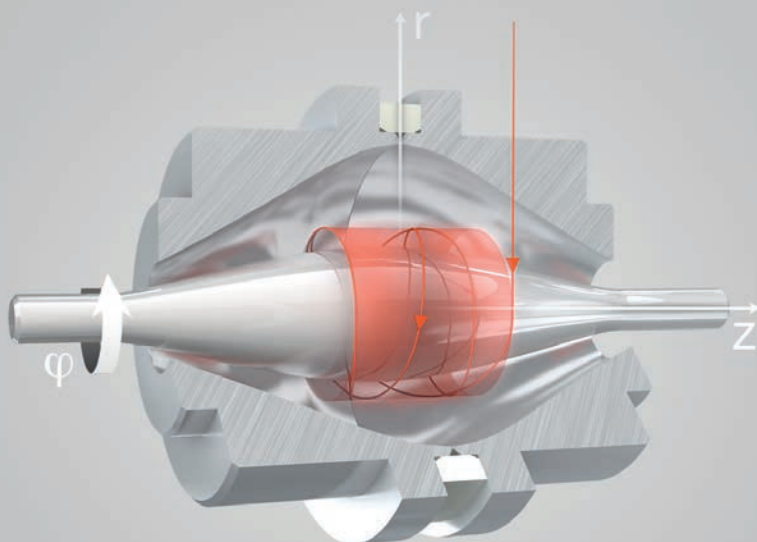




Q Exactive HF-X

Software Manual

Exactive Series 2.12

BRE0012262 Revision C March 2021

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Software Version: Exactive Series 2.12

For Research Use Only. Not for use in diagnostic procedures.

Read this First

Welcome to the Thermo Scientific Q Exactive HF-X system! Q Exactive™ HF-X is a member of the Thermo Scientific™ family of mass spectrometer (MS) detectors that are powered by Orbitrap™ technology.

About this Guide

This *Q Exactive HF-X Software Manual* provides reference information about the parameters in the Instrument Configuration window, the Instrument Setup window, and the Q Exactive HF-X Tune window. For information about the operating procedures for the Q Exactive HF-X mass spectrometer, we recommend that you read the *Exactive Series Operating Manual* in its entirety.

Who uses this Guide

This *Q Exactive HF-X Software Manual* is intended for all personnel that need to perform measurements with the Q Exactive HF-X mass spectrometer, especially the key operator. This manual should be kept near the instrument to be available for quick reference.

Scope of this Guide

The *Q Exactive HF-X Software Manual* includes the following chapters:

- [Chapter 1: “Instrument Configuration Window”](#) describes the Instrument Configuration window, which displays configuration information.
- [Chapter 2: “Q Exactive HF-X Readback Status Page for the Information View”](#) describes the page that allows controlling the instrument from the Roadmap view of the Xcalibur™ Home Page window.
- [Chapter 3: “Instrument Setup”](#) describes Instrument Setup, which is used to specify instrument settings.
- [Chapter 4: “Explore Q Exactive HF-X Tune”](#) provides information about Q Exactive HF-X Tune, its views, functions, and features.
- [Chapter 5: “Procedures in Q Exactive HF-X Tune”](#) provides information about procedures in Q Exactive HF-X Tune.

- [Chapter 6: “Reference Information”](#) provides information about various file types and other supplemental information.

Related Documentation

In addition to this guide, Thermo Fisher Scientific provides the following documents for the Q Exactive HF-X mass spectrometer:

- *Exactive Series Pre-Installation Requirements Guide*
- *Exactive Series Operating Manual*
- *Q Exactive HF-X QuickStart Guide*
- Manuals for the delivered ion sources and other software.

You can access PDF files of the documents listed above and of this guide from the data system computer. The Q Exactive HF-X Tune software also provides Help.

❖ To view product manuals

Go to **Start > Programs > Thermo Exactive Series > Manuals**.

❖ To open Help

- From the Q Exactive HF-X Tune window, choose **Help > Help Content**.
- If available for a specific window or dialog box, click **Help** or press **F1** for information about setting parameters.

For more information, including upcoming application notes, visit www.thermofisher.com.

Contacting Us

There are several ways to contact Thermo Fisher Scientific. You can use your smartphone to scan a QR Code, which opens your email application or browser.

Contact	Link / Remarks	QR Code
Brochures and Ordering Information	www.thermofisher.com/orbitrap	
Planet Orbitrap	PlanetOrbitrap.com is a scientific and community-based microsite that features detailed application workflows along with a searchable scientific library with links to peer-reviewed articles, product literature, and online presentations. This site also features technology, products, news, events, and community content.	
Patent Information	www.thermofisher.com/ms-patents	
Service Contact	www.unitylabservices.com	
Technical Documentation SharePoint	❖ To get user manuals for your product 1. With the serial number (S/N) of your instrument,* request access on our customer SharePoint as a customer at www.thermoscientific.com/Technicaldocumentation 2. For the first login, you have to create an account. Follow the instructions given on screen. Accept the invitation within six days and log in with your created Microsoft™ password. 3. Download current revisions of user manuals and other customer-oriented documents for your product. Translations into other languages may be available there as well. * You can find the serial number of your instrument on the name plate. Refer to the <i>Exactive Series Operating Manual</i> for the location.	

Contact	Link / Remarks	QR Code
Customer Feedback	❖ To suggest changes to this manual You are encouraged to report errors or omissions in the text or index. Send an email message to the Technical Editor at documentation.bremen@thermofisher.com. The PDF versions of our manuals allow adding comments with Adobe Acrobat Reader or other freely available PDF reader programs.	

Typographical Conventions

This section describes typographical conventions that have been established for Thermo Fisher Scientific manuals.

Signal Words

Make sure that you follow the precautionary statements presented in this manual. The special notices appear different from the main flow of text:

NOTICE

Points out possible material damage, data loss, impaired data quality and other important information in connection with the instrument.

Tip Highlights helpful information that can make a task easier.

Data Input

Throughout this manual, the following conventions indicate data input and output via the computer:

- Messages displayed on the screen are represented by capitalizing the initial letter of each word and by italicizing each word.
- Input that you enter by keyboard is identified by quotation marks: single quotes for single characters, double quotes for strings.
- For brevity, expressions such as “choose **File > Directories**” are used rather than “pull down the File menu and choose Directories.”
- Any command enclosed in angle brackets < > represents a single keystroke. For example, “press <F1>” means press the key labeled *F1*.
- Any command that requires pressing two or more keys simultaneously is shown with a plus sign connecting the keys. For example, “press <Shift> + <F1>” means press and hold the <Shift> key and then press the <F1> key.
- Any button that you click on the screen is represented in bold face letters. For example, “click **Close**.”

Topic Headings

The following headings are used to show the organization of topics within a chapter:

Chapter Name

Second Level Topics

Third Level Topics

Fourth Level Topics

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Instrument Configuration Window

Tip Do not change the settings in this window except during the installation of the instrument. Any changes in this window affect the data acquisition or the functionality of your instrument. A later change will rarely solve problems users have to face.

The Instrument Configuration window displays Q Exactive HF-X configuration information. See [Figure 1-1](#).

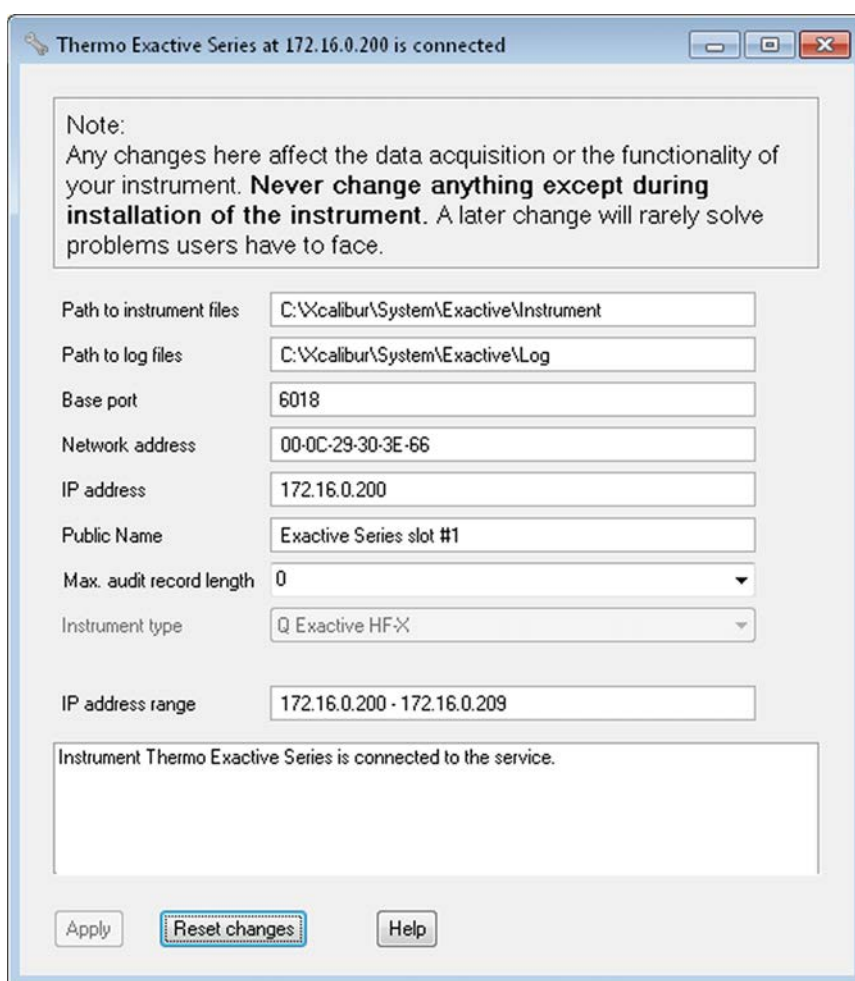


Figure 1-1. Instrument Configuration window

The Instrument Configuration window has the following parameters:

Parameter	Description
Path to instrument files	Displays the location of the instrument files. To change the path, click the folder button on the right side of the text box. A dialog box appears where you can select another location.
Path to log files	Displays the location of the log files. For information about the content of the log files, see “Log Files” on page 6-2 . To change the path, click the folder button on the right side of the text box. A dialog box appears where you can select another location.
Base port	Displays the first TCP/UDP port in use for this particular instrument. Leave the field empty for an automatic assignment.
Network address	Displays the hardware address of the network card installed in the instrument. Leave the field empty for an automatic assignment.
IP address	Displays the IP address. Leave the field empty for an automatic assignment.
Public Name	Displays the name that is shown in the About dialog box of Q Exactive HF-X Tune.
Max. audit record length	Use this list box to select the maximum audit record length. The following options are available: • 0 disables auditing • 50 is common for an Access audit database initialized by Platform’s Database Configuration • 255 is common for an Oracle audit database initialized by Platform’s Database Configuration • 1000 is common if auditing is done by Chromeleon. It is a compromise between size and readability
Instrument type	Displays the configured instrument type, that is Q Exactive HF-X.
IP address range	Displays the IP address or IP address range which should be assigned to the instrument during its starting phase. Use the numeric form, for example “172.16.2.1-172.16.2.15.” Tip Change only when advised by your network administrator.
Message box	Displays information about the instrument and connection status.
Buttons	
Apply	Saves your changes in this window.
Reset changes	Discards your changes in this window.
Help	Displays the Help for this window.

❖ To display this window

1. Choose **Programs > Thermo Foundation 3.1 > Instrument Configuration**.

2. From the Instrument Configuration window, click Q Exactive HF-X - Orbitrap MS in the Configured Devices area.
3. Click **Configure**.

Q Exactive HF-X Readback Status Page for the Information View

The readback status of each Xcalibur-configured instrument appears on the Status page of the Information view. When you click an instrument, Xcalibur™ displays current readings for the instrument on a page below the Run Manager pane. See [Figure 2-1](#).

Right-click any of the instruments to display a shortcut menu where you can switch your instrument to On, Off, or Standby mode.

Tip This view is normally displayed on the left side of the Home Page window. If this view is not displayed, the view has been turned off.

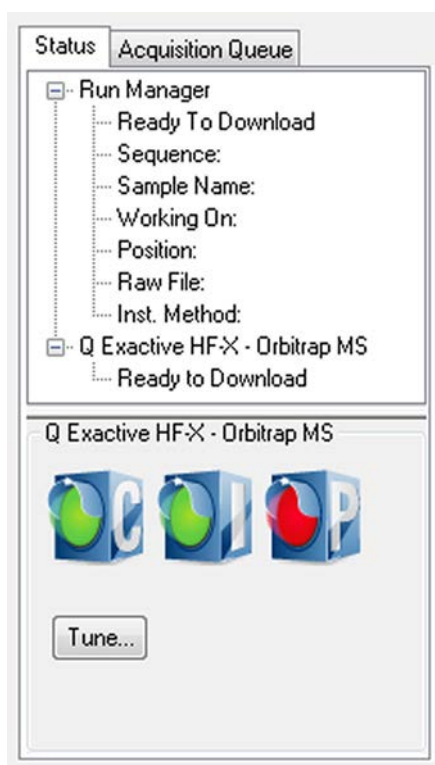


Figure 2-1. Q Exactive HF-X Readback Status Page for the Information View

The following functions are available:

Button		Description
	Communication Status	Shows the actual communication status of the system: • Green: communication with instrument is ok. • Yellow: only service is accessible (no instrument). • Red: communication is broken (no instrument, no service).
	Instrument Status	Shows the actual hardware status of the system (top instrument tree state): • Green: all readbacks are in specifications (green hooks). • Red: one or more readbacks are out of range.
	Performance Status	Shows the actual performance status of the system: • Green: the last evaluation/calibration was successful. • Yellow: last evaluation/calibration was successful, but is out of date. • Red: the evaluation/calibration was not successful.
Tune		Opens the Q Exactive HF-X Tune window.

❖ **To open this page**

1. From the Home Page window, choose **View > Info View** to display the Information view.
2. Click the **Status** tab.
3. Click **Q Exactive HF-X - Orbitrap MS**.

Instrument Setup

After you have selected in the Instrument Configuration program which instruments you want Xcalibur to control, use Instrument Setup to specify your instrument settings.

Contents

- [Instrument Setup Window](#)
- [Experiment Setup Page](#)
- [Summary Page](#)
- [Dialog Boxes of the Experiment Setup Page](#)

Instrument Setup Window

The Instrument Setup window displays the icons of the instruments that you have selected using the Instrument Configuration window. (See the View bar on the left side of the window.) See [Figure 3-1](#). If you have configured more instruments than can be displayed on your screen, a vertical scroll bar appears in the View bar. So, you can access all of the instruments.

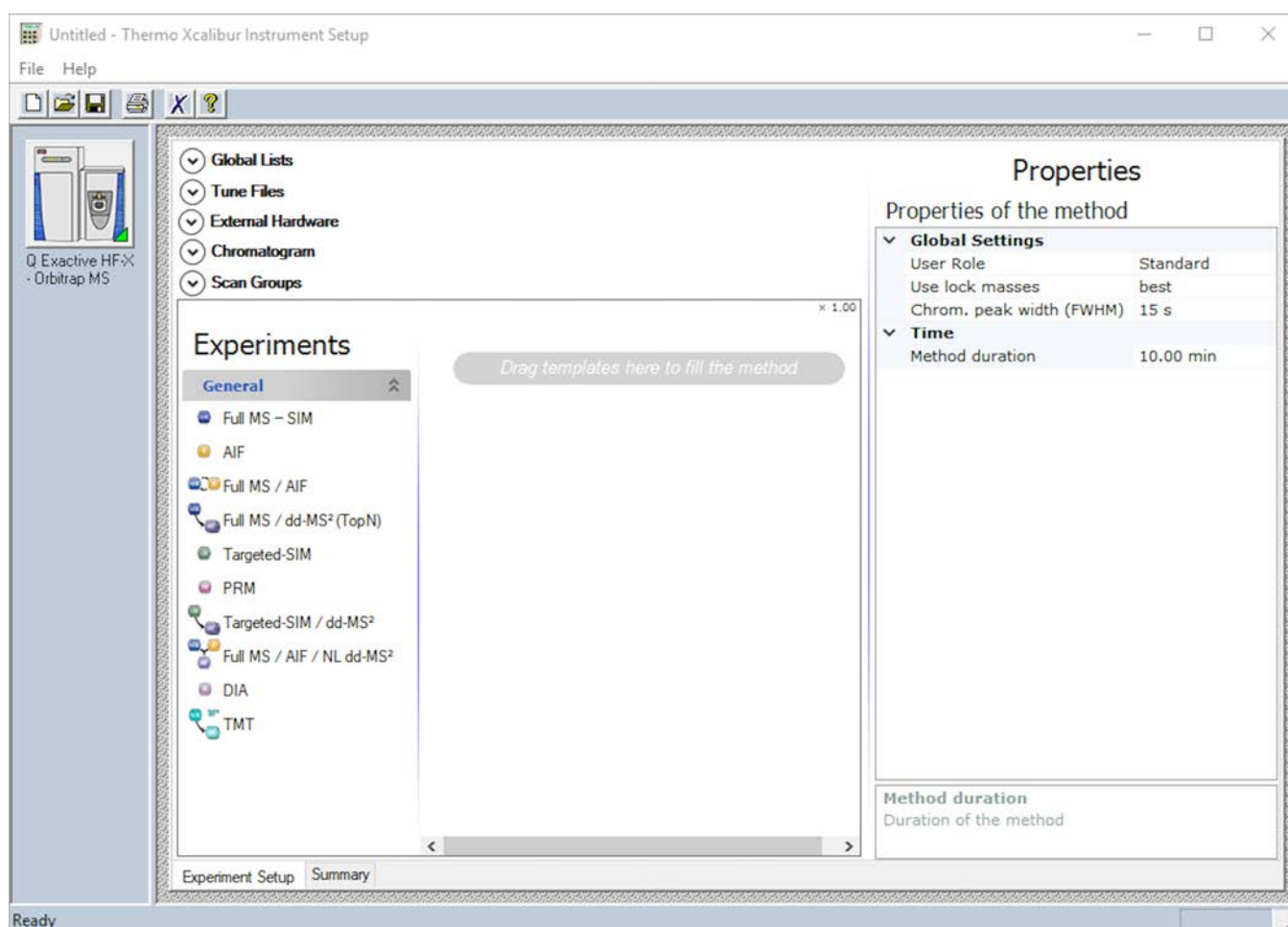


Figure 3-1. Instrument Setup window

To enter the setup parameters for a particular instrument, click the icon for that instrument. Xcalibur displays one or more pages of parameters to be set for the one you selected.

Tip Before you use the Instrument Setup window, use the Instrument Configuration program to select the instruments to be used for your experiment.

Use Instrument Setup to specify settings for your instruments after you have selected with the Instrument Configuration program the instruments that you want Xcalibur to control. The Instrument Setup window displays the setup parameters required for each instrument that

you select on the View bar. These might include your autosampler, LC pump, mass spectrometer, divert valves, syringe pump, contact closure timing sequence, and/or all other Xcalibur supported instruments that you have configured.

You can create new methods, modify existing methods, and save method files.

❖ **To display this window**



- Click  from the Roadmap view of the Home Page window.
- Or, choose **GoTo > Instrument Setup**.

View Bar

The View bar is a vertical bar on the left of the Instrument Setup window. It contains buttons for each of the instruments that you have selected by using the Instrument Configuration program.

Menus

Instrument Setup contains the following menus:

- [File Menu for the Instrument Setup Window](#)
- [Help Menu for the Instrument Setup Window](#)

Toolbar

[Instrument Setup Window Toolbar](#)

File Menu for the Instrument Setup Window

The File menu provides commands for file and program operations. It has the following commands:

	Command	Description
	New	Create a new method file having the appropriate extension.
	Open	Find and open a file that already exists.
	Save	Save the active method. Changes will be recorded in Audit Trail after the method is saved.

Command	Description
Save As	Edit user and description information, and view header information about the active file. Xcalibur opens the Save As dialog box. Changes will be recorded in Audit Trail after the method is saved.
Summary Information	Edit user and description information, and view header information about the active file.
Change Study Name	Select a dataset from a predefined list of names. The text of this menu item might be different if the administrator chose to use another name for a dataset. For example, this menu item might be Change Job Name.
Audit Trail	View all auditable events and changes made to data files in the current application.
 Print	Print the parameters in your instrument method.
Print Preview	View your page setup so that you can see what it looks like before printing it.
Print Setup	Select the following printing options: printer, form, orientation, and one-sided or two-sided printing.
Most Recently Used Files	View the paths and names of the last four files used. These are located above the Exit command. Both open and closed files are displayed. Click a displayed file to load it. If the selected file was closed, it will be opened.
Exit	Close the active window. If you exit before clicking OK from an active dialog box, Xcalibur asks if you want to save your changes.

Help Menu for the Instrument Setup Window

The Help menu lists the following commands:

Command	Description
Q Exactive HF-X - Orbitrap MS Help	Open the Configuration and Setup Help for the instrument.
Instrument Setup Help	Open Xcalibur Help and display Help for the Instrument Setup window.
Help On Current Item	View Help for the Instrument Setup page that is currently displayed.
Q Exactive HF-X - Orbitrap MS Contents and Index	View the Contents, Index, and Find Help pages for the selected instrument.
Xcalibur Help	Open Xcalibur Help.
Glossary	Open the Xcalibur glossary.

Command	Description
How to use Online Help	Open Help that describes how to use the Help viewer.
About Instrument Setup	View the version number of the Instrument Setup program and the Thermo Fisher Scientific copyright notice.

Instrument Setup Window Toolbar

The toolbar provides symbol shortcuts for frequently used commands. The following functions are available:

Button	Description
 New	Create a new instrument method.
 Open	Find and open an existing file.
 Save	If your method has not been saved before, clicking Save opens the Save As dialog box. Select the name and location for your instrument method. When you click Save , the File Summary Information Dialog Box opens. Enter header information for your instrument method. The file is saved when you click OK .
 Print	Print the parameters in your instrument method.
 Home Page	View the Home Page window—Roadmap view.
 Help	View Help for the Instrument Setup page that is currently displayed.

Method Editor

Use the Method Editor to specify the type of mass spectrometer experiment you plan to perform. See [Figure 3-2](#).

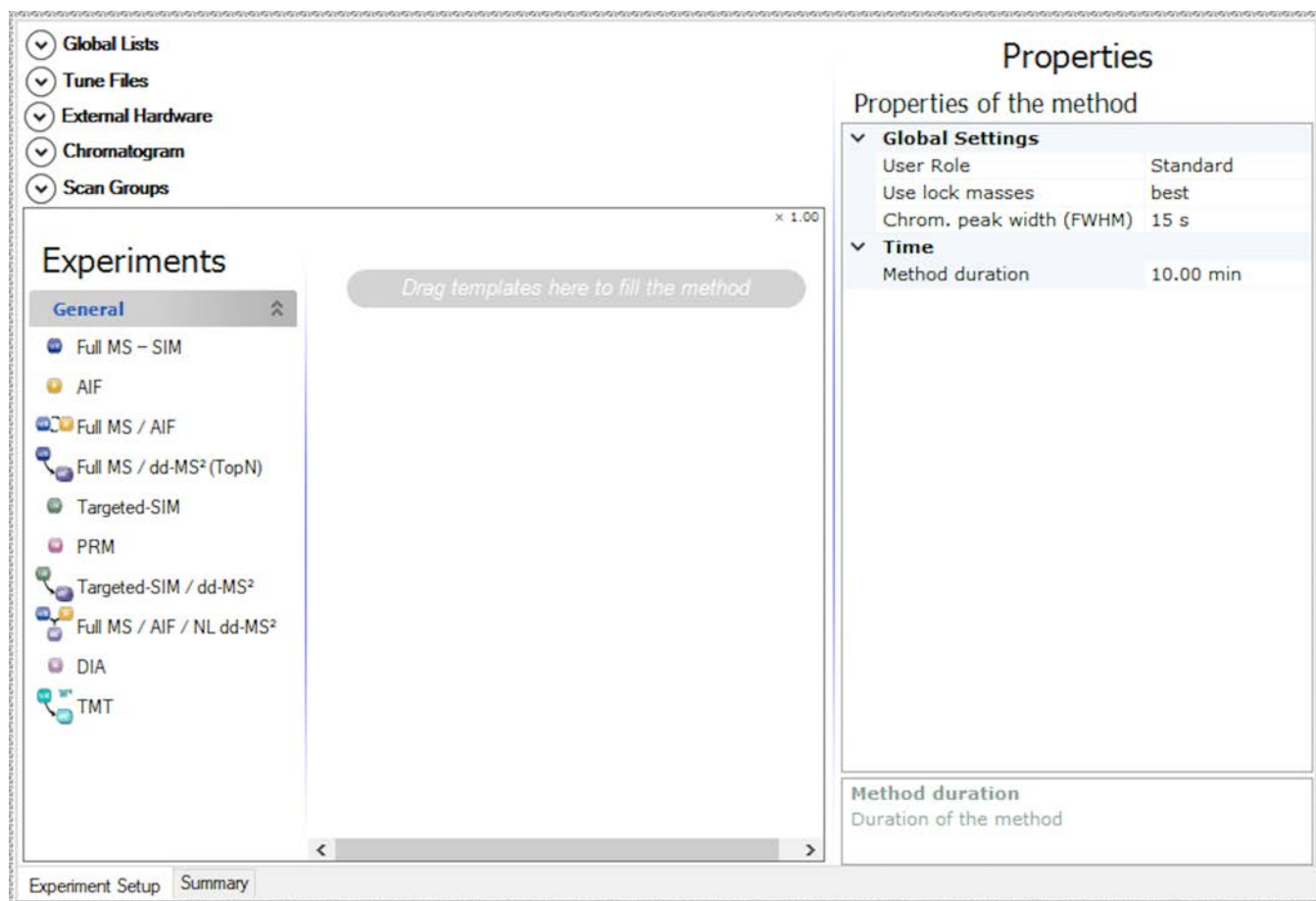


Figure 3-2. Method Editor

The Method Editor has the following pages:

- Experiment Setup Page
- Summary Page

❖ **To display this view**

Click **Instrument Setup** from the Roadmap View of the Home Page window or choose **GoTo > Instrument Setup**.

Experiment Setup Page

Use the Experiment Setup page to set up Q Exactive HF-X mass spectrometer experiments. You use this page to specify values for the Q Exactive HF-X parameters and save the parameters in an instrument method. See [Figure 3-3](#).

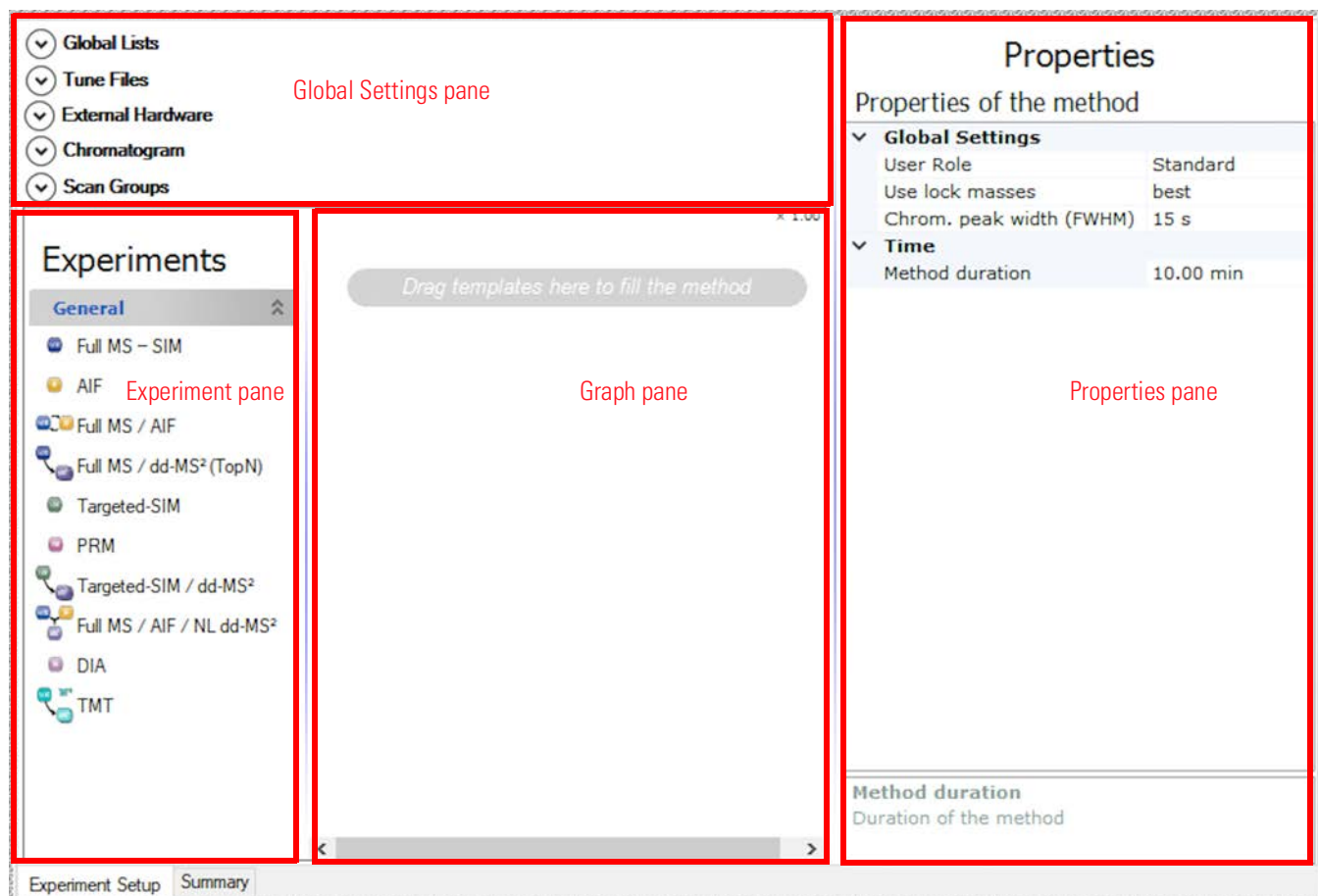


Figure 3-3. Method Editor—Experiment Setup page

The Experiment Setup page comprises four major windows:

- [Global Settings Pane](#)
- [Experiment Pane](#)
- [Graph Pane](#)
- [Properties Pane](#)

Global Settings Pane

The Global Settings pane is located on the top left side of the Experiment Setup page. It gives access to global lists, tune files, external hardware, chromatogram, and scan groups. See [Figure 3-4](#).

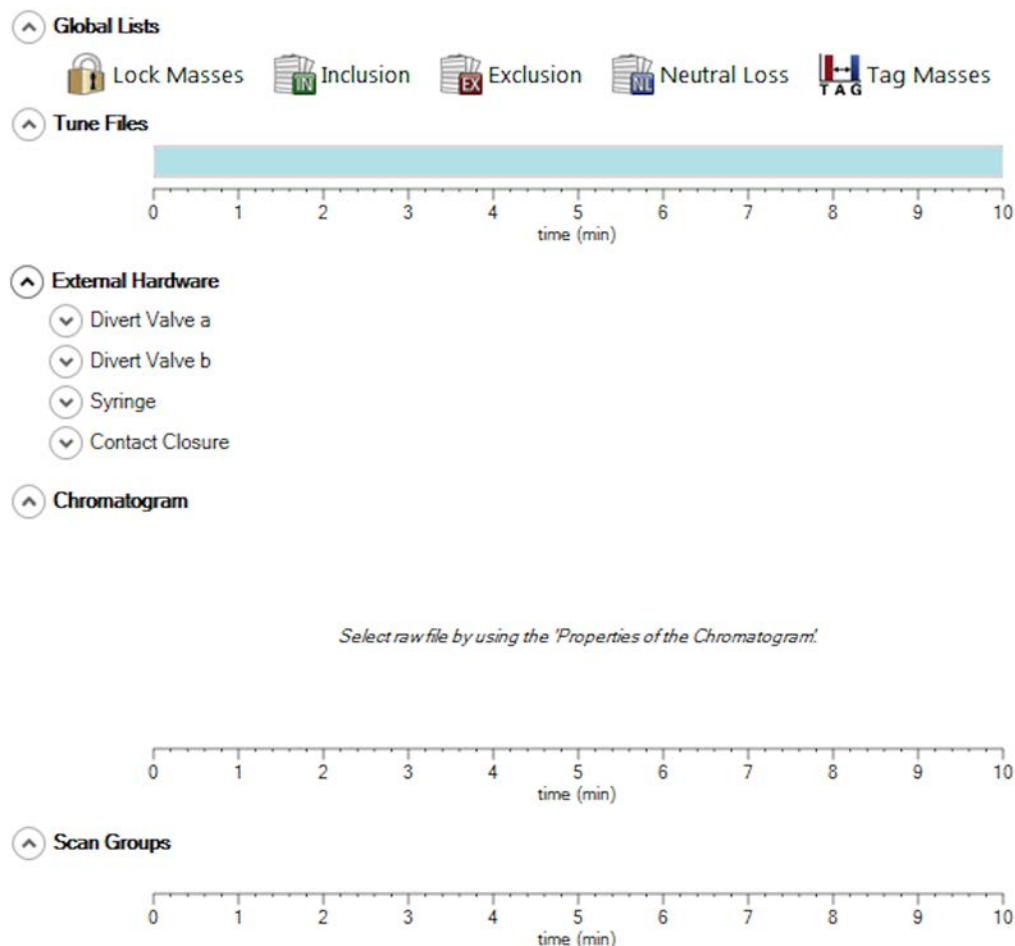


Figure 3-4. Method Editor—Global Settings pane

The Global Settings pane contains the following panes:

- [Global Lists](#)
- [Tune Files](#)
- [External Hardware](#)
- [Chromatogram](#)
- [Scan Groups](#)

Click the title bar of an individual pane to display it. Click again to hide it.

Global Lists

Use the Global Lists pane of the Experiment Setup page to perform intelligent automated MS/MS and SIM type experiments by efficiently utilizing the mass spectrometer to characterize parent ions independent of the “current segment” model. Use the Global Lists pane to specify parent, reject, and/or non-data dependent MS/MS and SIM masses with customizable and independent time windows. See [Figure 3-5](#). Scan events that reference the mass lists that you create here run only if there is a corresponding mass/time window at that particular retention time.



Figure 3-5. Method Editor—Global Lists pane

The following dialog boxes are available:

- [Lock Masses Dialog Box](#)
- [Inclusion List Dialog Box](#)
- [Exclusion List Dialog Box](#)
- [Neutral Losses Dialog Box](#)
- [Tag Masses Dialog Box](#)

To display a dialog box, click the respective icon.

Tune Files

The Tune Files pane shows a graphical representation of the tune files usage during the various phases of the experiment. See [Figure 3-6](#). In addition to the base tune file, you can specify up to 50 other tune files.

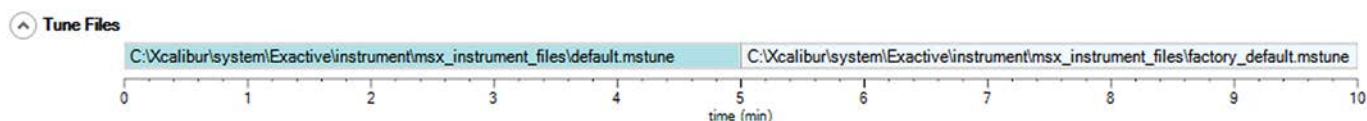


Figure 3-6. Method Editor—Tune Files

❖ To assign tune files

1. Do one of the following:
 - Point to a position on the time bar and right-click. Choose **Change to another tune file at <time at pointer position>** in the shortcut menu.

- Change the value of the Switch Count parameter in the Properties of Tunefiles pane.
2. In the Properties of Tunefiles pane, click the button next to the respective box of the Base Tunefile or New Tunefile parameter and browse for the new tune method file. See [Figure 3-7](#). Select the tune files and assign them to the experiment phases.

Properties of Tunefiles

General	
Switch Count	2
Base Tunefile	C:\Xcalibur\system\Exactive\instrument\msx_instrument_files\de
Element 1	
At	5.00
New Tunefile	C:\Xcalibur\system\Exactive\instrument\msx_instrument_files\fa
Element 2	
At	7.50
New Tunefile	

Figure 3-7. Properties of Tunefiles

The name and path way of the tune files will be shown on the respective time bar on the Tune Files pane.

❖ To change the starting time for tune files

- Position the cursor between adjacent tune files and drag the scan event along the time bar.
- In the Properties of Tunefiles pane, enter the time in the box of the At parameter of the respective Element.

❖ To remove a tune file

1. Position the cursor between adjacent tune files
2. Right-click to display the shortcut menu and choose **Remove change to tune file at <time at pointer position>**. The tune file to the right is removed.

❖ To zoom on the Tune Files pane

- Position the mouse pointer within the time axis area and drag the mouse across the time area of interest.
- To zoom in, position the mouse pointer within the pane and roll the mouse wheel forward.
- To zoom out, roll the wheel backward.
- To increase the zooming factor by two, keep the **<Shift>** key pressed while using the mouse wheel.

❖ **To unzoom the Tune Files pane**

Right-click in the pane to display the shortcut menu. Choose **Unzoom**.

❖ **To display this view**

On the External Hardware pane, expand the Tune Files item.

External Hardware

Use the External Hardware pane to configure and control optional hardware.

Divert Valve a / Divert Valve b

The Divert Valve items show graphic representations of the activities of the optional switching valves during the active acquisition. See [Figure 3-8](#). The normal LC flow through the switching valve (Position 1-2) is to the mass spectrometer. When the switching valve is activated (Position 1-6), LC flow is diverted to waste.

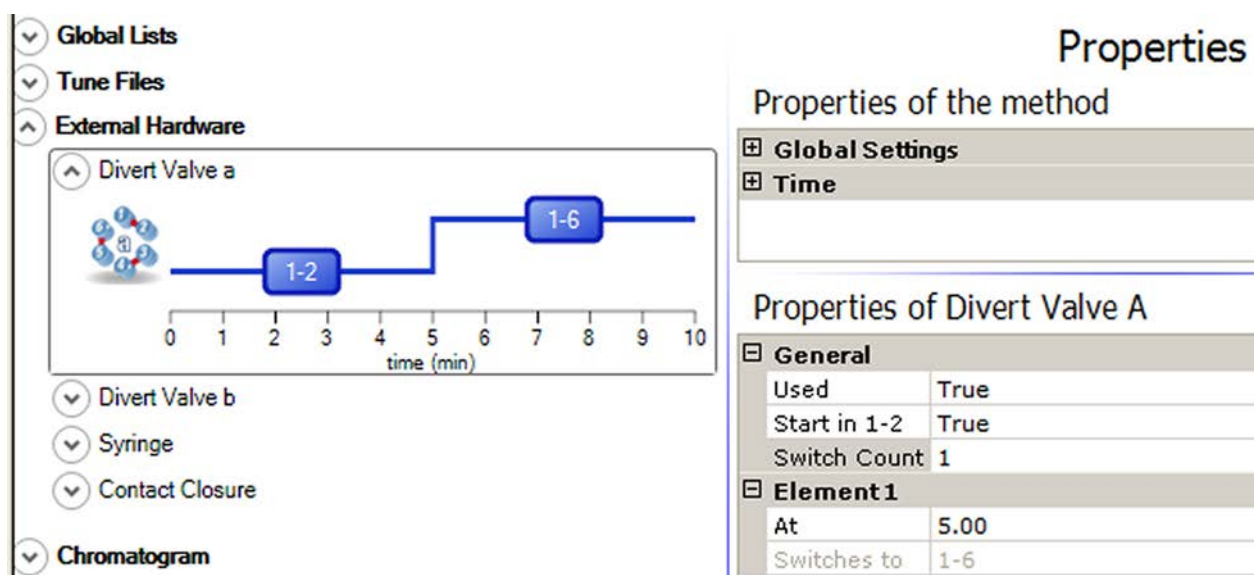


Figure 3-8. Properties of a switching valve that is used

❖ **To display this view**

On the External Hardware pane, expand the Divert Valve a or Divert Valve b item.

Use the shortcut menu of a Divert Valve item and the parameters of its Properties pane to control its activities:

❖ **To activate a switching valve**

- Right-click in the pane to display the shortcut menu. Choose **Activate**. The gray color  changes to the blue color . See [Figure 3-8](#).
- Click the valve symbol to select it. Set the Used parameter on the Properties pane to **True**.

❖ **To deactivate a switching valve**

- Right-click in the pane to display the shortcut menu. Choose **Deactivate**. The blue color changes to a gray color . See [Figure 3-9](#).
- Click the valve symbol to select it. Set the Used parameter on the Properties pane to **False**.

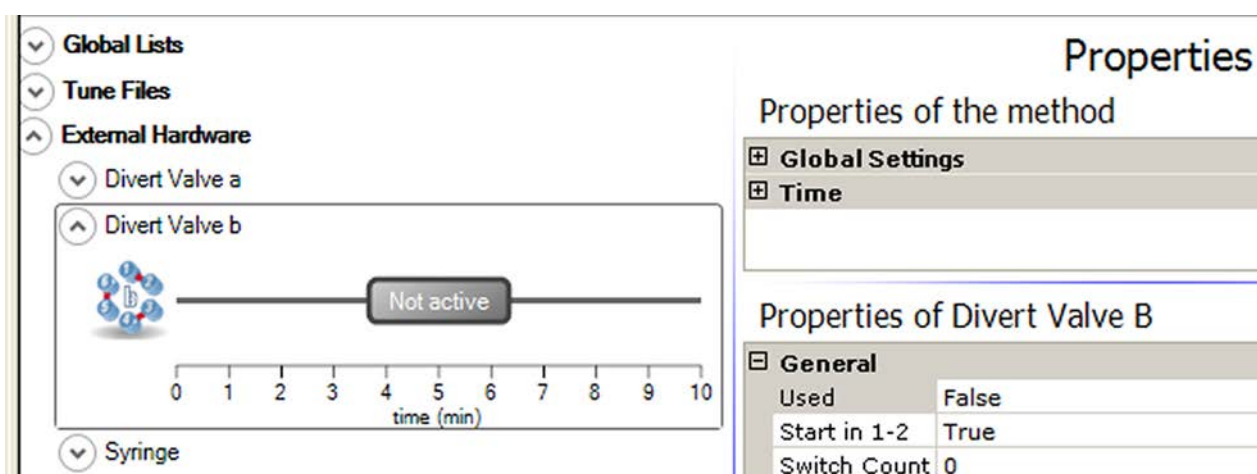


Figure 3-9. Properties of a switching valve that is not used

❖ **To change the start position of a switching valve**

- Right-click in the pane to display the shortcut menu. Depending on the active start position, choose **Start in 1-6** or **Start in 1-2**. The valve changes its start position.
- Click the valve symbol to select it. Depending on the active start position, set the Start in 1-2 parameter on the Properties pane to **True** or **False**.

❖ **To add a switch position for a switching valve**

1. Activate the switching valve as described above.

2. Do one of the following:
 - Use the mouse:
 - a. Move the mouse pointer to the position on the time line where you want to establish a switch position (5 minutes, for example).
 - b. Right-click in the pane to display the shortcut menu. Choose **Add switch at 5.00**.
 - Use the Properties pane:
 - a. Click the valve symbol to select it.
 - b. Set the Switch count parameter on the Properties pane to **1**.

A step in the line of the graphic representation indicates the new switch point. See [Figure 3-8](#).

3. To change the time of the switch position, do one of the following:
 - Drag the step that indicates the switch position to the new time.
 - On the Properties pane, set the At parameter of the respective Element to the new time.

❖ **To delete a switch position**

1. Move the mouse pointer to the switch position on the time line (at 5 minutes, for example).
2. Right-click in the pane to display the shortcut menu. Choose **Remove switch at 5.00**.

Syringe

The Syringe item shows a graphic representation of the activities of the optional syringe pump during the active acquisition. See [Figure 3-10](#).

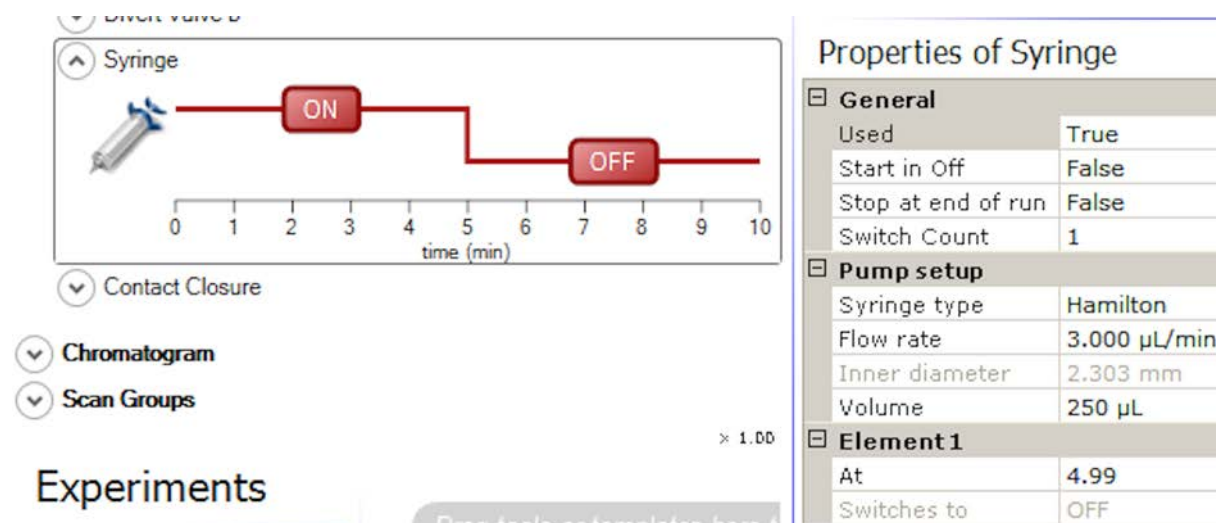


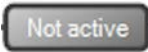
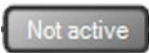
Figure 3-10. Syringe Pump pane

❖ To display this view

On the External Hardware pane, expand the Syringe Pump item.

Use the shortcut menu of the Syringe Pump item and the parameters of its Properties pane to control the activity of the syringe pump:

❖ To activate the syringe pump

- Right-click in the pane to display the shortcut menu. Choose **Activate**. The gray color  changes to the red color . See [Figure 3-10](#).
 - Click the valve symbol to select it. Set the Used parameter on the Properties pane to **True**.
- ### ❖ To deactivate the syringe pump
- Right-click in the pane to display the shortcut menu. Choose **Deactivate**. The red color changes to a gray color .
 - Click the valve symbol to select it. Set the Used parameter on the Properties pane to **False**.

❖ **To change the start position of the syringe pump**

- Right-click in the pane to display the shortcut menu. Depending on the active start position, choose **Start in ON** or **Start in OFF**. The pump changes its start position.
- Click the syringe symbol to select it. Depending on the active start position, set the Start in Off parameter on the Properties pane to **True** or **False**.

❖ **To add a switch position for the syringe pump**

1. Activate the syringe pump as described above.
2. Do one of the following:
 - Use the mouse:
 - a. Move the mouse pointer to the position on the time line where you want to establish a switch position (5 minutes, for example).
 - b. Right-click in the pane to display the shortcut menu. Choose **Add switch at 5.00**.
 - Use the Properties pane:
 - a. Click the syringe symbol to select it.
 - b. Set the Switch count parameter on the Properties pane to **1**.

A step in the line of the graphic representation indicates the new switch point. See [Figure 3-10](#).

3. To change the time of the switch position, do one of the following:
 - Drag the step that indicates the switch position to the new time.
 - On the Properties pane, set the At parameter of the respective Element to the new time.

❖ **To delete a switch position**

1. Move the mouse pointer to the switch position on the time line (at 5 minutes, for example).
2. Right-click in the pane to display the shortcut menu. Choose **Remove switch at 5.00**.

Contact Closure

The Contact Closure item shows a graphic representation of the contact closure activities during the active acquisition. See [Figure 3-11](#).

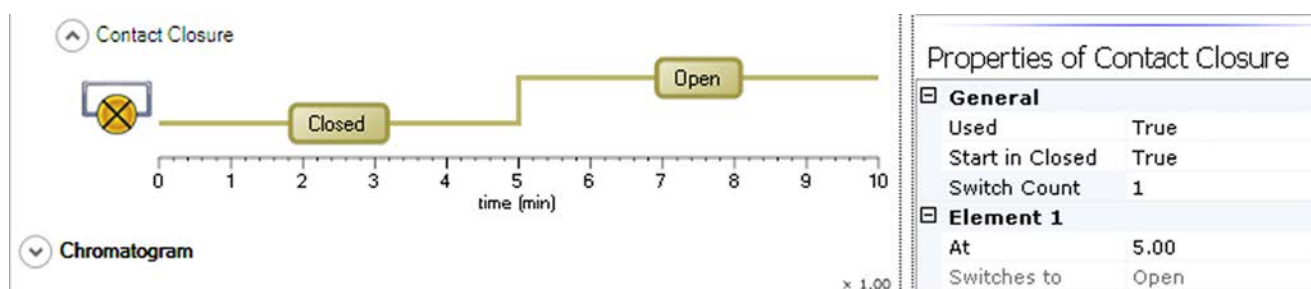


Figure 3-11. Contact closure

The settings of the Contact Closure item control the signals that the mass spectrometer transmits via the port labeled *Start Out* at its peripheral control output connection.

❖ To display this view

On the External Hardware pane, expand the Contact Closure item.

