



Carterra Ultra® Instrument User Manual

Ultra



Table of Contents

1. Introduction	4
1.1 Information About This Manual	4
1.2 Intended Purpose of Ultra	4
1.3 Regulatory Information	4
1.4 Associated Documentation	4
1.5 Glossary	4
2. Safety Instructions	6
2.1 Safety Precautions	6
2.2 Labels	6
2.3 Emergency Procedures	7
2.3.1 Emergency	7
2.3.2 Software Stop	7
2.3.3 Power Failure	7
2.4 Disposal	7
3. System Description	8
3.1 Instrument Components	8
3.2 Fluidics Systems	8
3.2.1 Cleaning Slides	9
3.2.2 Bulk Fluidics Reagents	9
3.2.3 Multichannel Fluidics	9
3.2.4 Single Channel Fluidics	9
3.3 Temperature Control	9
3.3.1 Interaction Temperature	9
3.3.2 Sample Deck Temperature	9
3.4 Sample Handling	10
3.5 Surface Plasmon Resonance Signal Detection and Processing	11
3.6 System Software	12
3.6.1 Navigator (Control Software)	12
3.6.2 Data Analysis Software	12
4. Operation	13
4.1 Starting the System	13
4.2 Navigator Pages and Related Actions	14
4.2.1 My Dashboard	14
4.2.2 Experiment Wizard	16
4.2.3 Experiment Manager	17
4.2.4 Experiment Runner	19
4.2.5 Chip Manager	23
4.2.6 Cleaning & Maintenance	25

5. Creating and Running an Experiment	27
5.1 Common Setup Tabs	27
5.1.1 Interaction Temperature and Chip Type	27
5.1.2 Regeneration Setup	27
5.1.3 Sample Information	29
5.1.4 Injections	31
5.1.5 Plate Quadrants	32
5.1.6 Injection Times	32
5.1.7 Summary	33
5.1.8 Experiment Actions	34
5.2 Common Options	34
5.2.1 MC cleaning	34
5.2.2 Calibration	34
5.2.3 Excluded Volume Correction (EVC)	36
5.2.4 50% DMSO Wash	37
5.2.5 Periodic Injections	38
5.2.6 Blocking Injections	39
5.3 Wizard Options	40
5.3.1 Surface Preparation Lawn	41
5.3.2 Surface Preparation Array	43
5.3.3 Capture Kinetics	45
5.3.4 Analyte Injections	49
5.3.5 Dual-Analyte Injections	53
5.3.6 Quantitation	56
5.4 Running an Experiment	59
6. Maintenance	61
6.1 User Maintenance	61
6.2 Clean MC Cleaning Station	61
6.3 aSFC and cPH Cleaning Procedure	62
7. Reference Information	64
7.1 Maintenance & Best Practices Guide, Troubleshooting and Support	64
7.2 Ultra Required Consumables	64
7.3 Chips	64
7.4 Carterra Consumables Ordering Information	64
7.5 Chemical Resistance of Wetted Parts	64

1. Introduction

1.1 Information About This Manual

The instructions contained in this document provide the information needed to operate and maintain Ultra properly. Additional documentation can be found at www.carterra-bio.com, or by contacting Customer Support at support@carterra-bio.com.

1.2 Intended Purpose of Ultra

Carterra Ultra® enables real-time, label-free analysis of molecular interactions. It is intended for research use only and not for use in diagnostic procedures. Do not expose the device to any external radiation. Using Ultra for purposes other than intended may invalidate the warranty.

1.3 Regulatory Information



The Ultra is intended for research use only and is not for use in diagnostic procedures.

1.4 Associated Documentation

The User Manual is supplied in PDF format on the instrument computer. Other resources, such as specification sheets, application notes, and technical literature, are available at www.carterra-bio.com.

1.5 Glossary

Advanced Single Flow Cell (aSFC)	Single-channel device that delivers solution to the sensor chip surface.
Analyte	Solution phase biomolecule injected across the chip surface.
Association Phase	Cycle phase in which an analyte is injected to assess its propensity to interact with the surface.
Baseline	Period of buffer flow before sample injection/association phase.
Capture	Non-covalent immobilization of a ligand to the chip surface.
Chip	The functionalized gold surface, prism, and mounting cartridge assembly.
Couple	Covalent immobilization of a ligand to the chip surface.
Custom Ultra 96-channel Print Head™ (cPH)	Multichannel print head that delivers multiple solutions to the sensor chip surface in parallel.
Cycle	Collection of phases that repeat for each line in the experimental method queue. For example, a regenerative kinetics cycle would consist of baseline, association, dissociation, regeneration, and stabilization.
Dissociation Phase	Cycle phase during which system buffer flows across the chip surface and the dissociation of bound analytes from the surface-deposited ligand is monitored over time.

Ligand	Biomolecule coupled or captured to the chip surface.
MC	Multichannel. The fluidics mode which uses the Custom Ultra 96-channel Print Head (cPH).
Phase	A distinct time segment of the assay cycle during which the experimental condition is constant.
Prism	Angular cut glass block used to direct incident laser light both to the chip surface and out to the charge-coupled device (CCD) camera detector.
Reference Region	Interspot ROIs used for local referencing.
Regeneration Phase	Removal of captured ligand(s) or bound analyte(s) from the chip surface by injection of a solution with, for example, low pH or high salt.
Response Unit (RU)	A unit of response on the sensorgram y-scale corresponding to a 0.1 millidegree shift in the SPR minima.
SC	Single Channel. The fluidics mode which uses the Advanced Single Flow Cell (aSFC).
Sensor	Surface Plasmon Resonance Imaging (SPRi) detection format consisting of a near-IR laser and a high-resolution charge-coupled device (CCD) camera detector.
Sensorgram	The time resolved signal recorded during an SPR experiment.
Region of Interest (ROI)	Area of the surface being monitored for binding. ROIs consist of locations with coupled or captured ligands as well as empty interspot locations used as references.
SPR	Surface Plasmon Resonance
Surface	Functionalized gold surface that provides a chemistry for attachment of biomolecules.




2. Safety Instructions

2.1 Safety Precautions

- Only properly trained personnel may operate and maintain Ultra.
- Do not operate the instrument in any way other than described in the User Manual.
- Ultra is not intended for use with flammable or corrosive substances.
- Take care that fingers are not trapped by moving parts. Pinch points are clearly marked within the system. Take additional precautions around these areas of the instrument, especially when the instrument is running.
- The two needle-based autosamplers are the main pinch-points and are labeled appropriately.
- Never place hands inside the instrument while it is in use. If doors are opened, the motors will continue through the last command and then stop. They will not move again until after the doors are closed. Do not open the doors while the instrument is running.
- Ultra is extremely heavy. Use four or more properly trained people, or suitable lifting equipment, when moving the instrument. Lifting equipment must not press on the instrument covers. Carterra strongly recommends that Ultra only be moved by Carterra Field Service Engineers. If Ultra needs to be moved, please contact Carterra.
- The instrument must always be connected to a grounded power outlet.
- Due to the size and power requirements of the instrument, it is unsafe to use any power cord other than the one supplied by Carterra. Please contact Customer Service to ensure that you have the correct power cord.
- Keep the power switch and power cord plug easily accessible at all times so they can be quickly disconnected if needed.
- All service and repair, with the exception of operations explicitly described in the User Manual, must be carried out by Carterra personnel. Do not open any covers or replace any parts unless specifically described in the User Manual.

2.2 Labels

The illustration below shows an example of the system serial number label. The label is attached to the main connector panel on the rear right of the instrument. In addition, the illustrations below show examples of hazard warning labels found on Ultra. These labels are designed to help users avoid injury when operating the instrument.


Symbol	Meaning
 <p>The image shows a rectangular label with the Carterra logo at the top. Below the logo, there are two fields: 'MODEL: Ultra' and 'SERIAL:'. Underneath these fields, there is a section for 'Power Input' with '100-240 VAC' and '20/30 Hz, 25A Max.' and a 'Research Use Only' warning. At the bottom, there is a CE mark and the text 'Carterra 50175-0001 Rev. 02/07 508-Low-City UT 80102 USA'.</p>	<p>System serial number label found on the back of the instrument.</p>
 <p>A yellow triangular warning symbol with a black border. Inside the triangle, there is a black silhouette of a hand being caught between two moving parts, with arrows indicating the direction of movement.</p>	<p>Caution - pinch point. Keep hands and fingers clear during operation.</p>
 <p>A yellow triangular warning symbol with a black border. Inside the triangle, there is a black lightning bolt symbol.</p>	<p>Electrical shock hazard. Disconnect power cord from electrical outlet before removing this panel or starting any service.</p>

2.3 Emergency Procedures

2.3.1 Emergency

To stop the system in an emergency, disconnect the main power from the instrument using the main switch on the rear top center panel.

2.3.2 Software Stop

Click the stop icon  in the experiment runner. The system will stop upon completion of the current action, which will potentially result in sample loss. If required, switch off power to the instrument using the power switch.

2.3.3 Power Failure

If the instrument shuts down unexpectedly, contact Customer Support at:

Telephone: 1-844-642-7635, Option 3

Email: support@carterra-bio.com

Web: www.carterra-bio.com/support

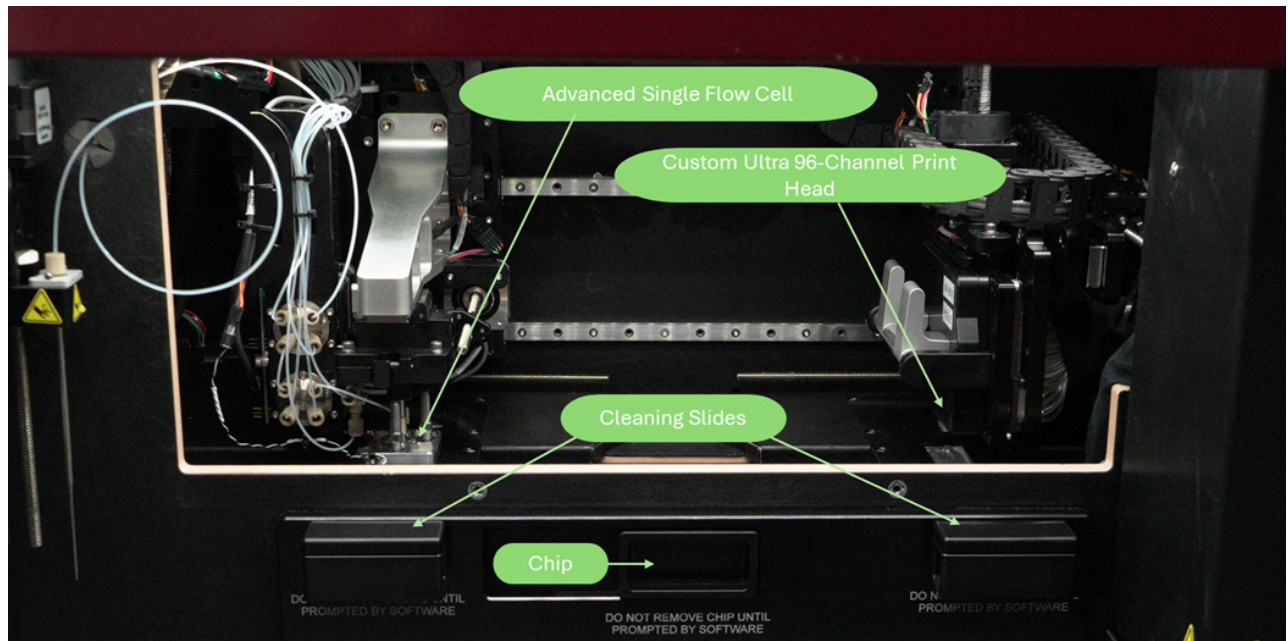
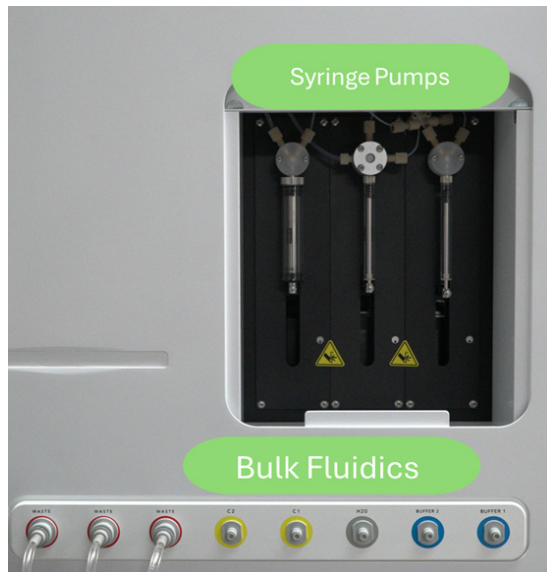
2.4 Disposal

The instrument must be decontaminated before decommissioning. All local laws and regulations must be followed for disposal and recycling of the various materials in Ultra. Electronic waste and electrical equipment must be collected separately and not disposed of as unsorted municipal waste.

3. System Description

3.1 Instrument Components

Ultra has two fluidic systems: 1) Multichannel (MC), and 2) Single Channel (SC). Each fluidic system is comprised of its own pumps, sample decks, reagent inlets, autosamplers, and cleaning stations.



3.2 Fluidic Systems

3.2.1 Cleaning Slides

A cleaning slide holder is located on the left and right sides of the instrument. When removing the slides, ensure that the instrument status reads Instrument Idle, confirming that both the Advanced Single Flow Cell (aSFC) and Custom Ultra 96-Channel Print Head (cPH) are undocked from the cleaning slides. Hold the slide-holder handle (black) and gently pull straight toward the body. Rinse a fresh 1.2 mm glass slide with water and isopropanol to eliminate dust and glass particles. Wipe with lint free wipes or lens paper and insert it into the slot, making sure to push the holder all the way in. Use re-cleaned or new cleaning slides each time before priming the flow cells on the cleaning slides. This avoids salt and contaminate build up on the interface of the aSFC and cPH.

3.2.2 Bulk Fluidics Reagents

System fluids are supplied to Ultra through a 5-port bulkhead located on the left side of the instrument. This bulkhead is connected via tubing to bottles for system buffers, 18 M Ω filtered water, and cleaning solutions. Three additional bulkhead ports are used to send waste fluids to the waste container located beneath the instrument. Chosen caps should restrict dust from entering the solutions and be vented to prevent pressure changes as fluid volume changes during operation.

3.2.3 Multichannel Fluidics

The multichannel (MC) fluidics path is principally comprised of the cPH that, when pressed against the sensor chip, creates 96 discrete channels. Each channel is linked, through peristaltic pumps, to one of 96-needles in an autosampler that can draw samples from microplates in Bays 3, 4, and 5 on the right-hand sample deck. During MC sample delivery, samples are drawn into fluidics and exposed to the chip surface using a back and forth motion, allowing for delivery of 96 samples with extended contact time using 200 μ L of each sample.

3.2.4 Single Channel Fluidics

The single channel (SC) fluidics path is principally comprised of the aSFC. When docked against the sensor surface, the aSFC creates a single large flow cell that covers all the ROIs simultaneously. Samples are drawn from Bays 1 & 2 and passed over all ROIs. Each analyte injection uses 180 μ L of sample. Analyte sample flows back and forth across the chip surface during an injection, enabling long contact times at high flow rates.

3.3 Temperature Control

3.3.1 Interaction Temperature

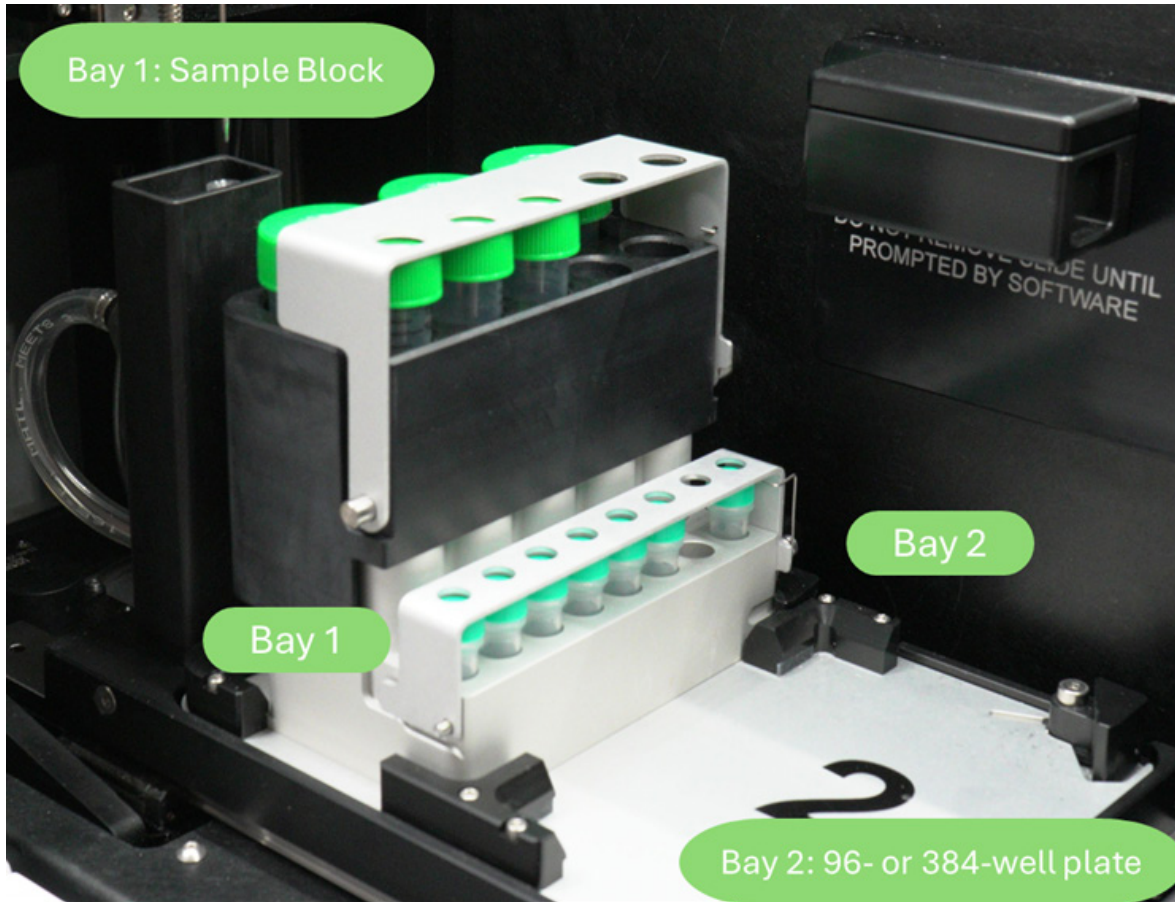
The temperature at the chip surface is referred to as the interaction temperature. The interaction temperature may be set from 10 °C to 40 °C in the Navigator software. Experiments will not start (unless specifically overridden by the user) until the actual temperature is equilibrated to within 2 °C of the set temperature.

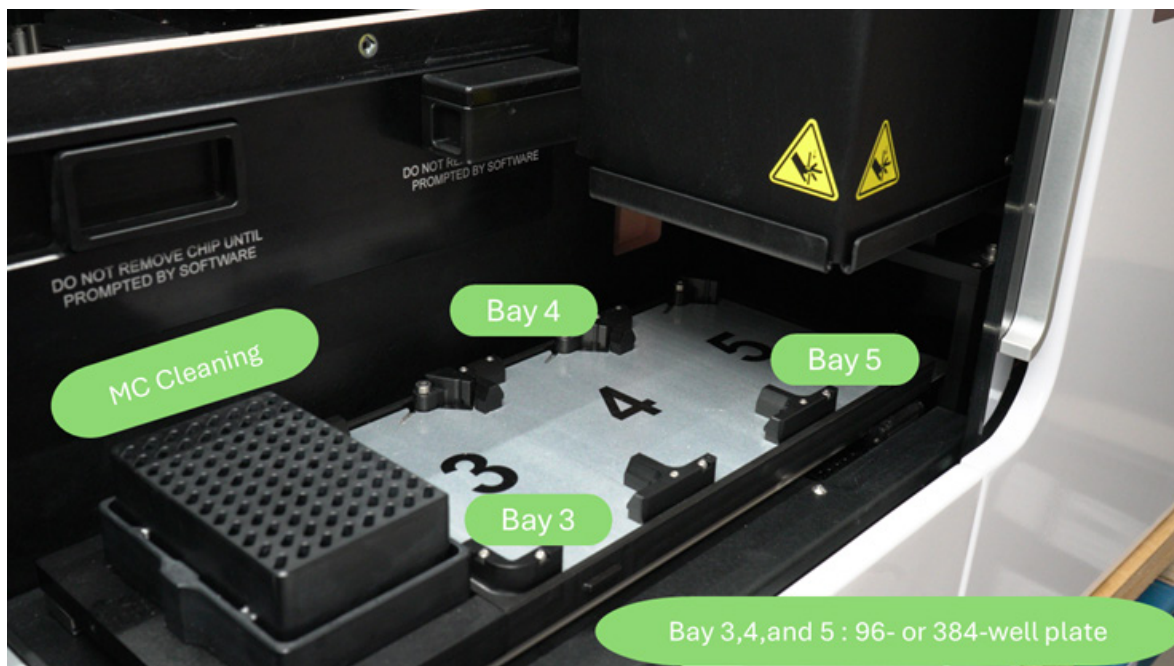
3.3.2 Sample Deck Temperature

The temperature of the sample decks is referred to as the sample deck temperature. The sample decks can be set from 10 °C to 20 °C (Although it should not be set below the dew point to avoid excessive condensation.) An experiment will start even if the sample deck has not achieved the set temperature in the program.

3.4 Sample Handling

Ultra provides two sample decks, one on the left side for the SC fluidics and one on the right for the MC fluidics. The SC side has two bays numbered 1 & 2, and the MC side has three bays numbered 3, 4, & 5.





All sample bays can hold 96- and 384-well microplates. Only Carterra-approved microplates should be used. To minimize sample evaporation over extended runs, it is recommended to use well plate covers.

Bay 1 on the SC side can accept the reagent sample block. It can hold up to 3 x 50 mL conical tubes, 5 x 15 mL conical tubes, and 8 x 1.5 mL vials. The required consumables table lists the approved labware for use with Ultra.

Each sample deck has a cleaning station. The MC cleaning station has a removable block that can be rinsed with 18 M Ω water only if salt buildup is present. See section 6.2 for the cleaning procedures. The SC cleaning station should not be removed for cleaning. If salt buildup is observed in or around the SC cleaning station, please contact Customer Support.

3.5 Surface Plasmon Resonance Signal Detection and Processing

Inside Ultra, molecular interactions are interrogated in real-time using surface plasmon resonance detection technology. Plasmons are electromagnetic surface waves induced in thin-film metals when illuminated at the total internal reflectance (TIR) angle. Plasmon resonance results in a narrow dip in the intensity of the reflected light at the SPR angle. Small changes in refractive index near the metal surface alter the SPR angle. When docked to a microfluidic flow cell, samples can be delivered to the surface by the fluidics subsystems. Binding partners can be attached to the sensor surface (ligands) and allowed to interact with molecules passed over the surface (analytes). Whenever ligand and analyte molecules bind, the accumulation of mass near the surface changes the SPR angle. The continuously monitored changes of this angle are converted to "Response Units" (RUs) and reported as a function of time.

Ultra divides a sensor chip into 192 regions of interest and monitors them simultaneously. For the highest quality data, Carterra recommends using up to 96 ROIs to contain ligand molecules while the other 96 serve as references whose response will be subtracted from the ligand regions during data reduction.

Ultra's light source is a near-infrared laser. The laser is reflected off a piezoelectric mirror that directs the beam in a rapid scanning pattern across the ROIs on the chip and at different angles. The light is recorded by a high-speed camera and directed to the computer through two video interlink cables. The segmentation and integration of the intensity over a range of angles allows for defining the SPR curve and its interpretation as RU. It is recommended that users do not run other programs on the computer during data collection to allow sufficient computational resources to handle the high-bandwidth data stream and its processing.

3.6 System Software

3.6.1 Navigator (Control Software)

The Navigator control software enables Ultra operation, acquires real-time data, and guides the user through the customization of provided wizards to configure and execute assays. Navigator is comprised of both the client software (GUI interface) and the Navigator server. Navigator generates results files that end with .sprdata.

3.6.2 Data Analysis Software

Carterra provides software packages for the analysis of data collected with Ultra.

