

Agilent MassHunter StreamSelect System

Quick Start Guide

For Research Use Only. Not to be used for diagnostic procedures.

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What is the Agilent MassHunter StreamSelect system?



The MassHunter StreamSelect system consists of a single Triple Quad LC/MS and two to four liquid chromatography systems running parallel, staggered analyses. The StreamSelect program is fully integrated into MassHunter Acquisition, and seamlessly controls all coordination between the individual HPLCs and LC/MS. The result is a very efficient and robust handling of the LC/MS analyses with data file integrity for every analysis.

The MassHunter StreamSelect System can increase the daily throughput of LC/MS analyses up to four-fold through highly efficient use of the analytical capabilities of the mass spectrometer, which results in higher productivity and cost effectiveness.

What's New in 8.0

- Support for Agilent StreamSelect RSI (PAL3) autosampler.
- Support for Windows 10.
- Support for Advanced Online Sample Cleanup.
- The order of the devices in the Method Editor window is the same as the order used in the Instrument Status window.

Where to Find More Information

For more information about the MassHunter StreamSelect System, see the *Agilent MassHunter StreamSelect Setup Guide*.

MassHunter StreamSelect Online Help

Refer to the online Help and tooltips available in these components of the MassHunter StreamSelect System:

- MassHunter StreamSelect Console
- MassHunter StreamSelect Instrument Configuration
- MassHunter StreamSelect Profile Editor

MassHunter StreamSelect Setup Guide

Use this guide to configure the plumbing of your MassHunter StreamSelect system.

MassHunter Data Acquisition Online Help

Refer to the MassHunter Data Acquisition for Triple Quad LC/MS online Help for help on the Tune Window. This online Help can be opened from the Tune Window. The Data Acquisition online Help also contains additional information for the Method Editor, Sample Run, and Worklist windows.

Where to Find More Information

MassHunter Data Acquisition Quick Start Guide

Refer to the *Agilent 6400 Series Triple Quad LC/MS System Quick Start Guide* for more information about the MassHunter Data Acquisition program. You can open the *Quick Start Guide* from Data Acquisition Resource App.

Agilent Web Site

To view support information for MassHunter StreamSelect and other Agilent products, visit http://www.agilent.com.

Where to Find More Information

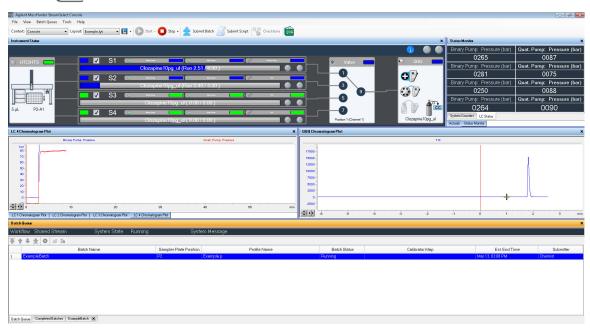
MassHunter StreamSelect Console

This program lets you submit, run, and monitor batches of samples for analysis.



To open the MassHunter StreamSelect Console

• Click the **StreamSelect** icon on the Desktop.



Tip The windows on the MassHunter StreamSelect Console can be resized, moved, or hidden to display only the information of interest. The layout can be saved; different layouts can be selected using the **Layout** controls on the toolbar or the menus. You can save a different layout for each **Context**.



Six Contexts

You select one of six contexts when you use StreamSelect. Each context has a different purpose, and each context has a different set of windows that are available. The toolbar and the menus also change depending on which context is selected. You select the **Context** in the toolbar.



