



## **LDMS for the Web - User Manual**

LDMS  
Version 11.0  
Web  
LS.0006

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## **Summary**

This manual explains how to use LDMS

# Contents

<b>Getting started.....</b>	<b>11</b>
About Frontier Science.....	11
About LDMS.....	11
General information.....	11
History.....	12
Windows and web versions.....	12
Migrating from Windows to web versions.....	12
System requirements.....	13
Signing in to LDMS.....	14
Acknowledgement of training.....	14
Changing users.....	16
Saving changes when automatically signed out.....	16
Downloading files.....	17
The LDMS user interface.....	17
Applying filters to a page.....	18
Specimen Filters Code Searching.....	20
Deleting Items.....	21
Using a List of Identifiers to Select Specimens.....	21
Challenge codes.....	22
<b>Specimen management.....</b>	<b>23</b>
Terms used in LDMS.....	24
Using the Specimen Management page.....	25
Entering specimen information (Overview).....	26
Participants.....	27
Participant identifiers.....	27
Adding participants using the Specimen Management page.....	27
Adding participants using Quick Add.....	29
Modifying a participant.....	29
Enrollments.....	30
Adding enrollments using the Specimen Management page.....	30
Modifying enrollments.....	31
Visits.....	32
Visit identifiers.....	33
Adding a visit to an enrollment.....	33
Modifying visits.....	34
Primary specimens.....	35
Specimen identifiers.....	35
Specimen identifiers in LDMS for Windows.....	36
Adding a primary specimen to a visit.....	37
Co-enrolling a primary specimen.....	38
Modifying a primary specimen.....	40
Aliquot specimens.....	41

Adding aliquots to a primary specimen.....	41
Entering cryopreservation information.....	43
Modifying aliquot specimens.....	43
Creating Subaliquots.....	44
Delete a specimen.....	45
Removing specimens from storage.....	45
Quick add.....	46
Adding specimens using Quick Add.....	47
Adding participants using Quick Add.....	48
Adding enrollments using Quick Add.....	49
TBD in quick add templates.....	49
Quick add templates.....	50
Differences between primaries and aliquots.....	51
Specimen availability.....	52
Specimen record details.....	53
Specimen conditions.....	57
Destroying a specimen.....	58
Procedural conditions.....	58
Specimen container conditions.....	59
Temperature conditions.....	60
Shipping conditions.....	60
Qualitative conditions.....	61
Quantitative conditions.....	61
Other conditions.....	62
Test assignment.....	63
Assigning tests to a specimen.....	63
Indicating that a test will not be performed.....	63
Deleting a test assignment.....	63

**Storage..... 64**

Navigation on the <b>Storage</b> page.....	64
The storage tree.....	65
Storage items.....	66
Icons and their meaning.....	68
Assigning storage locations.....	70
Adding a new storage unit.....	70
Adding a new level in a storage unit.....	72
Adding a container to a level.....	73
Assigning a storage location to specimens.....	75
Generating a printable list of what is in storage.....	77
Container report.....	77
Storage templates.....	78
Creating storage item templates.....	78
Modifying and removing storage templates.....	80
Moving items in storage.....	80
Moving Items in Storage - Filter Search.....	81
Consolidating storage containers.....	83
Listing specimens that moved in storage.....	83
Removing items from storage.....	84
Modifying the condition of stored specimens.....	85

Storage Action Report.....	86
----------------------------	----

**Shipping..... 86**

LDMS shipping file compatibility.....	87
Shipments are data transfer.....	87
Shipment numbers.....	88
New shipments.....	89
Creating new shipments.....	89
Sending a pending shipment.....	93
Generating a shipping manifest.....	94
Shipment Tracking Information.....	96
Supported shipping file formats.....	96
CSV shipping files.....	96
Cross-LIMS shipping files.....	99
SeraCare shipping files.....	101
Shipping container report.....	102
Shipment storage report.....	103
Receiving shipments.....	103
Shipping and projects.....	105
Import as is.....	105
Handling non-LDMS shipping files.....	105
Shipment QA/QC.....	105
Performing QA/QC.....	107
Shipment history.....	108
Removing a received shipment.....	109
Un-sending shipments.....	110
Re-downloading the shipping file of a sent shipment.....	110
Bulk Updating Condition Code and Comments of Shipments....	111
Shipment Evaluations.....	112

**Reports..... 113**

Custom Report Builder.....	113
Creating a custom report.....	114
Running a saved report.....	115
Modifying or deleting a saved report.....	116
Example custom report.....	116
Generating a report.....	117
Filter Reports Using a List of Specimens.....	118
Available report formats.....	119
Administrative reports.....	120
Anonymous Patients Map.....	120
Transaction Log Report.....	120
User Event Report.....	121
User permissions report.....	121
Barcode Reports.....	121
1D Barcodes Report.....	121
2D Barcodes Report.....	122
Exportable reports.....	122
Abbott SARS-COV-2 Quant Export Report.....	123

Abbott SARS-COV-2 Quant Export Report with Comments.....	123
Abbott SARS-COV-2 Quant Export Report with Sample Location.....	124
Aliquot count by primary report.....	124
Aliquot Inventory Report.....	125
CFAR export report.....	126
CFAR storage report.....	126
Database dump report.....	126
Database dump report 2.....	127
Exportable Abbott Assay Report.....	128
Laboratory 081 billing report.....	129
Laboratory 81 CNICS by date report.....	129
Laboratory 081 CNICS general report.....	129
Laboratory 188 storage report.....	130
Lab 40 LabKey report.....	130
Laboratory 48 billing report.....	131
Lab 485 aliquot report.....	132
Lab 485 specimen count report.....	132
Lab 485 specimen count with volume report.....	133
Primary specimen database dump report.....	133
Sample counts for specified project report.....	133
Specimen export report.....	134
Storage export report.....	134
Westat PK Export Report.....	135
Miscellaneous reports.....	135
Clinic contact report.....	135
LDMS abbreviated codes report.....	136
LDMS assay censor codes report.....	136
LDMS primary, additive, derivative, sub additive/derivative codes report.....	136
MWCCS.....	136
MWCCS Processing Report.....	136
Participant reports.....	137
Participant identifiers report.....	137
PK reports.....	137
Pharmacology Drug Count.....	137
Pharmacology Drug List.....	137
Pharmacology Proficiency Results.....	137
PK Drug Limits By Run.....	138
PK Participant Report.....	138
PK Summary Report.....	139
PK Summary with Assay Name.....	139
PK Summary with Assay Name (exportable).....	140
Quick Add Templates.....	140
Quick Add Template List Report.....	140
RPID Reports.....	141
Random PID Report.....	141
RPID Specimen Request Report.....	141
Shipping reports.....	141
Daily imported specimen log report.....	141
Detailed imported specimen report.....	142

Imported specimen report - summary.....	142
Lab 263 Summary Detail of Shipped Specimens.....	143
Shipped specimen report - detail report.....	143
Shipped specimen report - summary report.....	144
Shipping laboratory contact report.....	144
Specimens Marked for Shipping.....	144
Specimen reports.....	145
Cell yield QA/QC summary report.....	145
Lab 263 Processing Report.....	145
Lab 263 Summary of Specimens.....	146
Primary specimens received report.....	146
Specimen count report.....	147
Specimen log report.....	147
Specimen processing report.....	148
Specimens for a given project report.....	149
Specimens for a given project 2.....	149
Time to freeze QA/QC summary report.....	150
Time to process QA/QC summary report.....	150
Storage reports.....	151
Specimens in storage per PID report.....	151
Specimens not in storage report.....	151
Specimens remaining in storage report.....	151
Storage container location report.....	152
Storage count report by freezer.....	152
Storage detail report.....	152
Test Result Reports.....	153
Abbott Realtime HIV1 Assay Report.....	153
Abbott Realtime HIV1 Patient Report.....	153
Abbott Repeat and Censored Run/Samples.....	154
Abbott SARS-COV-2 Quant Assay Report.....	154
Abbott SARS-COV-2 Quant Patient Report.....	155
IQA Cryopreservation Patient Report.....	156
TaqMan HCV Repeat and Censored Run/Samples.....	156
TaqMan HIV-1 Repeat and Censored Run Samples.....	156
TaqMan Realtime HCV Assay Report.....	157
TaqMan Realtime HCV Patient Report.....	157
TaqMan Realtime HIV-1 Assay Report.....	158
TaqMan Realtime HIV-1 Patient Report.....	158
Taqman Realtime Qual Assay Report.....	159
TaqMan Realtime Qual Patient Report.....	159
WIHS.....	160
Processing Log - Lab 263.....	160

**Labels..... 160**

Label formats.....	160
Barcodes.....	161
Label sizes.....	161
How to use a barcode reader with LDMS.....	162
Printing labels anywhere.....	162
Support for LabelScape-generated Barcodes.....	163

Generating labels.....	163
Defining new label formats.....	165
Customizing label formats.....	166
Setting the default label format for a project.....	167

**Test Results.....167**

Test Results.....	167
Test Supported in LDMS.....	168
Running an assay means reading data.....	168
Test Results page.....	168
Locating assay runs.....	169
Censor Codes.....	169
Run Statuses.....	170
Creating New Test Result Runs.....	170
Assigning Results to Blinded Controls (Pellets).....	172
Reviewing a Run.....	172
Test History.....	173
Deleting assay runs.....	173
Restoring deleted runs.....	174
Test result reports.....	174
Entering PK Test Results.....	174
Completing PK Test Results.....	179
Reviewing a PK Test Run.....	180
PK Control Lots.....	180
Adding a New Lot.....	180
Editing or Deleting a Lot.....	181
PK Control Charting.....	181
Generating a Report.....	182
PK Templates.....	183
Adding a New Template.....	183
Updating an Existing Template.....	183

**Data Submission.....184**

Adding Submissions.....	184
Editing Submissions.....	185
Data Submission Filters.....	186

**Printers.....186**

Setting up the Brady IP300 printer.....	186
Setting up the Brady <sup>®</sup> MVP 300 printer.....	187
Setting up the LabXpert printer.....	188
Setting up the Zebra <sup>®</sup> GX 430t printer.....	189
Setting up the Brady BBP11-34L printer.....	190
Setting up the Brady <sup>®</sup> BBP33 printer.....	191
Setting up the Brady BMP53 printer.....	192
Setting up the Brady BP-PR 300 printer.....	192
Setting up the Zebra ZD620 Printer.....	193
Setting up other printers.....	193



<b>Preset projects.....</b>	<b>194</b>
ACTIV.....	194
ACTG/IMPAACT.....	195
AERAS.....	195
AIEDRP.....	196
AIS.....	197
AMC.....	197
ATN.....	198
BHP.....	198
BM.....	199
Botswana MOH.....	200
CEMALB.....	200
CHAVI.....	201
CIPRA-HT.....	201
CIPRA-ZA.....	201
CIPRA.....	202
CONTROL.....	202
CoVPN.....	203
CPCRA.....	203
CPQA.....	204
CP-CTNET.....	204
FACTS.....	205
HN.....	205
HPTN.....	206
IDCRC.....	206
IPREX.....	207
IQA.....	208
IRC.....	208
KENPHIA2.....	208
MACS.....	209
MATRIX.....	209
MAVRC.....	210
MOSAIC.....	210
mStudy.....	210
MTCT.....	211
MTN.....	211
MWCCS.....	212
NICHD-Westat.....	212
PHACS.....	212
PHIA.....	213
REPRIEVE.....	214
SHIMS.....	214
SNRP.....	215
TIES.....	215
VQA.....	215
VTN.....	216
WHIN.....	217
WIHS.....	217
WITS.....	218

WITSRepos.....	219
ZEBS.....	219
ZIP.....	220

**Administration..... 220**

Projects.....	221
Local projects.....	221
Government projects.....	224
Adding a Reagent.....	224
Adding Reagent Information.....	225
Linking Reagent to Sample in Specimen Management.....	226
Linking Reagent to Sample in Quick Add.....	227
Linking Additive to Reagent Lot.....	227
Reagent Lot Sample Details Report.....	227
Specimen Anonymization.....	227
Lab Settings.....	229
User Settings.....	229
User management.....	230
Changing your password.....	230
Password requirements.....	230
Dropdown Customization.....	231
RPID Requests.....	231
Adding a New RPID Request.....	232
Editing an RPID Request.....	233
Clear Filters.....	233

**Online Resources..... 233**

**Codes, units, and abbreviations..... 234**

Specimen type codes.....	234
Primary codes.....	234
Additive codes.....	241
Derivative codes.....	244
Sub additive/derivative codes.....	251
Condition codes.....	258
Unit codes.....	260
Measurement codes.....	260
Time unit codes.....	261
Visit codes.....	261
Assay Codes.....	263
Reasons for not running an assay censor codes.....	264
Immunology assay codes.....	264
Virology assay codes.....	264
Pharmacology assay codes.....	266

**Index..... 276**

## Getting started

This manual describes how to use LDMS for Web and is intended for users at laboratories.

### About Frontier Science

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Frontier Science develops and maintains LDMS, and provides data hosting for laboratories.

Frontier Science and Technology Research Foundation, Inc. is a not-for profit that provides data management services to research organizations. LDMS is one of those data management services.

Many organizations that utilize LDMS also utilize Frontier Science's *data management center* (often referred to as the DMC) in Amherst, New York for long term data storage. These organizations use LDMS as a mechanism for sending specimen data for studies to Frontier Science.

Frontier Science is involved in many other statistical research efforts beyond LDMS. To learn more about the work that Frontier Science does, visit <https://www.frontierscience.org>.

### About LDMS

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LDMS is a data management solution for laboratories managing biological medical specimens.

#### General information

LDMS is specifically designed for the needs of small and medium-sized research laboratories. It is available for Windows or as a web application. Laboratories generally use LDMS on one platform only. The Windows version must be installed on individual machines, but can utilize a centralized LDMS server installed at the laboratory. The web version does not require additional software to be installed and can be used in most web browsers. Users of the web version do not need to maintain a local database or create backups of data.

LDMS can perform many tasks, including the following:

- cataloging specimen information, such as its volume, additive, and current condition
- managing the transfer of specimen information between laboratories
- generating labels for specimens
- reading and entering assay result information
- keeping track of where specimens are located in storage units

Frontier Science manages data for laboratories using LDMS in a secure environment that meets the standards of 21 CFR Part 11 and NIST/FISMA guidelines.

## **History**

LDMS was initially released for Windows in 1998 to collect data for HIV-related clinical trials.

The first projects to use LDMS were the Adult and Pediatric AIDS Clinical Trials Groups (AACTG and PACTG, now known as ACTG and IMPAACT). While LDMS continues to be used heavily by projects that focus on HIV and related cohorts, it is also used for many other specialized research purposes, including hepatitis C (HCV) and influenza studies, proficiency testing programs, and specimen repositories.

In 2014, Frontier Science released the web version LDMS.

## **Windows and web versions**

Since the release of the web version of LDMS, Frontier Science has focused on the development of the web version.

The Windows version of LDMS continues to be maintained, and several updates to the Windows version have been released since the introduction of the web version. LDMS for Windows releases generally focus on improving existing features and project-specific changes. When possible, new laboratories should generally use the web version. When a new laboratory is set up, Frontier Science will guide the laboratory through the process of selecting and installing the appropriate version for their needs.

Laboratories are able to ship specimens to and receive specimens from other laboratories, regardless of which version of LDMS the laboratories are using. There may be other concerns when laboratories using the Windows and web versions need to work together. Frontier Science can work with laboratories to determine how to best handle different scenarios.

## **Migrating from Windows to web versions**

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Laboratories currently using LDMS for Windows may be able to migrate to the web version.

Migration from the Windows to web version must be approved and coordinated by Frontier Science. Frontier Science will typically invite laboratories to migrate when it is appropriate to do so. Issues that need to be considered when migrating a laboratory include the following:

- Are all projects that the laboratory participates in supported in the web version?
- Are the features the laboratory is currently using supported in the web version?
- Does the laboratory routinely work with laboratories using the Windows version?

It is possible to migrate a laboratory's existing LDMS for Windows data to the web version. To do this, the laboratory's Windows database must be obtained by LDMS User Support. Frontier Science will then convert the data to the appropriate format and test it internally for issues. If the database can be converted successfully, LDMS User Support will help get the laboratory setup with appropriate user accounts and training.

## System requirements

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These are the system requirements, along with recommended specifications, for using LDMS.

### Required

**Table 1: System requirements**

Component	Requirement
Web Browser	<ul style="list-style-type: none"> <li>• Firefox 54 or higher</li> <li>• Chrome 58 or higher</li> <li>• Edge 40 or higher</li> </ul> <p>JavaScript must be enabled for all browsers. Although most browsers will be able to use LDMS without issues, Frontier Science does not provide user support for web browsers that are not listed.</p>
Screen Resolution	1024 × 768
Networking	High-speed Internet connection
Input	Keyboard and 2-button mouse
Video	Monitor and video card capable of at least 1024 × 768 resolution and 16-bit color depth
Label Printing	Adobe Acrobat

### Recommended

**Table 2: System recommendations**

Component	Recommendation
Printer	Printers and barcode readers may have additional requirements. Consult your hardware's documentation for more information.
Barcode Reader	Compatible barcode scanner

### Other software

LDMS can generate reports and other types of files in several different formats. Most of these files can be opened by commonly used programs that are already on our computer.

**PDF viewer**      Needed to view and print reports. You can download many PDF viewers for free, such as Adobe Reader and

Evince. Many web browsers also have a built-in PDF viewer.



**Important:** An Adobe PDF viewer is required when printing labels.

**Spreadsheet viewer**

Needed to view exportable reports. Microsoft Excel or LibreOffice Calc can open these files.

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## Signing in to LDMS

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Sign in to LDMS by using your user name and password, and selecting a laboratory database.

### Prerequisites

You must have a user account before you can sign in to LDMS.

### Steps

1. In a web browser, go to [LDMS login](#).
2. In the upper-right corner of the page, click **LDMS Login**.
3. Enter your user name and password, and then click the **Login** button. The **Select Laboratory** page will open.
4. Select the laboratory from which you want to work from the **Select Lab[oratory]** box.  
You will be working out of the selected laboratory's database for your session. You will only be able to select a laboratory to which you have access.

### After you are finished

If you want to change to a different laboratory's database after signing in, click the **Change** link next to the laboratory name in the upper-right corner. To assign a default laboratory, hover over the **Administration** button and click **User Settings**. Click the drop-down box next to **Default Lab ID** and select the laboratory that you would like to make the default.

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## Acknowledgement of training

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If it is your first time logging into LDMS, you will be prompted to sign an acknowledgement of training after entering your username and password.

**Figure 1: Acknowledgment Form**



Please be advised that Frontier Science will require that all users be trained in the LDMS prior to using the system in accordance with 21 CFR Part 11. Acknowledgement of this training will be maintained electronically at Frontier Science.

**Please use the acknowledgment prompt below to indicate whether you, as an LDMS user, have been trained in the use of the LDMS. Training can include but is not limited to in person training from FSTRF or other qualified laboratory staff proficient in the use of LDMS, attending a webinar overview, reading the user manual or viewing other training materials available on the LDMS website ([www.ldms.org](http://www.ldms.org)).**

For those users who indicate “no,” or otherwise indicate that they have NOT received LDMS training, please be advised you will not be allowed into the program. All training materials are published on the LDMS website ([www.ldms.org](http://www.ldms.org)) and are available for you to complete this requirement. Please contact LDMS User Support with any questions or concerns regarding this requirement or access into the LDMS.

- No, I have not been trained
- Yes, I have been trained

Login ID

Password

Submit

If you have not been trained, you will not be allowed into the system. By selecting the option **Yes, I have been trained**, you are indicating that you have received training in the use of LDMS.

## Changing users

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To switch users from the same web browser, you must log out and log in as a different user.

### Background

Although multiple users can sign in and access data from one laboratory's database at the same time, you cannot sign in with multiple users from the same web browser on the same computer. For example, you can sign in as two different users on two different computers using Firefox, but you cannot open a new tab on the same computer and sign in as a different user. Doing so would cause problems with the tab in which you were originally signed in.

### Steps

1. In the upper-left corner of any page in LDMS, click the **Logout** button.
2. Sign in as a different user.

## Saving changes when automatically signed out

---

It is possible to save changes, even when automatically signed out of an idle session.

### Background

You will automatically be signed out of LDMS if you leave a page idle for 15 minutes. When this happens, you will receive a notification that you have been signed out. If you attempt to leave the current page, you will be directed back to the sign in page. If you had unsaved changes when you were automatically signed out, those changes will be lost when you are redirected to the sign in page. This is to prevent unauthorized users from saving changes from a session that is signed out.

It is possible to save unsaved changes on a page after being logged out by signing in using another tab in the same web browser.

### Steps

1. Without leaving the page with unsaved changes, open a new tab in your web browser.
2. In the new tab, go to the LDMS sign in page.
3. Sign in as the user with the unsaved changes.
4. Close the new tab.

### Result

The original tab with the unsaved changes will now be considered signed in. You will now be permitted to continue working and to save any changes made.



## Downloading files

Different web browsers have different way of handling file downloads.

Many modern web browsers are configured by default to try to open certain types of files automatically or download them to a default location. For example, by default Firefox will attempt to open PDF files using a built-in PDF viewer. Likewise, Chrome is configured by default to save file downloads to a default location without asking you where to save them.

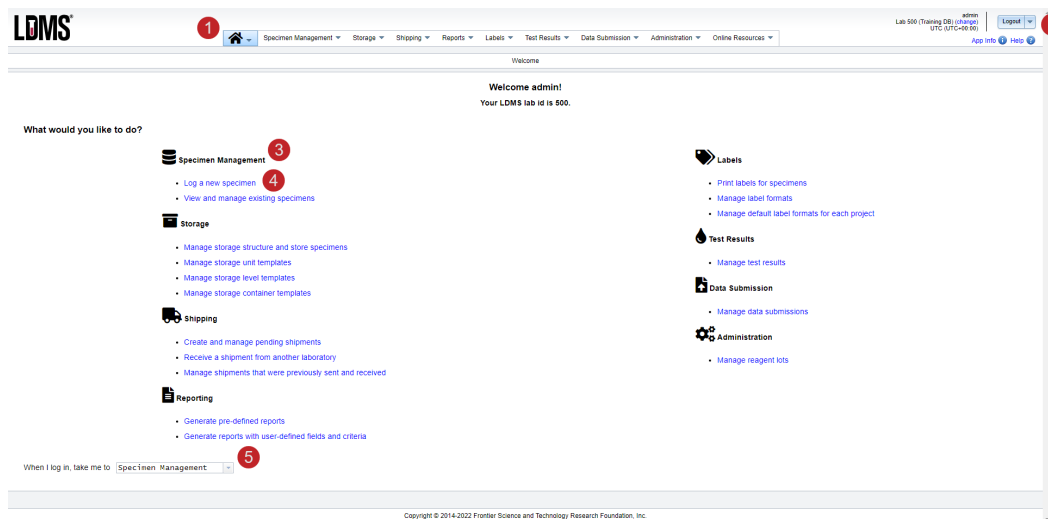
There are many times that LDMS will provide a file for you to download, such as a shipping file. Since you need to know where the file is on your computer in order to provide it to another laboratory, it is helpful to understand how your web browser handles file downloads.

How to view and modify your browser's behavior for downloading files or opening files automatically will vary by browser and version. For instructions, consult the help documentation for your web browser.

## The LDMS user interface

When you first log in, you will be brought to the LDMS Welcome Page unless you have set another page as your default login page.

**Figure 2: The LDMS Welcome page**



(1) The LDMS menu bar, (2) The action menu, (3) LDMS Module Section, (4) Module task quick-link, (5) Default login page setting

**LDMS menu bar** The menu bar is used to navigate between different tasks in LDMS. Hover the mouse pointer over a page to see its sub-pages.

**action menu** The action menu is used in various areas of LDMS to perform a major task. For example, on the **Specimen**

**Management** page, the action menu is used to create a new participant.

**signing out**

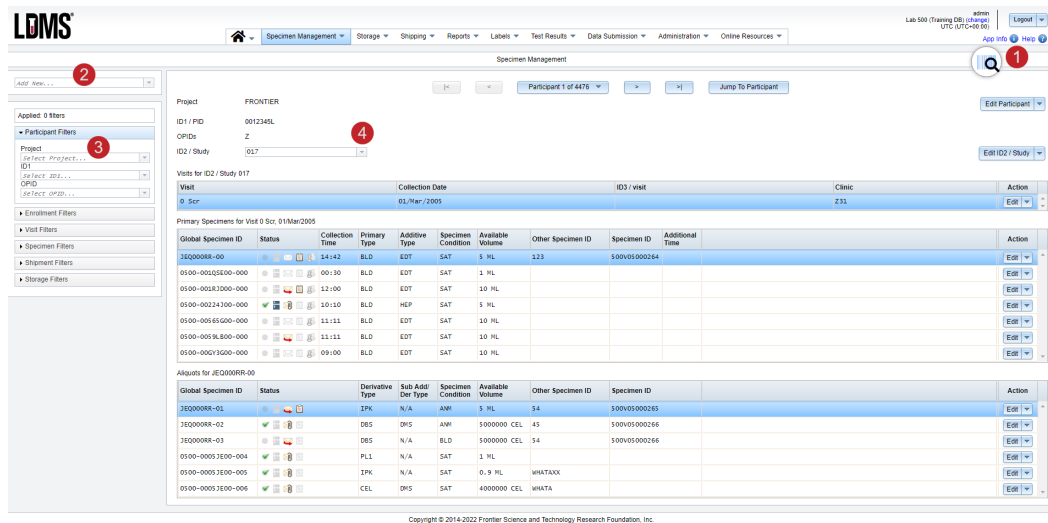
To sign out of LDMS as the current user, click the **Logout** button in the upper-right corner. This button is available on every page.

**change databases**

To change to a different laboratory database, click the **Change** link in the upper-right corner next to the laboratory name.

The LDMS user interface has many common elements across different pages.

**Figure 3: The main LDMS user interface**



(1) Barcode scanning available (2) An applied filter, (3) Currently viewed participant, (4) Specimens

**filters**

Filters are available on most pages and will limit the information that is displayed in the working area on the page. For example, if you are on the **Specimen Management** page and apply a filter with the value **FRONTIER** to the **Project** field, only participants enrolled in the **FRONTIER** project will be displayed. The filters that are available will vary, depending on the current page. To remove a filter after it has been applied, click on it.

**Applying filters to a page**

Filters are available on several pages and are used to narrow down the information that is displayed so that you can find something.

**Background**

On many pages in LDMS, all information for a particular task will be displayed together. For example, if you are on the Specimen Management page, all

participants in your laboratory's database will be displayed. If your laboratory has information for 200 participants, all 200 will be displayed by default and you would need to page through each one to find what you are looking for.

Filters can be used to temporarily limit the amount of participants shown so that only records of interest are displayed. This is the primary way to search for items in LDMS.

### Steps

1. Open a page with filters, such as the **Storage** or **Specimen Management** pages.  
Filters are displayed in the filters panel on the left side of the page, below the action menu.
2. Locate the desired filter.  
Filters are grouped into categories, such as visit filters and specimen filters. Some categories will be specific to the current page. For example, the storage container filters will only be available on the **Storage** page.

**Figure 4: The filters panel**

The screenshot shows a filters panel with the following elements:

- A box at the top indicating "Applied: 2 filters".
- A "Remove All Filters" button.
- A section for "Participant Filters" which is expanded. It contains:
  - A "Project" dropdown menu with the text "Select Project..." and a dropdown arrow. Below it, a blue button labeled "FRONTIER" with a close icon (X) is shown.
  - An "ID1" dropdown menu with the text "Select ID1..." and a dropdown arrow.
  - An "OPID" dropdown menu with the text "Select OPID..." and a dropdown arrow.
- Three collapsed filter sections: "Enrollment Filters", "Visit Filters", and "Specimen Filters".
- A section for "Shipment Filters" which is expanded. It contains:
  - A "Shipment Number" dropdown menu with the text "Select Shipment Number..." and a dropdown arrow.
  - An "Import Date" field with a dropdown arrow, a date input field containing "dd/MM/yyyy", and an "Add" button.
  - A blue button labeled "< 01/Aug/2016" with a close icon (X).
- A collapsed "Storage Filters" section at the bottom.

In this example, the FRONTIER filter has already been applied to **Project**. This means that only information for that project will be displayed.

3. Select or enter the information to be shown from the filter box.  
You can either select the information to filter from this list or enter it into the box. Filters will automatically show available options as you type.