The Kinetics Analysis Software opens any .sprdata file and provides tools for viewing any kind of experiment, and specifically for fitting for kinetic affinity, equilibrium affinity, collecting report points, quantitation, statistical data summaries, etc. Data analyzed with Kinetics will be saved as .kitx files.

The Carterra Epitope Analysis software is tailor-made for handling all the workflows related to Epitope mapping/binning, mutant mapping, and peptide mapping. Data analyzed with Epitope will be saved as .ebp files.

4. Operation







4.1 Starting the System

Power on the instrument using the main switch on the rear top center panel. Once the machine has powered on, start up the control computer and start Navigator.



4.2 Navigator Pages and Related Actions

Down the left side of the dashboard is a series of functional buttons that direct the user to further instrument functionality.

 <p>My Dashboard</p>	<p>Page with access to all the features available in the software.</p>
 <p>Experiment Wizard</p>	<p>Page for the experiment that is currently being designed/opened.</p>
 <p>Experiment Manager</p>	<p>Page with a list of all the user-created and saved Wizards containing customized run parameters.</p>
 <p>Experiment Runner</p>	<p>Page to review and check the planned experiment and see data collection while the experiment is running.</p>
 <p>Chip Manager</p>	<p>Page for chip management.</p>
 <p>Cleaning & Maintenance</p>	<p>Page for instrument maintenance, cleaning, and support.</p>

4.2.1 My Dashboard


Upon opening Navigator, the user is presented with the My Dashboard page. This window is divided into several sections, each of which is described in more detail below.

1. **Banner:** The banner across the top of the window provides important status and alert information to the user.



- a. **Instrument name and current state:** The left side of the banner contains the name of the instrument and a status message describing the instrument’s status. If a red hourglass is present, the user is being asked to wait for an action to be completed. A green hourglass means the instrument is idle and the user can initiate an action.
- b. The right side of the banner is **the status of the instrument’s thermals and sensor chip**. The on/off status indicates if thermal control is active or inactive for the interaction temperature (thermometer icon) and the sample decks (indicated by the plate icon). If the thermal system is on, a temperature value is displayed in green if the system is at or near the set temperature and red if it has not yet achieved the set temperature. If the thermal system is off, it will display “Off”. The user can type in a number for the desired temperature and press the green arrow to set the new temperature. Temperature control can be stopped by pressing the red circle with the white square in it. To the right is an icon indicating if a chip is docked or not and the type of chip (if currently docked).

- If the instrument is currently running, the **“Running Experiment”** section will list the details. Clicking the “Details” button will take the user to the Experiment runner tab.

 Experiment

20260211_Analyte_Injections

[Details](#)


Type **Analyte Injections**


Chip **20260211_CMDP_Chip (CMDP)**


Start **2/11/2026 11:50 AM**


Estimated End Time
2/11/2026 12:00 PM


- The **“Create New Experiment”** panel contains wizards covering the full experimental functionality of Ultra. Clicking on each one takes the user to that wizard and the user can begin designing the experiments.


 **Create New Experiment**



 Surface Prep Lawn


 Surface Prep Array



 Capture Kinetics


 Analyte Injections


 Dual-Analyte Injections


 Quantitation

- Activity History:** Allows the user to review all tasks Ultra has carried out recently, including wizards run, cleaning procedures, and primes. The list is searchable using the text box on the top right of the panel.

 **Activity History**
 Experiment
 Maintenance
 Prime

Activity	Type	Status	Start	End
> Prime System	Prime	Complete	8/6/2025 10:00 AM	8/6/2025 10:05 AM
> Quick prime	Prime	Complete	8/6/2025 10:12 AM	8/6/2025 10:13 AM
> conditioning 20250806	Experiment	Complete	8/6/2025 10:13 AM	8/6/2025 10:39 AM
> Prime	Prime	Complete	8/6/2025 10:51 AM	8/6/2025 10:57 AM
> Surface Prep Array 8/6/2025 10:41 AM	Experiment	Complete	8/6/2025 10:57 AM	8/6/2025 11:46 AM
> Prime System	Prime	Complete	8/6/2025 11:52 AM	8/6/2025 12:02 PM
> Quick prime	Prime	Complete	8/6/2025 12:07 PM	8/6/2025 12:08 PM
> 20250806_pH22RegenTest	Experiment	Complete	8/6/2025 12:08 PM	8/6/2025 12:57 PM
> Quick prime	Prime	Complete	8/6/2025 12:58 PM	8/6/2025 12:59 PM
> 20250806_EpitopeBinning	Experiment	Complete	8/6/2025 12:59 PM	8/6/2025 7:10 PM
Standby Flow	Maintenance	Complete	8/6/2025 7:10 PM	8/6/2025 7:21 PM
> Quick prime	Prime	Complete	8/6/2025 7:24 PM	8/6/2025 7:25 PM
> 20250806_Target2_CoupledKinetics	Experiment	Complete	8/6/2025 7:25 PM	8/7/2025 12:02 AM
> Prime System	Prime	Complete	8/7/2025 9:04 AM	8/7/2025 9:09 AM
> Prime Single Channel	Prime	Complete	8/7/2025 9:29 AM	8/7/2025 9:33 AM

- Standby Mode on Chip:** Start instrument standby by pressing the green button with the right arrow in it. This will direct Ultra to cycle buffer through the SC fluidics to prevent drying out of the liquid path or the chip.

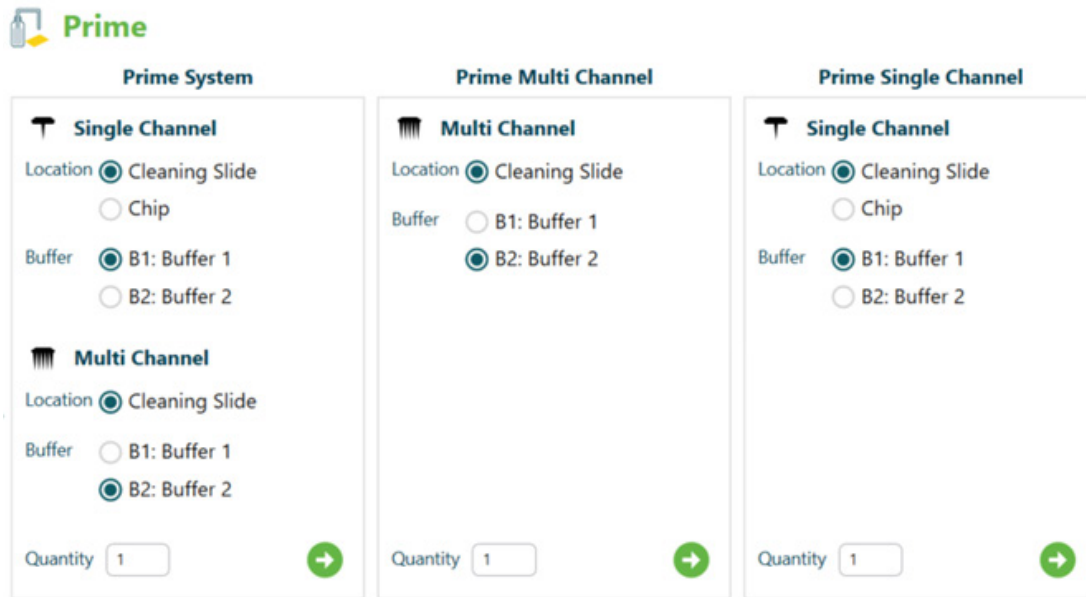
 **Standby Mode on Chip**

Standby Mode on Chip

➔
⏹

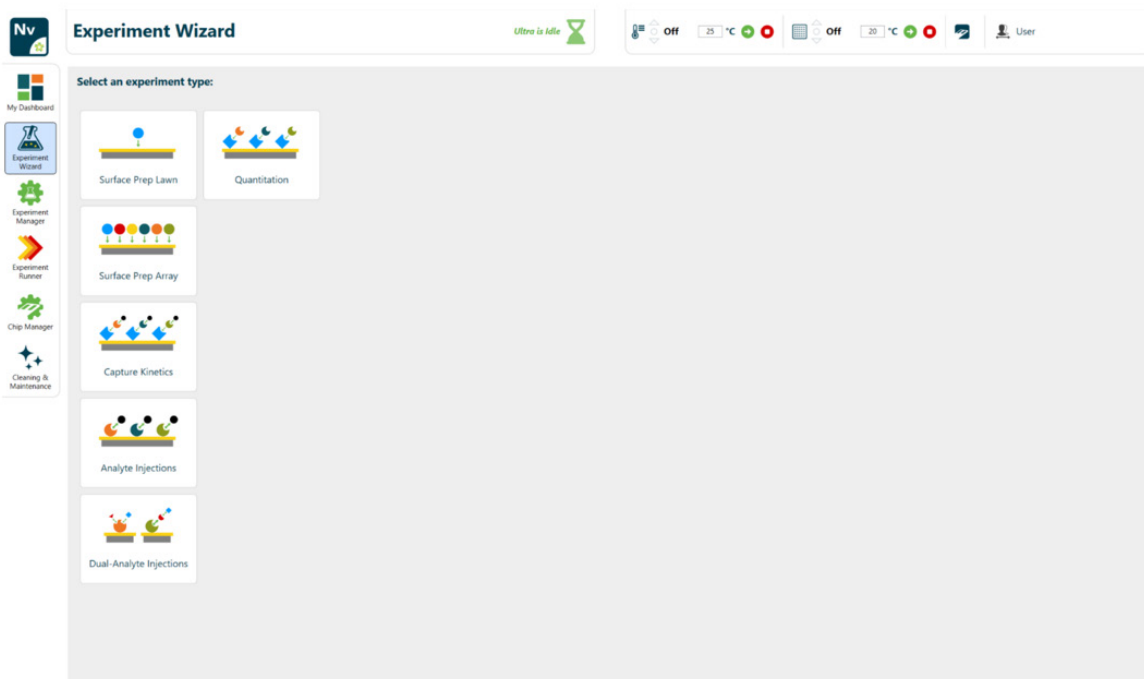
- Prime:** Ultra provides multiple priming options to prepare the instrument with running buffer before setup and experiments. Ultra supports two running buffers (B1 and B2). Each fluidic side (SC and MC) can be primed simultaneously or separately with B1 or B2 as selected in this tab. Priming can be performed on cleaning slides, which enables buffer exchange without wetting a chip. If a chip is docked and in use and the user wishes to prime the SC system without the chip drying out, they can select prime on chip.

The Prime section includes three panels to prime both sides, SC only or MC only. For each selection, choose B1 or B2 and whether to prime on chip or on the cleaning slide, and specify the number of prime cycles. The MC side will always prime on its cleaning slide; the SC side may be primed on either the cleaning slide or the chip.



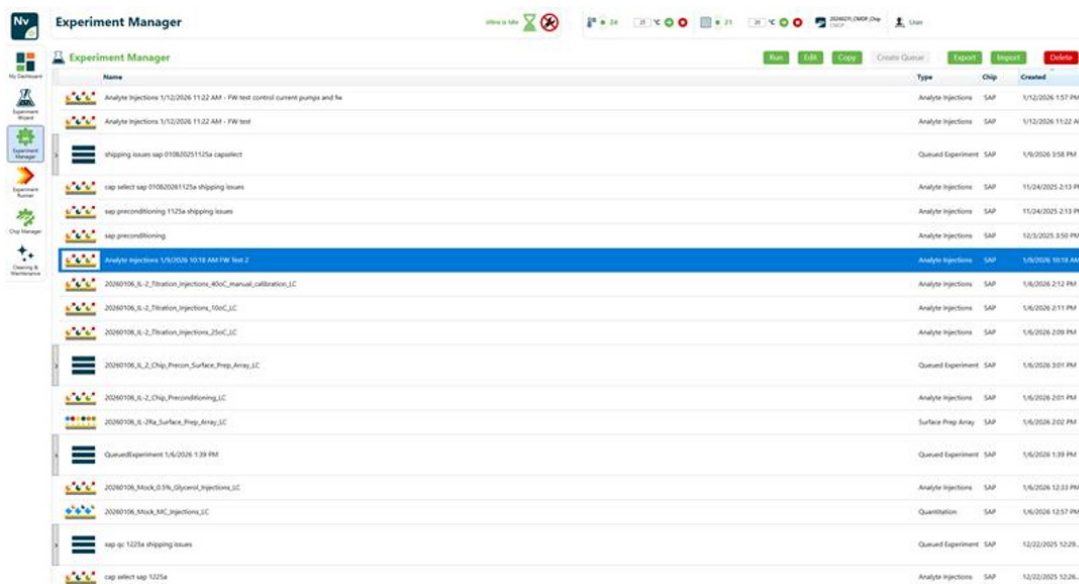
4.2.2 Experiment Wizard

This opens the experiment currently being created or edited. The user can configure a wizard while another program is running. For configuration details, see Chapter 5.



4.2.3 Experiment Manager

The Experiment Manager lists all user-created and saved wizards (experiments). From this menu, the user can run, edit, copy, export the experiment .cice file, import .cice files, delete experiments, and create queues. The list also displays the wizard type, selected chip, and creation date.



To edit an experiment, select it from the list and click Edit . This opens the Experiment Wizard where the user can modify run parameters, samples, and other settings. Carterra recommends saving any modified experiment with a new file name.

The Create Queue feature runs a group of experiments sequentially to increase unattended operation. Up to six experiments can be queued. The first experiment in the queue sets the interaction temperature and chip type for the entire queue. Conflicts are reported in the Validation window.

To create a queue, open Experiment Manager from the left task bar. Select the experiments to queue:

- Hold Ctrl and click to select non-adjacent experiments, or
- Hold Shift and click the first and last experiments to select a continuous range.

Click Create Queue to open the Create Queue window. Arrange experiments in the desired order, select intermediate priming options, review validation results, and click Run Queue to start the run.

Navigator validates each wizard before sending it to the Experiment Runner. For queued runs, Ultra evaluates the entire queue to estimate run time, sample usage, and buffer usage.

Example to create a queue: a three-experiment queue in which a 96-array is created using Surface Preparation Array, followed by kinetics and epitope binning using Analyte Injections and Dual-Analyte Injections, respectively.

1. Create the Surface Preparation Array experiment



2. Create the Analyte Injections experiment



3. Create the Dual Analyte Injections experiment



4. On the Experiment Manager page, select the 3 experiments.

Experiment Manager

Run Edit Copy Create Queue Export Import Delete

Name	Type	Chip	Created
Dual-Analyte Injections 2/11/2026 11:09 AM	Dual-Analyte Injections	CMDP	2/11/2026 11:10 AM
Analyte Injections 2/11/2026 11:08 AM	Analyte Injections	CMDP	2/11/2026 11:09 AM
Surface Prep Array 2/11/2026 11:07 AM	Surface Prep Array	CMDP	2/11/2026 11:08 AM
cmdp preconditioning	Analyte Injections	CMDP	1/26/2026 3:33 PM
20260114_GPCR1_CaptureKinetics w and w comp	Capture Kinetics	SAP	1/14/2026 6:25 PM

Create Queue

5. Review the queue for validation, experiment order, and select the type of intermediary primes. (A quick or regular prime will always be applied at the start of the queued experiment; intermediary primes are performed in addition to these primes.)

Experiment Queue

Experiment Queue Name: QueuedExperiment 2/11/2026 11:26 AM

Experiment	Prime	Qty
1 Surface Prep Array 2/11/2026 11:07 AM	Regular prime	1
2 Analyte Injections 2/11/2026 11:08 AM	Regular prime	1
3 Dual-Analyte Injections 2/11/2026 11:09 AM	Regular prime	1

Validation

No Errors Found

Summary

Temperature: 25 °C Selected Chip: CMDP

Estimate	Run Time	10 12h 34m
B1: Buffer 1	41	
B2: Buffer 2	321.1 ml	
C1: Cleaning 1	0	
C2: Cleaning 2	0	
H2O: Water	0	

Options: MC Cleaning: Disabled, Blocking: Disabled, Calibration: Enabled, 50% DMSO Wash: Disabled, Excluded Volume Correction: Disabled, Periodic Injections: Disabled

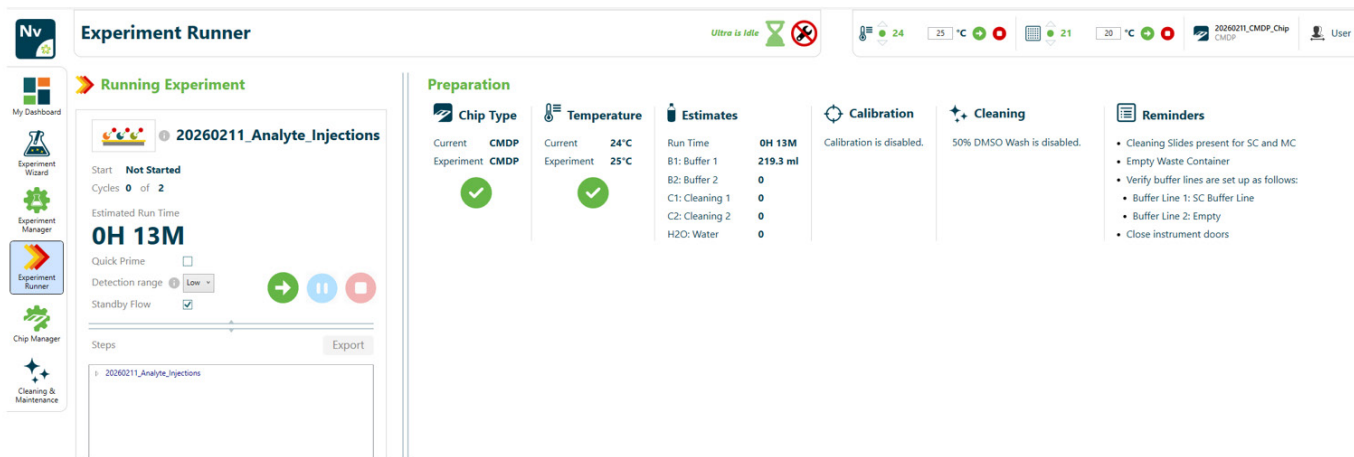
Deck: Bay 1: Sample Block loaded, Bay 2: 16d (2 no), Bay 3: 16d (20 d)

6. Save or Save & Run Queue.

Experiment Queue Name: Save Save & Run

4.2.4 Experiment Runner

Before an experiment begins, Navigator opens the Experiment Runner, where the user performs a final review of the planned experiment, including estimated run time and final reminders.

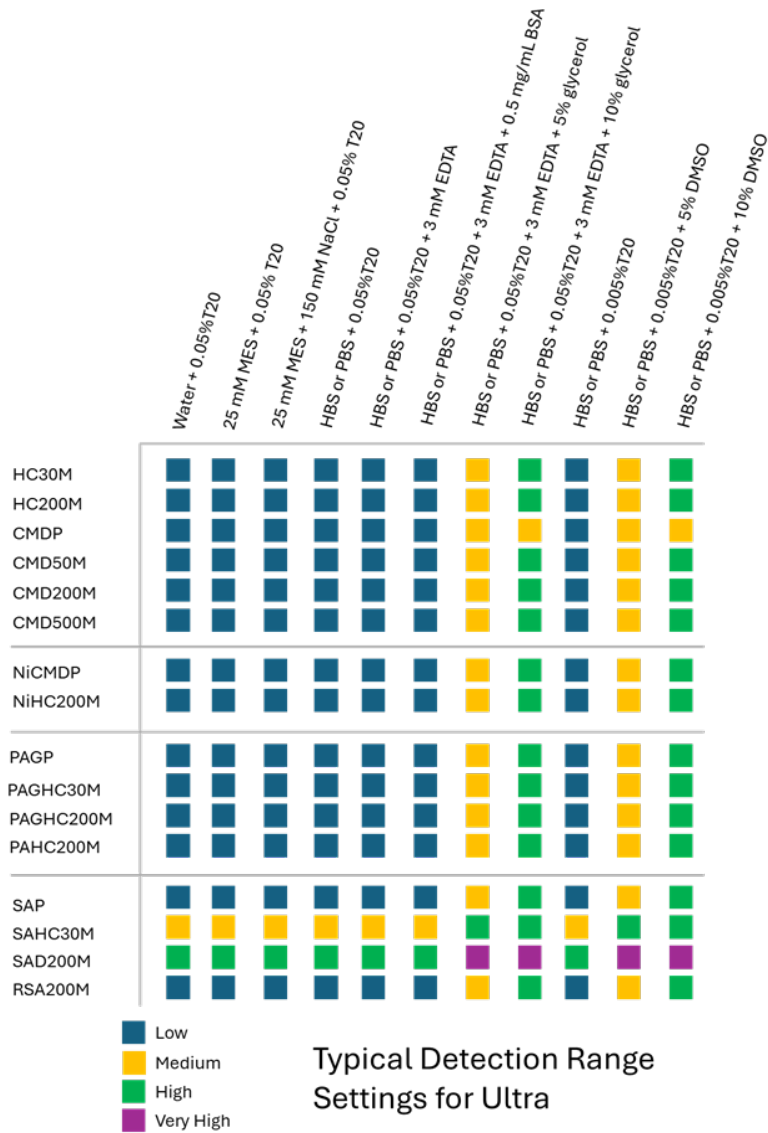


The top banner shows the current instrument status, current temperature, and chip status.

In the left panel, the user can select a Regular Prime (full prime) or enable Quick Prime. Quick Prime uses less buffer and is approximately one minute faster than a full Prime. A prime is required before every run and cannot be bypassed.

The user can also enable Standby Flow after the experiment is completed. Carterra recommends using Standby Flow between runs.

Before starting a run, the user must set the Detection Range. This setting is based on the experiment baseline response and depends on chip type, solvent components, and coupling density. The available settings, Low, Medium, High, and Very High, correspond to increasing baseline response. Guidance for selecting the correct range is available by hovering over the Detection Range setting.



Typical Detection Range Settings for Ultra



The right panel is the Preparation panel. See Section 5.4 for details.

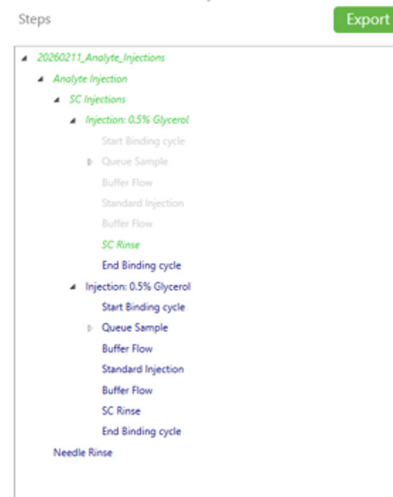
After all required settings are configured, start the experiment by clicking the green arrow ➔.

During an experiment, the Experiment Runner displays real-time information, including data from all 192 ROIs (updated every second), chip type, temperature, elapsed and estimated run time, and reminders.



