Notices

© Agilent Technologies, Inc. 2016

No part of this manual may be reproduced in any form or by any means (including electronic storage and retrieval or translation into a foreign language) without prior agreement and written consent from Agilent Technologies, Inc. as governed by United States and international copyright laws.

Manual Part Number

M8260-90031

Edition

3/2016

Agilent Technologies, Inc.

Software Revision

This guide is valid for revision A.02.01 of Sample Scheduler for OpenLAB CDS EZChrom Edition.

This version is compatible to OpenLAB CDS EZChrom Edition A.04.07 SR1 and A.04.07 SR2.

Warranty

The material contained in this document is provided “as is,” and is subject to being changed, without notice, in future editions. Further, to the maximum extent permitted by applicable law, Agilent disclaims all warranties, either express or implied, with regard to this manual and any information contained herein, including but not limited to the implied warranties of merchantability and fitness for a particular purpose. Agilent shall not be liable for errors or for incidental or consequential damages in connection with the furnishing, use, or performance of this document or of any information contained herein. Should Agilent and the user have a separate written agreement with warranty terms covering the material in this document that conflict with these terms, the warranty terms in the separate agreement shall control.

Technology Licenses

The hardware and/or software described in this document are furnished under a license and may be used or copied only in accordance with the terms of such license.

Restricted Rights Legend

If software is for use in the performance of a U.S. Government prime contract or subcontract, Software is delivered and licensed as “Commercial computer software” as defined in DFAR 252.227-7014 (June 1995), or as a “commercial item” as defined in FAR 2.101(a) or as “Restricted computer software” as defined in FAR 52.227-19 (June 1987) or any equivalent agency regulation or contract clause. Use, duplication or disclosure of Software is subject to Agilent Technologies’ standard commercial license terms, and non-DOD Departments and Agencies of the U.S. Government will receive no greater than Restricted Rights as defined in FAR 52.227-19(c)(1-2) (June 1987). U.S. Government users will receive no greater than Limited Rights as defined in FAR 52.227-14 (June 1987) or DFAR 252.227-7015 (b)(2) (November 1995), as applicable in any technical data.

Safety Notices

A CAUTION notice denotes a hazard. It calls attention to an operating procedure, practice, or the like that, if not correctly performed or adhered to, could result in damage to the product or loss of important data. Do not proceed beyond a CAUTION notice until the indicated conditions are fully understood and met.

A WARNING notice denotes a hazard. It calls attention to an operating procedure, practice, or the like that, if not correctly performed or adhered to, could result in personal injury or death. Do not proceed beyond a WARNING notice until the indicated conditions are fully understood and met.
Table of Content

Scheduler Overview 4

Scheduler interface 5

Application details 6

Analysis Management 6
States 6
Chromatogram and result files management 7

Analysis table: the laboratory analysis working list 8
Analysis table parameters 9
Analysis representation 11
Analysis table display options 11
Analysis table customization 12

Edit an analysis 12
Copy/Increment a parameter value 13
Use tokens for SampleId, ResultName and DataFileName 14
Change Instrument/Method used to perform the analysis 15

User actions 15

Quick Start 17

The sequence 17
Create a sequence by grouping a set of analysis 17
Sequence table customization 18
Edit a sequence 18
Copy/Increment the value of a sequence line parameter 19
Launch a sequence 19
Perform actions in sequence 20

Notifications 21
Invalid command 21

Options 21
Refresh 21
Open a chromatogram in the CDS from Sample Scheduler for OpenLAB CDS 21
Print 22
Save Layout 22
Reset analysis 22
Scheduler Overview

Sample Scheduler for OpenLAB CDS is an application designed to improve productivity of the chromatography laboratory by fully automating the chromatographic analyses. It is a powerful interface between a front-end platform such as a Laboratory Information Management System (LIMS), which sends analysis orders, and the OpenLAB CDS solution, which performs and processes the analyses.

The Scheduler application displays all the analyses to be performed on the instruments that you are authorized to use (configured in the OpenLAB Control Panel).

Each time a valid analysis order is received from the LIMS, it is displayed in the Scheduler application. The Scheduler manages the analysis: it sends the order to start the acquisition to OpenLAB CDS, and displays the status of the acquisition in real time. It chains the analyses to optimize instrument use.

You can edit the acquisition parameters of an analysis, and start or stop an acquisition, for example.

The Scheduler works in a Client/Server configuration. It communicates with OpenLAB CDS via OpenLAB Shared Services. In this way, the Scheduler can make use of the OpenLAB configuration in terms of users, projects, and instruments.

Several Scheduler installation configurations are supported. To learn more about supported configurations, refer to the Sample Scheduler for OpenLAB CDS EZChrom Edition Installation & Configuration Guide.