**Note:** Filters do not affect other filters. For example, if you select the FRONTIER project, then try to apply a filter for **ID1**, all ID1 values in the laboratory's database will be available for selection, even if they don't belong to the FRONTIER project.

### Result

The filter will be applied immediately once it is selected and the page will automatically refresh to remove any records that do not meet the filter's criteria. If two filters were selected, they will both be applied using "and" logic. For example, if you selected FRONTIER from the **Project** filter and BLD from the **Primary type** filter, only blood specimens for the FRONTIER project will be displayed..

### After you are finished

To remove a filter that has been applied, find it in the filter panel on the left side of the page and click on it. It will be removed immediately and the page will automatically be refreshed to reflect the change.

## Specimen Filters Code Searching

If using **Specimen Filters** options, contextual suggestions will appear when typing in the following fields:

- **Primary Type**
- **Additive**
- **Derivative Type**
- **Sub Add/Der Type**
- **Condition**

While other filter fields will display results as you type, these specific fields provide additional aid if uncertain of the *code abbreviation*. If unsure of the code abbreviation for DSE - Spray Dried Sodium EDTA, for example, then typing **EDTA** in the **Additive** field yields a list of possible codes containing the **EDTA**.

**Figure 5: Contextual results**

▼ Specimen Filters

Global Specimen ID

Specimen ID

Other Specimen ID

Primary Type

Additive

- DPE - Spray Dried EDTA
- DSE - Spray Dried Sodium EDTA
- EDT - EDTA
- LPE - Liquid Potassium EDTA
- LSE - Liquid Sodium EDTA
- PED - Potassium EDTA
- RBE - Royal blue - EDTA
- SED - Sodium EDTA
- SFE - Sodium Fluoride/Na<sub>2</sub>EDTA

Tech Initials

## Deleting Items

When a user deletes an item such as a specimen, storage item, shipment, or test run, the user will be required to specify why the item is being deleted. This reason is then displayed on the Transaction Log report to properly track the reason for deleting.

**Figure 6: Reason for Delete Window**

Reason for Delete

Enter the reason for deleting this aliquot.

OK Cancel

## Using a List of Identifiers to Select Specimens

You can use a list of identifiers to select a set of specimens

This feature is available in most places where specimens need to be selected including Custom Report Builder, Pending Shipments, Stored Samples, Test Results, and Print Labels using the **Upload Global Specimen Ids File** button. The file of identifiers must be a text file and must include one global specimen ID per line.

**Figure 7: Global ID List File Example**

```
0500-00ABCDE00-001
0500-00ABCDE00-002
0500-00FGHIJ00-001
0500-00FGHIJ00-002
0500-00FGHIJ00-003
0500-00KLMNP00-001
```

## Challenge codes

---

A challenge code is password that you must give to LDMS User Support to perform certain actions in LDMS.

Access to certain features in LDMS may be restricted for a number of reasons. For example, unimporting a received shipment can have very serious consequences. LDMS does not provide “undo” functionality to reverse such an action. A challenge code is a fail-safe mechanism that can prevent accidental changes to specimen data.

If you attempt to access a feature locked with a challenge code, LDMS will prompt you for the response code.

You must contact LDMS User Support and give them the **Challenge Code**. If appropriate, they will provide you with the response code which will then unlock the feature for your use. The code will change each time the feature is accessed, and will be needed even if the feature was previously unlocked.

**Figure 8: Prompt for challenge password**

Unimport Received Shipment

Continuing will unimport shipment number 543 which was imported from shipment 137 sent by lab 501.  
Unimporting a batch requires a challenge response from LDMS user support.

Challenge Code

Response Code

Unimport Cancel

In this example, you would provide LDMS User Support with the code `NOQEAS` and they will provide you with the **Response Code** to access this feature.

**⚠ Warning:** Do not close the challenge password window before you obtain the **Response Code**. Doing so will cause a new **Challenge Code** to be generated, which will require a different **Response Code**.

## Specimen management

The Specimen Management page is where you can manage the details of specimen records and related information for participant enrollments.

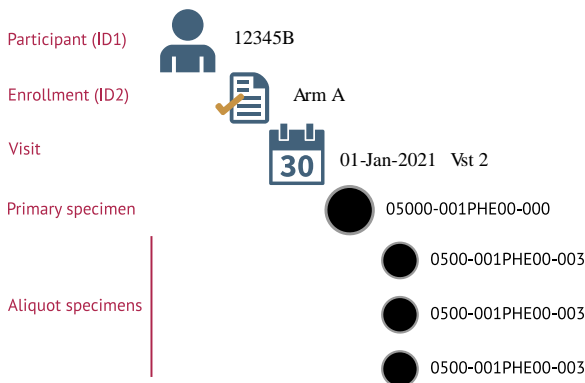
In LDMS, a participant, an enrollment, and specimens drawn from a participant (including the specimens derived from them) form a specimen record. Specimen records are added and displayed on the Specimen Management page.

## Terms used in LDMS

Specimen records are stored as a hierarchy of related participant, enrollment, and information. All of this information for a participant-project combination comprise a record in LDMS.

A *specimen record* in LDMS is the collection of specimen, study, and visit information for a specific participant.

**Figure 9: Contents of a specimen record**



The top of a specimen record represents the largest part, such as a clinical trials network; the right side of this image is an example of each item


- project** The organization that sponsors or conducts the study in which the participant is enrolled.
- participant** The person (or specimen source if the project doesn't work with human samples) that is participating in a given project. If a person is participating in more than one project, they will be considered two different participants in each project. Participants cannot be linked across projects.
- enrollment** The protocol or study in which the participant is enrolled.
- visit** A specific event at which a primary specimen was collected from a participant.
- primary specimen** The specimen that was collected from the participant, such as an unprocessed tube of blood
- aliquot** A specimen that was created by processing a primary specimen into a smaller specimen.



Each part of a specimen record is selected in sequence. For example, you must specify a project before enter participant information. Likewise, you must create the information for a visit event before you can add specimens that were drawn at that visit.

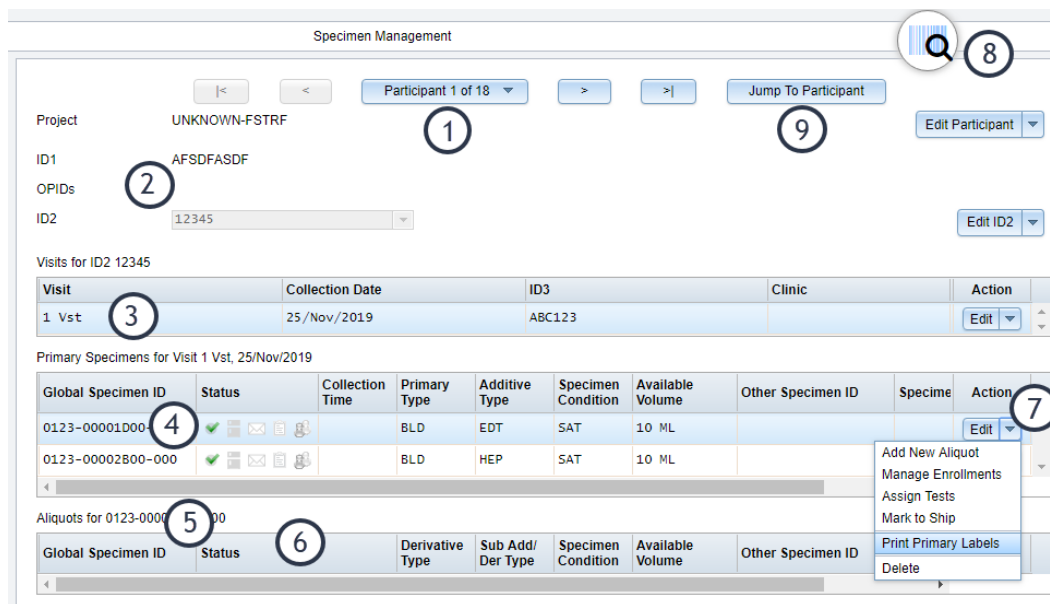
## Using the Specimen Management page

The **Specimen Management** page shows all of the visits for a specific participant and protocol combination.



 **Important:** The labels for certain buttons and menus in LDMS vary based on the project. For one participant, for example, the unique participant identifier (ID) may be called "PID"; for another project it may be "PanelID".

The main work area of the Specimen Management page will display the all the visits and associated specimens for a participant. Use the navigation buttons to change between different participants.

**Figure 10: The Specimen Management page**



- (1) Navigate between participants, (2) The current participant enrollment information, (3) Visits for the current participant, (4) Primary specimens for the currently selected visit, (5) Aliquot specimens derived from the currently selected primary specimen, (6) Specimen status indicators, (7) Actions for a primary (8) Indicator that you can scan a barcode to search for a record, (9) Jump directly to a participant

Status Icon	Meaning
	Specimen is available
	Specimen is assigned a storage location

Status Icon	Meaning
	Specimen has been marked to ship to another laboratory
	Specimen is on a pending shipment to another laboratory
	Specimen has been shipped to another laboratory
	Specimen has an additional enrollment
	Specimen has an additional enrollment

Objective	Action
Change participants	Click the navigation buttons at the top of the screen.
View the visits for a different study that the participant is enrolled in	Select the study from the <b>Study</b> drop-down box. If the <b>Study</b> box is disabled, then the participant is only enrolled in one study.
See the primary specimens associated with a visit	Click a visit from the <b>Visits</b> section of the page.
See the aliquots associated with a primary specimen	Click a primary in the <b>Primary Specimens</b> section.
Search for a specific participant	Use the filters on the left-side of the page.

## Entering specimen information (Overview)

Records are added to LDMS from the top-down, starting with the creation of a new participant.

### Background

Because records in LDMS are hierarchical, you need to enter information starting with a participant, and then work your way down to aliquot specimens.

There are two ways to enter participant, enrollment, and specimen in LDMS:

- Using the Quick Add feature (recommended)
- Adding new participant, enrollment, and specimen information one-by-one

For most data entry in LDMS, the Quick Add feature is strongly recommended since it allows you to enter all of the information at once. Adding individual items on the **Specimen Management** page is recommended for minor changes, such as adding a single aliquot specimen to a primary specimen.

Each of the steps below can be completed independently, provided that the previous steps were completed. For example, you can create a new participant in LDMS without enrolling that participant in any protocols or creating any associated visits, however you cannot create a generic enrollment that is not associated with a specific participant visit. Likewise, it

is also not possible to create a primary specimen without associating it with a specimen participant's visit.

### Steps

- 1.** Create a new participant.  
Participants are specific to a project. If a person is participating in more than one project, then they would be considered two different participants in LDMS and would be entered separately.
- 2.** Add an enrollment to the participant.  
This means that you are associating the participant with a specific protocol. Participants can be associated with multiple protocols.
- 3.** Add a visit to the participant.
- 4.** Add a primary specimen to the visit.
- 5.** Add aliquots that were processed from the primary specimen.

## Participants

---

A participant is the source for a specimen entered into LDMS.

The participant is typically a person enrolled in a study. Similar terms that you may be familiar with include "patient" and "source". In LDMS, a participant refers to all of these concepts. This means that a participant does not necessarily need to be a person. For example, a "participant" may be a control sample from which a specimen was created.

In LDMS, a participant will be the first thing that you create when adding a new *specimen record*. Newly created participants must be associated with a project and an ID1 (or participant identifier).

If a person is taking part in more than one project, that person will be considered two different participants in LDMS.

### Participant identifiers

A participant identifier is a series of numbers and letters that uniquely identifies a participant within a specific project.

A participant identifier is called "ID1" in LDMS until you select a project for the participant. Each project will have a different name for ID1. For one project, it may be called "PID"; for another project, it may be called "PANEL".

### Adding participants using the Specimen Management page

A new participant can be created on the **Specimen Management** page or the **Quick Add** page. This section explains how to add them on the Specimen Management page.

### Background

A new participant can be created two ways:

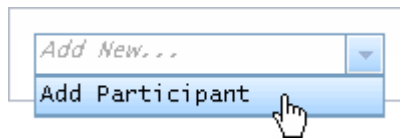
- If you want to create a new participant without any enrollments or visits, use the **Specimen Management** page.
- If you want to create a new participant allow with an associated visit and specimens, use the **Quick Add** feature.

The Quick Add feature requires you to enter at least one visit date with the participant. If the participant has not yet had a visit, you must use the Specimen Management page.

### Steps

1. From the LDMS menu bar, click **Specimen Management**.
2. From the action menu in the top-left of the page, click **Add Participant**.

**Figure 11: The action menu with Add Participant selected**



3. From the **Project** box, select a project.

### Example

**Figure 12: The Create Participant page**

A screenshot of the 'Create Participant' form. The form has the following fields and elements:

- Project:** A dropdown menu with '[Example Project]' selected and a red asterisk to its right.
- {ID1}:** A text input field containing '0111111C'.
- OPIDs:** A text input field with an 'Add OPID' button to its right.
- OPID Table:** A table with two columns: 'OPID' and 'Action'. It contains one row with the value '1693951990' in the 'OPID' column and a 'Delete' button in the 'Action' column.
- Buttons:** 'Save' and 'Cancel' buttons at the bottom.

4. In the **ID1** box, enter the participant's identifier.  
The label for the **ID1** box will vary by project. In the example above, ID1 is "PID".
5. Optional: In the **OPIDs** box, enter an *other participant identifier*, and then click **Add OPID**.  
More than one OPID can be added for the same participant. To remove an OPD that was added, click the **Delete** button to the right of it.
6. Click **Save**.

If the project has validation checks for ID1, they will be run at this time. If the ID1 that you entered is not valid for the project, you will be prompted to correct it before you can save the new participant.

If the project and participant identifier combination already exists, you will be asked if you want to view that participant instead.

### Result

The new participant will be created and added to the end of your laboratory's database. For example, if your laboratory previously had 250 participants, the new participant will be 251. LDMS will automatically open the record for the newly created participant so that you can add enrollment information.

## Adding participants using Quick Add

The Quick Add feature can be used to add a new participant, along with other information, on a single page.

### Background

If adding a participant in this way, at least one visit must have occurred as the date of the visit (the **Collection Date**) is required.

### Steps

1. From the LDMS menu bar, click **Specimen Management > Quick Add**.
2. Optional: Select a template for the participant visit.
3. Complete the information in the **Participant Information** section.
4. In the **Visit Information** section, enter the **Collection Date**.
5. At the bottom of the page, click **Add**.
6. Optional: Complete any additional enrollment, visit, or specimen information for this participant.

### Result

When the participant is successfully created, a note will appear at the top of the page. The participant will be available for select on the **Specimen Management** and **Quick Add** pages, where new enrollments, visits, and specimens can be added.

## Modifying a participant


Modify participants on the **Specimen Management** page.

### Background

A *participant* may need to be modified to correct an error in the ID1 that was entered, or to add and remove *OPIDs* as needed.

### Steps

1. Click **Specimen Management** from the LDMS menu.
2. Find the participant to be modified. This can be done by following one of the two sets of steps below:

- Use filters from the left side of the screen to narrow down the participants that are displayed.
  - Alternatively, click **Jump to Participant** and enter the appropriate project and participant ID, then click **Jump To**.
3. With the participant open in the work area, click the **Edit Participant** button.  
The **Edit Participant** window will open.
  4. Modify any participant information as needed.  
 **Note:** Edits made here will change all specimens associated with the participant.  
  
The **Enrollments** section of this window was not present when the participant was first created. It lists protocols in which the participant is enrolled, and provides a link to view and modify that enrollment, if needed.
  5. Click the **Save** button.  
If you modified the participant identifier, LDMS will check to ensure that it does not already exist for another participant.

---

## Enrollments

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An enrollment associates a participant with a protocol.

For example, a participant in the *Frontier* project may be participating in a study called F1526. The combination of that participant identifier on that study is called the *enrollment*.

A protocol is called ID2 in LDMS. Like ID1 for participant identifiers, the name for ID2 will vary, depending on the project. For example, a vaccine project may call the protocol box in LDMS "STUDY", whereas a pharmacology project may call it "TEST PANEL".

Also like ID1, a project may have rules for how its ID2 is formatted. For example, a vaccine project may require that protocols are in the format "STUDY 201", "STUDY 202", and so on; a pharmacology project may use "TEST PANEL A0003", "TEST PANEL A0004", etc. If the project has specified these rules, they will be enforced by LDMS.

A participant can be enrolled in more than one ID2 for a project, however because participants are specific to a project, they cannot be enrolled in protocols across multiple projects.

### **Adding enrollments using the Specimen Management page**

Enrollments are added to an existing participant, and associate that participant with a specific protocol.

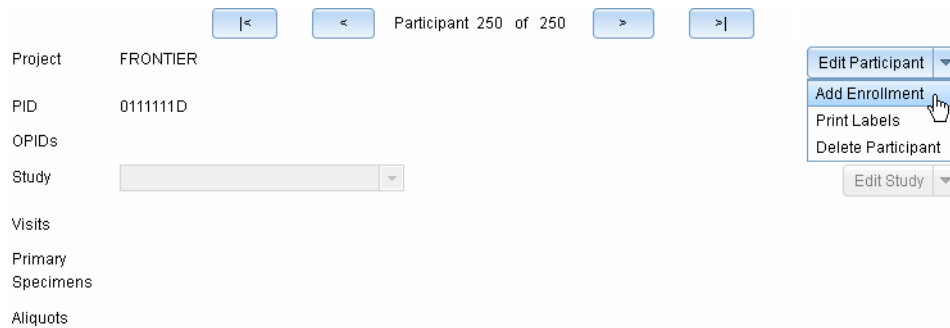
#### **Prerequisites**

The participant must already exist in LDMS before an enrollment can be added.

## Steps

1. From the LDMS menu bar, click **Specimen Management**.
2. Find the participant.  
Use filters from the left side of the page to narrow down the participants that are displayed.
3. From the **Edit Participant** menu, click **Add Enrollment**.

**Figure 13: Adding a new enrollment to a participant**



In this image, ID2 is called "Study"

The **Create Enrollment** window will open.

4. Select or enter an **ID2** in the box.  
The label for this box will vary, depending on the project. It is most commonly called **Study** or **Protocol**.
5. Click **Save**.

## Result

The participant is now enrolled in the protocol. You will see the protocol listed in the **ID2** box.

## After you are finished

If the participant is enrolled in more than one protocol for a project, you can create additional enrollments in the same way.

## Modifying enrollments

Participant enrollments can be modified or removed after they are created on the **Specimen Management** page.

## Prerequisites

- If removing an *enrollment* from a *participant*, the enrollment must not have any associated *visits*.
- If you accidentally added a visit and specimens to the enrollment in error and you want to preserve them, co-enroll the specimen(s) in another enrollment first so that the erroneous enrollment can be removed.

## Background

The only property of an enrollment is the associated *ID2*. If the incorrect *ID2* was selected when the enrollment was created, you can change it. Doing so will add the participant to a new enrollment, not change the existing. For example, if a participant is currently assigned an *ID2* of *STUDY3*, and you change it to *STUDY4*, this change will only affect this participant, not all participants in *STUDY3*. If the enrollment was added in error, it can be deleted instead.

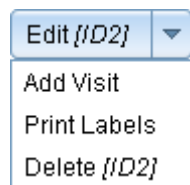


**Note:** Enrollments can also be modified using Quick Add.

## Steps

1. In the LDMS menu bar, click **Specimen Management**.
2. Find the participant with the enrollment to be modified.  
Use filters from the left side of the screen to narrow down the participants that are displayed.
3. Select the *ID2* from the **[ID2]** box.  
The label for the **[ID2]** box will depend on the project. Common labels are "study" and "protocol".
4. To modify the enrollment:
  - 4.1. Click **Edit [ID2]**, where "[Protocol]" is the appropriate label for the project.
  - 4.2. Modify the enrollment as needed.
  - 4.3. Click **Save**.
5. To remove the enrollment:
  - 5.1. From the **Edit [ID2]** menu, click **Delete [ID2]**.

**Figure 14: The Edit Study menu**



In this image, *ID2* is "Study"

- 5.2. Click **Delete**.

## Visits

A visit is a specimen collection event associated with an enrollment.

A visit typically involves the collection of specimens defined by the protocol. For example, a visit may specify that you collect 3 tubes of blood from the participant. In LDMS, you would add the visit to the participant, and then add the specimens to the visit.



## Visit identifiers

A visit identifier defines the type of visit.

A visit is identified by two pieces of information: the *visit value* and *visit unit*. The visit value is a sequential identifier, such as a number. The visit unit is the type of *visit*.

For example, a visit of “3 WK” indicates that it is the third visit of the week type. The 3 is the visit value, and WK is the visit unit. The protocol in which the participant is enrolled likely has defined specimen collections for this visit.


The available visit units are defined by various projects that use LDMS. Users cannot create their own visit units.

## Adding a visit to an enrollment

Visits are added to an enrollment on the **Specimen Management** page.

### Background

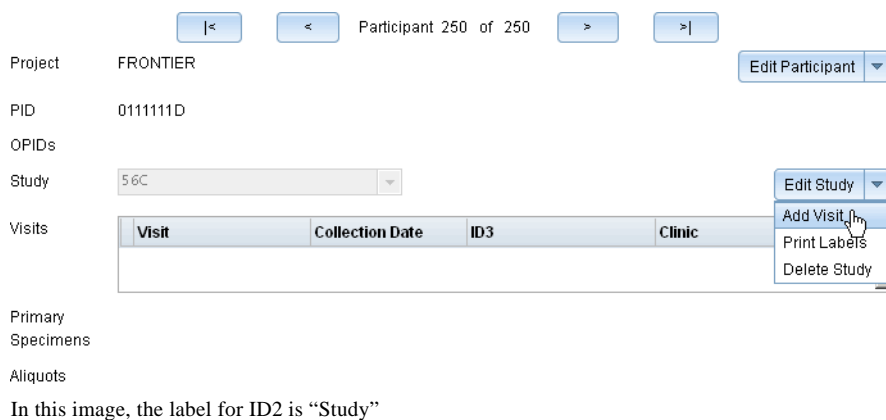
A visit must be created before you can enter specimen information in LDMS.

 **Tip:** If you want to create a new visit for a specimen that already exists, you should co-enroll the primary specimen instead of adding a new visit to the enrollment. During the co-enrollment process, you will have the opportunity to create a new visit.

### Steps



1. Click **Specimen Management** from the LDMS menu bar.
2. Find the participant to which a visit will be added.  
Use filters from the left side of the page to find the participant.
3. Select the **[ID2]** from the list.  
The label for the **[ID2]** box will depend on the project. Common labels are “study” and “protocol”.
4. Click the down arrow next to the **Edit [ID2]** button, and then click **Add Visit**.

**Figure 15: The Edit Study menu**



The **Add Visit** window will open.

**Figure 16: The Add Visit window**

5. Select the clinical site where the visit occurred from the **Clinic** list.  
If you want to know the name of the site, hover over it with the mouse pointer.  
 **Note:** The list of clinics and clinic ID numbers are maintained by Frontier Science and cannot be modified by users. For more information, contact LDMS User Support.
6. (If required by the project) Select the *ID3* from the **ID3** list.  
*ID3* is typically used for a sub-study or sub-protocol.
7. Select the date that the visit occurred or will occur from the **Collection Date** list.  
If the visit occurred or will occur over more than one day, you must add a new visit for each date.  
 **Note:** Future dates are allowed in the **Collection Date** field.
8. Enter the *visit value* and *visit unit* for the visit into the **Visit Value** boxes.  
If you want to see what a particular visit unit means, hover over it with the mouse pointer.
9. Click the **Save** button.

## Modifying visits

Visit information is modified or removed on the **Specimen Management** page.

### Background

You may need to modify a visit after it is created to correct an entry error (for example, using the incorrect clinic). If the visit was added in error, you can also remove it.

## Steps

1. Click **Specimen Management** > **Available Specimens** from the LDMS menu bar.
2. Find the participant with the visit to be modified.  
Use filters from the left side of the screen to narrow down the participants that are displayed.
3. Select the *protocol/ID2* associated with the visit from the **[Protocol]** box.  
The label for the **[Protocol]** box will depend on the project. Common labels are "study" and "protocol".
4. To modify the visit:
  - 4.1. Click the **Edit** button to the right of the visit.  
The **Edit Visit** window will open.
  - 4.2. Modify the visit information as needed.  
If a primary specimen has already been entered for the visit, it will be listed along with the visit information.
  - 4.3. Click the **Save** button.
5. To remove the visit, select **Delete** from the **Edit** menu to the right of the visit.  
In order to remove the visit, there must be no primary specimens added to it. If you want to remove a visit without deleting the primary specimens, you can co-enroll the primary specimen. This will allow you to associate the specimen with another visit.

## Primary specimens

---

A primary specimen is a specimen that was collected from a participant during a visit.

Primary specimens are generally larger specimens that are later processed into smaller specimens called aliquots. New primary specimens are added to LDMS on the **Specimen Management** page. They are always associated with at least one participant visit.

## Specimen identifiers

All specimens in LDMS are assigned a unique specimen identifier.

There are three types of specimen identifiers that can appear in LDMS:

**global specimen ID** This is a unique identifier assigned to all specimens.

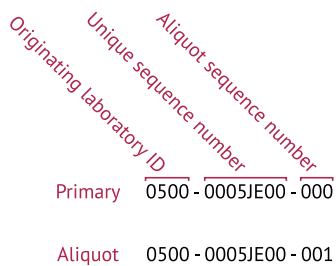
**specimen ID** This identifier may or may not be unique. It is only used by LDMS; LDMS will not assign a *specimen ID* to specimens added using LDMS.

**other specimen ID** This identifier is intended for laboratories to use to assign their own, internal-use identifiers as needed.

**Important:** LDMS for Windows and LDMS use different formats for the global specimen ID. The format used by LDMS is longer, and contains the originating laboratory’s ID. For example, the global specimen ID “0500-0005JE00-000” indicates that the specimen originated from LDMS laboratory 500.

The global specimen ID assigned by LDMS links a primary specimen to any aliquot specimens created from it. Primaries and aliquots derived from them will have the same global specimen ID up to the dash character. The last three numbers are the sequence number. A sequence number of “-000” indicates that the global specimen ID belongs to a primary specimen; any other number indicates that it belongs to an aliquot specimen.

**Figure 17: The global specimen ID of primary and aliquot specimens**



This image shows the relationship between a parent primary and aliquots derived from it.

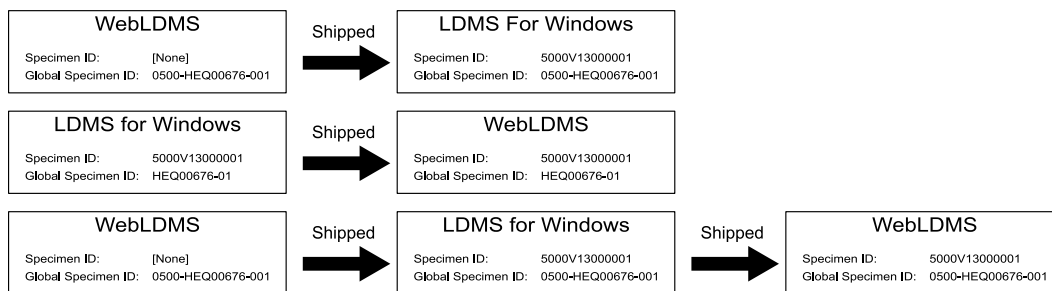
### Specimen identifiers in LDMS for Windows

LDMS for Windows handles specimen identifiers in a few ways that differ from LDMS.

Understanding the differences between the way LDMS and LDMS for Windows assign specimen identifiers is important if your laboratory does work with other laboratories.

LDMS will not assign a *specimen ID* to a specimen and will only assign a *global specimen ID*. LDMS for Windows will assign both. The format of the global specimen ID differs as well, depending on which system assigned it.

**Figure 18: Specimen ID and global specimen IDs interoperability**



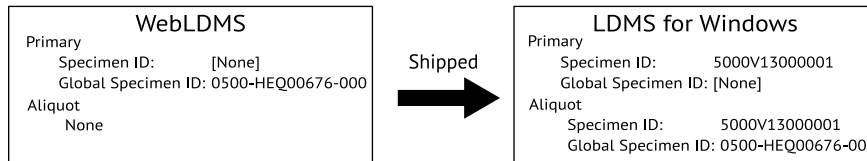
This image shows how specimen IDs and global specimen IDs are affected as specimens are shipped between LDMS and LDMS for Windows.

The global specimen ID of a primary specimen can be different. LDMS for Windows does not permit the shipping or storage of primary specimens;

these are features that are exclusive to LDMS. In LDMS for Windows, users would generally create aliquots (commonly called “ghost aliquots”) that were identical to the primary specimen; the aliquot (which was really just the primary) could then be shipped and stored.