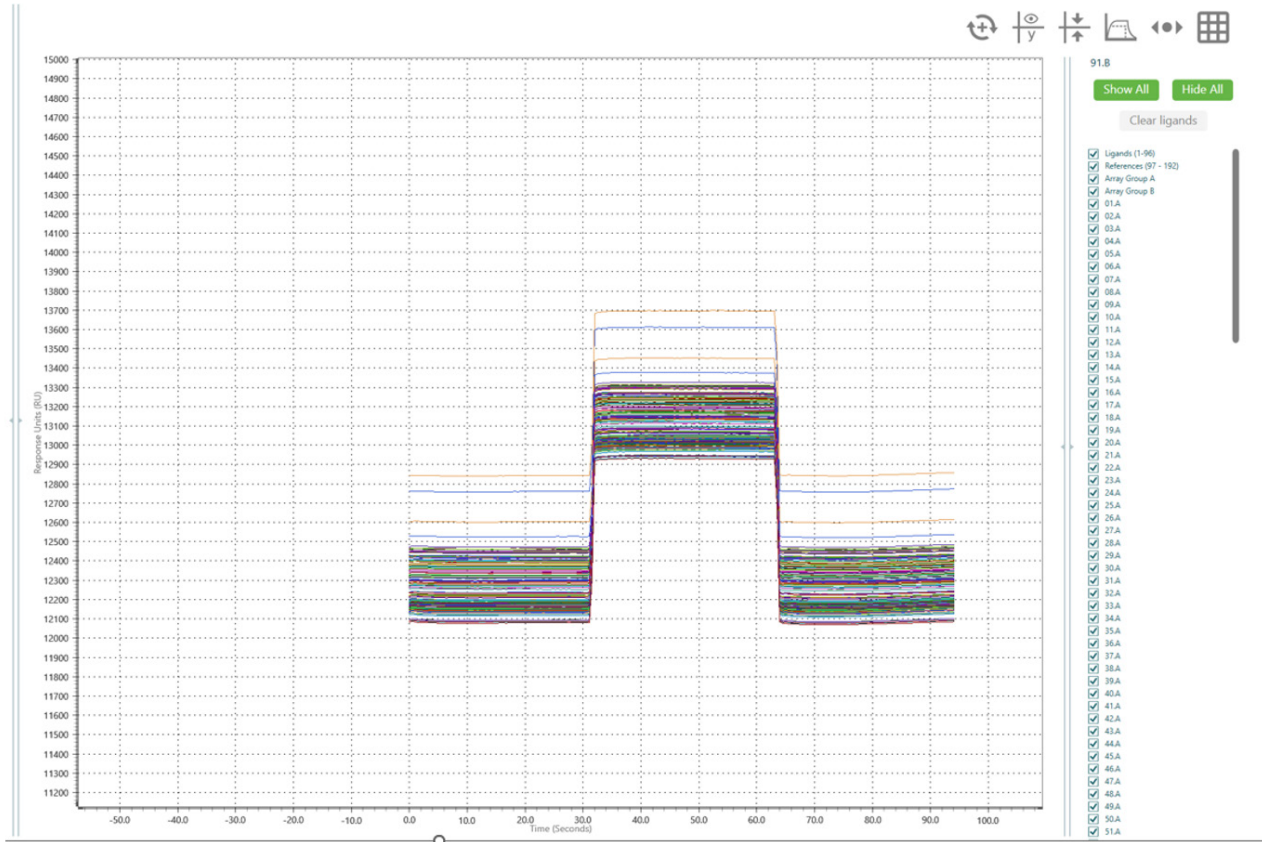
Once the run starts, this window updates to show the run end time instead of an estimated run time as well as the current cycle number and total cycles.

The Steps text box displays cycle information. Click the triangle icons to expand details for each cycle. Expanding the current cycle lists all actions executed in that cycle and highlights the action in progress. Selecting previous cycle updates the sensorgram display on the right to show data collected during that cycle.



The large panel in the lower-right of the Experiment Runner displays real-time data from all 192 ROIs. To zoom, click and drag from the upper-left to the lower-right of the region of interest. To reset zoom, click and drag from the lower-right to the upper-left anywhere on the plot.

This window also provides tools to simplify viewing during a run. By default, Ultra assigns the 96 ROIs in Array Group A as Ligands and the 96 ROIs in Array Group B as References; ROIs in each group are numbered 01-96. Use the Ligands and References toggles to show or hide each group. Use Show All and Hide All to quickly adjust visibility.



Function of other buttons in Experiment Runner:

	Caution: This button clears the ligand information for the current chip. Subsequent data files will not include ligand information unless you perform a new ligand deposition. Use this button only when necessary.
	This button resets the zoom. It will reset the window to the standard viewing window centered on the collected data after being zoomed in or out.
	This button shows/hides the Y-align bar. The Y-align bar should be set during the baseline injections.
	This button zeroes the whole set of sensorgrams to the location of the y-align bar by applying the Y-align function.
	Use this button to subtract the default reference array (Array Group B) from the default ligand array (Array Group A).
	This button enables/disables scrolling. Scrolling refers to the viewing window moving the view to capture the data currently being collected in the experiment. If you want to zoom in or out on a specific part of the sensorgram while the experiment is running, it is advised to disable scrolling.
	This button enables/disables the gridlines in the viewing window.

4.2.5 Chip Manager

In the Chip Manager page, the user can (1) load a new chip, (2) reload a previously used chip, or (3) unload a chip. To load a new chip, enter the Name, Serial Number, and Chip Type; Comments are optional. The chip table tracks the number of times each chip has been loaded. Although chips can be reused on Ultra, Carterra recommends using a new chip for each experiment to maintain the highest data quality.

To load a new chip, remove the chip from the freezer and allow it to warm to room temperature for 30 minutes to prevent condensation on the optics during loading. If an old chip is loaded, click "Unload Chip".

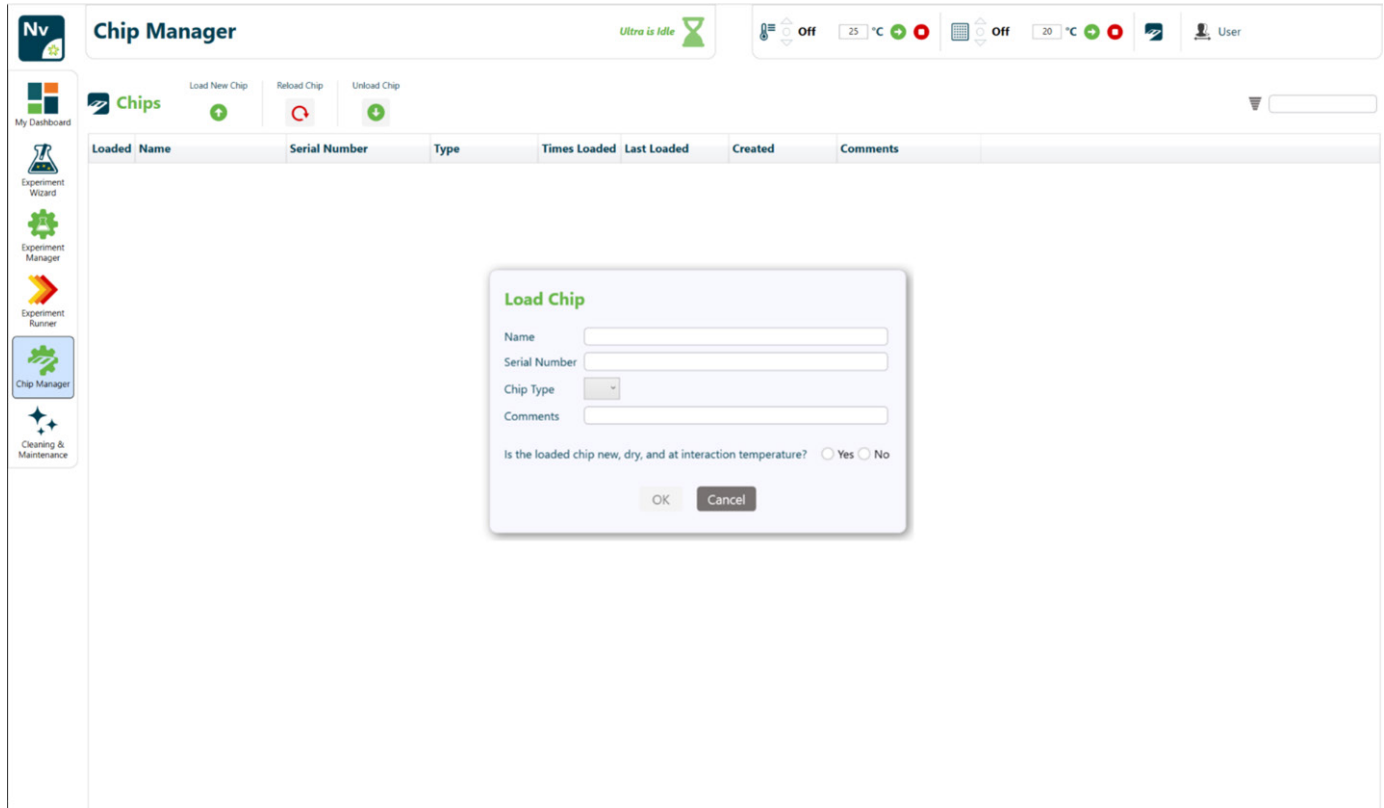
Unload Chip



Slide the chip door completely to the left, firmly grip the old chip, and pull it straight out of the instrument. Once the previous chip has been removed, open the new chip. The carrier sits inside a transparent plastic cylinder that suspends the assembly, so the prism and chip do not touch the container during shipping. Grab the chip and gently squeeze the top and bottom of the cylinder to release the chip and pull it straight out of the packaging, taking care not to touch or scratch any of the optical components. Slide the chip cover door completely to the left if closed and align the edge of the chip with the grooves in Ultra's housing. Slowly slide the chip all the way into the instrument. The user will feel a small 'bump' as it reaches the back. Make sure to push past this bump to completely and firmly seat the chip. Close the chip door completely to the right.

Wait 30 minutes after placing the chip for it to equilibrate to the instrument temperature. Once thermal equilibration is achieved, click “Load New Chip”:

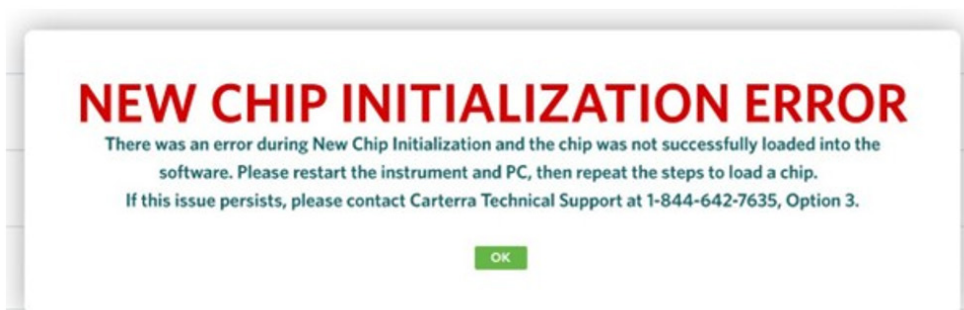
Load New Chip



The “Load New Chip” dialogue will appear, and the user can enter the chip name, serial number, comments, and select the chip type from the pull-down menu. Carterra highly recommends filling in a unique name, selecting the correct chip type, and entering the serial number. The load chip dialogue also asks whether the chip is new, dry, and at the interaction temperature. If the user can answer yes to all these questions and clicks the OK button, Ultra will perform a chip normalization procedure that provides for a uniform signal across the entire chip surface. Ultra performs this using the chip/air interface so no additional solutions or injections are required. This step can only be performed once, when the chip is new, dry, and at thermal equilibrium.

If your chip is being reused, select “No” to the question about the chip being new, dry, and thermally equilibrated. This will skip the normalization procedure, which could introduce artifacts into the optical correction if the chip surface is no longer uniform.

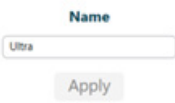
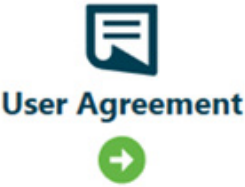

If there are issues during docking/normalizing of a chip, a warning will appear as shown below. If an error occurs, please retry the procedure one time. If the problem persists, please contact Customer Support.




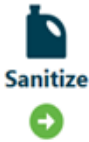



4.2.6 Cleaning & Maintenance

The cleaning & Maintenance page contains functions for instrument management, cleaning, and support:

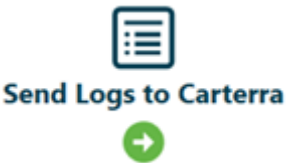
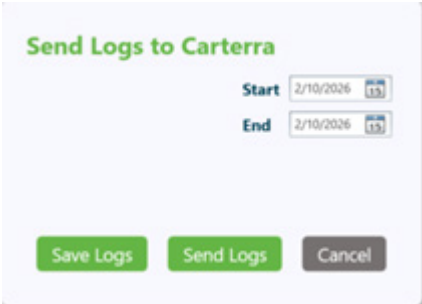
Instrument:

Options	Function										
	<p>Allows the user to set the name of their instrument.</p>										
<p>Serial Number 5211998</p>	<p>Shows the serial number of the instrument.</p>										
	<p>Takes the user to a PDF of the End User License Agreement.</p>										
	<p>Takes the user to a window with important general information about the instrument, such as the instrument installation date and the versions of the server, client, and scripts. It will also show hours and contact information for Carterra Service and Support. The user can also copy this information to the clipboard.</p> <div data-bbox="574 1247 1463 1598" style="border: 1px solid #ccc; padding: 10px; margin-top: 10px;"> <p>Ultra ☐ ×</p> <p>General Information</p> <table style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 60%;">Serial Number</td> <td>5211998</td> </tr> <tr> <td>Installation Date</td> <td>2019-08-09</td> </tr> <tr> <td>Server Version</td> <td>2.5.0.929</td> </tr> <tr> <td>Client Version</td> <td>2.5.0.929</td> </tr> <tr> <td>Scripts Version</td> <td></td> </tr> </table> <p>Carterra Service and Support (M – F, 8am – 6pm MT), 1-844-642-7635, Opt. 3 , support@carterra-bio.com</p> </div>	Serial Number	5211998	Installation Date	2019-08-09	Server Version	2.5.0.929	Client Version	2.5.0.929	Scripts Version	
Serial Number	5211998										
Installation Date	2019-08-09										
Server Version	2.5.0.929										
Client Version	2.5.0.929										
Scripts Version											

Cleaning:

Options	Function
	<p>The Clean procedure flows 3% Contrad, followed by a water rinse, through the internal fluidics of Ultra.</p>
	<p>The Sanitize procedure flows 3% Contrad, water, 0.1% sodium hypochlorite, and one final water rinse through the internal fluidics of Ultra.</p>
	<p>The Sanitize + Sleep completes the same cleaning procedure as Sanitize but finishes by airing out the fluidic lines of Ultra. This only needs to be performed when there is an extended period of time in which Ultra will not be used.</p>
	<p>The MC cleaning station (Waste Tray) can be accessed through the maintenance page for cleaning. Typically, these only need to be cleaned if residue buildup is apparent. The user can clean the MC cleaning station on their own using this function if they see buildup. The waste station should be cleaned with distilled water. If there is visible residue build up on the SC waste station, customers should contact Carterra support to schedule a maintenance visit.</p>
	<p>Flushes water followed by air through the buffer, water, and cleaning lines (B1, B2, H₂O, C1, and C2).</p>

Logs:

Options	Function
	<p>Allows user to save instrument logs to the PC or send the logs to Carterra Support. Users can set the date range for the logs.</p> 

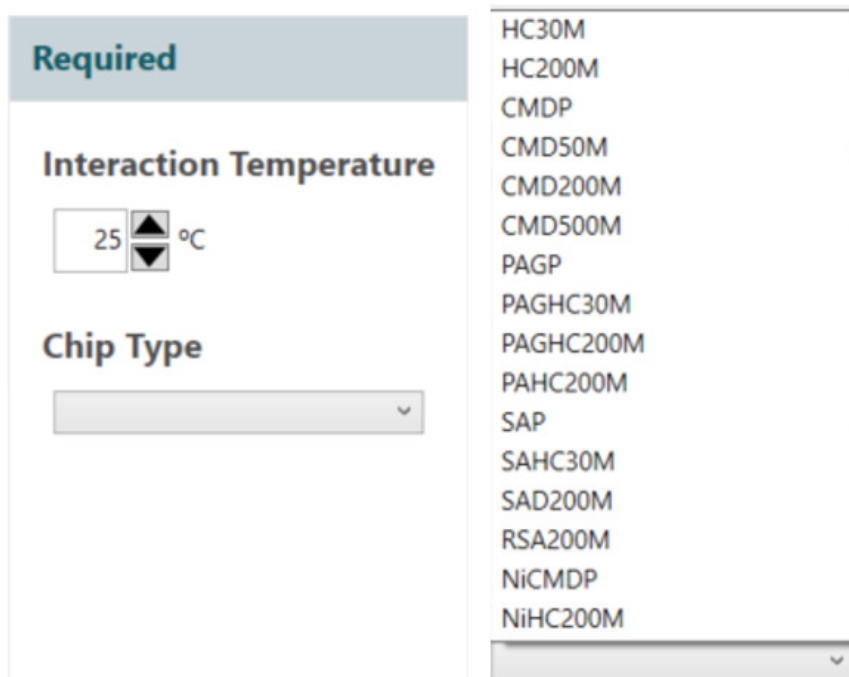
5. Creating and Running an Experiment

Building a method in the Navigator software is a simple process that starts with selecting the experiment type and navigating through a guided Wizard. Many of the same options are available for each experiment type and will be covered first. Later sections will cover the specific considerations for each Wizard option.

5.1 Common Setup Tabs

5.1.1 Interaction Temperature and Chip Type

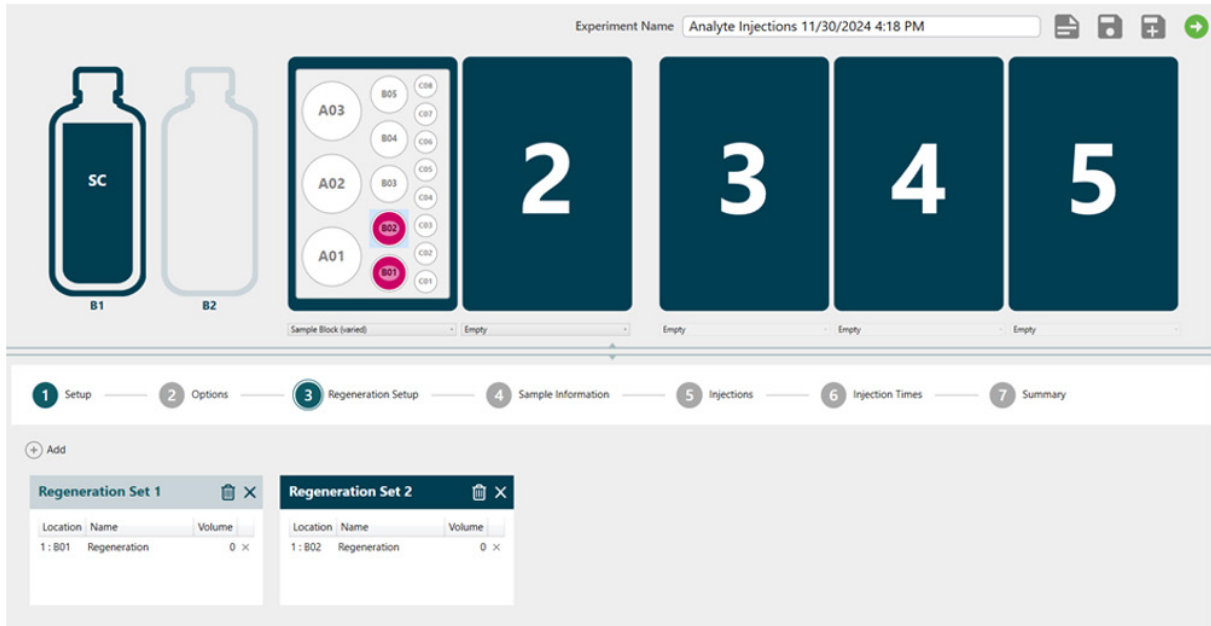
The user must set the interaction temperature (enter a value or use the up/down controls) and select the chip type (from the drop-down list) in each wizard on the Setup tab. The chip type should match the chip type that will be loaded for the experiment.



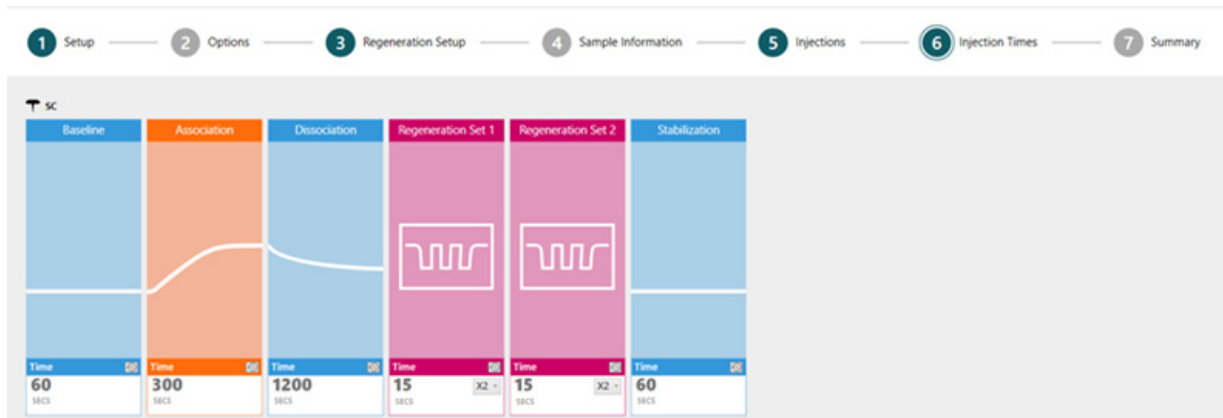
The image shows a software interface for setting up an experiment. On the left, under a 'Required' header, there are two fields: 'Interaction Temperature' and 'Chip Type'. The 'Interaction Temperature' field is a numeric input with a value of 25 and a unit of °C, accompanied by up and down arrow buttons. The 'Chip Type' field is a dropdown menu. To the right of the dropdown, a list of chip types is displayed, including HC30M, HC200M, CMDP, CMD50M, CMD200M, CMD500M, PAGP, PAGHC30M, PAGHC200M, PAHC200M, SAP, SAHC30M, SAD200M, RSA200M, NiCMDP, and NiHC200M.

5.1.2 Regeneration Setup

Some analyte/ligand interactions do not fully dissociate and may require regeneration before subsequent analysis. To facilitate their separation, Ultra can inject regeneration solutions using the aSFC. These solutions may contain high/low pH buffers, higher salinity salts, additives, competitors, etc., alone or in combination, that facilitate the removal of the analyte from the ligand without damaging the ligand material.



In the Regeneration Setup tab, click the (+) Add button to add the first regeneration set. Multiple regeneration sets can be added in cases where several sequential regeneration solutions are needed. Populate the regeneration solution location by clicking on the regeneration set and then the position in the reagent block. Additional vials or wells assigned within a region set will be treated as additional volume capacity, with Ultra injecting the number of times a full piece of labware will allow before incrementing to the next tube (380 µL of regeneration reagent is required per regeneration set, the maximum number of regenerations per labware [independent of pulse count] is 3 for a 1.5 mL vial, 39 for a 15 mL vial, 131 for a 50 mL vial, and 5 for a well in a 2 mL plate.). Regenerations from additional sets add a separate regeneration step to each cycle. In the injection times section, the contact time and number of pulses (1, 2, or 3) can be set separately for each regeneration set.



5.1.3 Sample Information

In the sample information tab, the user needs to specify the name, location/bay, and type of tube or plate for each sample in the experiment. The user also has the option to include additional information about the samples such as concentration, molecular weight, refractivity, or molecular volume. There is also a column for any other notes that the user might want to include. All the sample information added in Navigator will automatically be transferred to the .sprdata file produced by the experiment. It is best practice to include as much information as possible in this step.





The sample information tab makes use of both the interactive sample deck layout cartoon and the interactive written sample deck layout:



1/2) Buffer Bottles and Lines: the bottles (1) are a visual indication of how many buffers are needed for the experiment and which side of the instrument the buffer will be delivered to. Buffer and buffer line positions can be selected from the buffer box (2).

3/4) Bay 1 Sample Block: Bay 1 can only be accessed by the aSFC. Bay 1 will usually contain the sample block to hold samples in tubes. Positions A01 to A03 allow for 50 mL Septa cap tubes. Positions B01 to B05 allow for 15 mL Septa cap tubes. Positions C01 to C08 allow for 1.5 mL Septa cap tubes. Some wizards allow for the sample block in bay 1 to be switched out for a plate if desired by the user. Depending on the wizard and options the user has selected, some of the sample names will autofill. These sample names can be changed/edited.

5) Sample Names/Information Options: All Bays have the following options for adding sample names and information.

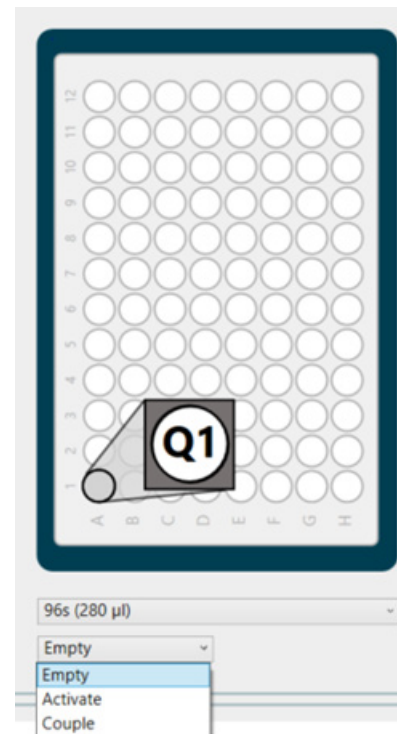
Button	Function
	Fill empty wells with Default well ID: this button will populate all empty sample names with the default bay/position (i.e. Sample Block location A01 will populate as 1A01).
	Copy sample information in template format to the clipboard: this button copies the sample information template to clipboard, which can then be pasted and edited in a spreadsheet. While sample names and information can be added directly in Navigator, this is an easy way to edit full plates of sample information all at once.
	Paste sample information from the clipboard in tab delimited format defined by the template: this button allows user to paste sample information from a spreadsheet that has been formatted using the sample information template. When copying and pasting information from another source into Navigator, make sure the column names are also included, or else the paste function will not work and induce an error message.
	Clear sample list: this button will delete all information in the sample list.