Use the shortcut menu of the Contact Closure item and the parameters of its Properties pane to control the contact closure activities:

❖ To activate the contact closure

- Right-click in the pane to display the shortcut menu. Choose **Activate**. The gray color  changes to the green color . See [Figure 3-11](#).
- Click the contact closure symbol to select it. Set the Used parameter on the Properties pane to **True**.

❖ To deactivate the contact closure

- Right-click in the pane to display the shortcut menu. Choose **Deactivate**. The green color changes to a gray color .
- Click the contact closure symbol to select it. Set the Used parameter on the Properties pane to **False**.

❖ To change the start position of the contact closure

- Right-click in the pane to display the shortcut menu. Depending on the active start position, choose **Start in Open** or **Start in Closed**. The contact closure changes its start position.

- Click the contact closure symbol to select it. Depending on the active start position, set the Start in Closed parameter on the Properties pane to **True** or **False**.

❖ **To add a switch position for the contact closure**

1. Activate the contact closure as described above.
2. Do one of the following:
 - Use the mouse:
 - a. Move the mouse pointer to the position on the time line where you want to establish a switch position (5 minutes, for example).
 - b. Right-click in the pane to display the shortcut menu. Choose **Add switch at 5.00**.
 - Use the Properties pane:
 - a. Click the contact closure symbol to select it.
 - b. Set the Switch count parameter on the Properties pane to **1**.

A step in the line of the graphic representation indicates the new switch point. See [Figure 3-10](#).

3. To change the time of the switch position, do one of the following:
 - Drag the step that indicates the switch position to the new time.
 - On the Properties pane, set the At parameter of the respective Element to the new time.

❖ **To delete a switch position**

1. Move the mouse pointer to the switch position on the time line (at 5 minutes, for example).
2. Right-click in the pane to display the shortcut menu. Choose **Remove switch at 5.00**.

Chromatogram

The chromatogram display shows the chromatogram for the selected raw file. See [Figure 3-12](#). If you have previously obtained a raw file (*.raw) of the chromatographic component separation, you can open this file.

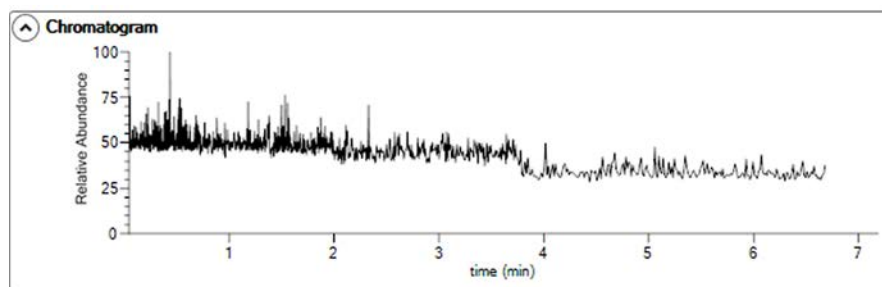


Figure 3-12. Chromatogram Display

❖ To display a chromatogram

1. In the Properties of Chromatogram pane, click into the empty field of the Rawfile parameter to display the  button. See [Figure 3-13](#).

Properties of Chromatogram



Figure 3-13. Selecting a rawfile

2. Click the  button to open a dialog box where you can browse for the raw file.
3. Select the raw file.
4. If available, select a scan filter.
5. Select a trace type. See [Figure 3-7](#).

Properties of Chromatogram

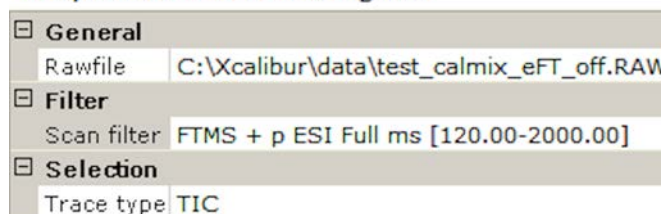


Figure 3-14. Properties of Chromatogram

The software updates the chromatogram immediately after a change.

❖ **To zoom on the chromatogram**

- Position the mouse pointer within the time axis area and drag the mouse across the time area of interest.
- To zoom in, position the mouse pointer within the chromatogram and roll the mouse wheel forward.
- To zoom out, roll the wheel backward.
- To increase the zooming factor by two, keep the <Shift> key pressed while using the mouse wheel.

❖ **To unzoom the chromatogram**

Right-click in the Scan Groups pane to display the shortcut menu. Choose **Unzoom**.

The chromatogram is also zoomed when the time axis of the Scan Groups is zoomed.

❖ **To display this view**

On the External Hardware pane, expand the Chromatogram item.

Scan Groups

In the Scan Groups pane, time bars represent the scan events during the acquisition. See [Figure 3-15](#). The Scan Groups pane is filled when you drag experiment symbols from the Experiment pane to the Graph pane.

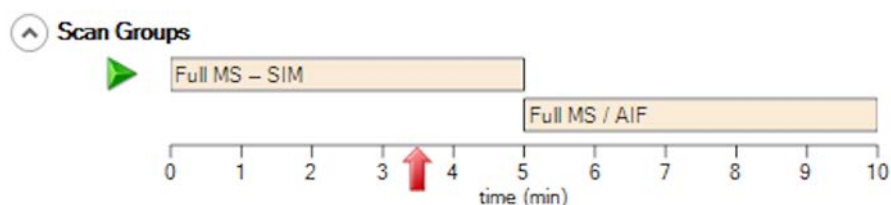


Figure 3-15. Scan Groups

Use the Properties pane of a scan event to control the activities during individual experiments. Red triangles (▶) to the left side of a time bar indicate active scan events.

❖ **To display the active scan events at a certain time**

Click the time line at the position. A red arrow (↑) indicates the selected time. A green triangle (▶) to the left side of the time bar indicates the active scan event. If scan events overlap at the selected time, green triangles appear for each active scan event. The bottom part of the Properties pane shows the parameters for the selected scan event.

❖ **To change start and end time of a scan event**

- Drag the left and right edges of the time bar to the desired positions on the time line.
- Enter the times in the Minimum and Maximum boxes of the runtime parameter on the Properties pane.

❖ **To zoom on the Scan Groups pane**

- Position the mouse pointer within the time axis area and drag the mouse across the time area of interest.
- To zoom in, position the mouse pointer within the pane and roll the mouse wheel forward.
- To zoom out, roll the wheel backward.
- To increase the zooming factor by two, keep the <Shift> key pressed while using the mouse wheel.

❖ **To unzoom the Scan Groups pane**

Right-click in the pane to display the shortcut menu. Choose **Unzoom**.

The Scan Groups pane is also zoomed when the time axis of the chromatogram display is zoomed.

❖ **To display this view**

On the External Hardware pane, expand the Scan Groups item.

Experiment Pane

The Experiment pane is located on the bottom left side of the Experiment Setup page. It gives access to predefined experiment templates. You cannot delete the experiment templates. You cannot combine experiment templates from different folders.

Every single experiment is associated with a descriptive icon. This icon can be dragged from the Experiment pane to the Graph pane. When selected, the icon gives an overview to the operator, which experiment and which associated options are active currently. Therefore, this icon changes dependent on the settings. Use the Properties pane to specify the values for your experiment parameters.

Tip Licenses installed on your instrument may affect the number of available experiments and the parameters used by them.

General Experiment Templates

The General folder contains predefined templates for experiments. See [Figure 3-16](#).

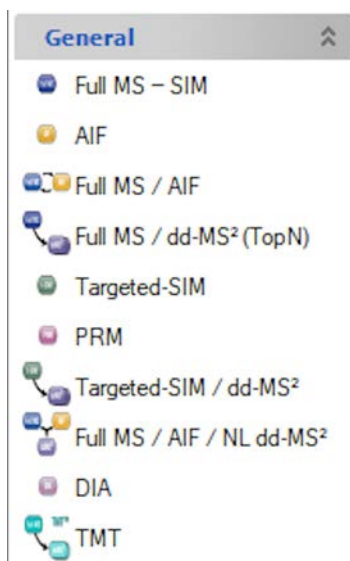


Figure 3-16. Available general templates

The Experiment Setup page allows using several system templates in an instrument method.

HMR Experiment Templates

The HMR folder contains predefined templates for experiments to be performed in High Mass Range (HMR) mode. See [Figure 3-17](#). This folder is available only on systems with a valid High Mass Range license.



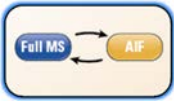
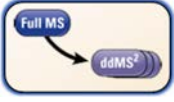
Figure 3-17. Available HMR templates

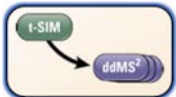
The Experiment Setup page allows using only one HMR template in an instrument method.

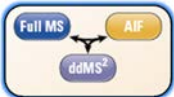
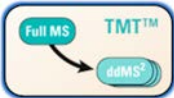
Tip An HMR Experiment can only be run with a tune file that was saved while HMR mode was active.

Experiment Symbols

The following experiment templates are available on the Experiment pane. Click the experiment symbol in the table to display an overview of the available parameters and values, which are displayed on the [Properties Pane](#).

Template	Experiment Symbol	Description
General Experiment Templates		
Full MS – SIM		This experiment comprises a full MS scan or SIM scan without HCD fragmentation. Special features: Segmented Master Scans
AIF		This All Ion Fragmentation (AIF) experiment will acquire MS/MS fragment scans with a wide isolation range. The set m/z range defines the quadrupole isolation as well as the analyzer detection window. Special features: Stepped Collision Energy (NCE)
Full MS / AIF		This experiment* comprises a full MS scan (without collision energy) followed by an AIF-scan (with a collision energy applied). Ions of the second scan event enter the HCD cell, ions of the first do not. Special features: Stepped Collision Energy (NCE) *This experiment is not available on systems with a valid High Mass Range license.
Full MS / dd-MS ² (TopN)		This experiment comprises a full MS scan (without collision energy) followed by a set of Data Dependent™ scans with a collision energy applied. Ions of the second scan event enter the HCD collision cell, ions of the first do not. Special features: - Auto value option: Dynamic Exclusion^a - Segmented Master Scans - Spectral Multiplexing (MSX) - Stepped Collision Energy (NCE) Tip Filters for triggering Data Dependent scans are listed under dd Settings.

Template	Experiment Symbol	Description
Targeted-SIM		This experiment acquires Single Ion Monitoring (SIM) scans depending on the entries of the global inclusion list, which is therefore mandatory and always activated. The mandatory inclusion list will be processed from first to last row without any automated sorting. Inclusion list entries with overlapping isolation windows are not multiplexed in the same scan event. Special features: - Spectral Multiplexing (MSX) - Inclusion list entries with overlapping isolation windows are not multiplexed in the same scan event. Here, triggering the second inclusion list candidate will be deferred to the next MSX scan event. - Use MSX ID of the inclusion list for user-defined sorting of single entries or user-defined multiplexing.
PRM		This Parallel Reaction Monitoring (PRM) experiment comprises MS/MS scans depending on the entries of the inclusion list. The mandatory inclusion list will be processed from first to last row without any automated sorting. Special features: - Spectral Multiplexing (MSX) - Stepped Collision Energy (NCE)
Targeted-SIM / dd-MS ²		This experiment comprises a targeted-SIM scan on precursor ions followed by a set of Data Dependent triggered MS/MS scans. Special features: - Auto value option: Dynamic Exclusion^a - Spectral Multiplexing (MSX) - Stepped Collision Energy (NCE) Tip Filters for triggering Data Dependent scans are listed under dd Settings.

Template	Experiment Symbol	Description
Full MS / AIF / NL dd-MS ²		This experiment* comprises a full MS scan followed by an All Ion Fragmentation (AIF) scan. When a user-defined <i>m/z</i> loss is recognized between one signal in the full MS scan and one signal in the subsequent AIF scan, a Data Dependent MS/MS scan will be triggered on the precursor ion of the full MS scan. The global Neutral Loss list is mandatory for this experiment. Special features: • Auto value option: Dynamic Exclusion^a • Spectral Multiplexing (MSX) • Stepped Collision Energy (NCE) *This experiment is available only when HMR mode and Protein mode are set to Off in the Tune file.
DIA		This Data Independent Acquisition (DIA) experiment covers the scan range by targeted HCD events with isolation windows defined in the inclusion list, which can also be acquired in multiplexing mode. The mandatory inclusion list will be processed from first to last row without any automated sorting. Special features: • Spectral Multiplexing (MSX) • Stepped Collision Energy (NCE) Tip Per multiplexed DIA scan event, isochronous injection times are used.
TMT		This Tandem Mass Tags (TMT) experiment comprises a full MS scan (without collision energy) followed by a set of Data Dependent™ scans with a collision energy applied. Ions of the second scan event enter the HCD collision cell, ions of the first do not. In contrast to all other experiments, Advanced Peak Detection is switched off. Special features: • Auto value option: Dynamic Exclusion^a • Segmented Master Scans • Spectral Multiplexing (MSX) • Stepped Collision Energy (NCE) Tip Filters for triggering Data Dependent scans are listed under dd Settings.

Template	Experiment Symbol	Description
HMR		
The parameter ranges of these experiments are modified to allow measuring intact proteins and protein complexes up to m/z 8000 under native/non-denaturing conditions. These experiments are available only on systems with a valid High Mass Range license.		
HMR - Full MS		The HMR - Full MS is an experiment to acquire full MS scans.
HMR - AIF		The HMR - AIF is an experiment to acquire HCD MS scans.

^aAuto value options: Depending on the experiment type, properties like “Dynamic Exclusion” can be set automatically by the software, dependent on the chromatographic peak width (FWHM).

Graph Pane

The Graph pane is located at the middle bottom side of the Experiment Setup window. It shows a graphic representation of the experiment during the acquisition. See [Figure 3-18](#).

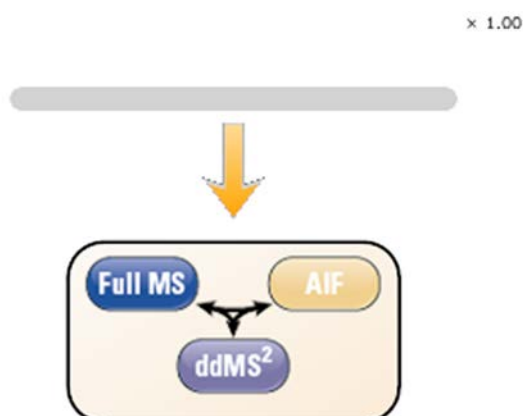


Figure 3-18. Graphic representation of the experiment

❖ To add an experiment to the active method

- Do one of the following:
 - Double-click an experiment symbol on the Experiment pane.
 - Drag an experiment symbol from the Experiment pane to the gray bar in the Graph pane.

In Xcalibur, the Scan Groups pane shows a corresponding time bar for each symbol.

- Use the Properties pane of an experiment to control the activities during individual experiments.

❖ **To delete an experiment**

1. Right-click the experiment symbol to display the shortcut menu.
2. Choose **Delete this <Name of Experiment>**.

❖ **To zoom in or out on the Graph pane**

- Position the mouse pointer within the pane and roll the mouse wheel forward to zoom in.
- Roll the wheel backward to zoom out.

The zoom factor ranges from 0.25 to 2. The actual zoom factor is displayed in the top right corner of the Graph pane.

Properties Pane

The Properties pane is located at the right side of the Experiment Setup page. See [Figure 3-19](#).

Properties	
Properties of the method	
Global Settings	
User Role	Standard
Use lock masses	best
Chrom. peak width (FWHM)	15 s
Time	
Method duration	10.00 min
Properties of Full MS — SIM	
General	
Runtime	0 to 10 min
Polarity	positive
Full MS — SIM	
Resolution	120,000
AGC target	3e6
Maximum IT	200 ms
Scan range	150 to 2000 m/z

Figure 3-19. Properties pane

The pane consists of two parts:

- [Properties of the Method](#)

The upper part is always available. It shows the properties of the active method.

The lower part depends on the item that is selected on the left side of the Experiment Setup page. One of the following tables is displayed:

- [Properties of Tunefiles](#)

The table shows the properties of the tune files selected in the Global Settings pane.

- [Properties of Divert Valve A / Divert Valve B](#)

The table shows the properties of the switching valve selected in the Global Settings pane.

- [Properties of Syringe](#)

The table shows the properties of the syringe pump selected in the Global Settings pane.

- [Properties of Contact Closure](#)

The table shows the properties of the contact closure selected in the Global Settings pane.

- The table shows the parameters for the experiment symbol selected in the Graph pane:

- [Properties of Full MS – SIM](#)
- [Properties of AIF](#)
- [Properties of Full MS / AIF](#)
- [Properties of Full MS / dd-MS² \(TopN\)](#)
- [Properties of Targeted-SIM](#)
- [Properties of PRM](#)
- [Properties of Targeted-SIM / dd-MS²](#)
- [Properties of Full MS / AIF / NL dd-MS²](#)
- [Properties of DIA](#)
- [Properties of TMT](#)

The following experiments are available only for systems with a valid High Mass Range license:

- [Properties of HMR - Full MS](#)
- [Properties of HMR - AIF](#)

Properties of the Method

The properties of the method include the following parameters:

Parameter	Description
Global Settings	
User Role	Use this field to specify whether the advanced parameters for scan events are displayed or not. To show the advanced parameters, set the field to Advanced . To hide the advanced parameters, set the field to Standard . Double-click into the field to change the status.
use lock masses	Use the list box to specify how lock masses are used in the active instrument method. The following options are available: - off No lock masses are used. - best Only the most intense lock mass of the global list that is found in the spectrum is used for a calibration. - if all present Lock masses are used only when all active masses of the global lock mass list are present at the same time. If timed lock masses are used, the mass spectrometer takes into account only those lock masses whose time windows cover the current retention time.
Lock mass injection ^a	If lock masses are used in the active instrument method, use this field to select the scan types for which lock mass will be additionally injected. The mass spectrometer will inject all lock masses of the active lock mass list to provide additional signals to improve mass accuracy. The decision whether found lock masses will be used for the mass correction is not affected and depends on the settings for the “use lock masses” parameter. Enter the scan types manually by using commas as separators for the strings. Or, click the down arrow to display a dialog box and select the corresponding check boxes. The following options are available: - Full MS - MS² - SIM

Parameter	Description
Chrom. peak width (FWHM)	Use this box to specify the estimated or determined chromatographic peak width at full width half maximum for the user's chromatographic setup. Based the value in this field, the mass spectrometer may calculate the values of other parameters to optimize the settings for HPLC or UHPLC if they are set to Auto: - Automatic pre-scanning for AGC AGC information will be updated automatically with a high frequency, when setting a lower FWHM (for fast chromatography) - Dynamic exclusion To change the peak width, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter the time in the spin box text field. The valid range for the peak width is from 1 to 10000 seconds.
Time	
Method duration	Use this box to specify the total mass spectrometer acquire time, in minutes, for the run. Q Exactive HF-X Tune rescales the Segments bar to correspond to the specified acquire time. To change the time, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter the time in the spin box text field. The valid range for the time is from 0.1 to 10000 minutes.
Customized Tolerances (+/-)^a	
Lock Masses Inclusion Exclusion Neutral Loss Mass Tags Dynamic Exclusion	Use the boxes in this group to adjust mass tolerances for global lists in different instrument methods. The tolerance can be set independently for each list type. The setting for Neutral Loss tolerances refers to the reference m/z and not to the mass difference $\Delta m/z$. To change a tolerance, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter the tolerance in the spin box text field. Available options are: – (use instrument default) 0.1–1000 ppm 0.1–50000 mmu When you directly enter a tolerance in the text field, you can use additional units. The software will convert it to ppm or mmu depending of its nature (absolute or relative definition). Accepted units are (for absolute definition: Da, Th, u, mmu; for a relative definition: ppt, ppb, ppm, %). An empty property value field as well as a set value of 0, -, or off will result in using the instrument default (displayed as -).

^aThis parameter is not available when User Role is set to **Standard**.

Properties of Tunefiles

The properties of the Tune Files item include the following parameters:

Parameter	Description
General	
Switch Count	Use this spin box to enter the number of switch positions that are to occur during a run. The valid range of positions is 0 through 50. Entering “0” results in the switch remaining either On or Off throughout the run. Enter a number between “1” and “50” to change the state from Off to On or On to Off at multiple specified times during a run. The number of positions on the Retention Time bar corresponds to the number of switch positions you specify using this spin box. When you enter a number different from 0, a corresponding number of Element parameter groups is displayed on the Properties pane.
Base Tunefile	Use this box to specify the current tune method file. To change the tune method file, click the button next to the box and browse for the new tune method file. A red dot in the left column indicates that no tune file is selected.
Elementn ($n=1-50$)	
Use the parameters of the Element groups to specify properties for the active item during individual switching events. The displayed parameters depend on the active item.	
At	Use this spin box to specify the time of the switching event. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
New Tunefile	Use this box to specify the tune method file for the new element. To change the tune method file, click the button next to the box and browse for the new tune method file. A red dot in the left column indicates that no tune file is selected.

❖ To show this view

Click the Tunefiles symbol in the Global Settings pane.

Properties of Divert Valve A / Divert Valve B

The properties of a switching valve include the following parameters:

Parameter	Description
General	
Used	Use this field to specify whether the switching valve is used during the acquisition or not. To use the switching valve, set the field to True . To not use the switching valve, set the field to False . Double-click into the field to change the status.

Parameter	Description
Start in 1-2	Use this field to specify whether the initial position of the switch at the start of a run is 1-2 or 1-6. To start the switching valve in position 1-2, set the field to True . To start the switching valve in position 1-6, set the field to False . Double-click into the field to change the status.
Switch Count	Use this spin box to enter the number of switch positions that are to occur during a run. The valid range of positions is 0 through 50. Entering “0” results in the switch remaining either On or Off throughout the run. Enter a number between “1” and “50” to change the state from Off to On or On to Off at multiple specified times during a run. The number of positions on the Retention Time bar corresponds to the number of switch positions you specify using this spin box.
Element n ($n=1-50$)	
Use the parameters of the Element groups to specify properties for the active item during individual switching events. The displayed parameters depend on the active item.	
At	Use this spin box to specify the time of the switching event. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
Switches to	This display field shows the status to which the contact closure is switched.

❖ **To show this view**

Click the Divert Valve a / Divert Valve b symbol in the External Hardware pane.

Properties of Syringe

The properties of the Syringe item include the following parameters:

Parameter	Description
General	
Used	Use this field to specify whether the syringe pump is used during the acquisition or not. To use the syringe pump, set the field to True . To not use the syringe pump, set the field to False . Double-click into the field to change the status.
Start in Off	Use this field to specify whether the initial state of the switch at the start of a run is On or Off. To start the acquisition with the syringe pump in Off status, set the field to True . To start the acquisition with the syringe pump in On status, set the field to False . Double-click into the field to change the status.
Stop at end of run	Use this field to have the mass spectrometer turn the syringe pump off when the run is completed. To turn the syringe pump off, set the field to True . To not have the mass spectrometer turn the syringe pump off after the run, set the field to False . Double-click into the field to change the status.

Parameter	Description
Switch Count	Use this spin box to enter the number of switch positions that are to occur during a run. The valid range of positions is 0 through 50. Entering “0” results in the switch remaining either On or Off throughout the run. Enter a number between “1” and “50” to change the state from Off to On or On to Off at multiple specified times during a run. The number of positions on the Retention Time bar corresponds to the number of switch positions you specify using this spin box.
Pump Setup	
Use the settings in this area to specify the syringe type and flow rate of the syringe pump.	
Syringe type	Use this list box to specify the syringe type (Hamilton, Unimetrics, or Other). If you select Hamilton or Unimetrics , you must specify the volume of the syringe in the Volume list box. If you select Other , you must specify the inside diameter of the syringe in the Inner diameter spin box.
Flow Rate	Use this spin box to set the volume of solvent solution passing through the syringe pump per unit time. The acceptable range of values depends on the selected syringe diameter. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
Inner diameter	Use this spin box to specify the inside diameter for syringes other than Hamilton and Unimetrics syringes. The acceptable range of values is 0.1 to 35 mm. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
Volume (µL)	Use this list box to specify the syringe volume for Hamilton and Unimetrics syringes. The acceptable values depend on the syringe type: - Hamilton: 0.5, 1, 2, 5, 10, 25, 50, 100, 250, and 500 µL. - Unimetrics: 10, 25, 50, 100, 250, 500, 1000, 2500, 5000, 10000, 25000, and 50000 µL.
Element n ($n=1-50$)	
Use the parameters of the Element groups to specify properties for the active item during individual switching events. The displayed parameters depend on the active item.	
At	Use this spin box to specify the time of the switching event. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
Switches to	This display field shows the status to which the syringe pump is switched.

❖ **To show this view**

Click the Syringe symbol in the External Hardware pane.

Properties of Contact Closure

The properties of the Contact Closure item include the following parameters:

Parameter	Description
General	
Used	Use this field to specify whether a timed contact closure program is used in an experiment method or not. To use the contact closure, set the field to True . To not use the contact closure, set the field to False . Double-click into the field to change the status.
Start in Closed	Use this field to specify whether the initial status of the contact closure at the start of a run is On or Off. To start the acquisition with the syringe pump in Closed status, set the field to True . To start the acquisition with the contact closure in Open status, set the field to False . Double-click into the field to change the status.
Switch Count	Use this spin box to select the number of switch positions that are to occur during a run. The valid range of positions is 0 through 50. Selecting “0” results in the switch remaining either Closed or Open throughout the run. Selecting a number between “1” and “50” allows you to change the state from Closed to Open or Open to Closed at multiple specified times during a run. The number of positions on the Retention Time bar corresponds to the number of switch positions you specify using this spin box.
Element n ($n=1-50$)	
Use the parameters of the Element groups to specify properties for the active item during individual switching events. The displayed parameters depend on the active item.	
At	Use this spin box to specify the time of the switching event. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
Switches to	This display field shows the status to which the contact closure is switched.

❖ To show this view

Click the Contact Closure symbol in the External Hardware pane.

Properties of Chromatogram

The properties of the Chromatogram item include the following parameters:

Parameter	Description
General	
Rawfile	Use this field to select a previously obtained raw data file corresponding to a similar chromatographic separation. Click the button next to the box and browse for the raw file. A red dot in the left column indicates that no raw file is selected.
Filter	
Scan filter	Use this field to select a scan description that tells the data system how to filter the raw data.
Selection	
Trace type	Use this field to select a chromatogram plot type. The software updates the chromatogram immediately after a change. The following options are available: • TIC Plots the sum of all the ion intensities. • Neutral Fragment Plots the sum of the ion intensities of the ions that produce a neutral fragment with a mass specified in the Neutral Fragment spin box. • Base Peak Plots the ion intensity of the most intense ion in the chromatogram. • Mass Range Plots the sum of the ion intensities only for ions in the mass range or ranges specified in the Range(s) box.
Neutral Fragment	This field is available when you have selected Neutral Fragment as trace type. To enter the m/z value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
Mass Ranges	Use this field to specify the range or ranges of mass-to-charge ratios (m/z) that the mass spectrometer can analyze. Use a dash (-) to separate the low and high masses of a range. Use a comma (,) to separate ranges. This field is not available when you have selected TIC as trace type.
Mass Tolerance	
Tolerance	For Neutral Fragment, Mass Range, and Base Peak plot types, use the spin box to specify the value of the mass tolerance. Enter a value in the range from 0 to 2000 and select the appropriate option in the Units field. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
Unit	Use this field to select the units that are used in processing the raw file. Select either the mmu (millimass units) option or the ppm (parts per million) option.

❖ **To show this view**

Click the Chromatogram symbol in the External Hardware pane.

Properties of Full MS – SIM

The properties of a Full MS – SIM experiment include the following parameters:

Parameter	Description
General	
Runtime	Use this box to specify the duration in minutes of the active scan event. Click into the field to display the spin boxes for the start time (Minimum) and the end time (Maximum) of the scan event. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range for the start time is from 0 to (end time minus 0.01) minutes. The valid range for the end time is from (start time plus 0.01) to 10000 minutes. Or, drag the left and right edges of the corresponding time bar to the desired positions on the time line in the Scan Groups pane.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity.
In-source CID ^a	Use this spin box to enter the in-source CID collision energy. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the CID collision energy to any value from 0 to 100 eV. A value of 0 eV means that the collision energy is switched off.
Full MS – SIM	
Use the parameters in this group to specify the properties of the master scan(s).	
Microscans ^a	Use this spin box to select the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.

Parameter	Description
Number of scan ranges ^a	Use this spin box to enter the number of segments in a segmented master scan. The segments can be defined independently from each other. They can be used to get a better S/N for specific areas and exclude matrix signals. The m/z ranges are acquired one after another and will result one scan for each range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. The valid range is from 1 to 8 scans.
Scan range n ($n=1-8$)	Use the spin boxes in this field to set values (in mass-to-charge ratio units) for Minimum, Maximum, Center, and Width for the current scan range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. • Minimum Select the minimum value for the scan range. You can enter any value from 50.0 to 2500.0. • Maximum Select the maximum value for the scan range. You can enter any value from 50.4 to 6000.0. • Center Select the center mass of the scan range. You can enter any value from 50.2 to 4250.0. • Width Select the width of the scan range. You can enter any value from 0.4 to 5600.0. The actual possible values are interdependent. For Minimum, the highest value is Maximum – 0.4. For Maximum, the lowest value is Minimum + 0.4 and the highest value is Minimum × 15.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.

^aThis parameter is not available when User Role is set to **Standard**.

❖ To show this view

Click the Full MS symbol in the Graph pane.

Properties of AIF

The properties of an AIF experiment include the following parameters:

Parameter	Description
General	
Runtime	Use this box to specify the duration in minutes of the active scan event. Click into the field to display the spin boxes for the start time (minimum) and the end time (maximum) of the scan event. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range for the start time is from 0 to (end time minus 0.01) minutes. The valid range for the end time is from (start time plus 0.01) to 10000 minutes. Or, drag the left and right edges of the corresponding time bar to the desired positions on the time line in the Scan Groups pane.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity.
In-source CID ^a	Use this spin box to enter the in-source CID collision energy. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the CID collision energy to any value from 0 to 100 eV. A value of 0 eV means that the collision energy is switched off.
AIF	
Microscans ^a	Use this spin box to select the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.

Parameter	Description
(N)CE / Stepped (N)CE	Use this box to specify either the absolute collision energy (CE) in eV or the normalized collision energy (NCE). The latter is a dimensionless number that is approximately equivalent to the HCD collision energy (in eV) for a reference ion of mass 500 and charge 1. The actual HCD energy is calculated on basis of mass and charge of either the selected precursor ion (Data Dependent MS2 or AIF scans) or the center mass of an isolation window (targeted MS2 or AIF scans). Specify whether absolute collision energy (CE) or normalized collision energy (NCE) is used. In the box, the software adds the prefix “ce:” or “nce:” to collision energy values (for example, ce:35) to indicate the selected energy type. If more than one value is entered, the mass spectrometer will perform a stepwise fragmentation on the precursor ion. All fragments created in the steps are collected and sent to the Orbitrap analyzer for one scan detection. Enter up to three values manually separated by blanks or the locally defined “list separator” (defined for Microsoft™ Windows™ via the „Region and Language“ settings). Or, click the down arrow to display a dialog box and select the corresponding number of check boxes. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 10 to 200.
Scan range	Use the spin boxes in this field to set values (in mass-to-charge ratio units) for Minimum, Maximum, Center, and Width for the current scan range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. • Minimum Select the minimum value for the scan range. You can enter any value from 50.0 to 2500.0. • Maximum Select the maximum value for the scan range. You can enter any value from 50.4 to 6000.0. • Center Select the center mass of the scan range. You can enter any value from 50.2 to 4250.0. • Width Select the width of the scan range. You can enter any value from 0.4 to 5600.0. The actual possible values are interdependent. For Minimum, the highest value is Maximum – 0.4. For Maximum, the lowest value is Minimum + 0.4 and the highest value is Minimum × 15.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.

^aThis parameter is not available when User Role is set to **Standard**.

❖ To show this view

Click the AIF symbol in the Graph pane.

Properties of Full MS / AIF

The properties of a Full MS / AIF experiment include the following parameters:

Parameter	Description
General	
Runtime	Use this box to specify the duration in minutes of the active scan event. Click into the field to display the spin boxes for the start time (minimum) and the end time (maximum) of the scan event. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range for the start time is from 0 to (end time minus 0.01) minutes. The valid range for the end time is from (start time plus 0.01) to 10000 minutes. Or, drag the left and right edges of the corresponding time bar to the desired positions on the time line in the Scan Groups pane.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity.
In-source CID ^a	Use this spin box to enter the in-source CID collision energy. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the CID collision energy to any value from 0 to 100 eV. A value of 0 eV means that the collision energy is switched off.
Full MS	
Use the parameters in this group to specify the properties of the master scan(s).	
Microscans ^a	Use this spin box to select the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.

Parameter	Description
Scan range	Use the spin boxes in this field to set values (in mass-to-charge ratio units) for Minimum, Maximum, Center, and Width for the current scan range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. • Minimum Select the minimum value for the scan range. You can enter any value from 50.0 to 2500.0. • Maximum Select the maximum value for the scan range. You can enter any value from 50.4 to 6000.0. • Center Select the center mass of the scan range. You can enter any value from 50.2 to 4250.0. • Width Select the width of the scan range. You can enter any value from 0.4 to 5600.0. The actual possible values are interdependent. For Minimum, the highest value is Maximum – 0.4. For Maximum, the lowest value is Minimum + 0.4 and the highest value is Minimum × 15.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.
AIF	
Microscans ^a	Use this spin box to select the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.

Parameter	Description
(N)CE / Stepped (N)CE	Use this box to specify either the absolute collision energy (CE) in eV or the normalized collision energy (NCE). The latter is a dimensionless number that is approximately equivalent to the HCD collision energy (in eV) for a reference ion of mass 500 and charge 1. The actual HCD energy is calculated on basis of mass and charge of either the selected precursor ion (Data Dependent MS2 or AIF scans) or the center mass of an isolation window (targeted MS2 or AIF scans). Specify whether absolute collision energy (CE) or normalized collision energy (NCE) is used. In the box, the software adds the prefix “ce:” or “nce:” to collision energy values (for example, ce:35) to indicate the selected energy type. If more than one value is entered, the mass spectrometer will perform a stepwise fragmentation on the precursor ion. All fragments created in the steps are collected and sent to the Orbitrap analyzer for one scan detection. Enter up to three values manually separated by blanks or the locally defined “list separator” (defined for Microsoft™ Windows™ via the „Region and Language“ settings). Or, click the down arrow to display a dialog box and select the corresponding number of check boxes. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 10 to 200.
Scan range	Use the spin boxes in this field to set values (in mass-to-charge ratio units) for Minimum, Maximum, Center, and Width for the current scan range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. • Minimum Select the minimum value for the scan range. You can enter any value from 50.0 to 2500.0. • Maximum Select the maximum value for the scan range. You can enter any value from 50.4 to 6000.0. • Center Select the center mass of the scan range. You can enter any value from 50.2 to 4250.0. • Width Select the width of the scan range. You can enter any value from 0.4 to 5600.0. The actual possible values are interdependent. For Minimum, the highest value is Maximum – 0.4; it cannot exceed the Minimum value for the Full MS scan range. For Maximum, the lowest value is Minimum + 0.4 and the highest value is Minimum × 15.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.

^aThis parameter is not available when User Role is set to **Standard**.

❖ To show this view

Click the Full MS / AIF symbol in the Graph pane.

Properties of Full MS / dd-MS² (TopN)

The properties of a Full MS / dd-MS² experiment include the following parameters:

Parameter	Description
General	
Runtime	Use this box to specify the duration in minutes of the active scan event. Click into the field to display the spin boxes for the start time (minimum) and the end time (maximum) of the scan event. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range for the start time is from 0 to (end time minus 0.01) minutes. The valid range for the end time is from (start time plus 0.01) to 10000 minutes. Or, drag the left and right edges of the corresponding time bar to the desired positions on the time line in the Scan Groups pane.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity.
In-source CID ^a	Use this spin box to enter the in-source CID collision energy. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the CID collision energy to any value from 0 to 100 eV. A value of 0 eV means that the collision energy is switched off.
Default charge state	Use this box to specify the default charge state for Data Dependent scans. The mass spectrometer uses the charge state to determine the highest mass-to-charge ratio and HCD energy for the Data Dependent MSⁿ scan. If the mass spectrometer cannot determine the charge state from the preceding scan, it uses the default charge state that you specify here. The valid range for the default charge state is 1 through 100. The default charge state is 2. For typical applications, a charge state of +2 is suitable for tryptic digests in which the peptide has a charge state of +2. If you are running a different experiment, you might want to change the default to a more appropriate value.
Inclusion	Use this field to enable the inclusion masses list that is attached to the active instrument method. Available options are on (inclusion list enabled) and – (inclusion list disabled). Default setting is –.
Exclusion	Use this field to enable the exclusion masses list that is attached to the active instrument method. Available options are on (exclusion list enabled) and – (exclusion list disabled). Default setting is –.
Tags	Use this field to enable the tag masses list for the active instrument method. Available options are on (list enabled) and – (list disabled). Default setting is –.
Full MS	
Microscans ^a	Use this spin box to enter the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.

Parameter	Description
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.
Number of scan ranges ^a	Use this spin box to enter the number of segmented master scans. Segmented master scans can be defined independently from each other. They can be used to get a better S/N for specific areas and exclude matrix signals. The scan ranges are acquired one after another and will result one scan for each range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. The valid range is from 1 to 8 scan ranges.
Scan range n ($n=1-8$)	Use the spin boxes in this field to enter values (in mass-to-charge ratio units) for Minimum, Maximum, Center, and Width for the current scan range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. - Minimum Select the minimum value for the scan range. You can enter any value from 50.0 to 2500.0. - Maximum Select the maximum value for the scan range. You can enter any value from 50.4 to 6000.0. - Center Select the center mass of the scan range. You can enter any value from 50.2 to 4250.0. - Width Select the width of the scan range. You can enter any value from 0.4 to 5600.0. The actual possible values are interdependent. For Minimum, the highest value is Maximum – 0.4. For Maximum, the lowest value is Minimum + 0.4 and the highest value is Minimum $\times$ 15.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.
dd-MS² / dd-SIM	
Microscans ^a	Use this spin box to enter the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.

Parameter	Description
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.
Loop count	Use this spin box to enter the number of repetitions of the corresponding scan event before continuing with the next scan event or experiment cycle. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no repetition) to 100 repetitions.
MSX count ^a	Use this spin box to enter the maximum number of precursors to be multiplexed in an scan event. In spectra multiplexing, multiple preselected precursors are collected in the C-Trap for simultaneous detection in the Orbitrap analyzer. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no spectral multiplexing) to 10 fillings.
TopN	This field displays the product of the selected values for Loop count and MSX count as maximum number of the most abundant precursors that will be selected.
Isolation window	Use this list box to enter the isolation width (in mass-to-charge ratio units) for the parent ion of interest. The mass range for the peak is centered at the parent mass and ranges one-half of the isolation width to either side of the parent mass. You can set the isolation window to any value from m/z 0.4 to 15 times the first mass of the Data Dependent scan. The default value is m/z 4.0. Too low a value results in loss of sensitivity because not all of the ions in a mass peak or in neighboring isotopic peaks are isolated. Too high a value causes interference from neighboring peaks.

Parameter	Description
Isolation offset ^a	Use this spin box to define an absolute offset by which the isolation window is shifted. The resulting window is non-symmetric with regard to the precursor m/z. Thus, more isotopes of a cluster might be covered, without the need of expanding the isolation window. Example: Precursor = m/z 524.265; Isolation window = 2.0 m/z; Isolation offset = +0.5 m/z; Resulting isolation window = m/z 523.765–525.765 To change the isolation offset, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the isolation offset to any value from m/z -50 to +50. Default is m/z 0.
Fixed first mass ^a	Use this box to specify whether to use a first mass of the Data Dependent scan. After an automated determination of the detection mass range, the first mass will be set to the defined fixed first mass. Because only masses up to 15 times the first mass can be trapped in the C-Trap, loss of ions in the upper detection range may occur. You can set Fixed first mass either to – (dynamic first mass) or to any m/z value between 50 and 2000. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Default is –.
(N)CE / Stepped (N)CE	Use this box to specify either the absolute collision energy (CE) in eV or the normalized collision energy (NCE). The latter is a dimensionless number that is approximately equivalent to the HCD collision energy (in eV) for a reference ion of mass 500 and charge 1. The actual HCD energy is calculated on basis of mass and charge of either the selected precursor ion (Data Dependent MS2 or AIF scans) or the center mass of an isolation window (targeted MS2 or AIF scans). Specify whether absolute collision energy (CE) or normalized collision energy (NCE) is used. In the box, the software adds the prefix “ce:” or “nce:” to collision energy values (for example, ce:35) to indicate the selected energy type. If more than one value is entered, the mass spectrometer will perform a stepwise fragmentation on the precursor ion. All fragments created in the steps are collected and sent to the Orbitrap analyzer for one scan detection. Enter up to three values manually separated by blanks or the locally defined “list separator” (defined for Microsoft™ Windows™ via the „Region and Language“ settings). Or, click the down arrow to display a dialog box and select the corresponding number of check boxes. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 10 to 200. Enter – for Data Dependent SIM scans.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.

Parameter	Description
dd Settings	
Use the parameters in this group to specify criteria for selecting one or more ions of interest on which to perform subsequent scans.	
Minimum AGC target	Use this box to specify a minimum value for the AGC target. If the mass peak of interest reaches this intensity within the Maximum IT, the mass spectrometer initiates a Data Dependent scan. Enter the value either as integer or in scientific notation with two decimal places (for example, 3.80e4) in the spin box text field. The valid range is from 0 to the value for the AGC target of the Data Dependent scan event.
Intensity threshold	This field displays the minimum intensity that a mass peak requires to initiate a Data Dependent scan.
Apex trigger	To obtain the highest quality data in the shortest period of time, it is best to defer data acquisition until near the apex of a chromatographic peak. Using the chromatographic peak apex detection provides numerous benefits for Data Dependent LC/MS/MS, including: • Improved MS/MS quality and signal levels • Shorter ion injection times • Reduced MS/MS acquisition of chemical background • Less dependence on static or dynamic exclusion lists • Reduced retriggering of scans on tailing chromatographic peaks Use this box to enter start (Minimum) and end (Maximum) of a retention time window in seconds relative to the occurrence of a precursor. If the mass spectrometer finds an apex within the window, it triggers a Data Dependent acquisition for the corresponding m/z or range of m/z. The mass spectrometer also triggers a Data Dependent scan when the end of the time window is reached without detecting an apex. The apex trigger always depends on other selection criteria (for example, intensity threshold). • Minimum Enter the minimum value for the time window (in seconds). You can enter any value from – (0) to 360. The default value is –. • Maximum Enter the maximum value for the time window (in seconds). You can enter any value from – (0) to 360 as long as it equals or exceeds the Minimum value. The default value is –.
Charge exclusion	Use the check boxes in this field to reject individual charge states or undetermined charge states as precursors for Data Dependent MS/MS scans. The following options are available: • – (charge exclusion disabled), • unassigned (charge state not determined) • 1–8 (at least one charge state is selected), • >8

Parameter	Description
Multiple charge states ^a	Use this field to decrease the number of redundant MS² spectra by limiting them to the most abundant charge state within a charge state distribution. All other criteria for dd-MS² properties must be met. The following options are available: • all (All charge states of a charge envelope are triggered.) • one charge state only (Only the most intense charge state of a charge envelope is triggered.)
Peptide match	Use this field to enable the mass spectrometer to select small molecules with peptide-like isotopic distributions for Data Dependent scanning. The mass spectrometer recognizes the monoisotopic mass of an isotopic distribution by comparing isotopic intensity ratios to typical peptide-like distributions. The following options are available: • on (peptide match enabled) • – (peptide match disabled) • preferred (peaks that are determined to belong to peptides are preferred and will be selected prior to those that are not, but still meeting all of the other Data Dependent filter criteria, for example, charge state and intensity) Default setting is preferred.
Exclude isotopes	Use this field to check whether the most intensive isotope of a cluster has been triggered in a Data Dependent scan event. All isotopes of that cluster will be then excluded. Available options are on (isotopes exclusion enabled) and – (isotopes exclusion disabled). Default setting is on. Isotopes exclusion is disabled for inclusion list entries.

Parameter	Description
Dynamic exclusion	Use this box to enter a time (in seconds) to prevent an ion from triggering a subsequent Data Dependent scan after it has already triggered a Data Dependent scan. The following input is possible: – (no dynamic exclusion) 0.1 to 50000 - auto [Dynamic exclusion = $2.5 \times \text{Chrom. peak width (FWHM)}$] Dynamic exclusion is valuable if the mass spectrometer has obtained enough data on an ion or if the base peak corresponds to a contaminant or an ion of non interest. If you enable dynamic exclusion, and if the mass spectrometer performs a Data Dependent scan on an ion, that ion is placed on the exclusion list (a temporary reject mass list) for a user-specified period of time. Then, when the mass spectrometer performs another Data Dependent scan on another ion, that ion is also placed on the exclusion list, and so on.
if idle	Use this field to select the behavior of the mass spectrometer when it has finished the Data Dependent scans that were triggered by a mass that meets the established criteria for Data Dependent actions. Available options are do not pick others and pick other. Default setting is do not pick others. This parameter is available only when at least one of the parameters Inclusion or Tags is set to on.

^aThis parameter is not available when User Role is set to **Standard**.

❖ To show this view

Click the Full MS / dd-MS² symbol in the Graph pane.

Properties of Targeted-SIM

The properties of a Targeted-SIM experiment include the following parameters:

Parameter	Description
General	
Runtime	Use this box to specify the duration in minutes of the active scan event. Click into the field to display the spin boxes for the start time (minimum) and the end time (maximum) of the scan event. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range for the start time is from 0 to (end time minus 0.01) minutes. The valid range for the end time is from (start time plus 0.01) to 10000 minutes. Or, drag the left and right edges of the corresponding time bar to the desired positions on the time line in the Scan Groups pane.

Parameter	Description
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity.
In-source CID ^a	Use this spin box to enter the in-source CID collision energy. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the CID collision energy to any value from 0 to 100 eV. A value of 0 eV means that the collision energy is switched off.
Inclusion	Because this experiment requires inclusion masses, this field is always set to on (inclusion list enabled).
SIM	
Microscans ^a	Use this spin box to enter the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.
Loop count	Use this spin box to enter the number of repetitions of the corresponding scan event before continuing with the next scan event or experiment cycle. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no repetition) to 100 repetitions.
MSX count ^a	Use this spin box to enter the maximum number of precursors to be multiplexed in an scan event. In spectra multiplexing, multiple preselected precursors are collected in the C-Trap for simultaneous detection in the Orbitrap analyzer. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no spectral multiplexing) to 10 fillings.
Isolation window	Use this list box to enter the isolation width (in mass-to-charge ratio units) for the parent ion of interest. The mass range for the peak is centered at the parent mass and ranges one-half of the isolation width to either side of the parent mass. You can set the isolation window to any value from m/z 0.4 to 15 times the first mass of the Data Dependent scan. The default value is m/z 4.0. Too low a value results in loss of sensitivity because not all of the ions in a mass peak or in neighboring isotopic peaks are isolated. Too high a value causes interference from neighboring peaks.

Parameter	Description
Isolation offset ^a	Use this spin box to define an absolute offset by which the isolation window is shifted. The resulting window is non-symmetric with regard to the precursor m/z. Thus, more isotopes of a cluster might be covered, without the need of expanding the isolation window. Example: Precursor = m/z 524.265; Isolation window = 2.0 m/z; Isolation offset = +0.5 m/z; Resulting isolation window = m/z 523.765–525.765 To change the isolation offset, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the isolation offset to any value from m/z -50 to +50. Default is m/z 0.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.

^aThis parameter is not available when User Role is set to **Standard**.

❖ To show this view

Click the Targeted-SIM symbol in the Graph pane.

Properties of PRM

The properties of a PRM experiment include the following parameters:

Parameter	Description
General	
Runtime	Use this box to specify the duration in minutes of the active scan event. Click into the field to display the spin boxes for the start time (minimum) and the end time (maximum) of the scan event. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range for the start time is from 0 to (end time minus 0.01) minutes. The valid range for the end time is from (start time plus 0.01) to 10000 minutes. Or, drag the left and right edges of the corresponding time bar to the desired positions on the time line in the Scan Groups pane.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity.
In-source CID ^a	Use this spin box to enter the in-source CID collision energy. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the CID collision energy to any value from 0 to 100 eV. A value of 0 eV means that the collision energy is switched off.

Parameter	Description
Dynamic RT ^a	Use this list box to enable the retention time correction for time windows of targeted compounds according to an internal standard (Pierce™ Peptide Retention Time Calibration Mixture, refer to www.fishersci.com, catalog numbers PI88320 and PI88321). If Dynamic RT is enabled, the time windows (start and end) that are entered in the inclusion list are corrected in real-time by a correction factor. This factor is calculated by comparing the expected RT to the actual RT of the internal standard during run-time. All 15 retention time standards will be recognized by the software. The standards that shall be used for correction must be entered in the inclusion list in addition to the target analytes. The center of the set retention time window for the standards reflects the expected RT. If the instrument method contains several PRM experiments, only those experiments use Dynamic RT where this parameter is set to on. The same correction factors are used for all PRM experiments in the instrument method (if Dynamic RT is activated). Available options are on (retention time correction enabled) and off (retention time correction disabled).
Default charge state	Use this box to specify the default charge state for Data Dependent scans. The mass spectrometer uses the charge state to determine the highest mass-to-charge ratio and HCD energy for the Data Dependent MSⁿ scan. If the mass spectrometer cannot determine the charge state from the preceding scan, it uses the default charge state that you specify here. The valid range for the default charge state is 1 through 100. The default charge state is 2. For typical applications, a charge state of +2 is suitable for tryptic digests in which the peptide has a charge state of +2. If you are running a different experiment, you might want to change the default to a more appropriate value.
Inclusion	Because this experiment requires inclusion masses, this field is always set to on (inclusion list enabled).
MS²	
Microscans ^a	Use this spin box to enter the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.