Figure 1. Six available Contexts in the toolbar

Batch Acquisition Context

The **Batch Acquisition** context is used to submit batches and scripts to the Batch Queue. You can also run a Checktune from this context. These windows are available in this context:

- "Instrument Status Window" on page 8
- "Status Monitor Window" on page 8
- "Chromatogram Plot Window" on page 9
- "Batch Queue Window" on page 10
- "Actuals Window" on page 13

Overlay Plot Context

The **Overlay Plot** context is used to examine the real-time plot. You can overlay the LC and MS plots for up to the last 25 runs. This window is available in this context:

"RTP Overlay Window" on page 14

Profile Editor Context

The **Profile Editor** context is used to edit a Profile. A Profile is a set of parameters that set how you want to do acquisitions. It includes the name of the acquisition method to use, warning and stopping limits for the pumps, data file naming rules, scripts to run before and after a batch, and the Batch Import Map File which determines the format that must be used when submitting a batch file. The Profile Editor Window has three different views. The following window is available in this context:

• "Profile Editor Window" on page 15

Six Contexts

System Settings Context

The **System Settings** context is used to set system parameters. You choose whether the system is executed as a **Shared Stream** or as a **Private Stream**. You also specify a script to execute when the Batch Queue starts running, plus you can specify an error script and a sleep script. The following window is available in this context:

"System Level Settings Window" on page 16

Method Development Context

The **Method Development** context is used to develop a data acquisition method. In this context, you can edit a method, run a sample, and run a worklist. You cannot switch to this context if the Batch Queue is running. The following windows are available in this context:

- "Chromatogram Plot Window" on page 9
- · "Instrument Status Window" on page 8
- "Actuals Window" on page 13
- "Method Editor Window" on page 17
- "Sample Run Window" on page 18
- "Worklist Window" on page 18

Tune Context

The **Tune** context is used to tune the instrument. You can run CheckTune and Autotune. You can also manually tune the instrument. The following windows are available in this context:

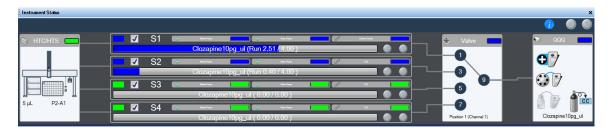
- "Tune Window" on page 19
- "Actuals Window" on page 13
- "Instrument Status Window" on page 8

Instrument Status Window

Instrument Status Window

The Instrument Status window is visible in the **Batch Acquisition** context, the **Method Development** context, and the **Tune** context.

This window in the MassHunter StreamSelect Console shows the status of the instrument components of all streams, such as autosampler, pump, column compartment, mass spectrometer, and valves. The progress of the current sample run is also shown for each stream.

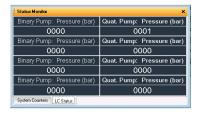


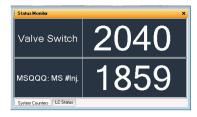
Status Monitor Window

The Status Monitor window is only visible in the **Batch Acquisition** context.

This window shows:

- actual values of key instrument parameters on the LC Status tab
- current counter values on the **System Counters** tab





To reset the counters, right-click the area, and then click **Reset** from the shortcut menu.

Chromatogram Plot Window

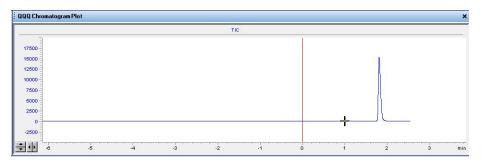
Chromatogram Plot Window

The Chromatogram Plot window is visible in the **Batch Acquisition** context and the **Method Development** context.

These windows in the MassHunter StreamSelect Console can be configured to plot data being acquired. The LC Chromatogram Plot windows are tabbed together by default. Each stream is shown in a different window. The initial plots are the Binary Pump pressure and Quat. Pump pressure. You can add or change the displayed plots in the **Edit Signal Plot** dialog box.



By default, the QQQ Chromatogram Plot contains the TIC for the mass spectrometer. You can add or change the displayed plots in the **Edit Signal Plot** dialog box which starts when you right-click the plot and click **Change**.



Batch Oueue Window

Batch Queue Window

The Batch Queue window is only visible in the **Batch Acquisition** context.