When a primary specimen is shipped to LDMS for Windows, an aliquot will automatically be created. This aliquot will have the global specimen ID of the primary specimen, and the primary specimen ID will have no global specimen ID.

**Figure 19: Primary specimens shipped to LDMS for Windows**



This image shows how a primary specimen without aliquots created in LDMS is converted to an aliquot if shipped to an LDMS for Windows laboratory.

In this situation, if the new aliquot is shipped to a laboratory that uses LDMS, it will recognize that the global specimen ID belongs to a primary specimen (and not an aliquot), and will turn it back into a primary specimen.

### Adding a primary specimen to a visit

A new primary specimen is added to a visit on the **Specimen Management** page.

#### Background

A primary specimen is added to an existing visit. The primary specimen can be added in LDMS even if it has not yet been processed into any aliquots.

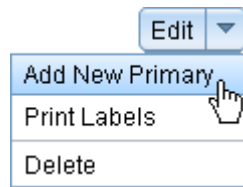
#### Steps

Locate and select the visit

1. Click **Specimen Management** from the LDMS menu.
2. Find the participant to which the primary specimen will be added. Use filters from the left side of the screen to narrow down the participants that are displayed.
3. Select the ID2 associated with the visit from the **[ID2]** box. The label for the **[ID2]** box will depend on the project. Common labels are “study” and “protocol”.

Add the new primary specimen

4. Click the down arrow next to the **Edit** button to the right of the visit to which the primary will be added, and then click **Add New Primary**.


**Figure 20: Adding a new primary to a visit**

The **Create Specimen** window will open.

5. Fill in the information for the new primary specimen.  
Items marked with a red \* are required.
6. Optional: Enter additional information about the primary specimens into the **Comments** box.  
Information that is typically included here includes details for specimens that were not collected, an explanation of a condition, or an explanation of why a specimen is not available.
7. Optional: Enter additional information about the primary specimens into the **Internal-only comments** box. These comments will be included if the specimen's information is shipped to another laboratory. Comments entered here is for your laboratory's use only. These comments will not be included if the specimen's information is shipped to another laboratory.
8. At the bottom of the window, click **Save**.  
The information you entered will be checked for completeness and validity. If there is an issue with one of your entries, it will be highlighted with a brief explanation of how to correct it.

### Result

A new primary specimen is now available. It will automatically be assigned a global specimen ID ending in "-00" by LDMS.

-  **Note:** The new primary will not have a specimen ID assigned to it. Specimen ID is only used by LDMS; LDMS uses the global specimen ID, not specimen ID, to identify specimens

### After you are finished

If the primary was collected for more than one protocol or project, you must also co-enroll the specimen so it is associated with each applicable visit.


### Co-enrolling a primary specimen

Co-enrolling is the process of associating a primary specimen with more than one visit or protocol.

## Background

A participant may be participating in two different protocols at the same time, and a single primary specimen might be collected to meet the needs of a visit from each protocol.

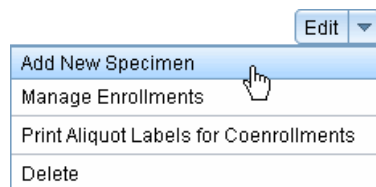
You can also co-enroll a primary specimen to move it between visits. This might happen, for example, if you selected the wrong visit for the primary specimen, and you want to move it to the correct visit rather than deleting it.

 **Note:** If a specimen is co-enrolled in a local project and a government project, when shipping specimens for the government project, information about the co-enrollment will not be included in the shipment.

## Steps

1. In the menu bar, click **Specimen Management**.
2. Local the specimen to be co-enrolled.  
Use filters from the left side of the screen to narrow down the participants that are displayed.
3. Click the down arrow next to the **Edit** button to the right of the primary to be co-enrolled, and then click **Manage enrollments**.

**Figure 21: The Edit button for a primary**



The **Manage Enrollments** window will open.

**Figure 22: The Manage Enrollments window**

Collection Date  \*

**1** Add Enrollment

Project	ID1	ID2	Visit Value	Action
FRONTIER <b>2</b>	123456	METABOLIC	0	Remove
FRONTIER	123456	56C	1	Remove

Selected Enrollment

Project  \*

**3** Note: specimens enrolled in only non-exportable projects may only be co-enrolled with other non-exportable projects.

PID  \*

Study  \*

Visit Value

Visit Units

ID3

Clinic

**4** Update

Aliquots **5**

Specimen ID	Global Specimen ID	Action
500V13000008	HEQ0067G-01	Edit
500V13000008	HEQ0067G-02	Edit
500V13000008	HEQ0067G-03	Edit

Save Cancel

(1) Add a blank enrollment row, (2) Enrollments for this primary specimen, (3) Details for currently selected enrollments, (4) Save changes to currently selected enrollment, (5) All aliquots derived from this primary, including all enrollments

- 4.** Click the **Add Enrollment** button.
- 5.** Select the blank row created in the previous step by clicking on it.
- 6.** Fill in the information in the **Selected Enrollment** section for the new enrollment.
- 7.** Click **Update**.  
The information for the enrollment will be updated in the list of enrollments.
- 8.** At the bottom of the window, click **Save**.

### Modifying a primary specimen

A primary specimen can be modified on the Specimen Management page.



## Background

After a primary has been created, it may need to be modified for a variety of reasons, such as correcting a data entry error or updating its current condition.

## Steps

1. Click **Specimen Management** from the LDMS menu.
2. Find the participant with the primary specimen to be modified.  
Use filters from the left side of the screen to narrow down the participants that are displayed.
3. Select the *protocol/ID2* associated with the *visit* from the **[Protocol]** box.  
The label for the **[Protocol]** box will depend on the project. Common labels are "study" and "protocol".
4. Click the **Edit** button to the right of the primary specimen to be modified.  
The **Edit Specimen** window will open.
5. Modify the primary specimen as needed.  
If any aliquot specimens were added for this primary, it will appear at the bottom of the window.
6. Click the **Save** button.  
If there are any issues with the changes that you made, such as an invalid entry, you will be prompted to correct it. An explanation will appear next to the information that needs to be corrected.

## Aliquot specimens

---

An aliquot is a specimen that is derived from a primary specimen

An *aliquot* is created by processing the specimen collected at a participant's visit into smaller specimens. For example, if 10 mL of blood was collected during a visit, that 10 mL tube is the *primary specimen*. It may be processed then into smaller, 1 mL tubes of double-spun plasma. These 1 mL specimens are the aliquots in LDMS.

### Adding aliquots to a primary specimen

An aliquot specimen is added to a primary specimen on the Specimen Management page.

## Background

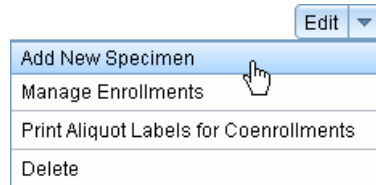
An aliquot is added to an existing primary.

## Steps

1. In the menu bar, click **Specimen Management**.

2. Find the participant by using filters on the left side of the screen.
3. Click the arrow next to the **Edit** button to the right of the primary to which the aliquots will be added, and then click **Add New Specimen**.

**Figure 23: Adding a new aliquot to a primary specimen**



The **Create Specimen** window will open.

4. Enter the number of aliquots that were created into the **Number of Aliquots** box.  
 When entering more than one aliquot together, all aliquots should have the same basic properties (such as the same volume). If you want to add multiple aliquots with different information, you can still do so, but you must edit the aliquots later. For example, if you have 3 aliquots that are identical, but one has a different **specimen condition**, you can add all three together, and then change the condition of the one aliquot when you are finished.
5. (If the primary is co-enrolled) Select the enrollment for the new aliquot from the **Enrollment** box.  
 An aliquot cannot be enrolled in more than one study.
6. Fill in the information for the new aliquot specimens.  
 Items marked with a red \* are required.
7. Optional: Enter additional information about the aliquot into the **Comments** box.  
 Information that is typically included here includes details for specimens that were not collected, an explanation of a condition, or an explanation of why a specimen is not available.
8. Optional: Enter additional information about the aliquot into the **Internal-only comments** box.  
 Comments entered here are for your laboratory's use only. These comments will not be included if the specimen's information is shipped to another laboratory.
9. At the bottom of the window, click **Save**.  
 The information you entered will be checked for completeness and validity. If there is an issue, it will be highlighted with a brief explanation of how to correct it.

### Result

The number of aliquots that you specified will be added to the participant visit. The primary specimen will automatically change to *unavailable* to indicate that the specimen was consumed during processing.

### After you are finished

If you added multiple aliquots and any of those aliquots differed from the others (such as one aliquot having a different condition), be sure to make those changes to the aliquot.

## Entering cryopreservation information

Cryopreservation information can be entered for aliquot specimens with the CEL derivative type (PBMC Cells, Viable).

### Steps

1. On the **Specimen Management** page, locate the specimen for which you are entering Cryopreservation information.
2. From the **Edit** button to the right of the specimen, click the down arrow, and then click **Cryopreservation**.  
This option will only be available for specimens with the derivative type CEL.
3. Do one of the following:
  - If results were obtained, select **Results Obtained**.
  - If results were not obtained, select the reason there are no results from the **Reason** list.
4. If results were obtained, complete the information in the **HIV Status**, **Primary Specimen Details**, **Aliquot Details**, and **Technician Details** sections
5. In the **Processing Tech Initials** box, enter the processing technician's initials.
6. In the **Data Entered By** box, enter your initials.
7. Click **Save**.

## Modifying aliquot specimens

You can modify individual aliquots specimens or modify multiple aliquot specimens together.

### Prerequisites

- All specimens to be modified must be from the same primary specimen.

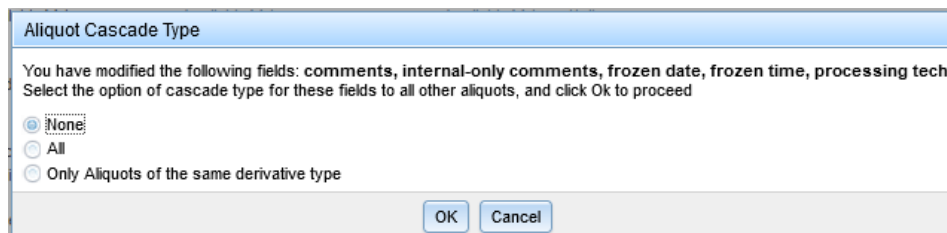
### Background

#### Steps

1. From the LDMS menu, click **Specimen Management**.
2. Locate the specimens you want to modify.
3. Select the aliquot specimens to modify.  
To select multiple aliquot specimens, press and hold the Ctrl key. To select multiple, contiguous specimens, press and hold the Shift key instead.

4. To the right of one of the selected specimens, click **Edit**.
5. (When editing multiple specimens only) In the **Edit Aliquots** window, select the check box next to any boxes you want to change.
6. Modify the specimen information as needed.
7. Optional: Making changes to **Frozen Date**, **Frozen Time**, **Processing Tech Initials**, **Comments** or **Internal Only Comments** for any single aliquot will give the user the option to cascade these changes to other aliquots. Changes can be cascaded to No other aliquots, All aliquots, Only aliquots having the same derivative type. Select an option and click **OK**.

**Figure 24: The Aliquot Cascade Type Window**



8. At the bottom of the **Edit Aliquots** window, click **Save**.

## Creating Subaliquots

Creating subaliquots is the process of making an aliquot from a pre-existing aliquot.

### Background

#### Steps

1. Scan the source aliquot barcode to find its record in **Specimen Management**.
2. In the **Visit** grid, click the **Edit** drop down menu, select **Add New Primary**.
3. In the **Create Primary Specimen** menu, add the following:
  - 3.1. Other Specimen ID - enter the Global Spec ID of the source aliquot into the field
  - 3.2. Additive
  - 3.3. Volume and Volume unit
  - 3.4. Collection Time
  - 3.5. Receive Time
  - 3.6. Adjust thaw counter
4. In the **Primary** grid, find the new Primary and use the **Edit** drop-down menu. Select **Add New Aliquot** and add the following in the **Create Aliquot** menu:
  - 4.1. Enter Derivative and Sub Add/Der Enter
  - 4.2. Volume and Volume unit



This option is only available if the specimen is assigned a storage location.

4. Optional: To change the specimen to *unavailable*, select **Set as Unavailable to be Stored Again**.
5. Click **Remove**.

## Quick add

---

The quick add feature allow you to create all of the specimens from a participant visit at once, and is the preferred method for entering new visits in LDMS.

If you add specimens to a participant on the **Specimen Management** page, you would need to add each primary and set of aliquots individually. The quick add feature allows you to select or create a participant and enrollment, create a new visit, and enter all of the specimens collected at that visit from one screen. For new visits, this significantly reduces the amount of time it takes to enter a new visit in LDMS. You can even create templates for common visits to save more time.

Once a template has been used, any visits or specimens that were created are not associated with the template. This means that if the template is later changed or removed, visits that were entered using the template won't be changed.

**Figure 25: Quick Add**

The screenshot shows the 'Quick Add' interface. On the left, there is a 'Template' dropdown (1) and 'Template Filters' (2) with options like 'Project', 'ID2', 'Visit', 'Visit Unit', and 'Visit Unit'. The main area is titled 'Template Comments' (3) and contains 'Participant Information' with fields for 'Project' (A000) (4), 'ID1' (with 'Add ID1' (5) and 'Upload ID1 File' (6) buttons), and 'OPIDs'. Below this is 'Enrollment Information' with an 'ID2' field, and 'Visit Information' with fields for 'ID3', 'Clinic', 'Collection Date', 'Visit Value', and 'Visit Units'. The 'Primary Information' section (8) includes an 'Add New' button (7) and a table for primary specimens:

#	Primary Type	Additive Type	Condition	Collection Time	Received Date	Received Time	Volume	Volume Units	Addit Time
1	BLD	ACD	SAT	HH:mm	24/Jun/2021	HH:mm			

Below the primary specimens table is an 'Aliquots for Primary #1' section with an 'Add New' button and a table for aliquots:

Total Aliquots	Derivative Type	Sub A/D Type	Condition	Volume	Volume Units	Other Specimen ID
1		N/A	SAT			

(1) Select and apply template for Quick Add entry, (2) Filter list of templates, (3) Instructions applicable to selected template appear here, (4) Select project and ID1, (5) Add ID1 button used to add multiple ID1s simultaneously, (6) Upload list of ID1s, (7) Add new primary specimen row, (8) Primary specimens, numbers for convenience

## Adding specimens using Quick Add

Quick Add is used to enter information for a participant, enrollments, and multiple specimens all on one page.

### Background

This is useful when you want to enter a lot of information for a participant at once. Templates (if available) can be used to fill in predefined information for you.

### Steps

1. From the LDMS menu bar, select **Specimen Management > Quick Add**.
2. Optional: From the **Template** list, select a template to apply.

Use the **Template Filters** to narrow down the list of templates. When you apply a template, a message with further instructions will appear.

**⚠ Warning:** Applying a template will clear any information you already entered on the **Quick Add** screen. In addition, once the template is applied, you cannot change projects unless you apply a different template or click **Clear Template**.

3. Optional: Complete the **Participant Information**.
  - 3.1. Select the project from the **Project** box.
  - 3.2. Select the **ID1** for the participant *or* enter a new ID1 if you are adding a new participant.
  - 3.3. To add multiple PIDs, click **Add ID1** or **Upload ID1 File** for each selected ID1
4. Complete the **Enrollment Information** by selecting an **ID2** *or* by entering a new ID2.
5. Complete the **Visit Information** section.
6. Optional: Add a primary specimen.
  - 6.1. In the **Primary Information** section, click **Add New**.
  - 6.2. In the row that appeared, enter the information for the primary specimen to be created.
  - 6.3. Optional: To view and modify all of the information for the primary, click **Edit** in the right column.
7. Optional: Add an aliquot specimen.
  - 7.1. Highlight the primary specimen for the aliquot.
  - 7.2. In the **Aliquot Information** section, click **Add New**.
  - 7.3. In the row that appeared, enter the information for the aliquot specimen to be created.
8. At the bottom of the page, click **Add**.

### **Adding participants using Quick Add**

The Quick Add feature can be used to add a new participant, along with other information, on a single page.

#### **Background**

If adding a participant in this way, at least one visit must have occurred as the date of the visit (the **Collection Date**) is required.

#### **Steps**

1. From the LDMS menu bar, click **Specimen Management > Quick Add**.
2. Optional: Select a template for the participant visit.
3. Complete the information in the **Participant Information** section.
4. In the **Visit Information** section, enter the **Collection Date**.
5. At the bottom of the page, click **Add**.



6. Optional: Complete any additional enrollment, visit, or specimen information for this participant.

### Result

When the participant is successfully created, a note will appear at the top of the page. The participant will be available for select on the **Specimen Management** and **Quick Add** pages, where new enrollments, visits, and specimens can be added.

## Adding enrollments using Quick Add

The Quick Add feature can be used to add an enrollment to an existing participant, along with other information.


### Prerequisites

The participant must already be added to LDMS before an enrollment can be added; enrollments cannot exist without being associated with at least one participant.

### Background

Using Quick Add to add an enrollment to a participant is especially useful if you want to enter other information at the same time, such as a visit or specimens.

### Steps

1. In the **LDMS** menu bar, click **Specimen Management > Quick Add**.
2. In the **Participation Information** section, select the **Project** and **ID1** for the participant.
3. In the **Enrollment Information** section, select or enter the enrollment.  
 **Note:** If you enter an ID2 that does not yet exist, it will be created.
4. Optional: Complete any additional visit or specimen information for this participant.
5. At the bottom of the page, click **Save**.

## TBD in quick add templates

The TBD code can be used in quick add templates for certain sections that might need to be completed when the template is used.

For example, you may need create a template for a visit where the additive time used for a primary specimen varies based on certain factors. In these situations, using the **TBD** code will require the user to select the correct code when the template is used.

### Places where TBD can be used in quick add templates

- Primary type

- Additive type
- Derivative type
- Sub A/D type

## Quick add templates

Quick add templates are predefined specimen entry scenarios (typically for specific study visits) that can be used to automatically create some default specimens.

Templates are best used for specific study visits to create the expected specimen collections for the visit. They can also be used to complete other information, such as the ID2 and project that would be the same whenever the template is applied.

There are two types of templates: templates created by Frontier Science and templates that are created by your laboratory. Templates created by Frontier Science are designed in collaboration with leadership for projects and cannot be modified by users. Templates created by users at your laboratory can be modified. User-created templates are only available at the laboratory where they were created; they are not shipped or sharable with other laboratories.

Regardless of the type, once a template is applied, you will be prevented from changing the participant's project (meaning you can't apply a template intended for one project, and then change the project, effectively using the template for a project for which it wasn't intended). In addition, when you apply a template, any information that you already entered on the Quick Add screen will be cleared. This means that the template must be applied first, before you enter any other information.

### Creating quick add templates

Create quick add templates by defining the information for the visit.

#### Steps

1. From the LDMS menu bar, click **Specimen Management > Quick Add Templates**.
2. Complete the **Template Information** section.  
The **Name** is the name of your template as it will appear when selecting it when using the quick add feature. The **Comments** is a brief description of the template that will appear when the template is selected, and can be used to provide the person entering data if additional information or instructions, such as a reminder to remove an optional specimen if it was not collected.
3. In the **Participant Information** section, select a **Project**.
4. Optional: In the **Enrollment Information** section, select an **ID2** to be applied.
5. Optional: In the **Visit Information** section, select an **ID3** to be applied.



**Important:** Either an ID2 or ID3 **must** be applied in order for the template to be created. Alternatively, both an ID2 and ID3

can be applied. These cannot be edited once the template has been triggered.

6. Optional: Add a primary specimen.
  - 6.1. In the **Primary Information** section, click **Add New**.
  - 6.2. In the row that appeared, enter the information for the primary specimen to be created.
  - 6.3. Optional: To view and modify all of the information for the primary, click **Edit** in the right column.
7. Optional: Add an aliquot specimen.
  - 7.1. Highlight the primary specimen for the aliquot.
  - 7.2. In the **Aliquot Information** section, click **Add New**.
  - 7.3. In the row that appeared, enter the information for the aliquot specimen to be created.
8. At the bottom of the page, click **Save Template**.

### **Modifying or deleting a quick add template**

Quick add templates can be changed or deleted without affecting specimens added using the template.

### **Background**

When a template is modified, the changes will be reflected when new visits are created using the template; existing entries will not be changed. If a template is deleted, it will be permanently removed, however any entries made using the template will remain.

### **Steps**

1. From the LDMS menu bar, click **Specimen Management > Quick Add Templates**.
2. In the **Saved Templates** box, select the template to be modified or deleted.
3. Do one of the following:
  - Make any changes to the template, and then click **Save Template** at the bottom of the page.
  - At the bottom of the page, click **Delete Template**.
  - Click "**Make Copy**" to make edits to a copy of the selected template while preserving the original template.

## **Differences between primaries and aliquots**

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This section describes the differences between how LDMS treats primaries and aliquots.

**Table 3: Primary and aliquot comparison**

	<b>Primary</b>	<b>Aliquot</b>
Global Specimen ID	Ends in -00	Ends in -01, -02, etc.
Processing date	Entered by user	Uses value from primary
Enrollment	Can be associated with more than one visit or protocol	Must select exactly one associated enrollment

Certain information can be cascaded from primaries to derived aliquots specimens, so that if the primary is updated users will be asked if they want to update the aliquots as well.

- Frozen date
- Frozen time
- Comments
- Internal comments
- Tech initials

If a comment is cascaded from a primary to an aliquot, it will be added to any existing comment the aliquot already has.


## Specimen availability

---

Availability refers to whether or not a specimen exists at a laboratory.

A specimen’s physical availability may change for a variety of reasons. For example, if a primary specimen was processed into aliquots, the primary specimen no longer exists and is thus not available. Likewise, if an aliquot’s tube was damaged and its contents could not be recovered, it is also not available.

If a specimen is available, it can be added to a shipment and it can be assigned a storage location. If it is not available, LDMS will prevent you from shipping or storing the specimen.

 **Note:** In LDMS for Windows, availability is called “never store”.

Availability is a property of both primary specimens and aliquot specimens. By default, new specimens are available until you change them to unavailable or a specific condition automatically changes them.

There are several times where LDMS will automatically modify a specimen’s availability. There are other places where you can manually change availability.

- You can manually change the availability of both primary and aliquot specimens, unless the specimen has been shipped.
- Specimens will automatically become unavailable if they are shipped.
- If a specimen’s volume changes to zero, it is automatically made unavailable.

- A primary specimen will automatically become unavailable after aliquots have been derived from it, and you cannot change it back to available unless the aliquots are deleted.
- Certain condition codes, such as DSR (destroyed) will automatically change a specimen to unavailable.

**Table 4: Specimen conditions that modify availability**


Code	Description
ANM	Sample Anonymized
ANP	Aliquot Not Prepared
CDT	Consumed During Testing
DSR	Destroyed
LSH	Lost Shipment
QNS	Quantity Not Sufficient
SNC	Sample Not Collected
SNP	Sample Not Processed
SNR	Sample Not Received

## Specimen record details

This section describes each specimen record entry box that appears on the Specimen Management page.





Field	Usage	Example	Notes
Additional Time	A value and a unit	4 Hrs	Used to indicate information such as the amount of time a participant was fasting. Typically used for Pharmacology specimens to indicate the amount of time after the last dosage was taken.
Additive Type	The additive in the primary collection tube	EDT	Selected from a pre-defined list of codified values. If there was no additive in the tube, use <b>NON</b> . Hover the mouse pointer over an additive for a more detailed description.
Additive Reagent			
Aliquots	List of any aliquots for the selected Primary Specimen	-	Displays the same specimen overview grid as seen on the <b>Specimen Management</b> page, specific to the primary's aliquots only. Aliquots can be edited from this window by clicking the <b>Edit</b> button.
Assigned Tests			

Field	Usage	Example	Notes
Available Volume	A value and a unit	1.00 ML	Used to indicate the volume of the sample available for use. Hover the mouse pointer over the units for a more detailed description.
Clinic	The clinical site where a visit occurred	102	Select from a pre-defined list. For a description of a clinic, such as its name, hover the mouse pointer over it.
Collection Date	The date that a visit occurred	02/Apr/2014	This will typically be one day. If a visit occurred over multiple days, each event will be considered a separate visit and listed as separately in LDMS. They will still, however, have the same visit value and visit unit.
Collection Time	The time that the specimen was collected	13:30	This time should be the local time for the clinical site, and be in 24-hour format. In LDMS for Windows, collection time is known as specimen time
Comments	Additional details about the specimen		Used to provide additional information, such as an explanation of a specimen's current condition. This comment will be included if the specimen data is shipped to another laboratory.
Derivative Type	The type of aliquot specimen created	PL2	Selected from a pre-defined list of codified values. Hover the mouse pointer over a type for a more detailed description.
Enrollment	The project-ID2 combination associated with an aliquot	project/ID2	The enrollment is in the format [project]/[ID2].
Frozen Date	The date the specimen was frozen	04/Jun/2014	This is generally used to indicate the date the freezing process began.
Frozen Time	The time the specimen was frozen	15:00	This is generally used to indicate the time the freezing process began.
Global Specimen ID	A unique identifier for the specimen	500-AEQ0052R-01	This will be unique for the specimen. LDMS will never generate the same global specimen ID, even at two different laboratories. Global specimen IDs for primaries always end in "-00"; global specimen IDs for aliquots will have the same ID as their parent primary, but end in "-01", "-02", and so forth. Specimens added in LDMS for the web will have the originating laboratory's ID number as the first 3 digits. Global specimen IDs generated by LDMS for Windows will lack this feature.

Field	Usage	Example	Notes
Harvest Date	Indicates the date that a culture derivative sample was harvested.	04/Jun/2014	-
ID3	A sub-protocol or study	A50250562I	Used by some projects to further identify the protocol. This is typically selected from a pre-defined list. For some protocols, a temporary value such as "NOSID" may be used until the exact value is assigned to the participant. For other protocols, this field may not be used or may be optional.
Imported	Indicates if the sample was received and if so, on what date.	Shipment 12 on 11/Aug/2005 or No	Link to <b>Received Shipment Review</b> page, if applicable.
Import Date	Date the shipment with the specimen was received	11/May/2016	If the specimen was not received in a shipment, this will be blank.
Internal-Only Comments	Additional details about the specimen		These comments will <i>not</i> be included if the specimen data is shipped to another laboratory.
Is Available	Indicates if the specimen is available		Availability means that the specimen exists and can be shipped, stored, and so forth. Reasons that a specimen might not exist include being destroyed or being shipped to another laboratory.
Owner Enrollment	The enrollment that "owns" a primary specimen	project/ID2	For primary specimens that have not been processed into aliquots, this is the enrollment that "owns" the specimen
Original Volume	Indicates the volume of the sample before any aliquots were created or tests were run	1.0 ML	-
Other Specimen ID	A laboratory-defined identifier		There are no rules or validation for this field; it can be used to assign a special identifier if needed by your laboratory.
Primary Type	The type of primary specimen	BLD	Selected from a pre-defined list of codified values. Hover the mouse pointer over a type for a more detailed description.
Processing Date	Date a primary specimen was processed into aliquot specimens	15/Oct/2012	Use local time. If present, the value entered for the parent primary specimen will be used for aliquots derived from the primary.

Field	Usage	Example	Notes
Processing Tech Initials	The initials of the person who processed a primary specimen into aliquot specimens	JD	If the processing tech initials are set for a primary, aliquots derived from the primary will receive those initials as well. You can change the initials for individual aliquots, if needed.
Processing Time	Time a primary specimen was processed into aliquot specimens	16:15	Use local 24-hour time. If present, the value entered for the parent primary specimen will be used for aliquots derived from the primary.
Reason Specimen Not Collected	Explanation of why an expected specimen was not collected during a visit	Specimen potentially compromised	Typically used in conjunction with a specimen condition code that indicates an issue with the specimen, such as "QNS" (quantity not sufficient). If necessary, use the <b>Comments</b> box for the specimen provide more details.
Received Date	The date the specimen was received by the processing laboratory where the primary was processed into aliquots	12/Mar/2014	-
Received Time	The time the specimen was received by the processing laboratory	14:45	Times should be entered in 24-hour local time.
Shipped	Whether the specimen has been shipped to another laboratory	Yes, no, or pending	Provides link to shipment, if applicable
Specimen Condition	The current condition of the specimen	SAT	Selected from a pre-defined list of codified values. Hover the mouse pointer over a condition for a more detailed description.
Specimen ID	A legacy specimen ID used only by LDMS	500V10000110	The specimen ID is an identifier for the specimen that was used by older laboratory management software. It will only be present for specimens that were entered or migrated from LDMS. Specimens created using LDMS will not be assigned a specimen ID.