While sample information can be typed directly into Navigator, the user is encouraged to use the buttons above to copy the sample information template and edit it in Excel or another spreadsheet.

6-8) Bays: Bays 1 and 2 can only be accessed by the aSFC. Bays 3, 4, and 5 can only be accessed by the cPH. All Bays may have a drop-down menu listing all plate options that can be loaded in these positions (see below).


96s (280 µl)
 96d (2 ml)
 384d (240 µl)
 384xd A (300 µl)
 384xd B (400 µl)
 Empty

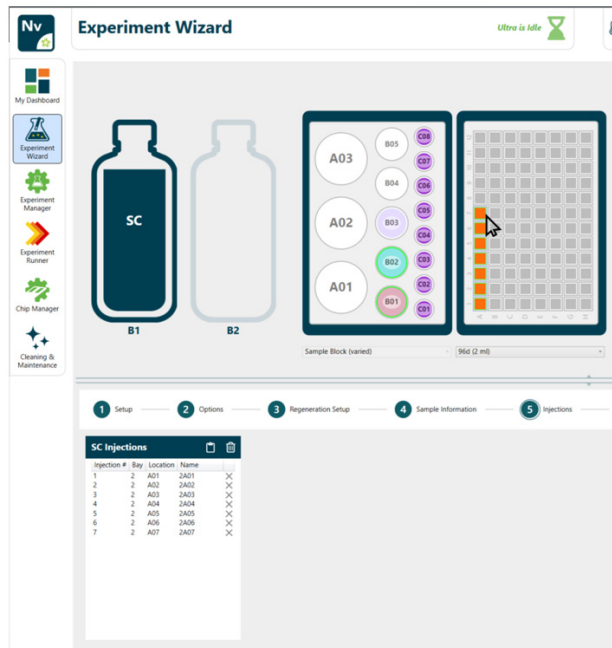
Depending on the experiment, Bays 3, 4, and 5 may have additional drop-down menus. For example, in the Surface Prep Array Wizard, there is an additional drop-down menu below; for this experiment, these options are used to indicate which bays will hold the activation plate or the coupling (ligand) plate.



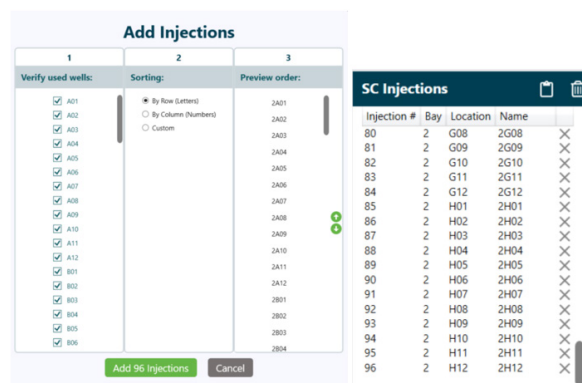
5.1.4 Injections


There are multiple options for injecting named samples in the Injections tab:

For a single injection, or just a few injections, the user can manually select the injections by clicking on each individual tube or well position. The order in which the injections are selected is how they will populate the injection set list. If an injection is selected in the incorrect order, click the X next to the sample name to delete it from the list. Select the trashcan button  to delete the entire injection set list. Depending on the volume capacity of the injection location, tubes and wells can be selected for multiple injections.



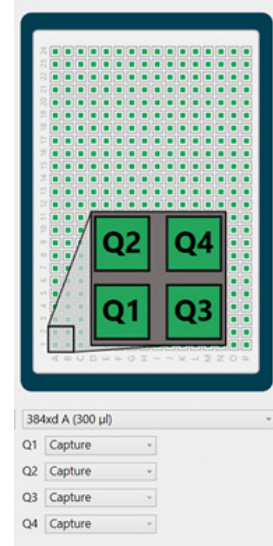
If many injections are desired, the user can select multiple injections at once by lassoing many wells at once. Once the desired wells have been lassoed, an Add injections window will pop up. There are three columns. Column 1 lists and allows the user to validate all the wells to be used for injections. Column 2 allows the user to sort the injections. By default, the injections will be sorted by row, but the injections can also be sorted by column or by a custom injection list (see below). Column 3 allows the user to preview the order of the injections. Clicking the Add Injections button will populate the injection set.



Additionally, selecting the clipboard button  in the injection set banner allows the user to paste in a custom injection list created in Excel or Google Sheets. The injection list must be formatted ([Bay] [Location]) to include the template column names.

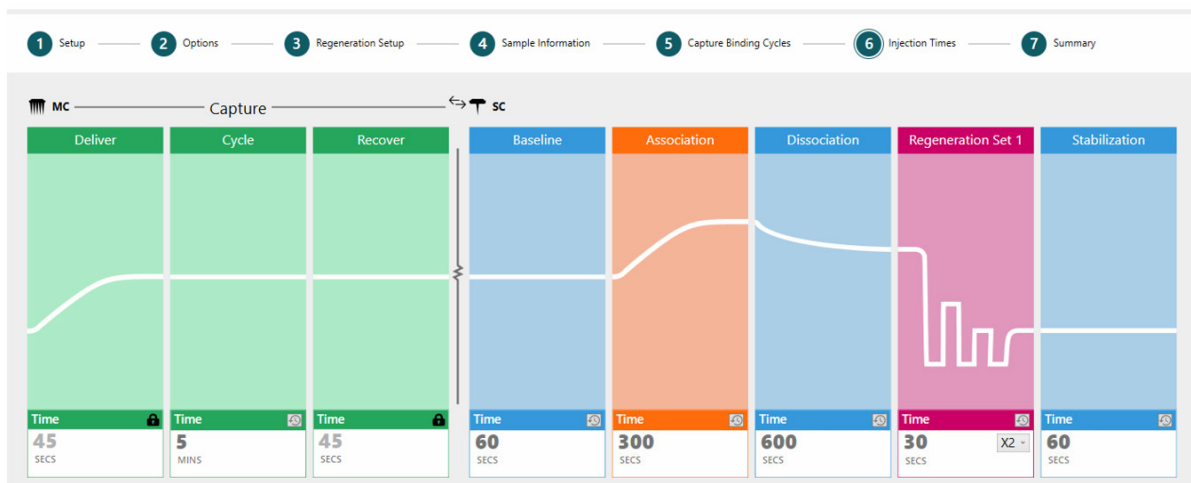
5.1.5 Plate Quadrants

384-well plates can be thought of as having four 96-well plates interlaced to fill the same dimensions. The Ultra’s needle array is positioned to center on the wells of a 96-well plate and they can access all the wells of a 384-well plate by addressing the plate in 4 shifted positions. Navigator software refers to these plate positions as quadrants, so a quadrant represents all the positions the 96-needle array can access simultaneously. The quadrant pattern simply skips a well in both the row and columns direction, so wells A01, A03, A05.... C01, C03, C05 are all wells in Quadrant 1. Quadrant 2 starts at well A02, Quadrant 3 starts at B01, and Quadrant 4 starts at B02. 96-well plates are listed as Q1 or quadrant 1, as there is only 1 position for the 96 needles.



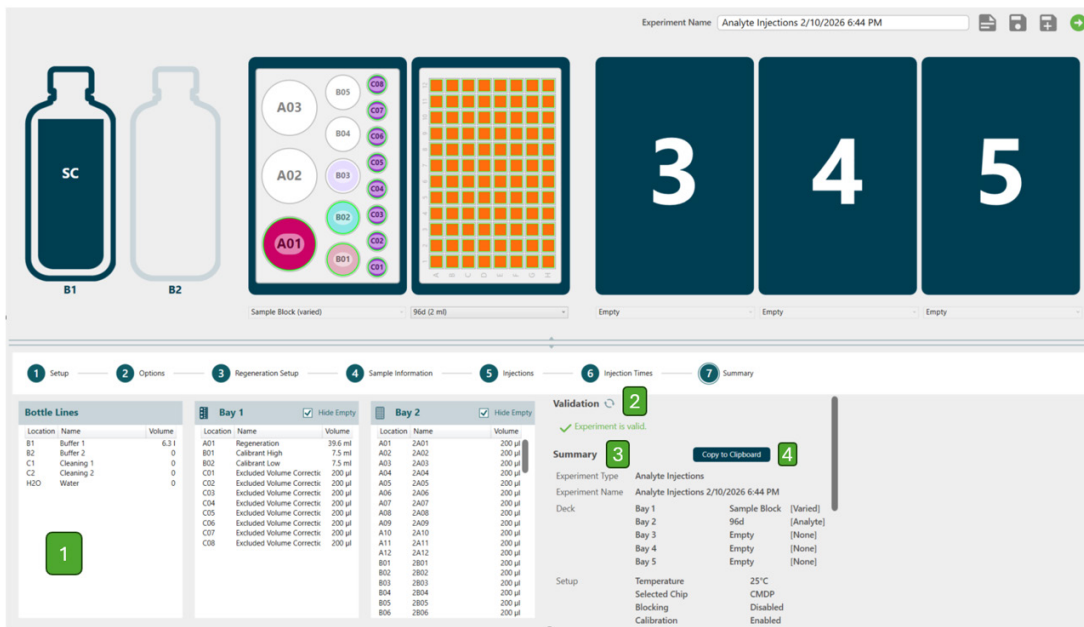
5.1.6 Injection Times

The user can set the time for each phase in a cycle in the injection times tab. Different injection types will be shown depending on the wizard and experiment options the user has selected. For some injections, including regeneration, there is a pulldown (shown below as 2x) indicating the number of times the regeneration pulse will be applied. The side of the instrument from which the injections are coming is specified in the top left corner (SC or MC).

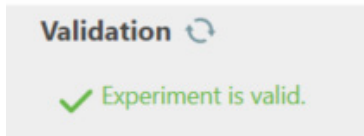


5.1.7 Summary

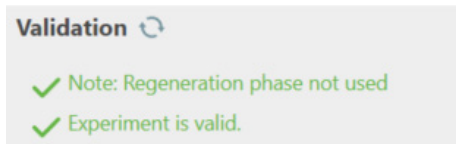
The summary tab summarizes and visually displays all vital experiment information and validates the experiment.



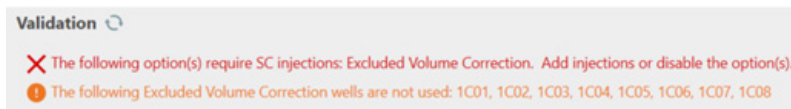
- 1. Bottle Lines and Bay Summaries:** This is where a user can double-check which Buffer Lines and Bays are being used in the experiment. It lists the specific location, name, and required volumes of every buffer and sample used in the experiment.
- 2. Validation:** If an experiment is valid and ready to run, this section will simply show a green message and check mark to indicate the experiment has been validated.



A green message other than “Experiment is valid” usually indicates that an optional step (such as regeneration) has not been selected for this experiment.

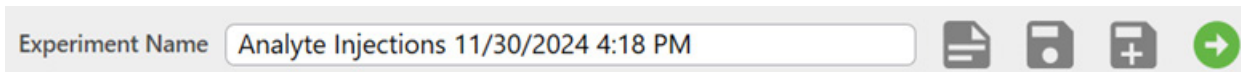


A red error message indicates that the experiment cannot be run until the changes in the message have been made. An orange message indicates that while the experiment can proceed without any changes, it might not run as intended. If changes are made, the validation status can be updated using the refresh button.



- 3. Summary:** This is a written summary of the whole experiment, including the experiment type, the experiment name, labware in use, setup information, injection times, and estimates of experiment run time and buffer usage. The estimates section does not account for the time or buffer used during primes prior to the experiment starting. Any changes made to the experiment setup will result in the summary updating to reflect the changes.
- 4. Copy to Clipboard button:** Clicking this button will copy all summary information to the clipboard for pasting into a spreadsheet.

5.1.8 Experiment actions



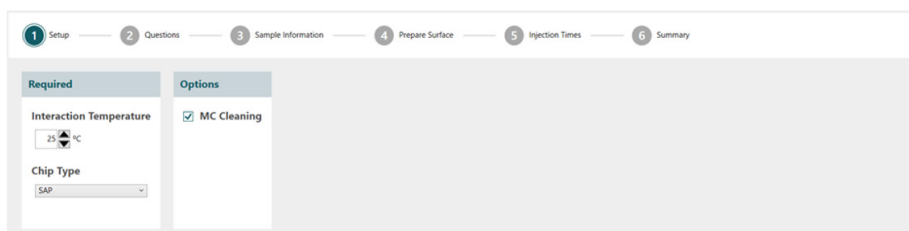
The experiment name is automatically populated based on the experiment wizard used to create the method. The user is encouraged to change the experiment names to include the experiment information. The buttons next to the experiment naming window are described in the table below.

Button	Function
	Show the experiment notes pane: this button will add a notes pane to the right side of all tabs of the experiment wizard.
	Overwrite the current experiment: this button will overwrite any saved changes made to a saved experiment method.
	Save the experiment as a new experiment: this button will save the experiment method as a new experiment in Experiment Manager.
	Send experiment to Experiment Runner: this button will save the experiment method and send it to the experiment runner if the experiment is valid. While hitting this button will save an experiment method, the user is always encouraged to save an experiment using the save/overwrite buttons prior to sending a method to the experiment runner.

5.2 Common Options

5.2.1 MC Cleaning

When available, MC cleaning performs additional cleaning of the multichannel head and fluidics using a solution from the C1 line to minimize sample-to-sample carryover. Enable this option when running MC across multiple cycles, especially when switching between different ligands with high concentrations. MC cleaning can be activated in the Wizard Setup tab. One MC cleaning consumes approximately 150 mL of MC Buffer and 130 mL of C1 Cleaning Buffer and adds about 9 minutes to the run time.



5.2.2 Calibration

In SPR experiments, the change in response is proportional to the change in refractive index of the solutions. However, this response isn't necessarily linear across the instrument's full dynamic range. The calibration procedure in Ultra restores full linearity for all 192 ROIs across the response range sampled by the calibration solutions, regardless of their relative coupling densities.

Ultra needs the user to provide two solutions and an empty mix tube for the calibration procedure. The “High” and “Low” calibrant solutions are comprised of running buffer aliquots whose refractive index is adjusted by the addition of high and low refractive index components to the experimental running buffer. These should be sufficiently high and low to span all the anticipated RI variance of all samples used in the run.

The user provides at least 7.5 mL of each of the high and low calibrant solutions in addition to an empty mix tube. When the calibration is executed, Ultra will draw samples of the high and low solutions in varying ratios, mix them in the mix tube, and inject them through the aSFC. The calibration procedure performs 12 injections, one each for the high and low solution and 10 intermediate mixed solutions. This procedure is the last to execute in an experiment and adds ~45 minutes to the runtime. Example solutions are given below. The below example produces 15 mL of each solution, providing enough for a second run and/or extra solutions for the Excluded Volume Correction procedure (see next section).

It is important that the calibrant series spans the full range of all observed data points throughout the rest of the experiment. If the calibration range was insufficient, prepare additional reagents with an appropriate range and execute an experiment wizard with at least one injection that includes the calibration procedure. The user can import these data into the calibration tab in Kinetics and Epitope.

Example solutions (for 15 mL of solution):

If using a non-DMSO running buffer:

Low RI = 4.5 mL water + 10.5 mL running buffer

High RI = 600 µL DMSO + 14.4 mL running buffer

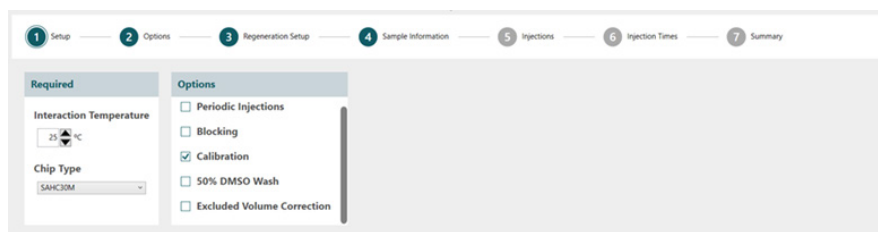
If using a running buffer with DMSO:

Low RI = 4.5 mL Buffer-DMSO (0% DMSO) + 10.5 mL running buffer with DMSO

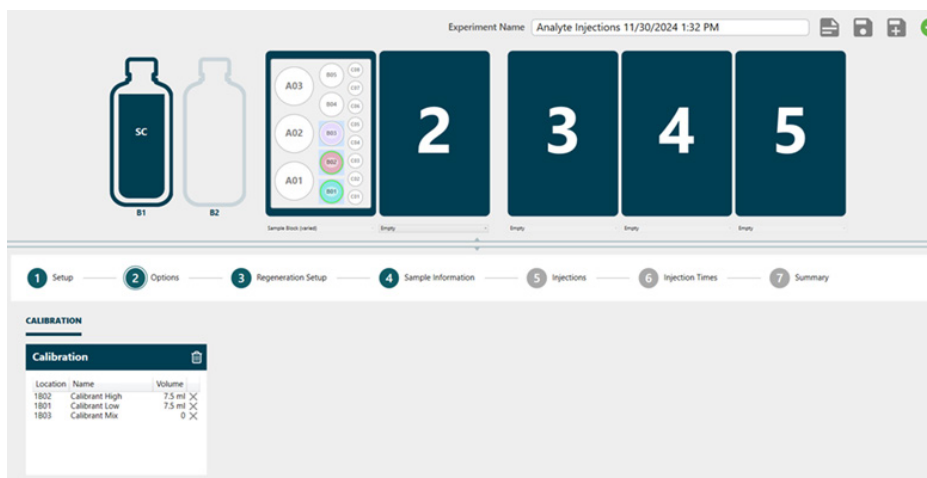
High RI = 600 µL DMSO + 14.4 mL running buffer with DMSO (makes a +4% DMSO solution)

Alternatives: +4% glycerol or +1 M NaCl can be used in place of DMSO.

To perform calibration, check the “Calibration” box in the options menu when it’s presented:



This will activate a “Calibration” box in the options menu:



The image above shows the “Options” submenu in a wizard setup. The user should click the calibration tab, then click the image of the sample block to indicate the desired locations for the Calibrant High, Calibrant Low, and Calibrant Mix tubes.

5.2.3 Excluded Volume Correction (EVC)

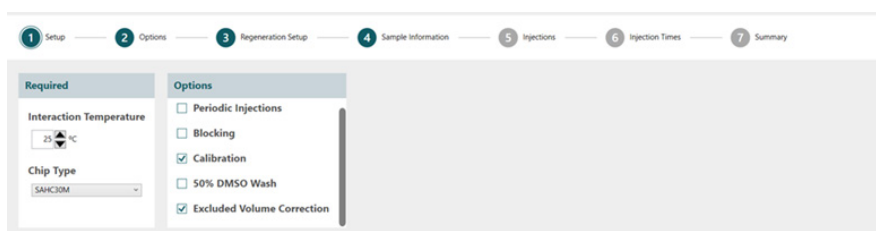
EVC corrects the difference in refractive index (RI) shift that arises between experimental and reference surfaces. This difference occurs because the deposited ligand material in the Ligand ROIs occupies space within the detection volume that, in the reference ROIs, is occupied by solvent leading to a larger buffer RI response than seen in occupied ligands. The deposited ligand molecules effectively exclude solvent molecules from entering the SPR detection region and therefore the excluded solvent molecules do not impact the bulk RI shift. As a result, ROIs with lower ligand density will show increased observed RI, and this difference in signal is unrelated to any binding event. When a reference ROI is subtracted from a ligand ROI during the referencing step of data processing, a negative signal may be produced if high refractive index buffers are being used and excluded volume correction is not properly applied. The magnitude of this effect is dependent on coupling densities and the degree of mismatch between the solvent components of an analyte solution and the running buffer. Solutions containing high refractive index components, such as DMSO and glycerol, are common examples of buffer systems requiring excluded volume correction. This correction is especially critical when kinetics are weak or absent. Without correction, binding responses and bulk RI shifts can overlap, making it difficult to distinguish genuine interactions from solvent effects.

To apply the EVC correction using Ultra, the user needs to provide a set of solutions spanning the RI range of the analytes in the experiment. For convenience, it is optimal to make 15 mL of the High Calibrant and Low Calibrant solutions (previous section), remove an aliquot, and dilute each 10% with the running buffer. This will ensure that the EVC solutions fall within the calibration range. The user is suggested to prepare at least 7 EVC solutions to construct a proper calibration curve, and the user will need at least 200 μ L of each solution. An example for preparing these solutions is below:

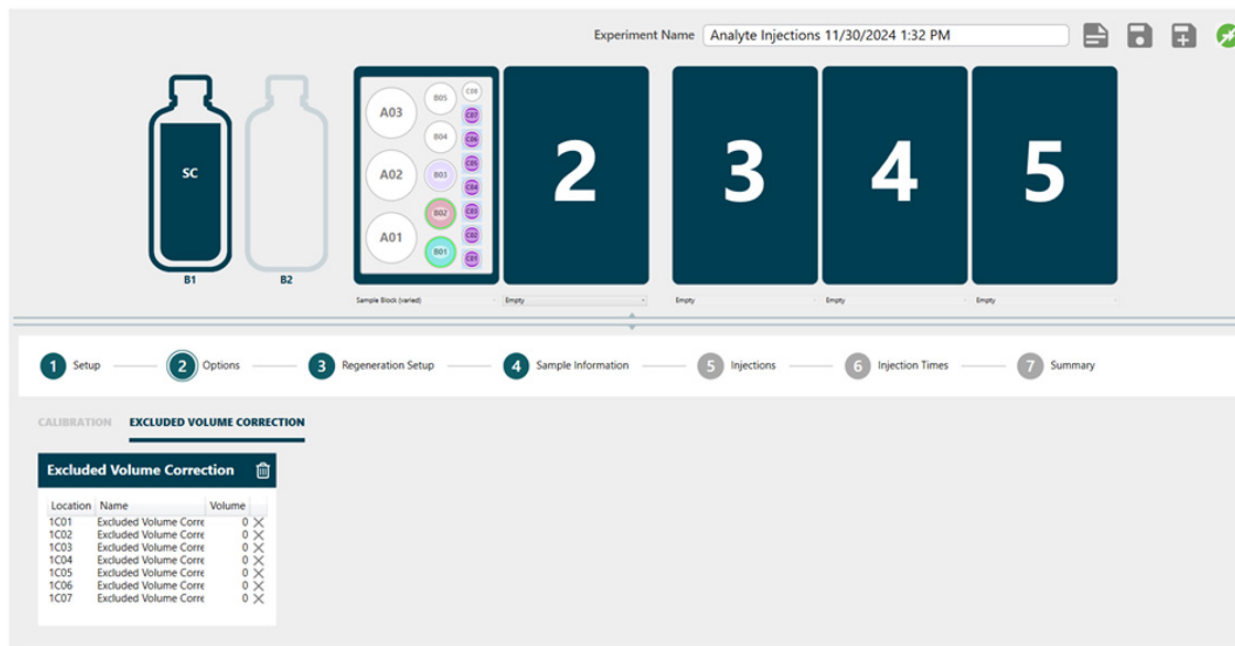
Place 7 labeled 1.5 mL screwcap vials (Simport Scientific #T341-4T and #T347AQX) compatible with the sample block in a holder. In tubes 2-6, place 300 μ L of running buffer. In tube 1 place 600 μ L of the High RI solution (after 10% dilution), and in tube 7 place 600 μ L of the Low RI solution (after dilution). Remove 300 μ L of the solution from tube 1 and dilute by thoroughly mixing with the solution in tube 2. Repeat this process by taking 300 μ L from tube 2 and mixing with tube 3. Discard the extra 300 μ L of solution in tube 3. Then mix 300 μ L from tube 7 into tube 6, and then mix 300 μ L of tube 6 into tube 5. Leave tube 4 alone as just running buffer and it will represent the zero-correction point when running buffer and EVC solution exactly match.