NOTE

We strongly advise you NOT to start an analysis from OpenLAB CDS or manually on an instrument that is currently being used by the Sample Scheduler for OpenLAB CDS (with an analysis scheduled on this instrument). If you do, the Scheduler’s analysis will be put into the CDS Run queue, which is not managed by the Scheduler.
Scheduler interface

The Sample Scheduler for OpenLAB CDS includes a simple and powerful interface consisting of:

- An **Analysis Table**, listing all the analyses sent by the LIMS, and their states. Each line of the table corresponds to the analysis of one sample on a specific instrument. You can edit the acquisition parameters and sample information before acquisition is performed. For example, you can modify the vial position or the injection volume.

- A **Sequence table**, listing all the analysis belonging to a sequence. Each line of the table corresponds to a sample. You can edit each line, and perform other actions such as changing the position of a line in the table, adding a new line, or removing a line.

- A list of action buttons, for example to stop an analysis or add an analysis.

Quick access to the Sample Scheduler Client is available from the **Start > All Programs > Agilent Technologies > Sample Scheduler for OpenLAB CDS** menu.

Once the application is launched, you have to log in by entering your OpenLAB user name and password (and, possibly, domain). This login acts as access control, allowing you to see only the analyses launched on instruments or projects you are authorized to use (as defined in the OpenLAB Control Panel).
Application details

The application displays the analyses to be performed. It can be used as a Worksheet, listing all analyses that are in progress, scheduled, or ended on all instruments of the laboratory. It gives useful information such as the position in the autosampler where the analyst has to put the vial.

Each time the LIMS submits an analysis order (a command), it is translated into an analysis. The Sample Scheduler for OpenLAB CDS manages the analysis from the submission to the CDS up to the end of the acquisition (performed by the CDS). The analysis states are displayed in the Scheduler interface along with other acquisition parameters.

Analysis Management

States

The analysis state evolves according to a logical workflow. It describes the analysis life cycle from the time it is created in the Scheduler database up to the end of its acquisition by the CDS.
The initial state of an analysis can be:

- **Waiting**: The analysis is associated with an instrument and a method. It is ready to be started; you can edit some parameters (the vial position, for example). It is then up to you to queue the analysis by clicking the **Schedule** button.

- **Scheduled**: The analysis is queued, it will start as soon as the instrument is idle and all the analyses with lower priority have been launched.

- **Holding**: The analysis is not associated with an instrument or method; it cannot be started. It is intended to be merged with another **Holding** analysis in the Scheduler client. Once merged, the two analyses are associated each to one tower of the instrument. Each of two 'merged' analyses will be injected on the defined tower. The aim is to optimize the instrument use by injecting two different samples on the same instrument simultaneously (using the same analytical method).

When the analysis is launched in the CDS, its state can be:

- **Submitted**: The analysis has been starting on the instrument.

- **In Progress**: The analysis is currently acquiring on the instrument. The acquisition is managed by the CDS.

- **Error**: The analysis has encountered an issue:
  - communication with instrument failed,
  - an error occurred on the instrument
  - an error occurred in the CDS

- **Waiting on error**: When several analyses are launched on the same instrument, one analysis is in acquisition (**Submitted** or **In Progress**) while the others are **Scheduled**. When an error occurs, the analysis currently being acquired switches to the **Error** state, and the **Scheduled** analyses switch to the **Waiting on error** state. It is your responsibility to restart the analyses when the issue is solved.

- **Stopping**: The analysis has been stopped in the Scheduler, and is currently stopping in the CDS. This state is transient.

- **Stopped**: The analysis has been stopped in the Scheduler.

- **Ended**: The analysis has been acquired; the results are available in the CDS.

- **Incomplete**: The analysis does not contain a value for all parameters that are required by the CDS to perform the acquisition (for example, instrument, project, method, injection volume, result name, data file name, sample id).

### Chromatogram and result files management

The files generated by a sample analysis are managed by the CDS. They are stored in the location specified in the OpenLAB Control Panel (Storage type/Storage path).

A **Result.rslt** folder, containing all the files generated by the CDS is created for each analysis.

The name of this result folder is specified either in the command sent by the LIMS, or by the user from the Scheduler interface. It corresponds to the **Result** Scheduler parameter.

The result folder name must be unique in order for the acquisition to be performed;
therefore, the Scheduler checks for the existence of the result name before starting an acquisition. If the result folder already exists, the Scheduler creates a new .rslt folder with the same Result name and including a Time Stamp. By this mechanism, all results are secured.

**Analysis table: the laboratory analysis working list**

The Analysis table displays a list of the analyses that are stored in the Sample Scheduler Database. The list shows the state of the analysis (*In progress*, *Scheduled*, *Ended*) and the instrument for which the analysis is scheduled.

The list of displayed analyses is user-dependent. The list is filtered according to the connected user, based on the OpenLAB user privileges: You see only the analyses associated with the instruments/projects you are authorized to use (see list of projects/instruments in OpenLAB Control Panel).