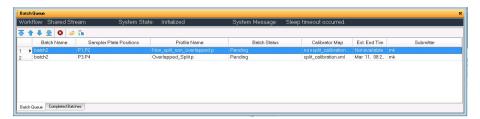
This window at the bottom of the MassHunter StreamSelect Console shows the following information:

Batch Status Pane

The pane at the top of the Batch Queue window shows status information for the Batch Queue, including the Workflow (Shared or Private Stream), System State, the currently running sample, the System Message, and any approaching event like sleep timeout or the command requested by the user.

Batch Queue Tab

The Batch Queue tab shows the batches that have been submitted. Batches are run in the order in the table. You can change the order of the batches in the Batch Queue using the buttons in the toolbar.



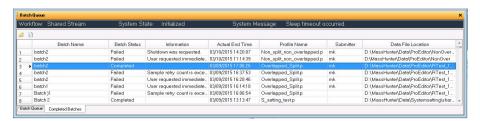
Batch Queue Window

Batch Queue Tab Toolbar

Toolbar Button	Action
₽	Move the selected batch to the top of the queue
Ŷ	Move the selected batch up one position in the queue
.	Move the selected batch down one position in the queue
₽	Move the selected batch to the bottom of the queue
8	Delete the selected batch or batches
Ġ	Open the data folder for the selected batch
(iii	View a list of samples in the selected batch. See "Completed Batches Tab Toolbar" on page 11.

Completed Batches Tab

The Completed Batches tab shows the batches that have been completed.



Completed Batches Tab Toolbar

Toolbar Button	Action
	Open the folder for the selected batch in File Explorer.
	Opens the Batch Log dialog box which shows information on events for the selected, completed batch.

Batch Oueue Window



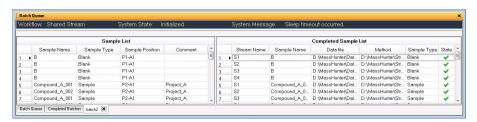
Sample List Tab

To view information about the samples in a batch, highlight the batch of interest in the Batch Queue tab, and then click the **View Sample List** () button. The Sample List tab opens and is labeled with the name of the selected batch. The Sample List tab has the following two panes of information:

- The **Sample List** pane shows the list of samples in the batch.
- The **Completed Sample List** pane shows the samples that have been run and tells which stream they ran on, the methods used, and the data file names.

You can select a different batch to display in the Sample List tab. You can only view 4 batches at a time in Sample List tabs. If you try to open a fifth batch, the first batch you opened is automatically closed.

You can close the Sample List tab by clicking the X in the tab.



Actuals Window

Actuals Window

The Actuals window is visible in the **Batch Acquisition** context, the **Method Development** context, and the **Tune** context.

The Actuals window contains two tables showing the current values of selected instrument parameters. The upper pane shows the values for different instrument parameters for different streams. The lower pane shows the values for instrument parameters that are the same for all streams.

You can customize the parameters that are displayed. You right-click in the window and click **Actual Settings**. The **Actuals Selection** dialog box is opened.



RTP Overlay Window

The RTP Overlay window is only visible in the Overlay Plot context.

You can see real-time plots in this window along with the previous data files. You can either see all streams combined into one plot (**Combined View** tab) or streams separated into different tabs (**Stream View** tab). The plots that you can see include an MS trace (a total ion chromatogram or TIC) and LC traces (Binary Pump trace and Quat. Pump trace). In this window you have options to change which traces are displayed, which streams are displayed, and which data files are displayed.

On the right side of this window, you can place two additional panes. By default these panes are hidden at the edge of the window. When you click the label for the pane, the pane is visible. When you move the cursor away from this pane, the pane is hidden again. You can make these panes be visible continuously when you click on the pin in the title of the pane.

These panes allow you to customize which data files are displayed. You mark the data files in the **Data file** pane. You select how many data files to show in the **Settings** pane. You can also remove the data files from the list when you click **Clear Data Files** on the **Settings** pane.