Analyte injections whose solvent RI falls outside the correction curve cannot be included. If this occurs, rerun the EVC protocol using the same chip and buffers from the prior experiment and a more appropriate range of EVC solutions. A separate EVC curve can be imported into the EVC dialogue in Kinetics and Epitope during data processing. (See the Kinetics and Epitope guides for more details.)

Users have the option to run the Excluded Volume Correction (EVC) by clicking that option in the Wizard Setup Tab as shown below:



When this option is selected, a submenu will appear in the option tab, allowing the user to specify the location and number of EVC solutions:



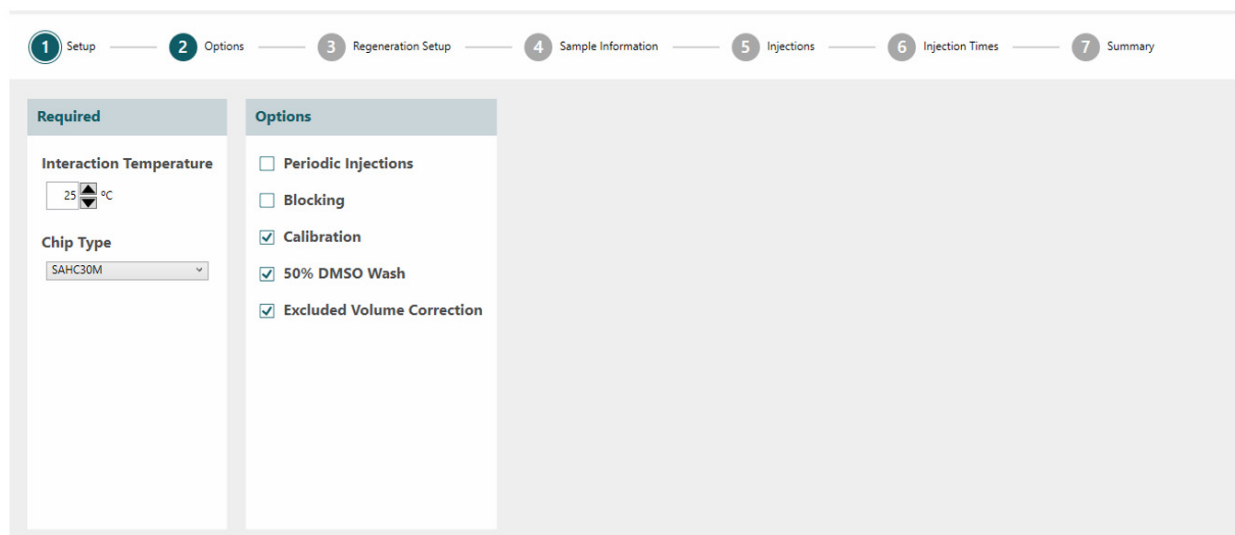
EVC injections must also be included in the Injections tab; otherwise, the EVC solutions won't be injected.

In the above case, seven solutions have been selected and populated into the 1.5 mL tube positions in the sample block. EVC can also be run from a microplate.

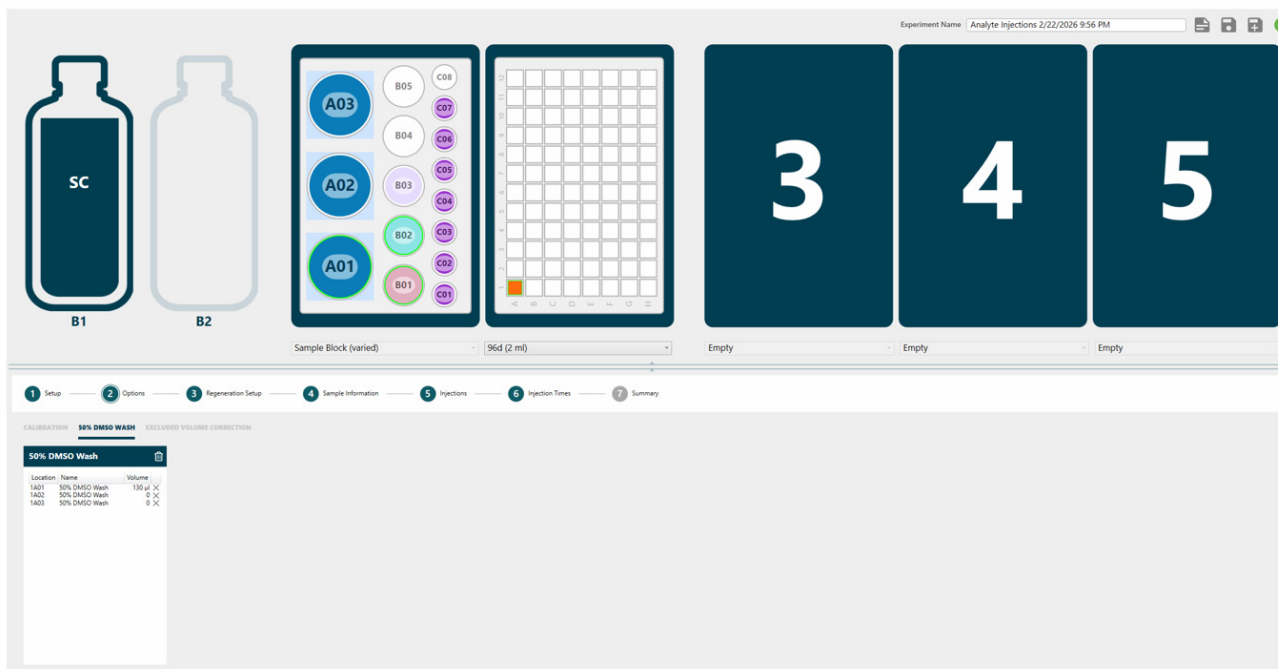
5.2.4 50% DMSO Wash

Ultra offers an extra cleaning procedure utilizing a user-provided cleaning solution. When activated, this procedure rinses the fluidic path of the SC side, excluding the aSFC and chip surface. This allows for a more stringent fluidic wash when the user is likely to encounter analyte carryover from injection to injection, which can cling to fluidic components such as the needle and tubing. The most frequent cleaning solution, especially in small-molecule work, is a 50% solution of DMSO. It is recommended to prepare this solution by mixing equal parts 100% DMSO with high purity water. Each cycle requires 130 µL of 50% DMSO, which adds approximately 2 minutes to the run time.

To activate the wash, check the 50% DMSO Wash box when available in Wizard Setup:

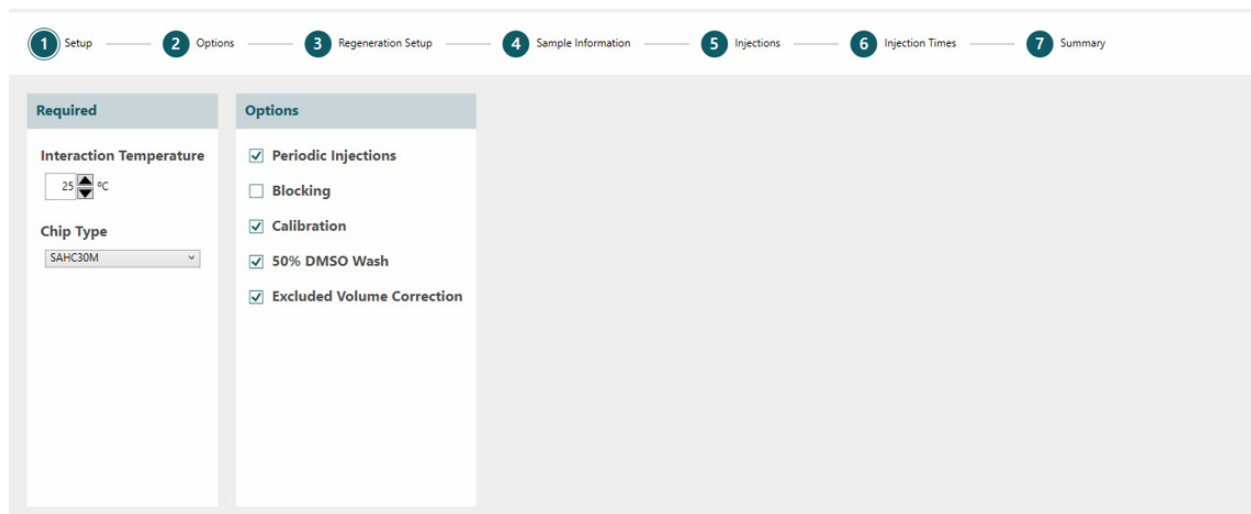


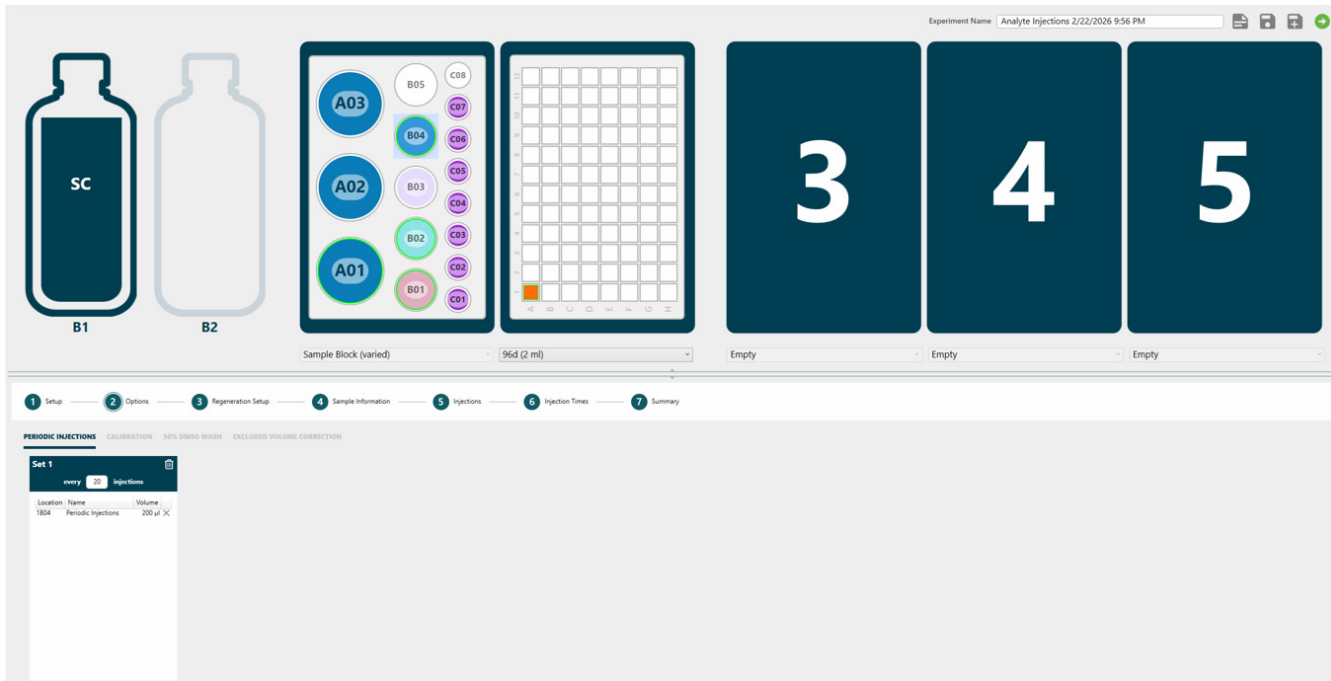
The wash solutions are drawn from tubes in the reagent rack. The locations can be specified in the Wizard Options tab. (In this example, all three 50 mL conical positions have been assigned as 50% DMSO wash.)



5.2.5 Periodic Injections

The Periodic Injection option directs Ultra to perform an analyte injection from a tube in the sample block at a regular interval specified in number of cycles. For example, in fragment screening it's useful to run a control injection every 10-20 cycles to ascertain the rate of decay of the various ligand proteins. 200 µL of sample will be used every time the cycle runs. Several different solutions can be specified, but each will be run at the same interval.



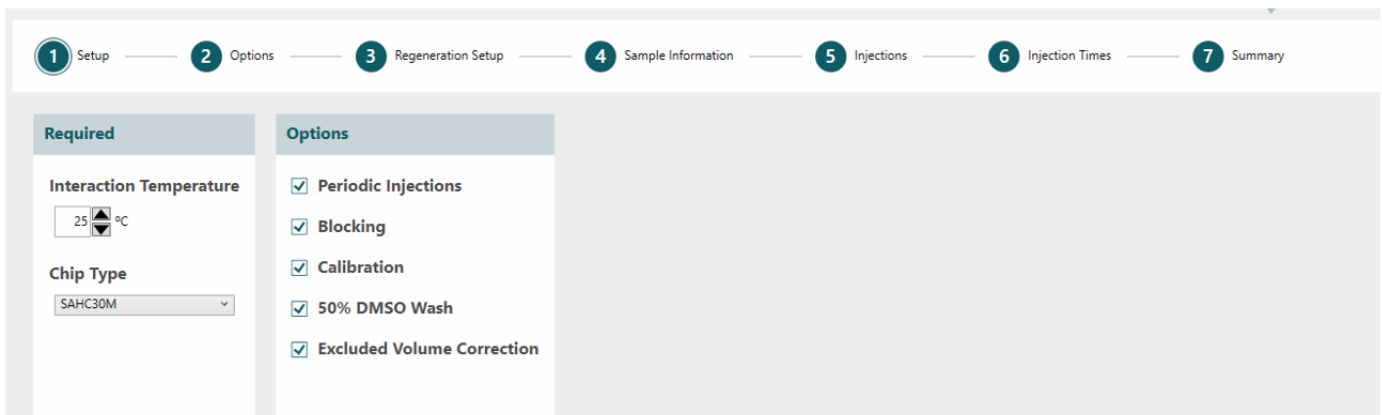


To activate periodic injections, select the Wizard Setup option. Under Wizard Options, the user can specify the periodic injection frequency and the sample location. These injections will automatically appear in Injection Sets in the correct interval once injections are chosen.

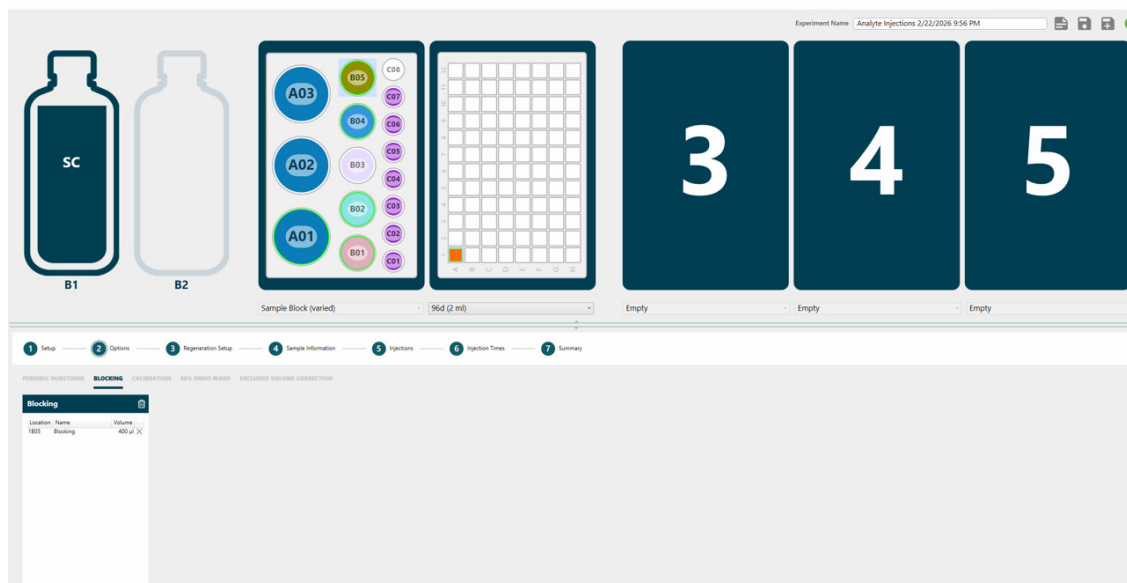
5.2.6 Blocking Injections

Blocking injections are useful in experiments where any unoccupied capture reagent could otherwise interact with subsequently injected analytes. For example, if the user captures and crosslinks antibodies via their Fc domain using an anti-human Fc antibody from crude samples, then a blocking injection of purified human IgG should be included before each epitope binning cycle to occupy any remaining free anti-human Fc sites and reduce non-specific interactions with analytes. 200 µL of the blocking solution is used for each cycle. The contact time is adjustable in the Injection Times tab.

The Blocking Injection option is activated by selecting that option in the Wizard Setup tab:









Details about the location of the blocking solution and required volumes can be found on the Wizard Options tab:



5.3 Wizard Options

There are 6 Wizard options in Navigator to let users build experiment methods:

 <p>Surface Prep Lawn</p>	<p>Coats the entire sensor chip surface with a uniform layer of biomolecules.</p>
 <p>Surface Prep Array</p>	<p>Creates an array of discretely deposited biomolecule locations on the sensor chip surface.</p>
 <p>Capture Kinetics</p>	<p>Enables multiple series (sets) of ligand capture and analyte injections for interaction analysis with one or more regeneration injections per set.</p>
 <p>Analyte Injections</p>	<p>Injects analyte over an array for interaction analysis. One or more regeneration injections can be added to each cycle.</p>
 <p>Dual-Analyte Injections</p>	<p>Sequentially injects 2 analytes without a wash step between them. One or more regeneration injections can be added to each cycle.</p>
 <p>Quantitation</p>	<p>This wizard used the cPH to measure the concentration of analytes in matrices.</p>

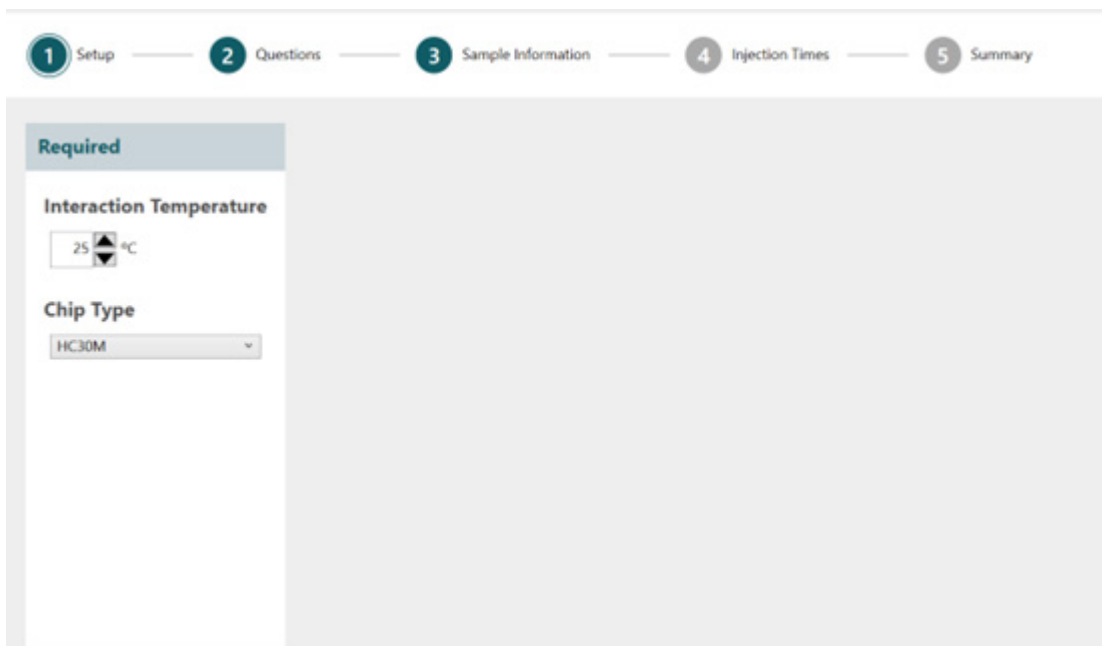
5.3.1 Surface Preparation Lawn

The Surface Preparation Lawn wizard coats, via coupled or captured, the entire sensor chip surface with a uniform layer of biomolecules. Typically, this uniform surface is then used to capture proteins/peptides/oligonucleotides using the Surface Preparation Array or capture kinetics wizard. In Surface Preparation Lawn, the aSFC docks on the sensor chip surface, primes the chip surface with the system running buffer, and passes SC injections across the surface. In doing so, biomolecules are covalently or noncovalently attached to the surface across all ROI and reference locations.

Immobilization can be done as a single injection, or co-immobilization can be performed when two biomolecules need to be immobilized serially. Using the capture option, the biomolecule can be captured on a pre-functionalized surface, such as a streptavidin surface, or the capture surface can be created as part of the application.

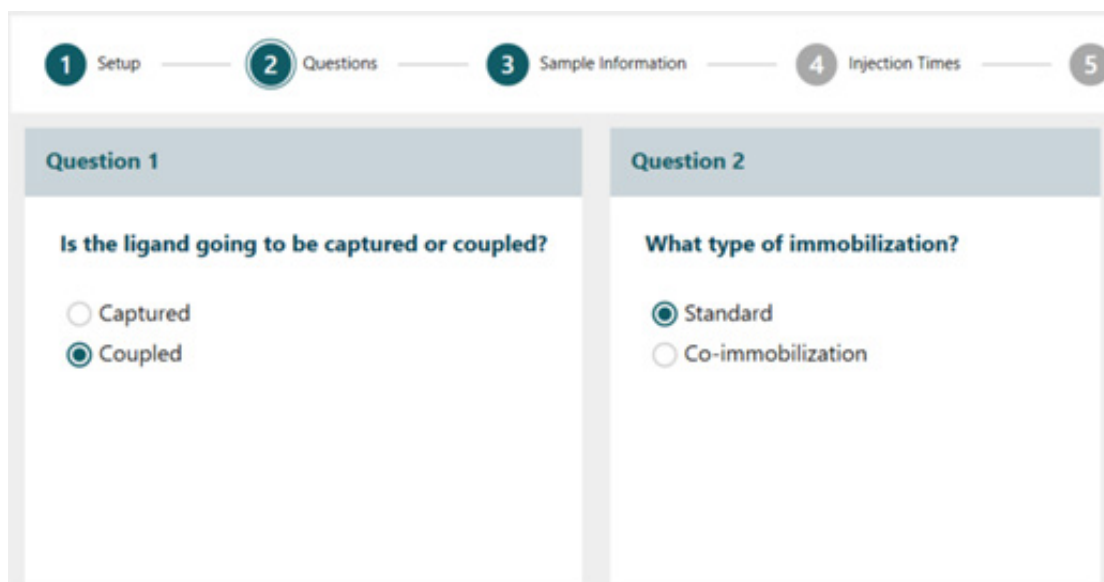
An example of setting up a standard amine coupling is provided below.

1. Choose the interaction temperature and chip type.



The screenshot shows the 'Required' section of the wizard. At the top, there is a progress bar with five steps: 1 Setup, 2 Questions, 3 Sample Information, 4 Injection Times, and 5 Summary. Step 1 is highlighted. Below the progress bar, the 'Required' section contains two fields: 'Interaction Temperature' with a value of 25 °C and a spin control, and 'Chip Type' with a dropdown menu set to 'HC30M'.

2. Select whether the ligand will be captured or coupled.



The screenshot shows the 'Questions' section of the wizard. At the top, the progress bar shows step 2 'Questions' highlighted. Below the progress bar, there are two question panels. 'Question 1' asks 'Is the ligand going to be captured or coupled?' with radio buttons for 'Captured' and 'Coupled', where 'Coupled' is selected. 'Question 2' asks 'What type of immobilization?' with radio buttons for 'Standard' and 'Co-immobilization', where 'Standard' is selected.