Parameter	Description
Loop count	Use this spin box to enter the number of repetitions of the corresponding scan event before continuing with the next scan event or experiment cycle. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no repetition) to 100 repetitions.
MSX count ^a	Use this spin box to enter the maximum number of precursors to be multiplexed in an scan event. In spectra multiplexing, multiple preselected precursors are collected in the C-Trap for simultaneous detection in the Orbitrap analyzer. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no spectral multiplexing) to 10 fillings.
MSX isochronous ITs ^a	When this parameter is set to on (enabled), all isolated windows are injected into the HCD cell with the same injection time for multiplexing scans. Thermo Fisher Scientific recommends that you set this parameter to – (disabled) when you use retention time correction (Dynamic RT).
Isolation window	Use this list box to enter the isolation width (in mass-to-charge ratio units) for the parent ion of interest. The mass range for the peak is centered at the parent mass and ranges one-half of the isolation width to either side of the parent mass. You can set the isolation window to any value from m/z 0.4 to 15 times the first mass of the Data Dependent scan. The default value is m/z 4.0. Too low a value results in loss of sensitivity because not all of the ions in a mass peak or in neighboring isotopic peaks are isolated. Too high a value causes interference from neighboring peaks.
Isolation offset ^a	Use this spin box to define an absolute offset by which the isolation window is shifted. The resulting window is non-symmetric with regard to the precursor m/z. Thus, more isotopes of a cluster might be covered, without the need of expanding the isolation window. Example: Precursor = m/z 524.265; Isolation window = 2.0 m/z; Isolation offset = +0.5 m/z; Resulting isolation window = m/z 523.765–525.765 To change the isolation offset, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the isolation offset to any value from m/z -50 to +50. Default is m/z 0.
Fixed first mass ^a	Use this box to specify whether to use a first mass of the Data Dependent scan. After an automated determination of the detection mass range, the first mass will be set to the defined fixed first mass. Because only masses up to 15 times the first mass can be trapped in the C-Trap, loss of ions in the upper detection range may occur. You can set Fixed first mass either to – (dynamic first mass) or to any m/z value between 50 and 2000. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Default is –.

Parameter	Description
(N)CE / Stepped (N)CE	Use this box to specify either the absolute collision energy (CE) in eV or the normalized collision energy (NCE). The latter is a dimensionless number that is approximately equivalent to the HCD collision energy (in eV) for a reference ion of mass 500 and charge 1. The actual HCD energy is calculated on basis of mass and charge of either the selected precursor ion (Data Dependent MS2 or AIF scans) or the center mass of an isolation window (targeted MS2 or AIF scans). Specify whether absolute collision energy (CE) or normalized collision energy (NCE) is used. In the box, the software adds the prefix “ce:” or “nce:” to collision energy values (for example, ce:35) to indicate the selected energy type. If more than one value is entered, the mass spectrometer will perform a stepwise fragmentation on the precursor ion. All fragments created in the steps are collected and sent to the Orbitrap analyzer for one scan detection. Enter up to three values manually separated by blanks or the locally defined “list separator” (defined for Microsoft™ Windows™ via the „Region and Language“ settings). Or, click the down arrow to display a dialog box and select the corresponding number of check boxes. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 10 to 200.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.

^aThis parameter is not available when User Role is set to **Standard**.

❖ To show this view

Click the PRM symbol in the Graph pane.

Properties of Targeted-SIM / dd-MS²

The properties of a Targeted-SIM / dd-MS² experiment include the following parameters:

Parameter	Description
General	
Runtime	Use this box to specify the duration in minutes of the active scan event. Click into the field to display the spin boxes for the start time (minimum) and the end time (maximum) of the scan event. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range for the start time is from 0 to (end time minus 0.01) minutes. The valid range for the end time is from (start time plus 0.01) to 10000 minutes. Or, drag the left and right edges of the corresponding time bar to the desired positions on the time line in the Scan Groups pane.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity.

Parameter	Description
In-source CID ^a	Use this spin box to enter the in-source CID collision energy. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the CID collision energy to any value from 0 to 100 eV. A value of 0 eV means that the collision energy is switched off.
Default charge state	Use this box to specify the default charge state for Data Dependent scans. The mass spectrometer uses the charge state to determine the highest mass-to-charge ratio and HCD energy for the Data Dependent MSⁿ scan. If the mass spectrometer cannot determine the charge state from the preceding scan, it uses the default charge state that you specify here. The valid range for the default charge state is 1 through 100. The default charge state is 2. For typical applications, a charge state of +2 is suitable for tryptic digests in which the peptide has a charge state of +2. If you are running a different experiment, you might want to change the default to a more appropriate value.
Inclusion	Because this experiment requires inclusion masses, this field is always set to on (inclusion list enabled).
SIM	
Microscans ^a	Use this spin box to enter the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.
Loop count	Use this spin box to enter the number of repetitions of the corresponding scan event before continuing with the next scan event or experiment cycle. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no repetition) to 100 repetitions.
MSX count ^a	Use this spin box to enter the maximum number of precursors to be multiplexed in an scan event. In spectra multiplexing, multiple preselected precursors are collected in the C-Trap for simultaneous detection in the Orbitrap analyzer. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no spectral multiplexing) to 10 fillings.

Parameter	Description
Isolation window	Use this spin box to enter the isolation width (in mass-to-charge ratio units) for the parent ion of interest. The mass range for the peak is centered at the parent mass and ranges one-half of the isolation width to either side of the parent mass. You can set the isolation window to any value from m/z 0.4 to 15 times the first mass of the Data Dependent scan. The default value is m/z 4.0. Too low a value results in loss of sensitivity because not all of the ions in a mass peak or in neighboring isotopic peaks are isolated. Too high a value causes interference from neighboring peaks.
Isolation offset ^a	Use this spin box to define an absolute offset by which the isolation window is shifted. The resulting window is non-symmetric with regard to the precursor m/z. Thus, more isotopes of a cluster might be covered, without the need of expanding the isolation window. Example: Precursor = m/z 524.265; Isolation window = 2.0 m/z; Isolation offset = +0.5 m/z; Resulting isolation window = m/z 523.765–525.765 To change the isolation offset, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the isolation offset to any value from m/z -50 to +50. Default is m/z 0.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.
dd-MS²	
Microscans ^a	Use this spin box to enter the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160. The valid range is from 1 to 3000 milliseconds.
Loop count	Use this spin box to enter the number of repetitions of the corresponding scan event before continuing with the next scan event or experiment cycle. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no repetition) to 100 repetitions.

Parameter	Description
MSX count ^a	Use this spin box to enter the maximum number of precursors to be multiplexed in a scan event. In spectra multiplexing, multiple preselected precursors are collected in the C-Trap for simultaneous detection in the Orbitrap analyzer. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no spectral multiplexing) to 10 fillings.
TopN	This field displays the product of the selected values for Loop count and MSX count as maximum number of the most abundant precursors that will be selected.
Isolation window	Use this spin box to enter the isolation width (in mass-to-charge ratio units) for the parent ion of interest. The mass range for the peak is centered at the parent mass and ranges one-half of the isolation width to either side of the parent mass. You can set the isolation window to any value from m/z 0.4 to 15 times the first mass of the Data Dependent scan. The default value is m/z 4.0. Too low a value results in loss of sensitivity because not all of the ions in a mass peak or in neighboring isotopic peaks are isolated. Too high a value causes interference from neighboring peaks.
Isolation offset ^a	Use this spin box to define an absolute offset by which the isolation window is shifted. The resulting window is non-symmetric with regard to the precursor m/z. Thus, more isotopes of a cluster might be covered, without the need of expanding the isolation window. Example: Precursor = m/z 524.265; Isolation window = 2.0 m/z; Isolation offset = +0.5 m/z; Resulting isolation window = m/z 523.765–525.765 To change the isolation offset, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the isolation offset to any value from m/z -50 to +50. Default is m/z 0.
Fixed first mass	Use this box to specify whether to use a first mass of the Data Dependent scan. After an automated determination of the detection mass range, the first mass will be set to the defined fixed first mass. Because only masses up to 15 times the first mass can be trapped in the C-Trap, loss of ions in the upper detection range may occur. You can set Fixed first mass either to – (dynamic first mass) or to any m/z value between 50 and 2000. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Default is –.

Parameter	Description
(N)CE / Stepped (N)CE	Use this box to specify either the absolute collision energy (CE) in eV or the normalized collision energy (NCE). The latter is a dimensionless number that is approximately equivalent to the HCD collision energy (in eV) for a reference ion of mass 500 and charge 1. The actual HCD energy is calculated on basis of mass and charge of either the selected precursor ion (Data Dependent MS2 or AIF scans) or the center mass of an isolation window (targeted MS2 or AIF scans). Specify whether absolute collision energy (CE) or normalized collision energy (NCE) is used. In the box, the software adds the prefix “ce:” or “nce:” to collision energy values (for example, ce:35) to indicate the selected energy type. If more than one value is entered, the mass spectrometer will perform a stepwise fragmentation on the precursor ion. All fragments created in the steps are collected and sent to the Orbitrap analyzer for one scan detection. Enter up to three values manually separated by blanks or the locally defined “list separator” (defined for Microsoft™ Windows™ via the „Region and Language“ settings). Or, click the down arrow to display a dialog box and select the corresponding number of check boxes. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 10 to 200.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.
dd Settings	
Use the parameters in this group to specify criteria for selecting one or more ions of interest on which to perform subsequent scans.	
Minimum AGC target	Use this box to specify a minimum value for the AGC target. If the mass peak of interest reaches this intensity within the Maximum IT, the mass spectrometer initiates a Data Dependent scan. Enter the value either as integer or in scientific notation with two decimal places (for example, 3.80e4) in the spin box text field. The valid range is from 0 to the value for the AGC target of the Data Dependent scan event.
Intensity threshold	This field displays the minimum intensity that a mass peak requires to initiate a Data Dependent scan.

Parameter	Description
Apex trigger	To obtain the highest quality data in the shortest period of time, it is best to defer data acquisition until near the apex of a chromatographic peak. Using the chromatographic peak apex detection provides numerous benefits for Data Dependent LC/MS/MS, including: • Improved MS/MS quality and signal levels • Shorter ion injection times • Reduced MS/MS acquisition of chemical background • Less dependence on static or dynamic exclusion lists • Reduced retriggering of scans on tailing chromatographic peaks Use this box to enter start (Minimum) and end (Maximum) of a retention time window in seconds relative to the occurrence of a precursor. If the mass spectrometer finds an apex within the window, it triggers a Data Dependent acquisition for the corresponding m/z or range of m/z. The mass spectrometer also triggers a Data Dependent scan when the end of the time window is reached without detecting an apex. The apex trigger always depends on other selection criteria (for example, intensity threshold). • Minimum Enter the minimum value for the time window (in seconds). You can enter any value from – (0) to 360. The default value is –. • Maximum Enter the maximum value for the time window (in seconds). You can enter any value from – (0) to 360 as long as it equals or exceeds the Minimum value. The default value is –.
Charge exclusion	Use the check boxes in this field to reject individual charge states or undetermined charge states as precursors for Data Dependent MS/MS scans. The following options are available: • – (charge exclusion disabled), • unassigned (charge state not determined), • 1–8 (at least one charge state is selected), • >8
Multiple charge states ^a	Use this field to decrease the number of redundant MS² spectra by limiting them to the most abundant charge state within a charge state distribution. All other criteria for dd-MS² properties must be met. The following options are available: • all (All charge states of a charge envelope are triggered.) • one charge state only (Only the most intense charge state of a charge envelope is triggered.)

Parameter	Description
Peptide match	Use this field to enable the mass spectrometer to select small molecules with peptide-like isotopic distributions for Data Dependent scanning. The mass spectrometer recognizes the monoisotopic mass of an isotopic distribution by comparing isotopic intensity ratios to typical peptide-like distributions. The following options are available: • on (peptide match enabled) • – (peptide match disabled) • preferred (peaks that are determined to belong to peptides are preferred and will be selected prior to those that are not, but still meeting all of the other Data Dependent filter criteria, for example, charge state and intensity) Default setting is preferred.
Exclude isotopes	Use this field to check whether the most intensive isotope of a cluster has been triggered in a Data Dependent scan event. All isotopes of that cluster will be then excluded. Available options are on (isotopes exclusion enabled) and – (isotopes exclusion disabled). Default setting is on. Isotopes exclusion is disabled for inclusion list entries.
Dynamic exclusion	Use this box to enter a time (in seconds) to prevent an ion from triggering a subsequent Data Dependent scan after it has already triggered a Data Dependent scan. The following input is possible: • – (no dynamic exclusion) • 0.1 to 50000 • auto [Dynamic exclusion = $2.5 \times \text{Chrom. peak width (FWHM)}$] Dynamic exclusion is valuable if the mass spectrometer has obtained enough data on an ion or if the base peak corresponds to a contaminant or an ion of non interest. If you enable dynamic exclusion, and if the mass spectrometer performs a Data Dependent scan on an ion, that ion is placed on the exclusion list (a temporary reject mass list) for a user-specified period of time. Then, when the mass spectrometer performs another Data Dependent scan on another ion, that ion is also placed on the exclusion list, and so on.

^aThis parameter is not available when User Role is set to **Standard**.

❖ To show this view

Click the Targeted-SIM / dd-MS² symbol in the Graph pane.

Properties of Full MS / AIF / NL dd-MS²

The properties of a Full MS / AIF / NL dd-MS² experiment include the following parameters:

Parameter	Description
General	
Runtime	Use this box to specify the duration in minutes of the active scan event. Click into the field to display the spin boxes for the start time (minimum) and the end time (maximum) of the scan event. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range for the start time is from 0 to (end time minus 0.01) minutes. The valid range for the end time is from (start time plus 0.01) to 10000 minutes. Or, drag the left and right edges of the corresponding time bar to the desired positions on the time line in the Scan Groups pane.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity.
In-source CID ^a	Use this spin box to enter the in-source CID collision energy. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the CID collision energy to any value from 0 to 100 eV. A value of 0 eV means that the collision energy is switched off.
Default charge state	Use this box to specify the default charge state for Data Dependent scans. The mass spectrometer uses the charge state to determine the highest mass-to-charge ratio and HCD energy for the Data Dependent MSⁿ scan. If the mass spectrometer cannot determine the charge state from the preceding scan, it uses the default charge state that you specify here. The valid range for the default charge state is 1 through 100. The default charge state is 2. For typical applications, a charge state of +2 is suitable for tryptic digests in which the peptide has a charge state of +2. If you are running a different experiment, you might want to change the default to a more appropriate value.
Neutral loss	This field is a reminder that the active experiment includes a neutral loss list.
Exclusion	Use this field to enable the exclusion masses list that is attached to the active instrument method. Available options are on (exclusion list enabled) and – (exclusion list disabled). Default setting is –.
Full MS	
Microscans ^a	Use this spin box to enter the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.

Parameter	Description
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.
Scan range	Use the spin boxes in this field to enter values (in mass-to-charge ratio units) for Minimum, Maximum, Center, and Width for the current scan range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. - Minimum Select the minimum value for the scan range. You can enter any value from 50.0 to 2500.0. - Maximum Select the maximum value for the scan range. You can enter any value from 50.4 to 6000.0. - Center Select the center mass of the scan range. You can enter any value from 50.2 to 4250.0. - Width Select the width of the scan range. You can enter any value from 0.4 to 5600.0. The actual possible values are interdependent. For Minimum, the highest value is Maximum – 0.4. For Maximum, the lowest value is Minimum + 0.4 and the highest value is Minimum × 15.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.
AIF	
Microscans ^a	Use this spin box to enter the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.

Parameter	Description
(N)CE / Stepped (N)CE	Use this box to specify either the absolute collision energy (CE) in eV or the normalized collision energy (NCE). The latter is a dimensionless number that is approximately equivalent to the HCD collision energy (in eV) for a reference ion of mass 500 and charge 1. The actual HCD energy is calculated on basis of mass and charge of either the selected precursor ion (Data Dependent MS2 or AIF scans) or the center mass of an isolation window (targeted MS2 or AIF scans). Specify whether absolute collision energy (CE) or normalized collision energy (NCE) is used. In the box, the software adds the prefix “ce:” or “nce:” to collision energy values (for example, ce:35) to indicate the selected energy type. If more than one value is entered, the mass spectrometer will perform a stepwise fragmentation on the precursor ion. All fragments created in the steps are collected and sent to the Orbitrap analyzer for one scan detection. Enter up to three values manually separated by blanks or the locally defined “list separator” (defined for Microsoft™ Windows™ via the „Region and Language“ settings). Or, click the down arrow to display a dialog box and select the corresponding number of check boxes. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 10 to 200.
Scan range	Use the spin boxes in this field to enter values (in mass-to-charge ratio units) for Minimum, Maximum, Center, and Width for the current scan range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. • Minimum Select the minimum value for the scan range. You can enter any value from 50.0 to 2500.0. • Maximum Select the maximum value for the scan range. You can enter any value from 50.4 to 6000.0. • Center Select the center mass of the scan range. You can enter any value from 50.2 to 4250.0. • Width Select the width of the scan range. You can enter any value from 0.4 to 5600.0. The actual possible values are interdependent. For Minimum, the highest value is Maximum – 0.4; it cannot exceed the Minimum value for the Full MS scan range. For Maximum, the lowest value is Minimum + 0.4 and the highest value is Minimum × 15.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.

Parameter	Description
MS²	
Microscans ^a	Use this spin box to enter the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.
Loop count	Use this spin box to enter the number of repetitions of the corresponding scan event before continuing with the next scan event or experiment cycle. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no repetition) to 100 repetitions.
MSX count ^a	Use this spin box to enter the maximum number of precursors to be multiplexed in a scan event. In spectra multiplexing, multiple preselected precursors are collected in the C-Trap for simultaneous detection in the Orbitrap analyzer. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no spectral multiplexing) to 10 fillings.
TopN	This field displays the product of the selected values for Loop count and MSX count as maximum number of the most abundant precursors that will be selected.
Isolation window	Use this list box to enter the isolation width (in mass-to-charge ratio units) for the parent ion of interest. The mass range for the peak is centered at the parent mass and ranges one-half of the isolation width to either side of the parent mass. You can set the isolation window to any value from m/z 0.4 to 15 times the first mass of the Data Dependent scan. The default value is m/z 4.0. Too low a value results in loss of sensitivity because not all of the ions in a mass peak or in neighboring isotopic peaks are isolated. Too high a value causes interference from neighboring peaks.

Parameter	Description
Isolation offset ^a	Use this spin box to define an absolute offset by which the isolation window is shifted. The resulting window is non-symmetric with regard to the precursor m/z. Thus, more isotopes of a cluster might be covered, without the need of expanding the isolation window. Example: Precursor = m/z 524.265; Isolation window = 2.0 m/z; Isolation offset = +0.5 m/z; Resulting isolation window = m/z 523.765–525.765 To change the isolation offset, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the isolation offset to any value from m/z -50 to +50. Default is m/z 0.
Fixed first mass	Use this box to specify whether to use a first mass of the Data Dependent scan. After an automated determination of the detection mass range, the first mass will be set to the defined fixed first mass. Because only masses up to 15 times the first mass can be trapped in the C-Trap, loss of ions in the upper detection range may occur. You can set Fixed first mass either to – (dynamic first mass) or to any m/z value between 50 and 2000. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Default is –.
(N)CE / Stepped (N)CE	Use this box to specify either the absolute collision energy (CE) in eV or the normalized collision energy (NCE). The latter is a dimensionless number that is approximately equivalent to the HCD collision energy (in eV) for a reference ion of mass 500 and charge 1. The actual HCD energy is calculated on basis of mass and charge of either the selected precursor ion (Data Dependent MS2 or AIF scans) or the center mass of an isolation window (targeted MS2 or AIF scans). Specify whether absolute collision energy (CE) or normalized collision energy (NCE) is used. In the box, the software adds the prefix “ce:” or “nce:” to collision energy values (for example, ce:35) to indicate the selected energy type. If more than one value is entered, the mass spectrometer will perform a stepwise fragmentation on the precursor ion. All fragments created in the steps are collected and sent to the Orbitrap analyzer for one scan detection. Enter up to three values manually separated by blanks or the locally defined “list separator” (defined for Microsoft™ Windows™ via the „Region and Language“ settings). Or, click the down arrow to display a dialog box and select the corresponding number of check boxes. To change a value, click the arrows in the spin box to increase [up arrow] or decrease [down arrow] the value. You can enter any value from 10 to 200.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.

Parameter	Description
dd Settings	
Use the parameters in this group to specify criteria for selecting one or more ions of interest on which to perform subsequent scans.	
Minimum AGC target	Use this box to specify a minimum value for the AGC target. If the mass peak of interest reaches this intensity within the Maximum IT, the mass spectrometer initiates a Data Dependent scan. Enter the value either as integer or in scientific notation with two decimal places (for example, 3.80e4) in the spin box text field. The valid range is from 0 to the value for the AGC target of the Data Dependent scan event.
Intensity threshold	This field displays the minimum intensity that a mass peak requires to initiate a Data Dependent scan.
Apex trigger	To obtain the highest quality data in the shortest period of time, it is best to defer data acquisition until near the apex of a chromatographic peak. Using the chromatographic peak apex detection provides numerous benefits for Data Dependent LC/MS/MS, including: • Improved MS/MS quality and signal levels • Shorter ion injection times • Reduced MS/MS acquisition of chemical background • Less dependence on static or dynamic exclusion lists • Reduced retriggering of scans on tailing chromatographic peaks Use this box to enter start (Minimum) and end (Maximum) of a retention time window in seconds relative to the occurrence of a precursor. If the mass spectrometer finds an apex within the window, it triggers a Data Dependent acquisition for the corresponding m/z or range of m/z. The mass spectrometer also triggers a Data Dependent scan when the end of the time window is reached without detecting an apex. The apex trigger always depends on other selection criteria (for example, intensity threshold). • Minimum Enter the minimum value for the time window (in seconds). You can enter any value from – (0) to 360. The default value is –. • Maximum Enter the maximum value for the time window (in seconds). You can enter any value from – (0) to 360 as long as it equals or exceeds the Minimum value. The default value is –.
Charge exclusion	Use the check boxes in this field to reject individual charge states or undetermined charge states as precursors for Data Dependent MS/MS scans. The following options are available: • – (charge exclusion disabled), • unassigned (charge state not determined) • 1–8 (at least one charge state is selected), • >8

Parameter	Description
Peptide match	Use this field to enable the mass spectrometer to select small molecules with peptide-like isotopic distributions for Data Dependent scanning. The mass spectrometer recognizes the monoisotopic mass of an isotopic distribution by comparing isotopic intensity ratios to typical peptide-like distributions. The following options are available: • on (peptide match enabled) • – (peptide match disabled) • preferred (peaks that are determined to belong to peptides are preferred and will be selected prior to those that are not, but still meeting all of the other Data Dependent filter criteria, for example, charge state and intensity) Default setting is preferred.
Dynamic exclusion	Use this box to enter a time (in seconds) to prevent an ion from triggering a subsequent Data Dependent scan after it has already triggered a Data Dependent scan. The following input is possible: • – (no dynamic exclusion) • 0.1 to 50000 • auto [Dynamic exclusion = $2.5 \times \text{Chrom. peak width (FWHM)}$] Dynamic exclusion is valuable if the mass spectrometer has obtained enough data on an ion or if the base peak corresponds to a contaminant or an ion of non interest. If you enable dynamic exclusion, and if the mass spectrometer performs a Data Dependent scan on an ion, that ion is placed on the exclusion list (a temporary reject mass list) for a user-specified period of time. Then, when the mass spectrometer performs another Data Dependent scan on another ion, that ion is also placed on the exclusion list, and so on.

^aThis parameter is not available when User Role is set to **Standard**.

❖ To show this view

Click the Full MS / AIF / NL dd-MS² symbol in the Graph pane.

Properties of DIA

The properties of a DIA experiment include the following parameters:

Parameter	Description
General	
Runtime	Use this box to specify the duration in minutes of the active scan event. Click into the field to display the spin boxes for the start time (minimum) and the end time (maximum) of the scan event. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range for the start time is from 0 to (end time minus 0.01) minutes. The valid range for the end time is from (start time plus 0.01) to 10000 minutes. Or, drag the left and right edges of the corresponding time bar to the desired positions on the time line in the Scan Groups pane.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity.
In-source CID ^a	Use this spin box to enter the in-source CID collision energy. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the CID collision energy to any value from 0 to 100 eV. A value of 0 eV means that the collision energy is switched off.
Default charge state	Use this box to specify the default charge state for Data Dependent scans. The mass spectrometer uses the charge state to determine the highest mass-to-charge ratio and HCD energy for the Data Dependent MSⁿ scan. If the mass spectrometer cannot determine the charge state from the preceding scan, it uses the default charge state that you specify here. The valid range for the default charge state is 1 through 100. The default charge state is 2. For typical applications, a charge state of +2 is suitable for tryptic digests in which the peptide has a charge state of +2. If you are running a different experiment, you might want to change the default to a more appropriate value.
DIA	
Microscans ^a	Use this spin box to enter the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.

Parameter	Description
Maximum IT	Use this list box to type or click a maximum allowed injection time (in milliseconds) to reach the AGC target value. You can enter either a number between 1 and 3000 or auto . If you enter auto , the mass spectrometer chooses a value that depends on the highest resolution of the active and the previous scan event.
Loop count	Use this field to enter the number of repetitions of the corresponding scan event before continuing with the next scan event or experiment cycle. The valid range is from 1 to 100. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
MSX count	Use this spin box to enter the maximum number of precursors to be multiplexed in an scan event. In spectra multiplexing, multiple preselected precursors are collected in the C-Trap for simultaneous detection in the Orbitrap analyzer. The following options are available: • 1 (no spectral multiplexing) The Method Editor sets the detection window to the isolation window. • 2–10 The Method Editor sets the detection window to the MSX scan range to show all of the multiplexed precursor mass ranges in one scan. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
MSX isochronous ITs	When this parameter is set to on, all isolated windows are injected into the HCD cell with the same injection time for multiplexing scans. The following options are available: • on (enabled) • – (disabled)
Isolation window	Use this list box to enter the isolation width (in mass-to-charge ratio units) for the parent ion of interest. The mass range for the peak is centered at the parent mass and ranges one-half of the isolation width to either side of the parent mass. You can set the isolation window to any value from m/z 0.4 to 15 times the first mass of the Data Dependent scan. Too low a value results in loss of sensitivity because not all of the ions in a mass peak or in neighboring isotopic peaks are isolated. Too high a value causes interference from neighboring peaks.

Parameter	Description
Isolation offset ^a	Use this spin box to define an absolute offset by which the isolation window is shifted. The resulting window is non-symmetric with regard to the precursor m/z. Thus, more isotopes of a cluster might be covered, without the need of expanding the isolation window. Example: Precursor = m/z 524.265; Isolation window = 2.0 m/z; Isolation offset = +0.5 m/z; Resulting isolation window = m/z 523.765–525.765 To change the isolation offset, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the isolation offset to any value from m/z -50 to +50. Default is m/z 0.
Fixed first mass	Use this box to specify whether to use a first mass of the Data Dependent scan. After an automated determination of the detection mass range, the first mass will be set to the defined fixed first mass. Because only masses up to 15 times the first mass can be trapped in the C-Trap, loss of ions in the upper detection range may occur. You can set Fixed first mass either to – (dynamic first mass) or to any m/z value between 50 and 2000. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Default is –.
(N)CE / Stepped (N)CE	Use this box to specify either the absolute collision energy (CE) in eV or the normalized collision energy (NCE). The latter is a dimensionless number that is approximately equivalent to the HCD collision energy (in eV) for a reference ion of mass 500 and charge 1. The actual HCD energy is calculated on basis of mass and charge of either the selected precursor ion (Data Dependent MS2 or AIF scans) or the center mass of an isolation window (targeted MS2 or AIF scans). Specify whether absolute collision energy (CE) or normalized collision energy (NCE) is used. In the box, the software adds the prefix “ce:” or “nce:” to collision energy values (for example, ce:35) to indicate the selected energy type. If more than one value is entered, the mass spectrometer will perform a stepwise fragmentation on the precursor ion. All fragments created in the steps are collected and sent to the Orbitrap analyzer for one scan detection. Enter up to three values manually separated by blanks or the locally defined “list separator” (defined for Microsoft™ Windows™ via the „Region and Language“ settings). Or, click the down arrow to display a dialog box and select the corresponding number of check boxes. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 10 to 200.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.

^aThis parameter is not available when User Role is set to **Standard**.

❖ To show this view

Click the DIA symbol in the Graph pane.

Properties of TMT

The properties of a TMT experiment include the following parameters:

Parameter	Description
General	
Runtime	Use this box to specify the duration in minutes of the active scan event. Click into the field to display the spin boxes for the start time (minimum) and the end time (maximum) of the scan event. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range for the start time is from 0 to (end time minus 0.01) minutes. The valid range for the end time is from (start time plus 0.01) to 10000 minutes. Or, drag the left and right edges of the corresponding time bar to the desired positions on the time line in the Scan Groups pane.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity.
In-source CID ^a	Use this spin box to enter the in-source CID collision energy. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the CID collision energy to any value from 0 to 100 eV. A value of 0 eV means that the collision energy is switched off.
Default charge state	Use this box to specify the default charge state for Data Dependent scans. The mass spectrometer uses the charge state to determine the highest mass-to-charge ratio and HCD energy for the Data Dependent MSⁿ scan. If the mass spectrometer cannot determine the charge state from the preceding scan, it uses the default charge state that you specify here. The valid range for the default charge state is 1 through 100. The default charge state is 2. For typical applications, a charge state of +2 is suitable for tryptic digests in which the peptide has a charge state of +2. If you are running a different experiment, you might want to change the default to a more appropriate value.
Inclusion	Use this field to enable the inclusion masses list that is attached to the active instrument method. Available options are on (inclusion list enabled) and – (inclusion list disabled). Default setting is –.
Exclusion	Use this field to enable the exclusion masses list that is attached to the active instrument method. Available options are on (exclusion list enabled) and – (exclusion list disabled). Default setting is –.
Tags	Use this field to enable the tag masses list for the active instrument method. Available options are on (list enabled) and – (list disabled). Default setting is –.
Full MS	
Microscans ^a	Use this spin box to enter the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.

Parameter	Description
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.
Number of scan ranges ^a	Use this spin box to enter the number of segmented master scans. Segmented master scans can be defined independently from each other. They can be used to get a better S/N for specific areas and exclude matrix signals. The scan ranges are acquired one after another and will result one scan for each range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. The valid range is from 1 to 8 scan ranges.
Scan range n ($n=1-8$)	Use the spin boxes in this field to enter values (in mass-to-charge ratio units) for Minimum, Maximum, Center, and Width for the current scan range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. - Minimum Select the minimum value for the scan range. You can enter any value from 50.0 to 2500.0. - Maximum Select the maximum value for the scan range. You can enter any value from 50.4 to 6000.0. - Center Select the center mass of the scan range. You can enter any value from 50.2 to 4250.0. - Width Select the width of the scan range. You can enter any value from 0.4 to 5600.0. The actual possible values are interdependent. For Minimum, the highest value is Maximum – 0.4. For Maximum, the lowest value is Minimum + 0.4 and the highest value is Minimum $\times$ 15.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.
dd-MS² / dd-SIM	
Microscans ^a	Use this spin box to enter the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.

Parameter	Description
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
AGC target	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT	Use this list box to type or click a maximum allowed injection time to reach the AGC target value. For example, type 160 . The valid range is from 1 to 3000 milliseconds.
Loop count	Use this spin box to enter the number of repetitions of the corresponding scan event before continuing with the next scan event or experiment cycle. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no repetition) to 100 repetitions.
MSX count ^a	Use this spin box to enter the maximum number of precursors to be multiplexed in an scan event. In spectra multiplexing, multiple preselected precursors are collected in the C-Trap for simultaneous detection in the Orbitrap analyzer. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 (no spectral multiplexing) to 10 fillings.
TopN	This field displays the product of the selected values for Loop count and MSX count as maximum number of the most abundant precursors that will be selected.
Isolation window	Use this list box to enter the isolation width (in mass-to-charge ratio units) for the parent ion of interest. The mass range for the peak is centered at the parent mass and ranges one-half of the isolation width to either side of the parent mass. You can set the isolation window to any value from m/z 0.4 to 15 times the first mass of the Data Dependent scan. Too low a value results in loss of sensitivity because not all of the ions in a mass peak or in neighboring isotopic peaks are isolated. Too high a value causes interference from neighboring peaks.

Parameter	Description
Isolation offset ^a	Use this spin box to define an absolute offset by which the isolation window is shifted. The resulting window is non-symmetric with regard to the precursor m/z. Thus, more isotopes of a cluster might be covered, without the need of expanding the isolation window. Example: Precursor = m/z 524.265; Isolation window = 2.0 m/z; Isolation offset = +0.5 m/z; Resulting isolation window = m/z 523.765–525.765 To change the isolation offset, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the isolation offset to any value from m/z -50 to +50. Default is m/z 0.
Fixed first mass ^a	Use this box to specify whether to use a first mass of the Data Dependent scan. After an automated determination of the detection mass range, the first mass will be set to the defined fixed first mass. Because only masses up to 15 times the first mass can be trapped in the C-Trap, loss of ions in the upper detection range may occur. You can set Fixed first mass either to – (dynamic first mass) or to any m/z value between 50 and 2000. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value.
(N)CE / Stepped (N)CE	Use this box to specify either the absolute collision energy (CE) in eV or the normalized collision energy (NCE). The latter is a dimensionless number that is approximately equivalent to the HCD collision energy (in eV) for a reference ion of mass 500 and charge 1. The actual HCD energy is calculated on basis of mass and charge of either the selected precursor ion (Data Dependent MS2 or AIF scans) or the center mass of an isolation window (targeted MS2 or AIF scans). Specify whether absolute collision energy (CE) or normalized collision energy (NCE) is used. In the box, the software adds the prefix “ce:” or “nce:” to collision energy values (for example, ce:35) to indicate the selected energy type. If more than one value is entered, the mass spectrometer will perform a stepwise fragmentation on the precursor ion. All fragments created in the steps are collected and sent to the Orbitrap analyzer for one scan detection. Enter up to three values manually separated by blanks or the locally defined “list separator” (defined for Microsoft™ Windows™ via the „Region and Language“ settings). Or, click the down arrow to display a dialog box and select the corresponding number of check boxes. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 10 to 200. Enter – for Data Dependent SIM scans.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.

Parameter	Description
dd Settings	
Use the parameters in this group to specify criteria for selecting one or more ions of interest on which to perform subsequent scans.	
Minimum AGC target	Use this box to specify a minimum value for the AGC target. If the mass peak of interest reaches this intensity within the Maximum IT, the mass spectrometer initiates a Data Dependent scan. Enter the value either as integer or in scientific notation with two decimal places (for example, 3.80e4) in the spin box text field. The valid range is from 0 to the value for the AGC target of the Data Dependent scan event.
Intensity threshold	This field displays the minimum intensity that a mass peak requires to initiate a Data Dependent scan.
Apex trigger	To obtain the highest quality data in the shortest period of time, it is best to defer data acquisition until near the apex of a chromatographic peak. Using the chromatographic peak apex detection provides numerous benefits for Data Dependent LC/MS/MS, including: • Improved MS/MS quality and signal levels • Shorter ion injection times • Reduced MS/MS acquisition of chemical background • Less dependence on static or dynamic exclusion lists • Reduced retriggering of scans on tailing chromatographic peaks Use this box to enter start (Minimum) and end (Maximum) of a retention time window in seconds relative to the occurrence of a precursor. If the mass spectrometer finds an apex within the window, it triggers a Data Dependent acquisition for the corresponding m/z or range of m/z. The mass spectrometer also triggers a Data Dependent scan when the end of the time window is reached without detecting an apex. The apex trigger always depends on other selection criteria (for example, intensity threshold). • Minimum Enter the minimum value for the time window (in seconds). You can enter any value from – (0) to 360. The default value is –. • Maximum Enter the maximum value for the time window (in seconds). You can enter any value from – (0) to 360 as long as it equals or exceeds the Minimum value. The default value is –.
Charge exclusion	Use the check boxes in this field to reject individual charge states or undetermined charge states as precursors for Data Dependent MS/MS scans. The following options are available: • – (charge exclusion disabled), • unassigned (charge state not determined) • 1–8 (at least one charge state is selected), • >8

Parameter	Description
Multiple charge states ^a	Use this field to decrease the number of redundant MS² spectra by limiting them to the most abundant charge state within a charge state distribution. All other criteria for dd-MS² properties must be met. The following options are available: • all (All charge states of a charge envelope are triggered.) • one charge state only (Only the most intense charge state of a charge envelope is triggered.)
Peptide match	Use this field to enable the mass spectrometer to select small molecules with peptide-like isotopic distributions for Data Dependent scanning. The mass spectrometer recognizes the monoisotopic mass of an isotopic distribution by comparing isotopic intensity ratios to typical peptide-like distributions. The following options are available: • on (peptide match enabled) • – (peptide match disabled) • preferred (peaks that are determined to belong to peptides are preferred and will be selected prior to those that are not, but still meeting all of the other Data Dependent filter criteria, for example, charge state and intensity) Default setting is preferred.
Exclude isotopes	Use this field to check whether the most intensive isotope of a cluster has been triggered in a Data Dependent scan event. All isotopes of that cluster will be then excluded. Available options are on (isotopes exclusion enabled) and – (isotopes exclusion disabled). Default setting is on. Isotopes exclusion is disabled for inclusion list entries.

Parameter	Description
Dynamic exclusion	Use this box to enter a time (in seconds) to prevent an ion from triggering a subsequent Data Dependent scan after it has already triggered a Data Dependent scan. The following input is possible: – (no dynamic exclusion) 0.1 to 50000 - auto [Dynamic exclusion = $2.5 \times \text{Chrom. peak width (FWHM)}$] Dynamic exclusion is valuable if the mass spectrometer has obtained enough data on an ion or if the base peak corresponds to a contaminant or an ion of non interest. If you enable dynamic exclusion, and if the mass spectrometer performs a Data Dependent scan on an ion, that ion is placed on the exclusion list (a temporary reject mass list) for a user-specified period of time. Then, when the mass spectrometer performs another Data Dependent scan on another ion, that ion is also placed on the exclusion list, and so on.
if idle	Use this field to select the behavior of the mass spectrometer when it has finished the Data Dependent scans that were triggered by a mass that meets the established criteria for Data Dependent actions. Available options are do not pick others and pick other. Default setting is do not pick others. This parameter is available only when at least one of the parameters Inclusion or Tags is set to on.

^aThis parameter is not available when User Role is set to **Standard**.

❖ To show this view

Click the TMT symbol in the Graph pane.

Properties of HMR - Full MS

The properties of an HMR - Full MS experiment¹ include the following parameters:

Parameter	Description
General	
Runtime	Use this box to specify the duration in minutes of the active scan event. Click into the field to display the spin boxes for the start time (Minimum) and the end time (Maximum) of the scan event. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range for the start time is from 0 to (end time minus 0.01) minutes. The valid range for the end time is from (start time plus 0.01) to 10000 minutes. Or, drag the left and right edges of the corresponding time bar to the desired positions on the time line in the Scan Groups pane.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity.
In-source CID ^a	Use this spin box to enter the in-source CID collision energy. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the CID collision energy to any value from 0 to 200 eV. This value range is fully applied for NSI sources. If another source is used, the maximum value will be reduced to 150 eV automatically. A value of 0 eV means that the collision energy is switched off.
Full MS	
Use the parameters in this group to specify the properties of the master scan(s).	
Microscans ^a	Use this spin box to select the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 17500, 35000, 45000, 70000, or 140000.
AGC target ^a	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT ^a	Use this list box to type or click a maximum allowed injection time (in milliseconds) to reach the AGC target value. You can enter either a number between 1 and 3000 or auto. If you enter auto , the mass spectrometer chooses a value that depends on the highest resolution of the active and the previous scan event.

¹. Available only for systems with a valid High Mass Range license.

Parameter	Description
Scan range	Use the spin boxes in this field to set values (in mass-to-charge ratio units) for Minimum, Maximum, Center, and Width for the current scan range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. - Minimum Select the minimum value for the scan range. You can enter any value from 350.0 to 2500.0. - Maximum Select the maximum value for the scan range. You can enter any value from 400.0 to 8000.0. - Center Select the center mass of the scan range. You can enter any value from 375.0 to 5250.0. - Width Select the width of the scan range. You can enter any value from 50.0 to 7650.0.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.

^aThis parameter is not available when User Role is set to **Standard**.

❖ To show this view

Click the HMR - Full MS symbol in the Graph pane.

Properties of HMR - AIF

The properties of an HMR - AIF experiment¹ include the following parameters:

Parameter	Description
General	
Runtime	Use this box to specify the duration in minutes of the active scan event. Click into the field to display the spin boxes for the start time (minimum) and the end time (maximum) of the scan event. To change a value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range for the start time is from 0 to (end time minus 0.01) minutes. The valid range for the end time is from (start time plus 0.01) to 10000 minutes. Or, drag the left and right edges of the corresponding time bar to the desired positions on the time line in the Scan Groups pane.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity.

¹. Available only for systems with a valid High Mass Range license.

Parameter	Description
In-source CID ^a	Use this spin box to enter the in-source CID collision energy. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the CID collision energy to any value from 0 to 200 eV. This value range is fully applied for NSI sources. If another source is used, the maximum value will be reduced to 150 eV automatically. A value of 0 eV means that the collision energy is switched off.
AIF	
Microscans ^a	Use this spin box to select the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Resolution	Use this list box to select the mass resolution used during the selected scan event. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 17500, 35000, 45000, 70000, or 140000.
AGC target ^a	Use this list box to select the AGC target value for the selected scan event. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, or 5e6.
Maximum IT ^a	Use this list box to type or click a maximum allowed injection time (in milliseconds) to reach the AGC target value. You can enter either a number between 1 and 3000 or auto. If you enter auto , the mass spectrometer chooses a value that depends on the highest resolution of the active and the previous scan event.
CE / Stepped CE	Use this box to specify the collision energy (CE) in eV. If more than one CE value is entered, the mass spectrometer will perform a stepwise fragmentation on the precursor ion. All fragments created in the steps are collected and sent to the Orbitrap analyzer for one scan detection. Enter up to three CE values manually separated by blanks or the locally defined "list separator" (defined for Microsoft™ Windows™ via the „Region and Language“ settings). Or, click the down arrow to display a dialog box and select the corresponding number of check boxes. To change a CE value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set CE to any value from 10 to 200. Default is 35.

Parameter	Description
Scan range	Use the spin boxes in this field to set values (in mass-to-charge ratio units) for Minimum, Maximum, Center, and Width for the current scan range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. • Minimum Select the minimum value for the scan range. You can enter any value from 350.0 to 2500.0. • Maximum Select the maximum value for the scan range. You can enter any value from 400.0 to 8000.0. • Center Select the center mass of the scan range. You can enter any value from 375.0 to 5250.0. • Width Select the width of the scan range. You can enter any value from 50.0 to 7650.0.
Spectrum data type ^a	Use this list box to toggle between Profile data format and Centroid data format.

^aThis parameter is not available when User Role is set to **Standard**.

❖ **To show this view**

Click the HMR - AIF symbol in the Graph pane.

Summary Page

The Summary page displays the parameters for mass spectrometer setup, syringe pump, divert valves, and contact closure that you specified on the Experiment Setup page.

❖ To zoom in or out on the Summary page

- Position the mouse pointer within the pane, press the <Ctrl> key, and roll the mouse wheel forward to zoom in.
- Position the mouse pointer within the pane, press the <Ctrl> key, and roll the wheel backward to zoom out.

The content of this page will be printed together with the information for other instruments.

❖ To display this page

In the Instrument Setup window, click the Summary tab.

Dialog Boxes of the Experiment Setup Page

This section provides a reference to the dialog boxes in the Experiment Setup page:

- Use the dialog boxes for global lists to define properties of masses that are used for setting up the experiments in the Experiment Setup page:
 - [Lock Masses Dialog Box](#)
 - [Inclusion List Dialog Box](#)
 - [Exclusion List Dialog Box](#)
 - [Neutral Losses Dialog Box](#)
 - [Tag Masses Dialog Box](#)
- [Mass Calculator](#)

Tip When you import data from csv files or txt files, pay attention to the following guidelines:

- Thermo Fisher Scientific recommends pasting the data from comma- or tab-separated files into a table instead of using the Import command. This way, the character encoding is usually transported and special letters like μ or ϵ or 3 appear as desired.
- Empty lines are ignored when pasting.
- The order and content of columns must match the table if no column headers are present. With column headers present, the order is taken from the headers.
- Missing columns enforce usage of the default value.

If a formula is present, the Method Editor always recalculates the m/z value of a compound. This prevents computational errors or missing significant fractional digits from being carried over.

Lock Masses Dialog Box

Use the Lock Masses dialog box to select a lock mass list for the active instrument method and to edit it. See [Figure 3-20](#). Lock masses are peaks in the spectrum that the mass spectrometer uses for internal mass calibration. Using lock masses improves the mass accuracy of the mass analyzer. If you do not specify any lock masses, the mass spectrometer uses the external mass calibration.

The dialog box allows defining a time window of activity for each lock mass (=timed lock masses). If Start or End is left blank, the lock mass is active from the beginning or until the end of the method, respectively. In the latter case, the End field displays “end.” The usage of lock masses during the active instrument method is specified on the Properties pane of the method.

The table shows the properties of the masses contained in the active lock mass list (*.lock-masses). To change the sort order, click the respective table column header. To invert the sort order, click again.



Figure 3-20. Method Editor—Lock Masses dialog box

The Lock Masses dialog box has the following parameters:

Parameter	Description
Mass [m/z]	Enter the mass-to-charge-ratio of the lock mass into the field (with a maximum of five decimals). To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity. During a scan, the mass spectrometer uses only the lock masses with a polarity that matches the active ion mode.
Start [min]	Enter the start time in minutes. Or, enter a time in seconds (by appending the letter <i>s</i>) or in hours (by appending the letter <i>h</i>). The software automatically converts your input into minutes.
End [min]	Enter the end time in minutes. Or, enter a time in seconds (by appending the letter <i>s</i>) or in hours (by appending the letter <i>h</i>). The software automatically converts your input into minutes.
Comment	Enter a comment for the lock mass into the field (for example, the compound name). This field is optional.

❖ **To display this dialog box**

1. In the Method Editor, expand the Global Lists pane.
2. Click the  **Lock Masses** button.

Title Bar

The title bar of a global list displays the name of the dialog box. A “modified” indicates a file with unsaved changes.

File Menu

The File menu provides commands for file operations. It has the following commands:

Command	Description
Import <Ctrl> + <I>	Opens a dialog box where you can select an existing mass collection. In addition to the program-specific data files, you can select *.csv or *.txt files that meet the requirements of the program. All available masses are replaced by the masses contained in the imported file. Click Open to import the file.
Export <Ctrl> + <S>	Opens a dialog box that you can use to save the active mass collection. In addition to using the program-specific data files, you can save the mass collection as tabulator-separated file (*.txt, for example) or comma-separated file (*.csv, for example). Enter a new file name, select the file type, and select the location (disk and directory) where you want to save it. Or, select an existing file. Click Save to save the file.
Export selected <Ctrl> + <Shift> + <S>	Opens a dialog box that you can use to save the selected masses. In addition to using the program-specific data files, you can save the mass collection as tabulator-separated file (*.txt, for example) or comma-separated file (*.csv, for example). Enter a new file name, select the file type, and select the location (disk and directory) where you want to save it. Or, select an existing file. Click Save to save the file. This command is available only when at least one line in the dialog box is selected.
Minimize <Ctrl> + <F4>	Closes the dialog box. Your edits will be retained. Or, click the Done button at the right side of the menu bar.

Edit Menu

The Edit menu provides commands for editing the active file. It has the following commands:

Command	Description
Undo until last save <Ctrl> + <Z>	Discards all changes to the active file that have not been saved.
Copy <Ctrl> + <C>	Copies the data of the selected mass to the clipboard.
Replace by clipboard <Ctrl> + <V>	Replaces the available masses by the content of the clipboard. The clipboard stores lock mass data as tabulator-separated text files. When the data in the clipboard are not in this format, the command is not available.

Help Menu

Displays the Help for this dialog box.

Inclusion List Dialog Box

Use the Inclusion List dialog box to edit a list of specific masses (inclusion masses) that can activate a Data Dependent action. See [Figure 3-21](#). The dialog box allows defining a time window of activity for each inclusion mass. If Start or End is left blank, the inclusion mass is active from the beginning or until the end of the method, respectively. In the latter case, the End field displays “end.”

To use an inclusion list in a experiment, set the Inclusion parameter on the Parameter pane to **on**. When a inclusion mass list is used in a Data Dependent experiment (Full MS / dd-MS², Targeted-SIM / dd-MS², Full MS /AIF / NL dd-MS²), the ions will be selected for the Data Dependent scan event, *only* if they are:

1. appearing in the referring master scan (mostly the full scan) and
2. fulfill all of the other defined selection criteria, such as Intensity Threshold.