Profile Editor Window

Profile Editor Window

The Profile Editor window is only visible in the Profile Editor context.

The Profile Editor window lets you create profiles for each type of analysis done in your lab to simplify daily operation. Profiles are based on representative data collected with MassHunter Data Acquisition.

Profile Editor Views

You click the appropriate icon in the left pane to display the view of interest for the parameters you want to set. For more information, see *MassHunter StreamSelect online Help*.



Acquisition view This view lets you view and edit method information, such as selecting reference data files, setting the LC run time and MS start and stop times for the TIC, and setting pressure warning and stopping limits. You select the method to use in this view.



Data File Naming view This view lets you specify options for naming the data files for MassHunter StreamSelect. You can specify a location for the root data file directory, select names for data subdirectories, and components to make up the data file names.



System view This view lets you specify batch import settings, calibration settings, event actions, plate settings, and other parameters, such as Wait Time for Ready and free disk threshold values.

Calibrator Map dialog box



You click the + button in the **Calibrator Map** section of the System View to open the **Calibrator Map dialog** box.

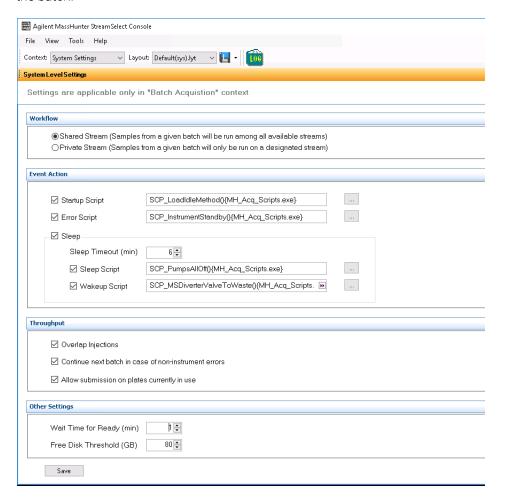
This dialog box lets you create or edit calibrator maps. Calibrator maps are listed in the Calibrator Map section of the **System** view. A subset of the calibrator maps that have been defined for the system can be selected for use in a particular MassHunter StreamSelect profile. Calibrator Maps are global; changes that are made to a calibrator map affect all profiles that reference that calibrator map.

System Level Settings Window

System Level Settings Window

The System Level Settings window is only visible in the **System Settings** context.

You set parameters that affect every user in this window. See the online Help for more information on this window. If you click **Shared Stream**, then samples from your batch are run on any available stream. If you click **Private Stream**, then all samples in your batch are run on the stream which you select when you submit the batch.

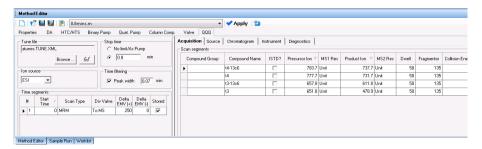


Method Editor Window

Method Editor Window

The Method Editor window is only visible in the **Method Development** context.

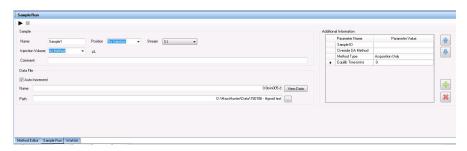
This window allows you to create a method that consists of setpoints for the instrument. The tabs that appear in the window are for only devices that are currently configured on the system. The Method Editor window is dynamic. It allows you to both view and change the current setpoints of the instrument. In addition, it has the **Apply** and **Reset** buttons. If a worklist is running, the setpoints change depending on which method is currently loaded on the instrument. You can get help on any tab in the Method Editor by pressing **F1**.



Sample Run Window

The Sample Run window is only visible in the **Method Development** context.

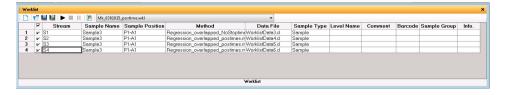
You can submit a single sample when you use this window. You specify the data file name and path, the position of the sample, the stream, the injection volume, and the name. You can also change some of the **Additional Information**.