Field	Usage	Example	Notes
Status	Icons indicating various properties about a specimen		 Specimen is available  Specimen is assigned a storage location  Specimen has been shipped to another laboratory  Specimen has an additional enrollment
Stored	Whether the specimen currently has a storage location assigned	Yes or no	Provides link to storage location
Sub-Additive/ Derivative			If the specimen does not have a sub-additive/derivative, select NON.
Thaw Count	The number of times the specimen has been frozen and thawed.	3	-
Total Cell Count	Total number of cells (in millions)	10	When entered, it will be multiplied by 1 million. For example, to indicate 10 million cells, enter 10; to indicate 500,000 cells, enter 0.5.
Tube Count	The number of primary tubes collected for the pooled sample	5	This field is used to record the number of primary tubes collected for the sample in scenarios where the tubes are pooled into a single sample when recording in LDMS.
Unavailable Date	The date the specimen is no longer available	12/Mar/2014	-
Visit Value	The protocol-defined identifier for a visit	1 Wk	This comprises of two boxes, a visit number and visit type. A visit value is typically a number or letter. The visit unit is selected from a pre-defined list. Hover the mouse pointer over a visit unit for a brief description.

## Specimen conditions

A specimen condition is a 3-letter code that indicates the status of a specimen.

Every *primary specimen* and *aliquot specimen* in LDMS has a condition assigned to it. The default condition for new specimens is SAT (satisfactory), but there are many others.

The majority of conditions indicate a deviation from the expected handling for a specimen. For example, if a specimen was supposed to be collected in one

type of tube but another was used, the INT (incorrect tube type) condition code could be used to indicate this.

There are several places where the condition of specimens can be changed:

- on the **Specimen Management** page, by editing an individual specimen
- when receiving specimen data from a shipping file
- on the storage page all specimens in a storage location can be modified

A common use for specimen conditions is indicating when an expected primary specimen was not collected. By setting the specimen's condition to an applicable code (such as QNS if not enough sample could be collected) and by entering descriptive comments, you can explain the omission of the expected specimens.


## Destroying a specimen

Specimen destruction is noted in LDMS by applying the `DSR` specimen condition.

### Background

When a specimen is destroyed, it is important to document that destruction in LDMS.

### Steps

1. From the menu bar, click **Specimen Management**.
2. Using filters on the left, locate the specimen to be destroyed.
3. To the right of the specimen, click **Edit**.
4. Change **Specimen Condition** to `DSR`.
5. (If the specimen has been assigned a storage location) Write down the storage location of the specimen, if it has not already been physically removed.  
 **Warning:** The specimen will automatically be un-assigned from its storage location in LDMS. This is your last chance to get the specimen's storage location.
6. In the **Comments** box, enter an explanation of why the specimen was destroyed.

### After you are finished

If you have not already done so, use the storage location that was noted by LDMS to find the specimen and physically remove it from storage. The specimen was automatically removed from storage in LDMS.

## Procedural conditions

These specimen condition codes describe issues that can occur in the collection and processing environment.

**Table 5: Procedural conditions**

Code	Description	Usage
ANP	Aliquot Not Prepared	Indicate that an expected aliquot was not processed, but no other more specific condition code applies. The <b>reason specimen not collected</b> box should be used in conjunction with ANP.
EQF	Equipment Failure	There was an issue with the processing equipment, such as a power failure during processing.
INV	Invalid	The specimen is not valid for testing purposes. Generally another condition code, such as LBE or PST, would be more appropriate.
LBE	Laboratory Error	The laboratory made a general error during processing, such as setting equipment up incorrectly or mislabeling specimens.
OPR	Outside Protocol Requirements	The specimen was drawn during the protocol-defined window, but not in a manner consistent with the protocol. For example, if a participant was supposed to be fasting but was not, this code would apply.
OSW	Outside Visit Window	The specimen was collected correctly, but outside the window for the visit as specified by the protocol.
PST	Processed After Specified Time	The specimen was collected and processed into aliquots, but the processing was done after the time frame specified by the protocol. This is commonly applicable for PBMC and pharmacology specimens.

### Specimen container conditions

These condition codes describe physical problems with the specimen's container. If there is a qualitative issue with the specimen as a result of the container issue, a qualitative code may be more appropriate.

**Table 6: Specimen container conditions**

Code	Description	Usage
BKV	Broken Vial	The container was broken beyond recovery, such as being dropped and shattered on the ground.
DMG	Damaged	The container is not leaking, but is damaged in another way, such as a tear in a label or a dent in a plastic container.
EXP	Expired	The additive in a container, or some other component used during specimen collection, was expired.
INT	Incorrect Tube	A tube type other than the one specified by the protocol was used, and the tube used was determined to be an acceptable alternative by the study team.
LKD	Leaked	The specimen leaked from the container, and it was placed inside another container and recovered.

## Temperature conditions

Temperature condition codes are typically applicable if there was an issue during shipping (such as sublimed dry ice) or if a piece of storage equipment failed. Other codes are applied as part of routine and expected handling of specimens. For example the FRO condition code can be used to indicate that a specimen intended to be stored ambient or refrigerated was frozen.

**Table 7: Temperature conditions**

Code	Description	Usage
DIM	Dry Ice Melted	The specimen was kept on dry ice, but the dry ice sublimed. This does not necessarily imply that the specimen was damaged or TNO.
FRO	Frozen	The temperature of the specimen has been lowered below its freezing point. This applies only to specimens that were not intended to be frozen, such as specimens that were shipped at ambient temperature during the winter.
REF	Refrigerated	The specimen is cooler than room temperature but not below its freezing point. This applies only to specimens that were not intended to be refrigerated.
TNO	Temperature Not Optimal	The specimen was stored or shipped at any temperature other than the temperature specified by the protocol.
TWD	Thawed	The specimen was frozen, and has been warmed so that it is no longer frozen. LDMS has a field to track a thaw count, which can be used to keep track of how many times the specimen has been thawed. This information can be found on the Details Window for the aliquot in Specimen Management.

## Shipping conditions

These condition codes apply to issues with a specimen shipment where the specimens are unaccounted for or were received late. If the shipping issue damaged the specimens, a temperature-related code such as DIM (dry ice melted) may be more appropriate.

**Table 8: Shipping conditions**

Code	Description	Usage
DSH	Delayed Shipment	A shipment did not occur on schedule, but there is no obvious damage to the specimens. If there was obvious damage, a more descriptive, temperature-related code (such as DIM or TNO) may be more appropriate.
LSH	Lost Shipment	A shipment was created and sent, but did not arrive at the receiving laboratory. Neither the shipping nor the receiving laboratory can locate it.
SNR	Sample Not Received	A data collection form, such as a CRF, was received, but a specimen listed on the form was not received. This differs from LSH in that only some specimens were not received, compared to an entire shipment.

## Qualitative conditions

These codes refer to the quality of a specimen. For example, if a blood specimen clotted, this is a qualitative issue that could prevent processing. If there was a qualitative or participant abnormality that would prevent processing but no other code is applicable, the SNP condition code can be used.

**Table 9: Qualitative conditions**

Code	Description	Usage
BLD	Bloody	The specimen, such as a throat swab, contained blood.
CLT	Clotted	The specimen has clotted, often because the additive did not mix correctly with the specimen.
CTM	Contaminated	The specimen is visibly contaminated.
DCG	Discharge present	A specimen, such as a vagina swab, that contains discharge material
HEM	Hemolyzed	A blood specimen that has hemolyzed.
HUM	Humidity	The specimen has been exposed to high humidity.
ICT	Icteric	There are excessive amounts of bilirubin in the specimen.
LIP	Lipemic	There is excessive fat content in the specimen.
LYS	Lysed	There has been a breakdown of cells in the specimen other than hemolyzation.
NQA	Real-time QA for viability and viable recovery not performed due to low volume of sample collected	Used by a Leukopak processing laboratory to indicate that the full specimen volume needed for PBMC viability and viable recovery QA could not be obtained.
SNP	Sample Not Processed	A generic code for when there is a qualitative issue that prevents an otherwise correctly collected primary from being processed into aliquots, but no other code applies. The Reason sample not collected field should be used in conjunction with SNP.
VPL	Viability percentage may be less than the expected parameter	Used by a processing laboratory to indicate that the PBMC viable percentage of the PBMC specimen may be lower than what's expected.
VRU	Viable recovery may be outside expected parameters (higher or lower)	Used by a processing laboratory to indicate that the PBMC viable recovery of the PBMC specimen may be outside what is expected.

## Quantitative conditions

These condition codes refer to the volume of specimen collected.

**Table 10: Quantitative conditions**

Code	Description	Usage
DFB	Difficult bleed	There was problems trying to obtain a blood specimen from the participant, typically resulting in a lower volume than was expected. This code is more specific than SHV, which does not indicate why the volume was low.
QNS	Quantity Not Sufficient	There was not enough specimen available to create the aliquot. For example, if specimen collected from the participant was supposed to be 10 mL but only 5 mL was collected, the aliquots that could not be created due to the low volume would be considered QNS. QNS means there is no volume at all for the aliquot, even though there was some volume for the primary.
SHV	Short Volume	The primary or aliquot specimen has at least some volume, but not the full expected volume.
SNC	Sample Not Collected	The primary specimen was not collected from the participant at all. This might happen if the participant declined to provide a specific sample.

### Other conditions

These condition codes are either automatically assigned to specimens or indicate some combination of issues. The default condition code that is assigned to all new specimens is SAT (satisfactory).

**Table 11: Other conditions**

Code	Description	Usage
ANM	Anonymized	The specimen was created using the anonymization tool in LDMS. This code is automatically assigned by LDMS and cannot be assigned manually.
COC	Combination of Codes	More than one condition code applies; the comments field in LDMS can be used to list the applicable codes.
DSR	Destroyed	The specimen has been destroyed.
OTH	Other	There is something noteworthy or unusual about the specimen, but no other available condition code applies.
SAT	Satisfactory	The default condition code for new specimens, indicating that the specimen was collected, processed, and handled as expected.
UNK	Unknown	Indicates that there is a significant gap in knowledge in the specimen's history. For example, if the specimen was collected by another laboratory that was not using LDMS and is several years old, and it may have been stored or treated improperly, this code may be appropriate.
YST	Did consent to storage	The participant has provided consent to storage of the specimen.
NST	Did not consent to storage	The participant did not provide consent to storage of the specimen.

## Test assignment

---

Specimens can be assigned tests to indicate a specific test that is expected.

While specimens cannot be tested in LDMS for the web, specimens may be shipped to a laboratory using a LDMS for Windows. The laboratory using LDMS for Windows may then enter results for the expected test.

### Assigning tests to a specimen

Expected tests can be assigned to a specimen, which will make it easier to locate the specimen when setting up assay test runs.

#### Steps

1. On the navigation menu, click **Specimen Management**.
2. Locate the specimen to have a test assigned. From that specimen's **Edit** menu, click **Assign Tests**.
3. In the **Test** list, select the test to assign.  
If **Other** was selected, enter the name of the test in the **Other Test Name** box.
4. Click **Assign Test**.

### Indicating that a test will not be performed

If an assay is expected but will not be performed, the test can be assigned and then indicated that it will not be tested.

#### Steps

1. On the navigation menu, click **Specimen Management**.
2. Locate the specimen to have a test assigned. From that specimen's **Edit** menu, click **Assign Tests**.
3. For the test, do the following:
  - 3.1. In the **Test Not Performed** column, select the check box.
  - 3.2. In the **Reason For No Result** column, select the appropriate code.  
Hover over a code to see a brief description.
  - 3.3. Optional: In the **Comment** column, enter more information about why the test was not performed.
4. Click **Save**.

### Deleting a test assignment

#### Background

A test assignment will typically only be deleted if it was added in error. If the test was expected but will not be run, the appropriate code could be assigned to the test instead.

### Steps

1. On the navigation menu, click **Specimen Management**.
2. Locate the specimen to have a test assigned. From that specimen's **Edit** menu, click **Assign Tests**.
3. In the **Action** column, click **Delete**.
4. Click **Save**.

## Storage

The Storage page is used to define how your real-world storage is set up and where individual specimens are stored.

The Storage page is organized into four sections:

<b>Stored specimens</b>	This is where you will actually perform storage work, such as creating a new storage unit or assigning a storage location to specimens.
<b>Storage unit templates</b>	This is where you can define templates for commonly used storage units.
<b>Level templates</b>	This is where you can define templates for commonly used <i>storage levels</i> .
<b>Container templates</b>	This is where you can define templates for commonly used storage containers.

### Navigation on the Storage page

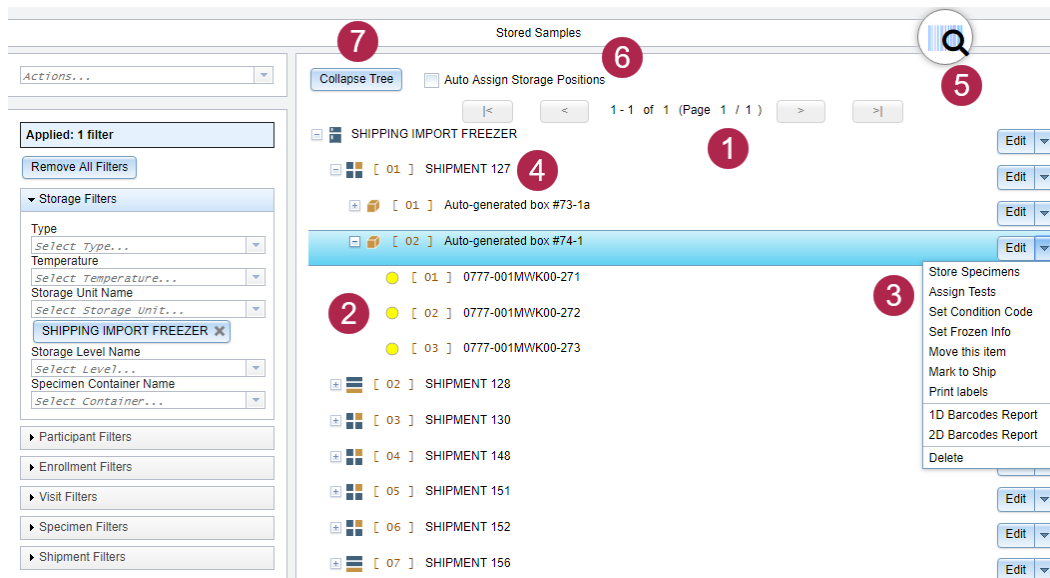
---

The **Storage** page shows a representation of your real-life storage as a collapsible tree.

This tree is called the storage tree view, and shows all of the items in storage as you have defined them in LDMS.



**Figure 26: The Storage page**



- (1) Navigate between pages (if your storage page does not fit on one).
- (2) The location of the specimen in “Auto-generated box #74-1”.
- (3) Edit menu for storage item named “Auto-generated box #74-1”.
- (4) The storage tree view.
- (5) Indicator that you can scan a barcode to add samples into a storage location.
- (6) The ability to automatically assign storage locations.
- (7) Close all units, levels, and containers.

The storage units in the storage tree are sorted alphabetically by name. The contents within storage units are sorted by position. Before expanding any storage items however, you can scan a barcode to search for a stored item automatically when the following icon is shown at the top of the page:



Click on the + button to the left of a storage item to open it. The contents in the square brackets next to the item’s name (such as [ 1, 2 ]) indicates that items position in its parent storage item. To the right of each storage menu is the **Edit** menu for that item. The options available from this menu will vary, depending on the type of storage item.

### The storage tree

The storage system in LDMS is a hierarchy of storage items.

There are several types of storage items in LDMS. From biggest to smallest, these are:

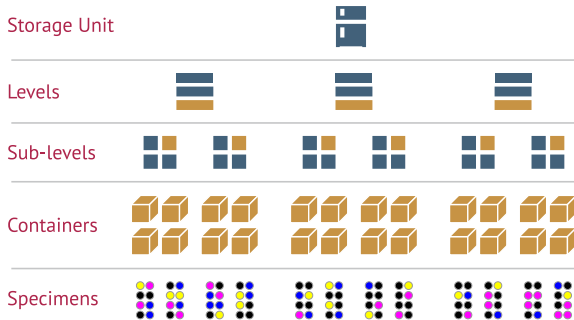
- storage unit** This is the main cooling unit used to store specimens, such as a freezer or a refrigerator.
- level** This is an intermediate part of a storage system, such as a shelf within a freezer. You can add an additional level to

another level. For example, you might have a shelf that contains racks of boxes, where the rack is a level on the shelf, which is a level in a freezer.

**container**

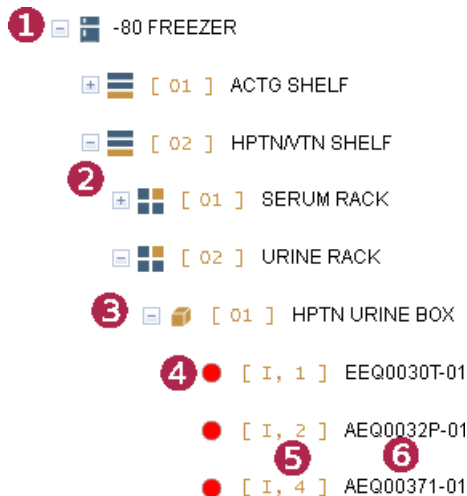
This is the storage item that holds specimens, such as a box.

**Figure 27: The LDMS storage hierarchy**



The storage hierarchy is visualized on the **Storage** page in LDMS as a tree.

**Figure 28: The storage tree on the Storage page**



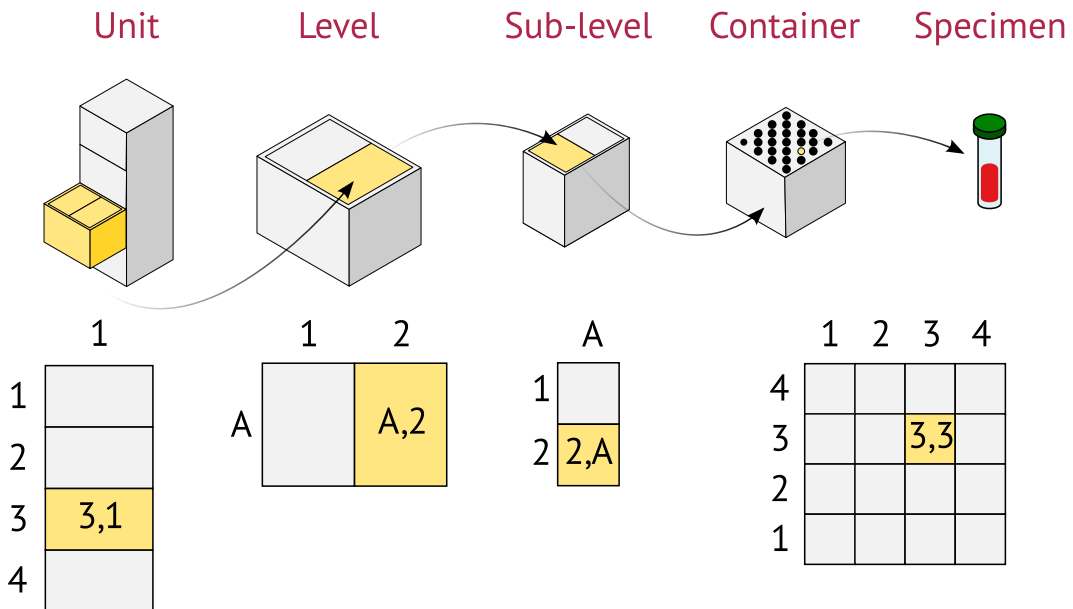
(1) A storage unit. (2) A level. (3) A container. (4) Specimens in the container. (5) The name for this specific storage unit. (6) The position of the item in its parent. (7) The global specimen ID for each specimen.

**Storage items**

Storage items in LDMS are represented as nested grids.

Each storage item contains rows and columns that represent individual locations within that storage item. For example, a shelf that can hold 10 boxes might have the dimensions of 2 x 5 (2 rows with 5 columns to represent each box). This is true of all storage items, from big storage units to small containers.

**Figure 29: Storage items as grids**



This visual illustrates the nested grid of storage items. Below each item is a grid showing where the highlighted item is positioned.

Rows and columns can be represented as either numbers or letters. Individual sections of a storage item can also be represented as a position number instead of coordinates. For example, if you have a 1 x 3 shelf, each position could be represented as 1, 2, and 3, rather than (1,1), (1,2), and (1,3).

Storage items can optionally have an *excluded position*. An excluded position is useful for determining which side of the storage item is the front and which is the back. For example, if you know that the upper-right corner of a container will be empty, you know where to start inserting specimens.

**Figure 30: Configuring a storage item layout**

Positions Only

Coordinate Order Row/Column

Column Labeling Alphabetic Left to Right

Row Labeling Alphabetic Top to Bottom

Fill Order Left to Right, Top to Bottom

Excluded Positions Corner(s) Upper Left

Preview

	A	B
A	A,A	A,B
B	B,A	B,B
C	C,A	C,B
D	D,A	D,B
E	E,A	E,B







The preview shows how these settings will be interpreted by LDMS. A,A (black) is an excluded position. A,B to C,A (gray) contain another storage item or specimen. C,B to E,B (tan) are empty positions.










All of these properties of storage items can be configured when adding new items to the storage tree. They can also be defined in advance by using a *storage template*.

### Icons and their meaning

The icons next to the items in the storage tree indicate the type of storage item, and special properties such as its additive or whether the item is part of a pending shipment.











**Table 12: Storage item icons**








Icon	Meaning
	Storage unit
	Storage unit that has been flagged 'mark to ship'
	Storage unit that is part of a pending shipment
	Level
	Level that has been flagged 'mark to ship'
	Level that is part of a pending shipment

Icon	Meaning
	Sub-level
	Sub-level that has been flagged 'mark to ship'
	Sub-level that is part of a pending shipment
	Container
	Container that has been flagged 'mark to ship'
	Container batched
	Specimen
	Specimen that has been flagged 'mark to ship'
	Specimen that is part of a pending shipment

**Table 13: Additives with colored tubes on the storage page**

Any additive not listed in this table uses a black icon.

Additive	Icon
ACD	
AHP	
DPE	
DSE	
EDT	
HEP	
LHG	
LHP	
LPE	
LSE	

Additive	Icon
NON	
PED	
SCI	
SED	
SFL	
SST	
THM	

## Assigning storage locations

### Adding a new storage unit

A storage unit is the largest type of storage item, and is used to hold levels.

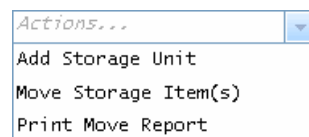
#### Background

A new *storage unit* is created by defining various properties for it, such as its size and temperature. You can manually define these properties for the storage unit as you create it, or you can use a template that applies default settings for you.

#### Steps

1. Click **Storage > Stored Specimens** from the LDMS menu bar.
2. From the action menu, select **Add storage unit**.

**Figure 31: The LDMS action menu**



The **Create storage unit** window will open.

3. Optional: Select a template to use for the new storage unit from the **From template** box.  
All settings from the template will be set for you. You can override any settings from the template if needed. Any changes made will only affect the new storage unit; the template will not be modified.
4. Optional: Click the **Empty Structure** button to remove any levels that were automatically added by a template.  
This is only necessary if you do not want to use the default levels (if present) from a template.  
All levels added by a template will be removed.

5. Enter a descriptive name for the new storage unit in to **Name** box.  
This is the name for the new storage unit as it will appear in the storage tree in LDMS.
6. Select the type of storage unit from the **Type** box.
7. Select the temperature of the new storage unit from the **Temperature** box.
8. Enter the number of rows and columns for the new storage unit into the **Number of rows** and **Number of columns** boxes.  
This represents the size and capacity of the new storage unit in terms of the number of *levels* that it can hold. For example, if you are creating a freezer that can hold 5 shelves vertically, you might have 1 column and 5 rows.
9. Select or deselect the **Positions only** option as desired.  
If the positions only option is selected, each item in the level in the new storage unit will be identified by a number. If it is not selected, each level will be identified by its coordinates.
10. (If **Positions only** is not selected) Define how levels in the new unit should be identified.
  - 10.1. Select either **Row/Column** or **Column/Row** from the **Coordinate order** box.  
If **Row/Column** is selected, each level's position will be identified in the format (row,column)
  - 10.2. Select how columns and rows are to be labeled from the **Column labeling** and **Row labeling** boxes.  
To use letters to identify rows or columns, select **Alphabetic**; to use numbers, select **numeric**.
  - 10.3. Select the fill order for the new unit from the **Fill order** box.  
Fill order can be used when adding a new level to the unit. While you must specify a fill order, you can override it when adding levels to the storage unit.
  - 10.4. Optional: Select a position(s) in the unit to be excluded from the **Excluded positions** box.  
Excluded positions are used to help identify the orientation of the container (meaning which side is the front and which is the back).
11. Review the **Preview** of the new unit.  
If any empty levels will automatically be added the new unit, they will be listed in the **Default Levels** section.
12. Optional: To save the current configuration as a new template, do the following.
  - 12.1. Select **Save As New Template**.
  - 12.2. In the **New Template Name** box, enter a name for the template.
13. Click the **Save** button.

**Result**

The new unit will have been added to the storage tree. The storage tree is in alphabetical order, so you may need to change pages in the storage tree to find your new storage unit.

**Adding a new level in a storage unit**

A new level is added to an existing storage unit or storage level.

**Prerequisites**

You must have created the storage unit before you can add levels to storage in LDMS. In other words, you cannot create a level that is not associated with a storage unit.

**Steps**

1. Click **Storage > Stored Specimens** from the LDMS menu bar.
2. Find the *storage unit* to which you are adding a *level*.  
If you want to add a sub-level to an existing level, find that level instead. You can use the filters on the left side of the page to help find the storage item.
3. Click the down arrow next to the **Edit** button to the right of the intended parent storage unit or level, and then click **Add new level**.

**Figure 32: The Edit Storage Unit button**



- The **Select position for new level** window will open.
4. Optional: Select a template to use for the new level from the **From template** box.  
All settings from the template will be set for you. You can override any settings from the template if needed. Any changes made will only affect the new level; the template will not be modified.
  5. Enter a descriptive name for the new level into the **Name** box.  
This is the name for the new level as it will appear in the storage tree in LDMS.
  6. Enter the number of rows and columns for the new level into the **Number of rows** and **Number of columns** boxes.  
This represents the size and capacity of the new level in terms of the number of levels or *containers* that it can hold. For example, if you are creating a shelf that can hold 5 boxes side-by-side, you might have 5 columns and 1 rows.
  7. Select or deselect the **Positions only** option as desired.



If the positions only option is selected, each item in the new level will be identified by a number. If it is not selected, each level will be identified by its coordinates.

- 8.** (If **Positions only** is not selected) Define how levels or containers in the new level should be identified.
  - 8.1.** Select either `Row/Column` or `Column/Row` from the **Coordinate order** box.

If `Row/Column` is selected, each level or container position will be identified in the format (row,column)
  - 8.2.** Select how columns and rows are to be labeled from the **Column labeling** and **Row labeling** boxes.

To use letters to identify rows or columns, select `Alphabetic`; to use numbers, select `numeric`.
- 9.** Select the fill order for the new level from the **Fill order** box.

Fill order can be used when adding a new level or container to the level. While you must specify a fill order, you can override it when adding items to the level.
- 10.** Optional: Select a position(s) in the level to be excluded from the **Excluded positions** box.

Excluded positions are used to help identify the orientation of the container (meaning which side is the front and which is the back).
- 11.** Review the **Preview** of the new storage item.
- 12.** Click the **Continue** button.

The **Select position** window will open.
- 13.** Specify the position within the storage unit for the new level by doing one of the following:
  - Select a position for the new level from the **Position** box.
  - Click on a position in the **Preview** section.

Positions that cannot be selected are either already occupied by another level or empty by exclusion rules for the storage unit. Gray positions are occupied; black positions are excluded.
- 14.** Optional: To save the current configuration as a new template, do the following.
  - 14.1.** Select **Save As New Template**.
  - 14.2.** In the **New Template Name** box, enter a name for the template.
- 15.** Click the **Save** button.

## Adding a container to a level

A new storage container is added to an existing level or sub-level.