Because target-based experiments or experiment parts (Targeted-SIM, PRM, Targeted-SIM / dd-MS²) are based on an inclusion list, the Inclusion parameter is always set to **on** for these experiments.

The table shows the properties of the masses contained in the active inclusion masses list (*.include-masses). To change the sort order, click the respective table column header. To invert the sort order, click again.

Method editor — Inclusion List										
File Edit Help			Done							
	Mass [m/z]	Formula [M]	Species	CS [z]	Polarity	Start [min]	End [min]	(N)CE	MSX ID	Comment
▶* 1					Positive					

Figure 3-21. Method Editor—Inclusion List dialog box

The Inclusion List dialog box has the following parameters:

Parameter	Description
Mass [m/z]	Enter the mass-to-charge-ratio of the inclusion mass into the field (with a maximum of five decimals). If you use the Mass Calculator to edit the Formula field, this field is automatically updated when you exit the editor.
Formula [M]	Use this field to describe the structure of the active compound. In addition to chemical formulas, you can enter amino acid sequences (one letter code) and peptide sequences (if they are structural terminated by H₂O). The different ways of definition are called formula types. You can either enter the formula directly or use the Mass Calculator. To display this editor, click the down arrow in this field. If more than one formula type for your input is possible, the Method Editor chooses the type with the highest priority (chemical formula > peptides > amino acids). Peptide sequences are marked by the prefix “p:” (for example, p: MRFA with $m/z = 524.26496$), amino acids by the prefix “aa:” (for example, aa: MRFA with $m/z = 506.25440$). Enter a prefix directly with the formula to ensure that the right type is applied. Pay attention to the following restrictions: • When you enter a valid formula, the Method Editor will set the default values for charge state (1) and Species (+H/-H). Then it will display an automatically calculated value in the Mass [m/z] field. • When you enter a formula that the Method Editor cannot interpret, the Mass [m/z] field will stay empty. When you save the method, the Method Editor will warn you that the method is not in the shape to be executed (due to the missing m/z value). When you reopen the method, the Method Editor will display exactly the formula that was entered. • When you enter a formula, The Method Editor requires a value for the charge state to calculate an m/z value. You can, however, save the method without specifying a charge state for the entry. When you save the method, the Method Editor will warn you that the method is not in the shape to be executed (due to the missing charge state). When you reopen the method, the Method Editor will display exactly the formula that was entered. • Entries of compounds with calculated m/z values outside the measurement specifications of the mass spectrometer ($m/z=50-6000$) can be saved in an instrument method. The instrument software, however, will ignore these entries when it executes the method. • When you change the m/z value that was calculated for the given set of formula, species and charge state, the Method Editor will clear the formula and species definition. The charge state will be preserved. • When you change the polarity for a set of calculated m/z, formula, species and charge state, the Method Editor will clear the Mass [m/z] field if the species definition is not valid for this polarity. You then need to change the species definition.

Parameter	Description
Species	Use this text field to define adducts or modifications of the active compound that are expected to be formed. The default value is +H for positive polarity and –H for negative polarity. The Method Editor will then recalculate the value in the Mass [m/z] field, if possible. The Species field can be used in two ways: - Click the down arrow to display a list of predefined adducts for each polarity: +H, +Na, +K, +NH₄ for positive polarity –H, +Cl, +OH, +HCOO for negative polarity - an empty entry to express adducts (for example, radical cations) for both polarities. The corresponding set will be displayed depending on the selected polarity. Selecting an adduct (A) will result in the strict behavior of applying one unit A to the compound and using “+H” or “–H” adduct depending on the charge state and active polarity. “+K” = $[M + K^+ + (z-1)H^+]^{z+}$; for example, MRFA, +K, CS=2, positive pol. = $[M + K^+ + H^+]^{2+}$ - Enter the modifications of the compound by using squared brackets and at least M as representation of the basic compound (for example, [M + Na + K] or [2M + Na]). The predefined adducts can be entered, too. This definition is used without additional auto dependencies, like adding protons. If you use the Mass Calculator to edit the Formula field, the Species field is automatically filled when you exit the editor.
CS [z]	Use this spin box to enter the charge state of the ion to be fragmented. The valid range is 1–100. The required collision energy for fragmenting an ion depends on its charge state. The higher the charge state, the lower the required collision energy. If this field is left blank, any charge state will be accepted, even unassigned. If you use the Mass Calculator to edit the Formula field, this field is automatically updated when you exit the editor.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity. During a scan, the mass spectrometer uses only the inclusion masses with a polarity that matches the active ion mode. If you use the Mass Calculator to edit the Formula field, this field is automatically updated when you exit the editor.
Start [min]	Enter the start of the time window (in minutes) that corresponds to the mass in this row. Or, enter a time in seconds (by appending the letter <i>s</i>) or in hours (by appending the letter <i>h</i>). The software automatically converts your input into minutes.
End [min]	Enter the end of the time window in minutes. Or, enter a time in seconds (by appending the letter <i>s</i>) or in hours (by appending the letter <i>h</i>). The software automatically converts your input into minutes.

Parameter	Description
(N)CE	Use the spin box to enter a potential gradient in the HCD cell used to fragment ions. The default collision energy is 35 eV. In the list box, specify whether absolute collision energy CE [eV] is used or normalized collision energy NCE is used. The valid range is 10 to 200 eV for CE or 10 to 200 for NCE. In the list, the software adds the prefix “ce:” to collision energy values (for example, ce:35). A high collision energy value results in more energy deposition (which generally leads to more fragmentation). A low collision energy value results in less energy deposition (which generally leads to less fragmentation).
MSX ID	Enter the number of the multiplexed scan event in which the inclusion mass was analyzed.
Comment	Enter a comment for the inclusion mass into the field (for example, the compound name). This field is optional.

❖ **To display this dialog box**

1. In the Method Editor, expand the Global Lists pane.
2. Click the  **Inclusion** button.

Title Bar

The title bar of a global list displays the name of the dialog box. A “modified” indicates a file with unsaved changes.

File Menu

The File menu provides commands for file operations. It has the following commands:

Command	Description
Import <Ctrl> + <I>	Opens a dialog box where you can select an existing mass collection. In addition to the program-specific data files, you can select *.csv or *.txt files that meet the requirements of the program. All available masses are replaced by the masses contained in the imported file. Click Open to import the file. When you want to import *.csv or *.txt files with entries that contain formulas, an extra third column "Formula type," which contains the prefix, must specify the formula type. Valid values for the fields that can be (re)interpreted are: - for Peptide type: "Peptide", "p", and "p:" (all case insensitive), - for Amino acid type: "Amino acid", "aa", "aa:" (all case insensitive), - for Chemical formula type: "Chemical formula", "c", "c:" (all case insensitive), and "" (empty).
Export <Ctrl> + <S>	Opens a dialog box that you can use to save the active mass collection. In addition to using the program-specific data files, you can save the mass collection as tabulator-separated file (*.txt, for example) or comma-separated file (*.csv, for example). Enter a new file name, select the file type, and select the location (disk and directory) where you want to save it. Or, select an existing file. Click Save to save the file. When you export *.csv or *.txt files with entries that contain formulas, an extra third column "Formula type" specifies the formula type. Values for the fields that are: - for Peptide type: "Peptide", - for Amino acid type: "Amino acid", - for Chemical formula type: "" (empty).
Export selected <Ctrl> + <Shift> + <S>	Opens a dialog box that you can use to save the selected masses. In addition to using the program-specific data files, you can save the mass collection as tabulator-separated file (*.txt, for example) or comma-separated file (*.csv, for example). Enter a new file name, select the file type, and select the location (disk and directory) where you want to save it. Or, select an existing file. Click Save to save the file. This command is available only when at least one line in the dialog box is selected.
Minimize <Ctrl> + <F4>	Closes the dialog box. Your edits will be retained. Or, click the Done button at the right side of the menu bar.

Edit Menu

The Edit menu provides commands for editing the active file. It has the following commands:

Command	Description
Undo until last save <Ctrl> + <Z>	Discards all changes to the active file that have not been saved.
Copy <Ctrl> + <C>	Copies the data of the selected mass to the clipboard.
Replace by clipboard <Ctrl> + <V>	Replaces the available masses by the content of the clipboard. The clipboard stores lock mass data as tabulator-separated text files. When the data in the clipboard are not in this format, the command is not available.

Help Menu

Displays the Help for this dialog box.

Exclusion List Dialog Box

Use the Exclusion List dialog box to edit a list of specific masses (exclusion masses) that will not trigger a subsequent Data Dependent scan even if they are present. See [Figure 3-22](#). The dialog box allows defining a time window of activity for each exclusion mass. If Start or End is left blank, the exclusion mass is active from the beginning or until the end of the method, respectively. In the latter case, the End field displays “end.”

To use an exclusion list in a experiment, set the Exclusion parameter on the Parameter pane to **on**.

The table shows the properties of the masses contained in the active exclusion masses list (*.exclude-masses). To change the sort order, click the respective table column header. To invert the sort order, click again.

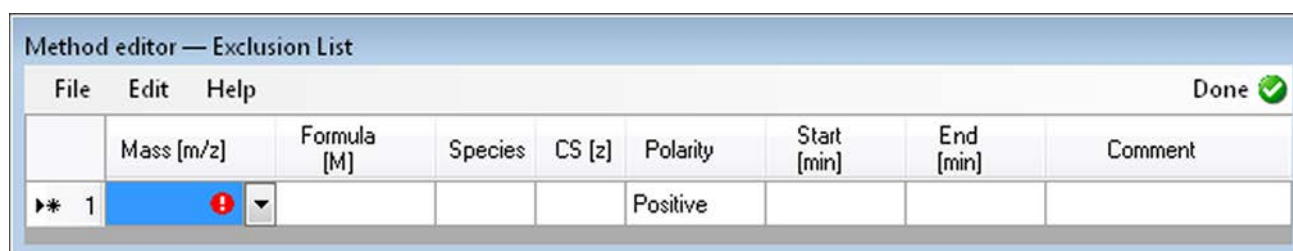


Figure 3-22. Method Editor—Exclusion List dialog box

The Exclusion List dialog box has the following parameters:

Parameter	Description
Mass [m/z]	Enter the mass-to-charge-ratio of the exclusion mass into the field (with a maximum of five decimals). If you use the Mass Calculator to edit the Formula field, this field is automatically updated when you exit the editor.
Formula [M]	Use this field to describe the structure of the active compound. In addition to chemical formulas, you can enter amino acid sequences (one letter code) and peptide sequences (if they are structural terminated by H₂O). The different ways of definition are called formula types. You can either enter the formula directly or use the Mass Calculator. To display this editor, click the down arrow in this field. If more than one formula type for your input is possible, the Method Editor chooses the type with the highest priority (chemical formula > peptides > amino acids). Peptide sequences are marked by the prefix "p:" (for example, p: MRFA with $m/z = 524.26496$), amino acids by the prefix "aa:" (for example, aa: MRFA with $m/z = 506.25440$). Enter a prefix directly with the formula to ensure that the right type is applied. Pay attention to the following restrictions: • When you enter a valid formula, the Method Editor will set the default values for charge state (1) and Species (+H/-H). Then it will display an automatically calculated value in the Mass [m/z] field. • When you enter a formula that the Method Editor cannot interpret, the Mass [m/z] field will stay empty. When you save the method, the Method Editor will warn you that the method is not in the shape to be executed (due to the missing m/z value). When you reopen the method, the Method Editor will display exactly the formula that was entered. • When you enter a formula, The Method Editor requires a value for the charge state to calculate an m/z value. You can, however, save the method without specifying a charge state for the entry. When you save the method, the Method Editor will warn you that the method is not in the shape to be executed (due to the missing charge state). When you reopen the method, the Method Editor will display exactly the formula that was entered. • Entries of compounds with calculated m/z values outside the measurement specifications of the mass spectrometer ($m/z=50-6000$) can be saved in an instrument method. The instrument software, however, will ignore these entries when it executes the method. • When you change the m/z value that was calculated for the given set of formula, species and charge state, the Method Editor will clear the formula and species definition. The charge state will be preserved. • When you change the polarity for a set of calculated m/z, formula, species and charge state, the Method Editor will clear the Mass [m/z] field if the species definition is not valid for this polarity. You then need to change the species definition.

Parameter	Description
Species	Use this field to define adducts or modifications of the active compound that are expected to be formed. The default value is +H for positive polarity and -H for negative polarity. The Method Editor will then recalculate the value in the Mass [m/z] field, if possible. The Species field can be used in two ways: - Click the down arrow to display a list of predefined adducts for each polarity: +H, +Na, +K, +NH₄ for positive polarity -H, +Cl, +OH, +HCOO for negative polarity - an empty entry to express adducts (for example, radical cations) for both polarities. The corresponding set will be displayed depending on the selected polarity. Selecting an adduct (A) will result in the strict behavior of applying one unit A to the compound and using “+H” or “-H” adduct depending on charge state and active polarity. “+K” = $[M + K^+ + (z-1)H^+]^{z+}$; for example, MRFA, +K, CS=2, positive pol. = $[M + K^+ + H^+]^{2+}$ - Enter the modifications of the compound by using squared brackets and at least M as representation of the basic compound (for example, [M + Na + K] or [2M + Na]). The predefined adducts can be entered, too. This definition is used without additional auto dependencies, like adding protons. If you select or define a species and the Formula field is empty, the species definition will stay grayed out. If you use the Mass Calculator to edit the Formula field, this field is automatically updated when you exit the editor.
CS [z]	Use the spin box to enter the charge state of the ion to be excluded. The valid range is 1–100. The required collision energy for fragmenting an ion depends on its charge state. The higher the charge state, the lower the required collision energy. If you use the Mass Calculator to edit the Formula field, this field is automatically updated when you exit the editor.
Polarity	Use this list box to toggle between positive ion polarity and negative ion polarity. During a scan, the mass spectrometer uses only the exclusion masses with a polarity that matches the active ion mode. If you use the Mass Calculator to edit the Formula field, this field is automatically updated when you exit the editor.
Start [min]	Enter the start of the time window (in minutes) that corresponds to the mass in this row. Or, enter a time in seconds (by appending the letter <i>s</i>) or in hours (by appending the letter <i>h</i>). The software automatically converts your input into minutes.

Parameter	Description
End [min]	Enter the end of the time window in minutes. Or, enter a time in seconds (by appending the letter <i>s</i>) or in hours (by appending the letter <i>h</i>). The software automatically converts your input into minutes.
Comment	Enter a comment for the exclusion mass into the field (for example, the compound name). This field is optional.

❖ **To display this dialog box**

1. In the Method Editor, expand the Global Lists pane.
2. Click the  **Exclusion** button.

Title Bar

The title bar of a global list displays the name of the dialog box. A “modified” indicates a file with unsaved changes.

File Menu

The File menu provides commands for file operations. It has the following commands:

Command	Description
Import <Ctrl> + <I>	Opens a dialog box where you can select an existing mass collection. In addition to the program-specific data files, you can select *.csv or *.txt files that meet the requirements of the program. All available masses are replaced by the masses contained in the imported file. Click Open to import the file. When you want to import *.csv or *.txt files with entries that contain formulas, an extra third column “Formula type,” which contains the prefix, must specify the formula type. Valid values for the fields that can be (re)interpreted are: • for Peptide type: “Peptide”, “p”, and “p:” (all case insensitive), • for Amino acid type: “Amino acid”, “aa”, “aa:” (all case insensitive), • for Chemical formula type: “Chemical formula”, “c”, “c:” (all case insensitive), and “” (empty).
Export <Ctrl> + <S>	Opens a dialog box that you can use to save the active mass collection. In addition to using the program-specific data files, you can save the mass collection as tabulator-separated file (*.txt, for example) or comma-separated file (*.csv, for example). Enter a new file name, select the file type, and select the location (disk and directory) where you want to save it. Or, select an existing file. Click Save to save the file. When you export *.csv or *.txt files with entries that contain formulas, an extra third column “Formula type” specifies the formula type. Values for the fields that are: • for Peptide type: “Peptide”, • for Amino acid type: “Amino acid”, • for Chemical formula type: “” (empty).

Command	Description
Export selected <Ctrl> + <Shift> + <S>	Opens a dialog box that you can use to save the selected masses. In addition to using the program-specific data files, you can save the mass collection as tabulator-separated file (*.txt, for example) or comma-separated file (*.csv, for example). Enter a new file name, select the file type, and select the location (disk and directory) where you want to save it. Or, select an existing file. Click Save to save the file.
	This command is available only when at least one line in the dialog box is selected.
Minimize <Ctrl> + <F4>	Closes the dialog box. Your edits will be retained. Or, click the Done button at the right side of the menu bar.

Edit Menu

The Edit menu provides commands for editing the active file. It has the following commands:

Command	Description
Undo until last save <Ctrl> + <Z>	Discards all changes to the active file that have not been saved.
Copy <Ctrl> + <C>	Copies the data of the selected mass to the clipboard.
Replace by clipboard <Ctrl> + <V>	Replaces the available masses by the content of the clipboard. The clipboard stores lock mass data as tabulator-separated text files. When the data in the clipboard are not in this format, the command is not available.

Help Menu

Displays the Help for this dialog box.

Neutral Losses Dialog Box

Use the Neutral Losses dialog box to edit neutral losses that can trigger a Data Dependent scan. See [Figure 3-23](#). The neutral losses are applied only in the Full MS /AIF / NL dd-MS² experiment. If a defined negative mass distance is found between a peak of the Full MS scan and those of the AIF scan, the corresponding peak of the Full MS scan will be isolated and fragmented to get the depending fragments.

The table shows the mass delta of the neutral loss and the charge state of the precursor ion. To change the sort order, click the respective table column header. To invert the sort order, click again.

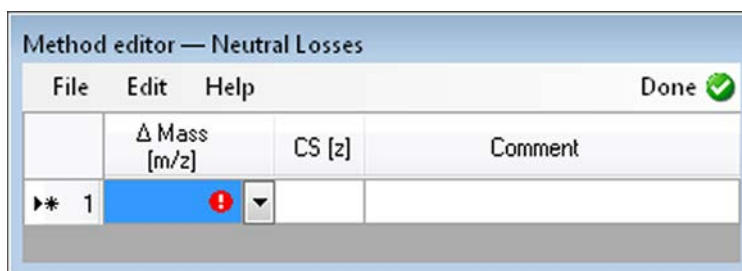


Figure 3-23. Method Editor—Neutral Losses dialog box

The Neutral Losses dialog box has the following parameters:

Parameter	Description
Δ Mass [m/z]	Use this spin box to enter the mass difference of the potential neutral loss (with a maximum of five decimals) as value independent of the method polarity. The valid range is 0.00001 to ±4000.00000.
CS [z]	Use this spin box to enter the charge state (CS) of the precursor ion. One entry must be defined per CS (for example, $m/z=18$, $CS=1$; $m/z=9$, $CS=2$; $m/z=4.5$, $CS=3$;...). The valid range is 1–100. If this field is left blank, any charge state is allowed, even an unassigned.
Comment	Enter a comment for the neutral loss into the field (for example, the compound name). This field is optional.

❖ **To display this dialog box**

1. In the Method Editor, expand the Global Lists pane.
2. Click the  **Neutral Loss** button.

Title Bar

The title bar of a global list displays the name of the dialog box. A “modified” indicates a file with unsaved changes.

File Menu

The File menu provides commands for file operations. It has the following commands:

Command	Description
Import <Ctrl> + <I>	Opens a dialog box where you can select an existing mass collection. In addition to the program-specific data files, you can select *.csv or *.txt files that meet the requirements of the program. All available masses are replaced by the masses contained in the imported file. Click Open to import the file.
Export <Ctrl> + <S>	Opens a dialog box that you can use to save the active mass collection. In addition to using the program-specific data files, you can save the mass collection as tabulator-separated file (*.txt, for example) or comma-separated file (*.csv, for example). Enter a new file name, select the file type, and select the location (disk and directory) where you want to save it. Or, select an existing file. Click Save to save the file.
Export selected <Ctrl> + <Shift> + <S>	Opens a dialog box that you can use to save the selected masses. In addition to using the program-specific data files, you can save the mass collection as tabulator-separated file (*.txt, for example) or comma-separated file (*.csv, for example). Enter a new file name, select the file type, and select the location (disk and directory) where you want to save it. Or, select an existing file. Click Save to save the file. This command is available only when at least one line in the dialog box is selected.
Minimize <Ctrl> + <F4>	Closes the dialog box. Your edits will be retained. Or, click the Done button at the right side of the menu bar.

Edit Menu

The Edit menu provides commands for editing the active file. It has the following commands:

Command	Description
Undo until last save <Ctrl> + <Z>	Discards all changes to the active file that have not been saved.
Copy <Ctrl> + <C>	Copies the data of the selected mass to the clipboard.
Replace by clipboard <Ctrl> + <V>	Replaces the available masses by the content of the clipboard. The clipboard stores lock mass data as tabulator-separated text files. When the data in the clipboard are not in this format, the command is not available.

Help Menu

Displays the Help for this dialog box.

Tag Masses Dialog Box

An MS/MS scan can be triggered by a mass that has a ‘partner’ mass a user-defined delta away. Use the Tag Masses dialog box to edit a list of such mass deltas. See [Figure 3-20](#). This is useful for applications where mass tags are used, or where mass pairs are known, and can greatly reduce the number of MS/MS scans on non-tagged species.

Tag masses can be used only in the Full MS / dd-MS² experiment. To use tag masses, set the Tags parameter on the Parameter pane to **on**.

The table displays the properties of the available tag masses. To change the sort order, click the respective table column header. To invert the sort order, click again.

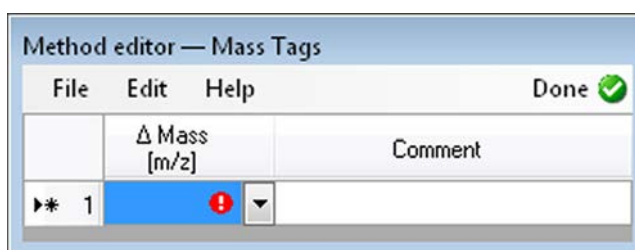


Figure 3-24. Method Editor—Tag Masses dialog box

The Tag Masses dialog box has the following parameters:

Parameter	Description
Δ Mass [m/z]	Use this spin box to enter the mass difference (with a maximum of five decimals). Depending on the sign, one precursor of the pair will be triggered. If you want to trigger on the heavy precursor (with a tag or isotope label), you need to enter a negative sign (for example, -6.02). It will be checked if an m/z distance towards lower m/z will be found. If so, the precursor at higher m/z will be selected. A positive m/z distance leads to the selection of the precursor with a lower m/z . If both precursors should be selected, two entries are needed, one with positive and one with negative sign. The valid range is 0.00001 to ± 4000.00000 .
Comment	Enter a comment into the field (for example, the compound name). This field is optional.

❖ To display this dialog box

1. In the Method Editor, expand the Global Lists pane.
2. Click the  Tag Masses button.

Title Bar

The title bar of a global list displays the name of the dialog box. A “modified” indicates a file with unsaved changes.

File Menu

The File menu provides commands for file operations. It has the following commands:

Command	Description
Import <Ctrl> + <I>	Opens a dialog box where you can select an existing mass collection. In addition to the program-specific data files, you can select *.csv or *.txt files that meet the requirements of the program. All available masses are replaced by the masses contained in the imported file. Click Open to import the file.
Export <Ctrl> + <S>	Opens a dialog box that you can use to save the active mass collection. In addition to using the program-specific data files, you can save the mass collection as tabulator-separated file (*.txt, for example) or comma-separated file (*.csv, for example). Enter a new file name, select the file type, and select the location (disk and directory) where you want to save it. Or, select an existing file. Click Save to save the file.
Export selected <Ctrl> + <Shift> + <S>	Opens a dialog box that you can use to save the selected masses. In addition to using the program-specific data files, you can save the mass collection as tabulator-separated file (*.txt, for example) or comma-separated file (*.csv, for example). Enter a new file name, select the file type, and select the location (disk and directory) where you want to save it. Or, select an existing file. Click Save to save the file. This command is available only when at least one line in the dialog box is selected.
Minimize <Ctrl> + <F4>	Closes the dialog box. Your edits will be retained. Or, click the Done button at the right side of the menu bar.

Edit Menu

The Edit menu provides commands for editing the active file. It has the following commands:

Command	Description
Undo until last save <Ctrl> + <Z>	Discards all changes to the active file that have not been saved.
Copy <Ctrl> + <C>	Copies the data of the selected mass to the clipboard.
Replace by clipboard <Ctrl> + <V>	Replaces the available masses by the content of the clipboard. The clipboard stores lock mass data as tabulator-separated text files. When the data in the clipboard are not in this format, the command is not available.

Help Menu

Displays the Help for this dialog box.

Mass Calculator

Use the Mass Calculator to specify the properties of compounds that are used in the Inclusion List dialog box and the Exclusion List dialog box.

	Mass [m/z]	Formula [M]
▶ 1	524.26496	p:MRFA

Compound

Formula:

Type:

Species:

Polarity: ☒ positive ☐ negative

m/z: Composition:

Figure 3-25. Mass Calculator (Method Editor)

When you display the Mass Calculator, its fields are filled with the values of the active list fields, if available. Otherwise, its fields are filled with the default values. The Method Editor applies the set and calculated values of the Mass Calculator to the active list fields, when you exit the editor by doing one of the following:

- Press **Enter** at any position.
- Click at any position outside of the editor.
- Click the down arrow in the Formula field again.

The Mass Calculator has the following parameters:

Parameter	Description
Compound	
Formula	Use the text field to specify the basic composition of the compound. Click the down arrow to display a list of the last entered compounds. The syntax rules and interpretation accept the kind of formula that is also accepted on the Spectrum Simulation page (Isotope Simulation area) of the Qual Browser.

Parameter	Description
Type	Use the Type list to specify the formula type used in the Formula field: • Chemical formula Formula is defined as the resulting elemental composition of the entered formula. This is the default selection. • Peptide Formula is defined as the sum of all of the entered amino acids additionally terminated with H at the N-terminus and OH at the C-terminus. • Amino Acid Formula is defined as the sum of all of the entered amino acids. Independent of the entry in the Species field, the elemental composition and the mass of the compound, Formula is completely determined by the given formula and selected formula type. Determined or defined formulas types are marked by the addition of a text prefix. For peptides it is “p:” (for example, “p: MRFA”); for amino acids it is “aa:” (for example, “aa: MRFA”). No prefix is displayed for chemical formulas.
Species	Use this text field to define adducts or modifications of the active compound that are expected to be formed. The default value is +H for positive polarity and –H for negative polarity. The Species field can be used in two ways: • Click the down arrow to display a list of predefined adducts for each polarity: - +H, +Na, +K, +NH₄ for positive polarity - -H, +Cl, +OH, +HCOO for negative polarity - an empty entry to express adducts (for example, radical cations) for both polarities. The corresponding set will be displayed depending on the selected polarity. Selecting an adduct (A) will result in the strict behavior of applying one unit A to the compound and using “+H” or “-H” adduct depending on the charge state and active polarity. “+K” = $[M + K^+ + (z-1)H^+]^{z+}$; for example, MRFA, +K, CS=2, positive pol. = $[M + K^+ + H^+]^{2+}$ • Enter the modifications of the compound by using squared brackets and at least M as representation of the basic compound (for example, [M + Na + K] or [2M + Na]). The predefined adducts can be entered, too. This definition is used without additional auto dependencies, like adding protons.
Charge state	Use the list box to select the resulting charge state. Available options are 1+ to 100+ for positive polarity and 1– to 100– for negative polarity. The default charge state is 1+ for positive polarity and 1– for negative polarity.
Polarity	Use the option buttons to select the applied polarity. The default polarity is positive.

Parameter	Description
m/z	This text field displays the calculated mass-to-charge ratio, with five decimal places (for example, 524.26496).
Composition	This text field displays the determined total formula (for example, C23 H38 N7 O5 S).

❖ **To display the Mass Calculator**

Click the down arrow in a Formula cell of the Inclusion List dialog box or the Exclusion List dialog box.

Instrument Setup

Dialog Boxes of the Experiment Setup Page

Explore Q Exactive HF-X Tune

This chapter provides information about Q Exactive HF-X Tune, its views, functions, and features.

Contents

- [Q Exactive HF-X Tune Overview](#)
- [Q Exactive HF-X Tune Menus](#)
- [Toolbar](#)
- [Tasks Panel](#)
- [Display Panel](#)
- [Dialog Boxes](#)

Q Exactive HF-X Tune Overview

The Q Exactive HF-X Tune program is used to operate the Q Exactive HF-X mass spectrometer. Figure 4-1 shows Q Exactive HF-X Tune. To access information about Q Exactive HF-X Tune, use the title bar, the toolbar, menu commands, display views, and Help.

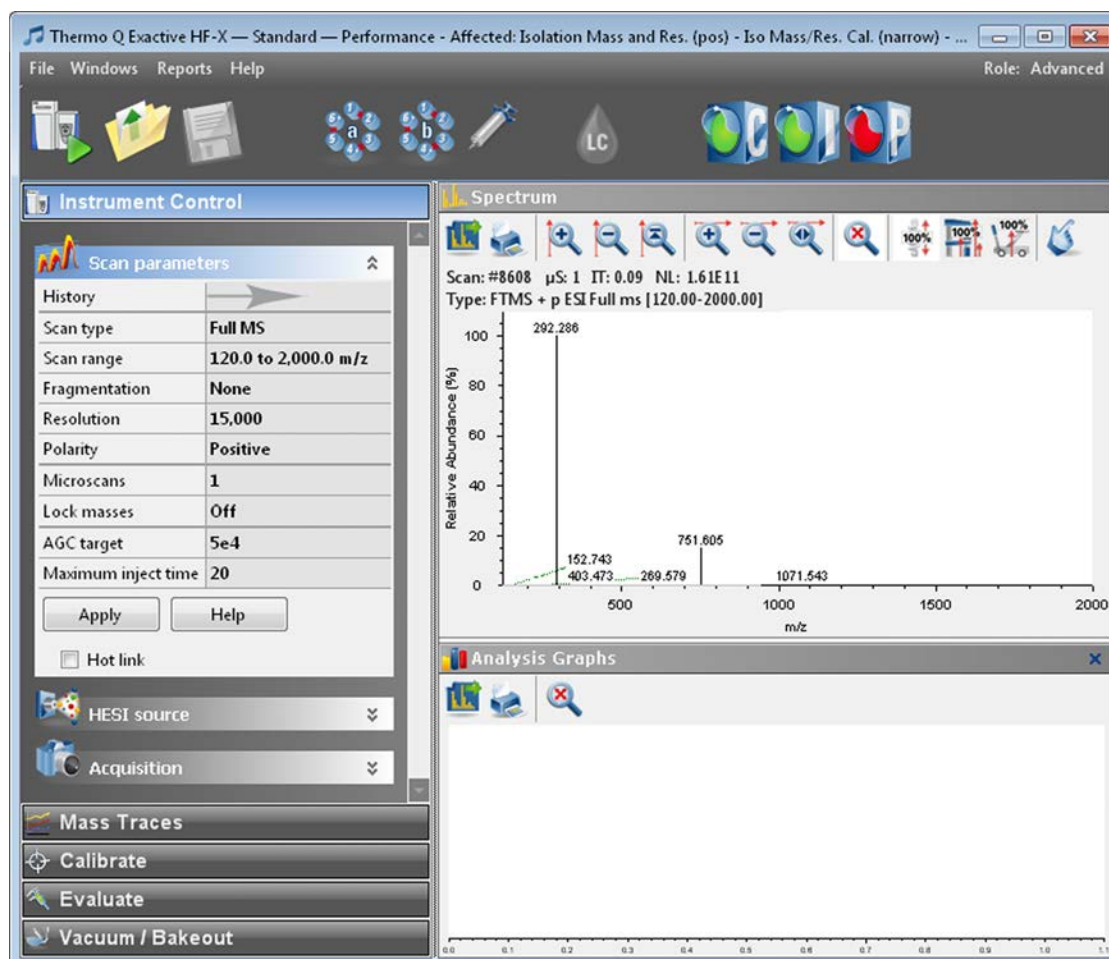


Figure 4-1. Q Exactive HF-X Tune

❖ To display this window

- Choose **Start > Programs > Thermo Exactive Series > Tune**, or
- Click  on the desktop.

When you are running Q Exactive HF-X Tune, an Q Exactive HF-X Tune icon () is displayed in the Microsoft™ Windows™ system tray. Double-click the  icon to display the Q Exactive HF-X Tune window when it is minimized. Right-click the  icon to display a shortcut menu that provides commands for restoring or terminating Q Exactive HF-X Tune.

Title Bar

The Q Exactive HF-X Tune title bar displays the name of the program, the name of the current Tune Method, and the instrument status. An asterisk indicates a Tune Method with unsaved changes.

Menus

The Q Exactive HF-X Tune menu bar displays the available menus. The Q Exactive HF-X Tune menus are as follows:

- [File Menu](#)
- [Windows Menu](#)
- [Reports Menu](#)
- [Help Menu](#)

On the far right side of the menu bar, the active user role is displayed.

Toolbar

The [Toolbar](#) provides symbol shortcuts for frequently used commands. It is located below the title bar of the Q Exactive HF-X Tune window.

Tasks Panel

The tasks panel on the left side of the Q Exactive HF-X Tune window comprises five windows:

- The [Instrument Control Window](#) on the left side of the Q Exactive HF-X Tune window comprises three windows:
 - [Scan Parameters Window](#) for defining a scan depending on the scan mode and scan type combination.
 - API Source window for displaying and editing parameters of the API source. The window adapts name and parameters of the currently detected source. At present, Q Exactive HF-X Tune provides the following API source windows:

[ESI Source Window](#)

[HESI Source Window](#)

[NSI Source Window](#)

[APCI Source Window](#)

[APPI Source Window](#)

[DART Source Window](#)

MALDI Source Window

- [Acquisition Window](#) for acquiring and storing measurement data.
- [Mass Traces Window](#) for selecting mass traces that are displayed in the Analysis Graphs Window.
- [Calibrate Window](#) for performing an automatic optimization of the calibration parameters.
- [Evaluate Window](#) for performing an automatic check of the instrument precision.
- [Vacuum / Bakeout Window](#) for displaying the pressure values at the vacuum gauges and performing an instrument bakeout.

Display Panel

The display panel on the right side of the Q Exactive HF-X Tune window comprises up to five windows:

- [Spectrum Window](#) for displaying a real-time data plot. The spectrum window is always visible.
- [Instrument Status Window](#) for displaying instrument parameters.
- [Messages Window](#) for displaying current status information about the instrument, the control service, or other programs.
- [Analysis Graphs Window](#) for displaying a real-time graph.
- [Debug Messages Window](#) for displaying messages that can be used during software development. The debug messages window is not available for standard users.

In addition to these five windows, the display panel may show additional windows for controlling other installed instruments.

Q Exactive HF-X Tune Menus

The Q Exactive HF-X Tune window has the following menus:

- [File Menu](#)
- [Windows Menu](#)
- [Reports Menu](#)
- [Help Menu](#)

User Role

On the far right side of the menu bar, the active user role is displayed. The user role specifies the number of parameters that are available for the active experiment. Standard User is the user role with the lowest number of available parameters.

Click the entry (Advanced, for example) to display a list that displays the available user roles. To change the active user role, click the respective entry. The number of available user roles depends on the installed licenses. See “[License Dialog Box](#)” on [page 4-64](#).

File Menu

The File menu provides commands for file and program operations. It has the following commands:

Command	Description
Load Tune File	Displays a dialog box that you can use to find and open a tune file (*.mstune) that already exists.
Save Tune File	Saves the active tune file with the current settings. Do not overwrite the default tune file <i>C:\Xcalibur\methods\HESI_Installation.mstune!</i>
Save Tune File as	Opens a dialog box that you can use to enter a new file name and to select the location (disk and directory) where you want to save it. Click Save to save the tune file with the current settings. Do not overwrite the default tune file <i>C:\Xcalibur\methods\HESI_Installation.mstune!</i>

Command	Description
Export System Settings	Opens a dialog box that you can use to save the current system settings (*.ini) to be imported on another computer that has no instrument attached and is intended for method editing. This computer has to have installed all needed software including Thermo Platform, Thermo Xcalibur and all instrument drivers like HPLC drivers installed. Imported values will be overwritten if an instrument will be attached later.
Terminate	Closes the active window. If the active tune file contains unsaved changes, a dialog box warns about losing data when you terminate the program.

Windows Menu

The Windows menu provides commands for customizing the information displayed in the Q Exactive HF-X Tune window. The system highlights the icon to the left of a command if the window is active. Deselect the command to hide the window.

The Windows menu has the following commands:

Command	Description
View > Show all	Displays all windows of Q Exactive HF-X Tune.
 Tooltips	Displays a short description of an item on the Q Exactive HF-X Tune window when you rest the mouse pointer over it.
 Spectrum	Displays the Spectrum window. The Spectrum Window is always visible.
 Instrument Status	Displays/Hides the Instrument Status window.
 Messages	Displays/Hides the Messages window.
 Analysis Graphs	Displays/Hides the Analysis Graphs window.
 Debug Messages	Displays/Hides the Debug Messages window. The debug messages window is not available for standard users.

Command	Description
 Mass Calculator	Displays the Mass Calculator, which helps you to calculate the mass of a compound of interest.
Installed instruments	Depending on the individual configuration of your system, additional commands may allow displaying windows for controlling other installed instruments (Accela™ AS or Accela Pump, for example.)

Tip Q Exactive HF-X Tune may open some windows (the analysis graphs window, for example) without user interaction if new important information is available.

Reports Menu

The Reports menu provides access to various calibration reports. The individual commands are available only when the respective reports have been created. If no reports exist (in a new system, for example), the Reports menu is shown grayed out and has no commands.

The Reports menu has the following commands:

Command	Description
Calibration > Latest	Opens the latest complete calibration report in PDF format.
Calibration > List	Displays the list of up to five (5) complete calibration reports. To open a report, double-click any of the calibration from the list.
Spectral Mass Calibration (neg) > Latest	Opens the latest negative mode calibration report in PDF format.
Spectral Mass Calibration (neg) > List	Displays the list of up to five (5) negative mode calibration reports. To open a report, double-click any of the spectral mass calibration from the list.
Spectral Mass Calibration (pos) > Latest	Opens the latest positive mode calibration report in PDF format.
Spectral Mass Calibration (pos) > List	Displays the list of up to five (5) positive mode calibration reports. To open a report, double-click any of the spectral mass calibration from the list.

Command	Description
Evaluation > Latest	Opens the latest complete evaluation report in PDF format.
Evaluation > List	Displays the list of up to five (5) complete evaluation reports. To open a report, double-click any of the items from the list.
Spectral Mass Evaluation (neg) > Latest	Opens the latest negative mode evaluation report in PDF format.
Spectral Mass Evaluation (neg) > List	Displays the list of up to five (5) negative mode evaluation reports. To open a report, double-click any of the items from the list.
Spectral Mass Evaluation (pos) > Latest	Opens the latest positive mode evaluation report in PDF format.
Spectral Mass Evaluation (pos) > List	Displays the list of up to five (5) positive mode evaluation reports. To open a report, double-click any of the items from the list.
All Reports	Opens a file manager window with a list of all previously acquired spectral mass calibration reports.

Help Menu

The Help menu groups commands that provide information about Q Exactive HF-X Tune. It has the following commands:

Command	Description
Help Overview	Displays Q Exactive HF-X Tune Help.
Help Content	Displays the table of contents for Q Exactive HF-X Tune Help.
Help Index	Displays the index for Q Exactive HF-X Tune Help.
About	Displays the About dialog box with information about the instrument and the current Q Exactive HF-X Tune version.

Toolbar

The Q Exactive HF-X Tune toolbar provides symbol shortcuts for frequently used commands. It is located below the title bar of the Q Exactive HF-X Tune window. To activate a toolbar function, click the corresponding toolbar button.

Some symbols provide information about the current statuses of respective instrument components either by their color or by displaying a tooltip when you rest the mouse pointer on them.

The following functions are available:

Button	Description
	General instrument state
	On / Standby / Off
	Run by Xcalibur
	
	Click to toggle between the instrument operating statuses On, Standby, and Off. The button reflects the instrument status: - When the mass spectrometer is On, Q Exactive HF-X Tune displays . - When the mass spectrometer is in Standby, Q Exactive HF-X Tune displays . - When the mass spectrometer is Off, Q Exactive HF-X Tune displays . The status of this button controls also the statuses of gas flow and syringe pump use (if present). If the mass spectrometer is controlled by an Xcalibur sequence, Q Exactive HF-X Tune displays . The acquisition can only be stopped from Xcalibur Sequence Setup View.
IMPORTANT When you start an acquisition while the instrument is in Off position, the instrument begins acquiring data after a delay of about 30 seconds.	
	Open
	Save
	Click to display a dialog box that you can use to find and open a *.mstune file that already exists. Or, choose File > Load Tune File. Click to open a dialog box that you can use to select the location (disk and directory) where you want to save the tune file. Or, choose File > Save Tune File as. This button is not available when the settings of the active tune file are not changed.

Button		Description
 	Divert Valve A Position 1 or Position 2	Click to switch the valve position directly. The button reflects the valve status (connected positions, Valve “a”).
 	Divert Valve B Position 1 or Position 2	Click to switch the valve position directly. The button reflects the valve status (connected positions, Valve “b”).
  	Syringe Pump Settings Syringe Pump On or Syringe Pump Off	Click to switch on/off the syringe pump (if present). A symbol in the lower right corner of the button indicates the current status of the syringe pump: - When the syringe pump is On, Q Exactive HF-X Tune displays . - When the syringe pump is Off, Q Exactive HF-X Tune displays . - When the syringe pump is in an unknown status, Q Exactive HF-X Tune displays . Click the down arrow to display the Syringe Pump Settings dialog box. Here, you can specify syringe pump parameters or manually operate the syringe pump.
	Direct Instrument Control	Click to display additional commands that allow displaying windows for controlling other installed instruments. The following systems are supported by instrument direct control: - Thermo Scientific Accela™ 1250 Pump - Thermo Scientific Accela Open AS autosampler - CTC PAL™ autosampler
  	Communication Status	Shows the actual communication status of the system: - Green: communication with instrument is OK. - Yellow: only service is accessible (no instrument). - Red: communication is broken (no instrument, no service).

Button		Description
	Hardware Status	Shows the actual hardware status of the system (top instrument tree state): - Green: all readbacks are in specifications (green hooks). - Red: one or more readbacks are out of range.
	Performance Status	Shows the actual performance status of the system: - Green: the last evaluation/calibration was successful. - Yellow: the last evaluation/calibration was successful, but is out of date. - Red: the evaluation/calibration was not successful. By default, the performance status icon turns yellow 25 hours after the last successful mass calibration or check. Advanced users can change this value in the System node of the instrument status window according to their mass accuracy requirements.
	Procedure active	If a procedure is active (for example, system bakeout or tune) Q Exactive HF-X Tune displays an animated icon next to the performance status button.
	Acquisition indicator	If the mass spectrometer is acquiring data, Q Exactive HF-X Tune displays an animated icon next to the performance status button.

Tasks Panel

Use the windows of the tasks panel to perform procedures that maintain the quality of measurements with the Q Exactive HF-X mass spectrometer.

The tasks panel is always visible. The windows in the tasks panel can be minimized or maximized. Click the title bar of an individual window to display it.

- [Instrument Control Window](#)
- [Mass Traces Window](#)
- [Calibrate Window](#)
- [Evaluate Window](#)
- [Vacuum / Bakeout Window](#)

Instrument Control Window

Use the windows of the Instrument Control window to enter individual physical settings and to acquire scans. The following windows are available:

- [Scan Parameters Window](#)
- API Source Window (one of the following)
 - [ESI Source Window](#)
 - [HESI Source Window](#)
 - [NSI Source Window](#)
 - [APCI Source Window](#)
 - [APPI Source Window](#)
 - [DART Source Window](#)
 - [MALDI Source Window](#)
- [Acquisition Window](#)

The Instrument Control window is always visible. Click the title bar of an individual window to display it. Click again to hide it. To change the order of windows within the Instrument Control window, drag individual windows by their title bars to the new places.

Scan Parameters Window

Use the Scan Parameters window to define a scan depending on the selected scan mode and scan type combination. See [Figure 4-2](#). The mass spectrometer updates the scan parameters only after you click **Apply** or select the Hot link check box.

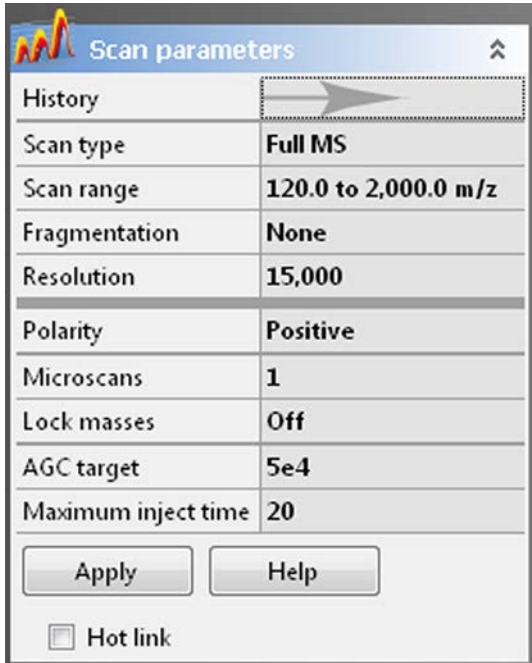


Figure 4-2. Scan Parameters window

The Scan Parameters window has the following parameters:

Parameter	Description
History	Click to display the Scan Parameters History dialog box. Here, select from a list of recent scans based on short scan descriptions. The maximum number of list items is 100. After a change of parameters, the history is updated when you click Apply or when you change the status of the Hot link check box.
Scan Type	Displays the current scan type. To change the settings, click into the field to display the Scan Type dialog box.
Scan Range	Displays the current scan range. To change the settings, click into the field to display the Scan Range dialog box.
Fragmentation	Displays the current settings for HCD fragmentation and in-source CID fragmentation. If no fragmentation type is selected, the text field shows <i>None</i> . To change the settings, click into the field to display the Fragmentation dialog box. Automatic tuning is disabled when in-source CID fragmentation is on.

Parameter	Description
Resolution	Use this list box to select the mass resolution for FTMS analysis. The mass resolution of the Orbitrap analyzer is proportional to $1/\sqrt{m/z}$. The scan time increases with increasing resolution and detect time. Available options are 7500, 15000, 30000, 45000, 60000, 120000, or 240000.
Polarity	Use this list box to toggle between positive ion and negative ion polarity.
Microscans	Use this spin box to select the number of averaged transients for one scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The valid range is from 1 to 10 microscans.
Lock masses	Displays the active lock masses. During a scan, the mass spectrometer uses only the lock masses with a polarity that matches the ion mode. If no lock masses are selected, the text field shows <i>Off</i>. To change the settings, click into the field to display the Lock Masses dialog box. Q Exactive HF-X Tune allows using active lock masses in user-defined calibration mass lists.
AGC target	Use this list box to select the AGC target value. The AGC target value controls the number of ions that are injected into the Orbitrap analyzer. Available options are 2e4, 5e4, 1e5, 2e5, 5e5, 1e6, 3e6, and 5e6.
Maximum inject time	Use this list box to type or click a maximum injection time for AGC. For example, type 160 . The valid range is from 1 to 3000 milliseconds.
Buttons	
Apply	Sends all changes to the instrument.
Help	Displays the Help for this window.
Hot Link	Select the Hot link check box to allow Q Exactive HF-X Tune to send any changes immediately to the instrument. A green frame around the parameter box indicates an active hot link.

❖ To display this window

Click the Scan Parameters window title bar in the Instrument Control window.

ESI Source Window

Use the ESI source window to specify electrospray ionization (ESI) source parameters. See [API Source Settings for Various LC Flow Rates](#) for recommended settings. The mass spectrometer updates the ESI source parameters only after you click **Apply** or with the Hot link check box being selected. See [Figure 4-3](#).

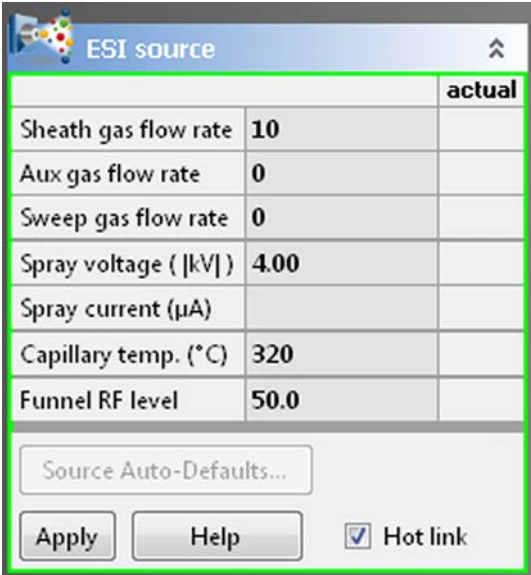


Figure 4-3. ESI source window

This window is available only when the mass spectrometer has detected an installed ESI source.

The ESI source window has the following parameters:

Parameter	Description
Sheath Gas Flow Rate	Displays the setpoint ESI source sheath gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Sheath Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the sheath gas flow rate to any value from 0 to 80 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sheath Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Aux Gas Flow Rate	Displays the setpoint ESI source auxiliary gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Aux Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 40 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Aux Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).