3. Enter or copy-paste sample information if desired. Default sample names are shown.

The screenshot shows the 'Sample Information' step of the software interface. On the left, there is a 'Sample Block (varied)' layout with wells A01, A02, A03, B01, B02, B03, B04, B05, C01, C02, C03, C04, C05, C06, C07, and C08. On the right, a table lists the sample locations and their properties:

Location	Name	Conc (M)	MW (Da)	Refractivity (Molecular Wt	Notes
A01		0.00E+0	0.00	0.0000	0.00	
A02		0.00E+0	0.00	0.0000	0.00	
A03		0.00E+0	0.00	0.0000	0.00	
B01		0.00E+0	0.00	0.0000	0.00	
B02		0.00E+0	0.00	0.0000	0.00	
B03		0.00E+0	0.00	0.0000	0.00	
B04		0.00E+0	0.00	0.0000	0.00	
B05		0.00E+0	0.00	0.0000	0.00	
C01	Activate	0.00E+0	0.00	0.0000	0.00	
C02	Couple	0.00E+0	0.00	0.0000	0.00	
C03	Quench	0.00E+0	0.00	0.0000	0.00	
C04	Wash	0.00E+0	0.00	0.0000	0.00	
C05		0.00E+0	0.00	0.0000	0.00	
C06		0.00E+0	0.00	0.0000	0.00	
C07		0.00E+0	0.00	0.0000	0.00	
C08		0.00E+0	0.00	0.0000	0.00	

4. Set injection times. (Activate, Couple, Quench ≥ 30 s; Wash ≥ 15 s/pulse)

The screenshot shows the 'Injection Times' step. It features a graph with four colored regions: Activate (green), Couple (orange), Quench (red), and Wash (blue). Below the graph, the time for each region is displayed in a box:

- Activate: 300 SECS
- Couple: 300 SECS
- Quench: 300 SECS
- Wash: 15 SECS (with a multiplier of X2)

5. Review summary.

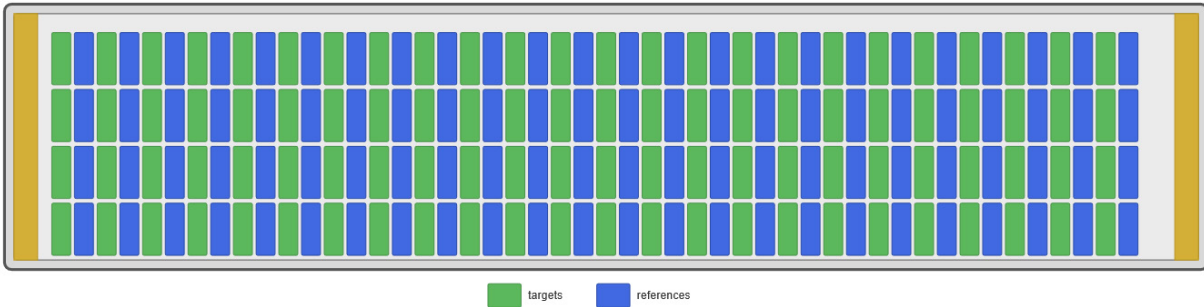
The screenshot shows the 'Summary' step. It includes a 'Validation' section with a green checkmark and the message 'Experiment is valid.' Below this is a 'Summary' section with a 'Copy to Clipboard' button. The summary details are as follows:

- Experiment Type: Surface Prep Lawn
- Experiment Name: Surface Prep Lawn 2/10/2026 1:05 PM
- Surface Prep Lawn Questions: Is the ligand going to be captured or coupled? Coupled
- What type of immobilization? Standard
- Deck:

Bay 1	Sample Block	[Varied]
Bay 2	Empty	[None]
Bay 3	Empty	[None]
Bay 4	Empty	[None]
Bay 5	Empty	[None]

5.3.2 Surface Preparation Array

Surface Preparation Array uses the cPH to create an array of discretely deposited biomolecule locations on the sensor chip surface. There are 2 main approaches to creating an array in Navigator: 1) captured and 2) coupled. The cPH docks on the sensor chip surface at one of two available positions, and solutions/samples from Bays 3, 4, or 5 are drawn up using the 96 sampling needles and delivered to the sensor chip surface. The wizard can create an array of up to 192 unique ROIs on the surface by printing 2 nested blocks of 96. When creating a coupled array, the surface can be activated with either the SC or MC side of the instrument.



An example of creating a full 192 array with single channel activation is provided below.

1. Choose the interaction temperature and chip type, as well as the optional MC cleaning.

2. Select whether the ligands will be captured or coupled.

3. Enter or copy-paste sample information. The user will also have to select which bay the ligand array will come from.

Bay 1

Location	Name	Conc (M)	MW (Da)	Refractivity (Molecular Vi	Notes
A01		0.00E+0	0.00	0.0000	0.00	
A02		0.00E+0	0.00	0.0000	0.00	
A03		0.00E+0	0.00	0.0000	0.00	
B01		0.00E+0	0.00	0.0000	0.00	
B02		0.00E+0	0.00	0.0000	0.00	
B03		0.00E+0	0.00	0.0000	0.00	
B04		0.00E+0	0.00	0.0000	0.00	
B05		0.00E+0	0.00	0.0000	0.00	
C01	Activate	0.00E+0	0.00	0.0000	0.00	
C02	Quench	0.00E+0	0.00	0.0000	0.00	
C03	Wash	0.00E+0	0.00	0.0000	0.00	
C04		0.00E+0	0.00	0.0000	0.00	
C05		0.00E+0	0.00	0.0000	0.00	
C06		0.00E+0	0.00	0.0000	0.00	
C07		0.00E+0	0.00	0.0000	0.00	
C08		0.00E+0	0.00	0.0000	0.00	

Bay 3

Location	Name	Conc (M)	MW (Da)	Notes
A01	Ligand_01	0.00E+0	0.00	
A02	Ligand_02	0.00E+0	0.00	
A03	Ligand_03	0.00E+0	0.00	
A04	Ligand_04	0.00E+0	0.00	
A05	Ligand_05	0.00E+0	0.00	
A06	Ligand_06	0.00E+0	0.00	
A07	Ligand_07	0.00E+0	0.00	
A08	Ligand_08	0.00E+0	0.00	
A09	Ligand_09	0.00E+0	0.00	
A10	Ligand_10	0.00E+0	0.00	
A11	Ligand_11	0.00E+0	0.00	
A12	Ligand_12	0.00E+0	0.00	
B01	Ligand_13	0.00E+0	0.00	
B02	Ligand_14	0.00E+0	0.00	
B03	Ligand_15	0.00E+0	0.00	
B04	Ligand_16	0.00E+0	0.00	
B05	Ligand_17	0.00E+0	0.00	
B06	Ligand_18	0.00E+0	0.00	
B07	Ligand_19	0.00E+0	0.00	
B08	Ligand_20	0.00E+0	0.00	
B09	Ligand_21	0.00E+0	0.00	
B10	Ligand_22	0.00E+0	0.00	
B11	Ligand_23	0.00E+0	0.00	
B12	Ligand_24	0.00E+0	0.00	
C01	Ligand_25	0.00E+0	0.00	

4. Select ligand deposition locations (Array Groups A and/or B).

Set 1

Multi Channel

Array Group A Bay 3

Array Group B None

Bay 3

Q1

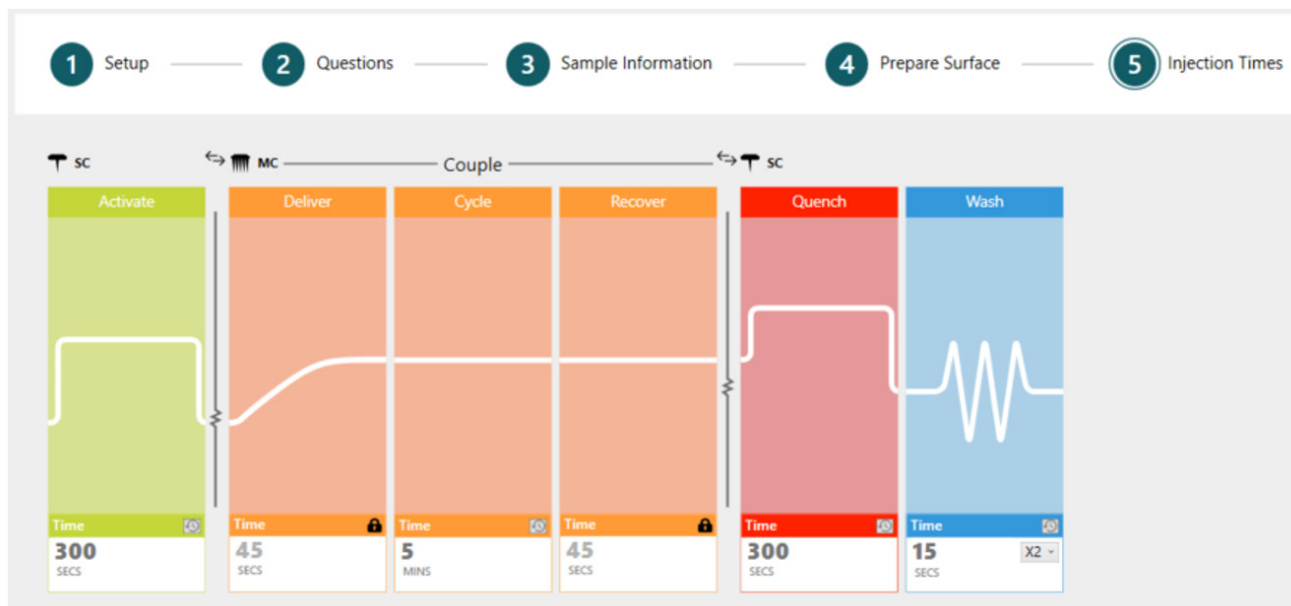
1 A

Bay 3

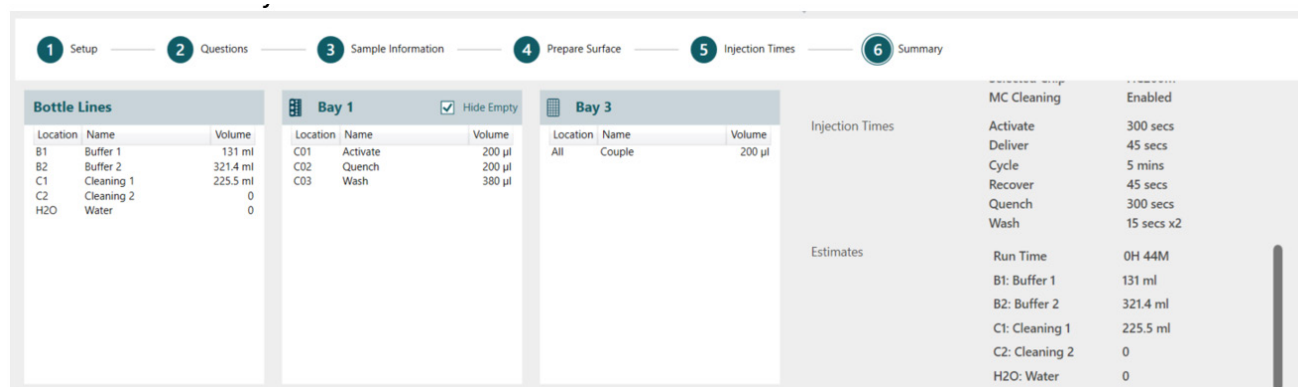
None

Bay 3

- Set injection times. (SC Activate or Quench ≥ 30 s; MC Couple - Deliver and Recover are fixed at 45 s, Cycle ≥ 1 min; SC Wash ≥ 15 s/pulse.)



- Review summary.



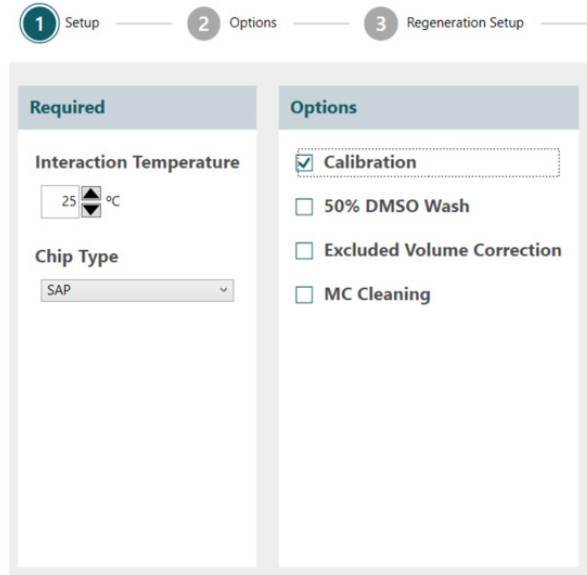
5.3.3 Capture Kinetics

The Capture Kinetics wizard enables the capture on an array followed by a series of analyte injections and one or more regeneration injections. In each Captured Kinetics "Set", the cPH docks on the sensor chip surface and captures an array of up to 192 locations, with samples being returned to the source plates when the array completes. Account for up to 20 μ l of volume loss per capture step for ligand samples. Then the aSFC docks on the surface and delivers a series of analyte injections with a profile consisting of baseline, association, and dissociation. After all the analyte injections within a "Set" have been performed, there is an option to regenerate the surface and make it suitable for another Capture Kinetics "Set". Typically, a series of injections of buffer blanks followed by analyte titrations will be performed and these data can be fit to derive rate constants and affinities.

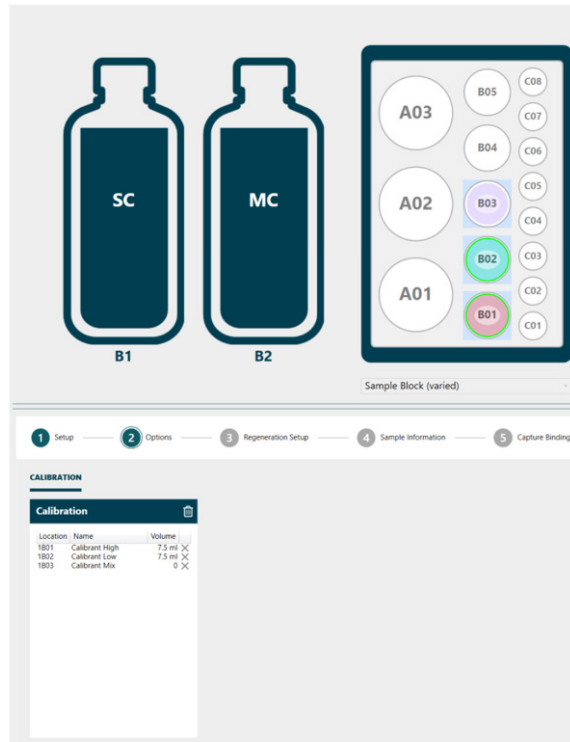
In Capture Kinetics, the building of an array is integrated with the SC injections. For each Kinetic Set, the MC injections create the array first, followed by all the SC injections in sequential order from the Single Channel Injections table. Multiple kinetic sets can be created to interrogate various ligand/analyte combinations or when regeneration is desired following each analyte. Regeneration is an additional option in Capture Kinetics.

An example of captured kinetics is shown below. This example demonstrates a set of ligands against analyte titration.

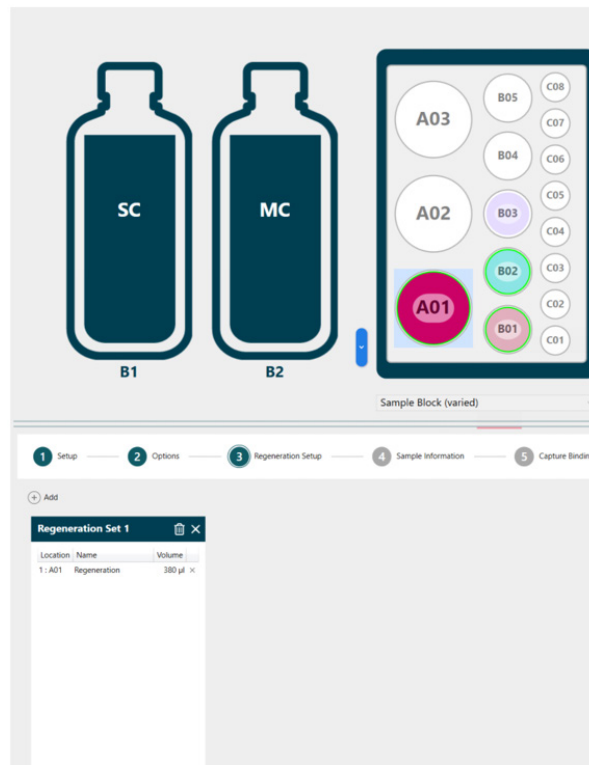
1. Set interaction temperature, chip type, and options. In this example, calibration is selected.



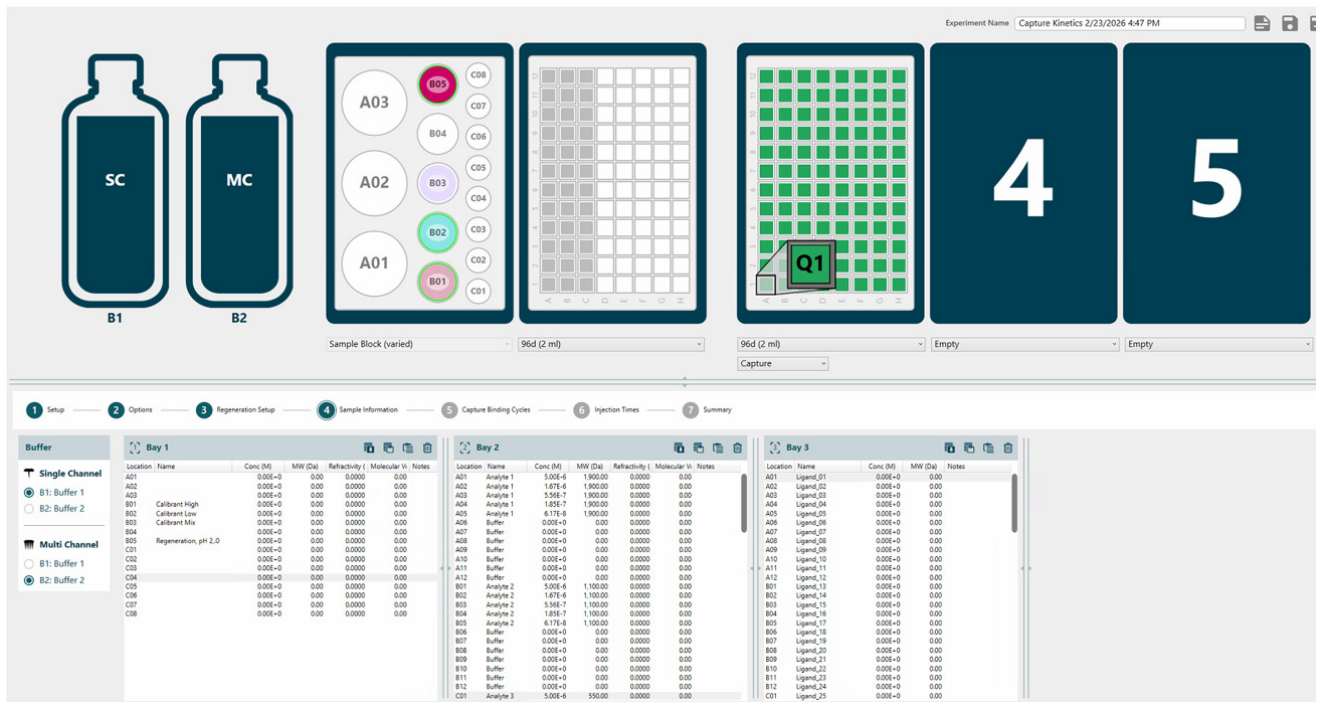
2. Select locations for the reagents needed for calibration.



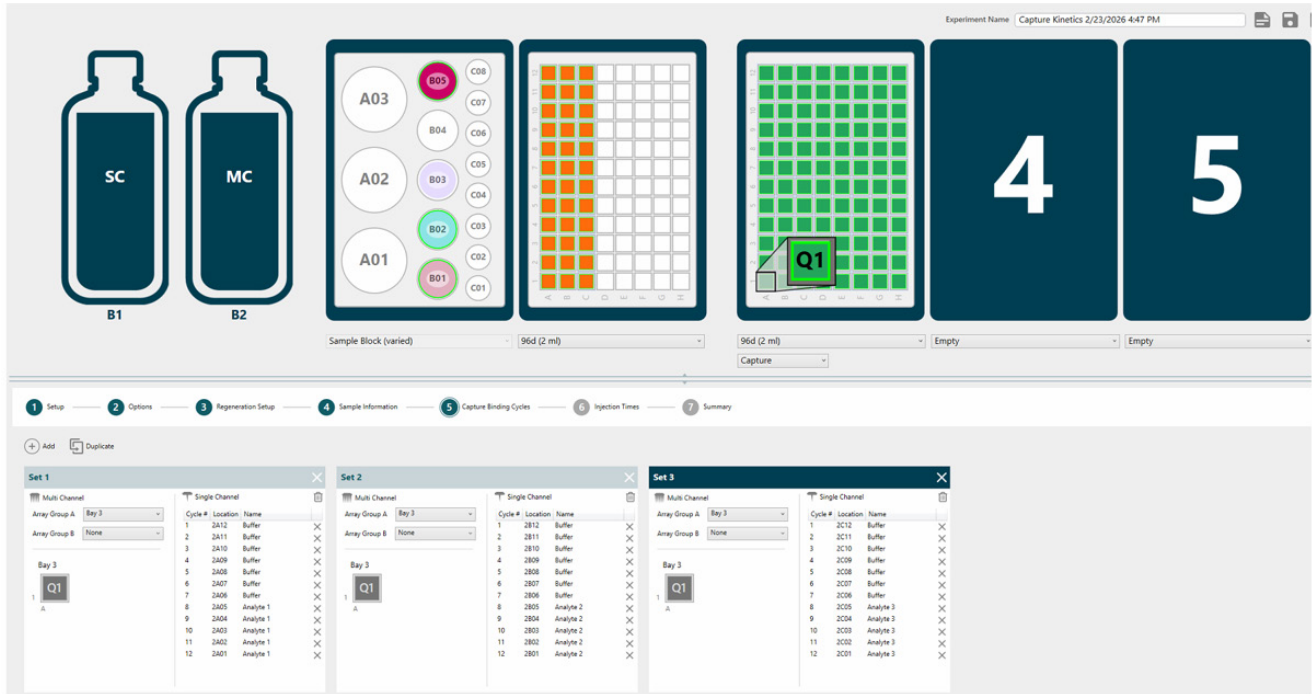
- Set up regeneration. Click  to add a regeneration set and select a location for the regeneration reagent.



- Enter sample information or copy-paste injection information. The user will also have to select which bay the capture reagent will come from.



- Define capture binding cycles. Create the capture kinetics sets for 96 ligands (MC) against a single antigen (SC) in Array Group A. Leave Array Group B empty to serve as a reference. For SC injections, click the sample positions in sequence on the virtual bays. Adding or duplicating a Set is allowed. In this example, a single plate of 96 ligands is tested against three different analytes over the course of three capture sets. Sets could be used to capture from different plates or plate quadrants across the different sets, increasing the number of ligands tested in an unattended run.



- Set injection times. (MC Capture - Deliver and Recover are fixed at 45 s, Cycle ≥ 1 min; SC Baseline, Association, Dissociation, or Stabilization ≥ 30 s; SC Regeneration ≥ 15s/pulse.)



7. Review summary.

The screenshot displays the 'Summary' step of the experiment setup process. At the top, a progress bar shows steps 1 through 7, with step 7 (Summary) highlighted. The main interface is divided into several sections:

- Bottle Lines:** A table listing reagents and their volumes.

Location	Name	Volume
B1	Buffer 1	2.1 l
B2	Buffer 2	260.8 ml
C1	Cleaning 1	0
C2	Cleaning 2	0
H2O	Water	0
- Bay 1:** A table listing locations and volumes for Bay 1.

Location	Name	Volume
B01	Calibrant High	7.5 ml
B02	Calibrant Low	7.5 ml
B05	Regeneration, pH 2.0	1.2 ml
- Bay 2:** A table listing locations and volumes for Bay 2.

Location	Name	Volume
A01	Analyte 1	200 µl
A02	Analyte 1	200 µl
A03	Analyte 1	200 µl
A04	Analyte 1	200 µl
A05	Analyte 1	200 µl
A06	Buffer	200 µl
A07	Buffer	200 µl
A08	Buffer	200 µl
A09	Buffer	200 µl
A10	Buffer	200 µl
A11	Buffer	200 µl
A12	Buffer	200 µl
B01	Analyte 2	200 µl
B02	Analyte 2	200 µl
B03	Analyte 2	200 µl
B04	Analyte 2	200 µl
B05	Analyte 2	200 µl
B06	Buffer	200 µl
B07	Buffer	200 µl
B08	Buffer	200 µl
B09	Buffer	200 µl
B10	Buffer	200 µl
B11	Buffer	200 µl
B12	Buffer	200 µl
C01	Analyte 3	200 µl
C02	Analyte 3	200 µl
C03	Analyte 3	200 µl
C04	Analyte 3	200 µl
C05	Analyte 3	200 µl
C06	Buffer	200 µl
C07	Buffer	200 µl
C08	Buffer	200 µl
C09	Buffer	200 µl
C10	Buffer	200 µl
C11	Buffer	200 µl
C12	Buffer	200 µl
- Bay 3:** A table listing locations and volumes for Bay 3.