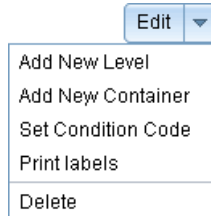
### Prerequisites

You must have created the storage units and levels for the container before adding the container. In other words, you cannot add a container to a freezer without a level, nor can you create a container that is not within a freezer.

## Steps

1. Click **Storage > Stored Specimens** from the LDMS menu bar.
2. Find the storage unit to which you are adding a level.  
If you want to add a sub-level to an existing level, find that level instead.
3. Click the down arrow next to the **Edit** button to the right of the level that will hold the container, and then click **Add New Container**.

**Figure 33: The Edit level button**



If the level has had sub-levels added, the **Add new container** option will not be available. A container cannot be added side-by-side with a sub-level.

The **Create container** window will open.

4. Enter the number of new *containers* to add in the **Number to add** box.
5. Optional: Select a template to use from the **From template** box. The information from the template will be populated into the remaining boxes. You can still modify this information, if needed. Any changes made will only affect the *containers* that you are creating.
6. Enter the number of rows and columns for the new container into the **Number of rows** and **Number of columns** boxes.

This represents the size and capacity of the new container in terms of the number of specimens that the container can hold. For example, if you are creating a box that can hold 25 specimens, you might have 5 columns and 5 rows.



**Note:** The system will warn the user when a box is outside the max 26x26 dimensions.

7. Select or deselect the **Positions only** option as desired.  
If the positions only option is selected, each specimen in the container will be identified by a number. If it is not selected, each specimen will be identified by its coordinates.
8. (If **Positions only** is not selected) Define how specimens in the new container should be identified.
  - 8.1. Select either *Row/Column* or *Column/Row* from the **Coordinate order** box.  
If *Row/Column* is selected, each specimen's position will be identified in the format (row,column)

- 8.2.** Select how columns and rows are to be labeled from the **Column labeling** and **Row labeling** boxes.  
To use letters to identify rows or columns, select `Alphabetic`; to use numbers, select `numeric`.
  - 8.3.** Select the fill order for the new level from the **Fill order** box.  
Fill order will be used when adding new specimens to the container, and you chose to use automatic positioning. While you must specify a fill order, using the automatic positioning feature is optional.
  - 8.4.** Optional: Select a position(s) in the container to be excluded from the **Excluded positions** box.  
Excluded positions are used to help identify the orientation of the container (meaning which side is the front and which is the back).
- 9.** Optional: To save the current configuration as a new template, do the following.
  - 9.1.** Select **Save As New Template**.
  - 9.2.** In the **New Template Name** box, enter a name for the template.
- 10.** Click the **Continue** button.  
The **Select position** window will open.
- 11.** Enter a descriptive name for the first container into the **Name** box.  
This is the label for the new container as it will appear in the storage tree.
- 12.** Specify the position for the new container on its parent level by doing one of the following:
  - Select a position for the new container from the **Position** box.
  - Click on a position in the **Preview** section.Positions that cannot be selected are either already occupied by another container or empty by exclusion rules for the parent level. Gray positions are occupied; black positions are excluded.
- 13.** Click the **Continue** button.  
You will need to specify the **Name** and position for each new container that you are creating.

### Result

The new *containers* will be created in the positions specified.

## Assigning a storage location to specimens

Individual specimens are added to containers on the **Storage** page.

### Prerequisites

You must create the specimens on the Specimen Management page prior to adding them to a container. You must also have created the *container* to which the specimens will be added.

## Background

Individual specimens are stored in containers. You cannot add specimens to a level or *storage unit* without a container.

## Steps

1. Click **Storage > Stored Samples** from the LDMS menu bar.
2. Find the storage container to which you want to add specimens in the storage tree.  
Use the filters on the left side of the screen to assist in finding the container.

3. From the **Edit** menu to the right of the container, select **Store specimens**.

**Figure 34: The Edit container menu**



The **Select Specimens** window will open.

4. Do one of the following:
  - Use filters to find specimens to limit the specimens displayed at the bottom of the page
  - Click **Upload File: Unique specimen IDs** (file must be a text file with one specimen ID per line)



**Note:** Supported ID formats include Specimen IDs, Other Spec IDs, Global Spec IDs, and Database IDs.

- Scan a specimen barcode
5. For each specimen to be stored, select the check box in the **Selected** column.

You can also click **Select All** to store all currently displayed specimens.

If you change filters at this point, any specimens selected will remain selected.

6. At the bottom of the Select Specimens window, click **Continue**. The **Select position for specimen** window will open.
7. Select the position where the first specimen will be stored from either the **Position** box or the **Preview** image.

The *global specimen ID* for the specimen will be displayed in the window. Positions that are gray are not available because a specimen already occupies that location. A position that is black is an *excluded position* in the container's configuration.

8. Optional: To place the remaining specimens to be stored automatically based on the container's fill order setting, select the **Auto-fill from selected position** option.
9. Click **Continue**.  
If there are more specimens to be stored and you did not select the **Auto-fill from selected position** option, you will be prompted to select a position for those specimens, otherwise, the window will close.

### Result

The specimens are now stored. If you look at the storage tree, you will see that they are now listed under the specified container.

### After you are finished

Generate the Storage Details and Container reports. These will help you know where the specimens need to physically be stored.

## Generating a printable list of what is in storage

The Storage Details and Container reports can be used to print a list of all the storage items or specimens in a specific location.

### Background

In addition to assigned specimens to a storage location in LDMS, you will need to actually put the real-life specimens in storage. The Storage Details and Container reports can assist you in putting storage items in the correct location. It is good practice to print them after making changes to storage in LDMS.

### Steps

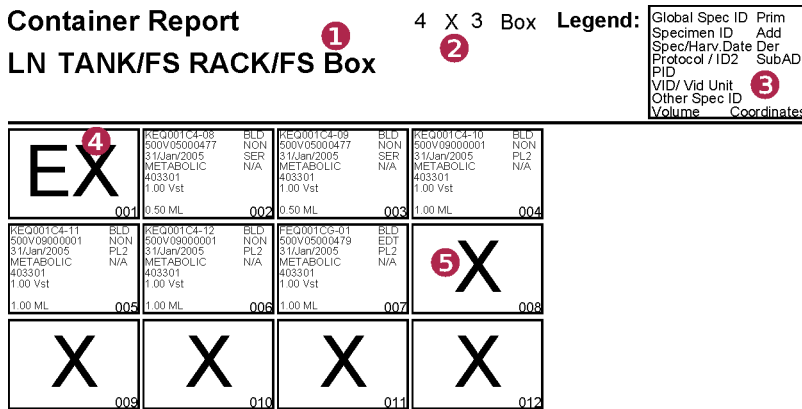
1. Click **Storage > Stored Samples** from the LDMS menu bar.
2. In the storage tree, locate the storage item for which you need to generate a report.
3. To the right of the storage item, click **Edit**.
4. Click the down arrow next to the **Reports** button, and then click either **Storage detail** or **Container**.
5. In the **File Type** box, select PDF (\*.pdf) and then click **Generate Report**.

## Container report

The Container report is a printable, graphic representation of the specimens within a storage container.

This report is useful for reconciling the storage locations assigned to specimens in LDMS and the actual real-life contents of a storage item. For example, if you initially assign specimens to a storage location in LDMS, you can print the container report and use it as a guide when inserting the actual specimens in the container.

**Figure 35: Container report**



(1) Storage location of container, (2) Dimensions of container, (3) Legend showing how to interpret the information for a specimen, (4) An excluded position, (5) An empty location

The top-right corner of the container report contains a key that shows how to interpret the details of a specimen listed on the report.

## Storage templates

Templates allow you to add commonly used storage items quickly by defining them in advance.

Template allow you to setup commonly used storage items, such as a box that your laboratory uses, and re-use the template as often as needed.

If you need to add a storage item that is a slight variation of an existing template, you can modify the template while creating the new storage item. For example, if you need to create a storage container that has an excluded corner that is not in the template, you can add it manually without needing to modify the template.

### Creating storage item templates

Storage item templates can be created for storage units, levels, and containers.

#### Background

These templates can be selected when adding storage items to LDMS to save time.

#### Steps

1. Hover the mouse pointer over **Storage** from the LDMS menu bar, and then click either **Storage unit templates**, **Level templates**, or **Container templates**, depending on the type of template you want to create.
2. Enter a name for the template into the **Name** box.

This is the name for the template as it will appear when creating new storage items.

3. (For storage units only) Select the type of storage unit from the **Type** box and the temperature from the **Temperature** box.
4. Enter the number of rows and columns for storage items based on this template into the **Number of rows** and **Number of columns** boxes.  
This represents the size and capacity of new storage items based on this template in terms of the number of levels or containers that it can hold. For example, if you are creating a shelf that can hold 5 boxes side-by-side, you might have 5 columns and 1 rows.
5. Select or deselect the **Positions only** option as desired.  
If the positions only option is selected, each item in storage items based on this template will be identified by a number. If it is not selected, each storage item will be identified by its coordinates.
6. (If **Positions only** is not selected) Define how *levels* or *containers* in storage items based on this template should be identified.
  - 6.1. Select either `Row/Column` or `Column/Row` from the **Coordinate order** box.  
If `Row/Column` is selected, each *level* or container position will be identified in the format (row,column)
  - 6.2. Select how columns and rows are to be labeled from the **Column labeling** and **Row labeling** boxes.  
To use letters to identify rows or columns, select `Alphabetic`; to use numbers, select `numeric`.
7. Select the fill order for storage items based on this template from the **Fill order** box.  
Fill order can be used when adding a new level or container to storage items based on this template. While you must specify a fill order, you can override it when add storage items.
8. Optional: Select a position(s) in storage items based on this template to be excluded from the **Excluded positions** box.  
Excluded positions are used to help identify the orientation of the container (meaning which side is the front and which is the back).
9. Review the **Preview** for storage items based on this template.
10. Optional: (For storage units only) Add default levels for new storage units based on this template.
  - 10.1. Click the **Add level** button.  
The **Add Level** window will open.
  - 10.2. Select a template from the **Saved Templates** box.  
The information for the template will be displayed, however you will not be able to modify it.
  - 10.3. Specify how many levels to add in the **Number to add** box.
  - 10.4. Click the **Continue** button.  
The **Select Position for Level** page will open.
  - 10.5. Select a position for the first storage item you are adding from either the **Position** box or on the **Preview**.

If you are adding more than one item, you can select the **Auto-fill all from selected position**. This option will place the remaining storage items based on the fill order of the storage item containing it. If you do not select this option, you will be prompted to manually position each storage item.

**10.6.** Click the **Continue** button.

The storage item(s) will now appear in the **Default Levels** list.

You can add sub-levels and containers to the default levels that you've added as needed.

**11.** Click the **Save template** button.

## Modifying and removing storage templates

Storage templates can be modified or removed after they have been created.

### Background

Changes to templates will only affect new storage items based on the template. Existing storage items that were based on the template will not be updated.

### Steps

**1.** Hover the mouse pointer over **Storage** from the LDMS menu bar, and then click either **Storage unit templates**, **Level templates**, or **Container templates**, depending on the type of template you want to modify.

**2.** Select the template to modify from the **Saved Templates** box.



**Note:** If you want to clear the screen so that you can create a new template instead of modifying the selected template, click the **Add new** button.

The settings for that template will be displayed.

**3.** Modify the template as needed.

If you want to remove the template, click the **Delete template** button. Deleting a template makes it unavailable to be used for new storage items. Existing storage items that were based on the template will not be affected.

**4.** Click the **Save template** button.

### Result

The template will be modified and any new storage items based on it will reflect the changes. Existing storage items that were based on the template will not be modified.

## Moving items in storage

---


Storage items can be moved to a different location or rearranged in their current location.



## Background

Any storage item can be moved to another location in LDMS. Moving a storage item will require you to specify its position in its new location. If you move a storage item from its current location to its current location, you will be given the opportunity to rearrange its contents.

## Steps

1. Click **Storage > Stored Samples** from the LDMS menu bar.  
Alternatively, you may use a barcode scanner to select the samples to be moved.
2. Click **Move this item** from the action menu.  
The **Move Selected to Storage Container** window will open.
3. From the list of storage containers, click the **Select** button to the right of the location where the selected item(s) should be moved to. The amount of free space is listed next to each container.  
The storage items selected must be moved to the same destination. You cannot move two storage items at once that cannot occupy the same location. For example, you cannot select to move a specimen and a level at the same time.  
The **Select Positions** window will open.
4. For each item being moved, select a position in the destination.  
If you want to automatically place the items being moved into the destination, select a position and then select the **Auto-fill all from selected position** option. This will cause all remaining storage items to be placed into the destination based on the destination's fill order.  
 **Note:** If samples are moved to a container that will not hold all selected samples, the remaining samples will remain selected to be moved to a different container.
5. Click the **Continue** button.

## Moving Items in Storage - Filter Search

### Background

Stored items can also be selected to be moved using various filters.

**Figure 36: Specimen Filter Screen**

Select Specimens

Remove All Filters **2**

**1** Participant Filters

Project  ACTG/IMPAACT **3**

ID1

OPID

Enrollment Filters

Visit Filters

Specimen Filters

Shipment Filters **6** **5** **3**

All  Selected **7** Clear Selected Select All Upload File: Unique specimen IDs

Selected <b>4</b>	Global Specimen Id	Specimen Id	Other Specimen Id	Primary Type	Additive	Derivative Type	Sub Add/Der Type
<input type="checkbox"/>	BEQ00002-05	500V05000002		BLD	EDT	PL2	N/A
<input type="checkbox"/>	JEQ0000G-03	500V05000006		BLD	SPO	PL1	N/A
<input type="checkbox"/>	BEQ0000L-05	500V05000009		BLD	EDT	PL2	N/A
<input type="checkbox"/>	DEQ00012-03	500V05000016		BLD	EDT	PL2	N/A
<input type="checkbox"/>	DEQ00012-04	500V05000016		BLD	EDT	PL2	N/A
<input type="checkbox"/>	DEQ00012-05	500V05000016		BLD	EDT	PL2	N/A
<input type="checkbox"/>	GEQ00017-01	500V05000019		BLD	EDT	PL2	N/A
<input type="checkbox"/>	GEQ00017-06	500V05000019		BLD	EDT	PL2	N/A

**8** Continue Cancel

(1) Various filters that can be applied to the list of specimens, (2) remove all specimens filters, (3) upload a unique specimen IDs file, (4) manually select specimens from filtered list to be moved, (5) select all specimens in filtered list to be moved, (6) clear selected specimens in filtered list, (7) filter list of specimens by selected only, (8) continue to Move Specimens screen

**Steps**

1. Navigate to the **Stored Samples** page under the **Storage** module.
2. In the **Actions** dropdown, select **Move Stored Specimens - Filter Search**. The **Select Specimens** screen will open.
3. Use the various filters to locate the specimens that need to be moved. The list of filtered specimens will appear below.
4. If not all specimens in the filtered list are intended to be moved, select the specimens that are to be moved and click the **Selected** radio button.
5. A global specimen IDs file can also be added to the list of filtered specimens by clicking **Upload File: Unique specimen IDs**.
6. Click **Continue**.

7. Use the dropdown menus on the following screen to find the location the specimens will be moved to and click **Select**.
8. Click **Continue** to confirm the move.

### Consolidating storage containers

Consolidating a storage container automatically moves specimens within a container based on its fill order to eliminate empty spaces.

#### Background

**Figure 37: Container consolidation**

	1	2	3	4	5	6	7	8	9
I	I,1	I,2	I,3	I,4	I,5	I,6	I,7	I,8	I,9
H	H,1	H,2	H,3	H,4	H,5	H,6	H,7	H,8	H,9
G	G,1	G,2	G,3	G,4	G,5	G,6	G,7	G,8	G,9
F	F,1	F,2	F,3	F,4	F,5	F,6	F,7	F,8	F,9
E	E,1	E,2	E,3	E,4	E,5	E,6	E,7	E,8	E,9
D	D,1	D,2	D,3	D,4	D,5	D,6	D,7	D,8	D,9
C	C,1	C,2	C,3	C,4	C,5	C,6	C,7	C,8	C,9
B	B,1	B,2	B,3	B,4	B,5	B,6	B,7	B,8	B,9
A	A,1	A,2	A,3	A,4	A,5	A,6	A,7	A,8	A,9

	1	2	3	4	5	6	7	8	9
I	I,1	I,2	I,3	I,4	I,5	I,6	I,7	I,8	I,9
H	H,1	H,2	H,3	H,4	H,5	H,6	H,7	H,8	H,9
G	G,1	G,2	G,3	G,4	G,5	G,6	G,7	G,8	G,9
F	F,1	F,2	F,3	F,4	F,5	F,6	F,7	F,8	F,9
E	E,1	E,2	E,3	E,4	E,5	E,6	E,7	E,8	E,9
D	D,1	D,2	D,3	D,4	D,5	D,6	D,7	D,8	D,9
C	C,1	C,2	C,3	C,4	C,5	C,6	C,7	C,8	C,9
B	B,1	B,2	B,3	B,4	B,5	B,6	B,7	B,8	B,9
A	A,1	A,2	A,3	A,4	A,5	A,6	A,7	A,8	A,9

The effect of container consolidation before (left) and after (right).

#### Steps

1. On the navigation menu, click **Storage**.
2. Locate the storage container to consolidate, and then click **Edit**.
3. Below the Preview section, click **Consolidate Container**.
4. At the bottom of the Edit Storage Container window, click **Save**.

### Listing specimens that moved in storage

After moving specimens in LDMS’s storage, you can print a list of these changes so that you can move the actual specimens.

#### Background

When specimens are moved in LDMS they also need to be moved in your actual specimen storage area so that the storage location assignments in LDMS remain accurate. To help you keep LDMS and your storage in sync, you can print a list of specimens that have been assigned new storage locations in LDMS.

#### Steps

1. In the menu bar, click **Storage > Stored Samples**

2. From the action menu in the upper-left corner, click **Print Move Report**.
3. Next to **Generate for**, select one of the following:
  - Select **This Login Session** if you want to see all specimens that you have moved while signed in.
  - Select **Date Range** if you want to see all specimens that have been moved during a given date range.
4. If using a date range, specify the **Start Date** and **End Date**
5. Leave the **File Type** as PDF (\*.pdf).  
This report is not intended to be generated in a format other than PDF.
6. Click **Generate Move Report**.

#### After you are finished

Each row in the *Storage Move Report* will represent one specimen that has changed locations, with its original location and its now location. Use the report to find the specimen in its original location so that it can be related to the new position.

## Removing items from storage


---

Storage items and specimens can be removed from storage

### Background

Removing a storage item removes all of the items that it contains. If the location being removed contains specimens, you will be given the opportunity to change their condition and apply comments to them, which can be accessed when viewing the specimens.

Removing a storage item that contains specimens does *not* delete the specimens. They will still be visible on the **Specimen Management** page, and (unless you chose to make them *unavailable*) they can be added to a different storage container.

 **Warning:** Removing a storage item cannot be undone.

### Steps

1. Click **Storage** from the LDMS menu bar.
2. Find the storage item or specimen that you want to remove.  
Use the filters on the left side of the **Storage** page to help locate the items to be removed.
3. From the **Edit** combo button to the right of the item, select **Delete**.



**Note:** For specimens, this option will be called **Remove** instead of Delete.

The **Delete [Item]** window will open.

- Optional: If you want to change the specimens that are stored at the location being removed to *unavailable*, select the **Unavailable** check box and add a date to the **Unavailable Date** field.

This means that the specimens will not be available to add to storage again. They will also not appear as available to ship when shipping specimen data to another laboratory. You will still be able to find the specimens, however, on the **Specimen Management** page.

If you do select this option, you will also be prompted to select a condition for the specimens and enter a comment. This comment will be applied to each specimen.

- Click the **Delete** or **Remove** button.

## Modifying the condition of stored specimens

The condition of all specimens in a specific storage location can be modified at once.

### Prerequisites

The storage location must not contain any specimens that are part of a pending shipment.

### Background

There will be occasions when you need to update the condition of all the specimens in a storage location at once. This might happen, for example, if there was an equipment failure and all of the specimens in a storage unit were thawed.

### Steps

- Click **Storage > Stored Specimens** from the LDMS menu bar.
- Locate the storage item that contains the specimens you want to modify.  
If you select a higher-level storage item, such as a *storage unit* or *storage level*, the specimens in all sub-levels and containers will be modified as well.
- From the edit menu to the right of the storage item, click **Set condition code**.

**Figure 38: The Edit container menu**



The **Set Condition Code** window will open.

4. Select the condition code to apply from the **Specimen condition** box.
5. Enter additional information about the specimens into the **Comments** box.  
Information that is typically included here includes details for specimens that were not collected, an explanation of a condition, or an explanation of why a specimen is not available.
6. Enter additional information about the specimens into the **Internal-only comments** box.  
Comments entered here are for your laboratory's use only. These comments will not be included if the specimen's information is shipped to another laboratory.
7. Click the **Save** button.

### Result

The condition code, comments, and internal-only comments for all of the specimens in the storage location will be updated as you specified.

## Storage Action Report

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The Storage Action Report shows you changes that have been made to your storage structure, such as adding specimens or containers.

### Steps

1. Click **Storage > Stored Samples** from the LDMS menu bar.
2. From the Action Menu, click **Print Storage Action Report**
3. Select the appropriate radio button for the **Generate for** field:
  - **This Login Session:** the report will display all changes made in Storage during the current login session.
  - **Events Since Your Last Printing of Report:** the report will display all changes made in Storage since the last time the Storage Action Report was run.
  - **Date Range:** the report will display all changes made in Storage during a selected date range. Select the date range using the **Start Date** and **End Date** fields.
4. Select the criteria for actions that will appear on the report.
5. Click **Generate Storage Action Report**.

## Shipping

The **Shipping** page in LDMS is where you create shipping data files and receive shipping data files from other laboratories.

The shipping page is organized into three sections:

<b>Pending shipments</b>	This page is where you create new data shipments, view and modify shipments that have been created but not yet sent, and generate <i>shipping files</i> .
<b>Receive shipments</b>	This page is where you will import shipping data files.
<b>Shipment history</b>	This page shows a record of all shipping files, created and received, for your laboratory. Shipments that are still pending will not be shown.

## **LDMS shipping file compatibility**

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LDMS shipping files are compatible with certain version of LDMS for Windows.

The format of the shipping files used by LDMS is an encrypted XML data file. LDMS for Windows support will vary based on the version of LDMS for Windows.

<b>LDMS for Windows version 10.0 or higher</b>	Can ship and receive shipping files with laboratories using LDMS without restriction
<b>LDMS for Windows version 9.x</b>	Can ship specimens to but not receive specimens from LDMS
<b>LDMS for Windows version 8.x or earlier</b>	No shipping compatibility with LDMS

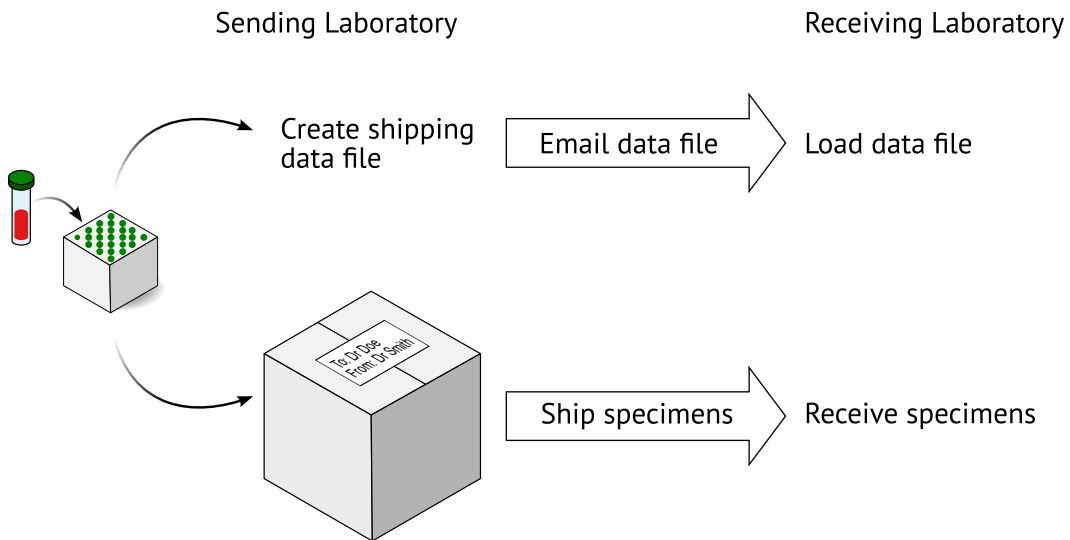
## **Shipments are data transfer**

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Shipping in LDMS is the process of transferring specimen information from one laboratory to another.

This is a parallel process to physically packaging and shipping specimens to another laboratory. As specimens are packaged, you will specify in LDMS that they are to be shipped. You will then generate a data file with the information for those specimens called a *shipping file*. Once created, you provide that file to the laboratory that will receive the specimens. In this sense, it is more accurate to think of "shipping" in LDMS as "data transfer" between two laboratories.

LDMS does *not* assist with the physical shipment of specimens. LDMS does not create postal labels for shipping boxes, track the progress of shipments of couriers, and other logistical tasks. Laboratories need to implement their own solutions for the actual shipping process.

**Figure 39: Shipping vs data transfer**

This figure illustrates how creating a shipping data file in LDMS and transferring it to a laboratory is a separate process from physically boxing and shipping the specimens to the recipient.

There are two ways to ship specimens using LDMS:

1. You can select individual specimens to be shipped, and then tell LDMS how you are going to put them in a shipping container.
2. You can assign the specimens to a container on the **Storage** page, then ship the container.

Both of these methods can be used together within the same shipment. Sending a container from LDMS storage is generally preferred over creating ad hoc shipping containers. By using a container that has already been organized and checked, you will save time and reduce the possibility of sending the wrong specimens.

## Shipment numbers

Shipment numbers are assigned to sent and received shipments as a way to identify it at your laboratory.

When a new shipment is created or received, it is assigned the next available shipment number by LDMS. For example, if the last shipment that you received had the shipment number 152, the next shipment (whether you receive it from another laboratory or create it to send) will be assigned the shipment number of 153.

Shipment numbers are *not* unique between laboratories, nor will they be the same at the laboratory that sent and shipment and the laboratory that received it. For example, if you create a shipping file, it may be assigned the number 153 at your laboratory. When the receiving laboratory receives the shipping data file, it will be assigned the next available shipment number at



*their* laboratory, which will probably be different from the shipment number at your laboratory.

For this reason, shipment numbers cannot be directly matched to shipments between laboratories. Instead, you would need to use the shipment setup date and other information to match a shipment that you sent to the same shipment received at another laboratory.

## New shipments

New shipments are created on the **Pending Shipments** page

The **Pending Shipments** page shows all data shipments that have been created but not yet sent. This page serves the following purposes:

1. Create new shipments
2. View or modify shipments that have been created but not yet sent.
3. "Ship" a shipment.

**Figure 40: The Pending Shipments page**

Shipment Number	Shipment Format	Destination Lab	Shipment Temperature	Setup Date	Ship Date	QA/QC	
119	LDMS	300	Dry Ice	08/Sep/2015	08/Sep/2015	Not Performed	Edit/Ship ▼
118	LDMS	1	Dry Ice	02/Sep/2015	02/Sep/2015	Not Performed	Edit/Ship ▼
117	LDMS	350	Ambient	02/Sep/2015	02/Sep/2015	Not Performed	Edit/Ship ▼
116	LDMS	350	Ambient	02/Sep/2015	02/Sep/2015	Not Performed	Edit/Ship ▼
115	LDMS	350	Cold Packs	02/Sep/2015	02/Sep/2015	Not Performed	Edit/Ship ▼
113		499		13/Aug/2012		Not Performed	Edit/Ship ▼
108		999001		01/Sep/2011		Not Performed	Edit/Ship ▼
102		17	Dry Ice	11/Jul/2011		Complete With Errors	Edit/Ship ▼
66		999001	Cold Packs	05/Apr/2010		Not Performed	Edit/Ship ▼
55		300	Cold Packs	25/Mar/2010		Not Performed	Edit/Ship ▼

The term "ship" in LDMS means that all of the specimens you want added to a shipment have been added and it is ready to be sent. When you ship a shipment, you will be prompted to save a shipping data file—*this file is the shipment*. In addition to sending a physical package of specimens to the receiving laboratory, you will need to provide the laboratory with the shipping data file. This is most commonly done using email, but you could also put the file on a disc or re-writable USB drive and include it with the physical shipment.