Parameter	Description
Sweep Gas Flow Rate	Displays the setpoint ESI source sweep gas flow rate. To change the setpoint flow rate, click the arrows in the Sweep Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 10 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sweep Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Spray Voltage	Displays the setpoint ESI source spray voltage (absolute value, in kilovolts). To change the setpoint spray voltage, click the arrows in the Spray Voltage spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the spray voltage to any value from 0.0 to 8.0 kV. The sign of the spray voltages changes automatically with the ion polarity mode: positive for positive ions and negative for negative ions. Or, enter a value in the spin box text field. The mass spectrometer changes the spray voltage when you click Apply or with the Hot link check box being selected. The Spray Voltage readback is to the right of the spin box. This readback displays the actual spray voltage (absolute value, in kilovolts).
Spray Current	This readback displays the actual ESI source spray current (in microamperes). The ESI spray current is typically less than 5 μA.
Capillary Temperature	Displays the setpoint ESI source heated capillary temperature (in degrees Celsius). To change the setpoint heated capillary temperature, click the arrows in the Capillary Temp spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the heated capillary temperature to any value from 0 to 450 °C. Or, enter a value in the spin box text field. The mass spectrometer changes the heated capillary temperature when you click Apply or with the Hot link check box being selected. The Capillary Temperature readback is to the right of the spin box. This readback displays the actual temperature (in degrees Celsius) of the heated capillary.

Parameter	Description
Funnel RF Level	Displays a numerical factor that the mass spectrometer uses, along with the lowest and highest mass, to calculate the Funnel RF amplitude. The magnitude of the Funnel RF level affects the mass spectrum as follows: - Decreasing the Funnel RF level will decrease the amount of fragmentation of fragile ions in the ion funnel. - Decreasing the Funnel RF level will decrease the transmission of high m/z ions through the ion funnel and increase the transmission of the low m/z ions. - Increasing the Funnel RF level will increase the amount of fragmentation of fragile ions in the ion funnel. - Increasing the Funnel RF level will increase the transmission of high m/z ions through the ion funnel and decrease the transmission of the low m/z ions. To change the Funnel RF level, click the arrows in the Funnel Level spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the Funnel RF level to any value from 0 to 100 (200)*. Or, enter a value in the spin box text field. The mass spectrometer changes the Funnel RF level when you click Apply or with the Hot link check box being selected. *The value in parentheses applies only to systems with a valid High Mass Range license. For stable ions, the default value, 50, provides a good starting point. By default, the Funnel RF level remains at 50 during all calibrations.
Buttons	
Source Auto-Defaults	This parameter is not available for this ion source type.
Apply	Sends all changes to the instrument.
Help	Displays the Help for this window.
Hot Link	Select the Hot link check box to allow Q Exactive HF-X Tune to send any changes immediately to the instrument. A green frame around the parameter box indicates an active hot link.

❖ To display this window

Click the ESI source window title bar in the Instrument Control window.

HESI Source Window

Use the HESI source window to specify heated-electrospray ionization (H-ESI) source parameters. See [API Source Settings for Various LC Flow Rates](#) for recommended settings. The mass spectrometer updates the H-ESI source parameters only after you click **Apply** or with the Hot link check box being selected. See [Figure 4-4](#).

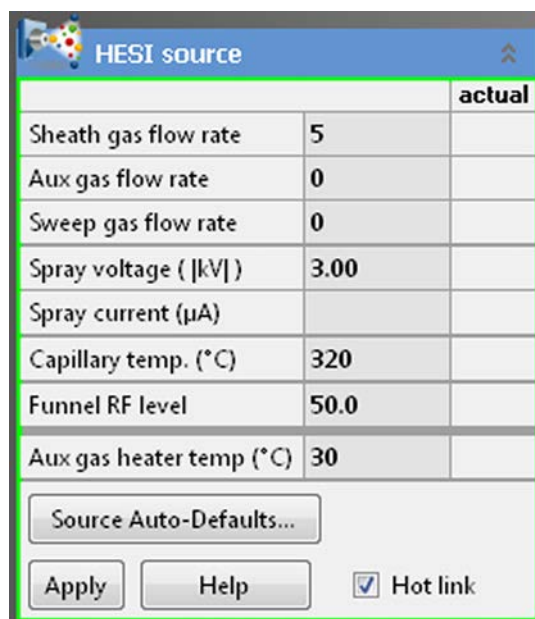


Figure 4-4. HESI source window

This window is available only when the mass spectrometer has detected an installed H-ESI source. The H-ESI source is the standard API source of the Q Exactive HF-X mass spectrometer.

The HESI source window has the following parameters:

Parameter	Description
Sheath Gas Flow Rate	Displays the setpoint H-ESI source sheath gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Sheath Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the sheath gas flow rate to any value from 0 to 80 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sheath Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Aux Gas Flow Rate	Displays the setpoint H-ESI source auxiliary gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Aux Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 40 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Aux Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).

Parameter	Description
Sweep Gas Flow Rate	Displays the setpoint H-ESI source sweep gas flow rate. To change the setpoint flow rate, click the arrows in the Sweep Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 10 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sweep Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Spray Voltage	Displays the setpoint H-ESI source spray voltage (absolute value, in kilovolts). To change the setpoint spray voltage, click the arrows in the Spray Voltage spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the spray voltage to any value from 0.0 to 8.0 kV. The sign of the spray voltages changes automatically with the ion polarity mode: positive for positive ions and negative for negative ions. Or, enter a value in the spin box text field. The mass spectrometer changes the spray voltage when you click Apply or with the Hot link check box being selected. The Spray Voltage readback is to the right of the spin box. This readback displays the actual spray voltage (absolute value, in kilovolts).
Spray Current	This readback displays the actual H-ESI source spray current (in microamperes). The H-ESI spray current is typically less than 5 μA.
Capillary Temperature	Displays the setpoint H-ESI source heated capillary temperature (in degrees Celsius). To change the setpoint heated capillary temperature, click the arrows in the Capillary Temp spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the heated capillary temperature to any value from 0 to 450 °C. Or, enter a value in the spin box text field. The mass spectrometer changes the heated capillary temperature when you click Apply or with the Hot link check box being selected. The Capillary Temperature readback is to the right of the spin box. This readback displays the actual temperature (in degrees Celsius) of the heated capillary.

Parameter	Description
Funnel RF Level	Displays a numerical factor that the mass spectrometer uses, along with the lowest and highest mass, to calculate the Funnel RF amplitude. The magnitude of the Funnel RF level affects the mass spectrum as follows: - Decreasing the Funnel RF level will decrease the amount of fragmentation of fragile ions in the ion funnel. - Decreasing the Funnel RF level will decrease the transmission of high m/z ions through the ion funnel and increase the transmission of the low m/z ions. - Increasing the Funnel RF level will increase the amount of fragmentation of fragile ions in the ion funnel. - Increasing the Funnel RF level will increase the transmission of high m/z ions through the ion funnel and decrease the transmission of the low m/z ions. To change the Funnel RF level, click the arrows in the Funnel Level spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the Funnel RF level to any value from 0 to 100 (200)*. Or, enter a value in the spin box text field. The mass spectrometer changes the Funnel RF level when you click Apply or with the Hot link check box being selected. *The value in parentheses applies only to systems with a valid High Mass Range license. For stable ions, the default value, 50, provides a good starting point. By default, the Funnel RF level remains at 50 during all calibrations.
Aux. Gas Heater Temperature	Displays the setpoint temperature (in degrees Celsius) of the H-ESI source heater, which heats the auxiliary gas. To change the setpoint vaporizer temperature, click the arrows in the Heater Temp spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the vaporizer temperature to any value from 0 to 600 °C. Or, enter a value in the spin box text field. The mass spectrometer changes the vaporizer temperature when you click Apply or with the Hot link check box being selected. The Heater Temperature readback is to the right of the spin box. This readback displays the actual temperature (in degrees Celsius) of the vaporizer.
Buttons	
Source Auto-Defaults	Displays the Autoselect ion source values dialog box.
Apply	Sends all changes to the instrument.
Help	Displays the Help for this window.
Hot Link	Select the Hot link check box to allow Q Exactive HF-X Tune to send any changes immediately to the instrument. A green frame around the parameter box indicates an active hot link.

❖ To display this window

Click the HESI source window title bar in the Instrument Control window.

NSI Source Window

Use the NSI source window to specify nanospray ionization (NSI) source parameters. See [Figure 4-5](#). The mass spectrometer updates the NSI source parameters only after you click **Apply** or with the Hot link check box being selected.

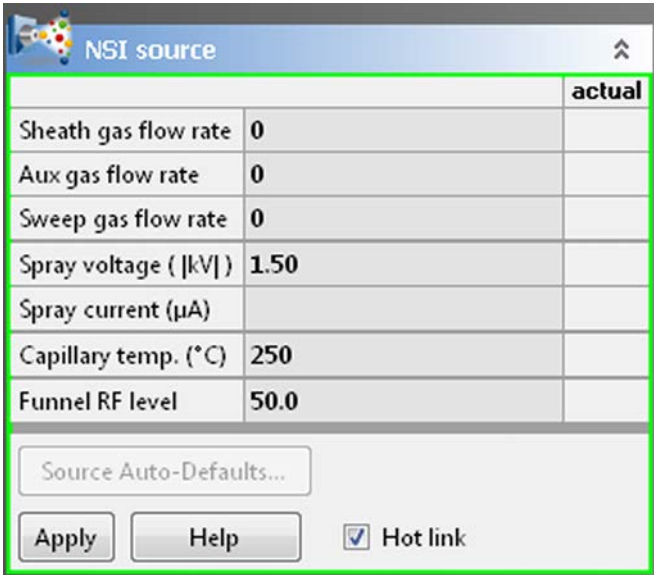


Figure 4-5. NSI source window

This window is available only when the Q Exactive HF-X mass spectrometer has detected an installed NSI source.

The NSI source window has the following parameters:

Parameter	Description
Sheath Gas Flow Rate	Displays the setpoint NSI source sheath gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Sheath Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the sheath gas flow rate to any value from 0 to 80 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sheath Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Aux Gas Flow Rate	Displays the setpoint NSI source auxiliary gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Aux Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 40 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Aux Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).

Parameter	Description
Sweep Gas Flow Rate	Displays the setpoint NSI source sweep gas flow rate. To change the setpoint flow rate, click the arrows in the Sweep Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 10 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sweep Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Spray Voltage	Displays the setpoint NSI source spray voltage (absolute value, in kilovolts). To change the setpoint spray voltage, click the arrows in the Spray Voltage spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the spray voltage to any value from 0.0 to 8.0 kV. The sign of the spray voltages changes automatically with the ion polarity mode: positive for positive ions and negative for negative ions. Or, enter a value in the spin box text field. The mass spectrometer changes the spray voltage when you click Apply or with the Hot link check box being selected. The Spray Voltage readback is to the right of the spin box. This readback displays the actual spray voltage (absolute value, in kilovolts).
Spray Current	This readback displays the actual NSI source spray current (in microamperes). NSI spray current is typically less than 5 μA.
Capillary Temperature	Displays the setpoint NSI source heated capillary temperature (in degrees Celsius). To change the setpoint heated capillary temperature, click the arrows in the Capillary Temp spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the heated capillary temperature to any value from 0 to 450 °C. Or, enter a value in the spin box text field. The mass spectrometer changes the heated capillary temperature when you click Apply or with the Hot link check box being selected. The Capillary Temperature readback is to the right of the spin box. This readback displays the actual temperature (in degrees Celsius) of the heated capillary.

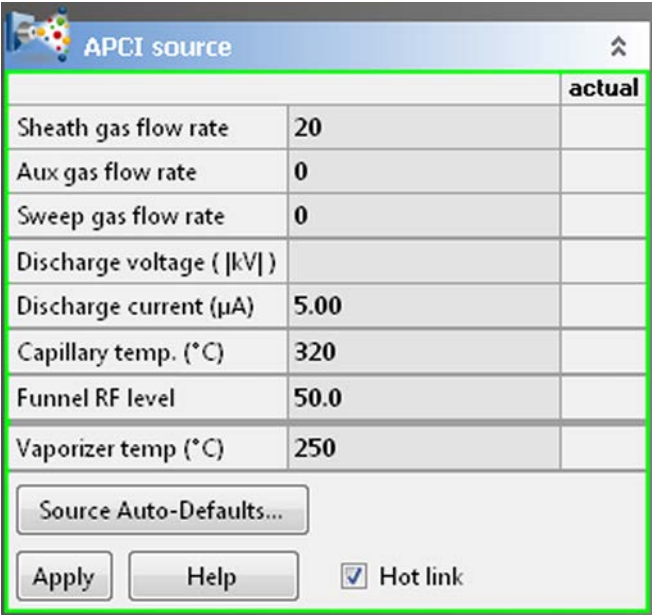
Parameter	Description
Funnel RF Level	Displays a numerical factor that the mass spectrometer uses, along with the lowest and highest mass, to calculate the Funnel RF amplitude. The magnitude of the Funnel RF level affects the mass spectrum as follows: - Decreasing the Funnel RF level will decrease the amount of fragmentation of fragile ions in the ion funnel. - Decreasing the Funnel RF level will decrease the transmission of high m/z ions through the ion funnel and increase the transmission of the low m/z ions. - Increasing the Funnel RF level will increase the amount of fragmentation of fragile ions in the ion funnel. - Increasing the Funnel RF level will increase the transmission of high m/z ions through the ion funnel and decrease the transmission of the low m/z ions. To change the Funnel RF level, click the arrows in the Funnel Level spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the Funnel RF level to any value from 0 to 100 (200)*. Or, enter a value in the spin box text field. The mass spectrometer changes the Funnel RF level when you click Apply or with the Hot link check box being selected. *The value in parentheses applies only to systems with a valid High Mass Range license. For stable ions, the default value, 50, provides a good starting point. By default, the Funnel RF level remains at 50 during all calibrations.
Buttons	
Source Auto-Defaults	This parameter is not available for this ion source type.
Apply	Sends all changes to the instrument.
Help	Displays the Help for this window.
Hot Link	Select the Hot link check box to allow Q Exactive HF-X Tune to send any changes immediately to the instrument. A green frame around the parameter box indicates an active hot link.

❖ To display this window

Click the NSI source window title bar in the Instrument Control window.

APCI Source Window

Use the APCI source window to set up an atmospheric pressure chemical ionization (APCI) experiment. See [API Source Settings for Various LC Flow Rates](#) for recommended settings. The mass spectrometer updates the APCI source parameters only after you click **Apply** or with the Hot link check box being selected. See [Figure 4-6](#).



The screenshot shows the 'APCI source' window with a table of parameters and their values. The 'actual' column is empty for all parameters. Below the table are buttons for 'Source Auto-Defaults...', 'Apply', and 'Help', along with a checked 'Hot link' checkbox.

		actual
Sheath gas flow rate	20	
Aux gas flow rate	0	
Sweep gas flow rate	0	
Discharge voltage (kV)		
Discharge current (μA)	5.00	
Capillary temp. (°C)	320	
Funnel RF level	50.0	
Vaporizer temp (°C)	250	

Source Auto-Defaults...
Apply Help ☒ Hot link

Figure 4-6. APCI source window

This window is available only when the mass spectrometer has detected an installed APCI source.

The APCI source window has the following parameters:

Parameter	Description
Sheath Gas Flow Rate	Displays the setpoint APCI source sheath gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Sheath Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the sheath gas flow rate to any value from 0 to 80 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sheath Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Aux Gas Flow Rate	Displays the setpoint APCI source auxiliary gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Aux Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 40 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Aux Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).

Parameter	Description
Sweep Gas Flow Rate	Displays the setpoint APCI source sweep gas flow rate. To change the setpoint flow rate, click the arrows in the Sweep Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 10 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sweep Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Discharge Voltage	Displays the actual APCI source discharge voltage (absolute value, in kilovolts).
Discharge Current	Displays the setpoint APCI source discharge current (in microamperes). To change the setpoint discharge current, click the arrows in the Discharge Current spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the discharge current to any value from 0 to 10 μA. (A typical value is 5 μA.) Or, enter a value in the spin box text field. The mass spectrometer changes the discharge current when you click Apply or with the Hot link check box being selected. The Discharge Current readback is to the right of the spin box. This readback displays the actual discharge current (in microamperes).
Capillary Temperature	Displays the setpoint APCI source heated capillary temperature (in degrees Celsius). To change the setpoint heated capillary temperature, click the arrows in the Capillary Temp spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the heated capillary temperature to any value from 0.00 to 300.00 $^{\circ}\text{C}$. Or, enter a value in the spin box text field. The mass spectrometer changes the heated capillary temperature when you click Apply or with the Hot link check box being selected. The Capillary Temperature readback is to the right of the spin box. This readback displays the actual temperature (in degrees Celsius) of the heated capillary.

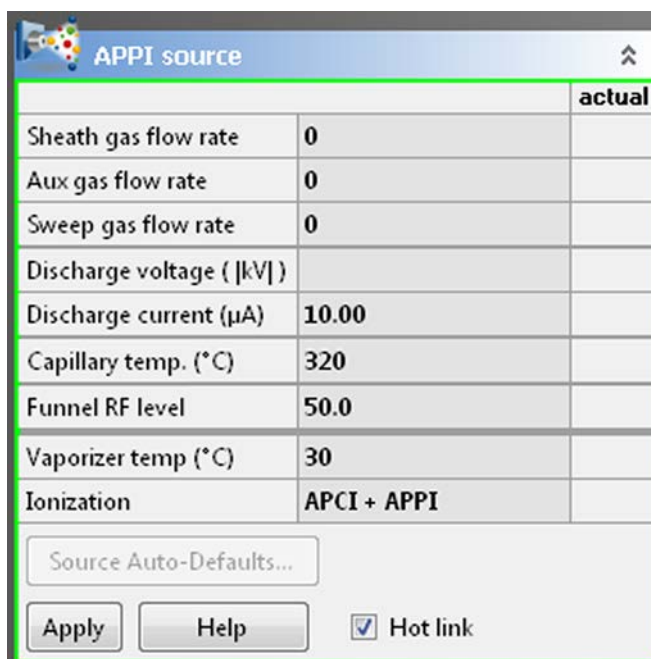
Parameter	Description
Funnel RF Level	Displays a numerical factor that the mass spectrometer uses, along with the lowest and highest mass, to calculate the Funnel RF amplitude. The magnitude of the Funnel RF level affects the mass spectrum as follows: - Decreasing the Funnel RF level will decrease the amount of fragmentation of fragile ions in the ion funnel. - Decreasing the Funnel RF level will decrease the transmission of high m/z ions through the ion funnel and increase the transmission of the low m/z ions. - Increasing the Funnel RF level will increase the amount of fragmentation of fragile ions in the ion funnel. - Increasing the Funnel RF level will increase the transmission of high m/z ions through the ion funnel and decrease the transmission of the low m/z ions. To change the Funnel RF level, click the arrows in the Funnel Level spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the Funnel RF level to any value from 0 to 100 (200)*. Or, enter a value in the spin box text field. The mass spectrometer changes the Funnel RF level when you click Apply or with the Hot link check box being selected. *The value in parentheses applies only to systems with a valid High Mass Range license. For stable ions, the default value, 50, provides a good starting point. By default, the Funnel RF level remains at 50 during all calibrations.
Vaporizer Temperature	Displays the setpoint APCI source vaporizer temperature (in degrees Celsius). To change the setpoint vaporizer temperature, click the arrows in the Vaporizer Temp. spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the vaporizer temperature to any value from 0 to 600 °C. Or, enter a value in the spin box text field. The mass spectrometer changes the vaporizer temperature when you click Apply or with the Hot link check box being selected. The Vaporizer Temperature readback is to the right of the spin box. This readback displays the actual temperature (in degrees Celsius) of the vaporizer.
Buttons	
Source Auto-Defaults	Displays the Autoselect ion source values dialog box.
Apply	Sends all changes to the instrument.
Help	Displays the Help for this window.
Hot Link	Select the Hot link check box to allow Q Exactive HF-X Tune to send any changes immediately to the instrument. A green frame around the parameter box indicates an active hot link.

❖ **To display this window**

Click the APCI source window title bar in the Instrument Control window.

APPI Source Window

Use the APPI source window to specify atmospheric pressure chemical ionization (APCI) source parameters and to turn on and off the atmospheric pressure photoionization (APPI) lamp. See [Figure 4-7](#). The mass spectrometer updates the APPI source parameters only after you click **Apply** or with the Hot link check box being selected.



The screenshot shows the 'APPI source' window with a table of parameters and their values. The 'actual' column is empty for all parameters. Below the table are buttons for 'Source Auto-Defaults...', 'Apply', 'Help', and a checked 'Hot link' checkbox.

		actual
Sheath gas flow rate	0	
Aux gas flow rate	0	
Sweep gas flow rate	0	
Discharge voltage (kV)		
Discharge current (μA)	10.00	
Capillary temp. (°C)	320	
Funnel RF level	50.0	
Vaporizer temp (°C)	30	
Ionization	APCI + APPI	

Source Auto-Defaults... ☒ Hot link

Figure 4-7. APPI source window

This window is available only when the mass spectrometer has detected an installed APPI source.

The APPI source window has the following parameters:

Parameter	Description
Sheath Gas Flow Rate	Displays the setpoint APPI source sheath gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Sheath Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the sheath gas flow rate to any value from 0 to 80 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sheath Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Aux Gas Flow Rate	Displays the setpoint APPI source auxiliary gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Aux Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 40 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Aux Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Sweep Gas Flow Rate	Displays the setpoint APPI source sweep gas flow rate. To change the setpoint flow rate, click the arrows in the Sweep Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 10 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sweep Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Discharge Voltage	When APPI is selected as ionization method, the actual discharge voltage displays '0'. When either APCI or APCI+APPI is selected as ionization method, the actual discharge voltage displays APCI voltage readback (absolute value, in kilovolts).
Discharge Current	Displays the setpoint source discharge current (in microamperes). To change the setpoint discharge current, click the arrows in the Discharge Current spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the discharge current to any value from 0 to 80 μA. (A typical value is 5 μA.) Or, enter a value in the spin box text field. The mass spectrometer changes the discharge current when you click Apply or with the Hot link check box being selected. When APPI is selected as ionization method, changes in discharge current have no effect. Discharge current changes are applied only when either APCI or APCI+APPI is selected as ionization method. The Discharge Current readback is to the right of the spin box. This readback displays the actual discharge current (in microamperes).

Parameter	Description
Capillary Temperature	Displays the setpoint APPI source heated capillary temperature (in degrees Celsius). To change the setpoint heated capillary temperature, click the arrows in the Capillary Temp spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the heated capillary temperature to any value from 0.00 to 450.00 °C. Or, enter a value in the spin box text field. The mass spectrometer changes the heated capillary temperature when you click Apply or with the Hot link check box being selected. The Capillary Temperature readback is to the right of the spin box. This readback displays the actual temperature (in degrees Celsius) of the heated capillary.
Funnel RF Level	Displays a numerical factor that the mass spectrometer uses, along with the lowest and highest mass, to calculate the Funnel RF amplitude. The magnitude of the Funnel RF level affects the mass spectrum as follows: • Decreasing the Funnel RF level will decrease the amount of fragmentation of fragile ions in the ion funnel. • Decreasing the Funnel RF level will decrease the transmission of high m/z ions through the ion funnel and increase the transmission of the low m/z ions. • Increasing the Funnel RF level will increase the amount of fragmentation of fragile ions in the ion funnel. • Increasing the Funnel RF level will increase the transmission of high m/z ions through the ion funnel and decrease the transmission of the low m/z ions. To change the Funnel RF level, click the arrows in the Funnel Level spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the Funnel RF level to any value from 0 to 100 (200)*. Or, enter a value in the spin box text field. The mass spectrometer changes the Funnel RF level when you click Apply or with the Hot link check box being selected. *The value in parentheses applies only to systems with a valid High Mass Range license. For stable ions, the default value, 50, provides a good starting point. By default, the Funnel RF level remains at 50 during all calibrations.
Vaporizer Temperature	Displays the setpoint APPI source vaporizer temperature (in degrees Celsius). To change the setpoint vaporizer temperature, click the arrows in the Vaporizer Temp. spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the vaporizer temperature to any value from 0 to 500 °C. Or, enter a value in the spin box text field. The mass spectrometer changes the vaporizer temperature when you click Apply or with the Hot link check box being selected. The Vaporizer Temperature readback is to the right of the spin box. This readback displays the actual temperature (in degrees Celsius) of the vaporizer.

Parameter	Description
Ionization	Use this list box to select the ionization method. The following options are available: • APCI APCI alone • APPI Photoionization • APCI + APPI APCI in combination with APCI
Buttons	
Source Auto-Defaults	This parameter is not available for this ion source type.
Apply	Sends all changes to the instrument.
Help	Displays the Help for this window.
Hot Link	Select the Hot link check box to allow Q Exactive HF-X Tune to send any changes immediately to the instrument. A green frame around the parameter box indicates an active hot link.

❖ **To display this dialog box**

Click the APPI source window title bar in the Instrument Control window.

DART Source Window

Use the DART source window to specify direct analysis in real time (DART™) source parameters. See [Figure 4-8](#). The mass spectrometer updates the DART source parameters only after you click **Apply** or with the Hot link check box being selected.

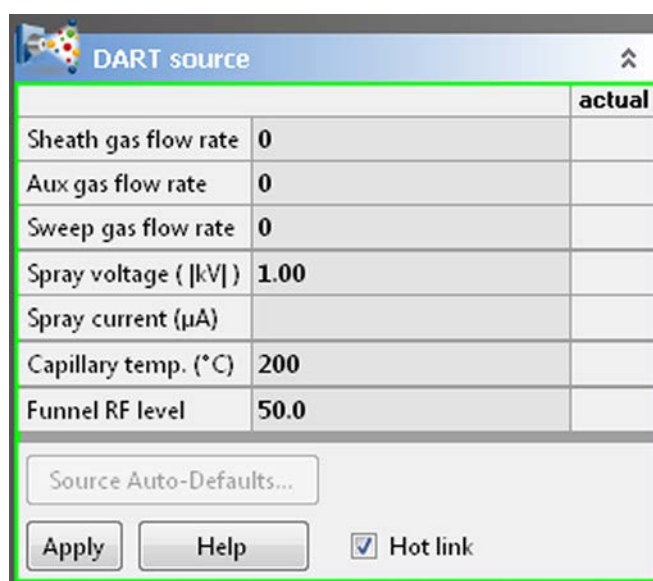


Figure 4-8. DART source window

Using a DART ion source increases the gas input into the UHV region. As a result, the pressure might exceed the instrument status warning level. This is indicated by a yellow LED in the Vacuum / Bakeout window. Advanced users can enable the DART ion source compatibility in the Instrument Status window to increase the UHV warning level.

This window is available only when the mass spectrometer has detected an installed DART source.

The DART source window has the following parameters:

Parameter	Description
Sheath Gas Flow Rate	Displays the setpoint DART source sheath gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Sheath Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the sheath gas flow rate to any value from 0 to 80 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sheath Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Aux Gas Flow Rate	Displays the setpoint DART source auxiliary gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Aux Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 40 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Aux Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Sweep Gas Flow Rate	Displays the setpoint DART source sweep gas flow rate. To change the setpoint flow rate, click the arrows in the Sweep Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 10 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sweep Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).

Parameter	Description
Spray Voltage	Displays the setpoint DART source spray voltage (absolute value, in kilovolts). To change the setpoint spray voltage, click the arrows in the Spray Voltage spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the spray voltage to any value from 0.0 to 8.0 kV. The sign of the spray voltages changes automatically with the ion polarity mode: positive for positive ions and negative for negative ions. Or, enter a value in the spin box text field. The mass spectrometer changes the spray voltage when you click Apply or with the Hot link check box being selected. The Spray Voltage readback is to the right of the spin box. This readback displays the actual spray voltage (absolute value, in kilovolts).
Spray Current	This readback displays the actual DART source spray current (in microamperes). DART spray current is typically less than 5 μA.
Capillary Temperature	Displays the setpoint DART source heated capillary temperature (in degrees Celsius). To change the setpoint heated capillary temperature, click the arrows in the Capillary Temp spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the heated capillary temperature to any value from 0.00 to 450.00 $^{\circ}$C. Or, enter a value in the spin box text field. The mass spectrometer changes the heated capillary temperature when you click Apply or with the Hot link check box being selected. The Capillary Temperature readback is to the right of the spin box. This readback displays the actual temperature (in degrees Celsius) of the heated capillary.
Funnel RF Level	Displays a numerical factor that the mass spectrometer uses, along with the lowest and highest mass, to calculate the Funnel RF amplitude. The magnitude of the Funnel RF level affects the mass spectrum as follows: - Decreasing the Funnel RF level will decrease the amount of fragmentation of fragile ions in the ion funnel. - Decreasing the Funnel RF level will decrease the transmission of high m/z ions through the ion funnel and increase the transmission of the low m/z ions. - Increasing the Funnel RF level will increase the amount of fragmentation of fragile ions in the ion funnel. - Increasing the Funnel RF level will increase the transmission of high m/z ions through the ion funnel and decrease the transmission of the low m/z ions. To change the Funnel RF level, click the arrows in the Funnel Level spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the Funnel RF level to any value from 0 to 100 (200)*. Or, enter a value in the spin box text field. The mass spectrometer changes the Funnel RF level when you click Apply or with the Hot link check box being selected. *The value in parentheses applies only to systems with a valid High Mass Range license. For stable ions, the default value, 50, provides a good starting point. By default, the Funnel RF level remains at 50 during all calibrations.

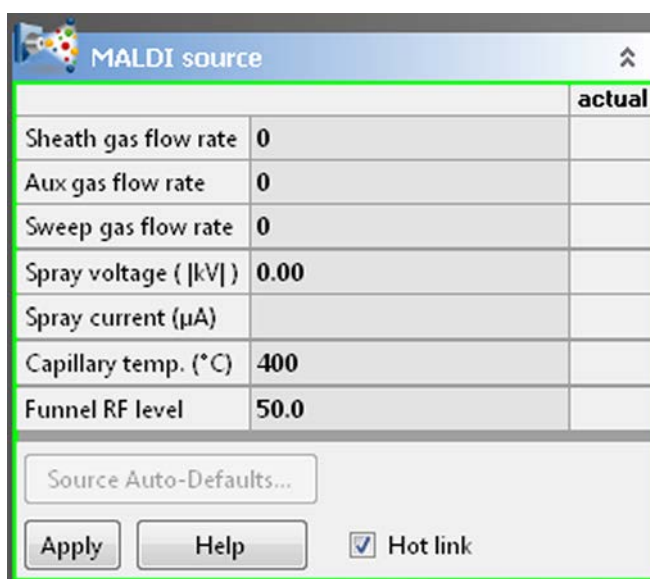
Parameter	Description
Buttons	
Source Auto-Defaults	This parameter is not available for this ion source type.
Apply	Sends all changes to the instrument.
Help	Displays the Help for this window.
Hot Link	Select the Hot link check box to allow Q Exactive HF-X Tune to send any changes immediately to the instrument. A green frame around the parameter box indicates an active hot link.

❖ To display this dialog box

Click the DART source window title bar in the Instrument Control window.

MALDI Source Window

Use the MALDI source window to specify matrix-assisted laser desorption/ionization (MALDI) source parameters. See [Figure 4-9](#). The mass spectrometer updates the MALDI source parameters only after you click **Apply** or with the Hot link check box being selected.



The screenshot shows the 'MALDI source' dialog box. It has a title bar with a small icon and the text 'MALDI source'. Below the title bar is a table with parameters and their values. The table has three columns: parameter name, value, and 'actual'. The parameters are: Sheath gas flow rate (0), Aux gas flow rate (0), Sweep gas flow rate (0), Spray voltage ([kV]) (0.00), Spray current (μA), Capillary temp. (°C) (400), and Funnel RF level (50.0). Below the table is a 'Source Auto-Defaults...' button. At the bottom are 'Apply' and 'Help' buttons, and a 'Hot link' checkbox which is checked.

		actual
Sheath gas flow rate	0	
Aux gas flow rate	0	
Sweep gas flow rate	0	
Spray voltage ([kV])	0.00	
Spray current (μA)		
Capillary temp. (°C)	400	
Funnel RF level	50.0	

Source Auto-Defaults...

Apply Help ☒ Hot link

Figure 4-9. MALDI source window

This window is available only when the mass spectrometer has detected an installed MALDI source.

The MALDI source window has the following parameters:

Parameter	Description
Sheath Gas Flow Rate	Displays the setpoint MALDI source sheath gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Sheath Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the sheath gas flow rate to any value from 0 to 80 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sheath Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Aux Gas Flow Rate	Displays the setpoint MALDI source auxiliary gas flow rate (in arbitrary units). To change the setpoint flow rate, click the arrows in the Aux Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 40 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Aux Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Sweep Gas Flow Rate	Displays the setpoint MALDI source sweep gas flow rate. To change the setpoint flow rate, click the arrows in the Sweep Gas Flow Rate spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the flow rate to any value from 0 to 10 units. Or, enter a value in the spin box text field. The mass spectrometer changes the flow rate when you click Apply or with the Hot link check box being selected. The Sweep Gas Flow Rate readback is to the right of the spin box. This readback displays the actual flow rate (in arbitrary units).
Spray Voltage	Displays the setpoint MALDI source spray voltage (absolute value, in kilovolts). To change the setpoint spray voltage, click the arrows in the Spray Voltage spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the spray voltage to any value from 0.0 to 8.0 kV. The sign of the spray voltages changes automatically with the ion polarity mode: positive for positive ions and negative for negative ions. Or, enter a value in the spin box text field. The mass spectrometer changes the spray voltage when you click Apply or with the Hot link check box being selected. The Spray Voltage readback is to the right of the spin box. This readback displays the actual spray voltage (absolute value, in kilovolts).
Spray Current	This readback displays the actual MALDI source spray current (in microamperes). MALDI spray current is typically less than 5 μA.

Parameter	Description
Capillary Temperature	Displays the setpoint MALDI source heated capillary temperature (in degrees Celsius). To change the setpoint heated capillary temperature, click the arrows in the Capillary Temp spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the heated capillary temperature to any value from 0.00 to 450.00 °C. Or, enter a value in the spin box text field. The mass spectrometer changes the heated capillary temperature when you click Apply or with the Hot link check box being selected. The Capillary Temperature readback is to the right of the spin box. This readback displays the actual temperature (in degrees Celsius) of the heated capillary.
Funnel RF Level	Displays a numerical factor that the mass spectrometer uses, along with the lowest and highest mass, to calculate the Funnel RF amplitude. The magnitude of the Funnel RF level affects the mass spectrum as follows: - Decreasing the Funnel RF level will decrease the amount of fragmentation of fragile ions in the ion funnel. - Decreasing the Funnel RF level will decrease the transmission of high m/z ions through the ion funnel and increase the transmission of the low m/z ions. - Increasing the Funnel RF level will increase the amount of fragmentation of fragile ions in the ion funnel. - Increasing the Funnel RF level will increase the transmission of high m/z ions through the ion funnel and decrease the transmission of the low m/z ions. To change the Funnel RF level, click the arrows in the Funnel Level spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the Funnel RF level to any value from 0 to 100 (200)*. Or, enter a value in the spin box text field. The mass spectrometer changes the Funnel RF level when you click Apply or with the Hot link check box being selected. *The value in parentheses applies only to systems with a valid High Mass Range license. For stable ions, the default value, 50, provides a good starting point. By default, the Funnel RF level remains at 50 during all calibrations.
Buttons	
Source Auto-Defaults	This parameter is not available for this ion source type.
Apply	Sends all changes to the instrument.
Help	Displays the Help for this window.
Hot Link	Select the Hot link check box to allow Q Exactive HF-X Tune to send any changes immediately to the instrument. A green frame around the parameter box indicates an active hot link.

❖ **To display this dialog box**

Click the MALDI source window title bar in the Instrument Control window.

Acquisition Window

Use the Acquisition window to enter parameters for acquiring and storing scan data as well as to monitor the progress of the active acquisition. See [Figure 4-10](#).

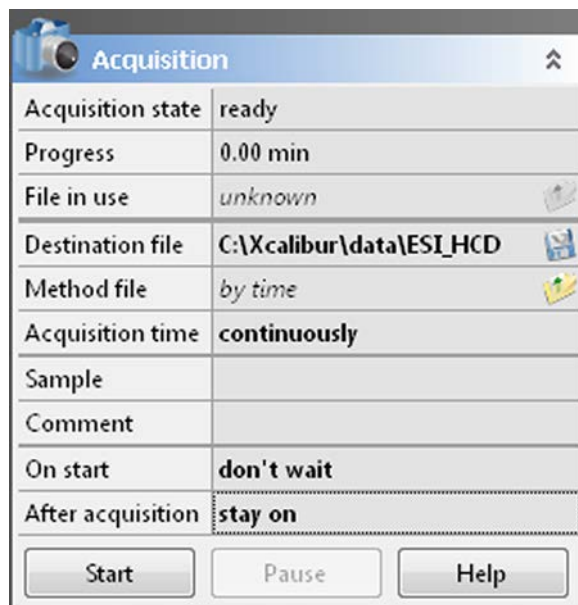


Figure 4-10. Acquisition window

The Acquisition window has the following parameters:

Parameter	Description
Acquisition state	Displays the status of the current acquisition.
Progress	Displays the elapsed time of the current acquisition.
File in use	Displays the name of the raw file to be acquired to disk for the current sample. To display the file in Qual Browser, click the  button. This value is up to date even when Q Exactive HF-X Tune is acquiring data under control of Xcalibur.
Destination file	Displays the full path of the folder where your *.raw files will be saved. To change the path, type the full path (Drive:\path) in the text box or click the  button to the right of the text box to browse your directories and select the folder where your *.raw files should be saved. Saving raw files on network drives typically causes problems. Preferably select a local path (for example, C:\Xcalibur\data).

Parameter	Description
Method file	Displays the name of the instrument method (*.meth) to be used during the current acquisition. The tune file used in that instrument method will be used for your scan but other devices configured in that instrument method will not be included. Type in the name of the instrument method, or click the  button to the right of the text box to browse your computer for an instrument method file (typically saved in C:\Xcalibur\methods). When the active acquisition is controlled by the settings of the parameter Acquisition time, this parameter is not available. Instead, the text field shows <i>by time</i>.
Sample	Displays the name of the current sample. To change the sample name, type the new name in the text field.
Comment	Displays a comment on the current sample, if available. To change the comment, type the new name in the text field.
Acquisition time	Displays the duration of the acquisition time. Use the option buttons to select one of the following settings: • Continuously The acquisition, once it is started, will continue until you stop (Stop button) or pause (Pause button) it. • Scans Specify the number of scans for the current acquisition. You can set the number of scans to any value from 1 to 10000. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. • Minutes Specify the time in minutes for the current acquisition. You can set the acquisition time from 0.01 to 15000.00 minutes. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. When the active acquisition is controlled by a method file, this parameter is not available. Instead, the text field shows <i>by method</i>.
On start	Use the list box to set the start mode of the data acquisition. The options are as follows: • don't wait Initiates acquisition of the raw file immediately when you click Start in the Acquisition window. • wait for contact closure When you click Start in the Acquisition window, the acquisition pauses. Q Exactive HF-X Tune initiates acquisition of the raw file either when it receives a contact closure signal (for example, from an analog autosampler) or when you click Resume.

Parameter	Description
After acquisition	Use the list box to set the instrument mode after the data acquisition has stopped. The options are as follows: • stay on The instrument remains On when the current acquisition is completed. • enter standby mode Sets the instrument to Standby when the current acquisition is completed. • switch off Switches Off the instrument when the current acquisition is completed.
Buttons	
Start / Stop	Use this button to start and stop the data acquisition. When no acquisition is in progress, Q Exactive HF-X Tune displays Start. When an acquisition is in progress, Q Exactive HF-X Tune displays Stop. To start an acquisition, click Start. To stop an acquisition, click Stop. To pause an acquisition, click the Pause / Resume button. No Q Exactive HF-X Tune controlled data acquisition is possible if the instrument is controlled by Xcalibur or Pathfinder. IMPORTANT When you start an acquisition while the instrument is in Off position, the instrument begins acquiring data after a delay of about 30 seconds.
Pause / Resume	Use this button to pause and resume an acquisition in progress. When no acquisition is in progress, the button is inactive (gray). When an acquisition is in progress, Q Exactive HF-X Tune displays Pause. When an acquisition is paused, Q Exactive HF-X Tune displays Resume. To pause an acquisition in progress, click Pause. To resume an acquisition that is paused, click Resume. To stop an acquisition in progress, click the Start / Stop button. The acquisition can be started by clicking Resume if the mass spectrometer is waiting for contact closure.
Help	Displays the Help for this window.

❖ To display this window

Click the Acquisition window title bar in the Instrument Control window.

Mass Traces Window

Use the Mass Traces window to display mass traces for the total ion current and up to five m/z values in the Analysis Graphs window. See [Figure 4-11](#). You can plot mass traces when manually adjusting source parameters like gas flows or spray voltage. You can also optimize collision energy/normalized collision energy or in-source CID energy.

Tip Make sure that you tune your instrument for both ion modes if you want to use a switching method! Settings for both polarity modes are saved in the same tune file!

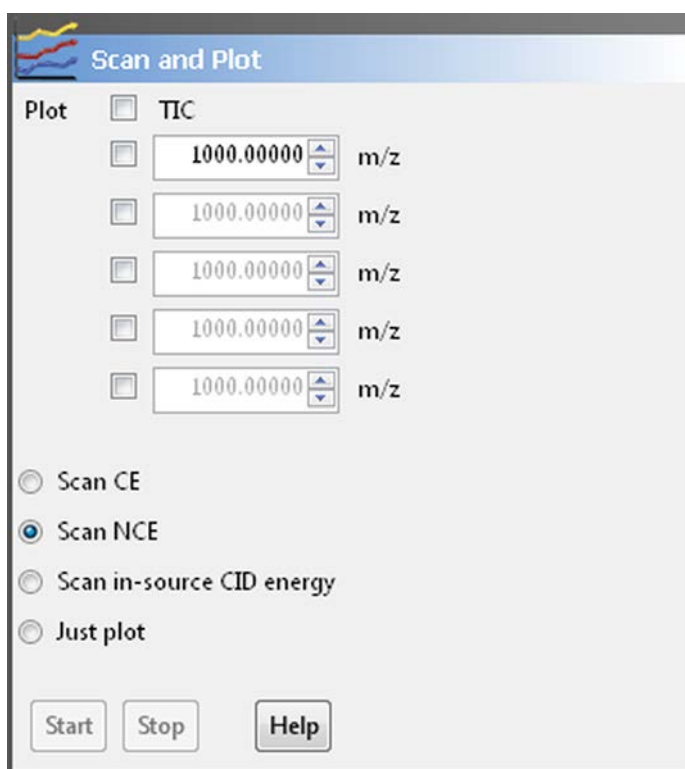


Figure 4-11. Mass Traces window

The Mass Traces window has the following parameters:

Parameter	Description
Plot	
TIC	Select this check box to plot the total ion current.
Masses to plot	Select a check box for each m/z value that you want to plot (up to five). When you select a check box, the spin box becomes active. The spin box displays the mass-to-charge ratio to plot. You can set the mass-to-charge ratio to any value from m/z 50 to m/z 6000 (m/z 8000)*. *The value in parentheses applies only to systems with a valid High Mass Range license. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
Scan CE	Select this option button to optimize the collision energy on the total ion current.
Scan NCE	Select this option button to optimize the normalized collision energy on the total ion current.
Scan in-source CID energy	Select this option button to optimize the in-source CID energy on the total ion current.
Just plot	Select this option button to plot the mass trace without optimization.

Parameter	Description
Buttons	
Start	Click Start to start plotting the mass traces. The instrument needs to be in On status to start a plotting procedure. When plotting is in progress, the Q Exactive HF-X Tune displays Stop .
Stop	Click Stop to stop plotting the mass traces.
Help	Displays the Help for this window.

Calibrate Window

Use the Calibrate window of the tasks panel to perform an automatic optimization of the calibration parameters. See [Figure 4-12](#). Calibration parameters are instrument parameters whose values do not vary with the type of experiment.

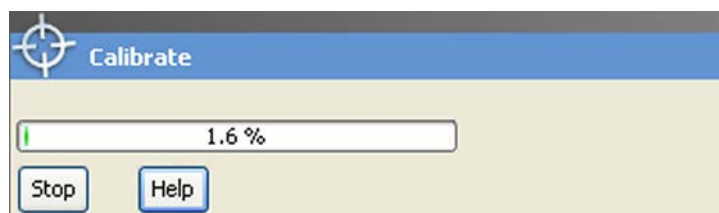


Figure 4-12. Calibrate window

Standard users can choose the ion mode they want to calibrate in the Calmix Calibration window. Advanced users can use the Calmix Calibration window to calibrate the instrument with the standard calibration solution (calmix). Or, they can use the Customized Calibration window to enter parameters for a calibration with a calibration solution of their choosing.

Tip If the system was in Off mode before, it is necessary to put the instrument into On mode for at least 90 minutes before a mass calibration is performed.

The calibrating procedure requires that you introduce calibration solution into the mass spectrometer at a steady rate for several minutes (or longer). You can introduce the solution directly from the syringe pump. Refer to the *Exactive Series Operating Manual* for information.

The Calibrate window has the following parameters:

Parameter	Description
Progress bar	Displays the elapsed percentage of the current calibration procedure.

Parameter	Description
Buttons	
Calibrate	Click Calibrate to start an automatic calibration of the mass spectrometer. The instrument needs to be in On status to start a calibration. The duration of the automatic calibration depends on the selected check boxes; a complete automatic calibration requires about four minutes. When calibration is in progress, Q Exactive HF-X Tune displays Stop .
Stop	Click Stop to stop a calibration in progress.
Help	Displays the Help for this window.

❖ **To display this window**

Click  **Calibrate** in the tasks panel.

Calmix Calibration Window

Use the Calmix Calibration window to select parameters and ion modes when performing an automatic calibration with the standard calibration solution (calmix). See [Figure 4-13](#) and [Figure 4-14](#). The window displays the current statuses of the individual calibration items on the right side.

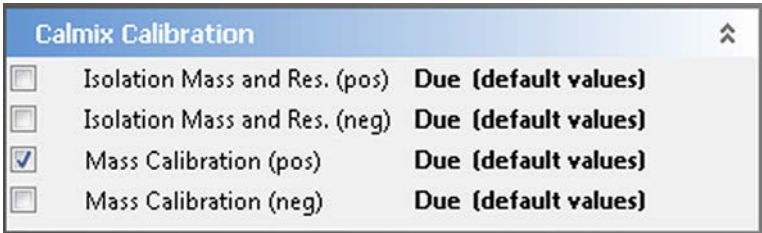


Figure 4-13. Calmix Calibration window (for standard users)



Figure 4-14. Calmix Calibration window (for advanced users)

The Calmix Calibration window has the following parameters:

Parameter	Description
In a hierarchical list of items in a tree view, advanced users can select individual parameters that they want to calibrate. If the check box is not selected, no subentry is selected. If the check box is selected, all subentries are selected. If the check box is filled, some subentries are selected.	
Base Calibration	The Base Calibration item displays a hierarchical list of items in a tree view. This parameter is not available for standard users.
Isolation Mass and Res. (pos) Isolation Mass and Res. (neg)	Select this check box to perform an automatic calibration for isolation mass and resolution of the quadrupole in the respective ion mode.
Mass Calibration (pos) Mass Calibration (neg)	Select this check box to perform an automatic calibration for all calibration parameters in the respective ion mode. Use the applicable calibration solution for the selected ion mode. Refer to the <i>Exactive Series Operating Manual</i> or the <i>Q Exactive HF-X QuickStart Guide</i> for information.
HMR Mode Calibration (pos) ^a HMR Mode Calibration (neg)	Select this check box to perform automatic calibrations for the High Mass Range (HMR) in the respective ion mode. Running these calibrations is not possible when HMR mode is set to Off in the instrument status window. Use a calibration solution of ammonium hexafluorophosphate (AHFP).
-HMR eFT Parameters (pos) ^a -HMR eFT Parameters (neg)	Select this check box to perform an automatic eFT calibration using the HMR mass list. This parameter is not available for standard users.
-HMR Mass Calibration (pos) ^a -HMR Mass Calibration (neg)	Select this check box to perform an automatic mass calibration using the HMR mass list. If necessary, the instrument changes the scan parameters used for this calibration.

^aThese calibrations are available only on systems with a valid High Mass Range license.

Customized Calibration Window

Use the Customized Calibration window to perform a mass calibration with a user-defined calibration solution. Enter the m/z values on which to calibrate. See [Figure 4-15](#). This window is not available for standard users.

The screenshot shows the 'Customized Calibration' window. It has a title bar with the text 'Customized Calibration' and a maximize button. Below the title bar, there are two sections: 'List of positive ions to handle' and 'List of negative ions to handle'. Each section contains a list of m/z values, each preceded by a checkbox and followed by 'm/z'. The values are displayed in a text box with up and down arrows for adjustment.

Section	m/z Value
List of positive ions to handle	2000.00000
	195.08765
	524.26496
	1121.99702
	1221.99064
	1321.98425
	1421.97786
	1521.97148
	1621.96509
	1721.95870
List of negative ions to handle	265.14790
	514.28440
	1279.99721
	1379.99083
	1479.98444
	1579.97805
	1679.97166
	1779.96528
	1000.00000
	1000.00000

Figure 4-15. Customized Calibration window

Tip Use this window for (positive and negative) mass calibration only! For all other calibration procedures, use the standard calibration solution (calmix)!