You can also edit an analysis from this table.
## Analysis table parameters

<table>
<thead>
<tr>
<th>Parameter name</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Run status</td>
<td>CDS acquisition status: idle, running, etc.</td>
</tr>
<tr>
<td>Run time</td>
<td>The current acquisition time over the total acquisition time. It is displayed only when analysis is in <em>In Progress</em> state.</td>
</tr>
<tr>
<td>ECustomi</td>
<td>Up to five Scheduler ECustom variables can be defined for the analysis (sample information). These variables can be assigned a value in the command, or edited in the Analysis table and the Sequence. If pre-defined values have been specified in the Sample Scheduler Configuration, they can be selected from a combo box. They can be used as tokens to name the Sample id, Result and Data File.</td>
</tr>
<tr>
<td>Calibration mode</td>
<td>Used to define the calibration mode when the sample is a standard: Clear all calibration, Clear calibration for level, Clear replicates, Average replicates.</td>
</tr>
<tr>
<td>Comments</td>
<td>User comments. This information is displayed on screen, to allow you to enter information on the sample. It is not stored in the generated chromatogram file.</td>
</tr>
<tr>
<td>Data file</td>
<td>Name of the generated chromatogram (.dat). It can be composed of pre-defined parameters (for example, &lt;I&gt; for instrument, &lt;U&gt; for user) or Scheduler variables parameters (for example, &lt;E1&gt;, &lt;T5&gt;) and text. You can select the token from a list.</td>
</tr>
<tr>
<td>Description</td>
<td>Sample description. For information purposes.</td>
</tr>
<tr>
<td>Dilutor</td>
<td>Dilutor factor. Used by the CDS for quantity computation. The default value is 1. 0 is not a valid value.</td>
</tr>
<tr>
<td>Tower</td>
<td>The tower position where the sample is injected (Front or Back). Scheduler manages single- and dual-tower instruments, but for dual-tower instruments, the injection can be performed only on one of the towers.</td>
</tr>
<tr>
<td>Inj.volume</td>
<td>Injection volume. Mandatory if Method inj.vol. is not selected.</td>
</tr>
<tr>
<td>Instrument</td>
<td>The name of the instrument that performs the analysis.</td>
</tr>
<tr>
<td>TCustomi</td>
<td>Up to 10 Scheduler TCustom variables can be defined. They can be used as tokens to name the Result and Data File. These variables can be assigned a value in the command or edited in the Analysis table and the Sequence. If pre-defined values have been specified in the Sample Scheduler Configuration, they can be selected from a combo box.</td>
</tr>
<tr>
<td>ISTD_i amount</td>
<td>The amount of the first ISTD defined in the peaks/groups table of the CDS method. The default value is 1. 0 is not a valid value.</td>
</tr>
<tr>
<td>ISTD_i amount unit</td>
<td>The units of the ISTD amount. For information purposes.</td>
</tr>
<tr>
<td>Last modification by</td>
<td>Name of the last user that has modified the analysis acquisition parameters. If the analysis is generated by the LIMS, and you have made no modifications in the Scheduler client, ‘LIMS’ is displayed.</td>
</tr>
<tr>
<td>Application details</td>
<td></td>
</tr>
<tr>
<td>---------------------</td>
<td></td>
</tr>
<tr>
<td><strong>If</strong> the analysis is generated from a Quick start, or has been modified by a user in the Scheduler client, the name of the connected user is displayed.</td>
<td></td>
</tr>
<tr>
<td><strong>Last modification date</strong></td>
<td>The date when the analysis parameters were last modified. If no modification was done from Scheduler client, the analysis creation Date/Time is displayed (Date/Time the analysis entered into Scheduler Database).</td>
</tr>
<tr>
<td><strong>Level</strong></td>
<td>If the sample is a standard, define its level (as defined in the CDS method).</td>
</tr>
<tr>
<td><strong>Method</strong></td>
<td>The CDS method used to perform the analysis.</td>
</tr>
<tr>
<td><strong>Method inj.vol.</strong></td>
<td>Use the injection volume defined in the selected method. Do not select this option if no injection volume is defined in the CDS method (for example, for an instrument without autosampler). For an analysis generated by the LIMS, this column is displayed only if the CanUseMethodInjectionVolume parameter is assigned the ‘true’ value in the command. So according to the selected analysis, this column can be displayed or not.</td>
</tr>
<tr>
<td><strong>Multiplier</strong></td>
<td>Multiplier factor. Used by the CDS for quantity computation. The default value is 1.</td>
</tr>
<tr>
<td><strong>Alternative Inst/Meth</strong></td>
<td>Instrument/method that could be used to perform the analysis instead of the main Instrument and Method. Options are defined in the XML command (Not available for analyses generated from Quick Start).</td>
</tr>
<tr>
<td><strong>Priority</strong></td>
<td>Priority of the analysis. It displays the order in which scheduled analysis will be performed. Priority order is defined by instrument and corresponds to the order the analysis generated by the LIMS.</td>
</tr>
<tr>
<td><strong>Project</strong></td>
<td>The OpenLAB project associated with the analysis. It defines the folder where results are stored. The project properties, defined in OpenLAB Control Panel, are applied.</td>
</tr>
<tr>
<td><strong>Result</strong></td>
<td>Name of the CDS result folder where analysis files are stored. When the analysis is added in the Scheduler, it is assigned a result name. If a result folder with the same name already exists when the acquisition starts, the result name is renamed: result-timestamp.rslt. The result name can be composed of the CDS pre-defined parameters (for example, &lt;I&gt; for instrument, &lt;U&gt; for user) or Scheduler variables (for example, &lt;E1&gt;, &lt;T5&gt;) and text. You can select the tokens from a list.</td>
</tr>
<tr>
<td><strong>Sample id</strong></td>
<td>Each analysis is assigned a Sample id. The Sample id can be composed of the CDS pre-defined parameters (for example, &lt;I&gt; for instrument, &lt;U&gt; for user) or Scheduler Variables (for example, &lt;E1&gt;, &lt;T5&gt;) and text.</td>
</tr>
<tr>
<td><strong>Sample mass</strong></td>
<td>Mass of the sample, used by the CDS for quantity computation. The default value is 1. 0 is an invalid value.</td>
</tr>
<tr>
<td><strong>Sample mass unit</strong></td>
<td>Units of the sample mass. For information purposes.</td>
</tr>
<tr>
<td><strong>Sample type</strong></td>
<td>Specifies whether the sample is a Sample or a Cal.Std.</td>
</tr>
<tr>
<td><strong>Sequence name</strong></td>
<td>Specifies the name of the sequence.</td>
</tr>
</tbody>
</table>
State