Location	Name	Volume
All	Capture	200 µl
- Summary Panel:** A panel on the right providing a high-level overview of the experiment.
 - Experiment Type:** Capture Kinetics
 - Experiment Name:** Capture Kinetics 2/23/2026 4:47 PM
 - Deck:** Bay 1 (Sample Block [Varied]), Bay 2 (96d [Analyte]), Bay 3 (96d [Capture]), Bay 4 (Empty [None]), Bay 5 (Empty [None]).
 - Setup:** Temperature (25°C), Selected Chip (SAP), Calibration (Enabled), 50% DMSO Wash (Disabled), Excluded Volume Correction (Disabled), MC Cleaning (Disabled).
 - Injection Times:** Deliver (45 secs), Cycle (5 mins), Recover (45 secs), Baseline (60 secs), Association (300 secs), Dissociation (1200 secs), Regeneration Set 1 (20 secs x3), Stabilization (60 secs).
 - Capture Sets:** Set 1 (Injections: 12, Array Group A: Bay 3, Array Group B: None), Set 2 (Injections: 12, Array Group A: Bay 3, Array Group B: None), Set 3 (Injections: 12, Array Group A: None, Array Group B: None).
 - Estimates:** Run Time (18H 19M), B1: Buffer 1 (2.1 l), B2: Buffer 2 (260.8 ml), C1: Cleaning 1 (0), C2: Cleaning 2 (0), H2O: Water (0).

5.3.4 Analyte Injections

The Analyte Injections wizard injects a series of analytes. The array should have already been prepared using the Surface Preparation Array wizard. Unlike the Capture Kinetics wizard, there is no building of the array during the method. The aSFC docks on the sensor chip and delivers an injection profile consisting of baseline, association, and dissociation, with an option for regeneration. Samples are from any locations in Bay 1 or 2. The aSFC remains docked throughout the experiment. The analyte binding responses can then be fit to a kinetic model to determine rate constants and affinity or analyzed for any other binding features.

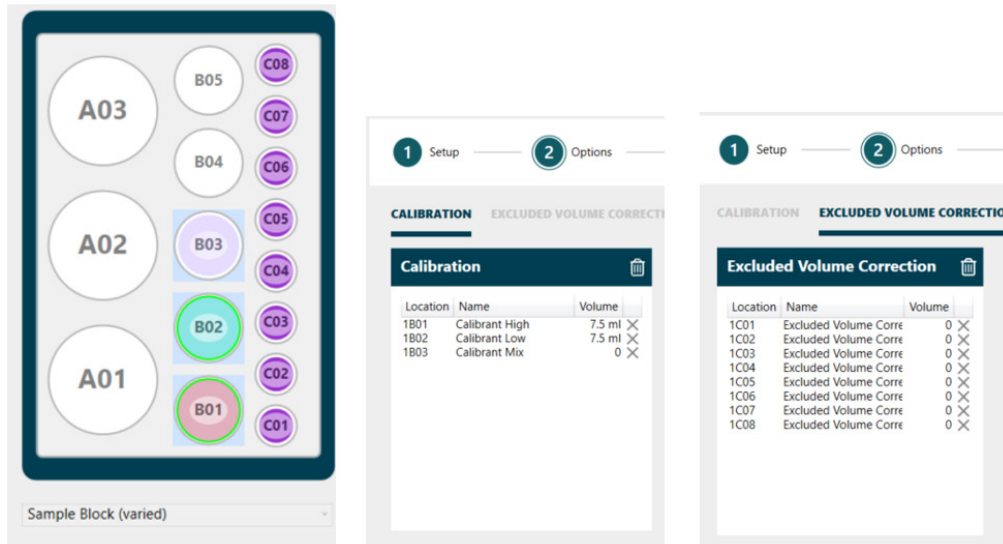
An example of Analyte Injections from a 96-well plate in Bay 2 is provided below.

1. Set interaction temperature, chip type, and options. In this example, calibration and EVC are selected.

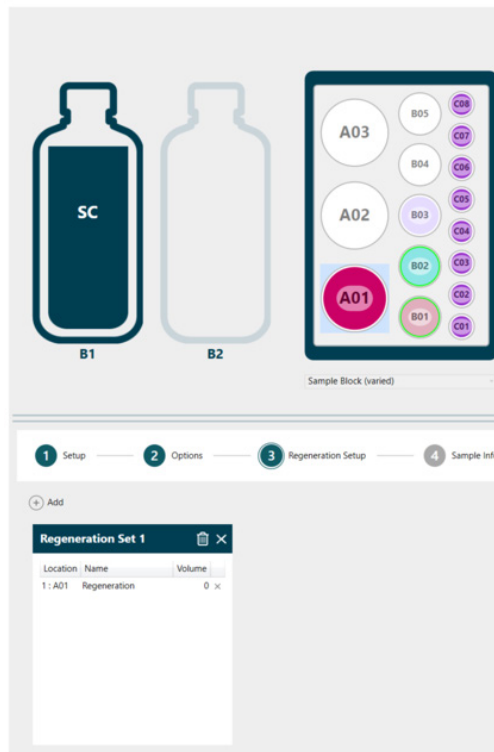
The screenshot shows the 'Options' step of the experiment setup. The progress bar at the top indicates steps 1 (Setup), 2 (Options), and 3 (Regeneration Setup), with step 2 (Options) highlighted. The interface is divided into two main sections:

- Required:**
 - Interaction Temperature:** A numeric input field set to 25 °C.
 - Chip Type:** A dropdown menu set to CMDP.
- Options:** A list of checkboxes for additional settings.
 - Periodic Injections
 - Blocking
 - Calibration
 - 50% DMSO Wash
 - Excluded Volume Correction

2. Select locations for the reagents needed for the selected options.



3. Set up regeneration.



4. Enter sample information, or copy-paste injection information.

The screenshot displays the 'Sample Information' step of the instrument's software. At the top, there are visual representations of sample blocks B1 and B2, and a grid of injection positions labeled A01-A03 and C01-C08. Below these is a data table for Bay 1 and Bay 2.

Location	Name	Conc (M)	MW (Da)	Refractivity (cm ³ /mol)	Molecular Wt.	Notes
A01	Regeneration	0.00E+0	0.00	0.0000	0.00	
A02		0.00E+0	0.00	0.0000	0.00	
A03		0.00E+0	0.00	0.0000	0.00	
B01	Calibrant High	0.00E+0	0.00	0.0000	0.00	
B02	Calibrant Low	0.00E+0	0.00	0.0000	0.00	
B03	Calibrant Mix	0.00E+0	0.00	0.0000	0.00	
B04		0.00E+0	0.00	0.0000	0.00	
B05		0.00E+0	0.00	0.0000	0.00	
C01	Excluded Volume Correction	0.00E+0	0.00	0.0000	0.00	
C02	Excluded Volume Correction	0.00E+0	0.00	0.0000	0.00	
C03	Excluded Volume Correction	0.00E+0	0.00	0.0000	0.00	
C04	Excluded Volume Correction	0.00E+0	0.00	0.0000	0.00	
C05	Excluded Volume Correction	0.00E+0	0.00	0.0000	0.00	
C06	Excluded Volume Correction	0.00E+0	0.00	0.0000	0.00	
C07	Excluded Volume Correction	0.00E+0	0.00	0.0000	0.00	
C08	Excluded Volume Correction	0.00E+0	0.00	0.0000	0.00	

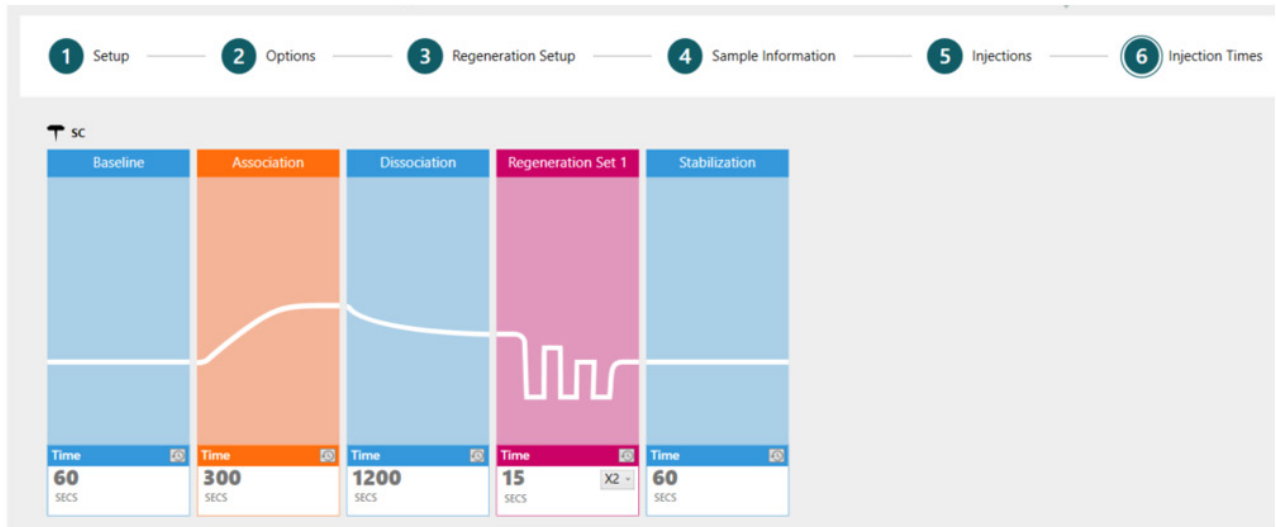
Location	Name	Conc (M)	MW (Da)	Refractivity (cm ³ /mol)	Molecular Wt.	Notes
A01	Compound_1	1.00E-4	385.00	0.0000	0.00	
A02	Compound_2	1.00E-4	352.00	0.0000	0.00	
A03	Compound_3	1.00E-4	255.00	0.0000	0.00	
A04	Compound_4	1.00E-4	418.00	0.0000	0.00	
A05	Compound_5	1.00E-4	432.00	0.0000	0.00	
A06	Compound_6	1.00E-4	225.00	0.0000	0.00	
A07	Compound_7	1.00E-4	473.00	0.0000	0.00	
A08	Compound_8	1.00E-4	245.00	0.0000	0.00	
A09	Compound_9	1.00E-4	345.00	0.0000	0.00	
A10	Compound_10	1.00E-4	417.00	0.0000	0.00	
A11	Compound_11	1.00E-4	476.00	0.0000	0.00	
A12	Compound_12	1.00E-4	511.00	0.0000	0.00	
B01	Compound_13	1.00E-4	317.00	0.0000	0.00	
B02	Compound_14	1.00E-4	350.00	0.0000	0.00	
B03	Compound_15	1.00E-4	209.00	0.0000	0.00	
B04	Compound_16	1.00E-4	503.00	0.0000	0.00	
B05	Compound_17	1.00E-4	522.00	0.0000	0.00	
B06	Compound_18	1.00E-4	348.00	0.0000	0.00	
B07	Compound_19	1.00E-4	312.00	0.0000	0.00	
B08	Compound_20	1.00E-4	288.00	0.0000	0.00	
B09	Compound_21	1.00E-4	323.00	0.0000	0.00	
B10	Compound_22	1.00E-4	304.00	0.0000	0.00	
B11	Compound_23	1.00E-4	596.00	0.0000	0.00	
B12	Compound_24	1.00E-4	279.00	0.0000	0.00	
C01	Compound_25	1.00E-4	551.00	0.0000	0.00	
C02	Compound_26	1.00E-4	354.00	0.0000	0.00	

5. Set up SC injections. Click the sample positions in sequence on the virtual bays. Include the EVC injections at the end of the sequence.

The screenshot displays the 'Injections' step of the instrument's software. At the top, there are visual representations of sample blocks B1 and B2, and a grid of injection positions labeled A01-A03 and C01-C08. Below this is a table for SC Injections.

Injection #	Bay	Location	Name
88	2	H04	2H04
89	2	H05	2H05
90	2	H06	2H06
91	2	H07	2H07
92	2	H08	2H08
93	2	H09	2H09
94	2	H10	2H10
95	2	H11	2H11
96	2	H12	2H12
97	1	C01	Excluded Vc
98	1	C02	Excluded Vc
99	1	C03	Excluded Vc
100	1	C04	Excluded Vc
101	1	C05	Excluded Vc
102	1	C06	Excluded Vc
103	1	C07	Excluded Vc
104	1	C08	Excluded Vc

6. Set injection times. (SC Baseline, Association, Dissociation, or Stabilization ≥ 30 s; SC Regeneration ≥ 15s/pulse.)



7. Review summary.

The screenshot displays the 'Summary' configuration interface. At the top, a progress bar shows steps 1 through 7, with step 7 'Summary' highlighted. The interface is divided into several sections:

- Bottle Lines:** A table listing locations and volumes.

Location	Name	Volume
B1	Buffer 1	0
B2	Buffer 2	0
C1	Cleaning 1	0
C2	Cleaning 2	0
H2O	Water	0
- Bay 1:** A table listing locations, names, and volumes.

Location	Name	Volume
A01	Regeneration	39.2 ml
B01	Calibrant High	7.5 ml
B02	Calibrant Low	7.5 ml
C01	Excluded Volume Correctic	200 µl
C02	Excluded Volume Correctic	200 µl
C03	Excluded Volume Correctic	200 µl
C04	Excluded Volume Correctic	200 µl
C05	Excluded Volume Correctic	200 µl
C06	Excluded Volume Correctic	200 µl
C07	Excluded Volume Correctic	200 µl
- Bay 2:** A table listing locations, names, and volumes.

Location	Name	Volume
A01	Compound_1	200 µl
A02	Compound_2	200 µl
A03	Compound_3	200 µl
A04	Compound_4	200 µl
A05	Compound_5	200 µl
A06	Compound_6	200 µl
A07	Compound_7	200 µl
A08	Compound_8	200 µl
A09	Compound_9	200 µl
A10	Compound_10	200 µl
A11	Compound_11	200 µl
A12	Compound_12	200 µl
B01	Compound_13	200 µl
B02	Compound_14	200 µl
B03	Compound_15	200 µl
B04	Compound_16	200 µl
B05	Compound_17	200 µl
B06	Compound_18	200 µl
B07	Compound_19	200 µl
B08	Compound_20	200 µl
B09	Compound_21	200 µl
B10	Compound_22	200 µl
B11	Compound_23	200 µl
B12	Compound_24	200 µl
C01	Compound_25	200 µl
C02	Compound_26	200 µl
C03	Compound_27	200 µl
C04	Compound_28	200 µl
C05	Compound_29	200 µl
C06	Compound_30	200 µl
- Validation:** A green checkmark indicates 'Experiment is valid.'
- Summary:** A 'Copy to Clipboard' button is present.
- Experiment Details:**
 - Experiment Type: Analyte Injections
 - Experiment Name: Analyte Injections 2/23/2026 5:31 PM
 - Deck: Bay 1 (Sample Block [Varied]), Bay 2 (96s [Analyte]), Bay 3 (Empty [None]), Bay 4 (Empty [None]), Bay 5 (Empty [None])
 - Setup: Temperature (25°C), Selected Chip (CMDP), Blocking (Disabled), Calibration (Enabled), 50% DMSO Wash (Disabled), Excluded Volume Correction (Enabled), Periodic Injections (Disabled)
 - Injection Times: Baseline (60 secs), Association (300 secs), Dissociation (1200 secs), Regeneration Set 1 (15 secs x2), Stabilization (60 secs)

5.3.5 Dual-Analyte Injections

The dual-injection wizard allows the sequential injection of two analytes without a wash step between them. The most common use case is classical epitope binning. Classical Binning is a competitive epitope characterization technique where antibodies are assessed for their ability to bind to antigen already bound by other antibodies, often referred to as “sandwiching”. Collectively, this data enables classification of antibodies based on whether they bind to similar regions of an antigen. Classical binning is set up using Bay 1 and/or Bay 2 for the sandwiching antibody, with the assumption that the array has been previously built using Surface Preparation Array. For every cycle, the antigen will be injected, followed by an antibody in the SC injection tables.

An example of a dual-analyte injection experiment for classical binning is shown below.

1. Set interaction temperature, chip type, and options. In this example, periodic injections is selected for antigen then buffer control cycles.

The screenshot shows two side-by-side panels. The 'Required' panel on the left contains:

- Interaction Temperature:** A numeric input field set to 25 with a degree Celsius symbol and a small up/down arrow icon.
- Chip Type:** A dropdown menu currently showing 'HC30M'.

 The 'Options' panel on the right contains four checkboxes:

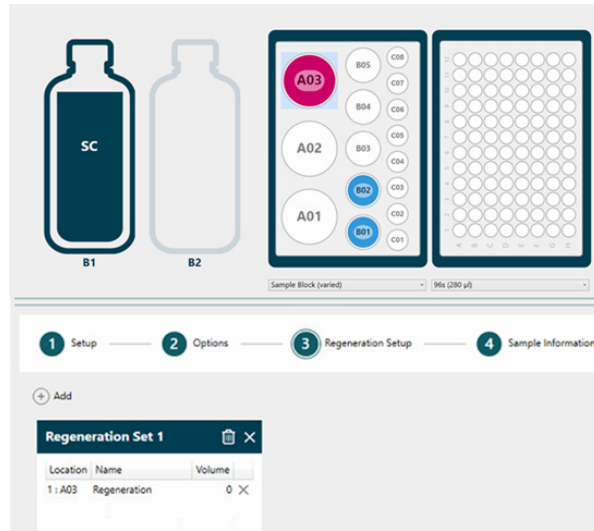
- Periodic Injections**
- Blocking**
- Calibration**
- 50% DMSO Wash**
- Excluded Volume Correction**

2. Select locations for the reagents needed for the selected options.

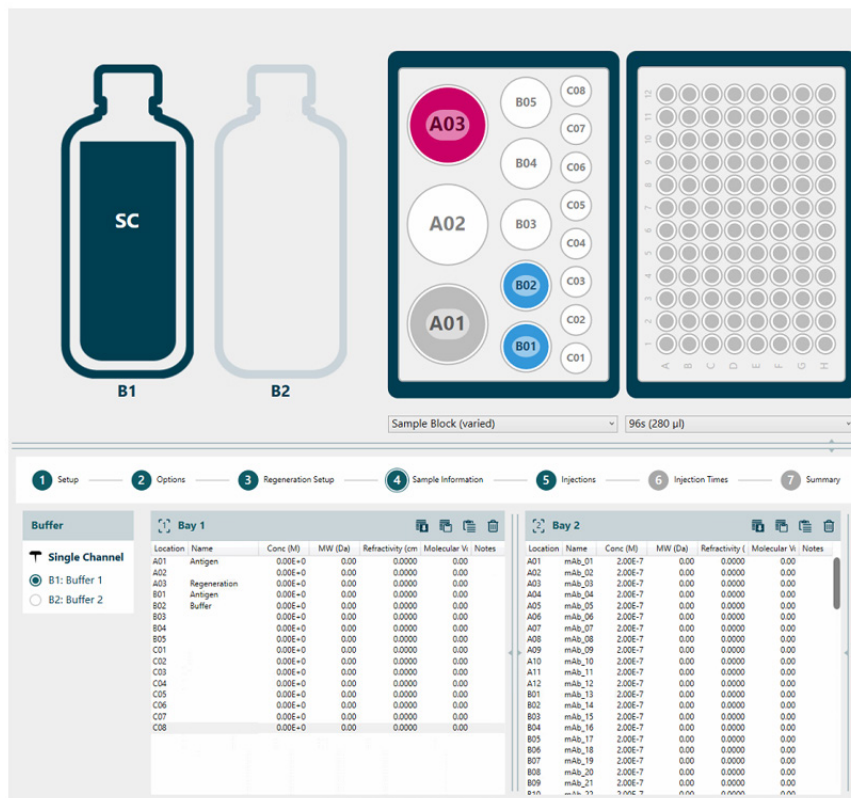
The screenshot shows a multi-step configuration interface. At the top, there are two vial icons labeled B1 and B2, and a 96-well plate grid. A legend below the grid shows colored circles for A01, A02, A03, B01-B05, and C01-C05. Below this is a progress bar with four steps: 1 Setup, 2 Options, 3 Regeneration Setup, and 4 Sample. The 'PERIODIC INJECTIONS' section is active, showing two injection sets:

- Set 1:** every 10 injections. Location 1B01, Name: Antigen, Volume: 0 µl.
- Set 2:** every 10 injections. Location 1B02, Name: Buffer, Volume: 0 µl.

3. Set up regeneration.



4. Enter sample information, or copy-paste injection information.



5. Select the injection order for each injection set.

The screenshot displays the 'Injections' setup screen. At the top, there are two bottle icons labeled B1 and B2. To their right is a circular selection grid with injection sets A01, A02, A03, B01, B02, B03, B04, B05, C01, C02, C03, C04, C05, C06, C07, and C08. Below this is a 96-well plate diagram. A progress bar at the bottom shows steps 1-5, with step 5 'Injections' highlighted.

Below the progress bar are two tables for injection sets:

SC Injection 1				
Injection #	Bay	Location	Name	
1	1	B01	Per. Antigen	
2	1	A01	Antigen	X
3	1	A01	Antigen	X
4	1	A01	Antigen	X
5	1	A01	Antigen	X
6	1	A01	Antigen	X
7	1	A01	Antigen	X
8	1	A01	Antigen	X
9	1	A01	Antigen	X
10	1	A01	Antigen	X
11	1	A01	Antigen	X
12	1	B01	Per. Antigen	
13	1	A01	Antigen	X
14	1	A01	Antigen	X
15	1	A01	Antigen	X
16	1	A01	Antigen	X
17	1	A01	Antigen	X
18	1	A01	Antigen	X
19	1	A01	Antigen	X
20	1	A01	Antigen	X
21	1	A01	Antigen	X
22	1	A01	Antigen	X
23	1	B01	Per. Antigen	
24	1	A01	Antigen	X
25	1	A01	Antigen	X

SC Injection 2				
Injection #	Bay	Location	Name	
1	1	B02	Buffer	
2	2	A01	mAb_01	X
3	2	A02	mAb_02	X
4	2	A03	mAb_03	X
5	2	A04	mAb_04	X
6	2	A05	mAb_05	X
7	2	A06	mAb_06	X
8	2	A07	mAb_07	X
9	2	A08	mAb_08	X
10	2	A09	mAb_09	X
11	2	A10	mAb_10	X
12	1	B02	Buffer	
13	2	A11	mAb_11	X
14	2	A12	mAb_12	X
15	2	B01	mAb_13	X
16	2	B02	mAb_14	X
17	2	B03	mAb_15	X
18	2	B04	mAb_16	X
19	2	B05	mAb_17	X
20	2	B06	mAb_18	X
21	2	B07	mAb_19	X
22	2	B08	mAb_20	X
23	1	B02	Buffer	
24	2	B09	mAb_21	X
25	2	B10	mAb_22	X

6. Set injection times, including the amount of regeneration pulses desired. (All phases other than Regeneration ≥ 30 s; Regeneration ≥ 15 s/pulse.)

The screenshot shows the 'Injection Times' setup screen. A progress bar at the top highlights step 6 'Injection Times'. Below it is a chromatogram plot with the following phases and times:

Phase	Time (SECS)
Baseline	30
Association 1	300
Association 2	300
Dissociation	60
Regeneration Set 1	30 (x2 pulses)
Stabilization	60

7. Review summary.

Validation
 ✓ Experiment is valid.