The Customized Calibration window has the following parameters:

Parameter	Description
Masses to calibrate	Select a check box for each m/z value that you want to plot (up to ten for each ion mode). When you select a check box, the spin box becomes active. The spin box displays the mass-to-charge ratio to plot. You can set the mass-to-charge ratio to any value from m/z 50 to m/z 6000 (m/z 8000)*. *The value in parentheses applies only to systems with a valid High Mass Range license. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.

Evaluate Window

Use the Evaluate window of the tasks panel to perform an automatic check of the instrument calibration. See [Figure 4-16](#).

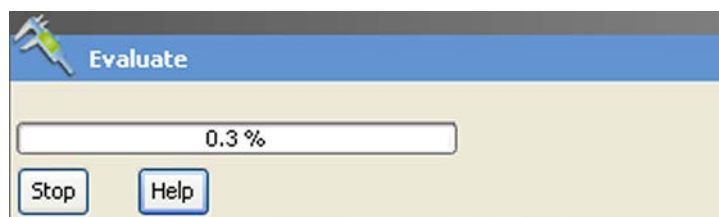


Figure 4-16. Evaluate window

To enable an evaluation, standard users must select at least one check box in the Calmix Evaluation window. Advanced users must select at least one check box either in the Calmix Evaluation window or in the Customized Evaluation window.

The evaluation procedure requires that you introduce calibration solution (calmix) into the mass spectrometer at a steady rate for several minutes (or longer). You can introduce the solution directly from the syringe pump. Refer to the *Exactive Series Operating Manual* for information.

The Evaluate window has the following parameters:

Parameter	Description
Progress bar	Displays the elapsed percentage of the current evaluation procedure.

Parameter	Description
Buttons	
Evaluate	Click Evaluate to start an automatic evaluation of calibration parameters. The instrument needs to be in On status to start an evaluation. When evaluation is in progress, Q Exactive HF-X Tune displays Stop .
Stop	Click Stop to stop an evaluation in progress.
Help	Displays the Help for this window.

Calmix Evaluation Window

Use the Calmix Evaluation window to enable the evaluation with the standard calibration solution (calmix). See [Figure 4-17](#).

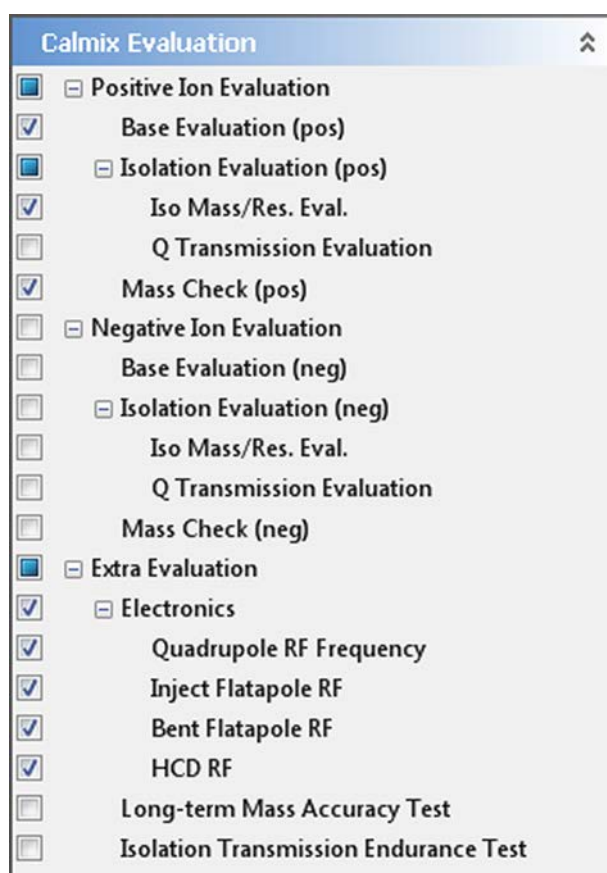


Figure 4-17. Calmix Evaluation window (for advanced users)

The Calmix Evaluation window has the following parameters:

Parameter	Description
In a hierarchical list of items in a tree view, you can select individual parameters that you want to evaluate. If the check box is not selected, no subentry is selected. If the check box is selected, all subentries are selected. If the check box is filled, some subentries are selected.	
Positive Ion Evaluation	
Select the check boxes to evaluate various parameters for the positive ion mode.	
-Base Evaluation (pos)	Evaluates the basic performance of the instrument in positive ion mode.
-Isolation Evaluation (pos)	Evaluates the performance of the quadrupole in positive ion mode.
--Iso Mass/Res. Eval. (pos)	Evaluates the instrument performance for quadrupole isolation and resolution in positive ion mode. This parameter is not available for standard users.
--Q Transmission Evaluation (pos)	Evaluates the quadrupole transmission against minimum requirements in positive ion mode. This evaluation requires a calibrated quadrupole and a stable calmix spray. This parameter is not available for standard users.
-Mass Check (pos)	Evaluates the m/z accuracy of the Orbitrap analyzer in positive ion mode.
-HMR Mode Check (pos) ^a	Evaluates the basic performance of the instrument in HMR mode.
--HMR Spectral Mass Accuracy Test (pos) ^a	Performs a mass accuracy test for the HMR mode. This parameter is not available for standard users.
Negative Ion Evaluation	
Select the check boxes to evaluate various parameters for the negative ion mode.	
-Base Evaluation (neg)	Evaluates the basic performance of the instrument in negative ion mode.
-Isolation Evaluation (neg)	Evaluates the performance of the quadrupole in negative ion mode.
--Iso Mass/Res. Eval. (neg)	Evaluates the instrument performance for quadrupole isolation and resolution in negative ion mode. This parameter is not available for standard users.
--Q Transmission Evaluation (neg)	Evaluates the quadrupole transmission against minimum requirements in negative ion mode. This evaluation requires a calibrated quadrupole and a stable calmix spray. This parameter is not available for standard users.
-Mass Check (neg)	Evaluates the m/z accuracy of the Orbitrap analyzer in negative ion mode.
-HMR Mode Check (neg) ^a	Evaluates the basic performance of the instrument in HMR mode.

Parameter	Description
--HMR Spectral Mass Accuracy Test (neg) ^a	Performs a mass accuracy test for the HMR mode. This parameter is not available for standard users.
Extra Evaluation	
Select the check boxes to evaluate various parameters that are not contained in the standard evaluations.	
Electronics	Evaluates the performance of electronic components.
-Quadrupole RF Frequency	Checks the quadrupole RF voltage. This parameter is not available for standard users.
-Inject Flatapole RF	Checks the inject flatapole RF voltage. This parameter is not available for standard users.
-Bent Flatapole RF	Checks the bent flatapole RF voltage. This parameter is not available for standard users.
-HCD RF	Checks the RF voltage of the collision cell. This parameter is not available for standard users.
Long-term Mass Accuracy Test	Performs a mass accuracy test over an extended period. This parameter is not available for standard users.
Isolation Transmission Endurance Test	Tests the behavior of the mass isolation optic elements under permanent ion load. The procedure requires a stable calmix signal with TIC > 5.0E+08; it will run for about 16 minutes. This parameter is not available for standard users.

^aThese evaluations are available only on systems with a valid High Mass Range license.

Customized Evaluation Window

Use the Customized Evaluation window to enter the m/z values on which to evaluate by using a user-defined calibration solution. See [Figure 4-15](#). This window is not available for standard users.

Customized Evaluation

List of positive ions to handle

☐	m/z
☐	2000.00000
☐	195.08765
☐	524.26496
☐	1121.99702
☐	1221.99064
☐	1321.98425
☐	1421.97786
☐	1521.97148
☐	1621.96509
☐	1721.95870

List of negative ions to handle

☐	m/z
☐	265.14790
☐	514.28440
☐	1279.99721
☐	1379.99083
☐	1479.98444
☐	1579.97805
☐	1679.97166
☐	1779.96528
☐	1000.00000
☐	1000.00000

Duration min

Figure 4-18. Customized Evaluation window

The Customized Evaluation window has the following parameters:

Parameter	Description
Masses to evaluate	Select a check box for each m/z value that you want to plot (up to ten for each ion mode). When you select a check box, the spin box becomes active. The spin box displays the mass-to-charge ratio to plot. You can set the mass-to-charge ratio to any value from m/z 50 to m/z 6000 (m/z 8000)*. *The value in parentheses applies only to systems with a valid High Mass Range license. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
Duration	The spin box displays the duration (in minutes) of the evaluation procedure. You can set the duration to any value from 0.2 to 2160 minutes. The default duration is 0.5 minutes. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.

❖ **To display this window**

Click  Evaluate in the Tasks window.

Vacuum / Bakeout Window

The Vacuum / Bakeout window of the tasks panel reads back the pressure values at the vacuum gauges and allows performing an instrument bakeout. See [Figure 4-19](#).

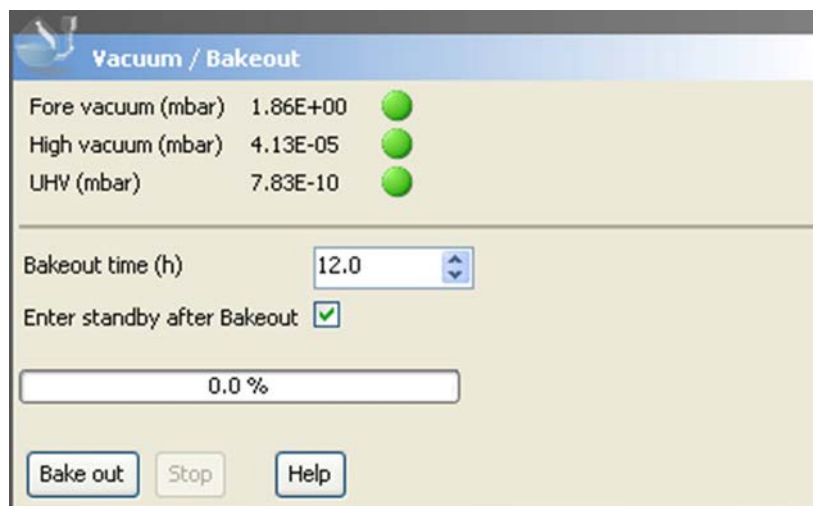


Figure 4-19. Vacuum / Bakeout window

Tip After the bakeout time has expired, the instrument requires a cooling and stabilization time of about three hours.

The Vacuum / Bakeout window has the following parameters:

Parameter	Description
Vacuum	
Green LEDs indicate that the readback values are sufficient for operating the mass spectrometer. If an LED indicates a vacuum problem, use the instrument status window for error diagnosis.	
Fore vacuum	This readback displays the actual pressure (in mbar) in the forevacuum line and ion source region as read by the Pirani gauge.
High vacuum	This readback displays the actual pressure (in mbar) in the high vacuum chamber as read by the ion gauge. This parameter is visible only when the ion gauge in the high vacuum chamber is switched on. Advanced users can switch on this gauge by using the shortcut menu of the Vacuum System node of the instrument status window.
UHV	This readback displays the actual pressure (in mbar) in the Orbitrap chamber as read by the ion gauge.

Parameter	Description
Bakeout	
Bakeout time	Enter the desired baking duration (in hours) into the spin box. The range is 4 to 30 hours. When you click Bake out, the mass spectrometer starts the baking routine. The baking script is stopped after the preset duration. Click Stop to abort the baking routine. The instrument has to cool down for another three hours before it can be used.
Enter standby after Bakeout	Select the check box to set the instrument to standby mode after the bakeout procedure is finished.
Progress bar	Displays the elapsed percentage of the current baking procedure.
Bake out	Click Bake out to start the bakeout routine. To stop a bakeout in progress, click the Stop button. Bakeout is possible only when the instrument status is Off.
Stop	Click Stop to abort the bakeout routine. The instrument has to cool down for another three hours before it can be used.
Help	Displays the Help for this window.

❖ **To display this window**

Click  **Vacuum / Bakeout** in the tasks panel.

Display Panel

The windows in the display panel provide real-time information about the instrument status, the Q Exactive HF-X Tune software, or other programs.

The following windows are available:

- [Spectrum Window](#)
- [Instrument Status Window](#)
- [Messages Window](#)
- [Analysis Graphs Window](#)
- [Debug Messages Window](#)

The spectrum window is always visible. The debug messages window is not available for standard users.

Depending on the individual configuration of your system, additional windows may allow controlling other installed instruments (Accela™ AS or Accela Pump, for example.)

Q Exactive HF-X Tune offers various ways to arrange windows in the display panel:

❖ **To display a window in the display panel**

Choose the respective command in the Windows menu.

❖ **To hide a window in the display panel**

- Choose the respective command in the Windows menu.
- Right-click the title bar of a window to display the shortcut menu. Choose **Hide**.

❖ **To change the position of a window in the display panel**

- Use the mouse to drag the window by its title bar to the new location, which can be even outside the Q Exactive HF-X Tune window.
- Within the display panel, you can dock the window to any one of the four sides. While you drag the window, Q Exactive HF-X Tune displays icons to indicate the available docking positions.
- Right-click the title bar of a *docked* window to display the shortcut menu. Choose **Floating** to undock the window.

Or, double-click on the title bar of the window.

- Right-click the title bar of an *undocked* window to display the shortcut menu. Choose **Floating** to dock the window to its last docking position.

Or, double-click the title bar of the window.

Spectrum Window

The spectrum window displays real-time data generated during calibration, tuning, and diagnostic tests. See [Figure 4-20](#). The spectrum window is always visible.

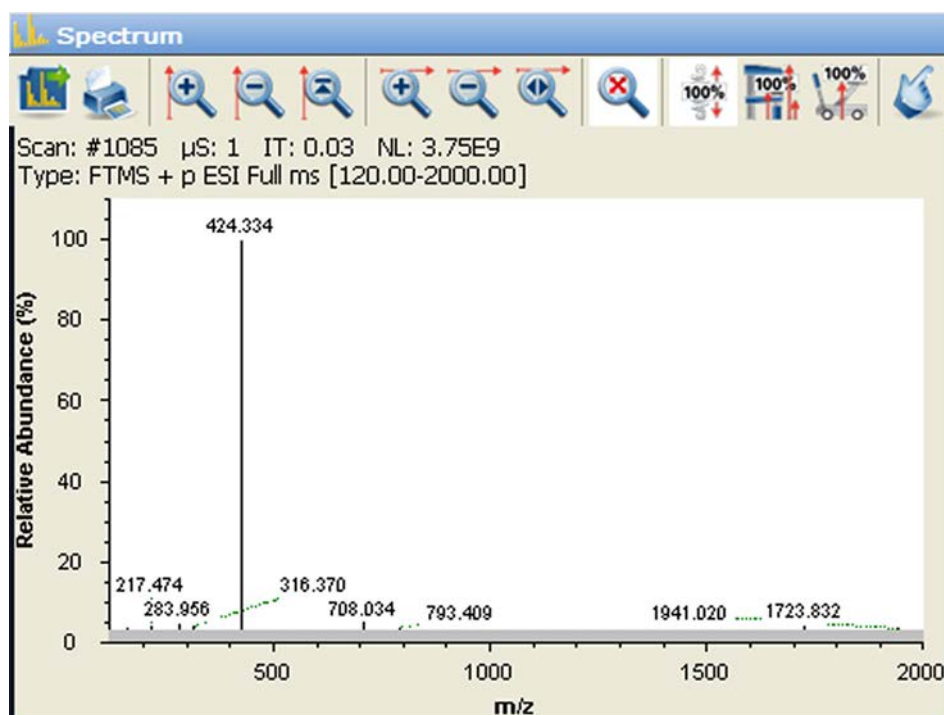


Figure 4-20. Spectrum window

The spectrum window allows using the mouse for zooming.

❖ To zoom in or out on a spectrum

- Click and drag with the left mouse button (hand cursor) from the beginning to the end of the portion you want to see enlarged.
- Or, use the mouse wheel for zooming. Position the mouse pointer within the spectrum and roll the wheel forward to zoom in on the spectrum area.
- To zoom in on the spectrum with respect to one axis only, position the mouse pointer within the axis area and roll the mouse wheel forward. Roll the wheel backward to zoom out.

- To increase the zooming factor by two, keep the **<Shift>** key pressed while using the mouse wheel.

To return to a display of the full spectrum, click the  button in the toolbar or choose **Unzoom** in the shortcut menu.

Press the **<Shift>** key to enable mouse panning. When mouse panning is active (mouse pointer changes to hand cursor), you can shift the spectrum along the X-axis while keeping the left mouse button pressed.

The spectrum window has the following parameters:

Parameter	Description
Header	
Scan #	The number of scans since the beginning of the last acquisition (or since the last time the mass spectrometer was rebooted)
μS	Number of microscans
IT	Inject time (in milliseconds)
NL	Normalization level
Type	Scan type The scan type information comprises ion polarity, source type, fragmentation type and energy (if active), and scan range. When the acquisition is controlled by an instrument method, the information includes the current scan segment and the current scan event.

❖ To display this window

Choose **Windows > Spectrum**.

Toolbar

Use the buttons in the toolbar to manipulate the spectrum display.

The toolbar of the spectrum window has the following parameters:

Parameter	Description
	Click to copy the current spectrum into the clipboard.
	Click to plot the current spectrum. You can view a print preview before the spectrum is printed. In a Page Setup dialog box, you can set up printer's parameters (paper size and orientation, for example).

Parameter	Description
	Click to zoom in on the Y-axis (factor 2).
	Click to zoom out on the Y-axis (factor 2).
	Click to normalize the Y scale: Q Exactive HF-X Tune always displays the largest peak in the spectrum at full scale (vertical scale = largest peak in spectrum).
	Click to zoom in on the X-axis (factor 2).
	Click to zoom out on the X-axis (factor 2).
	Click to display the entire mass range.
	Click to normalize the display (X-axis, Y-axis).
	Click to set to fixed mode: the height of the Y-axis is set equal to the height of the largest peak in the current spectrum and remains fixed even if larger peaks occur.
	Click to set the Y-axis to the height of the highest peak so that the largest peak in the spectrum is always displayed at full scale.
	Click to set to creep mode: the Y scale of the mass spectrum automatically increases if the peak intensity increases, but does not decrease if the peak intensity decreases.
	Click to toggle between mouse panning and mouse zooming: - When mouse panning is active, you can shift the spectrum along the X-axis while keeping the left mouse button pressed (hand cursor). - When mouse zooming is active, you can zoom in the spectrum by using the mouse.

Shortcut Menu

Right-click the spectrum window to display the shortcut menu. It has the following commands:

Command	Description
Save Image As	Saves the current graph as image file. A Save As dialog opens and you can enter the file name, file type, and the directory.

Command	Description
Unzoom	Reverts the zoom action.
Display options	Opens the Display Options dialog box.

Instrument Status Window

The instrument status window displays real-time status information for the instrument components. All parameters are arranged in a tree view. See [Figure 4-21](#). The Control node and the System node are not available for standard users.

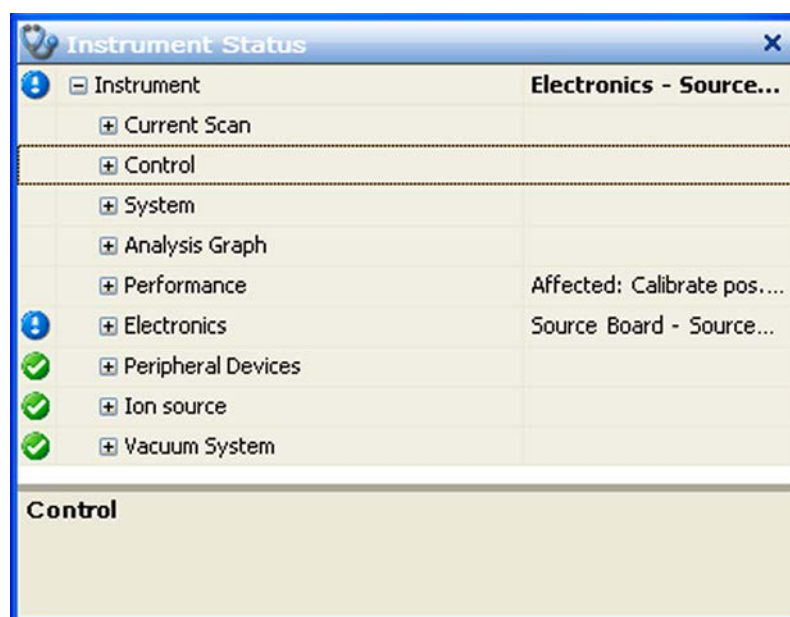


Figure 4-21. Instrument status window

In addition to showing numerical values of parameters, the instrument status window uses icons to indicate the statuses of system components. Thus, you can use the instrument status window for a quick error diagnosis.

When expanded, some nodes provide shortcut menus that are displayed when you right-click an item. The available commands depend on the selected node and the user privileges. Generally, the shortcut menus allow changing the current settings.

Tip For normal operation, it is not necessary to change the settings in the instrument status window. It just allows monitoring the system in more detail (more readbacks etc.) than the other windows.

❖ To display this window

Choose **Windows > Instrument Status**.

Messages Window

The messages window displays real-time information about the statuses of the instrument, the control service, or other programs. For further analysis, you can copy the content of the messages window to a text editor.

❖ To copy content from the messages window to a text editor

1. Select part of the content with the mouse, or press **<Ctrl> + <A>** to select the complete content of the messages window.
2. Press **<Ctrl> + <C>** to copy the text to the clipboard.
3. Open a document in the text editor.
4. Press **<Ctrl> + <V>** to insert the copied text into the document.

The messages window has the following parameters:

Parameter	Description
The messages are sorted with respect to time. To change the sort order, click the respective table column header. To invert the sort order, click again.	
Priority	The message priority is indicated by symbols:  Info; status is normal / command successful  Warning; no user action required  Error; user action required  Fatal error; program cannot proceed
Source	The message source is indicated by symbols:  Message from Q Exactive HF-X Tune program  Message from instrument  Message from service
Time	Time and date of the message
Description	Displays the message text.

❖ To display this window

Choose **Windows > Messages**.

Analysis Graphs Window

The analysis graphs window displays real-time data generated during calibration, tuning, and diagnostic tests. See Figure 4-22. To save data displayed in the window, choose **Save Image As** in the shortcut menu of the window.

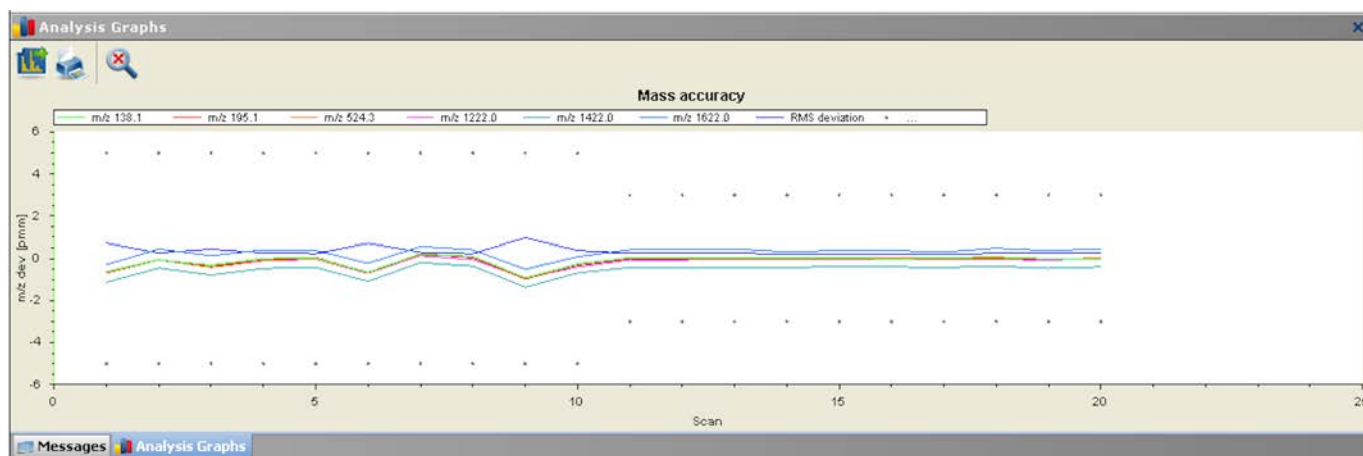


Figure 4-22. Analysis Graphs window

The analysis graphs window allows using the mouse for zooming.

❖ To zoom in or out on an analysis graph

- Click and drag with the left mouse button (hand cursor) from the beginning to the end of the portion you want to see enlarged.
- Or, use the mouse wheel for zooming. Position the mouse pointer within the graph and roll the wheel forward to zoom in on the graph area.
- To zoom in on the graph with respect to one axis only, position the mouse pointer within the axis area and roll the mouse wheel forward. Roll the wheel backward to zoom out.
- To increase the zooming factor by two, keep the **<Shift>** key pressed while using the mouse wheel.

To return to a display of the full spectrum, click the  button in the toolbar or choose **Unzoom** in the shortcut menu.

Press the **<Shift>** key to enable mouse panning. When mouse panning is active (mouse pointer changes to hand cursor), you can shift the graph along both axes while keeping the left mouse button pressed.

❖ To display this window

Choose **Windows > Analysis Graphs**.

Toolbar

The toolbar of the analysis graphs window has the following parameters:

Parameter	Description
	Click to copy the current graph into the clipboard.
	Click to plot the current graph. You can view a print preview before the graph is printed. In a Page Setup dialog box, you can set up printer's parameters (paper size and orientation, for example).
	Click to normalize the display (X-axis, Y-axis).

Shortcut Menu

Right-clicking on the analysis graphs window displays the shortcut menu. It has the following commands:

Command	Description
Save Image As	Saves the current graph as image file. A Save As dialog opens and you can enter the file name, file type, and the directory.
Unzoom	Reverts the zoom action.

Debug Messages Window

The debug messages window displays messages that can be used during method development. The debug messages window is not available for standard users. For further analysis, you can copy the content of the debug messages window to a text editor.

❖ To copy content from the debug messages window to a text editor

1. Select part of the content with the mouse, or press **<Ctrl> + <A>** to select the complete content of the messages window.
2. Press **<Ctrl> + <C>** to copy the text to the clipboard.
3. Open a document in the text editor.
4. Press **<Ctrl> + <V>** to insert the copied text into the document.

The debug messages window has the following parameters:

Parameter	Description
The messages are sorted with respect to time. To change the sort order, click the respective table column header. To invert the sort order, click again.	
Priority	The message priority is indicated by symbols:  Debugging message  Info; status is normal / command successful  Warning; no user action required  Error; user action required  Fatal error; program cannot proceed
Source	The message source is indicated by symbols:  Message from Q Exactive HF-X Tune program.  Message from instrument.  Message from service.
Time	Time and date of the message
Description	Displays the message text.

❖ To display this window

Choose **Windows > Debug Messages**.

Shortcut Menu of the Debug Messages Window

The debug messages window has a shortcut menu that is displayed when you right-click into the window. Use the commands of the shortcut menu to configure the scope of the messages displayed in the window. Click a command to activate it; click it again to deactivate it.

The following message priorities can be displayed:

- Debug
- Log
- Info
- Warning
- Error
- Fatal

For each message priority, the following message sources are available:

- Instrument
- Service
- Application

A  icon in front of a message source shows that it is selected. A  icon in front of a message priority shows that it is shown for all three message sources. A  icon in front of a message priority shows that it is shown for one or two message sources.

In addition to the commands for configuring the content of the debug messages window, the **Clear list** command allows removing the complete content of the window.

Dialog Boxes

This section provides a reference to the dialog boxes in Q Exactive HF-X Tune.

Dialog Boxes Displayed from the Menu Bar

- [About Dialog Box](#)
- [License Dialog Box](#)
- [Mass Calculator](#)

Dialog Boxes Displayed from the Toolbar

- [Syringe Pump Settings Dialog Box](#)

Dialog Boxes Displayed from the Scan Parameters Window

- [Fragmentation Dialog Box](#)
- [Scan Parameters History Dialog Box](#)
- [Scan Range Dialog Box](#)
- [Scan Type Dialog Box](#)

Dialog Boxes for Editing Lock Masses

- [Collection Modification Dialog Box](#)
- [Delete Lock Mass Collection Dialog Box](#)
- [Lock Masses Dialog Box](#)
- [Lock Mass Removal Dialog Box](#)
- [Lock Mass Replacement Dialog Box](#)
- [Name Change Dialog Box](#)
- [New Lock Mass Collection Dialog Box](#)

Dialog Boxes Displayed from the Spectrum Window

- [Display Options Dialog Box](#)

About Dialog Box

Use the About dialog box to display information about the instrument, the current Q Exactive HF-X Tune version, and the active licenses. To copy the instrument identification to the clipboard, click the  button.

The About dialog box has the following parameters:

Parameter	Description
Buttons	
OK	Saves your changes and closes the dialog box.
Add license	Displays the License dialog box.
Back / Next	Display various dialog boxes with legal information and information about third party licenses used by Q Exactive HF-X Tune.
Help	Displays the Help for this dialog box.

❖ To display this dialog box

Choose **Help > About**.

Autoselect Ion Source Values Dialog Box

Use the Autoselect ion source values dialog box to automatically apply suitable parameters for a HESI ion source or APCI ion source in dependence on a LC flow rate. See [Figure 4-24](#).

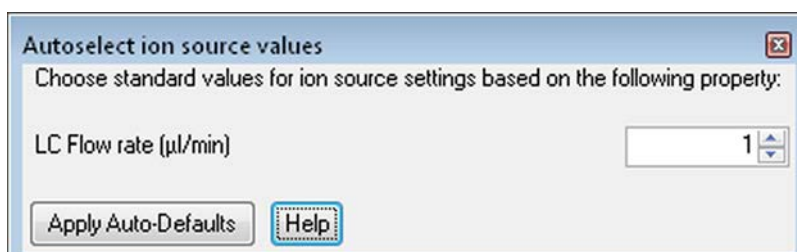


Figure 4-23. Autoselect ion source values dialog box

See “[Default Parameters and Ranges for HESI-2 and APCI](#)” on [page 6-6](#) for a list of the involved parameters and their values.

The Autoselect ion source values dialog box has the following parameters:

Parameter	Description
LC Flow rate (µl/min)	Use this spin box to specify the volume of solvent solution passing through the liquid chromatography system per unit time (in microliters per minute). To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field. The acceptable range of values is 0 to 2000.
Buttons	
Apply Auto-Defaults	Applies suitable values for the following source parameters: • Capillary temperature • Vaporizer temperature • Sheath gas flow • Auxiliary gas flow • Sweep gas flow • Spray voltage (for HESI) • Discharge Current (for APCI)

❖ **To display this dialog box**

On the HESI source window or the APCI source window, click **Source Auto-Defaults**.

License Dialog Box

Use the License dialog box to enter licenses that activate additional features. See [Figure 4-24](#).



Figure 4-24. License dialog box

The License dialog box has the following parameters:

Parameter	Description
License key	Use the text box to enter the license key.
Buttons	
OK	Saves your changes and closes the dialog box.
Cancel	Discards your changes and closes the dialog box.
Help	Displays the Help for this dialog box.

❖ **To display this dialog box**

1. Choose **Help > About** to display the About dialog box.
2. In the About dialog box, click **Add license**.

Mass Calculator

Use the Mass Calculator to calculate the exact mass of an compound of interest.

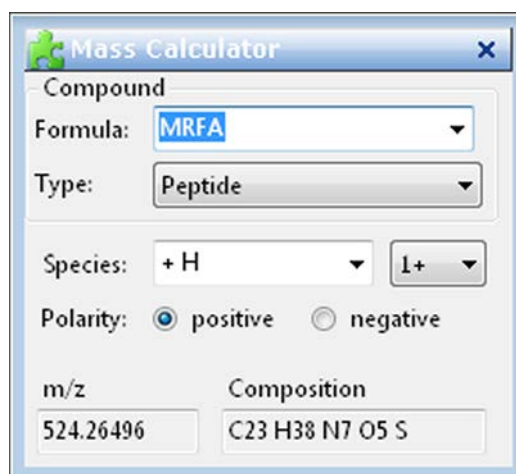


Figure 4-25. Mass Calculator (Tune)

The Mass Calculator has the following parameters:

Parameter	Description
Compound	
Formula	Use the text field to specify the basic composition of the compound. Click the down arrow to display a list of the last entered compounds. The syntax rules and interpretation accept the kind of formula that is also accepted on the Spectrum Simulation page (Isotope Simulation area) of the Qual Browser.

Parameter	Description
Type	Use the Type list to specify the formula type used in the Formula field: • Chemical formula Formula is defined as the resulting elemental composition of the entered formula. This is the default selection. • Peptide Formula is defined as the sum of all of the entered amino acids additionally terminated with H at the N-terminus and OH at the C-terminus. • Amino Acid Formula is defined as the sum of all of the entered amino acids. Independent of the entry in the Species field, the elemental composition and the mass of the compound, Formula is completely determined by the given formula and selected formula type.
Species	Use this text field to define adducts or modifications of the active compound that are expected to be formed. The Species field can be used in two ways: • Click the down arrow to display a list of predefined adducts for each polarity: - +H, +Na, +K, +NH₄ for positive polarity - -H, +Cl, +OH, +HCOO for negative polarity - an empty entry to express adducts (for example, radical cations) for both polarities. The corresponding set will be displayed depending on the selected polarity. Selecting an adduct (A) will result in the strict behavior of applying one unit A to the compound and using “+H” or “-H” adduct depending on the charge state and active polarity. “+K” = $[M + K^+ + (z-1)H^+]^{z+}$; for example, MRFA, +K, CS=2, positive pol. = $[M + K^+ + H^+]^{2+}$ • Enter the modifications of the compound by using squared brackets and at least M as representation of the basic compound (for example, [M + Na + K] or [2M + Na]). The predefined adducts can be entered, too. This definition is used without additional auto dependencies, like adding protons.
Charge state	Use the list box to select the resulting charge state. Available options are 1+ to 100+ for positive polarity and 1– to 100– for negative polarity. The default charge state is 1+ for positive polarity and 1– for negative polarity.
Polarity	Use the option buttons to select the applied polarity. The default polarity is positive.
m/z	This text field displays the calculated mass-to-charge ratio, with five decimal places (for example, 524.26496).
Composition	This text field displays the determined total formula (for example, C₂₃ H₃₈ N₇ O₅ S).

❖ **To display the Mass Calculator**

Choose **Windows > Mass Calculator**.

Syringe Pump Settings Dialog Box

Use the Syringe Pump Settings dialog box to specify parameters of the syringe and the syringe pump. See [Figure 4-26](#). Additionally, use the dialog box to manually operate the syringe pump.

Syringe type	Other
Volume (µL)	10
Syringe inner diameter (mm)	2.300
Flow rate (µL / min)	5.000
Apply Help	
Manual control Start Stop	

Figure 4-26. Syringe Pump Settings dialog box

Tip Advanced users can select the syringe pump type and enter parameters for the syringe pump in the instrument status window.

The Syringe Pump Settings dialog box has the following parameters:

Parameter	Description
Syringe type	Use this list box to specify the syringe type (Hamilton, Unimetrics, or Other). If you select Hamilton or Unimetrics, you must specify the volume of the syringe in the Volume list box. If you select Other, you must specify the inside diameter of the syringe in the Syringe inner diameter spin box.
Volume (µL)	Use this list box to specify the syringe volume for Hamilton and Unimetrics syringes. The acceptable values depend on the syringe type: - Hamilton: 0.5, 1, 2, 5, 10, 25, 50, 100, 250, and 500 µL. - Unimetrics: 10, 25, 50, 100, 250, 500, 1000, 2500, 5000, 10000, 25000, and 50000 µL.
Syringe inner diameter (mm)	Use this spin box to specify the inside diameter for syringes other than Hamilton and Unimetrics syringes. The acceptable range of values is 0.1 to 35 mm. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.

Parameter	Description
Flow rate (µL/min)	Use this spin box to specify the volume of solvent solution passing through the syringe pump per unit time (in microliters per minute). The acceptable range of values depends on the selected syringe volume or syringe inner diameter. To change this value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. Or, enter a value in the spin box text field.
Buttons	
Apply	Sends all changes to the instrument.
Help	Displays the Help for this window.
Manual Control	Sets the syringe pump to manual control. Use the buttons on the syringe pump to switch it on and off. When the syringe pump is under manual control, Q Exactive HF-X Tune displays .
Start	Switches on the syringe pump. When the syringe pump is On, Q Exactive HF-X Tune displays .
Stop	Switches off the syringe pump. When the syringe pump is Off, Q Exactive HF-X Tune displays .

❖ To display this dialog box

In the toolbar, right-click the  symbol.

Scan Parameters History Dialog Box

Use the Scan Parameters History dialog box to select from a list of recent scans based on short scan descriptions. See [Figure 4-27](#). Select a scan from the list to populate all scan parameters in the Scan Parameters window with the parameters from that scan.

If the Hot link check box is selected in the Scan Parameters window, selecting another list item immediately changes the instrument parameters.

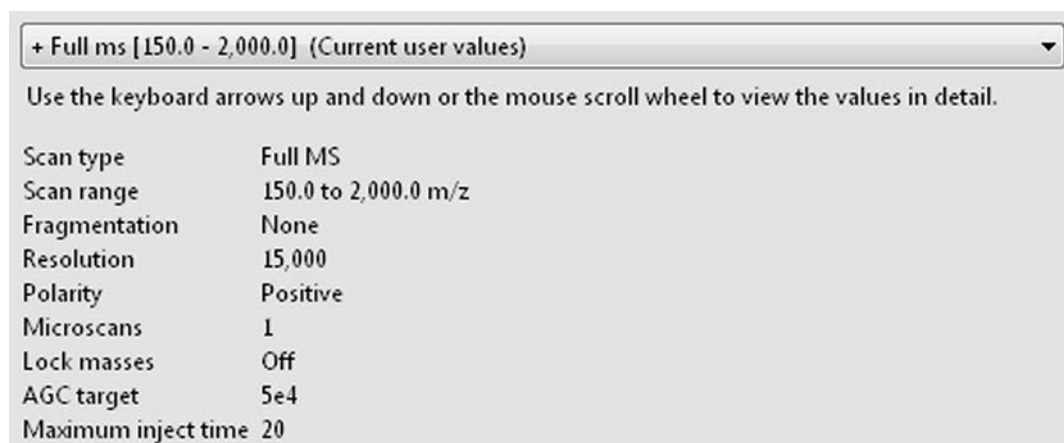


Figure 4-27. Scan Parameters History dialog box

❖ **To display this dialog box**

In the Scan Parameters window, click the History field.

Scan Type Dialog Box

Use the Scan Type dialog box to select the scan type to be used during the currently selected scan event. See [Figure 4-28](#).

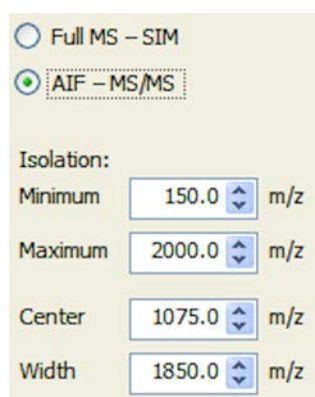


Figure 4-28. Tune—Scan Type dialog box

The Scan Type dialog box has the following parameters:

Parameter	Description
Full MS - SIM	Select this option to enable a Full MS scan (isolation width > 10 amu) or a selected ion monitoring (isolation width ≤ 10 amu) scan type.
AIF - MS/MS	Select this option to enable All Ion Fragmentation (isolation width > 10 amu) or the MS/MS scan type (isolation width ≤ 10 amu). When you select this option, the Isolation area becomes available. When you select this option, Q Exactive HF-X Tune automatically selects the NCE check box in the Fragmentation dialog box.
Isolation	
Use the Isolation area to set the scan range of the selected scan type.	
Minimum	Use this spin box to select the minimum value for the scan range (in mass-to-charge ratio units) used during the currently selected scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 50.0 to 2500 (7950.0) ^a .
Maximum	Use this spin box to select the maximum value for the scan range (in mass-to-charge ratio units) used during the currently selected scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 50.4 to 6000.0 (100.0 to 8000.0) ^a .
Center	Use this spin box to select the center mass (in mass-to-charge ratio units) of the scan range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 50.2 to 4250.0 (75.0 to 7975.0) ^a .
Precursor	Use this spin box to select the mass of a precursor ion of interest. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from <i>m/z</i> 50.2 to 4000 (75.0 to 7975.0) ^a .
Width	Use this spin box to select either the width of the scan range (in mass-to-charge ratio units) used for a SIM scan or the isolation width for the precursor ion of interest during an MS/MS scan. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. For Full MS scans and AIF scans, you can enter any value from <i>m/z</i> 0.4 to 5600.0 (50.0 to 7950.0) ^a . For SIM and MS/MS scans, you can enter any value from <i>m/z</i> 0.4 to 10.

^aThe values in parentheses apply only to systems with a valid High Mass Range license.

❖ To display this dialog box

In the Scan Parameters window, click the Scan type field.

Scan Range Dialog Box

Use the Scan range dialog box to specify the scan range of the data acquisition. See [Figure 4-29](#). The scan range affects the amount of stored and transmitted data.

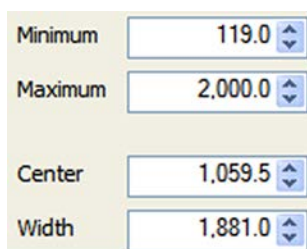


Figure 4-29. Scan range dialog box

The Scan Range dialog box allows setting either minimum and maximum or center and width of the scan range. If you change one pair of values, the other pair is changed accordingly.

Tip The ratio for maximum-to-minimum should not exceed 15. If necessary, Q Exactive HF-X Tune will correct the settings automatically. This rule does not apply to systems with a valid High Mass Range license.

The Scan range dialog box has the following parameters:

Parameter	Description
Minimum	Use this spin box to select the minimum value for the scan range (in mass-to-charge ratio units) used during the currently selected scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 50.0 to 2500.0.
Maximum	Use this spin box to select the maximum value for the scan range (in mass-to-charge ratio units) used during the currently selected scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 50.4 to 6000.0 (100.0 to 8000.0)^a.

Parameter	Description
Center	Use this spin box to select the center mass (in mass-to-charge ratio units) of the scan range. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 50.2 to 4250.0 (75.0 to 7975.0)^a.
Width	Use this spin box to select the width of the scan range (in mass-to-charge ratio units) used during the currently selected scan event. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 0.4 to 5600.0 (50.0 to 7950.0)^a.

^aThe values in parentheses apply only to systems with a valid High Mass Range license.

❖ To display this dialog box

In the Scan Parameters window, click the Scan range field.

Fragmentation Dialog Box

Use the Fragmentation dialog box to activate a fragmentation with in-source CID or the HCD collision cell. You can specify the fragmentation voltages to be used. See [Figure 4-30](#).

Figure 4-30. Tune—Fragmentation dialog box

The Fragmentation dialog box has the following parameters:

Parameter	Description
In-source CID	Activates the in-source CID. To change the CID collision energy, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can set the CID collision energy to any value from 0.1 to 100 eV.* *On instruments with a valid High Mass Range license, a maximum CID collision energy of 150 eV is possible, with an installed NSI source even 200 eV. Automatic tuning is disabled when in-source CID fragmentation is on. To use automatic tuning, clear this check box.
HCD	
Activates the HCD collision cell. When you select this check box, Q Exactive HF-X Tune automatically changes the scan type, if necessary.	
When HCD fragmentation is on, automatic tuning comprises only HCD relevant parameters.	
NCE / CE	Use the option buttons to specify whether to use normalized collision energy (NCE) or collision energy (CE) for HCD fragmentation. Thus, you can apply the same absolute HCD collision energy for internal standards (ISTDs) and the corresponding analytes. NCE is a dimensionless number that is approximately equivalent to the HCD collision energy (in eV) for a reference ion of mass 500 and charge 1. The actual HCD energy is calculated on basis of mass and charge of the selected precursor ion. To change the value, click the arrows in the spin box to increase [up arrow] or to decrease [down arrow] the value. You can enter any value from 10 to 200.
Charge	Enter the charge state of the ion to be fragmented. The available range is 1 to 5. The required collision energy for fragmenting an ion depends on its charge state. The higher the charge state, the lower the required collision energy. The algorithm for calculating the absolute collision energy is based on empirical data taken from measurements on peptides. For example, the required absolute collision energy to fragment a $[M+2H]^{2+}$ ion is about 90 percent of that of the corresponding $[M+H]^+$ ion. For a $[M+3H]^{3+}$ ion, the value decreases to 85 percent. The spin box is active only if the HCD check box is selected.

❖ **To display this dialog box**

In the Scan Parameters window, click into the Fragmentation field.

Collection Modification Dialog Box

Use this dialog box to modify a lock mass collection by importing lock masses from an xml file. See [Figure 4-33](#). This dialog box appears only when the xml file contains information about lock mass collections that differs from the available lock mass collections.

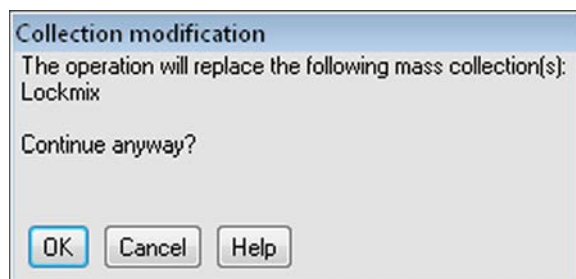


Figure 4-31. Collection Modification dialog box

The Collection Modification dialog box has the following parameters:

Parameter	Description
OK	Saves your changes and closes the dialog box. The lock mass collection is updated with the data contained in the xml file.
Cancel	Discards your changes and closes the dialog box.
Help	Displays the Help for this dialog box.

❖ To display this dialog box

1. Choose **Import > Merge with file content** in the shortcut menu of the Lock Masses dialog box.
2. In the file selection dialog box, select an xml file to import from.

Lock Masses Dialog Box

Use the Lock Masses dialog box to edit lock mass lists. See [Figure 4-32](#). The table shows all available lock masses. Lock mass collections store information about lock mass usage.

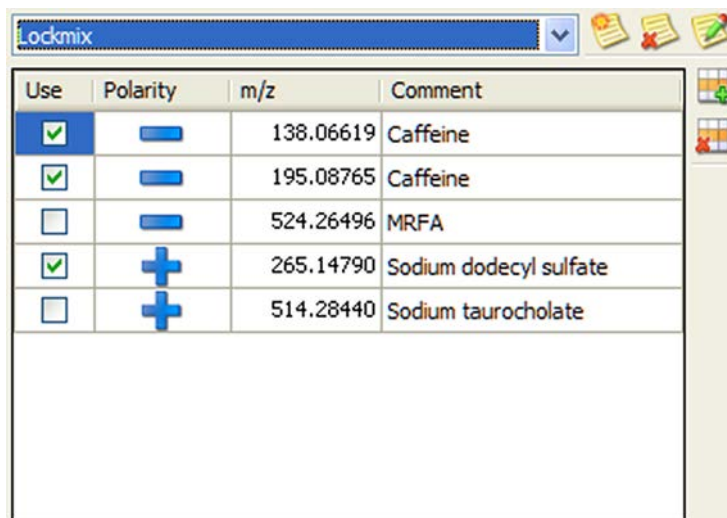


Figure 4-32. Tune—Lock Masses dialog box

The Lock Masses dialog box has the following parameters:

Parameter	Description
Lock mass lists	
Lock mass lists	Use the list box to select an existing lock mass collection.
	Displays the New Lock Mass Collection dialog box where you can enter the name for a new lock mass collection.
	Deletes the active lock mass collection. The lock masses themselves are still available. This button is not available when no lock mass collection is selected.
	Displays the Name Change dialog box where you can edit the name of the active lock mass collection. This button is not available when no lock mass collection is selected.

Parameter	Description
Available lock masses	
The table displays the properties of the available lock masses and whether they are used in the selected lock mass collection. To change the sort order, click the respective table column header. To invert the sort order, click again.	
Lock mass table	• Use Select the check box to use the lock mass. A ☒ indicates that the lock mass is used in the active lock mass collection. The lock mass is displayed in the Lock masses field of the Scan Parameters window. • Polarity Click the symbol to change the polarity of the lock mass. During a scan, the mass spectrometer uses only the lock masses with a polarity that matches the active ion mode. • m/z Enter the mass of the lock mass into the field (with a maximum of five decimals). • Comment Enter a comment for the lock mass into the field. This field is optional.
	Creates a new lock mass.
	Deletes the selected lock masses.

❖ To display this dialog box

In the Scan Parameters window, click into the Lock Masses field.

Shortcut Menu of the Lock Masses dialog box

The Lock Masses dialog box has a shortcut menu that is displayed when you right-click into the dialog box.

It has the following commands:

Command	Description
Select all masses in use	Selects all masses used in the active lock mass collection. This command is not available when no lock mass is used.
Import > Merge with clipboard	Appends the content of the clipboard to the available lock masses. The clipboard stores lock mass data as tabulator-separated text files. When the data in the clipboard are not in this format, the command is not available.
Import > Replace by clipboard	Replaces the available lock masses by the content of the clipboard. The clipboard stores lock mass data as tabulator-separated text files. When the data in the clipboard are not in this format, the command is not available.