Corresponds to the state of the analysis:
Waiting, Scheduled, In Progress, Ended, Error, Stopping, Stopped, Holding.

Task state

State of the task: Ready, started, finished, error. A task corresponds to one
instrument.
Analyses that are performed on two coupled instruments are composed of
two tasks, where one task corresponds to one instrument. Some parameters
are to be defined by instrument: Vial, injection volume, etc.

User

Name of the OpenLAB user who is assigned the analysis. For analyses
launched by the LIMS, the user name is the one defined in the command. If
no user is defined in the command, 'LIMS' is displayed.

Vial

The autosampler position where the sample is set.
If the instrument uses a valve instead of a sampler, and does not require a
vial position to be defined, you can leave the Vial field empty.

Note that if you update an OpenLAB parameter (add/delete a user, a project, an
instrument, a method) you must restart the Scheduler Client to update the corresponding
parameter list.

Analysis representation

The following analysis types are represented into the Analysis table:

Single tower analysis:
An analysis launched in the Scheduler on a single-tower instrument is displayed
on a single line in the Analysis table.

Dual towers analysis:
An analysis launched in the Scheduler on a dual-tower instrument is displayed on
a double line in the Analysis table. The parameters relative to the Sample are
displayed in merged cells (Sample id, Instrument, Result, Method, etc.) whereas the
others (relative to the tower) are displayed in spit cells (Vial, Data file).

Dual instruments analysis (Dual tasks):
An analysis launched in the Scheduler on two coupled instruments is displayed on
a double line in the Analysis table. The parameters common to the two instruments
are displayed in merged cells (Sample id, State, Priority, Project, User, Last
modification date, Last modified by). Parameters specific to each Instrument are
displayed in split cells (for example, Instrument, Run status, Run time, Task State,
Method, Result, Data file, vial).

Analysis table display options

You can organize the analyses in the table as follows:

- Filter the information by clicking the \( \checkmark \) button in the column header and selecting
  the filter from a list. A filter can be applied on several parameters (for example,
  display all analysis performed on instrument Agilent7890_1 in Scheduled state).
This option can be used to filter the analyses by user, providing you with a working list.

The applied filters are listed in the footer of the Sample Scheduler Client.

To clear all the filters, click the button on the left top corner of the Analysis table.

- Sort the content of a column by alphabetic order or increasing/decreasing number by clicking the associated / button in the column header.

### Analysis table customization

You can customize the parameters to be displayed in the Analysis table.

- You can select the parameters to display in the View tab. Parameters are grouped into four categories: **Analysis Info, Acquisition, Quantification** and **Custom info**. In each category, select the parameters you want to display, by checking the corresponding parameter names:

  ![Acquisition parameters](image)

If you need to see all the parameters of the category, the Acquisition parameters for example, when adding a new analysis (quick start) click on the category button. Then, to redisplay only the selected parameters of the category, click on the category name again.

- You can modify the column position by simply dragging and dropping the column header from one position to another.