## Creating new shipments

Creating a shipment means defining which specimens will be sent and where they are going to be sent.

### Prerequisites

- The specimens must have already been entered into LDMS

- If you want to ship a storage container with specimens, you must have already assigned the specimens to the container in LDMS.

## Background



**Note:** You can save an incomplete shipment (such as leaving the destination blank), however you will need to complete the shipment before it can be sent.

## Steps

1. Click **Shipping > Pending Shipments** from the LDMS menu bar. The Pending Shipments page will open.
2. From the LDMS action menu, click **Create Shipment**. The **Pending Shipment Preview** window will open.
3. Complete the information on the **General** tab.  
All information on this tab is required.
  - shipment date** This is the date that the physical shipment was (if it was already shipped) or will be shipped. If you do not know when you will be shipping the specimens, select an approximate date—it can be changed before the shipping file is generated.
  - format** This is the type of shipping file you are creating. Unless the destination does not use LDMS, select **LDMS**.
  - temperature** This will be the method of temperature control for the specimens during transport.
4. Complete the information on the **Shipping Destination** tab. Existing laboratories that are using LDMS and LDMS are already available for selection. The contact information for these laboratories is maintained by Frontier Science.
  - 4.1. Select either **Contact, Lab Number, or Lab Name**.  
This is how you will select the laboratory. **Contact** is the shipping contact person on file for the laboratory. **Lab Number** is the laboratory's LDMS ID. **Lab Name** will show each laboratory in alphabetical order.
  - 4.2. Select a laboratory from the drop-down box below.  
If you selected **Contact or Lab Name**, the number in parenthesis next to each laboratory's name is the laboratory's LDMS ID number.
  - 4.3. Select or enter the person to receive the shipment at the receiving laboratory from the **Contact Person** box.  
Laboratories can be added to LDMS. These will only appear as available for selection by your laboratory. Since all laboratories that use LDMS and LDMS are already listed, the new laboratory is assumed to be using some other laboratory management system.

- 4.1.** Select **New lab**.
  - 4.2.** Complete all the boxes in the **Shipping Destination** and **Contact Information** sections.
  - 4.3.** Optional: If you want to save this laboratory for future use, select the **Save address** box.
- 5.** Complete the information on the **Contact at sending lab** tab.  
This is where you enter the information for the person at your laboratory who should be contacted if there is an issue with the shipment.
- 6.** Optional: Complete the information on the **Shipment notes** tab.  
The **Comment** and **Disclaimer** will appear on the shipping manifest and will be shown to the receiving laboratory when they load the shipping file. These comments are in addition to comments that were entered for individual specimens. Use the **Comment** box for general information about the shipment. The **Disclaimer** box can be used to provide information about the restrictions placed on the specimens' usage.  
The **Shipment Carrier** and **Tracking Number** will *not* appear on the shipping manifest and are not included in the shipping file.
- 7.** Add specimens to the shipment on the **Shipment Contents** tab.
  - Add a container already setup on the **Storage** page to the shipment from the **Storage Containers** list.
  - Add specimens to a single use shipping container in the **Shipping Containers** section.
- 8.** Add storage containers to the shipment.
  - 8.1.** Click the **Add New** button to the right of the **Storage Containers** list.  
The **Storage Containers** window will open.
  - 8.2.** For each storage item to be shipped, select the check box next to it.
  - 8.3.** Click **Add Selected to Shipment**.
- 9.** Add individual specimens to the shipment.
  - 9.1.** Click the **Add New** button to the right of **Shipping Containers**.  
The **Create Shipping Container** window will open.
  - 9.2.** Enter the number of rows and columns for the container into the **Number of rows** and **Number of columns** boxes.  
This represents the size and capacity of the container. For example, a container with 8 columns and 5 rows could hold up to 40 specimens. The container as it is currently defined will appear in the **Preview** section.
  - 9.3.** Select or deselect the **Positions only** option as desired.  
If the positions only option is selected, each specimen in the shipping container will be identified by a number. If it is not selected, each specimen will be identified by its coordinates.

**9.4.** (If **Positions only** is not selected) Define how specimens in the container should be organized.

**coordinate order** This is how the specimens position will be identified, such as (8,5) or (5,8).

**column labeling and row labeling** This is how rows and columns will be named in the container. Alphabetic uses letters while numeric uses numbers. The second option specifies where labeling should start.

**9.5.** Select the fill order for the shipping container from the **Fill order** box.

The fill order is the logic that is used to determine where specimens will be placed in the container.

**9.6.** Select the sort order for the container from the **Primary Sort Order** box.

This is how specimens will be sorted before they are put into the container.

**9.7.** (If **Prot/ID2** was selected for primary sort order) Select a **Secondary Sort Order**.

**9.8.** Click the **Add Specimens** button.

**9.9.** Do one of the following:

- In the list of specimens, select the check box next to each specimen to be shipped. Use the available filters to find the specimens you need.

Or:

- Click the **Upload File: Unique specimen IDs** button to upload a file of samples to be included in the shipment.

**9.10.** In the list of specimens, select the check box next to each specimen to be shipped.

Use the available filters to find the specimens you need.

**9.11.** At the bottom of the Select Specimens to Ship window, click **Continue**.

The **Preview** section for the shipping container will indicate the positions that now hold specimens. If you added more specimens than could fit in the container, multiple containers will have been created. You can switch between these containers using the arrow buttons in the **Preview** section.

**9.12.** Click the **Add** button.

The shipping container will appear in the **Shipping boxes** list.

**10.** Do one of the following:

- To save the shipment so that it can be modified again before the shipping file is generated, click the **Save** button.
- To generate the shipping file now and change the shipment status to shipped, click the **Ship** button.

### Result

If the shipment was saved, a new shipment will be added to the **Pending Shipments** page. It will appear at the top of the list and will have been assigned the next available shipment number.

### After you are finished

You should perform QA/QC on the shipment after it has been created before sending it.

## Sending a pending shipment

Sending a shipment is the process of generating a shipping data file on the **Pending Shipments** page.

### Background

The shipping file can either be in LDMS format or CSV format. The file that is created will need to be transferred to the laboratory to add the specimens to their database.


### Steps


1. Click **Shipping > Pending Shipments** from the LDMS menu bar.
2. Locate the pending shipment to be sent.
3. Click the **Edit/Ship** button to the right of the shipment. The **Pending Shipment Preview** window will open.
4. Click the **Ship** button.

LDMS will warn you that this is your last chance to generate the Shipment Storage Report. If you want to view this report, click the **Cancel** button. On the **Shipment Contents** tab, click the **Shipment Storage Report** button to generate the report.

LDMS will check that the information for the shipment has been fully completed. If there are any issues, it will be highlighted in red and you will be prompted to correct it before continuing.
5. When asked to confirm if you want to send the shipment, click the **OK** button.

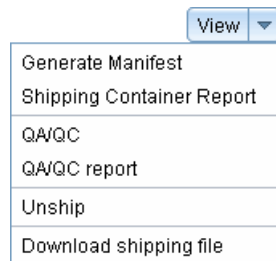
The shipping file will be generated. When it is ready, you will be prompted to save it to your computer.

 **Warning:** Do not close the window until the shipping file has been saved.

 **Note:** If there is an error in the shipment information, it can be corrected directly from the **Validation Error** page.
6. Click the **Close** button to go back to the **Pending Shipments** page.
7. Optional: Generate a shipping manifest.
  - 7.1. Click **Shipping > Shipment History** from the LDMS menu bar.
  - 7.2. Locate the shipment that you sent.

- 7.3.** Click the arrow next to the **View** button, and then click **Generate Manifest**.

**Figure 41: Generate Manifest**



### Result

The shipping file is now saved at the location you specified on your computer.

### After you are finished

This is the file you will need to transfer to the laboratory that will be receiving the specimens. You can either email this file to the receiving laboratory or provide it on removable media (such as a USB drive) with the physical shipment of specimens.

## Generating a shipping manifest

Shipping manifests contain an overview of the contents of a shipment, and are intended to be printed and included with shipments.

### Background

A shipping manifest should be printed and included with all shipments. This will help the laboratory receiving the shipment to identify its contents and match it to the shipping file that you provided to them. You can also save the manifest as a PDF file, and then send it to the receiving laboratory long with the shipping file.

The shipping manifest can be generated before or after a shipment is sent.

**Figure 42: A typical shipping manifest**

**Shipping Manifest**  
**QA/QC Not Performed**

Setup Date: 18/Feb/2022 2

**Batch Number: 527** 1

Shipped: No    Ship Date: 18/Feb/2022

<p><b>Shipped From:</b> Lab ID: 500                  Lab Name: Frontier Laboratories                  4033 Maple Road                  Amherst NY 14226 <span style="border: 1px solid black; border-radius: 50%; padding: 2px;">3</span></p> <p><b>Country:</b> United States  <b>Contact:</b> Jon Doe  <b>Phone #:</b> (444) 444-4444  <b>Fax #:</b> (555) 555-5555  <b>E-mail:</b> jdoe@gmail.com</p>	<p><b>Shipped To:</b> <span style="border: 1px solid black; border-radius: 50%; padding: 2px;">5</span>                  Lab ID: 1                  Lab Name: Partners AIDS Research Center                  Room 435, Room: 1                  65 Landsdowne St.                  Cambridge MA 02139</p> <p><b>Country:</b> United States  <b>Contact:</b> Colin McManus  <b>Phone #:</b> (617) 768-8298  <b>Fax #:</b> (617) 768-8299  <b>E-mail:</b> cmcmanus4@bwh.harvard.edu</p>
<p><b>Number of Specimens:</b> 4 <span style="border: 1px solid black; border-radius: 50%; padding: 2px;">4</span>  <b>Comments:</b>  <b>Carrier:</b> FedEx  <b>Tracking #:</b> 123456789</p>	

**Shipping Manifest** **Box Name: Box #1-1** 6

**Box Sort Order:** Prot/ID2, Specimen ID

**Batch Number:** 527      **Setup Date:** 18/Feb/2022      **Shipped:** No      **Ship Date:** 18/Feb/2022

Spec ID	Global Spec ID	Project/Prot	PID/ID1	VID	Clinic	Collection / Harvest Date	Spec Time	Prim	Add	Der	Sub A/D	Volume	Pos
500V11000009	AEQ005NZ-06	ACTG/IMPAACT A5001	01111111C	1 Wk	5043	23/Mar/2011	07:40	BLD	EDT	PL1	N/A	1 ML	1
500V11000009	AEQ005NZ-07	ACTG/IMPAACT A5001	01111111C <span style="border: 1px solid black; border-radius: 50%; padding: 2px;">7</span>	1 Wk	5043	23/Mar/2011	07:40	BLD	EDT	PL1	N/A	1 ML	2
500V11000009	AEQ005NZ-08	ACTG/IMPAACT A5001	01111111C	1 Wk	5043	23/Mar/2011	07:40	BLD	EDT	PL1	N/A	1 ML	3
500V11000009	AEQ005NZ-09	ACTG/IMPAACT A5001	01111111C	1 Wk	5043	23/Mar/2011	07:40	BLD	EDT	PL1	N/A	1 ML	4

(1) The shipment number, (2) The date that the shipment was initially created, (3) Sending laboratory’s contact information, (4) Shipment carrier and tracking information (5) Receiving laboratory’s contact information, (6) Name of shipping container, (7) Specimens in the shipping container

**Steps**

1. Do one of the following:
  - For pending shipments, click **Shipping > Pending Shipments** from the menu bar.
  - For sent shipments, click **Shipping > Shipment History** from the menu bar.
2. Locate the shipment for which you want to generate a manifest.
3. Click the arrow next to the **View** button to the right of the shipment, and then click **Generate Manifest**.
4. Select PDF from the **File type** box.  
 Because manifests are intended to be printed, they have been designed with PDF output in mind only. If you select a different file format for the manifest, you may experience formatting issues.

**Result**

You will be prompted to save the manifest or it may open automatically, depending on the default behavior of your web browser.

## Shipment Tracking Information

Information about a shipping carrier and the tracking number can be entered into LDMS at any point by both a sending a receiving laboratory.

The **Shipping Carrier** and **Tracking Number** are on the **Shipment Notes** tab when viewing a shipment. This information can be updated at any time for any shipment, including shipments that have already been sent or received by your laboratory.

Shipment tracking information will not appear on printed shipping manifests and will not be included in shipping files.

## Supported shipping file formats

These are the file formats that are supported for sending and receiving shipping files.

**Table 14: Supported shipping file formats**

Format	Encrypted?	Intended destination
LDMS	Yes	Laboratories using LDMS (both web and windows version)
CSV	No	Laboratories not using LDMS
SeraCare	No	Specimens being sent to the Precision Bioscience Repository
Cross-LIMS Manifest	No	Laboratories not using LDMS

### CSV shipping files

LDMS can generate and accept CSV (comma separated value) shipping files that meet these requirements.

- The file must be a comma delimited text file with the .csv file extension.
- The first line in the file must be a header row.
- The file must contain, at minimum, all required columns (in any order) to be processed by LDMS.
- When a CSV shipping file is generated by LDMS, all columns listed in the following table will be included.



**Note:** Field headers in the file are not case-sensitive.

Column Label	Example Value	Column Required in File	Must be Defined in File	Notes
Shipment Number	145	No	No	ID number for the shipment.
Sending Lab	500	Yes	Yes	ID number for the laboratory sending the shipping file.



Column Label	Example Value	Column Required in File	Must be Defined in File	Notes
Receiving Lab	143	No	No	ID number for the laboratory receiving the shipping file.
Setup Date	05/Jan/2016	No	No	Date shipping file was created. Must be in the format dd/Mmm/YYYY.
Ship Date	05/Jan/2016	No	No	Date specimens were shipped. Must be in the format dd/Mmm/YYYY.
Temperature	Dry Ice	No	No	Temperature of the shipment.
Shipment Comment	This is a comment	No	No	Notes about the shipment.
Container	Box #1-1	No	No	Name of container holding specimen.
Row	1	No	No	Position of specimen in container. Alpha and numeric coordinates are allowed.
Column	1	No	No	Position of specimen in container. Alpha and numeric coordinates are allowed.
QA Performed	--	No	No	Whether shipping file was compared to the actual shipment to ensure specimens were correct and included in the correct container locations.
project	FRONTIER	Yes	Yes	Name of project for which the specimen was collected.
ID1	0111111C	Yes	Yes	Participant or specimen source ID.
ID2	F5309	Yes	Yes	Protocol ID.
ID3	--	Yes	No	Sub-protocol ID.
Visit	1	Yes	No	Visit value.
Visit Unit	WK	Yes	No	Unit for visit. Must be a valid LDMS visit unit code.
Clinic	701	Yes	No	Clinical site where specimen was collected.
Specimen Date	05/Jan/2016	Yes	Yes	Collection date. Must be in the format dd/Mmm/YYYY.
Specimen Time	15:20	Yes	No	Collection time. Must be in 24-hour format.
Received Date	05/Jan/2016	Yes	Yes	Date specimen was received by laboratory. Must be in the format dd/Mmm/YYYY.
Received Time	15:20	No	No	24-hour time specimen was received by laboratory. Must be in 24-hour format.
Specimen ID	500V0500001	No	No	Specimen ID (used for specimens entered in LDMS for Windows only).
Global Spec ID	CEQ0000P-03	No	No	If not specified, a global specimen ID will be generated automatically when the shipping file is received in LDMS.

Column Label	Example Value	Column Required in File	Must be Defined in File	Notes
Other Spec ID	--	No	No	Other specimen ID.
Primary	BLD	Yes	Yes	Specimen primary type. Must be a valid LDMS primary code.
Additive	EDT	Yes	Yes	Specimen additive. Must be a valid LDMS additive code.
Derivative	PL2	Yes	No	Specimen derivative. Must be a valid LDMS derivative.
Sub A/D	N/A	No	No	Specimen sub-additive/derivative. Must be a valid LDMS sub-additive/derivative code. If not specified, will default to N/A.
Volume	1.5	Yes	Yes	Volume of specimen
Volume Units	ML	Yes	Yes	Units used for specimen volume.
Condition	SAT	No	No	Three letter code representing specimen's current condition. If not specified, will default to SAT.
Comments	This is a comment	No	No	Notes about the specimen
Tests	--	No	No	Assays assigned to the specimen
Processing Date	05/Jan/2016	No	No	
Processing Time	15:20	No	No	
Frozen Date	05/Jan/2016	No	No	
Frozen Time	15:20	No	No	
Total Cell Count		No	No	
Processing Tech		No	No	
Second condition code		No	No	
Freezer		No	No	
Level 1		No	No	
Level 2		No	No	
Harvest Date	05/Jan/2016	No	No	
Additional Time	15:20	No	No	

Column Label	Example Value	Column Required in File	Must be Defined in File	Notes
Additional Time Unit		No	No	
Thaw Count		No	No	
Internal comments	This is a comment	No	No	Import this field if it's in the file, but do NOT ship it out from WebLDMS
Reason not collected		No	No	
Primary Database ID	12345	No	No	Primary Specimen's Database ID value. Must be sourced from a primary specimen that already exists in the database. Setting this value will ensure new aliquots are organized under the specified primary specimen provided other dependent values are properly matched. Value can be determined from Custom Report Builder or from the primary's Edit Primary Specimen popup URL in Specimen Management.

### Cross-LIMS shipping files

LDMS can generate and accept cross-LIMS shipping files that meet these requirements.

- The file must be a tab delimited text file with the .txt file extension.
- The first line in the file must be a header row.
- The file must contain, at minimum, all required columns (in any order) to be processed by LDMS.
- When a cross-LIMS shipping file is generated by LDMS, all columns listed in the following table will be included.
- If additional columns are present in a cross-LIMS file, those columns will be ignored.
- Cross-LIMS shipping import sets the clinic value for VTN records based on the PID. This allows LDMS labs to receive cross-LIMS shipments of VTN samples if needed.

Column Label	Example Value	Required	Notes
SHIP_ID	0500-0999-0000000147	Yes	In the format <i>[Sending_Lab_ID]-Receiving_Lab_ID]-[Shipment_ID]</i> leading zeros must be added to make the ID the correct length (for example 500-19-147 is not valid, but 0500-0019-0000000147 is valid)
SHIP_DATE	06-Jan-16	No	Date shipped. Date must be in the format dd-Mmm-yy

Column Label	Example Value	Required	Notes
RECIPIENT	999	Yes	Receiving laboratory's ID
SHIPPED_FROM	500	Yes	Sending laboratory's ID
GLOBAL_ID	GEQ00017-03	No	A valid LDMS global specimen ID
project	FRONTIER	Yes	The project for which the specimen was collected.
PROTOCOL	F5309	Yes	The protocol (ID2) for which the specimen was collected
PID	0777777F	Yes	The participant identifier (ID1)
VID	7	Yes	The visit value
VID_UNIT	Day	Yes	The visit unit. Must be a valid LDMS visit code
COLL_DT_TM	17-Jan-05 09:12	Yes	Collection date and time, in the format dd-Mmm-yy HH:mm, using 24-hour clock
PRIM	BLD	Yes	Primary type. Must be a valid LDMS primary code.
DER	PL2	Yes	Derivative type. Must be a valid LDMS derivative code.
SUBDER	N/A	Yes	Sub-additive/derivative type. Must be a valid LDMS sub-additive/derivative code.
ADD	EDT	Yes	Additive type. Must be a valid LDMS additive code
QTY	1	Yes	Volume of the specimen collected.
QTY_UNIT	ML	Yes	Volume unit. Must be a valid LDMS volume unit code.
CONDITION	SAT	No	Condition of the specimen. Must be a valid LDMS condition code.

Column Label	Example Value	Required	Notes
OTHERSPECID	VTN	No	Other Specimen ID. Must be alpha/numeric with a max field length of 17 characters.
TIME	0.00	No	Must include the Additional Time. Format must be numeric/decimal with precision to two decimals.
TIMEUNIT	HRS, TR, or RAN	No	Must include Additional Time Unit Abbreviation. The field must be three characters long.
COMMENT	This is a comment	No	A comment about the specimen.
BOX	#1-1	No	Name of shipping container
ROW	1	No	Row in shipping container (from top-to-bottom)
COL	1	No	Column in shipping container (from left-to-right)

**SeraCare shipping files.**

LDMS can generate (but not receive) "SeraCare" shipping files that meet these requirements.

Column Label	Example Value	Notes
Global Spec ID	0777-001MWK00-286	
project	FRONTIER	The project for which the specimen was collected.
PID	0111111C	Participant ID (ID1)
VID	8	Visit value.
VID Unit	Vst	Visit unit.
Collection Date	1-Mar-13	Collection date
Collection Time	1:00	Collection time.
Prim	BLD	Primary type.
Der	BLD	Derivative type.
Add	ACD	Additive type.
Other Spec ID	PLORQ	--
Volume	1	--
Volume Unit	ML	--



## Shipment storage report

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This report lists the specimens in a shipment and their assigned storage location.

This report is intended to be printed and be used to help locate and pull specimens from storage. This would only be applicable if you assigned a storage location to the specimens being shipped on the **Storage** page.

You can generate the Shipment Storage Report when generating a shipping file. After a shipping file has been created, you can access the report from the **Shipment History** page by clicking the drop-down next to the **View** button for the shipment and selecting **Shipment Storage Report**.

### Information displayed on report

- Shipment number
- Shipment setup date
- Specimen ID
- Global specimen ID
- Other specimen ID
- project/ID2
- ID1
- Visit
- Collection date
- Collection time
- Primary
- Additive
- Derivative
- Sub additive/derivative
- Volume
- Storage location
- Original storage location

## Receiving shipments

---

Receiving a shipment is the process of importing specimen information from laboratory into your laboratory.

### Background

Once you have the shipping file from the laboratory sending you the specimens, you can import the specimen information into LDMS.

### Steps

1. From the menu bar, click **Shipping > Receive Shipments**.
2. Click **Select File**.

A window will open to select the shipping file. The shipping file will generally be named `ship-[your laboratory ID number].xml` for LDMS shipping files or `lab[your laboratory ID number].csv` for CSV files.



**Note:** Supported ID formats include Specimen IDs, Other Spec IDs, Global Spec IDs, and Database IDs.

3. Optional: If you want specimens to automatically be assigned storage locations, select **Import directly into storage**.
4. Optional: To apply RPID to the specimens being imported, select **Import as RPID**. This will anonymize the imported specimen data. This feature is disabled by default and must be activated by LDMS User Support, and the feature can only be applied to specimens for the ACTG or IMPAACT projects.
5. Click **Preview Shipment**.
6. On the **Confirm Temperature** list, select the temperature of the shipment as you received it.
7. **Optional:** Click the **Edit Condition Codes** button to update information of specimens on the shipping file before receiving the shipment.
  - 7.1. After clicking the **Edit Condition Codes** button, the **Set Condition Codes** window will open.
  - 7.2. Select specimen(s) from the table.
  - 7.3. Apply condition codes, set as unavailable, or add comments as needed.
  - 7.4. Click **Update Selected Specimens**.
  - 7.5. When finished, click **Save**.
8. Review the shipment to ensure it is correct.

It is a good idea to check that the shipping destination is your laboratory, and that the specimens are what you were expecting. Click the **View** button next to shipment containers to see what specimens are in the shipment. By checking the shipment at this stage, you can avoid potential errors, such as receiving the wrong shipping file.
9. Click **Receive Shipment**.



**Note:** If the shipping temperature you indicated differs from the temperature indicated in the shipping file, you will be asked if you want to override the shipping temperature. This means the temperature you selected will be saved in your database instead of the temperature from the sending laboratory.

### Result

LDMS will assign the next available shipment number to the shipment.

### After you are finished

Go to the **Shipment History** page to view the newly received shipment and perform additional actions, such as QA/QC.



## Shipping and projects

During shipping import, users will be notified if the file contains a new project that does not exist in their database. If the new project is not expected, the import can be cancelled.

### Import as is

When receiving a shipping file, it is possible to take shipping and storage items in the shipment and automatically assign them to your laboratory's storage. The option to do this is provided when receiving a shipping file.

The items on the shipment will be placed in your storage based on what it is.

Item	Where it will go in storage
Storage unit	Added as a new storage unit
Level or container	In the <b>SHIPPING IMPORT FREEZER</b> , on a level with the shipment number

If the item was a storage item at the sending laboratory, it will retain its original name in your storage. If the item was a storage container created for the shipment, it will be placed in the **SHIPPING IMPORT FREEZER** on a level with the shipment number. These containers will generally have names like "Auto-generated box #76-1" in your storage. The shelf name also includes the sending lab ID.

Once the items are added to your storage, you are not restricted to how you use them. You can retain containers, move them to different storage units, and so forth.

### Handling non-LDMS shipping files

Shipping files that did not originate from LDMS may not contain the global specimen ID needed by LDMS. Such specimens will receive special handling when they are received.

- All specimens without a global specimen ID will be treated like aliquot specimens and assigned to a new primary specimen.
- All specimens without a global specimen ID will be assigned one
- Specimens with the same project, ID1, ID2, visit, collection date, collection time, primary type, and additive time will be grouped until the same primary specimen.

## Shipment QA/QC

---

Shipment QA/QC is the process of comparing actual specimens in a shipping container to the specimen that is expected in that container position by LDMS. This should be done for shipments before they are sent and after they are received.

You can view the current QA/QC status of a shipment on the **Pending Shipments** or **Shipment History** page.

QA/QC Status	Action Needed
Complete	None
In Progress	Finish QA/QC
Complete with Errors	Investigate the specimens that did not pass QA/QC
Not Performed	Start QA/QC

To perform QA/QC, you need to look at the global specimen ID on a physical specimen, and then compare it to the global specimen ID in LDMS. If they match, the specimen has passed, otherwise it has failed. QA/QC should be performed by scanning the specimen's barcode, which will read the global specimen ID and do the comparison for you. This is the recommended process. If you do not have a barcode scanner, you can manually compare the two global specimen IDs instead.

**Figure 44: The QA/QC Entry page**

QA/QC Entry, Shipment Number 623

Select a container 1 Box #1-1

Container 1 of 1

	?	?	?	?	?	?	?

Performed By 3 ADM  
 Date 30/Dec/2024  
 Fill Order Left to Right, Top to Bottom  
 Container Type Shipment

Alternative Scanning

Scan barcodes with alternative identifiers

Match Scan Against Global Specimen ID

Field

Scan Input (Alt+I)

Position (Absolute) 1

Global Specimen ID 0500-00JZVJ00-001

Scanned ID

Correct Coordinates

Performed By

Other Specimen ID

Comments 5

7

Specimen ID

Primary BLD

Additive EDT

Derivative PL2

Sub Add/Der N/A

Project FRONTIER

ID1 / PID DDD

ID2 / Study WWW

ID3 / visit

Collection / Harvest Date 23/Dec/2024

Collection Time

Additional Time

Visit 2 Vst

Volume 1 ML

(1) Containers in the shipment, (2) Currently selected specimen, (3) Manually pass or fail selected specimen, (4) Currently selected specimen's global specimen ID, (5) Modifiable boxes, (6) Indicator showing that you can scan a barcode to complete shipment QA/QC automatically, (7) Print the current label

If the shipment contains multiple containers, you will need to change containers during QA/QC, since each container must be reviewed separately.

While performing QA/QC, you have the option to modify each specimen's other specimen ID and comments. If you do so, these changes will be reflected in the specimen information on the **Specimen Management** page.


**Performing QA/QC**

QA/QC is performed by scanning or comparing each specimen's label with the expected specimen information, and indicating if it is correct or incorrect.

## Background

QA/QC should be performed after creating a pending shipment but before creating the shipping file. It should also be performed on shipments from other laboratories after they have been received.

## Steps

1. Do one of the following:
  - To QA/QC a pending shipment, on the navigation menu, hover over **Shipping**, and then click **Pending Shipments**.
  - To QA/QC a pending shipment, on the navigation menu, hover over **Shipping**, and then click **Shipment History**.
2. On the **Edit/Ship** (for pending) or **View** (for received) menu in the right column, click **QA/QC**.
3. Optional: Enter the initials of the person that performed QA/QC and the date that it was completed in the **Performed By** and **Date** boxes.
4. With the first specimen select (which is the default), do one of the following:
  - Scan the specimen barcode (recommended). After scanning the barcode, one of two sounds will play, depending on whether the sample passes or fails.
    -  **Note:** Users can QA/QC shipments by scanning non-LDMS generated barcodes. The value in the scanned barcode must match to the value set in Other Specimen ID or ID1/PID field for QA to pass.
  - Manually compare the **global specimen ID** on the screen with the global specimen ID on the specimen label. If they match, click **Pass Specimen**, otherwise click **Fail Specimen**.
5. (If there are multiple shipment containers) After each specimen in the container has been reviewed, select the next item from the **Select a Container** list.
6. After all specimens in the shipment have been reviewed, click **Save** at the bottom of the page.