Command	Description
Import > Merge with file content	Opens a dialog box so that you can select a .csv, .txt, or .xml file that contains a list of lock masses. The content of the file is appended to the available lock masses. See Exporting and Importing Lock Masses for information about the format of lock mass files.
Import > Replace by file content	Opens a dialog box so that you can select a .csv, .txt, or .xml file that contains a list of lock masses. All available lock masses are replaced by the masses contained in the imported file. The present lock masses are removed from all existing lock mass lists. You have to confirm your action in the Lock mass replacement dialog box. See Exporting and Importing Lock Masses for information about the format of lock mass files.
Export > Copy selected to clipboard	Copies the data of the selected lock mass to the clipboard.
Export > Copy all to clipboard	Copies the data of all available lock masses to the clipboard.
Export > Copy selected to file	Opens the dialog box, where you can save the data of the selected lock mass(es) as a .csv, .txt, or .xml file. See Exporting and Importing Lock Masses for information about the format of lock mass files.
Export > Copy all to file	Opens the dialog box, where you can save the data of all available lock masses as a .csv, .txt, or .xml file. See Exporting and Importing Lock Masses for information about the format of lock mass files.

Lock Mass Removal Dialog Box

Use this dialog box to delete one or more lock masses that are selected in the Lock Masses dialog box. See [Figure 4-33](#).

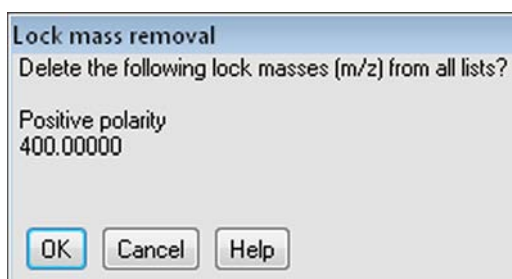


Figure 4-33. Lock Mass Removal dialog box

The Lock Mass Removal dialog box has the following parameters:

Parameter	Description
OK	Saves your changes and closes the dialog box. The lock masses are now removed from the table in the Lock Masses dialog box.
Cancel	Discards your changes and closes the dialog box.
Help	Displays the Help for this dialog box.

❖ **To display this dialog box**

In the Lock Masses dialog box, click the  button.

Lock Mass Replacement Dialog Box

Use this dialog box to replace all available lock masses by masses contained either in a csv, txt, or xml file or in the clipboard. See [Figure 4-33](#).

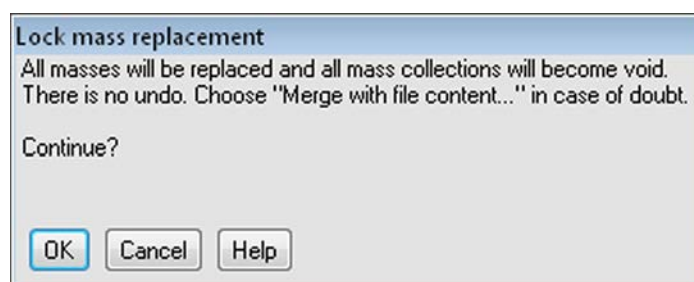


Figure 4-34. Lock Mass Replacement dialog box

The Lock Mass Replacement dialog box has the following parameters:

Parameter	Description
OK	Removes the lock masses and replaces them by the imported lock masses. The present lock mass collections become void.
Cancel	Closes the dialog box.
Help	Displays the Help for this dialog box.

❖ **To display this dialog box**

Choose **Import > Replace by file content** or **Import > Replace by clipboard** in the shortcut menu of the Lock Masses dialog box.

New Lock Mass Collection Dialog Box

Use this dialog box to enter a name for the lock mass collection that is displayed in the Lock Masses dialog box. See [Figure 4-35](#).

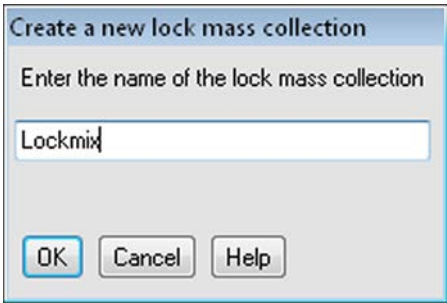


Figure 4-35. New Lock Mass Collection dialog box

The New Lock Mass Collection dialog box has the following parameters:

Parameter	Description
Name of lock mass collection	Use this text field to enter the name for the new lock mass collection.
Buttons	
OK	Saves your changes and closes the dialog box. The name of the lock mass collection is now displayed in the list box of the Lock Masses dialog box.
Cancel	Discards your changes and closes the dialog box.
Help	Displays the Help for this dialog box.

❖ **To display this dialog box**

In the Lock Masses dialog box, click the  button.

Delete Lock Mass Collection Dialog Box

Use this dialog box to delete an existing lock mass collection. See [Figure 4-36](#). The lock masses themselves are not deleted.

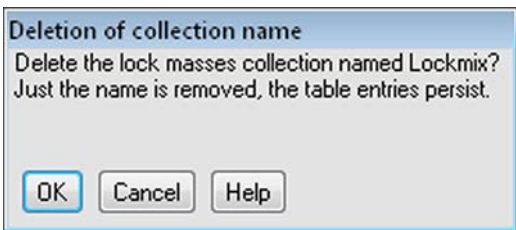


Figure 4-36. Delete Lock Mass Collection dialog box

The Delete Lock Mass Collection dialog box has the following parameters:

Parameter	Description
OK	Saves your changes and closes the dialog box. The name of the lock mass collection is now removed from the list box of the Lock Masses dialog box.
Cancel	Discards your changes and closes the dialog box.
Help	Displays the Help for this dialog box.

❖ **To display this dialog box**

In the Lock Masses dialog box, click the  button.

Name Change Dialog Box

Use this dialog box to change the name of an existing lock mass collection. See [Figure 4-37](#).

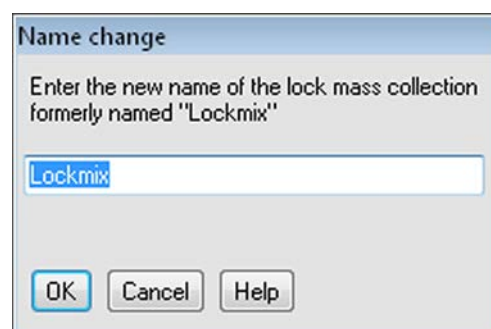


Figure 4-37. Name Change Dialog Box

The Name Change dialog box has the following parameters:

Parameter	Description
Name of lock mass collection	Use this text field to enter the new name for the lock mass collection.
Buttons	
OK	Saves your changes and closes the dialog box. The name of the lock mass collection is now displayed in the list box of the Lock Masses dialog box.
Cancel	Discards your changes and closes the dialog box.
Help	Displays the Help for this dialog box.

❖ **To display this dialog box**

In the Lock Masses dialog box, click the  button.

Display Options Dialog Box

Use this dialog box to modify the appearance of the displayed mass spectrum in the spectrum window. See [Figure 4-38](#).

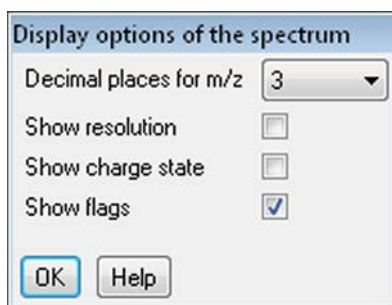


Figure 4-38. Display Options Dialog Box

The Display Options dialog box has the following parameters:

Parameter	Description
Decimal places for m/z	Use this list box to set how many decimal places of precision are shown when mass positions are annotated on mass spectra. The valid range is 0 to 5.
Show resolution	Select this check box to have Q Exactive HF-X Tune annotate mass peaks with the mass resolution.
Show charge state	Select this check box to have Q Exactive HF-X Tune annotate mass peaks with the charge state.
Show flags	Select this check box to have Q Exactive HF-X Tune indicate peaks that are contained in the active lock mass collection. The scan parameters window must show entries for lock masses.
Buttons	
OK	Saves your changes and closes the dialog box.
Help	Displays the Help for this dialog box.

❖ **To display this dialog box**

In the shortcut menu of the spectrum window, choose **Display options**.

Procedures in Q Exactive HF-X Tune

This chapter describes procedures that you may need when using Q Exactive HF-X Tune.

Contents

- [Adding a License](#)
- [Using Lock Masses and Lock Mass Collections](#)
- [Performing a System Bakeout](#)
- [Changing Default Settings of Q Exactive HF-X Tune](#)
- [Using License-Specific Settings in Q Exactive HF-X Tune](#)

Adding a License

Use the License dialog box to enter licenses that activate additional features.

❖ To add a license

1. Copy the license key that you received from Thermo Fisher Scientific to the clipboard.
2. In Q Exactive HF-X Tune, choose **Help > About** to display the About dialog box.
3. In the About dialog box, click **Add license** to display the License dialog box.
4. Paste the license code from the clipboard into the text field.
5. Click **OK** to save your input and close the License dialog box.

The About dialog box now displays the expiration date of the new license.

Using Lock Masses and Lock Mass Collections

This section provides instructions for using lock masses and lock mass collections.

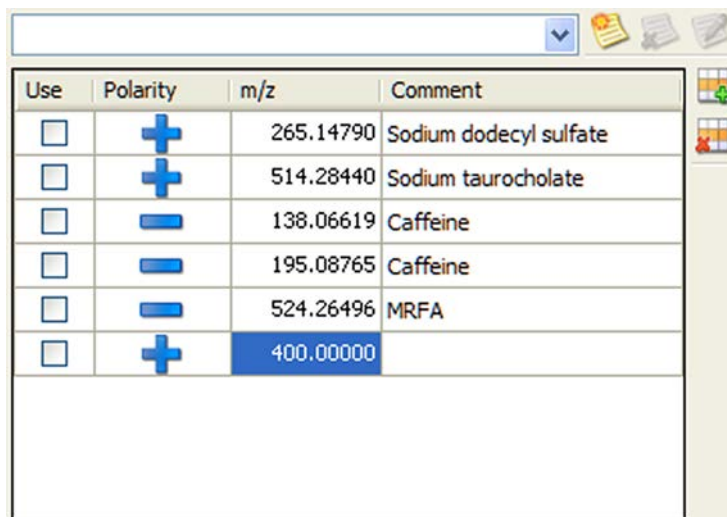
The following topics are available:

- [Adding a Lock Mass](#)
- [Deleting Lock Masses](#)
- [Exporting and Importing Lock Masses](#)
- [Creating a new Lock Mass Collection](#)
- [Renaming a Lock Mass Collection](#)
- [Adding a Lock Mass to a Lock Mass Collection](#)
- [Removing a Lock Mass from a Lock Mass Collection](#)
- [Deleting a Lock Mass Collection](#)

Adding a Lock Mass

❖ To add a lock mass

1. In the Lock Masses dialog box, click the  button. A new row appears at the end of the lock mass table. See [Figure 5-1](#).



Use	Polarity	m/z	Comment
☐	+	265.14790	Sodium dodecyl sulfate
☐	+	514.28440	Sodium taurocholate
☐	-	138.06619	Caffeine
☐	-	195.08765	Caffeine
☐	-	524.26496	MRFA
☐	+	400.00000	

Figure 5-1. Adding a new lock mass

2. Enter the data for the new lock mass into the new table row:
 - a. Select the Use check box if you want to use the new lock mass in the active lock mass collection.

- b. Click the cell in the Polarity column until the correct sign appears:  for positive or  for negative.
- c. Enter the m/z value for the new lock mass (with a maximum of five decimals).
- d. Optionally, enter a comment for the new lock mass.

The new lock mass is now available to be used.

Deleting Lock Masses

❖ To delete lock masses

1. In the Lock Masses dialog box, select one lock mass or several lock masses:
 - To select a single lock mass, click into the respective table row.
 - To select adjacent lock masses, click the first table row. Then hold down the **<Shift>** key while you click the last row.
 - To select nonadjacent lock masses, click the first table row. Then hold down the **<Ctrl>** key while you click the other rows that you want to add to the selection.
2. Click the  button. The Lock Mass Removal dialog box appears and requests your confirmation for deleting the listed lock masses.
3. Click **OK** to confirm your input and to close the dialog box. All selected lock masses are removed from the list in the Lock Masses dialog box.

Exporting and Importing Lock Masses

Q Exactive HF-X Tune allows exporting lock mass data to the clipboard or to a file. Other applications can then use the data. You can also copy the export files to other computers where Q Exactive HF-X Tune is installed. So you can reuse the lock masses without having to recreate them. To reuse the lock masses, import the data either from the clipboard or from a lock mass file.

With a spreadsheet, a text editor, or an XML editor, you can create lock mass files even without using Q Exactive HF-X Tune.

Lock Mass Files

Q Exactive HF-X Tune uses the following file formats for exporting and importing lock mass data:

- Comma-separated value lists (.csv)

- Tabulator-separated text files (.txt)
- XML files (.xml)

Lock mass data are stored in the following order:

1. Usage status: True for used, False for unused
2. Ion polarity: positive mode or negative mode
3. m/z: up to five decimals
4. Comment: optional

The clipboard stores lock mass data as tabulator-separated text files. In contrast to .csv and .txt files, .xml files additionally store information about lock mass collections and lock mass usage.

Exporting Lock Masses

Q Exactive HF-X Tune allows exporting lock mass data to the clipboard or to a file.

❖ To export selected lock masses to the clipboard

1. In the Lock Masses dialog box, select the lock masses you want to export:
 - To select a single lock mass, click into the respective table row.
 - To select adjacent lock masses, click the first table row. Then hold down the **<Shift>** key while you click the last row.
 - To select nonadjacent lock masses, click the first table row. Then hold down the **<Ctrl>** key while you click the other rows that you want to add to the selection.
2. Right-click into the dialog box to display the shortcut menu.
3. Choose **Export > Copy selected to clipboard** to copy the selected lock mass to the clipboard.

❖ To export all lock masses to the clipboard

1. In the Lock Masses dialog box, right-click into the dialog box to display the shortcut menu.
2. Choose **Export > Copy all to clipboard** to copy all available lock mass to the clipboard.

❖ **To export some lock masses to a file**

1. In the Lock Masses dialog box, select the lock masses you want to export:
 - To select a single lock mass, click into the respective table row.
 - To select adjacent lock masses, click the first table row. Then hold down the <Shift> key while you click the last row.
 - To select nonadjacent lock masses, click the first table row. Then hold down the <Ctrl> key while you click the other rows that you want to add to the selection.
2. Right-click into the dialog box to display the shortcut menu.

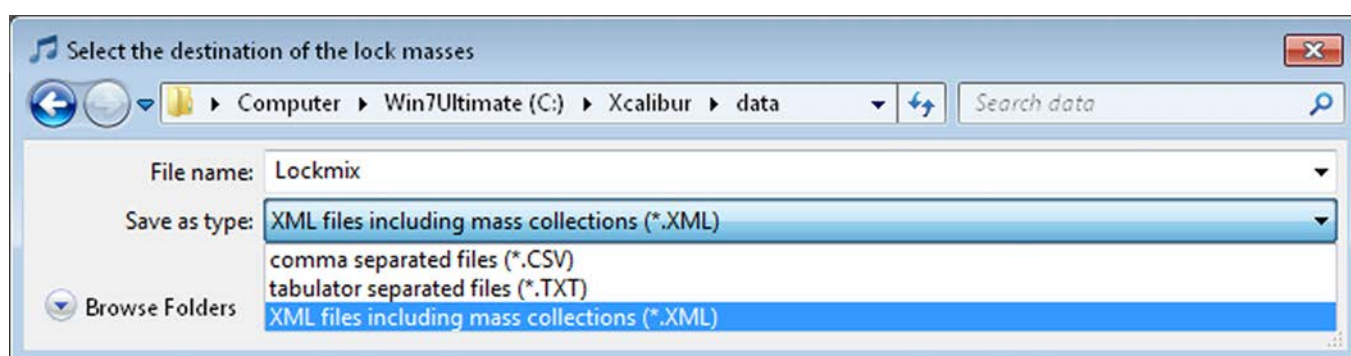


Figure 5-2. Selecting the lock mass export file

3. Choose **Export > Copy selected to file** to open the file selection dialog box. See [Figure 5-2](#).
 - a. Browse to the destination of the export file.
 - b. Select the format of the export file.
 - c. Enter a new name for the export file or select an existing file.
 - d. Click **Save** to export the selected lock masses to the file. If you want to overwrite an existing file, you have to confirm your action in a dialog box. The file selection dialog box is closed.

❖ **To export all lock masses to a file**

1. In the Lock Masses dialog box, right-click into the dialog box to display the shortcut menu.

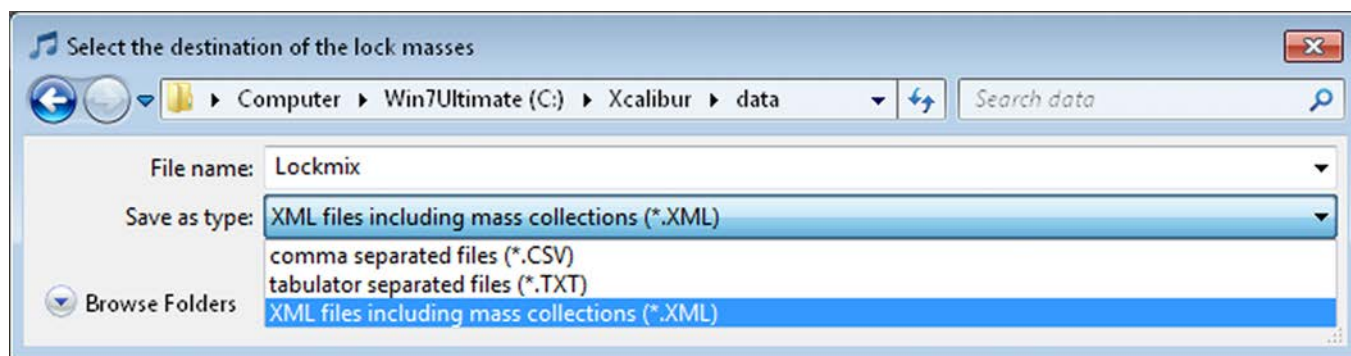


Figure 5-3. Selecting the lock mass export file

2. Choose **Export > Copy all to file** to open the file selection dialog box. See [Figure 5-3](#).
 - a. Browse to the destination of the export file.
 - b. Select the format of the export file.
 - c. Enter a new name for the export file or select an existing file.
 - d. Click **Save** to export the lock masses to the file. If you want to overwrite an existing file, you have to confirm your action in a dialog box. The file selection dialog box is closed.

Importing Lock Masses

Q Exactive HF-X Tune allows importing lock mass data from the clipboard or from a file. The imported lock masses either are added to the present lock masses or they replace them.

❖ To add lock masses from the clipboard

1. Copy lock mass data in an appropriate format to the clipboard. See [Lock Mass Files](#) for information about the requirements.
2. In the Lock Masses dialog box, right-click into the dialog box to display the shortcut menu.
3. Choose **Import > Merge with clipboard** to import the lock mass data from the clipboard to the lock mass table.

The clipboard stores lock mass data as tabulator-separated text files. When the data in the clipboard are not in this format, the command is not available.

4. The lock mass list in the Lock Masses dialog box displays additional rows for the imported lock masses.

❖ **To add lock masses from a file**

1. In the Lock Masses dialog box, right-click into the dialog box to display the shortcut menu.
2. Choose **Import > Merge with file content** to open the file selection dialog box. See [Figure 5-4](#).
 - a. Browse to the destination of the import file.
 - b. Select the format of the import file.
 - c. Select one of the displayed files.
 - d. Click **Open** to import the lock masses to Q Exactive HF-X Tune. The dialog box is closed.

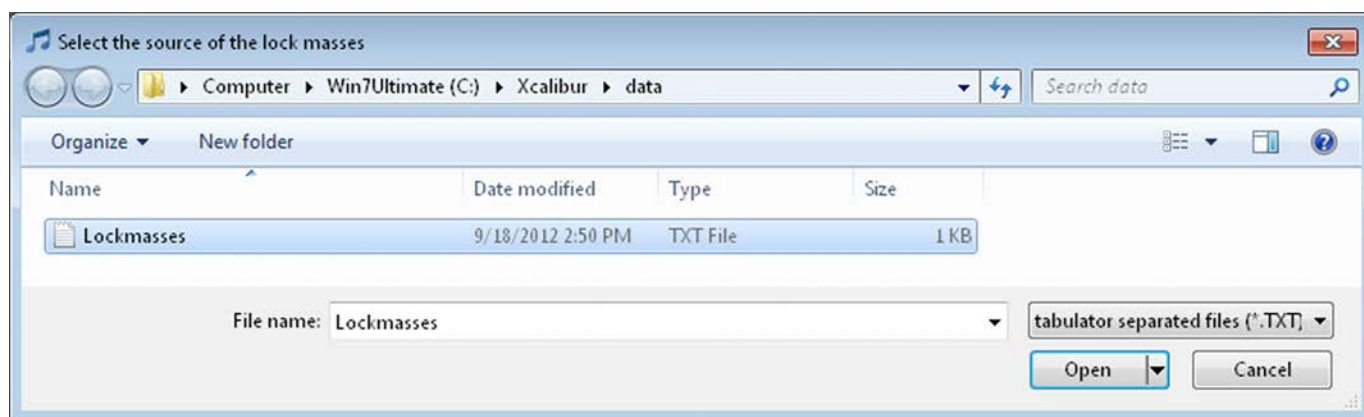


Figure 5-4. Selecting the lock mass import file

3. If you are importing an xml file that contains information about lock mass collections that differs from the present lock mass collections, the Collection modification dialog is displayed. Click **OK** to confirm the operation and to close the dialog box.
4. The lock mass list in the Lock Masses dialog box displays additional rows for the imported lock masses.

❖ **To replace all lock masses by clipboard data**

1. Copy lock mass data in an appropriate format to the clipboard. See [Lock Mass Files](#) for information about the requirements.
2. In the Lock Masses dialog box, right-click into the dialog box to display the shortcut menu.
3. Choose **Import > Replace by clipboard** to import the lock mass data from the clipboard to the lock mass table.

The clipboard stores lock mass data as tabulator-separated text files. When the data in the clipboard are not in this format, the command is not available.

4. The Lock Mass Replacement dialog box is displayed. Click **OK** to confirm the import.
5. The Lock Mass Replacement dialog box is closed. The lock mass list in the Lock Masses dialog box displays only the imported lock masses.

❖ **To replace all lock masses from a file**

1. In the Lock Masses dialog box, right-click into the dialog box to display the shortcut menu.
2. Choose **Import > Replace by file content**.
3. The Lock Mass Replacement dialog box is displayed. Click **OK** to confirm the import.

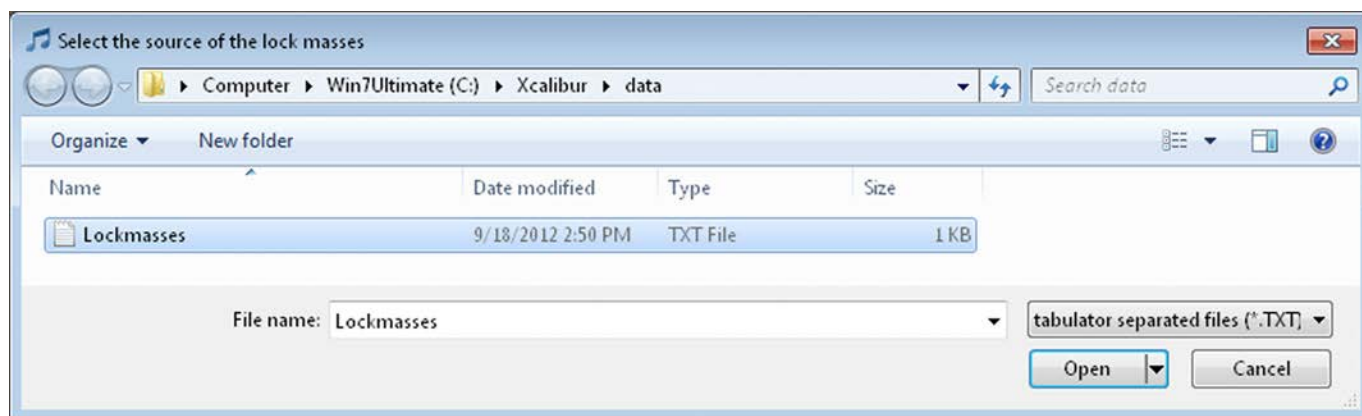


Figure 5-5. Selecting the lock mass import file

4. The Lock Mass Replacement dialog box is closed. The file selection dialog box is displayed. See [Figure 5-5](#).
 - a. Browse to the destination of the import file.
 - b. Select the format of the import file.
 - c. Select one of the displayed files.
 - d. Click **Open** to import the lock masses to Q Exactive HF-X Tune. The dialog box is closed.
5. The lock mass list in the Lock Masses dialog box displays only the imported lock masses.

If you have imported lock mass data from an xml file that contained information about lock mass collections and lock mass usage, the dialog box displays the corresponding information.

Creating a new Lock Mass Collection

❖ To create a lock mass collection

1. In the Lock Masses dialog box, click the  button.
2. In the New Lock Mass Collection dialog box, enter a name for the new lock mass collection. See [Figure 5-6](#).

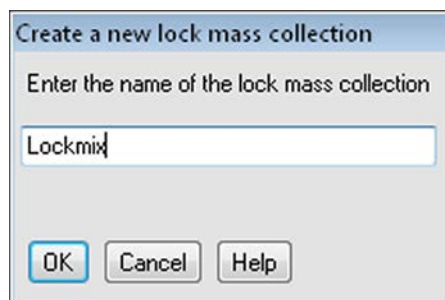


Figure 5-6. Creating a lock mass collection

3. Click **OK** to confirm your input and to close the dialog box.
4. The name of the new lock mass collection appears in the list box of the Lock Masses dialog box.

Renaming a Lock Mass Collection

❖ To rename a lock mass collection

1. In the Lock Masses dialog box, select an existing lock mass collection in the list box.
2. Click the  button. The Name Change dialog box is displayed. See [Figure 5-7](#).

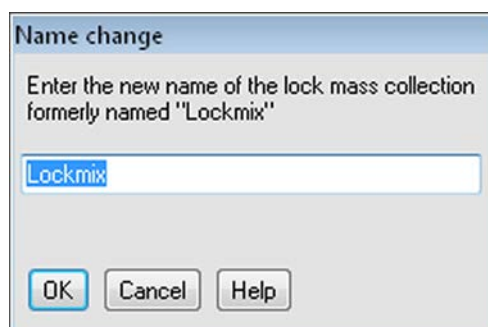


Figure 5-7. Changing the name of a lock mass collection

3. In the text field, replace the old name of the lock mass collection with the new name.

4. Click **OK** to confirm your input and to close the dialog box.
5. In the Lock Masses dialog box, the new lock mass collection is displayed in the list box.

Adding a Lock Mass to a Lock Mass Collection

❖ To add a lock mass to a lock mass collection

1. In the Lock Masses dialog box, select an existing lock mass collection in the list box.
2. Select the Use check box in the table row of the lock mass.
3. A ☒ indicates that the lock mass is used in the active lock mass collection.

Removing a Lock Mass from a Lock Mass Collection

❖ To remove a lock mass from a lock mass collection

1. In the Lock Masses dialog box, select an existing lock mass collection in the list box.
2. Clear the Use check box in the table row of the lock mass.
3. A ☐ indicates that the lock mass is not used in the active lock mass collection.

Deleting a Lock Mass Collection

❖ To delete a lock mass collection

1. In the Lock Masses dialog box, select an existing lock mass collection in the list box.
2. Click the  button.
3. In the Delete Lock Mass Collection dialog box, click **OK** to confirm your action and to close the dialog box.
4. The name of the lock mass collection is removed from the list box of the Lock Masses dialog box.

Performing a System Bakeout

The system bakeout of the mass spectrometer removes unwanted gases or molecules (collected or remaining) from the high vacuum region of the instrument. Ions can collide with those gases or molecules resulting in lower overall sensitivity. Therefore, Thermo Fisher Scientific recommends baking out the instrument if the high vacuum decreases noticeable during routine operation.

Bakeout is mandatory after maintenance or service work is performed in the analyzer region where the system is vented. You should bake out an instrument that has been vented for at least twelve hours (12 hours) before you can start using it again.

In case the system has been vented during a power failure, it is necessary to bake out the system to obtain the operating vacuum.

Tip Before you start the bakeout, make sure that the pumps are up and running at their operating speed. If you have just switched on the mass spectrometer, this will take about 10 minutes. To check the pump speed, open the Instruments Status window and expand the Vacuum System node of the Instrument tree.

❖ To perform a system bakeout



1. In the Q Exactive HF-X Tune window, click on the **On/Standby** button to put the instrument in Off condition. (See image in margin.)
2. In the Tasks panel, click  **Vacuum / Bakeout** to display the Vacuum / Bakeout window.
3. Enter the baking duration (in hours) into the spin box. The range is 4 to 30 hours. See [Figure 5-8](#).

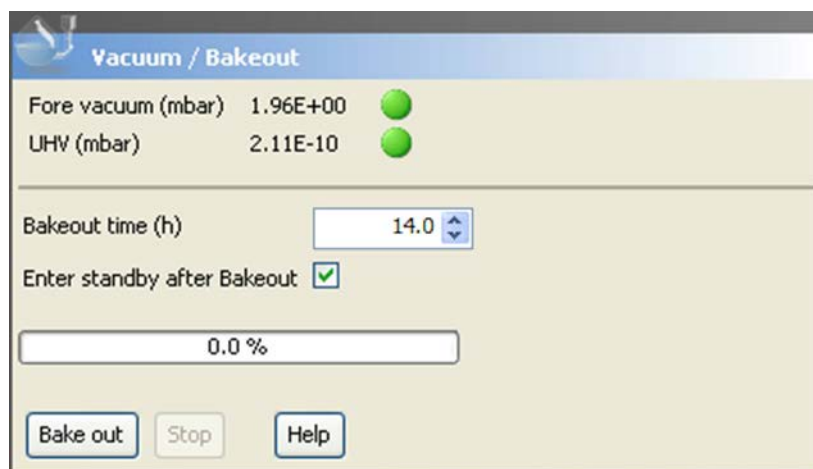


Figure 5-8. Vacuum / Bakeout window

4. Click **Bake out**. A dialog box shows the duration of the baking procedure. See [Figure 5-9](#). Click **Yes** to confirm the message.

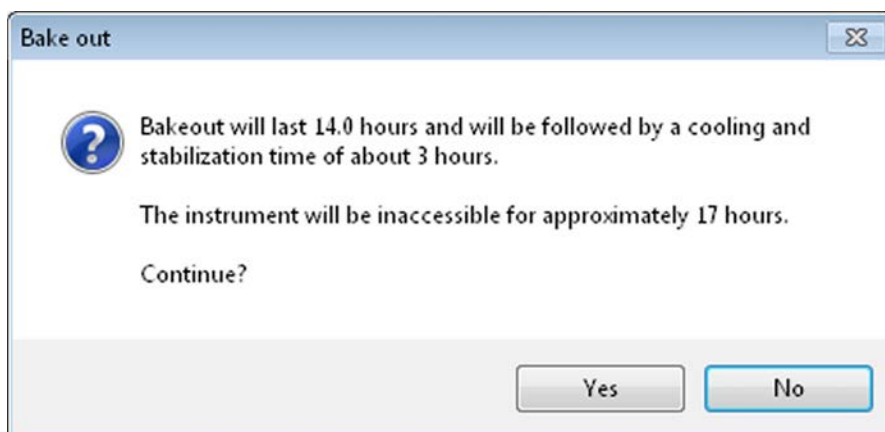


Figure 5-9. Bakeout message box

5. The message box disappears and the baking procedure starts. The instrument indicates the active bakeout procedure by a flashing Vacuum LED at the front side. Additionally, the Q Exactive HF-X Tune software displays a corresponding message box.
6. The baking of the instrument stops after the preset duration. The Vacuum LED keeps flashing until the cooling and stabilization time (of about 3 hours) is finished.

Click **Stop** in the Vacuum / Bakeout window to abort the baking routine before the preset time.

Changing Default Settings of Q Exactive HF-X Tune

Advanced users can use the instrument status window to change default settings of Q Exactive HF-X Tune.

Contents

- [Displaying the High Vacuum Readback](#)
- [Entering Parameters for the Syringe Pump](#)
- [Changing the Settings for the Performance Status Check](#)
- [Enabling the DART Ion Source Compatibility](#)
- [Changing the Sweep Gas Flow in Standby Mode](#)

Displaying the High Vacuum Readback

The High Vacuum readback in the Vacuum / Bakeout window is visible only when the ion gauge in the high vacuum chamber is switched on. Advanced users can switch on this gauge manually.

❖ To switch on the High Vacuum readback in the Vacuum / Bakeout window

1. Click   in the tasks panel to display the Vacuum / Bakeout window.
2. If the instrument status window is not visible, choose **Windows > Instrument Status**.
3. In the instrument status window, click **Instrument > Vacuum System**.
4. Right-click the High Vacuum parameter to display the shortcut menu.
5. Choose **Turn on** to switch on the ion gauge in the high vacuum chamber.
6. The Vacuum / Bakeout window now displays the High Vacuum readback.

To extend the lifetime of the ion gauge in the high vacuum chamber, it is switched off again after a preset time of about thirty minutes.

Entering Parameters for the Syringe Pump

The syringe contact of the Q Exactive HF-X mass spectrometer allows controlling established syringe pumps by Q Exactive HF-X Tune by means of the RS-232 serial interface. Suitable syringe pumps are the Chemyx Fusion 100 pump (available from Thermo Fisher Scientific) and the Harvard Apparatus Model 11 Plus Advanced pump. Advanced users can select the syringe pump type and enter parameters for the syringe pump in the instrument status window.

❖ To enter parameters for the syringe pump

1. If the instrument status window is not visible, choose **Windows > Instrument Status**.
2. In the instrument status window, click **Instrument > System > Configuration settings > Peripherals**. The Peripherals node displays parameters for the syringe pump. See [Figure 5-10](#).

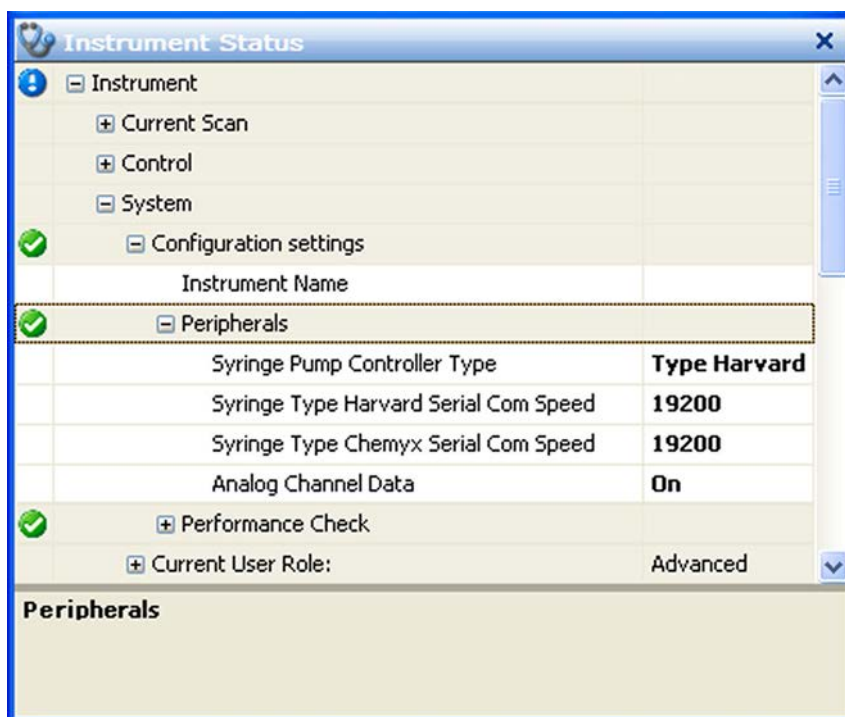


Figure 5-10. Instrument status window—Peripherals node

3. To change the settings for a parameter, right-click the parameter entry to display the shortcut menu. If necessary, change the values of the following parameters:
 - Syringe Pump Controller Type: In the list box, select either **Type Harvard** (for Harvard Apparatus Model 11 Plus Advanced pump) or **Type Chemyx** (for Chemyx Fusion 100 pump).

- Syringe Type Harvard Serial Com Speed: Enter the baud rate for the interface into the input field. Available options are 1200, 2400, 4800, 9600, and 19200 bauds. Press the **<Enter>** key to confirm your input.
- Syringe Type Chemyx Serial Com Speed: Enter the baud rate for the interface into the input field. Available options are 1200, 2400, 4800, 9600, and 19200 bauds. Press the **<Enter>** key to confirm your input.

See the manual that came with the syringe pump for the correct baud rate.

Changing the Settings for the Performance Status Check

By default, the performance status icon on the toolbar turns yellow 25 hours after the last successful mass calibration or check. Advanced users can change this value in the System node of the instrument status window according to their mass accuracy requirements.

❖ To change the settings for the performance status check

1. If the instrument status window is not visible, choose **Windows > Instrument Status**.
2. In the instrument status window, click **Instrument > System > Configuration settings > Performance Check**. The Mass calibration due time (h) field displays the current validity period of the mass calibration (25 hours, for example). See [Figure 5-11](#).

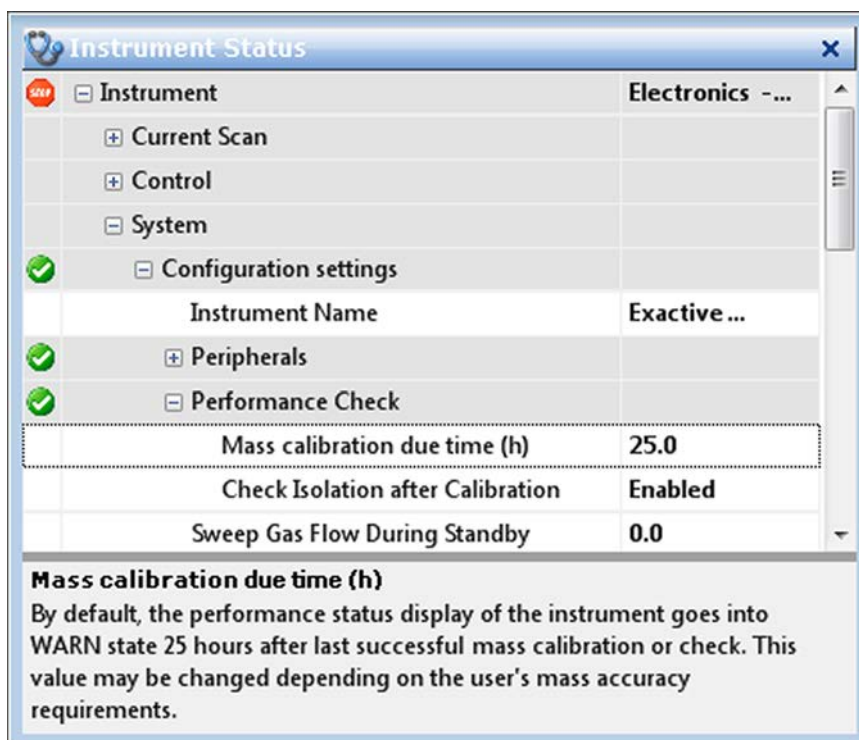


Figure 5-11. Instrument status window—Performance Check node

- To change the value, right-click the number in the text field to display the shortcut menu.
- In the Set text field, enter the new validity period (40, for example). See [Figure 5-12](#). You can enter a value between 1 and 500 hours.



Figure 5-12. Changing the calibration validity period

- Press the **<Enter>** key to confirm your input. The shortcut menu disappears and the new value is displayed in the instrument status window.

Enabling the DART Ion Source Compatibility

Using a DART ion source increases the gas input into the UHV region. As a result, the pressure might exceed the instrument status warning level. This is indicated by a yellow LED in the Vacuum / Bakeout window. Advanced users can enable the DART ion source compatibility in the Instrument Status window to increase the UHV warning level to 5E-09 mbar.

❖ **To enable the DART ion source compatibility**

1. If the instrument status window is not visible, choose **Windows > Instrument Status**.
2. In the instrument status window, click **Instrument > System > Configuration settings > Performance Check > DART Ion Source Compatibility**.
3. To change the value, right-click the entry in the text field to display the shortcut menu.
4. In the Set text field, select **Enabled**. See Figure 5-13. The shortcut menu disappears and the new value is displayed in the instrument status window.

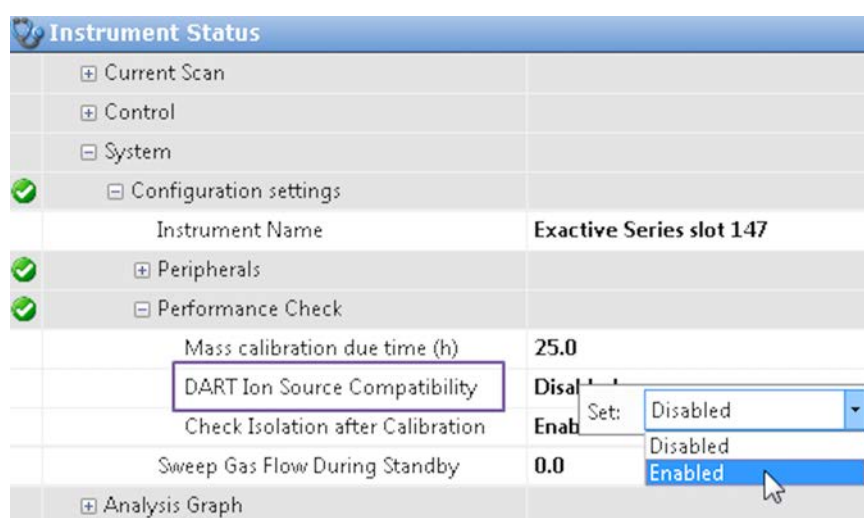


Figure 5-13. Instrument status window—DART Ion Source Compatibility

Changing the Sweep Gas Flow in Standby Mode

Advanced users can leave some sweep gas on during standby to positively pressurize the ion source. Studies have shown that this can reduce the amount and size of the particles that get into the system and onto the ion optics.

Tip Users who use nitrogen gas from a limited supply (gas bottles, for example) may want to switch off the sweep gas flow during standby.

❖ **To change the sweep gas flow during standby**

1. If the instrument status window is not visible, choose **Windows > Instrument Status**.
2. In the instrument status window, click **Instrument > System > Configuration settings > Sweep Gas Flow During Standby**.

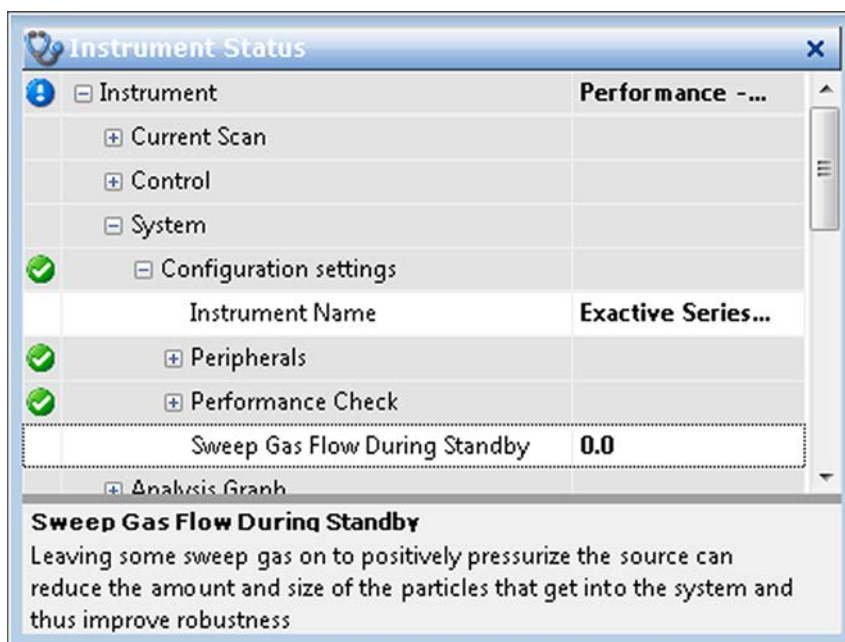


Figure 5-14. Instrument status window—Sweep gas flow during standby

3. To change the value, right-click the number in the text field to display the shortcut menu.
4. In the Set text field, enter the new value (2, for example). See [Figure 5-15](#). You can enter a value between 0 (no sweep gas) and 10 arbitrary units.



Figure 5-15. Changing the sweep gas flow

5. Press the **<Enter>** key to confirm your input. The shortcut menu disappears and the new value is displayed in the instrument status window.

Using License-Specific Settings in Q Exactive HF-X Tune

For advanced users, the instrument status window provides various parameters that are available only when the corresponding license is installed.

Disabling the HMR Mode or the Intact Protein Mode

On instruments with a valid High Mass Range license or Intact Protein license, advanced users can use the instrument status window to temporarily disable the features that are provided by the corresponding mode.

If both licenses are installed on your system, only the following settings are available:

Mode	Setting		
High Mass Range (HMR) Mode	Off	On	Off
Intact Protein Mode	Off	Off	On

The following instruction for disabling the HMR mode works in the same way for the Protein mode.

❖ To disable the HMR Mode

1. If the instrument status window is not visible, choose **Windows > Instrument Status**.
2. In the instrument status window, click **Instrument > Control > Settings > HMR mode**.

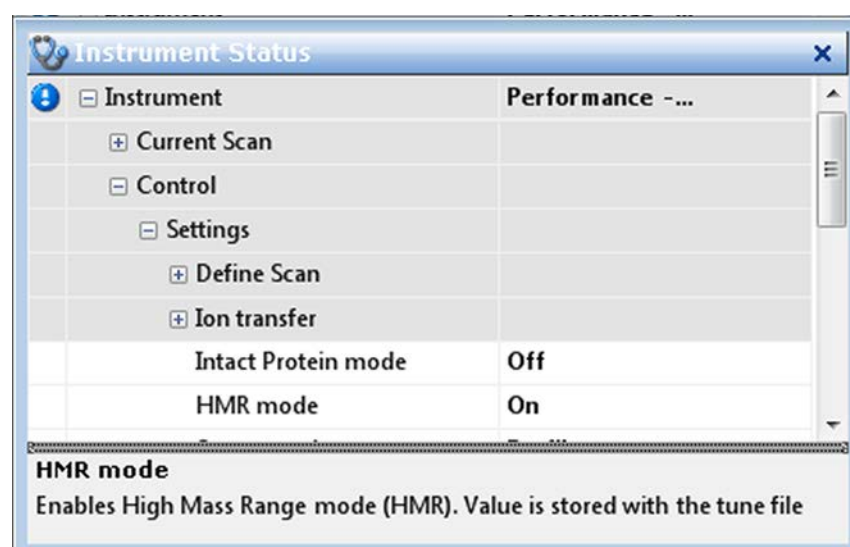


Figure 5-16. Instrument status window—HMR mode

3. To change the value, right-click the text field to display the shortcut menu.
4. In the Set list box, select **Off**. The shortcut menu disappears and the new value is displayed in the instrument status window.

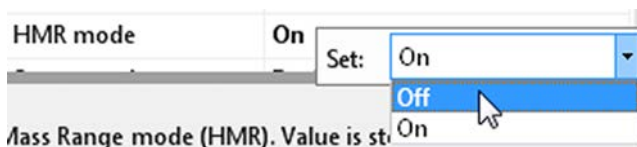


Figure 5-17. Switching off the HMR mode

To enable the HMR mode again, select **On** in the shortcut menu.

Setting the HCD Trapping Gas Pressure

HCD trapping enables a better trapping of large molecules. It is available on instruments with a valid High Mass Range license or Intact Protein license.

The trapping gas pressure is normalized to the standard operating pressure difference in the trapping region. A value <1 decreases the pressure compared to the standard pressure, a value >1 increase the pressure compared to the standard pressure. The default value for Intact Protein mode is 0.2 and the default value for HMR mode is 1.0.

❖ To change the HCD trapping gas pressure

1. If the instrument status window is not visible, choose **Windows > Instrument Status**.
2. In the instrument status window, do one of the following:
 - Click **Instrument > Control > Settings > Intact Protein mode**.
 - Click **Instrument > Control > Settings > HMR mode**.
3. Right-click the text field to display the shortcut menu. In the Set list box, select **On**. The shortcut menu disappears and the new value is displayed in the instrument status window. If the other mode option is available, it is set to Off.

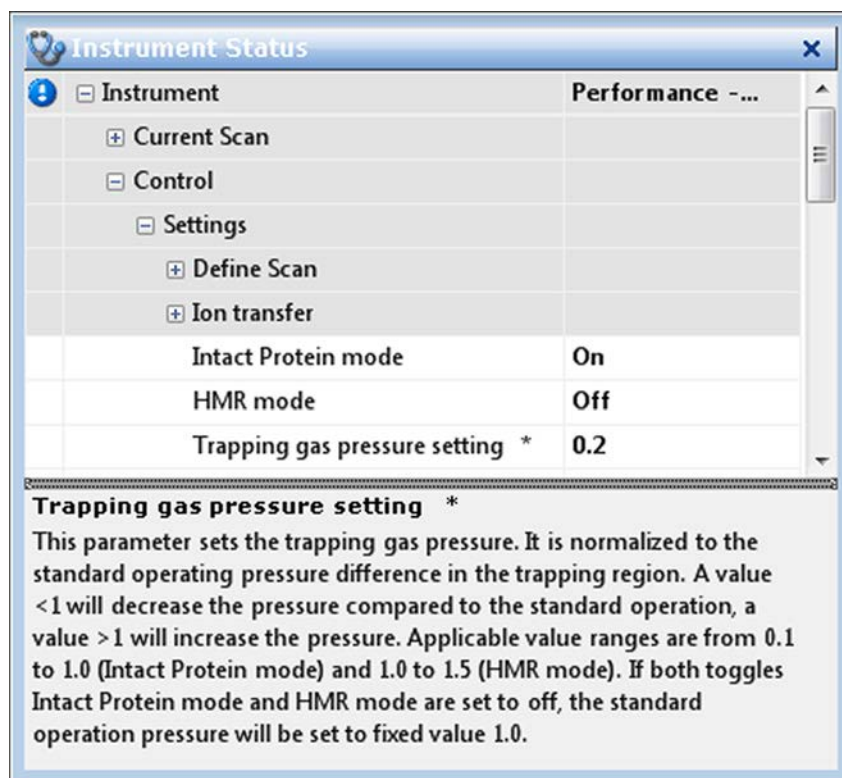


Figure 5-18. Instrument status window—Trapping gas pressure

4. Right-click **Trapping gas pressure setting** to display the shortcut menu.
5. In the Set rel. pressure field, enter the new value (1, for example).
For Intact Protein mode, you can enter a value between 0.1 and 1.
For HMR mode, you can enter a value between 1 and 1.5.