- You can customize the width of the columns.

- You can group the analyses by parameter. To group analyses by instrument, for example, drag the Instrument column header into the dedicated area just above the Analysis table. It is possible to define several group levels (Instrument/State/User) by successively dragging and dropping several column headers into the dedicated area. To ungroup the analyses, drag the header back into the table.

  You can expand all analyses or collapse all analyses by clicking the Collapse all/Expand all buttons in the View tab.

To save the user-specific layout; click the Save Layout button in the Options ribbon.

### Edit an analysis

Only analyses in the **Waiting** or **Incomplete** state can be edited.

To edit an analysis, select the cell of the analysis to modify in the Analysis table and
enter a value (or double click into the cell). The analysis is then switched into the **Edited by user name** state to inform the other users that the analysis is currently edited.

The analysis stays in **Edition** until you click the cell of another analysis or the **Save** button. Until you select a cell of the same analysis, the analysis stays in **Edition**. In this way, you can successively modify all the parameters of the same analysis before exiting the **Edition** mode.

All the parameters are editable except:

- **Last modification by**
- **Last modification date**
- **Priority**
- **Run status**
- **Run time**
- **id**
- **State**
- **Task state**

Once you have completed the edition of an analysis, controls are performed by the Sample Scheduler to ensure that the analysis is valid.

- If an erroneous value has been defined for an OpenLAB parameter (Project, user, instrument, method), you are prompted to define a valid value.

- If no value is assigned to a parameter required by the CDS to perform the analysis (for example, injection volume, Data File name, Result name), the analysis switches into the **Incomplete** state. You can click on the state cell of the analysis to get a list of missing values. The $i$ symbol, on the state cell, indicates that you can access information by clicking this position.

- If all parameter values are valid, the analysis switches into the **Waiting** state.

**NOTE**

Only one analysis can be edited per session, and an analysis cannot be edited simultaneously by two users.

**Copy/Increment a parameter value**

You can copy or increment (one by one) the value of an analysis parameter for a selection of analyses.

Define the value to duplicate or increment for one analysis, select this analysis and the analyses to modify, and select the **Copy** or **Increment** option in the context menu. The value of the first selected analysis is duplicated/incremented for the other analyses.

For a dual-tower instrument, the copy/increment is performed by tower (that is, the value of the front tower is applied to all front-tower analyses, and value of the back tower is applied to all back-tower analysis.

The copy/increment options are available only for **Waiting/Incomplete/Waiting on error** analysis states.
Use tokens for SampleId, ResultName and DataFileName

It is possible to use predefined identifiers to generate the Sample id, Result name and Data file name.

Two kinds of token are accepted:
- EZChrom CDS tokens
- Sample Scheduler variables.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Pre-defined identifiers &lt;X&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>SampleId</td>
<td>UserName &lt;U&gt;</td>
</tr>
<tr>
<td>(EZChrom Sample id)</td>
<td>MethodName &lt;M&gt;</td>
</tr>
<tr>
<td></td>
<td>Instrument name &lt;I&gt;</td>
</tr>
<tr>
<td></td>
<td>Date &amp;Time &lt;D&gt;</td>
</tr>
<tr>
<td></td>
<td>Vial &lt;V&gt;</td>
</tr>
<tr>
<td></td>
<td>ECustomN [N=1 to 5] &lt;E1&gt; to &lt;E5&gt;</td>
</tr>
<tr>
<td>DataFileName</td>
<td>User Name &lt;U&gt;</td>
</tr>
<tr>
<td>(EZChrom Data File.dat)</td>
<td>Method Name &lt;M&gt;</td>
</tr>
<tr>
<td></td>
<td>Instrument Name &lt;I&gt;</td>
</tr>
<tr>
<td></td>
<td>Date &amp;Time &lt;D&gt;</td>
</tr>
<tr>
<td></td>
<td>SampleId &lt;ID&gt;</td>
</tr>
<tr>
<td></td>
<td>Vial &lt;V&gt;</td>
</tr>
<tr>
<td></td>
<td>ECustomN [N=1 to 5] &lt;E1&gt; to &lt;E5&gt;</td>
</tr>
<tr>
<td></td>
<td>TCustom [N=1 to 10] &lt;T1&gt; to &lt;T10&gt;</td>
</tr>
<tr>
<td>ResultName</td>
<td>SampleId &lt;ID&gt;</td>
</tr>
<tr>
<td>(EZChrom .rslt folder and .rst file)</td>
<td>UserName &lt;U&gt;</td>
</tr>
<tr>
<td></td>
<td>Method Name &lt;M&gt;</td>
</tr>
<tr>
<td></td>
<td>Datafile Name &lt;F&gt;</td>
</tr>
<tr>
<td></td>
<td>Instrument Name &lt;I&gt;</td>
</tr>
<tr>
<td></td>
<td>Date &amp;Time &lt;D&gt;</td>
</tr>
<tr>
<td></td>
<td>Vial &lt;V&gt;</td>
</tr>
<tr>
<td></td>
<td>ECustomN [N=1 to 5] &lt;E1&gt; to &lt;E5&gt;</td>
</tr>
<tr>
<td></td>
<td>TCustom [N=1 to 10] &lt;T1&gt; to &lt;T10&gt;</td>
</tr>
</tbody>
</table>
To facilitate the use of tokens in the sample Scheduler Client, the list of available tokens is proposed in the relevant cells.