## After you are finished

Confirm that QA/QC has been completed for the shipment by looking at the **QA/QC** column on the **Pending Shipments** or **Received Shipments** page.

---

## Shipment history

A record of shipments sent and received can be found on the **Shipment History** page.

In terms of LDMS, a shipment received is one for which you have uploaded a shipping data file from another laboratory in LDMS, and a shipment sent is when you have generated the shipping data file.

**Figure 45: The Shipment History page**

Shipment Number	Shipment Type	Shipment Format	Destination Lab	Sending Lab	Sending Lab Shipment Number	Shipment Temperature	Setup Date	Shipment Date	Received Date	QA/QC	Shipment Evaluation	
536	Received	LDMS	213	501	21	Liquid Nitrogen			28/Nov/2022	Not Performed	<input checked="" type="checkbox"/>	View
535	Received	CSV	10	673	1389	Dry Ice			21/Nov/2022	Not Performed	<input type="checkbox"/>	View
534	Received	LDMS	15	5005	1515	Ambient			16/Nov/2022	Not Performed	<input type="checkbox"/>	View
533	Received	LDMS	15	501	12	Ambient			25/Oct/2022	Not Performed	<input checked="" type="checkbox"/>	View

1 - 4 of 4 results

- Generate Manifest
- Shipment Storage Report
- Shipping Container Report
- Print labels
- Edit Shipment Evaluation
- Delete Shipment Evaluation
- Download Shipment Evaluation Form
- QA/QC
- QA/QC report
- 1D Barcodes Report
- 2D Barcodes Report
- Set Condition Code
- Unimport

- Shipment number** An internal shipment number assigned to the shipment at your laboratory
- Shipment type** Indicates whether the shipment was **sent** to another laboratory or **received** from another laboratory
- Shipment format** The type of shipping file
- Destination laboratory** The laboratory ID of the destination that is indicated within the shipping file
- Sending laboratory** The laboratory that generated the shipping file.
- Sending lab shipment number** Original shipment number assigned by lab that sent shipment
- Shipment temperature** The shipment temperature that was indicated in the shipping file
- Setup date** The date the shipping file was created
- Shipment date** The date that the shipping file was generated
- Received date** The date that your laboratory loaded the shipping file in LDMS (only applicable to shipments that you received)
- QA/QC** This indicates whether or not QA/QC was performed on the shipping file
- Shipment Evaluation** This Indicates whether or not a Shipment Evaluation has been performed for the shipment

**Removing a received shipment**

**Background**

If a shipping file was received and loaded into LDMS in error, it may need to be removed. Because multiple laboratories may be affected and the quality of specimen data affected, the ability to unload a shipping file that was received requires you to contact LDMS User Support.

### Steps


1. Contact LDMS User Support.  
This should be done first because if your session is idle for too long and you are logged out, a new challenge code will be generated.
2. In the menu bar, click **Shipping > Shipment History**.
3. On the **View** button to the right of the shipment, click the arrow and select **Unimport**.
4. Provide LDMS User Support with the **Challenge Code**.
5. In the **Response Code** box, enter the code provided LDMS User Support.
6. Click **Unimport**.

### Un-sending shipments

After a shipping file has been generated and a shipment changed to sent in LDMS, it is possible to change the shipment back to a pending state.

### Background

This would be necessary if you need to modify the shipment and re-generate the shipping file. This could happen, for example, if you discovered there were more specimens to be shipped and the shipment hasn't left your laboratory yet.

 **CAUTION:** A shipment should not be un-sent if the receiving laboratory has received and loaded the shipping file. Doing so would cause the specimens to appear at both laboratories. Contact the receiving laboratory and ensure that have not yet loaded the shipping file before continuing.

### Steps

1. In the menu bar, click **Shipping > Shipment History**.
2. On the **View** button to the right of the shipment, click the arrow and select **Unship**.
3. Click **Unship**.

### Re-downloading the shipping file of a sent shipment

It is possible to re-download the shipping file of a previously sent shipment.

### Background

When you send a pending shipment, you will be prompted to download the shipping file that you will need to supply to the receiving laboratory. If this file becomes lost or damaged, it is possible to download it again. This file will be identical to the shipping file that was previously downloaded.

### Steps

1. In the menu bar, click **Shipping > Shipment History**.

2. On the **View** button to the right of the shipment, click the arrow and select **Download shipping file**.
3. When prompted, save the shipping file.

## Bulk Updating Condition Code and Comments of Shipments

Users have the ability to bulk update the Condition Code and Comments for all specimens in a shipment. This is accessed through the **Shipping** menu.

### Background

#### Steps

1. From the menu bar, click **Shipping**, and then click **Shipment History**.
2. Find the shipment that needs updating and click the arrow next to **View**.
3. From the dropdown menu, click **Set Condition Code**. The **Set Condition Code** window will appear.

Set Condition Code

---

**Note: The following values will be applied to all specimens within this shipment.**

Specimen Condition  \*

Comments

Internal-Only Comments

Unavailable

Unavailable Date

---

4. In the new window, select the specimen condition from the dropdown menu.
5. Add any comments or mark as unavailable as needed.
6. Click **Save**.

## Shipment Evaluations

Users can create new shipment evaluations for received shipments and update existing ones.

**Figure 46: Create Shipment Evaluation Screen**

Create Shipment Evaluation

---

Sending Lab  \*

Sending Lab Batch #  \*

Did the received shipment have any reportable problems?  Yes  No \*

Comments

Problem Codes

Problem Code	Comments	Select ID2s	ID2s	Action
102 - Missing Paper Shipping Manifest	<input type="text"/>	1 item(s) selected	IB853	<input type="button" value="Delete"/>
201 - LDMS Shipping File Does Not Import	<input type="text"/>	0 item(s) selected		<input type="button" value="Delete"/>

Is this shipment considered resolved?

Evaluation Form

(1) Add or update the sending lab batch number, (2) indicate whether the shipment had any reportable problems, (3) add any comments, (4)\* select a problem code from a dropdown, (5)\* add more dropdowns for additional problem codes, (6)\* remove a listed problem code, (7)\* Associate comments and ID2s to individual problem codes, (8)\* indicate whether the shipment is considered resolved, (9) upload a shipment evaluation form, (10) create the shipment evaluation

\*Only available if user selects **Yes** for the question **Did the received shipment have any reportable problems?**

### Creating a New Shipment Evaluation

1. From the LDMS menu, navigate to **Shipping**, then select **Shipment History**.
2. In the dropdown menu of a received shipment, select **Add New Shipment Evaluation**.
3. On the **Create Shipment Evaluation** screen, indicate whether the received shipment had any reportable problems, and enter a comment and attach an evaluation form as needed.



4. If the user indicates that the shipment did have reportable problems, at least one problem code must be added. The user may also indicate whether the shipment is considered resolved.
5. Click **Create** to create the evaluation.

### **Editing an Existing Shipment Evaluation**

Users may edit or delete a shipment evaluation or evaluation form as needed.

- To update an existing Shipment Evaluation form, click **Edit Shipment Evaluation** in the dropdown next to a received shipment. Make changes as needed and then click **Edit**.
- To delete an existing Shipment Evaluation form, click **Delete Shipment Evaluation** in the dropdown next to a received shipment. In the bottom of the **Delete Shipment Evaluation** window, click **Delete**.

## **Reports**

The **Reports page** is where you can retrieve data that is stored in your laboratory's LDMS database.

While you can browse specimen information for individual participant visits on the **Specimen Management page**, you can't control what is displayed and how. For example, suppose you need a list of participant identifiers for all participants at your laboratory, and what project those participants belong to. You can't quickly get this information from the Specimen Management page.

This is where reports are helpful. The Reports page allows you to generate pre-defined reports about data in your laboratory's LDMS database. While the content of these reports are predetermined, you can often add criteria to filter what will be displayed. For example, you could generate a report that lets you see all participant identifiers at your laboratory, but only for a specific project.

### **Custom Report Builder**

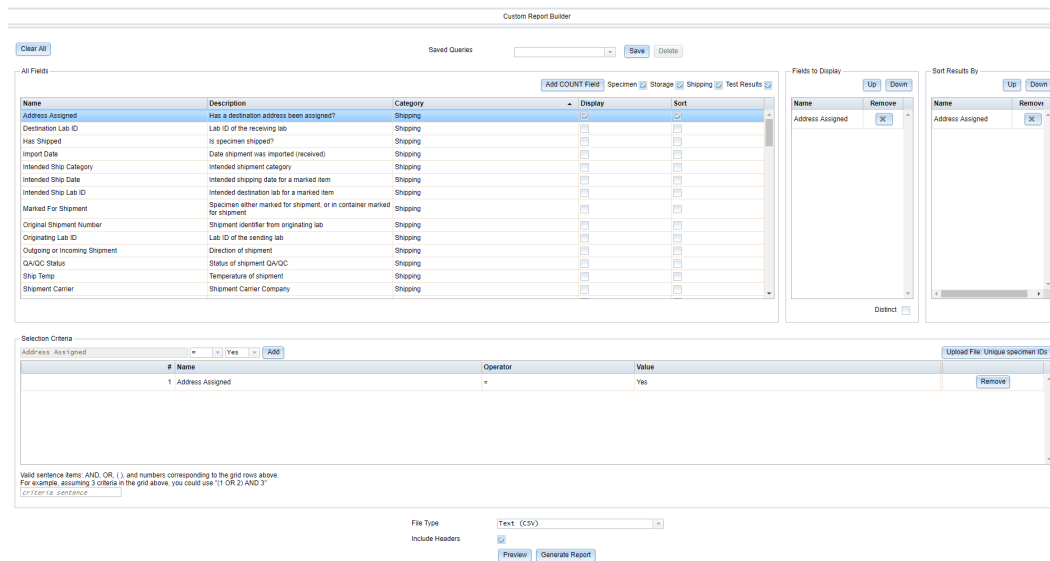
---

The Custom Report Builder allows you to export specimen data from LDMS into a wide variety of formats.

The custom report builder allows you to do the following:

- specify what data to use to select specimens to appear on the report
- the information to appear on the report
- how to sort information on the report
- apply complex logic to reports
- save custom reports so they can be re-used

**Figure 47: The Custom Report Builder**



## Creating a custom report

Custom reports are created by indicating the information that should appear on the report, how the report should be sorted, and any special logic for selecting specimens.

### Steps

1. From the menu bar, click **Reports > Custom Report Builder**.
2. In the **All Fields** section, do the following:
  - For items that you want to *appear* on the report, select the check box under **Display**.
  - For items that you want to use to *sort* records on the report, select the check box under **Sort**.
3. Optional: Use the **Add COUNT Field** to provide aggregate counts on the report.
  - 3.1. Click the **Add COUNT Field** button in the **All Fields** section. The **Add COUNT Field** window will open.
  - 3.2. Select the field, enter the label, and mark as distinct as needed.
  - 3.3. Click **OK**.
4. In the **Fields to display** and **Sort results by** section, use the **Up** and **Down** buttons to set the order of items.
 

Fields displayed on the report will be shown from left-to-right in the order you specify. Results will be sorted in the order specified. An item can be removed by clicking the **X** next to it or deselecting the check box.

**Example**

If you sort by **Destination Lab ID** and **Ship Date**, the records on the report will first be sorted by the destination laboratory, and *then* by the shipment date.

5. Optional: To remove duplicate records, under **Fields to display**, select **Distinct**.  
Any rows on the report that have the same values across all displayed fields will only appear on the report once.
6. Optional: Apply a filter to your report in the **Selection criteria** section.  
If no selection criteria is specified, all data from your laboratory will be included.
  - 6.1. In the **All Fields** section, click an item to select it.
  - 6.2. In the **Selection criteria** section, select an operator and value for your filter.
  - 6.3. Click **Add**.
  - 6.4. In the box below the filters, enter logic for applying the filter using the numbers next to each item.  
If you leave this box blank, filters will be applied as 1 AND 2 AND ... (etc.).

**Example**

For example, if you want to apply filter #1 and either filters #2 or #3, enter 1 AND (2 OR 3).

**Example**

To apply a filter that excludes specimens that originated from laboratory 500, select **Source Lab ID** in the **All Fields** section, the **<>** operator, and enter 500.



**Note:** LDMS accepts wildcard values (\*). Wildcard values can be used for the Like and Not Like qualifiers.

7. In the **File Type** list, select the format for your report output.
8. Optional: If you do not want a header row with the name of each column to appear on your report, deselect **Include Headers**.
9. Do one of the follow:
  - To save your report so that it can be run later, enter a name for your report into the **Saved Queries** box at the top of the page, and then click **Save**.
  - To view the first 100 records of the report in your browser, click **Preview**.
  - To generate and save the report in the indicated file type, click **Generate Report**.

**Running a saved report**

Saved custom report can be run at any time.

### Steps

1. From the menu bar, click **Reports > Custom Report Builder**.
2. In the **Saved Queries** box, select the report you want to run.
3. Optional: Make any changes needed to the report's fields, sort order, or selection criteria.  
Changes will *not* be permanently saved unless you click **Save** at the top of the page.
4. Do one of the following:
  - To view the first 100 records of the report in your browser, click **Preview**.
  - To generate and save the report in the indicated file type, click **Generate Report**.

### Modifying or deleting a saved report

A saved custom report can be modified and re-saved or deleted.

### Steps

1. From the menu bar, click **Reports > Custom Report Builder**.
2. In the **Saved Queries** box, select the report you want to run.
3. Do one of the following:
  - To remove the saved report, click the **Delete** button.
  - To modify the report, make changes to its fields, sort order, or selection criteria, and then click **Save**.
  - To modify the report and save it as a new report, enter a new name into the **Saved Queries** box, and then click **Save**.

### Example custom report

This is an example of a custom report for tracking specimens on shipments that have not been sent.

This report will find all specimens in your laboratory's database that are part of a shipment and are still available. It filters by specimens that are available and have a shipment setup date (all specimens with a shipment setup date will meet the "before 30/Sep/2099" criteria, since that date is in the future). This report would be useful for identifying specimens that you are expected to ship but still have in your possession.

- Fields to display**
- Global specimen ID
  - Batch number
  - QA/QC status
  - Shipment setup date
  - Destination laboratory ID

- Sort results by**
- Destination laboratory ID
  - Batch number

**Selection criteria**

- Available = Yes
- Destination laboratory ID <> *Your\_Laboratory\_ID*
- Shipment setup date < 30/Sep/2099

## Generating a report

All reports are generated by following this procedures

### Background

By default, any report is generated using all available data in laboratory’s database. If you want to narrow down the records that will appear on a report, you must apply filters. If more than one filter is applied, only records that met *all* of the filters will appear on the report.

**Figure 48: The Reports page**

Report Categories  1

Report

Filter Criteria

Volume Unit  ML 2

#	Field	Operator	Value	
1	Primary	=	BLD	<input type="button" value="Delete"/>
2	Primary	=	ART	<input type="button" value="Delete"/>
3	Volume	>	10	<input type="button" value="Delete"/>
4	Volume Unit	=	ML	<input type="button" value="Delete"/>

Valid sentence items: AND, OR, (), and numbers corresponding to the grid rows above.

3

File Type  4


In this example, the report that will be generated will contain all BLD or ART specimens that also have a volume greater than 10 mL. (1) Report categories, (2) Add criteria to table below, (3) Logic for generating report, (4) File format for the report

### Steps

1. On the LDMS menu bar, click **Reports > Standard Reports**.
2. In the **Report categories** box, select a broad category for the report you want to generate.
3. In the **Report** box select a report.

4. Optional: Add one or more filter to narrow down the information displayed on the report.
  - 4.1. Select a data item to filter by from the box below **Filter Criteria**.


Additional boxes will appear to specify the details for the filter.
  - 4.2. Select an operator from the middle box.

 **Note:** The <> operator means “not equal to”.
  - 4.3. Select a value for the filter from the third box.

The values available will be dependent on the filter. For example, if you are filtering by *Additive*, only valid additives in LDMS will be displayed.
  - 4.4. Click the **Add** button.

Your criteria will be added to the list of filters. If you want to remove it after it has been added, click the **Delete** button to its right.
5. Optional: Specify logic for the report in the box below the filter criteria.

The logic is formed by using the numbers in the **#** column in the filter criteria, along with the words *AND*, *OR*, or parenthesis.
6. Select a format for the report from the **File Type** box.
7. Click the **Generate** button.

 **Note:** If no filter criteria is entered, LDMS will alert the user that the report may take a long time to generate.

### Result

The report will be generated in the format that you specified. You may be asked to open or download the report, depending on your web browser's default behavior.

---

## Filter Reports Using a List of Specimens

---

You can use a list of identifiers to select a set of specimens.

The Specimen List feature is an available filter criteria on select reports. The filter criteria allows users to select specific specimens for display using a list of IDs. The file of identifiers must be a text file and must include one Global Specimen ID per line.

### Figure 49: Global ID List File Example

```
0500-00ABCDE00-001
0500-00ABCDE00-002
0500-00FGHIJ00-001
0500-00FGHIJ00-002
0500-00FGHIJ00-003
0500-00KLMNP00-001
```

## Available report formats

This section describes the file formats in which LDMS can generate reports.

- If you are generating a report from the **Exportable** reports category, the **Microsoft Excel Workbook Data-only** file type should be used.
- Reports in any category other than **Exportable** are designed for **PDF**.
- Use other file types for reports may result an unexpected formatting, depending on the report. There may also be variations in the file type's format, depending on the specific report.

**Table 15: File types for LDMS reports**

File type	Extension	Description	Opened by...
Crystal Reports	.rpt	Do not use	N/A
PDF	.pdf	A formatted report intended to be printed on letter size paper (preferred)	A PDF viewer, such as Adobe Reader
Character separated values	.csv	A text file with all information separated by comma characters	A text editor, such as Notepad
Microsoft Excel (97-2003)	.xls	A workbook for versions of Excel prior to Excel 2007; this version contains a header row for each column	Microsoft Excel or LibreOffice Calc
Microsoft Excel (97-2003) Data-only	.xls	Same as above, but usually without a header row	Microsoft Excel or LibreOffice Calc
Microsoft Excel Workbook Data-only	.xlsx	A workbook that will work in Excel 2007 or later (preferred for exportable reports)	Microsoft Excel 2007 or later, or LibreOffice Calc
Microsoft Word (97-2003)	.doc	A Word document with formatting, such as tables and headers; can be difficult to modify, depending on the report	Microsoft Word or LibreOffice Writer
Microsoft Word (97-2003) Editable	.rtf	A rich-text file that can be edited by many word processors; uses less formatting, which makes it easier to modify	Microsoft Wordpad
Rich Text Format	.rtf	Same as Microsoft Word (97-2003) format, but compatible with RTF word processors	Microsoft Wordpad
XML	.xml	A Crystal Reports XML file. The scheme for this format <a href="#">is available</a>	An advanced text editor, such as Notepad++
Tab-separated Text	.ttx	A text file with information separated by tab characters.	A text editor, such as Notepad

## Administrative reports

### Anonymous Patients Map

Provides a list of all anonymized specimens with their anonymized ID1s mapped to their source ID1s.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• Anonymized Date</li> <li>• Anonymized ID1</li> <li>• Original ID1</li> </ul>	<ul style="list-style-type: none"> <li>• Source ID1</li> <li>• Anon ID1</li> <li>• Source Specimen ID</li> <li>• Source Global Specimen ID</li> <li>• Anon Global Spec ID</li> <li>• Source Specimen Date</li> <li>• Anon Specimen Date</li> </ul>

### Transaction Log Report

On the Reports page, select **Report Categories > Admin**, then from the **Report** dropdown, select **Transaction Log Report**.

You may add start and end date filters as well as any others as desired.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• End Date</li> <li>• Global Spec ID</li> <li>• Start Date</li> <li>• Transaction Type</li> <li>• User</li> </ul>	<ul style="list-style-type: none"> <li>• User</li> <li>• Date/Time</li> <li>• Table</li> <li>• Transaction Type</li> <li>• Old Data</li> <li>• New Data</li> <li>• LDMS Transaction ID</li> </ul>

Figure 50: The Transaction Log Report

User	Date/Time	Table	Transaction Type	Old Data	New Data	LDMS Transaction ID
Moz	06/Nov/2023 12:36:42 EST	Patients	Add		ID1 = 123654; Group ID = 1300005	32,549
Moz	06/Nov/2023 12:36:42 EST	Enrollments	Add		ID2 = APRICOT	32,550
Moz	06/Nov/2023 12:36:42 EST	Visits	Add		Visit Value = ; Visit Unit = ; ID3 = ; Clinic =	32,551
Moz	06/Nov/2023 12:36:42 EST	VisitSamples	Add		Global Specimen ID = KEQ0078L-00	32,552
Moz	06/Nov/2023 12:50:03 EST	Samples	Update	Global Specimen ID = KEQ0078L-01; Specimen ID = 500V15000003; OriginalVolume	OriginalVolume = 4	32,553
Moz	06/Nov/2023 12:54:31 EST	VisitSamples	Delete	Global Specimen ID = KEQ0078L-06		32,554
Moz	06/Nov/2023 12:54:31 EST	Samples	Add	Global Specimen ID = KEQ0078L-06; Specimen ID = 500V15000003		32,555
Moz	06/Nov/2023 12:54:41 EST	Samples	Update	Global Specimen ID = KEQ0078L-04; Specimen ID = 500V15000003; OriginalVolume	OriginalVolume = 13	32,556
Moz	06/Nov/2023 12:55:12 EST	Samples	Add		Global Specimen ID = -NEW-GU-; Specimen ID =	32,558
Moz	06/Nov/2023 12:55:12 EST	VisitSamples	Add		Global Specimen ID = 0500-001MCA00-007	32,559
Moz	06/Nov/2023 12:55:12 EST	Samples	Update	Global Specimen ID = KEQ0078L-00; Specimen ID = 500V15000001; SubSamplesCr	SubSamplesCreated = 7	32,560
Moz	06/Nov/2023 12:55:12 EST	Samples	Update	Global Specimen ID = -NEW-GU-; Specimen ID = ; GlobalSpecimenId = -NEW-GU-; f	GlobalSpecimenId = 0500-001MCA00-007; AliquotSeque	32,561
Moz	06/Nov/2023 12:58:54 EST	VisitSamples	Delete	Global Specimen ID = 0500-001MCA00-007		32,562
Moz	06/Nov/2023 12:58:54 EST	Samples	Delete	Global Specimen ID = 0500-001MCA00-007; Specimen ID =		32,563
Moz	06/Nov/2023 12:59:28 EST	Samples	Update	Global Specimen ID = KEQ0078L-04; Specimen ID = 500V15000003; OriginalVolume	OriginalVolume = 11	32,564
Moz	06/Nov/2023 12:59:38 EST	Samples	Update	Global Specimen ID = KEQ0078V-00; Specimen ID = 500V15000001; OriginalVolume	OriginalVolume = 45	32,565
Moz	06/Nov/2023 13:01:34 EST	Samples	Add		Global Specimen ID = -NEW-GU-; Specimen ID =	32,566
Moz	06/Nov/2023 13:01:34 EST	VisitSamples	Add		Global Specimen ID = 0500-00257C00-000	32,567
Moz	06/Nov/2023 13:01:34 EST	Samples	Update	Global Specimen ID = -NEW-GU-; Specimen ID = ; RootSampleId = ; GlobalSpecime	RootSampleId = 10830; GlobalSpecimenId = 0500-00257	32,568
admin	06/Nov/2023 15:15:59 EST	Samples	Update	Global Specimen ID = 0777-001MWK00-276; Specimen ID = ; Condition = 10412; C	Condition = 10424; Comments = Received_TESTING_AB	32,570
admin	06/Nov/2023 15:15:59 EST	Samples	Update	Global Specimen ID = 0777-001MWK00-277; Specimen ID = ; Condition = 10412; C	Condition = 10424; Comments = Received_TESTING_AB	32,571
admin	06/Nov/2023 15:15:59 EST	Samples	Update	Global Specimen ID = 0777-001MWK00-278; Specimen ID = ; Condition = 10412; C	Condition = 10424; Comments = Received_TESTING_AB	32,572
admin	06/Nov/2023 15:15:59 EST	Samples	Update	Global Specimen ID = 0777-001MWK00-281; Specimen ID = ; Condition = 10412; C	Condition = 10424; Comments = Received_TESTING_AB	32,573
admin	06/Nov/2023 15:15:59 EST	Samples	Update	Global Specimen ID = 0777-001MWK00-282; Specimen ID = ; Condition = 10412; C	Condition = 10424; Comments = Received_TESTING_AB	32,574
admin	06/Nov/2023 15:19:45 EST	Samples	Update	Global Specimen ID = 0500-001NV000-001; Specimen ID = ; Condition = 10412; C	Condition = 10413; Comments = Sent_TESTING_AB; Int	32,575
admin	06/Nov/2023 15:19:45 EST	Samples	Update	Global Specimen ID = 0500-001NV000-003; Specimen ID = ; Condition = 10412; C	Condition = 10413; Comments = Sent_TESTING_AB; Int	32,576



## User Event Report

Provides a report of user events, such as adding, updating, or deleting information in LDMS.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• Event Date</li> <li>• Event Type</li> <li>• Login ID</li> <li>• Module</li> <li>• Transaction ID</li> </ul>	<ul style="list-style-type: none"> <li>• Login ID</li> <li>• Event Date/Time</li> <li>• Module</li> <li>• Event Type</li> <li>• Description</li> <li>• Reason</li> <li>• Item Name</li> <li>• Item ID</li> <li>• Min Transaction ID</li> <li>• Max Transaction ID</li> </ul>

## User permissions report

Shows each user account associated with your LDMS laboratory, and the user's access to specific pages in LDMS.

### Example

**Figure 51: The User Permission Report**

#### User Permissions Report

<b>jdoe</b>	Full	View
Specimen	X	
DataRetrieval	X	
Reports	X	
Administration	X	
Account		
Labels	X	
Shipping	X	
Storage	X	

#### System Administrator

(1) The user's name. (2) The user's permissions by page. (3) Only present if the user has system administrator privileges.

## Barcode Reports

---

### 1D Barcodes Report

Displays a line listing of specimens along with a series of 1D barcodes. Each specimen row will include a 1D barcode that encodes the specimens Global Spec ID, ID1, and Other Spec ID. This reports can be printed and used to scan groups of specimens into applications outside of LDMS that may use 1D barcodes to input information such as Global Spec ID, ID1, or Other Spec ID.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG Protocol</li> <li>• Additive</li> <li>• Clinic ID</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG PID/ID2</li> <li>• Primary</li> <li>• Project</li> <li>• Received Date</li> <li>• Run ID</li> <li>• Shipment Number</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Visit Unit</li> <li>• Visit Value</li> </ul>	<ul style="list-style-type: none"> <li>• Global Spec ID</li> <li>• Project</li> <li>• ID2</li> <li>• Id1</li> <li>• Collection Date</li> <li>• Vid</li> <li>• Vid Unit</li> <li>• Other Spec ID</li> <li>• Global Spec ID Barcode</li> <li>• ID1 Barcode</li> <li>• Other Spec ID Barcode</li> </ul>

## 2D Barcodes Report

Displays a line listing of specimens along with a series of 2D barcodes. Each specimen row will include a 2D barcode that encodes the specimens Global Spec ID, ID1, and Other Spec ID. This reports can be printed and used to scan groups of specimens into applications outside of LDMS that may use 2D barcodes to input information such as Global Spec ID, ID1, or Other Spec ID.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG Protocol</li> <li>• Additive</li> <li>• Clinic ID</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG PID/ID2</li> <li>• Primary</li> <li>• Project</li> <li>• Received Date</li> <li>• Run ID</li> <li>• Shipment Number</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Visit Unit</li> <li>• Visit Value</li> </ul>	<ul style="list-style-type: none"> <li>• Global Spec ID</li> <li>• Project</li> <li>• ID2</li> <li>• Id1</li> <li>• Collection Date</li> <li>• Vid</li> <li>• Vid Unit</li> <li>• Other Spec ID</li> <li>• Global Spec ID Barcode</li> <li>• ID1 Barcode</li> <li>• Other Spec ID Barcode</li> </ul>

## Exportable reports

Exportable reports are designed to be generated for spreadsheet and CSV formats so that the data can be manipulated manually.

### Abbott SARS-COV-2 Quant Export Report

Displays specimen details and results from Abbott SARS-COV-2 Quant runs in the Test Results module.