Worklist Window

The Worklist window is only visible in the **Method Development** context.

The Worklist window allows you to create a list of samples to run. When you are developing a new method, you can create a worklist to run the method multiple times with different samples. You can use the menus to change the worklist. You can also use the shortcut menus in the Worklist window. The shortcut menu changes depending on where you clicked on the table: a cell, a row, a column, or the upper left empty box.

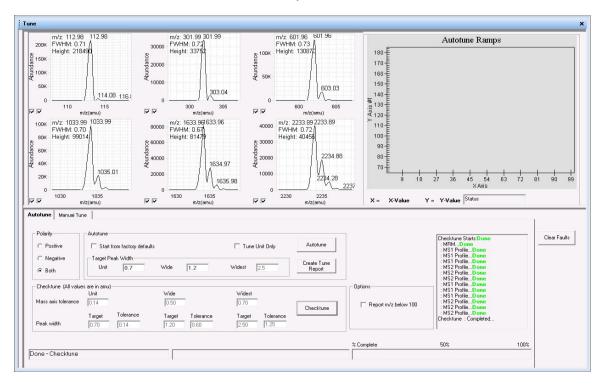


Tune Window

Tune Window

The Tune window is visible only in the **Tune** context.

You can run an Initial Autotune, an Autotune, or a Checktune from the Tune window. You can also manually tune the instrument from this window.



Tune Window

Batch Sample Submission and Data Acquisition Method Setup

This section describes how to submit batches of samples in Agilent MassHunter StreamSelect System, set up data acquisition methods for your analyses, and do a checktune on the instrument.

Before you start

- If methods have not yet been set up for your analysis, see "To set up methods for Data Acquisition" on page 23.
- Create or change a profile for your analysis in the Profile context. MassHunter StreamSelect profiles can be developed for each type of analysis done in your lab to simplify daily operation. MassHunter StreamSelect profiles are based on representative data collected.

See "Profile Editor Window" on page 15 for a description of the Profile Editor window

NOTE

You specify the profile when you submit a batch.

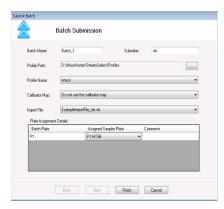
• Do a checktune on the instrument to verify performance as necessary. See "To do a checktune on the instrument" on page 28.

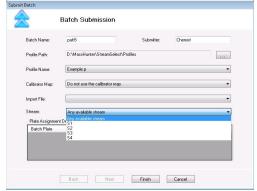
To submit batches

- 1 Open the MassHunter StreamSelect Console. See "To open the MassHunter StreamSelect Console" on page 5.
- 2 If necessary, set the Context to Batch Acquisition.



3 Click **Submit Batch** on the toolbar of the MassHunter StreamSelect Console. If you select **Shared Stream** in the System Settings context, then the **Stream** parameter is not included in this dialog box.





- **4** On the Submit Batch dialog box, enter the following information:
 - **Batch Name:** Enter a name for the batch, which is used to determine where the batch folder is created based on Batch Naming settings.
 - **Submitter**: The field is optional, but may be used in batch folder naming.
 - Profile Path and Profile Name: Select a profile for the type of analysis that you are doing.
 - Calibrator Map: Select a Calibrator map from the list. Calibrator maps are created and assigned to a profile in the MassHunter StreamSelect Profile Editor; see page 15 for more information. If you select Do not use Calibrator Map, then the samples in the Import File are either run on the stream which you selected (if you clicked Private Stream in the System Level Settings window) or run on alternating streams in the order they appear in the list (if you click Shared Stream in the System Level Settings window). For example on a Shared Stream system, sample line 1 runs on Stream 1, sample line 2 runs on Stream 2, and so on. If one stream shuts down during the run, then the remaining samples for that stream run or will run on a different stream.

