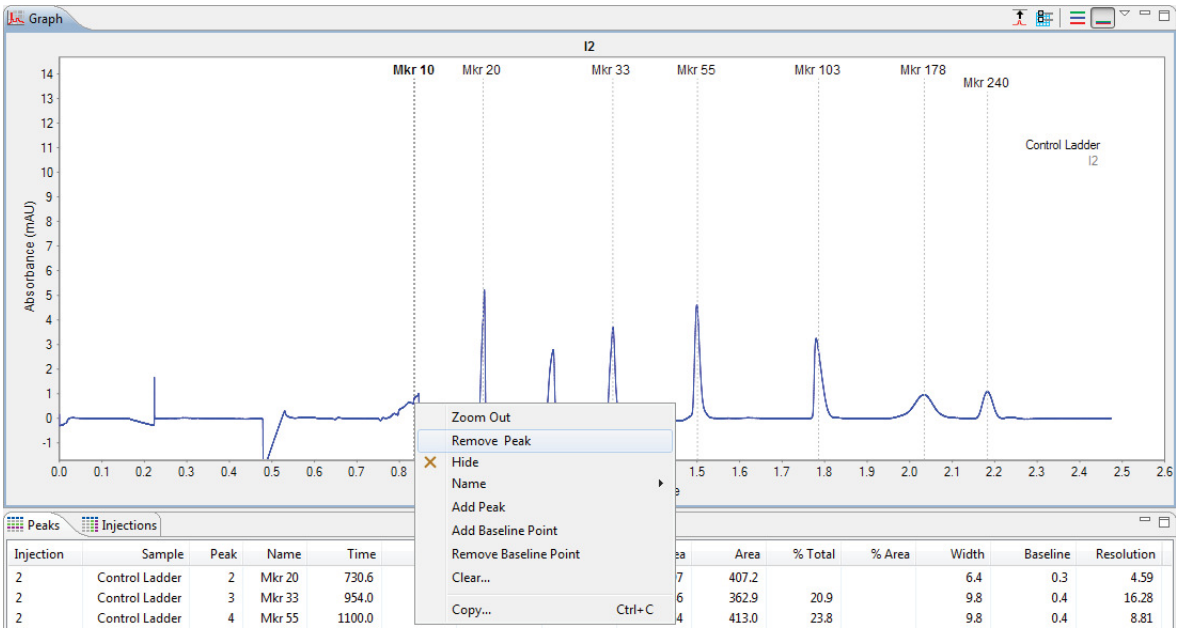
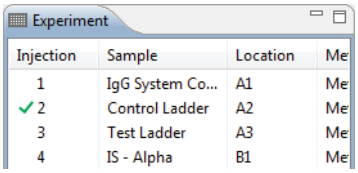
*NOTE: To remove MW Marker peak assignments that were made manually, right click on the peak in the electropherogram or Peaks table and click **Clear**.*

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.

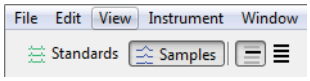


Step 3: Checking Sample Peaks

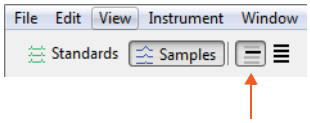
All detected peaks will be labeled automatically with the RMT (default) or apparent MW (if the CE-SDS MW Markers were run).

To make sure your sample proteins are identified correctly:

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

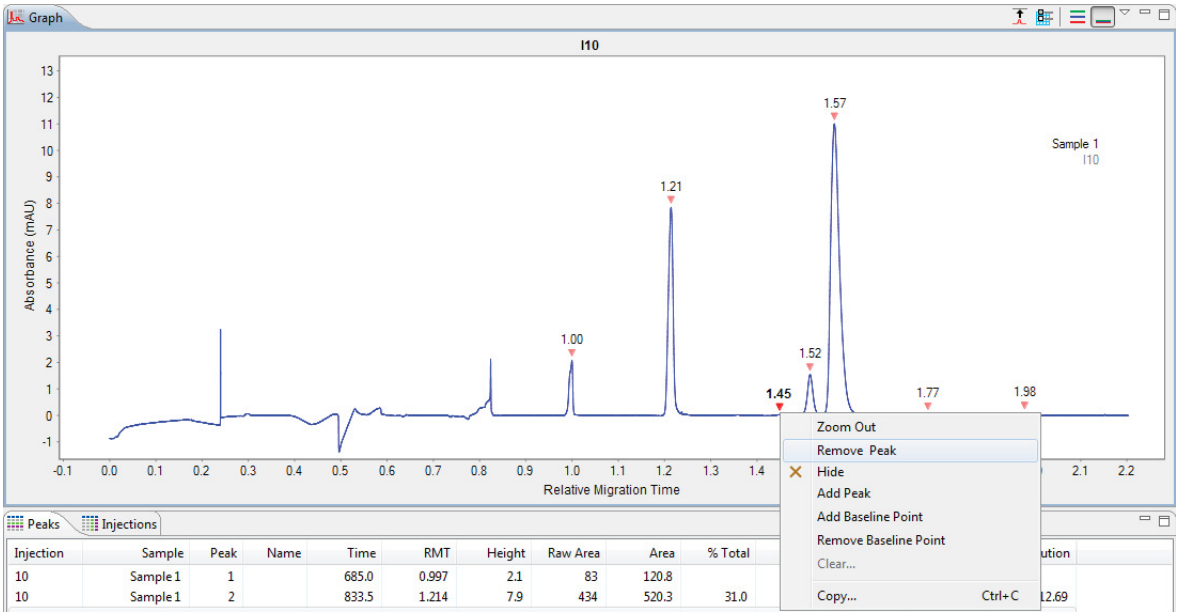


2. Click the **Single View** icon in the View bar.

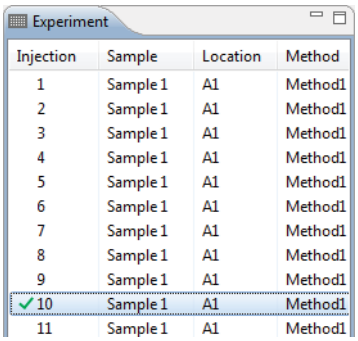


3. Click **Injection 1** in the Experiment pane.
4. If your sample peaks aren't identified correctly, here's how to manually correct them:

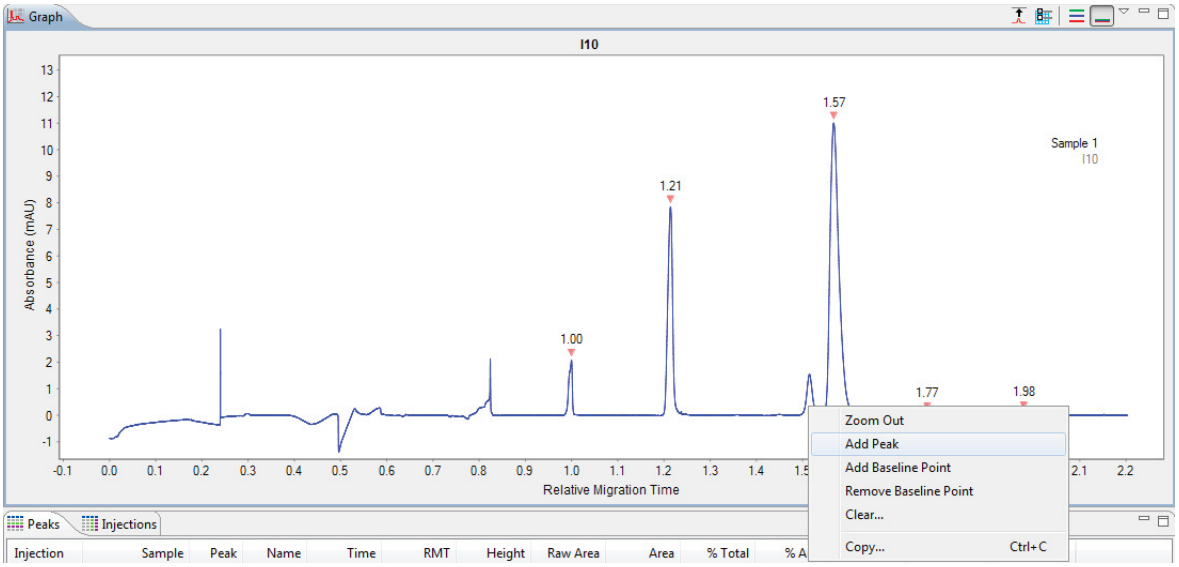
   If a peak is incorrectly identified as a sample peak: Right-click the peak in the electropherogram or Peaks table and select **Remove Peak**. Compass will no longer identify it as a sample peak in the electropherogram and the peak data will be removed in the results table.



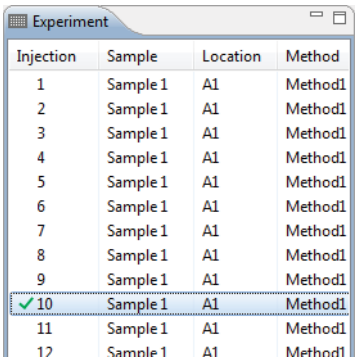
A check mark will appear next to the injection in the Experiment pane to indicate a manual correction was made.



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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*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**.*

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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.