**Change Instrument/Method used to perform the analysis**

Each analysis is assigned an instrument/method, used to perform the analysis. You can edit both the instrument and the method parameters in the Analysis table, and select values.

If several methods have been developed in the laboratory to analyze the same product on different instruments, in order to avoid difficulties caused by an instrument error or an overloaded instrument, you can provide an alternative solution by defining them in the XML command used to generate an analysis.

When such an analysis exists, you can change the instrument and method from the Analysis table in a single step. You have simply to select the desired instrument/method pair in the Alternative Inst/Meth column. The Instrument and Method cells are then assigned the corresponding values.

Note that this option is not available for analyses generated by a Quick Start.

**User actions**

You can add a new analysis, modify the order in which the analysis are launched, stop a running analysis, or delete one or several analyses.

The list of actions is described in the following table:

<table>
<thead>
<tr>
<th>Actions</th>
<th>Details</th>
</tr>
</thead>
<tbody>
<tr>
<td>Schedule</td>
<td>Allows you to switch <strong>Waiting</strong> analyses/sequence(s) into the <strong>Scheduled</strong> state.</td>
</tr>
<tr>
<td>Waiting</td>
<td>Allows you to switch <strong>Scheduled</strong> analyses/sequence(s) into the <strong>Waiting</strong> state.</td>
</tr>
<tr>
<td>Restart Analysis</td>
<td>Allows you to restart <strong>Ended</strong>, <strong>Error</strong>, and <strong>Stopped</strong> analyses/sequence(s). The restarted analysis switches into the <strong>Waiting</strong> state. You have to schedule it manually (using the <strong>Schedule</strong> button).</td>
</tr>
<tr>
<td>Stop</td>
<td>Allows you to <strong>Stop a Submitted</strong> or <strong>In Progress</strong> analysis/sequence.</td>
</tr>
<tr>
<td></td>
<td>When <strong>Stop</strong> is used with a sequence, the entire sequence is stopped. The In progress analysis of the sequence switches into <strong>Stopped</strong> state, the subsequent ones switch into the <strong>Waiting</strong> state in the sequence table. The sequence state switches into the <strong>Stopped</strong> state in the Analysis table.</td>
</tr>
<tr>
<td>Stop instrument</td>
<td>Allows you to <strong>Stop</strong> all acquisitions performed on an instrument: the <strong>Submitted</strong> or <strong>In Progress</strong> analysis is stopped; the <strong>Scheduled</strong> ones switch into the <strong>Waiting</strong> state.</td>
</tr>
</tbody>
</table>
You need only select an analysis (in **Submitted**, **In Progress** or **Scheduled** state) associated with the instrument to stop and then click the **Stop instrument** button. If you select analyses associated with different instruments, all analyses launched on those instruments are stopped.

<table>
<thead>
<tr>
<th>Delete</th>
<th>Allows you to delete selected analyses/sequence(s), that is, remove them from the sample Scheduler database. All analysis can be deleted except those in <strong>Submitted</strong>, <strong>In Progress</strong> and <strong>Edited by</strong> states.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Merge</td>
<td>This option is available only when two <strong>Holding</strong> state analyses are selected. It is intended for injecting two samples simultaneously on a dual-tower instrument, one sample on each tower.</td>
</tr>
<tr>
<td>Split</td>
<td>This option is available only when a <strong>Merged</strong> analysis is selected. It allows you to split the two merged analyses into two <strong>Holding</strong> analyses.</td>
</tr>
<tr>
<td>Quick Start</td>
<td>Allows you to create analyses from the Scheduler client, without an XML command. See LIMS command: the analysis order generated by the LIMS in Sample Scheduler for OpenLAB CDS EZChrom Edition Installation &amp; Configuration Guide for more information.</td>
</tr>
<tr>
<td>Create Sequence</td>
<td>This option is available only when selected analyses are in the <strong>Waiting</strong> or <strong>Incomplete</strong> state, and they are assigned the same Project, Instrument, Method, Tower. It allows you to group analyses in a Sequence. <strong>Incomplete</strong> analyses, with no value assigned to Project, Instrument or Method, can be grouped into a sequence.</td>
</tr>
<tr>
<td>Assign User</td>
<td>Allows you to assign a set of analyses to a user. Select the analyses/sequences in the Analysis table, and click the <strong>Assign User</strong> button.</td>
</tr>
<tr>
<td>Validate Edition</td>
<td>Allows you to validate the edition of an analysis or sequence.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Priority</th>
<th>Allows you to decrease the position of the analysis in the order. The priority order goes from N to N-1. It can be useful for analyzing an urgent sample, for example.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sooner</td>
<td>Allows you to increase the position of the analysis in the order. The priority order goes from N to N+1.</td>
</tr>
</tbody>
</table>