To start, stop, and resume batches

- Import File: Select the file that contains the list of samples for the batch.
- **Stream**: If you select **Private Stream**, then you also need to select which Stream to use.
- 5 In the Plate Assignments Details table, assign a position in the autosampler to the plates in the Import File and Calibrator Map. By default, only plates that are not currently in use by any other batches can be assigned. See "System Level Settings Window" on page 16 to learn how to be allowed to use plates that are currently in use by other batches.
- 6 Click Finish.

The batch appears in the Batch Queue window.

To start, stop, and resume batches

Use this procedure to manage the Batch Queue.

- 1 If the queue has stopped, restart it with one of the following options:
 - Click Batch Queue > Start > Start Batch.
 - Click Batch Queue > Start > Resume Batch.
- 2 If you need to reorder the batches in the queue, use the arrow buttons on the Batch Queue tab.



- 3 If you need to stop the batch before completion:
 - Click Batch Queue > Stop> Stop Batch.
 - Click Batch Queue > Stop> Stop after Current Sample.
 - Click Batch Queue > Stop> Stop after Current Batch.
- **4** Monitor baseline and adjust plot in the Chromatogram Plot windows, as described in MassHunter StreamSelect Console online Help.
- **5** To view information about the samples in a batch, highlight the batch of interest, and then click the **View Sample List** button.



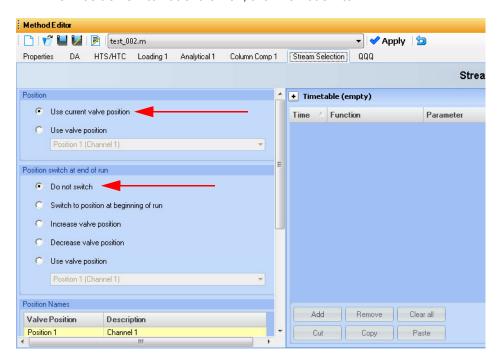
The sample information is shown in the Sample List tab of the Batch Queue window.

To set up methods for Data Acquisition

To set up methods for Data Acquisition

You use the **Method Development** context to set acquisition method parameters. If the Batch Queue is running, you cannot select the **Method Development** context.

- 1 Select **Method Development** for the **Context**.
- 2 Click the Method Editor window.
- 3 On the Valve tab in the Method Editor window:
 - For Position, click Use current valve position.
 - For Position switch at end of run, click Do not switch.



Note that tab names can be customized; your system may have different labels.

- **4** Set the **Stoptime** for devices in the **Method Editor** window:
 - On the Pump and QQQ tabs, set the Stoptime to the same values.
 - For all other devices, such as TCC, set the Stoptime to the default value of As Injector/No Limit.

To set up methods for Data Acquisition

- **5** Set CTC autosampler parameters:
 - **a** For HTC/HTS autosampler, on the **HTS/HTC** tab in the **Method Editor** window, select a cycle from the **Available Cycles** list. See **Figure 2.**
 - **b** For PAL3 RSI autosampler, on the **PAL3 Sampler** tab, select a script from the drop-down list. See **Figure 3**.
 - **c** Review the other parameters on this tab.

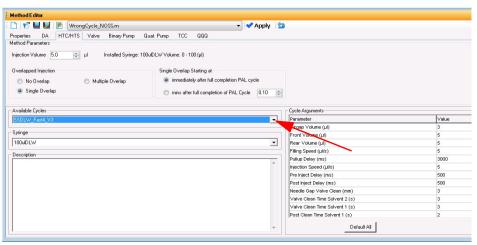


Figure 2. HTC/HTS tab to set cycle parameters

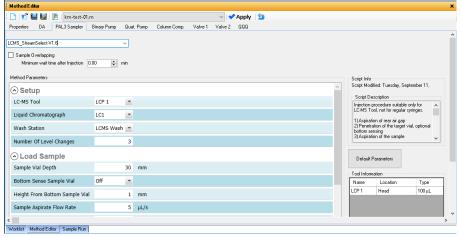


Figure 3. PAL3 Sampler tab to set script parameters

To set up methods for Data Acquisition

6 Set additional method parameters on the **Column Comp.** tab in the **Method Editor** window.

For information on setting Acquisition method parameters, see the *online Help* for MassHunter Workstation Data Acquisition software.