Summary Copy to Clipboard

Experiment Type: Dual-Analyte Injections
 Experiment Name: Dual-Analyte Injections 2/23/2026 5:43 PM

Deck	Bay	Sample Block	Notes
Deck	Bay 1	96s	[Analyte 2]
	Bay 2	Empty	[None]
	Bay 3	Empty	[None]
	Bay 4	Empty	[None]
	Bay 5	Empty	[None]

Setup

Temperature	25°C
Selected Chip	HC30M
Blocking	Disabled
Calibration	Disabled
50% DMSO Wash	Disabled
Excluded Volume Correction	Disabled
Periodic Injections	Enabled

Injection Times

Baseline	60 secs
Association 1	300 secs

5.3.6 Quantitation

The Quantitation wizard is designed to estimate concentrations of analytes and can be performed in complex matrices such as supernatants. In this wizard, the cPH first docks onto the sensor chip with a uniform capture surface, which was either previously prepared using the Surface Preparation Lawn method or a premade surface such as Protein A, Protein A/G, or NTA. Then up to 96 samples, including a series of standards of known concentrations, are drawn up and cycled across the surface. At the end of the cycle, the samples are returned to the well plate and, optionally, the aSFC docks on the chip to regenerate the surface. Using either binding responses or slope, the known standards can then be used to calculate the concentrations of the unknown samples. Quantitation cycles are created by selecting Sets of 96 samples, up to 2 captures per cycle, followed by a regeneration of the surface. Using 384-well plates, up to 1152 unique samples (including standards) can be tested in the quantitation wizard.

An example of quantitation from a 96-well plate in Bay 3 is provided below.

1. Set interaction temperature, chip type, and options of calibration and MC cleaning.

Required

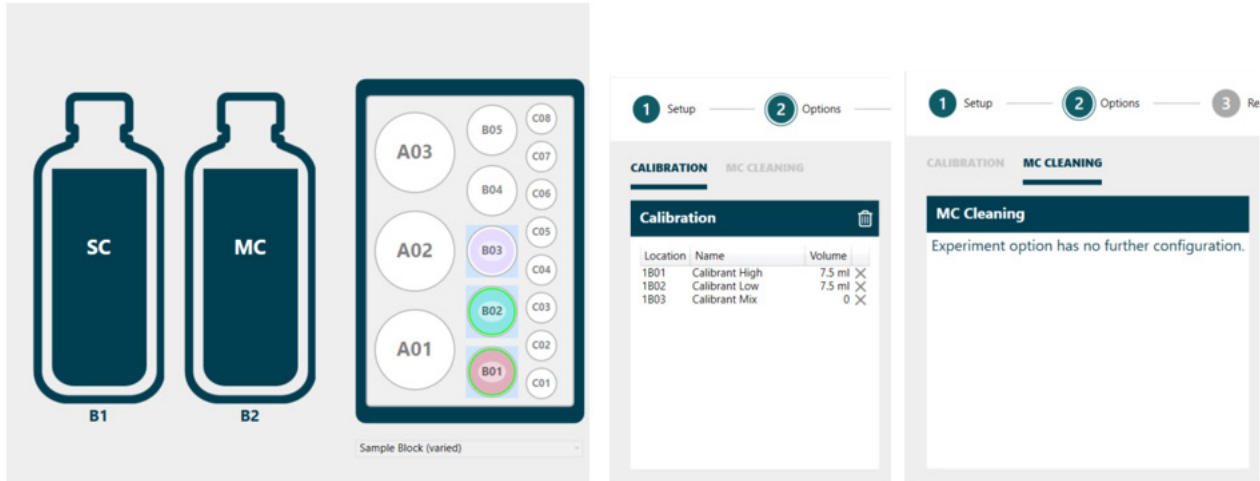
Interaction Temperature: 25 °C

Chip Type: CMDP

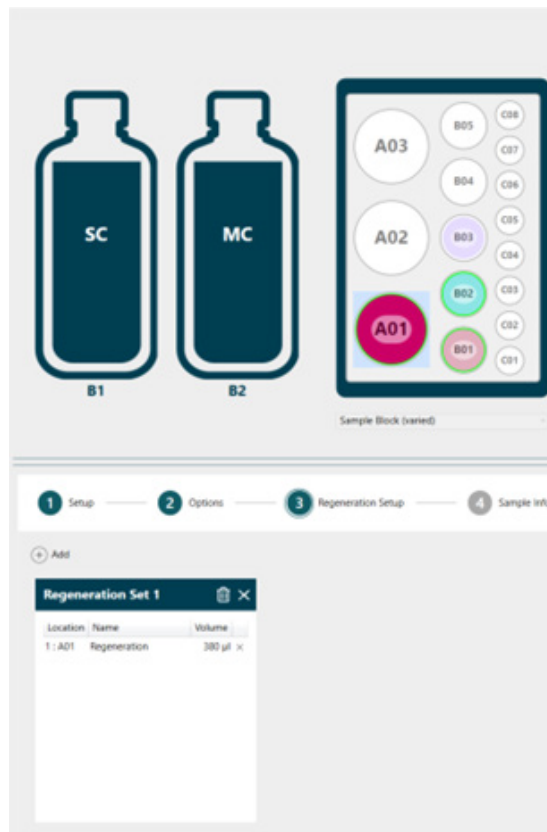
Options

- Calibration
- MC Cleaning

2. Select locations for the reagents needed for the selected options. MC cleaning requires no additional steps or selections. Calibration injections will be applied automatically.



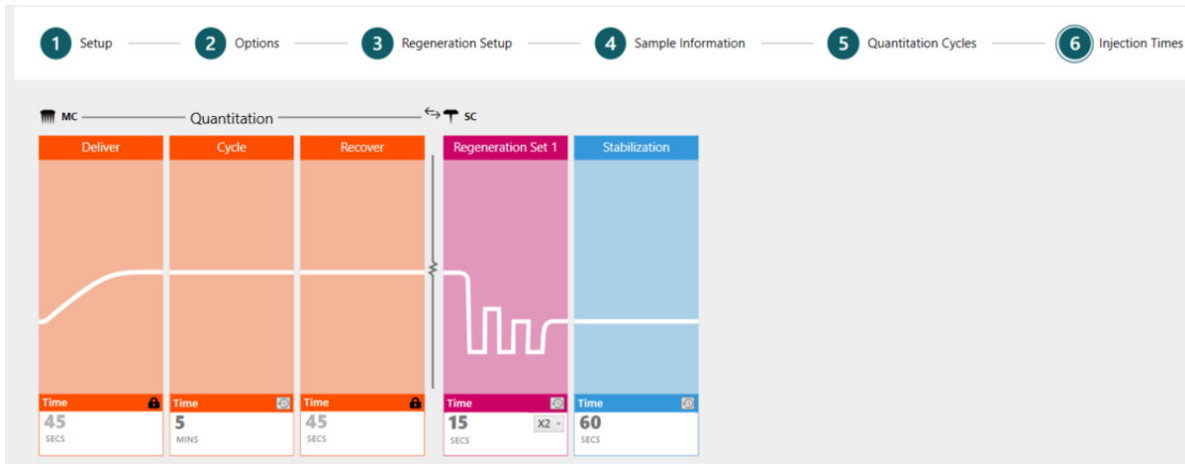
3. Set up regeneration.



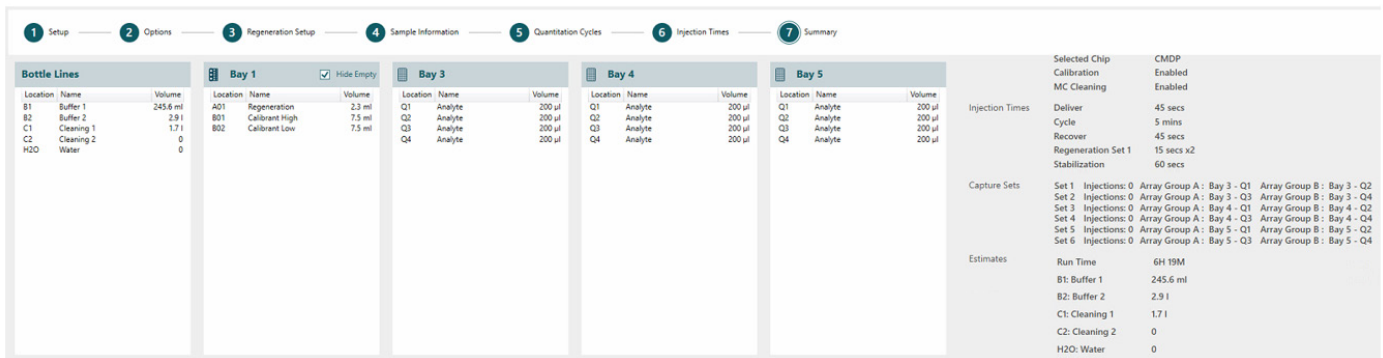
4. Enter or copy-paste injection information.

5. Set up quantitation cycles by selecting which Array Group (A or B) the analyte injections will come from.


- Set up injection times. (MC – Quantitation: Deliver and Recover are fixed at 45 s, Cycle ≥ 1 min; SC Regeneration ≥ 15s/pulse, Stabilization ≥ 30 s.)



- Review summary.



5.4 Running an Experiment

After a method is created, saved and sent over to the Experiment Runner via the Save and Run icon , the sample decks will move out into position for access to all 5 bays. At this point, it is appropriate to load all well plates and the sample block (if applicable). This is also a good time to check the waste stations for any salt accumulation that may warrant removing them for rinsing before running an experiment.

Before starting the experiment, check each of the steps from the Preparation panel (right side of Experiment Runner) to make sure that the specified chip, cleaning slides, and reagents are in place, empty the waste container, and check the temperature setting.

Preparation

Chip Type

Current **CMDP**
Experiment **CMDP**



Temperature

Current **24°C**
Experiment **25°C**



Estimates

Run Time **1D 12H 39M**
B1: Buffer 1 **4.1 l**
B2: Buffer 2 **465.3 ml**
C1: Cleaning 1 **0**
C2: Cleaning 2 **0**
H2O: Water **0**

Calibration




Calibration is enabled.

Cleaning

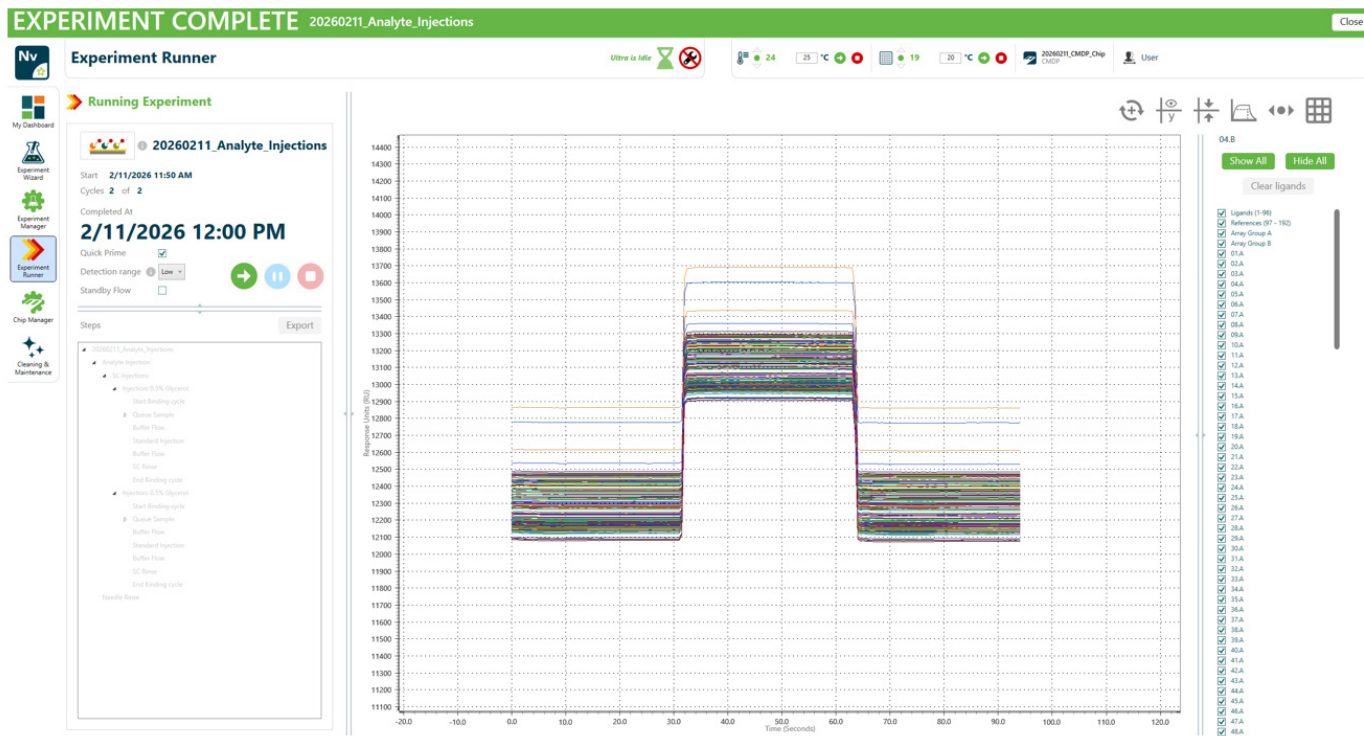
50% DMSO Wash is disabled.
MC Cleaning is disabled.

Reminders

- Cleaning Slides present for SC and MC
- Empty Waste Container
- Close instrument doors

Once all reagents are in place, use the Run Experiment icon  to start the experiment. The Pause button  allows the current running experiment to be temporarily halted and takes effect at the conclusion of the current cycle. To restart from Pause, select the Run Experiment icon. To completely stop an experiment, select the Stop icon . Once the currently running actions are completed, this will end the experiment.

When the experiment is completed, depending on selections made during setup, either an Experiment Complete or Standby Flow pop-up banner will be present. Data from the experiment remains in the Experiment Runner chart at the conclusion of the experiment until the next experiment is loaded. Data is continuously saved to the .sprdata file in the Experiment Data folder. It can then be processed in the Kinetics or Epiteo Data Analysis Software.



This message displayed at the top of the page while in Standby mode.



Ultra has a feature called Maintenance Mode that actuates the instrument fluidics every two hours to ensure optimal performance. This action only occurs when the instrument is idle. Maintenance Mode takes approximately 3 min and moves the cPH to the cleaning slide location as well as placing the Multichannel needles in the waste block. "Maintenance Mode is Running" will be displayed on the upper view of Navigator. Please wait until this action completes before using the instrument.

6. Maintenance

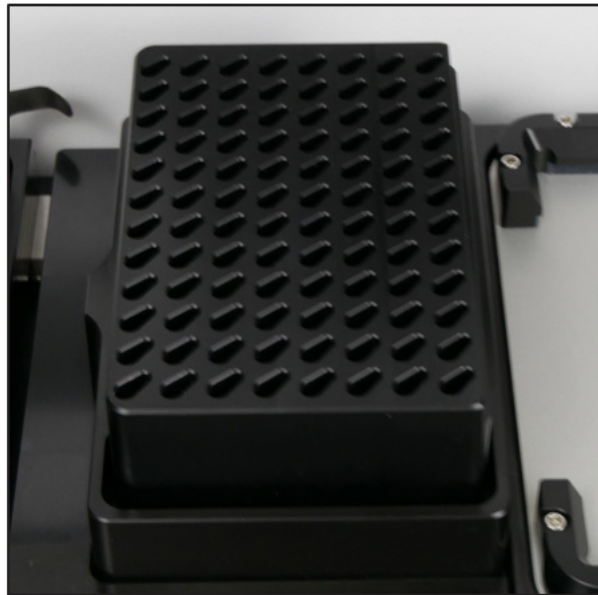
6.1 User Maintenance

Proper instrument maintenance is crucial to maintain instrument performance and the generation of quality data. Cleaning and Maintenance can be accessed through the side navigation panel of Navigator. Use the "Send Logs to Carterra" function to either save or send the logs during a user-defined period. Ultra should be cleaned regularly according to the Ultra Maintenance & Best Practices Guide. Failure to do so may result in poor data quality, instrument malfunctions, and voiding of warranty. Selecting the maintenance function from the list of options under the maintenance tab will allow the user to run each of the cleaning procedures.

6.2 Clean MC Cleaning Station

The MC cleaning station (Waste Tray) can be accessed through the maintenance page for cleaning. Typically, this only needs to be cleaned if residue buildup is apparent. The orientation is specific and the wash block is keyed, so use caution when removing and reinstalling to ensure proper orientation.

Use the software selections under cleaning to access the waste stations. Never put hands into the instrument to remove the waste stations until the software indicates it is safe to do so.



MC Cleaning Station (Waste Tray)

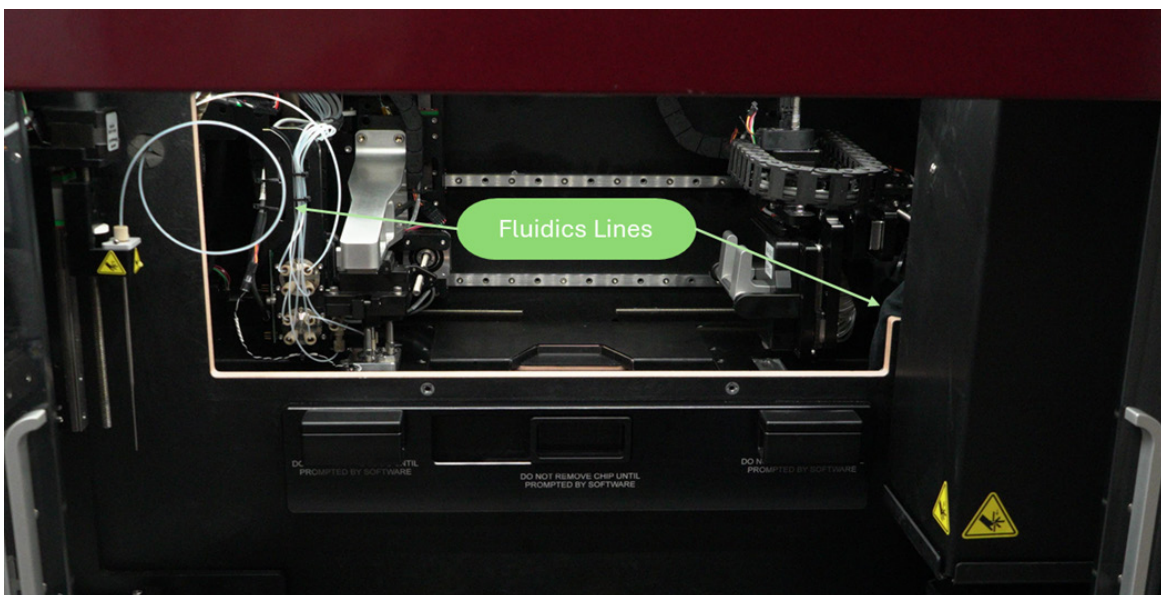
6.3 aSFC and cPH Cleaning Procedure

Users need to clean the face of the aSFC and cPH before starting their next experiments to ensure a proper seal of the aSFC gasket and to avoid stamping contaminants onto the chip surface from the cPH using the following procedure:

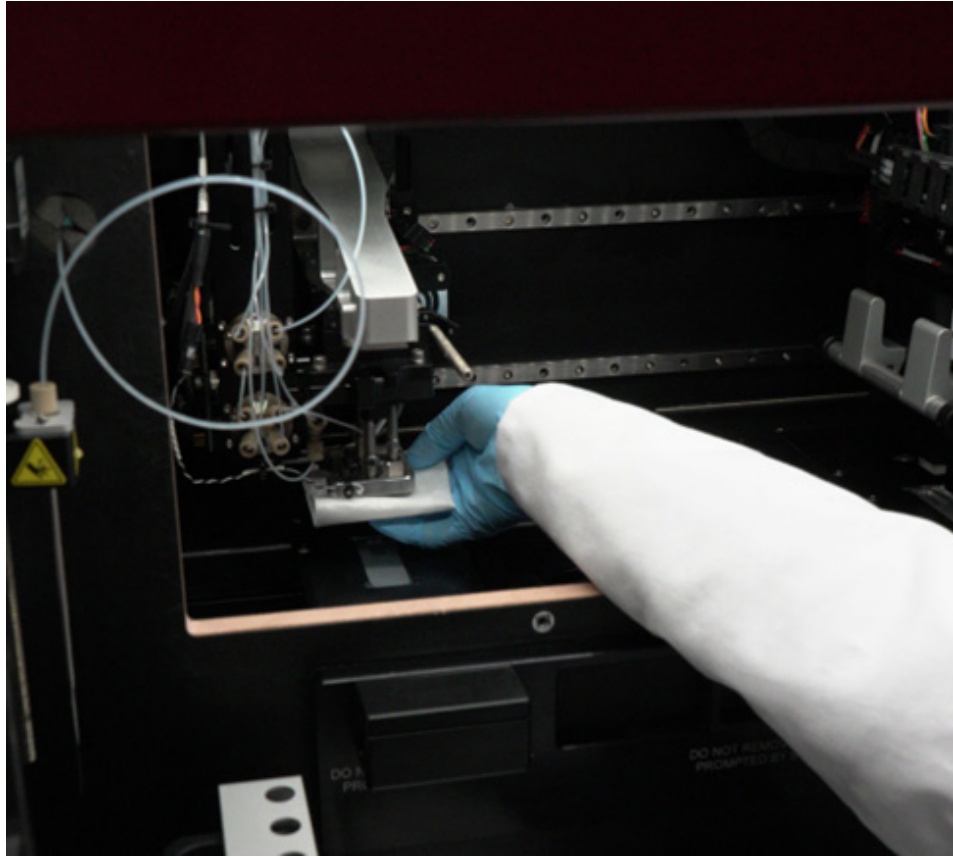
1. Make sure that no program is running and that standby flow has been turned off.
2. Ensure that the instrument status reads Instrument Idle, confirming that both the aSFC and cPH are undocked from the chip and cleaning slides.
3. Open the front doors and identify the black insulated panel covering the interior front wall, which is secured using four thumb screws. For convenience, the screws will not come out of the panel.



4. Loosen the screws until they detach from the inner wall. Be careful to hold the panel so it does not fall against the sample deck.
5. Carefully dislodge the panel and remove it from the interior, taking care not to catch the left or right side of it on the single-channel or multichannel tubing. Set the panel aside on a nearby bench. (Do not place it on top of the instrument.)



6. Use a 18 M Ω water-soaked TechniCloth (or lint-free) wipe to gently blot and wipe the underside/gasket of the aSFC and cPH to remove any salt buildup.



7. Reattach the panel to the front wall of the instrument using the thumb screws. Take care not to pinch the single channel or multichannel tubing between the panel and the instrument. Once the panel is attached, make sure the tubing is free and not under the panel.
8. Opening the instrument interior can disrupt thermal equilibrium. After closing the interior, allow sufficient time for the system temperature to re-equilibrate before starting high-quality data collection.

7. Reference Information

7.1 Maintenance & Best Practices Guide, Troubleshooting and Support

The Maintenance & Best Practices Guide is available upon request from Customer Support. If you encounter any issues or would like assistance with troubleshooting procedures, contact Customer Support at support@carterra-bio.com or by calling 1-844-642-7635, Option 3.

7.2 Ultra Required Consumables

Ultra required consumables can be found at <https://info.carterra-bio.com/hubfs/Downloads/Required%20Consumables.pdf>

7.3 Chips

Chips can be found at <https://carterra-bio.com/biosensor-chips/>

7.4 Carterra Consumables Ordering Information

Consumables and reagents can be found at www.carterra-bio.com/store

7.5 Chemical Resistance of Wetted Parts

Concentrated organic solvents should not contact Ultra unless indicated in the table below. Long-term exposure to extremes of pH and/or high salt solutions should be avoided. Short term compatibility means the solutions can be used for injections for cleaning or maintenance. Long term compatibility means the solutions can be used for assays, including in the running buffer. They should never be used as an undiluted running buffer. Contact Carterra Technical Support for further questions on chemical compatibility.

Solution	Concentration	Exposure Limit
DMSO	5%	Long Term
DMSO	50%	Short Term
Glycerol	5%	Long Term
Sodium Chloride	1 M	Long Term
Sodium Chloride	3 M	Short Term
Contrad-70	3%	Short Term
Sodium Dodecyl Sulfate	0.5%	Long Term
Sodium Hypochlorite	<1%	Long Term
Magnesium Chloride	0.1 M	Short Term
Hydrochloric Acid	50%	Short Term
Phosphoric Acid	5 M	Short Term
Sodium Hydroxide	0.2 M	Short Term
Glycine	10 mM	Short Term

Carterra technology is protected by the following patents and other patents pending:
8,210,119, 8,211,382, 8,383,059, 8,999,726, 9,682,372, 9,682,396, 10,825,548

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