**Merge/Split:**

The **Merge** option is available only when two **Holding** state analyses are selected. It is intended for injecting two samples simultaneously on a dual-tower instrument, one sample on each tower. In this way, the productivity of the instrument is optimized.
Select the two **Holding** analyses in the Analysis table and click the **Merge** button. Select the dual-tower instrument, project, method to be used, and specify which sample will be analyzed on which tower in the **Merge analysis** screen.

Define the acquisition parameters/Sample information in the Analysis table, and validate the analysis. A new **Merge** analysis, with two Sample ids, is displayed in the Analysis table. It is ready to be started.

If you make a mistake when merging two analyses, you can **Split** the merged analysis to recover the two initial **Holding** analyses by clicking the **Split** button.

**Quick Start**

The Scheduler is designed to perform analyses launched by the LIMS via commands. An alternative way is to add a new analysis directly from the Sample Scheduler Client.

When you click the **Quick Start** button, a **Quick Start** screen is displayed. You have to select/define:

- The project to be associated with the acquisition from the list of authorized projects.
- The instrument used to perform the acquisition from the list of instruments you are authorized to use.
- The Tower(s) to be used to perform the acquisition: Front, Back or Dual. The Scheduler is not aware of the instrument configuration (1 or 2 Towers). You must select a valid value for the Tower parameter, given the instrument configuration.
- The method to use from the list of methods defined for the selected project. You must select a method compatible with the selected Instrument/Tower.
- The number of replicates. A maximum of 99 replicates can be defined.

A new analysis is added to the Analysis table in the Edition state.

Assign values to the acquisition parameters, the calibration parameters, etc.

When the edition has been validated, the replicates are generated. The new analyses are assigned the following Sample id: ‘User_Name_DateTime#QS#_i’ (where i is the replicate number), or ‘User_Name_DateTime#QS#’ if replicates equals 1.

**The sequence**

You can create and launch a sequence of analyses from the Sample Scheduler for OpenLAB CDS, as in the CDS.

All the analyses of the sequence are launched on the same instrument, using the same tower, and the same method, in the same OpenLAB Project.

Sample Scheduler for OpenLAB CDS, manages sequences created manually from the Scheduler client interface (group of analysis).

**Create a sequence by grouping a set of analysis**

To create a sequence, select the **Waiting/Incomplete** analyses to group (with same project, instrument, method, tower) in the Analysis table, then click the **Create sequence** button.

A sequence line appears in the Analysis table. Only the parameters that are common to
all the analyses belonging to the sequence are displayed (Sequence name, Project, Instrument, Method, Tower, State, Result, Priority, User, Alternative Inst/Meth, Last modified by, Last modification date).

**NOTE**

If some of the selected analyses are not assigned a Project and/or Instrument and/or Method, once grouped into sequence, they are assigned the value of the other ‘complete’ analyses. If the tower position is not defined for a dual-tower analysis, you cannot group the analyses in a sequence. You must first assign the Front and Back Tower positions to the analyses.

When you select a sequence in the Analysis table, its content is displayed below, in the **Sequence Table**.

**Sequence table customization**

You can customize the parameters to be displayed in the Sequence table.

- You can select the parameters to display. Parameters are grouped into four categories: **Analysis Info**, **Acquisition**, **Quantification** and **Custom info**. In each category you select the parameters you want to display by checking the corresponding parameter names:

  ![Acquisition Table](image)

  If you need to see all the parameters of the category, click on the category button. If you want to redisplay only the default parameters of the category (the checked ones), click on the category name again.

- You can modify the column position by simply dragging and dropping the column header from one position to another.

- You can customize the width of the columns.

To save the user-specific layout, click the **Save Layout** button in the **Options** ribbon of the Analysis table.

**Edit a sequence**

You can edit the sequence parameters to assign them a value in the Analysis table; for example, you can assign a name to the sequence.

You can also edit the sequence parameters in the Sequence table.
You can edit the parameters of each analysis of the sequence by editing the corresponding cell in the sequence table. Once all parameters are defined, validate the sequence either by clicking the Validate button or by selecting another analysis in the Analysis table. All the changes are then saved.

Copy/Increment the value of a sequence line parameter

You can copy or increment (one by one) the value of a sequence line parameter to a selection of lines.

Select the value to duplicate or implement for one line, select this line and the lines to modify, and select the Copy or Increment option in the context menu. The value of the first selected line is copied/incremented to the other lines.