- **7** Set other LC parameters.
- 8 Set the parameters on the **QQQ** tab.
- **9** Set the parameters on the **DA** tab.
- **10** Set the parameters on the **Properties** tab.
- 11 Save the method.
- **12** Set up a worklist to verify the method for your analysis as explained in the next section.

To verify an acquisition method using a single sample

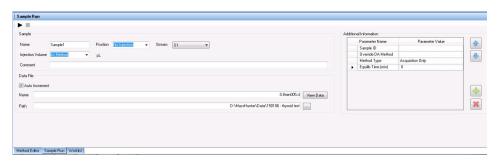
To verify an acquisition method using a single sample

You use the **Method Development** context to run a single sample as follows.

This task helps you test the new method you created in "To set up methods for Data Acquisition" on page 23.

For more information on running samples, see the *online Help* for MassHunter Workstation Data Acquisition software.

- 1 Set the Context to Method Development.
- 2 Click the Sample Run tab. If this tab is not visible, click View > Sample Run.



- **3** Enter the following information:
 - Name (Sample)
 - Position
 - Stream
 - Injection volume
 - Name (Data File)
- 4 If necessary, change other parameters under **Additional Information**.
- 5 Click Sample > Run or press F5.
- **6** (optional) Examine the real-time plots in the Chromatogram Plot window or switch to the **Overlay Plot** context and view the real-time plots in that context.

To verify an acquisition method using a worklist

To verify an acquisition method using a worklist

You use the **Method Development** context to set up a worklist as follows.

You can test the new method you created in "To set up methods for Data Acquisition" on page 23 by creating a worklist. For more information on setting up worklists, see the *online Help* for MassHunter Workstation Data Acquisition software.

- 1 If necessary, select **Method Development** for the **Context**.
- 2 Set up a worklist as follows. The worklist runs your sample of interest on two LC streams.
 - **a** Add the first sample to the worklist:
 - Click Add Sample from the Worklist menu. A new sample row is added to the Worklist table.
 - Select a Stream to use for this sample in the Worklist. You select the Stream in the Stream column in the worklist table.
 - Fill out the information for this sample, using the **Method** you developed in the previous steps of this procedure.
 - **b** Add additional sample rows to the Worklist table:
 - Click Add Sample from the Worklist menu. A new sample row is added to the Worklist table.
 - Select a Stream to use for this row in the Worklist
 - Fill out the information for this second sample, using the same **Sample Position** and **Method** as used for the first sample.
 - **c** Click **Worklist Run Parameters** from the Worklist menu to set parameters on the Worklist Run Parameters dialog box.
 - **d** (optional) Save the worklist.
- **3** Place the sample in the proper location if it is not already there.
- 4 Run the worklist and evaluate the results.
 - a Click Worklist > Run or press F4.
 - **b** When the analyses are completed, compare the results in MassHunter Qualitative Analysis to make sure the method gives the expected results for all LC streams.
 - **c** Change the method parameters if necessary.
 - **d** Save the method if you make any changes.

To do a checktune on the instrument

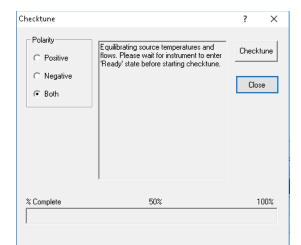
You are now ready to use the Batch Queue. See "To submit batches" on page 21.

To do a checktune on the instrument

Run the Checktune procedure as needed to verify the performance of the Triple Quad LC/MS. Checktune checks the mass axis tolerance and the peak width for three different peak widths and displays the result. You can also run a Checktune from the Tune context. See "Tune Window" on page 19.