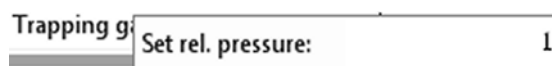


Figure 5-19. Changing the trapping gas pressure

6. Press the **<Enter>** key to confirm your input. The shortcut menu disappears and the new value is displayed in the instrument status window.

Averaging Spectra

On instruments with a valid High Mass Range license or Intact Protein license, advanced users can use the instrument status window to enable the rolling averaging of the acquired spectra. This increases the signal-to-noise ratio at the expense of the speed of signal changes. Averaging can be used only when either HMR mode or Intact Protein mode is enabled.

❖ **To enable the averaging of spectra**

1. If the instrument status window is not visible, choose **Windows > Instrument Status**.
2. In the instrument status window, click **Instrument > Control > Settings > Define Scan > Averaging**.

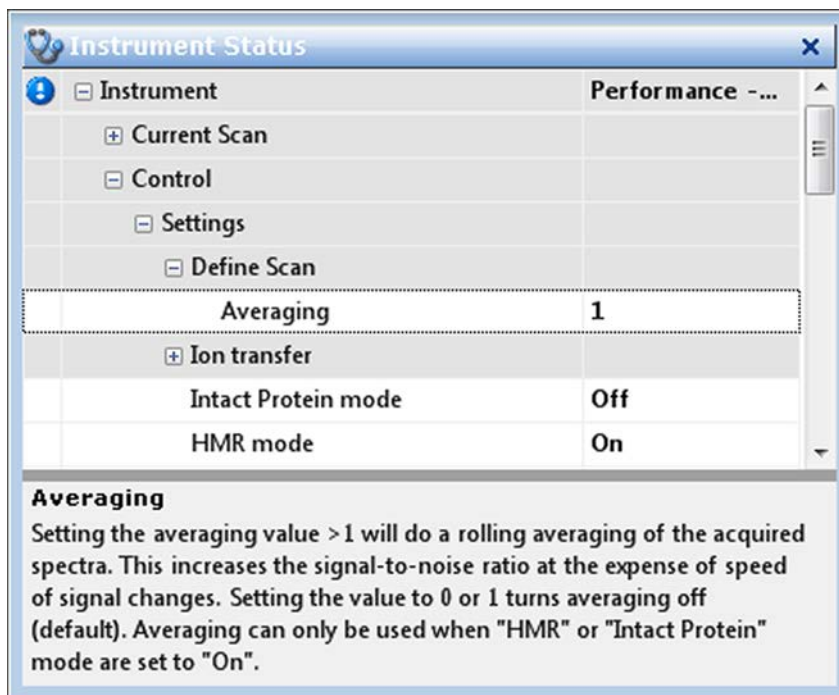


Figure 5-20. Instrument status window—Averaging

3. To change the value, right-click the number in the text field to display the shortcut menu.
4. In the Set text field, enter the new value (100, for example). You can enter either 0 or 1 (no averaging) or an integer between 2 and 1000.



Figure 5-21. Enabling averaging spectra

5. Press the **<Enter>** key to confirm your input. The shortcut menu disappears and the new value is displayed in the instrument status window.

Performing Calibrations and Evaluations for HMR Mode

The mass calibration for the HMR mode supports values up to m/z 8000. Ammonium hexafluorophosphate (AHFP) ions can be detected up to m/z 8000 and are suitable for mass calibrations and evaluations in HMR mode.

Tip AHFP is corrosive. Read the MSDS for further information.

❖ To prepare a calibration or an evaluation in the HMR mode

1. Prepare an HMR calibration solution containing 1 mg/mL ammonium hexafluorophosphate (AHFP or NH_4PF_6) in isopropanol:water 50:50.
2. In the instrument status window, make sure that HMR mode is set to On.
3. In the Scan parameters window, use these settings:

Scan range	630.0 to 6670.0 m/z
In-source CID	100 eV
Resolution	140000
AGC target	3e6

Also, the m/z values of the ions contained in the HMR mass list are used.

4. In the HESI source window, use these settings:

Sheath gas flow rate	5
Spray voltage	3.8 kV
Capillary temperature	320 °C
S-lens RF level	200

❖ To calibrate in the HMR mode

1. In the Calmix Calibration window, do the following:
 - Select the **HMR Mode Calibration (pos)** check box to calibrate in the positive ion mode.

and/or
 - Select the **HMR Mode Calibration (neg)** check box to calibrate in the negative ion mode.
2. Start injecting the AFHP solution.
3. In the Calibrate window, click **Calibrate** to start the calibration.

❖ **To evaluate in the HMR mode**

1. In the Calmix Evaluation window, do the following:
 - Expand the Positive Ion Evaluation node and select the **HMR Mode Check (pos)** check box to evaluate in the positive ion mode.
 - and/or
 - Expand the Negative Ion Evaluation node and select the **HMR Mode Check (neg)** check box to evaluate in the negative ion mode.
2. Start injecting the AFHP solution.
3. In the Calibrate window, click **Evaluate** to start the evaluation.

Tip The high concentration of the AFHP solution might cause the contamination of the ion source. Try to spray this solution as short as possible. Rinse and spray the source with pure solvent or calmix right afterwards.

Displaying the Mass Calibration Lists for the HMR Mode

On instruments with a valid High Mass Range license, advanced users can use the instrument status window to display the list of masses used for mass calibrations and evaluations in HMR mode. They can also change the used masses, if necessary.

❖ **To display the HMR mass list**

1. If the instrument status window is not visible, choose **Windows > Instrument Status**.
2. In the instrument status window, click **Instrument > Control > Procedures > HMR Mass List**.
 - Expand the **Positive ions** node to display a list of seven masses in the range between m/z 670 and m/z 6049.
 - Expand the **Negative ions** node to display a list of seven masses in the range between m/z 633 and m/z 6501.9.

Procedures in Q Exactive HF-X Tune

Using License-Specific Settings in Q Exactive HF-X Tune

Reference Information

This chapter provides reference information for the following:

Contents

- [Log Files](#)
- [Tune Files and Calibration Files](#)
- [API Source Settings for Various LC Flow Rates](#)
- [One-Letter Abbreviations for Amino Acids](#)

Log Files

Log files (*.log) are created for a Q Exactive HF-X mass spectrometer. The default directory for the log files is C:\Xcalibur\system\Exactive\log. The Instrument Configuration window shows the actual path.

Additional log files are created every time the Exactive window service starts. The file name shows date and time of the service start, as shown in the following example:

Thermo Exactive--2008-10-22--08-17-22.log

The system automatically deletes all log files that are older than 18 months.

Each line in a log file is a message. A message has several properties that are listed at the beginning of the line, followed by the message body.

Properties are enclosed in brackets. A property is a property name followed by an equal sign followed by the property value. These properties exist:

Abbreviation	Meaning
Time	Time of the message. The current local time is displayed followed by the time offset to UTC.
Acc	Windows™ account name that caused this message; “(none)” is used for an instrument source. Other known values are “ExactiveUser” and “Xcalibur_System”.
User	User name description of the Windows account
Comp	Computer name on which this message was caused, “(none)” is used for an instrument source.
App	Application name that caused this message; “(none)” is used for an instrument source.
PID	Process identifier of the application process
Inst	Instrument affected
Conn	Connection in charge for the communication with the instrument
Type	Type of the message. Message types are “info”, “warning”, “error” and “FATAL error”

Access to the log files is regulated by the Microsoft™ Windows user account or group account. Full access to the log files is granted to Administrators. Members of the Power User group can read, delete, and modify these files. Standard users can read these files.

Tune Files and Calibration Files

Tune files and calibration files contain information for operating the instrument.

Tune Files

Tuning optimizes voltage settings for API source and ion transfer optics to ensure highest sensitivity. The resulting tune file (*.mstune) is specific to a particular analyte and solvent flow rate.

During installation of the instrument, the service engineer creates a tune file HESI_Installation.mstune in the folder C:\Xcalibur\methods\. Use this file as a starting point for optimizing the mass spectrometer for your specific measurement requirements. Use this folder to store your personal tune files.

Tip Do not overwrite the default tune file
C:\Xcalibur\methods\HESI_Installation.mstune!

Calibration File

After having tuned the Q Exactive HF-X mass spectrometer, calibrate the instrument to ensure the mass accuracy of the measurement results. Calibration parameters are instrument parameters whose values do not vary with the type of experiment. They are stored *automatically* in a calibration file (*.mscal) in the folder
C:\Xcalibur\system\Exactive\instrument\msx_instrument_files\.

The file master_cal.mscal contained in this folder is the calibration file used for operating the instrument. It will be overwritten with new calibration values every time a calibration procedure is successful.

Tip Never save or change files in the folder
C:\Xcalibur\system\Exactive\instrument\msx_instrument_files\! Files in this folder are automatically managed by the instrument software.

API Source Settings for Various LC Flow Rates

The ESI, H-ESI, and HESI-II probes can generate ions from liquid flows of 1 $\mu\text{L}/\text{min}$ to 1.0 mL/min . With this flow rate range you can use a variety of separation techniques: capillary LC, microbore LC, and analytical LC. An optional nanospray ion source is available for sub-microliter analysis. The APCI probe can generate ions from liquid flows as low as 50 $\mu\text{L}/\text{min}$, but typical flow rates are from 0.2 to 2.0 mL/min . Within this range of flow rates, you can use separation techniques such as microbore LC, analytical LC, and semi-preparative LC.

As you change the rate of flow of solvents entering the mass spectrometer, you must adjust several of the mass spectrometer parameters:

- For ESI, adjust the temperatures of the ion transfer tube and adjust the gas flow rates for the sheath gas and auxiliary gas.
- For H-ESI, adjust the temperatures of the ion transfer tube and the vaporizer, and adjust the gas flow rates for the sheath gas and auxiliary gas.
- For APCI, adjust the temperatures of the ion transfer tube and the vaporizer, and adjust the gas flow rates for the sheath gas and auxiliary gas.

In general, the higher the rate of liquid flowing into the mass spectrometer, the higher the temperature of the ion transfer tube (and vaporizer) and the higher the gas flows.

Table 6-1 provides guidelines for setting H-ESI operating parameters for various LC solvent flow rates. Table 6-2 provides guidelines for setting ESI operating parameters. Table 6-3 provides guidelines for setting APCI operating parameters.

Table 6-1. Guidelines for setting operating parameters for LC/H-ESI/MS

Liquid flow rate ($\mu\text{L}/\text{min}$)	Capillary (ion transfer tube) temperature ($^{\circ}\text{C}$) ^a	Vaporizer temperature ($^{\circ}\text{C}$) ^b	Sheath gas pressure (arbitrary units)	Auxiliary gas flow (arbitrary units)	Spray voltage (V)
5	275	Off to 50	5	0 to 10 ^c	+3500 (-2500) ^d
200	275	300 to 400	45	30 (H-ESI probe) 10 (HESI-II probe)	+3500 (-2500)

Table 6-1. Guidelines for setting operating parameters for LC/H-ESI/MS, continued

Liquid flow rate (μL/min)	Capillary (ion transfer tube) temperature (°C) ^a	Vaporizer temperature (°C) ^b	Sheath gas pressure (arbitrary units)	Auxiliary gas flow (arbitrary units)	Spray voltage (V)
500	300	300 to 400 (H-ESI probe) 300 to 500 (HESI-II probe)	55	50 (H-ESI probe) 15 (HESI-II probe)	+3500 (-2500)
1000	325	350 to 450 (H-ESI probe) 500 (HESI-II probe)	65	60 (H-ESI probe) 20 (HESI-II probe)	+3500 (-2500)

^aAlways optimize the Funnel RF voltage when you change the temperature of the ion transfer tube.

^bCompound dependent

^cAux gas flow must be greater than 0 if the vaporizer is on.

^dNegative ion mode

Table 6-2. Guidelines for setting operating parameters for LC/ESI/MS

Liquid flow rate (μL/min)	Suggested column ID size (mm)	Spray voltage (V)	Capillary temperature (°C)	Sheath gas (arbitrary units)	Auxiliary gas (arbitrary units)
less than 10	Capillary	3000 (-2500) ^a	200 to 250	5 to 30	Off
50 to 100	1.0	3000 (-2500)	250 to 300	10 to 30	5 to 10
200 to 400	2.1 to 4.6	3500 (-2500)	300 to 350	20 to 40	10 to 20
greater than 400	4.6	4000 (-3500)	350	30 to 75	10 to 40

^aNegative ion mode

Table 6-3. Guidelines for setting operating parameters for LC/APCI/MS

Liquid flow rate (μL/min)	Capillary temperature (°C)	APCI vaporizer temperature (°C)	Sheath gas (arbitrary units)	Auxiliary gas (arbitrary units)	Corona discharge current (μA)
200	250	350	25	5	+4 (-10) ^a
1000	250	450	45	5	+4 (-10)

^aNegative ion mode

Default Parameters and Ranges for HESI-2 and APCI

Table 6-4 and Table 6-5 list the parameters and values that Q Exactive HF-X Tune uses when you click **Source Auto-Defaults** in the HESI source window or the APCI source window.

Table 6-4. Default Parameters and Ranges for HESI-2

Liquid flow rate (μL/min)	Capillary temp. (°C)	Vaporizer temp. (°C)	Sheath gas press. (arbitrary units)	Auxiliary gas flow (arbitrary units)	Sweep gas flow (arbitrary units)	Spray voltage (V)
5	275	50	5	3	0	+3500 (-2500)
10	275	100	15	5	0	+3500 (-2500)
50	275	150	30	10	1	+3500 (-2500)
100	275	200	35	10	1	+3500 (-2500)
200	275	400	45	10	2	+3500 (-2500)
600	300	450	55	15	3	+3500 (-2500)
1000	325	500	65	20	4	+3500 (-2500)

Tip Spray Voltage is a “tunable” parameter, which can optimize at low voltages (for example, 500–1000 V) for some compounds.

Table 6-5. Default Parameters and Ranges for APCI

Liquid flow rate (mL/min)	Capillary temp. (°C)	Vaporizer temp. (°C)	Sheath gas press. (arbitrary units)	Auxiliary gas flow (arbitrary units)	Sweep gas flow (arbitrary units)	Discharge Current (μA)
0.2	225	350	20	5	0	4 ^a (20 ^b)
0.6	250	400	25	5	0	4 ^a (40 ^b)
1.0	275	450	30	5	0	4 ^a (60 ^b)

^aPositive ion mode

^bNegative ion mode

Tip The APCI Discharge Current in negative ion mode generally requires a higher current than positive ion mode. This parameter should be optimized for the target compound up to a maximum of 100 μA.

One-Letter Abbreviations for Amino Acids

The following table assists you in using the Mass Calculator.

One letter	Name	Formula
A	Alanine	C ₃ H ₅ NO
C	Cysteine	C ₃ H ₅ NOS
D	Aspartate	C ₄ H ₅ NO ₃
E	Glutamate	C ₅ H ₇ NO ₃
F	Phenylalanine	C ₉ H ₉ NO
G	Glycine	C ₂ H ₃ NO
H	Histidine	C ₆ H ₇ N ₃ O
I	Isoleucine	C ₆ H ₁₁ NO
K	Lysine	C ₆ H ₁₂ N ₂ O
L	Leucine	C ₆ H ₁₁ NO
M	Methionine	C ₅ H ₉ NOS
N	Asparagine	C ₄ H ₆ N ₂ O ₂
O	Ornithine	C ₅ H ₁₁ N ₂ O
P	Proline	C ₅ H ₇ NO
Q	Glutamine	C ₅ H ₈ N ₂ O ₂
R	Arginine	C ₆ H ₁₂ N ₄ O
S	Serine	C ₃ H ₅ NO ₂
T	Threonine	C ₄ H ₇ NO ₂
V	Valine	C ₅ H ₉ NO
W	Tryptophan	C ₁₁ H ₁₀ N ₂ O
Y	Tyrosine	C ₉ H ₉ NO ₂

Reference Information

One-Letter Abbreviations for Amino Acids

Glossary

This section lists and defines terms used in this manual. It also includes acronyms, metric prefixes, symbols, and abbreviations.

A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

- A**
- A** ampere
- AC** alternating current
- ADC** analog-to-digital converter; a device that converts data from analog to digital form.
- adduct ion** An ion formed by the joining together of two species, usually an ion and a molecule, and often within the ion source, to form an ion containing all the constituent atoms of both species.
- AGC** See [Automatic Gain Control \(AGC\)](#).
- APCI** See [atmospheric pressure chemical ionization \(APCI\)](#).
- APCI corona discharge current** The ion current carried by the charged particles in the APCI source. The voltage on the APCI corona discharge needle supplies the potential required to ionize the particles. The APCI corona discharge current is set; the APCI corona discharge voltage varies, as required, to maintain the set discharge current.
- See also [corona discharge](#) and [APCI corona discharge voltage](#).
- APCI corona discharge voltage** The high voltage that is applied to the corona discharge needle in the APCI source to produce the APCI corona discharge. The corona discharge voltage varies, as required, to maintain the set APCI spray current.
- See also [APCI spray current](#).
- APCI manifold** The manifold that houses the APCI sample tube and nozzle, and contains the plumbing for the sheath and auxiliary gas.
- APCI needle, corona discharge** A needle to which a sufficiently high voltage (typically ± 3 to ± 5 kV) is applied to produce a chemical ionization plasma by the corona discharge mechanism.
- See also [chemical ionization \(CI\)](#), [chemical ionization \(CI\) plasma](#), [atmospheric pressure chemical ionization \(APCI\)](#), and [corona discharge](#).
- APCI nozzle** The nozzle in the APCI probe that sprays the sample solution into a fine mist.
- See also [atmospheric pressure chemical ionization \(APCI\)](#).
- APCI sample tube** A fused silica tube that delivers sample solution to the [APCI nozzle](#). The APCI sample tube extends from the sample inlet to the APCI nozzle.
- See also [atmospheric pressure chemical ionization \(APCI\)](#), and [API stack](#).
- APCI source** Contains the APCI probe assembly, APCI manifold, and API stack.
- See also [atmospheric pressure chemical ionization \(APCI\)](#), [APCI manifold](#), and [API stack](#).
- APCI spray current** The ion current carried by the charged particles in the APCI source. The [APCI corona discharge voltage](#) varies, as required, to maintain the set spray current.
- APCI vaporizer** A heated tube that vaporizes the sample solution as the solution exits the sample tube and enters the atmospheric pressure region of the APCI source.
- See also [atmospheric pressure chemical ionization \(APCI\)](#).

API See [atmospheric pressure ionization \(API\)](#).

API atmospheric pressure region The first of two chambers in the API source. Also referred to as the spray chamber.

API capillary-skimmer region The area between the capillary and the skimmer, which is surrounded by the tube lens. It is also the area of first-stage evacuation in the API source.

API heated capillary A tube assembly that assists in desolvating ions that are produced by the ESI or APCI probe.

See also [API heated capillary voltage](#).

API heated capillary voltage The DC voltage applied to the heated capillary. The voltage is positive for positive ions and negative for negative ions.

See also [API source](#) and [API heated capillary](#).

API ion transfer capillary A tube assembly that assists in desolvating ions that are produced by the ESI, NSI, or APCI probe.

See also [API ion transfer capillary offset voltage](#) and [API ion transfer capillary temperature](#).

API ion transfer capillary offset voltage A DC voltage applied to the ion transfer capillary. The voltage is positive for positive ions and negative for negative ions.

See also [API source](#) and [API ion transfer capillary](#).

API ion transfer capillary temperature The temperature of the ion transfer capillary, which should be adjusted for different flow rates.

See also [API source](#) and [API ion transfer capillary](#).

API source The sample interface between the LC and the mass spectrometer. It consists of the API probe (ESI or APCI) and API stack.

See also [atmospheric pressure ionization \(API\)](#), [ESI source](#), [APCI source](#), [ESI probe](#), and [API stack](#).

API spray chamber The first of two chambers in the API source. In this chamber the sample liquid exits the probe and is sprayed into a fine mist (ESI or NSI) or is vaporized (APCI) as it is transported to the entrance end of the ion transfer capillary.

API spray shield A stainless steel, cylindrical vessel that, in combination with the ESI or APCI flange, forms the atmospheric pressure region of the API source.

See also [atmospheric pressure ionization \(API\)](#).

API stack Consists of the components of the API source that are held under vacuum and includes the [API spray shield](#), [API ion transfer capillary](#), [API tube lens](#), [skimmer](#), the ion transfer capillary mount, and the tube lens and skimmer mount.

See also [atmospheric pressure ionization \(API\)](#) and [API source](#).

API tube lens A lens in the API source that separates ions from neutral particles as they leave the ion transfer capillary. A potential applied to the tube lens focuses the ions toward the opening of the skimmer and helps to dissociate adduct ions.

See also [API tube lens offset voltage](#), [API source](#), [API ion transfer capillary](#), and [adduct ion](#).

API tube lens and skimmer mount A mount that attaches to the heated capillary mount. The tube lens and skimmer attach to the tube lens and skimmer mount.

API tube lens offset voltage A DC voltage applied to the tube lens. The value is normally tuned for a specific compound.

See also [API tube lens](#), [adduct ion](#), and [source CID](#).

AP-MALDI See [atmospheric pressure matrix-assisted laser desorption/ionization \(AP-MALDI\)](#).

APPI See [Atmospheric Pressure Photoionization \(APPI\)](#).

ASCII American Standard Code for Information Interchange

atmospheric pressure chemical ionization (APCI) A soft ionization technique done in an ion source operating at atmospheric pressure. Electrons from a corona discharge initiate the process by ionizing the mobile phase vapor molecules. A reagent gas forms, which efficiently produces positive and negative ions of the analyte through a complex series of chemical reactions.

See also [electrospray ionization \(ESI\)](#).

atmospheric pressure ionization (API) Ionization performed at atmospheric pressure by using [atmospheric pressure chemical ionization \(APCI\)](#), [electrospray ionization \(ESI\)](#), or [nanospray ionization \(NSI\)](#).

atmospheric pressure matrix-assisted laser desorption/ionization (AP-MALDI) Matrix-assisted laser desorption/ionization in which the sample target is at atmospheric pressure.

See also [matrix-assisted laser desorption/ionization \(MALDI\)](#).

Atmospheric Pressure Photoionization (APPI) A soft ionization technique in which an ion is generated from a molecule when it interacts with a photon from a light source.

atomic mass unit Atomic Mass Unit (u) defined by taking the mass of one atom of carbon-12 as being 12u; unit of mass for expressing masses of atoms or molecules.

Automatic Gain Control (AGC) Sets the ion injection time to maintain the optimum quantity of ions for each scan. With AGC on, the scan function consists of a prescan and an analytical scan.

See also [ion injection time](#).

auxiliary gas The outer-coaxial gas (nitrogen) that assists the sheath (inner-coaxial) gas in dispersing and/or evaporating sample solution as the sample solution exits the APCI, ESI, or H-ESI nozzle.

auxiliary gas flow rate The relative rate of flow of [auxiliary gas](#) (nitrogen) into the API source reported in arbitrary units.

auxiliary gas inlet An inlet in the API probe where auxiliary gas is introduced into the probe.

See also [auxiliary gas](#) and [atmospheric pressure ionization \(API\)](#).

auxiliary gas plumbing The gas plumbing that delivers outer coaxial nitrogen gas to the ESI or APCI nozzle.

auxiliary gas valve A valve that controls the flow of auxiliary gas into the API source.

B

b bit

B byte (8 b)

baud rate data transmission speed in events per second

BTU British thermal unit, a unit of energy

C

°C degrees Celsius

CE central electrode (of the Orbitrap analyzer);

European conformity. Mandatory European marking for certain product groups to indicate conformity with essential health and safety requirements set out in European Directives.

centroid data Data used to represent mass spectral peaks in terms of two parameters: the centroid (the weighted center of mass) and the intensity. The data is displayed as a bar graph. The normalized area of the peak provides the mass intensity data.

cfm cubic feet per minute

chemical ionization (CI) The formation of new ionized species when gaseous molecules interact with ions. The process can involve transfer of an electron, proton, or other charged species between the reactants.

chemical ionization (CI) plasma The collection of ions, electrons, and neutral species formed in the ion source during chemical ionization.

See also [chemical ionization \(CI\)](#).

CI See [chemical ionization \(CI\)](#).

CID See [collision-induced dissociation \(CID\)](#).

cm centimeter

cm³ cubic centimeter

collision gas A neutral gas used to undergo collisions with ions.

collision-induced dissociation (CID) An ion/neutral process in which an ion is dissociated as a result of interaction with a neutral target species.

comma-separated values text file A comma-delimited text file. The extension of a comma-separated values text file is csv. This file format can be read by a text editor program, such as Microsoft™ Notepad, or by a spreadsheet program, such as Microsoft Excel™.

consecutive reaction monitoring (CRM) scan type A scan type with three or more stages of mass analysis and in which a particular multi-step reaction path is monitored.

Convectron™ gauge A thermocouple bridge gauge that is sensitive to the pressure as well as the thermal conductivity of the gas used to measure pressures between X and Y.

corona discharge In the APCI source, an electrical discharge in the region around the corona discharge needle that ionizes gas molecules to form a chemical ionization (CI) plasma, which contains CI reagent ions.

See also [chemical ionization \(CI\) plasma](#) and [atmospheric pressure chemical ionization \(APCI\)](#).

CPU central processing unit (of a computer)

CRM See [consecutive reaction monitoring \(CRM\) scan type](#).

C-Trap curved linear trap

<Ctrl> control key on the terminal keyboard

D

d depth

Da dalton

DAC digital-to-analog converter

damping gas Helium gas introduced into the ion trap mass analyzer that slows the motion of ions entering the mass analyzer so that the ions can be trapped by the RF voltage fields in the mass analyzer.

DART Direct Analysis in Real Time

data-dependent scan A scan mode that uses specified criteria to select one or more ions of interest on which to perform subsequent scans, such as MS/MS or ZoomScan.

DC direct current

divert/inject valve A valve on the mass spectrometer that can be plumbed as a divert valve or as a loop injector.

DS data system

DSP digital signal processor

E

ECD See [electron capture dissociation \(ECD\)](#).

EI electron ionization

electron capture dissociation (ECD) A method of fragmenting gas phase ions for tandem mass spectrometric analysis. ECD involves the direct introduction of low energy electrons to trapped gas phase ions.

See also [electron transfer dissociation \(ETD\)](#) and [infrared multiphoton dissociation \(IRMPD\)](#).

electron multiplier A device used for current amplification through the secondary emission of electrons. Electron multipliers can have a discrete dynode or a continuous dynode.

electron transfer dissociation (ETD) A method of fragmenting peptides and proteins. In electron transfer dissociation (ETD), singly charged reagent anions transfer an electron to multiply protonated peptides within the ion trap mass analyzer. This leads to a rich ladder of sequence ions derived from cleavage at the amide groups along the peptide backbone. Amino acid side chains and important modifications such as phosphorylation are left intact.

See also [fluoranthene](#).

electrospray ionization (ESI) A type of atmospheric pressure ionization that is currently the softest ionization technique available to transform ions in solution into ions in the gas phase.

EMBL European Molecular Biology Laboratory

<Enter> Enter key on the terminal keyboard

ESD ElectroStatic Discharge. Discharge of stored static electricity that can damage electronic equipment and impair electrical circuitry, resulting in complete or intermittent failures.

ESI See [electrospray ionization \(ESI\)](#).

ESI flange A flange that holds the [ESI probe](#) in position next to the entrance of the heated capillary, which is part of the API stack. The ESI flange also seals the atmospheric pressure region of the API source and, when it is in the engaged position against the spray shield, compresses the high-voltage safety-interlock switch.

ESI probe A probe that produces charged aerosol droplets that contain sample ions. The ESI probe is typically operated at liquid flows of 1 $\mu\text{L}/\text{min}$ to 1 mL/min without splitting. The ESI probe includes the ESI manifold, sample tube, nozzle, and needle.

ESI source Contains the ESI probe and the API stack.

See also [electrospray ionization \(ESI\)](#), [ESI probe](#), and [API stack](#).

ESI spray current The flow of charged particles in the ESI source. The voltage on the ESI spray needle supplies the potential required to ionize the particles.

ESI spray voltage The high voltage that is applied to the spray needle in the ESI source to produce the ESI spray current. In ESI, the voltage is applied to the spray liquid as it emerges from the nozzle.

See also [ESI spray current](#).

ETD See [electron transfer dissociation \(ETD\)](#).

eV Electron Volt. The energy gained by an electron that accelerates through a potential difference of one volt.

Extensible Markup Language See [XML \(Extensible Markup Language\)](#).

external lock mass A lock that is analyzed in a separate MS experiment from your sample. If you need to run a large number of samples, or if accurate mass samples will be intermingled with standard samples, you might want to use external lock masses. These allow more rapid data acquisition by eliminating the need to scan lock masses during each scan.

See also [internal lock mass](#).

F

f femto (10^{-15})

°F degrees Fahrenheit

.fasta file extension of a SEQUEST™ search database file

ft foot

Fast Fourier Transform (FFT) An algorithm that performs a Fourier transformation on data. A Fourier transform is the set of mathematical formulae by which a time function is converted into a frequency-domain function and the converse.

FFT See [Fast Fourier Transform \(FFT\)](#).

fluoranthene A reagent anion that is used in an [electron transfer dissociation \(ETD\)](#) experiment.

firmware Software routines stored in read-only memory. Startup routines and low-level input/output instructions are stored in firmware.

forepump The pump that evacuates the foreline. A rotary-vane pump is a type of forepump.

Fourier Transform - Ion Cyclotron Resonance Mass Spectrometry (FT-ICR MS) A technique that determines the mass-to-charge ratio of an ion by measuring its cyclotron frequency in a strong magnetic field.

fragment ion A charged dissociation product of an ionic fragmentation. Such an ion can dissociate further to form other charged molecular or atomic species of successively lower formula weights.

fragmentation The dissociation of a molecule or ion to form fragments, either ionic or neutral. When a molecule or ion interacts with a particle (electron, ion, or neutral species) the molecule or ion absorbs energy and can subsequently fall apart into a series of charged or neutral fragments. The mass spectrum of the fragment ions is unique for the molecule or ion.

FT Fourier Transformation

FT-ICR MS See [Fourier Transform - Ion Cyclotron Resonance Mass Spectrometry \(FT-ICR MS\)](#).

FTMS Fourier Transformation Mass Spectrometry

full-scan type Provides a full mass spectrum of each analyte or parent ion. With the full-scan type, the mass analyzer is scanned from the first mass to the last mass without interruption. Also known as single-stage full-scan type.

FWHM See [peak width at half height](#).

G

g gram

G Gauss; giga (10^9)

GC gas chromatograph; gas chromatography

GC/MS gas chromatography / mass spectrometer

GUI graphical user interface

H

h hour

h height

handshake A signal that acknowledges that communication can take place.

HCD See [higher energy collision-induced dissociation \(HCD\)](#).

header information Data stored in each data file that summarizes the information contained in the file.

H-ESI probe Heated-electrospray ionization (H-ESI) converts ions in solution into ions in the gas phase by using [electrospray ionization \(ESI\)](#) in combination with heated [auxiliary gas](#).

higher energy collision-induced dissociation (HCD)

Collision-induced dissociation that occurs in the HCD cell of the [Orbitrap mass analyzer](#). The HCD cell consists of a straight multipole mounted inside a collision gas-filled tube. A voltage offset between C-Trap and HCD cell accelerates parent ions into the collision gas inside the HCD cell, which causes the ions to fragment into product ions. The product ions are then returned to the Orbitrap analyzer for mass analysis. HCD produces triple quadrupole-like product ion mass spectra.

high performance liquid chromatography (HPLC)

Liquid chromatography in which the liquid is driven through the column at high pressure. Also known as high pressure liquid chromatography.

HPLC See [high performance liquid chromatography \(HPLC\)](#).

HV high voltage

Hz hertz (cycles per second)

I

ICR ion cyclotron resonance

ID inside diameter

IEC International Electrotechnical Commission

IEEE Institute of Electrical and Electronics Engineers

in. inch

infrared multiphoton dissociation (IRMPD) In infrared multiphoton dissociation (IRMPD), multiply charged ions consecutively absorb photons emitted by a infrared laser until the vibrational excitation is sufficient for their fragmentation. The fragments continue to pick up energy from the laser pulse and fall apart further to ions of lower mass.

See also [electron capture dissociation \(ECD\)](#).

instrument method A set of experiment parameters that define Xcalibur operating settings for the autosampler, liquid chromatograph (LC), mass spectrometer, divert valve, syringe pump, and so on. Instrument methods are saved as file type .meth.

internal lock mass A lock that is analyzed during the same MS experiment as your sample and is contained within the sample solution or infused into the LC flow during the experiment. Internal lock masses provide the most accurate corrections to the data.

See also [external lock mass](#).

I/O input/output

ion gauge Measures the pressure in the mass analyzer region (high vacuum region) of the vacuum manifold.

ion injection time The amount of time that ions are allowed to accumulate in the ion trap mass analyzer when AGC is off. With AGC on, the ion injection time is set automatically (up to the set maximum ion injection time) based on the AGC target value.

See also: [Automatic Gain Control \(AGC\)](#).

ion optics Focuses and transmits ions from the API source to the mass analyzer.

ion source A device that converts samples to gas-phase ions.

ion sweep cone A removable cone-shaped metal cover that fits on top of the [API ion transfer capillary](#) and acts as a physical barrier to protect the entrance of the capillary.

ion sweep gas Extra nitrogen gas that flows along the axis of the API ion transfer capillary (between the ion sweep cone and the capillary block) towards the API spray. The sweep gas flow is thus countercurrent to the flow of the ions.

See also [ion sweep gas pressure](#).

ion sweep gas pressure The rate of flow of the sweep gas (nitrogen) into the API source. A measurement of the relative flow rate (in arbitrary units) to provide the required flow of nitrogen gas out from the Ion Sweep cone towards the API spray.

See also [ion sweep gas](#).

IRMPD See [infrared multiphoton dissociation \(IRMPD\)](#).

K

k kilo (10³, 1000)

K kilo (2¹⁰, 1024)

KEGG Kyoto Encyclopedia of Genes and Genomes

kg kilogram

L

l length

L liter

LAN local area network

lb pound

LC See [liquid chromatography \(LC\)](#).

LC/MS See [liquid chromatography / mass spectrometry \(LC/MS\)](#).

LED light-emitting diode

LHe liquid helium

liquid chromatography (LC) A form of elution chromatography in which a sample partitions between a stationary phase of large surface area and a liquid mobile phase that percolates over the stationary phase.

liquid chromatography / mass spectrometry (LC/MS) An analytical technique in which a high-performance liquid chromatograph (LC) and a mass spectrometer (MS) are combined.

LN2 liquid nitrogen

lock mass A known reference mass in the sample that is used to correct the mass spectral data in an accurate mass experiment and used to perform a real-time secondary mass calibration that corrects the masses of other peaks in a scan. Lock masses with well-defined, symmetrical peaks work best. You can choose to use [internal lock mass](#) or [external lock mass](#).

log file A text file, with a log file extension, that is used to store lists of information.

M

μ micro (10⁻⁶)

m meter; milli (10⁻³)

M mega (10⁶)

M⁺ molecular ion

MALDI See [matrix-assisted laser desorption/ionization \(MALDI\)](#).

matrix-assisted laser desorption/ionization (MALDI) A method of ionizing proteins where a direct laser beam is used to facilitate vaporization and ionization while a matrix protects the biomolecule from being destroyed by the laser.

See also [atmospheric pressure matrix-assisted laser desorption/ionization \(AP-MALDI\)](#).

MB Megabyte (1 048 576 bytes)

MH⁺ protonated molecular ion

microscan One mass analysis (ion injection and storage or scan-out of ions) followed by ion detection. Microscans are summed, to produce one scan, to improve the signal-to-noise ratio of the mass spectral data. The number of microscans per scan is an important factor in determining the overall scan time.

min minute

mL milliliter

mm millimeter

MRFA A peptide with the amino acid sequence methionine–arginine–phenylalanine–alanine.

MS mass spectrometer; mass spectrometry

MS scan modes Scan modes in which only one stage of mass analysis is performed. The scan types used with the MS scan modes are [full-scan type](#) and [selected ion monitoring \(SIM\) scan type](#).

MSDS Material Safety Data Sheet

MS/MS Mass spectrometry/mass spectrometry, or tandem mass spectrometry is an analytical technique that involves two stages of mass analysis. In the first stage, ions formed in the ion source are analyzed by an initial analyzer. In the second stage, the mass-selected ions are fragmented and the resultant ionic fragments are mass analyzed.

MSⁿ scan mode The scan power equal to 1 to 10, where the scan power is the power *n* in the expression MSⁿ. MSⁿ is the most general expression for the scan mode, which can include the following:

- The scan mode corresponding to the one stage of mass analysis in a single-stage full-scan experiment or a selected ion monitoring (SIM) experiment
- The scan mode corresponding to the two stages of mass analysis in a two-stage full-scan experiment or a selected reaction monitoring (SRM) experiment
- The scan mode corresponding to the three to ten stages of mass analysis (*n* = 3 to *n* = 10) in a multi-stage full-scan experiment or a consecutive reaction monitoring (CRM) experiment

See also [MS scan modes](#) and [MS/MS](#).

multipole A symmetrical, parallel array of (usually) four, six, or eight cylindrical rods that acts as an ion transmission device. An RF voltage and DC offset voltage are applied to the rods to create an electrostatic field that efficiently transmits ions along the axis of the multipole rods.

m/z Mass-to-charge ratio. An abbreviation used to denote the quantity formed by dividing the mass of an ion (in u) by the number of charges carried by the ion. For example, for the ion C₇H₇²⁺, *m/z* = 45.5.

N

n nano (10⁻⁹)

nanospray ionization (NSI) A type of electrospray ionization (ESI) that accommodates very low flow rates of sample and solvent on the order of 1 to 20 nL/min (for static nanospray) or 100 to 1000 nL/min (for dynamic nanospray).

NCBI National Center for Biotechnology Information (USA)

NIST National Institute of Standards and Technology (USA)

NMR Normal Mass Range

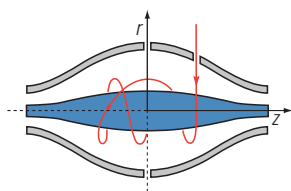
NSI See [nanospray ionization \(NSI\)](#).

O

octapole An octagonal array of cylindrical rods that acts as an ion transmission device. An RF voltage and DC offset voltage applied to the rods create an electrostatic field that transmits the ions along the axis of the octapole rods.

OD outside diameter

Orbitrap mass analyzer The Orbitrap™ mass analyzer consists of a spindle-shape central electrode surrounded by a pair of bell-shaped outer electrodes. Ions inside the mass analyzer orbit in stable trajectories around the central electrode with harmonic oscillations along it.



Two detection electrodes record an image current of the ions as they undergo harmonic oscillations. A Fourier transformation extracts different harmonic frequencies from the image current. An ion's mass-to-charge ratio m/z is related to the frequency f of its harmonic oscillations and to the instrumental constant k by: $m/z = k/f^2$

OT Orbitrap

See [Orbitrap mass analyzer](#).

OVC outer vacuum case

Ω ohm

P

p pico (10^{-12})

Pa pascal

parent ion An electrically charged molecular species that can dissociate to form fragments. The fragments can be electrically charged or neutral species. A parent ion can be a molecular ion or an electrically charged fragment of a molecular ion. Also called a precursor ion.

parent mass The mass-to-charge ratio of a parent ion. The location of the center of a target parent-ion peak in mass-to-charge ratio (m/z) units. Also known as precursor mass.

See also [parent ion](#).

PCB printed circuit board

PDA detector Photodiode Array detector is a linear array of discrete photodiodes on an integrated circuit chip. It is placed at the image plane of a spectrometer to allow a range of wavelengths to be detected simultaneously.

PE protective earth

peak A maximum in a graph of intensity versus time or intensity versus mass. The position of the maximum is said to be the position of the peak.

peak end The end of a chromatographic peak occurs when the detection signal decreases to a value less than the current threshold criteria.

See also [peak start](#).

peak height (peak dimension) The distance from the peak maximum to the peak base, measured perpendicular to the ordinate.

peak start The start of a chromatograph peak occurs when the detection signal increases to a value greater than the current threshold criteria.

See also [peak end](#).

peak width The distance across a peak measured at a selected peak-height level, in minutes or mass units. The peak-height level is usually specified as a percentage of the maximum peak height.

See also [peak width at half height](#).

peak width at half height The full width of a peak at half its maximum height, sometimes abbreviated FWHM.

See also [peak width](#) and [peak end](#).

PID proportional / integral / differential

P/N part number

p-p peak-to-peak voltage

ppm parts per million

PQD pulsed-Q dissociation

precursor ion An electrically charged molecular species that can dissociate to form fragments. The fragments can be electrically charged or neutral species. A precursor ion (PR) can be a molecular ion or an electrically charged fragment of a molecular ion. Also known as parent ion.

precursor mass Mass of the corresponding precursor (or parent) ion or molecule.

profile data Data representing mass spectral peaks as point-to-point plots, with each point having an associated intensity value.

psig pounds per square inch, gauge

PTM posttranslational modification

pulsed Q dissociation (PQD) Collision-induced dissociation that involves precursor ion activation at high Q, a time delay to allow the precursor to fragment, and then a rapid pulse to low Q where all fragment ions are trapped. The fragment ions can then be scanned out of the ion trap mass analyzer and detected. PQD eliminates the “1/3 Rule” low mass cut-off for MS/MS data.

Q

quadrupole A symmetrical, parallel array of four hyperbolic rods that acts as a mass analyzer or an ion transmission device. As a mass analyzer, one pair of opposing rods has an oscillating radio frequency (RF) voltage superimposed on a positive direct current (DC) voltage. The other pair has a negative DC voltage and an RF voltage that is 180 degrees out of phase with the first pair of rods. This creates an electrical field (the quadrupole field) that efficiently transmits ions of selected mass-to-charge ratios along the axis of the quadrupole rods.

R

RAM random access memory

raw data Uncorrected liquid chromatograph and mass spectrometer data obtained during an acquisition. Xcalibur and Xcalibur-based software store this data in a file that has a .raw file extension.

resolution The ability to distinguish between two points on the wavelength or mass axis.

retention time (RT) The time after injection at which a compound elutes. The total time that the compound is retained on the chromatograph column.

RF radio frequency

RF lens A multipole rod assembly that is operated with only radio frequency (RF) voltage on the rods. In this type of device, virtually all ions have stable trajectories and pass through the assembly.

RF voltage An AC voltage of constant frequency and variable amplitude that is applied to the ring electrode or endcaps of the mass analyzer or to the rods of a multipole. Because the frequency of this AC voltage is in the radio frequency (RF) range, it is referred to as RF voltage.

RMS root mean square

ROM read-only memory

rotary-vane pump A mechanical vacuum pump that establishes the vacuum necessary for the proper operation of the turbomolecular pump. (Also called a roughing pump or forepump.)

RS-232 An accepted industry standard for serial communication connections. This Recommended Standard (RS) defines the specific lines and signal characteristics used by serial communications controllers to standardize the transmission of serial data between devices.

RT An abbreviated form of the phrase *retention time (RT)*. This shortened form is used to save space when the retention time (in minutes) is displayed in a header, for example, RT: 0.00-3.75.

S

s second

scan mode and scan type combinations A function that coordinates the three processes in the MS detector: ionization, mass analysis, and ion detection. You can combine the various scan modes and scan types to perform a wide variety of experiments.

selected ion monitoring (SIM) scan type A scan type in which the mass spectrometer acquires and records ion current at only one or a few selected mass-to-charge ratio values.

See also [selected reaction monitoring \(SRM\) scan type](#).

selected reaction monitoring (SRM) scan type A scan type with two stages of mass analysis and in which a particular reaction or set of reactions, such as the fragmentation of an ion or the loss of a neutral moiety, is monitored. In SRM a limited number of product ions is monitored.

SEM secondary electron multiplier

Serial Peripheral Interface (SPI) hardware and firmware communications protocol

serial port An input/output location (channel) for serial data transmission.

sheath gas The inner coaxial gas (nitrogen), which is used in the API source to help nebulize the sample solution into a fine mist as the sample solution exits the ESI or APCI nozzle.

sheath gas flow rate The rate of flow of sheath gas into the API source. A measurement of the relative flow rate (in arbitrary units) that needs to be provided at the sheath gas inlet to provide the required flow of [sheath gas](#) to the ESI or APCI nozzle.

sheath gas inlet An inlet in the API probe where [sheath gas](#) is introduced into the probe.

sheath gas plumbing The gas plumbing that delivers [sheath gas](#) to the ESI or APCI nozzle.

sheath gas pressure The rate of flow of sheath gas (nitrogen) into the API source. A measurement of the relative flow rate (in arbitrary units) that needs to be provided at the sheath gas inlet to provide the required flow of inner coaxial nitrogen gas to the ESI or APCI nozzle. A software-controlled proportional valve regulates the flow rate.

See also [sheath gas](#).

sheath gas valve A valve that controls the flow of [sheath gas](#) into the API source. The sheath gas valve is controlled by the data system.

signal-to-noise ratio (S/N) The ratio of the signal height (S) to the noise height (N). The signal height is the baseline corrected peak height. The noise height is the peak-to-peak height of the baseline noise.

SIM See [selected ion monitoring \(SIM\) scan type](#).

skimmer A vacuum baffle between the higher pressure capillary-skimmer region and the lower pressure region. The aperture of the skimmer is offset with respect to the bore of the ion transfer capillary.

source CID A technique for fragmenting ions in an [atmospheric pressure ionization \(API\)](#) source. Collisions occur between the ion and the background gas, which increase the internal energy of the ion and stimulate its dissociation.

SPI See [Serial Peripheral Interface \(SPI\)](#).

SRM See [selected reaction monitoring \(SRM\) scan type](#).

sweep gas Nitrogen gas that flows out from behind the sweep cone in the API source. Sweep gas aids in solvent declustering and adduct reduction.

See also [sweep gas flow rate](#).

sweep gas flow rate The rate of flow of sweep gas into the API source. A measurement of the relative flow rate (in arbitrary units) to provide the required flow of nitrogen gas to the sweep cone of the API source.

See also [sweep gas](#).

syringe pump A device that delivers a solution from a syringe at a specified rate.

T

T Tesla

target compound A compound that you want to identify or quantitate or that a specific protocol (for example, an EPA method) requires that you look for. Target compounds are also called analytes, or target analytes.

TIC See [total ion current \(TIC\)](#).

TMP See [turbomolecular pump](#).

Torr A unit of pressure, equal to 1 mm of mercury and 133.32 Pa.

total ion current (TIC) The sum of the ion current intensities across the scan range in a mass spectrum.

tube lens offset The voltage offset from ground that is applied to the tube lens to focus ions toward the opening of the skimmer.

See also [source CID](#).

Tune Method A defined set of mass spectrometer tune parameters for the ion source and mass analyzer. Tune methods are defined by using the instrument software's tune window and saved as tune file.

A tune method stores tune parameters only. (Calibration parameters are stored separately, not with the tune method.)

tune parameters Instrument parameters whose values vary with the type of experiment.

turbomolecular pump A vacuum pump that provides a high vacuum for the mass spectrometer and detector system.

TWA time weighted average

U

u atomic mass unit

UHV ultra high vacuum

ultra-high performance liquid chromatography (U-HPLC) See [high performance liquid chromatography \(HPLC\)](#).

Ultramark 1621 A mixture of perfluoroalkoxycyclotriphosphazenes used for ion trap calibration and tuning. It provides ESI singly charged peaks at m/z 1022.0, 1122.0, 1222.0, 1322.0, 1422.0, 1522.0, 1622.0, 1722.0, 1822.0, and 1921.9.

UMR Universal Mass Range

V

V volt

VAC volts alternating current

VDC volts direct current

vacuum manifold A thick-walled, aluminum chamber with machined flanges on the front and sides and various electrical feedthroughs and gas inlets that encloses the API stack, ion optics, mass analyzer, and ion detection system.

vacuum system Components associated with lowering the pressure within the mass spectrometer. A vacuum system includes the vacuum manifold, pumps, pressure gauges, and associated electronics.

vent valve A valve that allows the vacuum manifold to be vented to air or other gases. A solenoid-operated valve.

vol volume

W

w width

W watt

WEEE European Union Waste Electrical and Electronic Equipment Directive. Provides guidelines for disposal of electronic waste.

X

XML (Extensible Markup Language) A general-purpose markup language that is used to facilitate the sharing of data across different information systems, particularly via the Internet.

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