For a dual-tower instrument, the copy/increment is performed by tower.

The copy/increment options are available only for the Waiting/Incomplete/Waiting on error/Edited by analysis states.

Launch a sequence

Launch the sequence by clicking the Schedule button.

The sequence state is updated in the Analysis table, and the states of the sequence analyses are updated in the sequence table.

When the sequence is started, the data file names of all the analyses are updated: automatic suffix #i is added, where ‘i’ represents the analysis position order in the sequence.
For example, the data file name of the third sequence analysis is ‘Data’ in the sequence table; when the sequence is launched it evolves to ‘Data #3.dat’.

NOTE
When the CDS ‘date’ token <D> is used in the Data file name definition of the sequence analyses, all the analyses are assigned the date /time the sequence is launched, and not the date/time each analysis is launched.

Perform actions in sequence
You can do the following:

<table>
<thead>
<tr>
<th>Action</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Add</td>
<td>Add a new line at the end of the sequence.</td>
</tr>
<tr>
<td>Delete</td>
<td>Delete the selected line(s) of the sequence. If all the lines of the sequence have been deleted, the sequence line is also deleted in the Analysis table.</td>
</tr>
<tr>
<td>Convert into analysis</td>
<td>Remove the selected line(s) of the sequence and convert them into analyses displayed in the Analysis table. This action is not available while the sequence is in edition.</td>
</tr>
<tr>
<td>Sooner</td>
<td>Decrease the line one position (for example, from 3 to 2)</td>
</tr>
</tbody>
</table>
Later
Increase the line one position (for example, from 3 to 4)

Print
Print the sequence as it is displayed on screen.

Notifications

Invalid command

When an invalid command is generated by the LIMS, it is automatically trashed by the Sample Scheduler. To ensure users are informed of the command trash, a notification is sent into the Scheduler Client. To display the list of notifications, click the Notifications/Show all button. The trashed commands are listed with the date/time of the trash and the list of errors present in the command. You can acknowledge one or several notification(s) to remove it/them from the list.

Note that only the users who have been defined in the Scheduler Configuration Home/Notifications/On screen receive the notifications.

Options

Refresh

An automatic refresh is performed every timed period defined in the Sample Scheduler Configuration. You can force a refresh of the Analysis table by clicking the Refresh button.

Open a chromatogram in the CDS from Sample Scheduler for OpenLAB CDS

You can open a chromatogram in the CDS from the Scheduler if you need to check the peak integration or results.

As the chromatogram name can be complex (for example, when using CDS and Scheduler tokens to generate data file names), it can take time to find/open it from the CDS. The Sample Scheduler for OpenLAB CDS offers the possibility to directly open the chromatogram from the Scheduler interface.

Double-click the line corresponding to the chromatogram in the Analysis table, or select it and click the Open Data button to open it in the CDS. An EZChrom Offline session is opened automatically with the same credentials as in the Sample Scheduler for OpenLAB CDS: user, project, and instrument.

You can open only one chromatogram (.DAT) per instrument/computer. If you successively open two chromatograms acquired on the same instrument from the same computer, the first chromatogram is opened in a CDS session, then the open session is closed before it is reopened with the second chromatogram.

For an instrument with two towers, select the line corresponding to the Front or Back tower in the Analysis table and double-click it, or click the Open Data button to open the corresponding chromatogram(s).
If several signals are associated with one tower, the **Open Data** option opens the chromatograms of all signals.

**NOTE** When opening a chromatogram, no refresh is performed in the Scheduler interface, no action can be taken (Edition, Quick Start, etc.).

### Print

You can print the Analysis table by clicking the **Print** button in the **Options** ribbon. The printing matches information displayed into the Scheduler client, using the same columns, position, grouping, sorting and filtering.

This option allows you to print the working list, which can be referred to when you have to put all the samples in the correct instrument/autosampler position.

### Save Layout

You can customize both the Analysis table and Sequence Table layouts, for example, the columns to display, their positions and widths.

To save the user-specific layout; click the **Save Layout** button in the **Options** ribbon.

One layout can be saved per user.

### Reset analysis

The purpose of the reset analysis feature is to unblock an analysis that is blocked in the Sample Scheduler database. It can be used, for example, to restore an analysis that has been blocked in **Edited by** state in the database following a crash of the Scheduler Client.

This function is available only for Sample Scheduler administrators (Is an administrator (Sample Scheduler) rights).

Select the analysis to reset, click the **Reset** button in Administration.

Resetting an analysis switches it into either the **Waiting** or the **Incomplete** state, according to its content. You can subsequently manage it as a normal analysis.
In This Book

This manual describes the following:

- Sample Scheduler presentation
- Sample Scheduler Interfaces
- Application details
- Analysis management
- Analysis table
- Analysis edition
- Quick Start
- The Sequence
- Notifications
- Options