- 1 Open the MassHunter StreamSelect Console. See "To open the MassHunter StreamSelect Console" on page 5.
- 2 Set Context to Batch Acquisition.
- **3** If the mass spectrometer is in standby, right-click the **QQQ** device pane in the Instrument Status window and click **On** to turn it on.
- 4 Click Checktune in the toolbar.



- 5 On the Checktune dialog box:
 - **a** Set the **Polarity** to use during Checktune:
 - Positive
 - Negative
 - Both (positive and negative polarities)



To do a checktune on the instrument

b Click Checktune.

When you start Checktune, the mass spectrometer may go to a "Not Ready" state. Checktune parameters take time to stabilize. Checktune begins automatically when the Triple Quad LC/MS is ready and can take up to 15 minutes to run.

NOTE

- The system automatically runs the correct Checktune, depending on whether a standard tune file or a fast scan tune file is loaded.
- The Checktune for a Fast Scan autotune file only checks the MS2 operation and reports only the MS2 operation.

When Checktune is finished:

- If the Checktune passes, a message is displayed stating that it passed.
- If the Checktune does *not* pass, a message is displayed that says that Autotune is recommended.
- A Checktune Report appears in the Print Preview dialog box.
- **6** If the Checktune does *not* pass, select the **Tune** context, and run an Autotune on the QQQ.

Reference

MassHunter Workstation Programs

Reference

MassHunter Workstation Programs

MassHunter StreamSelect Instrument Configuration

The MassHunter StreamSelect Instrument Configuration lets you configure instruments for MassHunter StreamSelect. See "MassHunter StreamSelect Instrument Configuration" on page 31. For more information, see the MassHunter StreamSelect Setup Guide.

MassHunter Data Acquisition

Several of the windows in the Method Development context are very similar to windows in the MassHunter Data Acquisition program, such as the Worklist or the Sample Run window. Refer to the user guides for the MassHunter Data Acquisition program for additional help.

MassHunter Qualitative Analysis

In the MassHunter Qualitative Analysis program, to identify the stream that was used to acquire a data file:

- **1** Open the MassHunter Qualitative Analysis program.
- 2 Open the data file.
- 3 Open the Sample Information window.

The stream is shown in the **Stream Name** information.

MassHunter Quantitative Analysis

In the MassHunter Quantitative Analysis program, to identify the stream that was used to acquire a data file:

- 1 Open the MassHunter Quantitative Analysis program.
- **2** Create a batch. Select the data file to be part of the batch.
- 3 Add the **Sample Group** column, which is part of the **Sample** columns.
- 4 Click **View > Toolbars > Filtering** to display the filtering toolbar.
- **5** Filter which streams are displayed in the table.

Reference

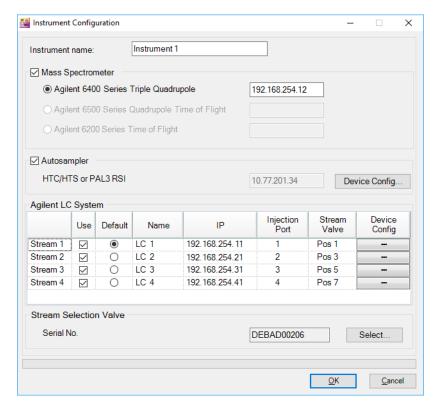
MassHunter StreamSelect Instrument Configuration

MassHunter StreamSelect Instrument Configuration

This dialog box lets you configure instruments for MassHunter StreamSelect. For more information, see the MassHunter StreamSelect Setup Guide.



To display the MassHunter StreamSelect Instrument Configuration window, click the **Instrument Configuration** icon on the Desktop.



In this Book

The *Quick Start Guide* helps you get started using the Agilent MassHunter StreamSelect System.

This guide supports MassHunter StreamSelect Software 8.0.

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