Sorting	Available filters	Information on report
-	<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Additive</li> <li>• Assay Date</li> <li>• Clinic ID</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>• Group</li> <li>• Protocol</li> <li>• PID</li> <li>• Secondary ID</li> <li>• Qualitative Result</li> <li>• Quantitative Result (Log copies/mL)</li> <li>• Dilution Factor</li> <li>• Final Quantitative Result (Log copies/mL)</li> <li>• m2000 Error Code/description</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Sub Add/Der</li> <li>• Visit</li> <li>• Clinic</li> <li>• Collection Date/Time</li> <li>• Other Specimen ID</li> <li>• Global Specimen ID</li> <li>• Run ID</li> <li>• Assay Date</li> </ul>

### Abbott SARS-COV-2 Quant Export Report with Comments

Displays specimen details and results from Abbott SARS-COV-2 Quant runs in the Test Results module. Report includes Specimen comments for each result.

Sorting	Available filters	Information on report
-	<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Additive</li> <li>• Assay Date</li> <li>• Clinic ID</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>• Group</li> <li>• Protocol</li> <li>• PID</li> <li>• Secondary ID</li> <li>• Qualitative Result</li> <li>• Quantitative Result (Log copies/mL)</li> <li>• Dilution Factor</li> <li>• Final Quantitative Result (Log copies/mL)</li> <li>• m2000 Error Code/description</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Sub Add/Der</li> <li>• Visit</li> <li>• Clinic</li> </ul>

Sorting	Available filters	Information on report
		<ul style="list-style-type: none"> <li>Collection Date/Time</li> <li>Other Specimen ID</li> <li>Global Specimen ID</li> <li>Run ID</li> <li>Assay Date</li> <li>Condition</li> <li>Comments</li> </ul>

### Abbott SARS-COV-2 Quant Export Report with Sample Location

Displays specimen details and results from Abbott SARS-COV-2 Quant runs in the Test Results module. Report includes specimen location field from the Abbott result file.

Sorting	Available filters	Information on report
-	<ul style="list-style-type: none"> <li>ACTG PID</li> <li>ACTG Protocol</li> <li>ACTG Protocol Type</li> <li>Additive</li> <li>Assay Date</li> <li>Clinic ID</li> <li>Derivative</li> <li>Global Spec ID</li> <li>Non ACTG PID/ID1</li> <li>Non ACTG Prot/ID2</li> <li>Other Specimen ID</li> <li>Primary</li> <li>Project</li> <li>Run ID</li> <li>SID/ID3</li> <li>Specimen Date</li> <li>Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>Group</li> <li>Protocol</li> <li>PID</li> <li>Secondary ID</li> <li>Qualitative Result</li> <li>Quantitative Result (Log copies/mL)</li> <li>Dilution Factor</li> <li>Final Quantitative Result (Log copies/mL)</li> <li>m2000 Error Code/description</li> <li>Primary</li> <li>Additive</li> <li>Derivative</li> <li>Sub Add/Der</li> <li>Visit</li> <li>Clinic</li> <li>Collection Date/Time</li> <li>Other Specimen ID</li> <li>Global Specimen ID</li> <li>Run ID</li> <li>Assay Date</li> <li>Sample Location</li> </ul>

### Aliquot count by primary report

Shows the number of aliquots processed from each primary specimen.

Sorting	Filter criteria	Information displayed on report
This report is sorted by ID1 and ID2	<ul style="list-style-type: none"> <li>Additive</li> <li>Global spec ID</li> <li>Non ACTG PID/ID1</li> <li>Non ACTG Prot/ID2</li> <li>Other specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>Additive</li> <li>Global specimen ID</li> <li>ID1</li> <li>ID2</li> <li>Other specimen ID</li> </ul>

Sorting	Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>• Primary</li> <li>• project</li> <li>• Specimen date</li> <li>• Visit unit</li> <li>• Visit value</li> </ul>	<ul style="list-style-type: none"> <li>• Primary</li> <li>• project</li> <li>• Specimen date</li> <li>• Visit value and unit</li> <li>• Primary volume</li> <li>• Aliquot volume</li> <li>• Number of aliquots</li> </ul>

### Aliquot Inventory Report

Provides a specimen listing with a custom set of header values as shown below.

Sorting	Available filters	Information on report
-	<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG Protocol</li> <li>• Additive</li> <li>• Clinic ID</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Import Date</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Received Date</li> <li>• Shipment Number</li> <li>• Specimen Date</li> <li>• Sub Add/Der</li> <li>• Visit Unit</li> <li>• Visit Value</li> </ul>	<ul style="list-style-type: none"> <li>• PID</li> <li>• Collection Date</li> <li>• Collection Date</li> <li>• Collection Date</li> <li>• Col time (hrs)</li> <li>• Collection time (min)</li> <li>• Visit Value</li> <li>• Visit Unit</li> <li>• Study name</li> <li>• Global Specimen ID</li> <li>• Primary Type</li> <li>• Additive Type</li> <li>• Derivative Type</li> <li>• Sub add/der type</li> <li>• Volume</li> <li>• Volume Unit</li> <li>• Primary Volume</li> <li>• Vol Unit</li> <li>• Processing Time</li> <li>• Processing Month</li> <li>• Processing Day</li> <li>• Processing Year</li> <li>• Frz date</li> <li>• Frz time</li> <li>• Cell Count</li> <li>• Condition</li> <li>• Is sample Available</li> <li>• Is sample stored</li> <li>• Stored month</li> <li>• Stored Day</li> <li>• Stored Year</li> <li>• Storage temp</li> <li>• Is sample shipped</li> <li>• Sample Comments</li> <li>• Storage Freezer</li> <li>• Storage Rack</li> <li>• Storage container</li> </ul>

Sorting	Available filters	Information on report
		<ul style="list-style-type: none"> <li>Storage Box position</li> </ul>

### CFAR export report

Shows specimens stored at the laboratory.

Sorting	Filter criteria	Information displayed on report
This report is sorted by specimen ID	<ul style="list-style-type: none"> <li>project</li> </ul>	<ul style="list-style-type: none"> <li>Specimen ID</li> <li>project</li> <li>Global specimen ID</li> <li>ID2</li> <li>OPID</li> <li>Visit value and unit</li> <li>Primary</li> <li>Additive</li> <li>Derivative</li> <li>Sub additive/derivative</li> <li>Volume</li> <li>Volume unit</li> <li>Stored date</li> <li>Specimen date</li> <li>Storage location</li> </ul>

### CFAR storage report

Provides a summary of storage items at the laboratory.

Sorting	Filter criteria	Information displayed on report
This report is sorted by storage container and specimen ID	<ul style="list-style-type: none"> <li>Import date</li> <li>project</li> <li>Received date</li> <li>Specimen date</li> </ul>	<ul style="list-style-type: none"> <li>Container</li> <li>Specimen ID</li> <li>project</li> <li>ID2</li> <li>ID1</li> <li>Global specimen ID</li> <li>Visit</li> <li>Primary</li> <li>Additive</li> <li>Derivative</li> <li>Sub-additive/derivative</li> <li>Volume</li> <li>Specimen date</li> <li>Position</li> </ul>

### Database dump report

A general report that provides information from all specimens in a laboratory's LDMS database.

Sorting	Available filters	Information on report
-	<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Additive</li> <li>• Clinic ID</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• project</li> <li>• Received Date</li> <li>• Ship to Lab Number</li> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Sub Add/Der</li> <li>• Visit Unit</li> <li>• Visit Value</li> <li>• Volume</li> <li>• Volume Unit</li> </ul>	<ul style="list-style-type: none"> <li>• project</li> <li>• PID/ID1</li> <li>• Protocol/ID2</li> <li>• SID/ID3</li> <li>• Visit</li> <li>• Visit Unit</li> <li>• Clinic</li> <li>• Rec Date</li> <li>• Rec Time</li> <li>• Collection Date</li> <li>• Collection Time</li> <li>• Import Date</li> <li>• Spec ID</li> <li>• Global Spec ID</li> <li>• PRI</li> <li>• ADD</li> <li>• DER</li> <li>• SUB</li> <li>• VOL</li> <li>• VOL Unit</li> <li>• Cond</li> <li>• Time</li> <li>• Time Unit</li> <li>• Other Spec ID</li> <li>• Test</li> <li>• Comments</li> <li>• Ship Date</li> <li>• Ship Batch Number</li> <li>• Ship to Lab</li> </ul>

## Database dump report 2

A general report that provides information from all specimens in a laboratory's LDMS database.

Sorting	Available filters	Information on report
-	<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG Protocol</li> <li>• Additive</li> <li>• Clinic ID</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Import Date</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• project</li> <li>• Received Date</li> <li>• Shipment Number</li> <li>• Specimen Date</li> <li>• Sub Add/Der</li> </ul>	<ul style="list-style-type: none"> <li>• LDMS laboratory ID</li> <li>• Primary unique ID</li> <li>• Aliquot unique ID</li> <li>• project</li> <li>• ID1</li> <li>• Collection date (month, day, and year)</li> <li>• Received date (month, day, and year)</li> <li>• Collection time</li> <li>• Visit (value and unit)</li> <li>• ID2</li> <li>• ID3</li> <li>• Global specimen ID</li> <li>• Specimen ID</li> <li>• Other specimen ID</li> </ul>

Sorting	Available filters	Information on report
	<ul style="list-style-type: none"> <li>• Visit Unit</li> <li>• Visit Value</li> </ul>	<ul style="list-style-type: none"> <li>• Primary code</li> <li>• Additive code</li> <li>• Derivative code</li> <li>• Sub-additive/derivative code</li> <li>• Enrollment</li> <li>• Aliquot volume (value and unit)</li> <li>• Primary volume (value and unit)</li> <li>• Processing time</li> <li>• Processing date (month, day, and year)</li> <li>• Processing tech initials</li> <li>• Frozen date (month, day, year)</li> <li>• Frozen time</li> <li>• Total cell count</li> <li>• Specimen condition</li> <li>• Availability</li> <li>• Additional time (value and unit)</li> <li>• Status (not stored and available, stored, and unavailable)</li> <li>• Storage date (month, day, year)</li> <li>• Storage temperature</li> <li>• Shipping status</li> <li>• Destination laboratory</li> <li>• Shipment number</li> <li>• Shipment temperature</li> <li>• Shipment date (month, day, year)</li> <li>• Sending laboratory</li> <li>• Received shipment number</li> <li>• Received temperature</li> <li>• Date shipment received (month, day, year)</li> <li>• Clinic</li> <li>• Comments</li> <li>• Whether a quick add template was used</li> <li>• Reason specimen not collected</li> <li>• Storage unit</li> <li>• Storage level</li> <li>• Storage sub-level</li> <li>• Storage container</li> <li>• Position</li> <li>• System date</li> <li>• Date last changed</li> </ul>

### Exportable Abbott Assay Report



Sorting	Available filters	Information on report
-	<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Assay Date</li> <li>• Global Spec ID</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Primary</li> <li>• Project</li> <li>• Run ID</li> <li>• Specimen Date</li> <li>• Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>• PID</li> <li>• ID2/Pro</li> <li>• ID3</li> <li>• Visit</li> <li>• PRI</li> <li>• Specimen ID</li> <li>• Global Spec ID</li> <li>• Spec Date</li> <li>• Rec Date</li> <li>• Import Date</li> <li>• Assay Date</li> <li>• RUN ID</li> <li>• Dilution</li> <li>• Result</li> <li>• System Censor</li> <li>• User Censor</li> <li>• Run System Censor</li> <li>• Run User Censor</li> </ul>

### Laboratory 081 billing report

Report request by laboratory 81 (but can be used for other purposes).

Sorting	Filter criteria	Information displayed on report
This report is sorted by project, ID2, and ID1.	<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Derivative</li> <li>• Global specimen ID</li> <li>• project</li> <li>• Specimen date</li> </ul>	<ul style="list-style-type: none"> <li>• project</li> <li>• ACTG protocol</li> <li>• PID/ID1</li> <li>• Specimen date</li> <li>• Derivative</li> <li>• Global specimen ID</li> </ul>

### Laboratory 81 CNICS by date report

Report requested by laboratory 81 (but can be used by any laboratory).

Sorting	Filter criteria	Information displayed on report
This report is sorted by specimen date	<ul style="list-style-type: none"> <li>• Non ACTG prot/ID2</li> <li>• Primary</li> <li>• project</li> <li>• Received date</li> <li>• Specimen date</li> <li>• Volume</li> <li>• Volume unit</li> </ul>	<ul style="list-style-type: none"> <li>• project</li> <li>• Non ACTG protocol/ID2</li> <li>• Specimen date</li> <li>• Received date</li> <li>• Primary</li> <li>• Volume</li> <li>• Volume units</li> </ul>

### Laboratory 081 CNICS general report

Report requested by laboratory 81 (but can be used by any laboratory).

Sorting	Filter criteria	Information displayed on report
This report is sorted by ID1	<ul style="list-style-type: none"> <li>• Additive</li> <li>• Derivative</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Received date</li> <li>• Specimen date</li> <li>• Specimen time</li> <li>• Sub additive/derivative</li> <li>• Volume</li> <li>• Volume unit</li> </ul>	<ul style="list-style-type: none"> <li>• Non ACTG protocol/ID2</li> <li>• PID/ID1</li> <li>• Specimen date</li> <li>• Specimen time</li> <li>• Received date</li> <li>• Additive</li> <li>• Derivative</li> <li>• Sub additive/derivative</li> <li>• Volume</li> <li>• Volume units</li> </ul>

### Laboratory 188 storage report

Provides a summary a summary of stored and not stored specimens, useful for determining what specimens still needs to be assigned a storage location in LDMS.

Sorting	Filter criteria	Information displayed on report
This report is sorted by global specimen ID	<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Additive</li> <li>• Condition</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• OPID</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• project</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Specimen Time</li> <li>• Time</li> <li>• Time Unit</li> <li>• Visit Unit</li> <li>• Visit Value</li> <li>• Volume</li> <li>• Volume Unit</li> </ul>	<ul style="list-style-type: none"> <li>• Global specimen ID</li> <li>• Other specimen ID</li> <li>• Freezer</li> <li>• Shelf</li> <li>• Rack</li> <li>• Container</li> <li>• Position</li> </ul>

### Lab 40 LabKey report

Short reference description.

Sorting	Filter criteria	Information displayed on report
This report is sorted by specimen ID	<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG Protocol</li> </ul>	<ul style="list-style-type: none"> <li>• GlobalSpecID</li> <li>• Laboratory Name</li> </ul>

Sorting	Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>• ACTG Protocol Type</li> <li>• Additive</li> <li>• Clinic ID</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Import Date</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Primary</li> <li>• project</li> <li>• Received Date</li> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Sub Add/Der</li> <li>• Visit Unit</li> <li>• Visit Value</li> </ul>	<ul style="list-style-type: none"> <li>• Clinic</li> <li>• PTID</li> <li>• Specimen Date</li> <li>• Receipt Date</li> <li>• LDMS Spec ID</li> <li>• project</li> <li>• Visit</li> <li>• Protocol</li> <li>• Visit Unit</li> <li>• Volume</li> <li>• Volume Unit</li> <li>• Storage Date</li> <li>• Ship Date</li> <li>• Ship Lab</li> <li>• Sub additive/derivative</li> <li>• Comments</li> <li>• Primary</li> <li>• Derivative</li> <li>• Additive</li> <li>• Condition</li> <li>• Storage unit</li> <li>• Level 1</li> <li>• Level 2</li> <li>• Container</li> <li>• Position</li> <li>• Frozen Time</li> <li>• Processing Tech Initials</li> <li>• Processing Date</li> <li>• Total Cell Count</li> <li>• Other Spec ID</li> <li>• ID3</li> <li>• OPID</li> <li>• Processing time</li> <li>• Frozen date</li> <li>• Primary Volume</li> <li>• Primary Vol Units</li> <li>• Received Time</li> <li>• Mark for Shipping</li> </ul>

### Laboratory 48 billing report

Report that provides specimen information.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Additive</li> <li>• Clinic ID</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• project</li> </ul>	<ul style="list-style-type: none"> <li>• Specimen ID</li> <li>• project/Protocol</li> <li>• PID</li> <li>• Visit/Unit</li> <li>• Specimen Date</li> <li>• Additive</li> </ul>

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Visit Unit</li> <li>• Visit Value</li> </ul>	

### Lab 485 aliquot report

Similar to the Specimen Export Report, but sorts the results differently.

Sorting	Filter criteria	Information displayed on report
<ol style="list-style-type: none"> <li>1. project</li> <li>2. Non-ACTG Protocol</li> <li>3. Non-ACTG PID</li> <li>4. Visit Value</li> <li>5. Primary</li> <li>6. Additive</li> <li>7. Derivative</li> </ol>	<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Additive</li> <li>• Derivative</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Primary</li> <li>• project</li> <li>• Sub Add/Der</li> <li>• Visit Unit</li> <li>• Visit Value</li> </ul>	<ul style="list-style-type: none"> <li>• project</li> <li>• PID/ID1</li> <li>• Protocol</li> <li>• SID/ID3</li> <li>• Visit</li> <li>• Visit [Unit]</li> <li>• Clinic</li> <li>• Received Date</li> <li>• Collection Date</li> <li>• Collection Time</li> <li>• Import Date</li> <li>• Specimen ID</li> <li>• Global Specimen ID</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Sub Additive/Derivative</li> <li>• Volume</li> <li>• Volume Unit</li> <li>• Condition</li> <li>• Time</li> <li>• Time Unit</li> <li>• Other Specimen ID</li> <li>• Test</li> <li>• Comments</li> <li>• Ship Date</li> <li>• Ship Batch</li> <li>• Ship to Laboratory</li> </ul>

### Lab 485 specimen count report

Provides the number of specimens with a unique primary-additive-derivative-sub A/D combination.

Sorting	Filter criteria	Information displayed on report
<ol style="list-style-type: none"> <li>1. project and study combination</li> <li>2. Participant</li> <li>3. Visit</li> </ol>	<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Additive</li> <li>• Derivative</li> </ul>	<ul style="list-style-type: none"> <li>• PID</li> <li>• Visit</li> <li>• Visit Unit</li> <li>• Primary</li> <li>• Additive</li> </ul>

Sorting	Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Primary</li> <li>• project</li> <li>• Sub Add/Der</li> <li>• Visit Unit</li> <li>• Visit Value</li> <li>• Volume</li> <li>• Volume unit</li> </ul>	<ul style="list-style-type: none"> <li>• Derivative</li> <li>• Sub Additive/Derivative</li> <li>• Count</li> </ul>

### Lab 485 specimen count with volume report

Provides the number of specimens with a unique primary-additive-derivative-sub A/D combination, along with total volume.

Sorting	Filter criteria	Information displayed on report
<ol style="list-style-type: none"> <li>1. project and study combination</li> <li>2. Participant</li> <li>3. Visit</li> </ol>	<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Additive</li> <li>• Derivative</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Primary</li> <li>• project</li> <li>• Sub Add/Der</li> <li>• Visit Unit</li> <li>• Visit Value</li> </ul>	<ul style="list-style-type: none"> <li>• PID</li> <li>• Visit</li> <li>• Visit Unit</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Sub Additive/Derivative</li> <li>• Volume</li> <li>• Volume Unit</li> <li>• Count</li> </ul>

### Primary specimen database dump report

Provides a list of specimen ID numbers for primaries, along with draw dates and received dates.

Sorting	Filter criteria	Information displayed on report
This report is sorted by specimen ID	None	<ul style="list-style-type: none"> <li>• Specimen ID</li> <li>• Other specimen ID</li> <li>• Collection date</li> <li>• Received date</li> </ul>

### Sample counts for specified project report

Shows how many specimens for a given derivative type are available for each project locally.

Sorting	Filter criteria	Information displayed on report
This report is organized by project	<ul style="list-style-type: none"> <li>• Derivative</li> <li>• project</li> </ul>	<ul style="list-style-type: none"> <li>• Derivative type</li> </ul>

Sorting	Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>Received date</li> <li>Specimen date</li> </ul>	<ul style="list-style-type: none"> <li>Description of derivative type</li> <li>Count (number of specimens)</li> </ul>

### Specimen export report

Designed for pulling information for local groups that have been shipped.

Sorting	Filter criteria	Information displayed on report
This report is sorted by project, then by participant identifier (ID1), and then by specimen ID	<ul style="list-style-type: none"> <li>Shipped batch number</li> </ul>	<ul style="list-style-type: none"> <li>Protocol</li> <li>project</li> <li>Primary type</li> <li>Derivative type</li> <li>Additive</li> <li>Sub additive/derivative type</li> <li>Collection date</li> <li>Visit value</li> <li>Visit unit</li> <li>Global specimen ID</li> <li>Original volume</li> <li>Original volume unit</li> <li>Available volume</li> <li>Available volume unit</li> <li>Clinic</li> <li>Time</li> <li>Received date</li> <li>Participant identifier (ID1)</li> <li>Protocol identifier (ID2)</li> <li>Source laboratory</li> <li>Draw time</li> <li>Received time</li> </ul>

### Storage export report

Provides a summary of specimens and their storage location in a laboratory's local database.

Sorting	Filter criteria	Information displayed on report
-	<ul style="list-style-type: none"> <li>ACTG PID/ID1</li> <li>ACTG protocol</li> <li>ACTG protocol type</li> <li>Additive</li> <li>Derivative</li> <li>Non ACTG PID/ID1</li> <li>Non ACTG Prot/ID2</li> <li>OPID</li> <li>Other specimen ID</li> <li>Primary</li> </ul>	<ul style="list-style-type: none"> <li>Specimen ID</li> <li>project/Prot</li> <li>PID/ID1</li> <li>OPID</li> <li>Primary</li> <li>Additive</li> <li>Derivative</li> <li>Sub additive/derivative</li> <li>Specimen Date</li> <li>Visit ID</li> </ul>

Sorting	Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>project</li> <li>Specimen date</li> <li>Specimen ID</li> <li>Sub add/der</li> <li>Visit unit</li> <li>Visit value</li> <li>Volume</li> <li>Volume unit</li> </ul>	<ul style="list-style-type: none"> <li>Volume</li> <li>Time</li> <li>Shipped no.</li> <li>Other specimen ID</li> <li>Storage location + position</li> </ul>

### Westat PK Export Report

Used to transfer PK results to Westat data management team.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>Assay Date</li> <li>Non ACTG PID/ID1</li> <li>Non ACTG Prot/ID2</li> <li>Project</li> <li>Run ID</li> <li>Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>Specimen ID</li> <li>PID/ID1</li> <li>Other Spec ID</li> <li>VID</li> <li>Spec Date</li> <li>Spec Time</li> <li>Time/Unit</li> <li>Assay Date</li> <li>Run ID</li> <li>Add</li> <li>Der</li> <li>Drug</li> <li>Conc</li> <li>Units</li> <li>Censors</li> <li>Reviewed</li> </ul>

### Miscellaneous reports

#### Clinic contact report


Provides contact information for clinics by clinic ID number.

Sorting	Filter criteria	Information displayed on report
This report is sorted by clinic ID	<ul style="list-style-type: none"> <li>Clinic ID</li> </ul>	<ul style="list-style-type: none"> <li>Clinic ID</li> <li>Clinic name</li> <li>Address</li> <li>Telephone number</li> <li>Fax number</li> <li>Contact(s) [including name, phone number, fax number, and email address]</li> </ul>

### LDMS abbreviated codes report

Provides a list of LDMS unit, visit, time, specimen condition codes used in LDMS and their meaning.

#### Information displayed on report

 **Note:** The information on this report is identical to the hover text that appears throughout LDMS.

- Measurement codes
- Visit unit codes
- Time unit codes
- Specimen condition codes

### LDMS assay censor codes report

Provides a list of assay censor codes.


#### Information displayed on report

- Censor codes
- Code descriptions

### LDMS primary, additive, derivative, sub additive/derivative codes report

Provides a list of LDMS primary, additive, derivative, and sub additive/derivative codes throughout LDMS.

#### Information displayed on report

 **Note:** The information on this report is identical to the hover text that appears throughout LDMS.

- Primary codes
- Additive codes
- Derivative codes
- Sub additive/derivative codes

## MWCCS

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### MWCCS Processing Report

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• Non-ACTG PID/ID1</li> <li>• Project</li> <li>• Specimen Date</li> <li>• Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>• Global Spec ID</li> <li>• Der</li> <li>• Other Spec ID</li> <li>• Volume</li> <li>• Number of Aliquots</li> <li>• Study</li> <li>• Processing Instructions</li> </ul>



Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>• Cell count</li> <li>• Amt</li> <li>• Storage</li> <li>• Processor's Initials</li> <li>• Date/Time Processed/Frozen</li> <li>• Unused Tubes</li> </ul>

## Participant reports

### Participant identifiers report

Provides a list of participants in your database by project.

Sorting	Filter criteria	Information displayed on report
This report is sorted by project, and then by ID1	<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• OPID</li> <li>• project</li> <li>• SID/ID3</li> </ul>	<ul style="list-style-type: none"> <li>• project</li> <li>• ID1</li> <li>• ID2</li> <li>• ID3</li> <li>• OPID</li> <li>• Clinic</li> </ul>

## PK reports

### Pharmacology Drug Count

Displays a result count by analyte per study/ protocol.

#### Filter Criteria

- ACTG Protocol
- ACTG Protocol Type
- Assay Date
- Clinic ID
- Project
- Specimen Date

### Pharmacology Drug List

List of pharmacology drugs and their associated codes.

### Pharmacology Proficiency Results

Displays results of Pharmacology proficiency testing

**Filter Criteria**

- Round Number

**PK Drug Limits By Run**

PK drug limits sorted by run.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• Assay Date</li> <li>• Drug</li> <li>• Run ID</li> </ul>	<ul style="list-style-type: none"> <li>• Run ID</li> <li>• Drug</li> <li>• Drug Lower Limit</li> <li>• Drug Upper Limit</li> <li>• Run Lower Limit</li> <li>• Run Upper Limit</li> <li>• Units</li> </ul>

**PK Participant Report**

An individualized report per specimen showing associated participant details along with detailed test results including censor codes, run limits, and a final calculated result.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG Protocol</li> <li>• Assay Date</li> <li>• Clinic ID</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Received Date</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>• Participant</li> <li>• Project / ID2</li> <li>• ID3</li> <li>• Collection Date</li> <li>• Visit</li> <li>• Clinic Name</li> <li>• Fax</li> <li>• Testing Lab</li> <li>• Specimen ID</li> <li>• Global Spec ID</li> <li>• Other Spec ID</li> <li>• Received Date</li> <li>• Received Time</li> <li>• Sample Condition</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Run ID</li> <li>• Detection Platform</li> <li>• Run Type</li> <li>• Test Date</li> <li>• Tech Initials</li> <li>• Analyte</li> <li>• Description</li> <li>• Unit</li> <li>• Concentration</li> <li>• Lower Limit</li> <li>• Upper Limit</li> <li>• Censors</li> <li>• Review Comment</li> </ul>

Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>Sample Comment</li> </ul>

## PK Summary Report

PK Summary Report sorted by protocol

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>ACTG PID</li> <li>ACTG Protocol</li> <li>ACTG Protocol Type</li> <li>Additive</li> <li>Assay Date</li> <li>Derivative</li> <li>Drug</li> <li>Global Spec ID</li> <li>Non ACTG PID/ID1</li> <li>Non ACTG Prot/ID2</li> <li>OPID</li> <li>Other Specimen ID</li> <li>Primary</li> <li>Project</li> <li>Received Date</li> <li>Run ID</li> <li>Specimen Date</li> <li>Specimen ID</li> <li>Specimen Time</li> <li>Time</li> <li>Time Unit</li> <li>Visit Unit</li> <li>Visit Value</li> </ul>	<ul style="list-style-type: none"> <li>PID/ID1</li> <li>Specimen ID</li> <li>Global Specimen ID</li> <li>Other Spec ID</li> <li>Spec Date</li> <li>VID</li> <li>Spec Time</li> <li>Time/Unit</li> <li>Assay Date</li> <li>Run ID</li> <li>Pri</li> <li>Add</li> <li>Der</li> <li>Drug</li> <li>Conc</li> <li>Cens</li> <li>Rev by</li> <li>Rev Date</li> </ul>

## PK Summary with Assay Name

Same as PK Summary Report but with additional Assay Name column

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>ACTG PID</li> <li>ACTG Protocol</li> <li>ACTG Protocol Type</li> <li>Additive</li> <li>Assay Date</li> <li>Derivative</li> <li>Drug</li> <li>Global Spec ID</li> <li>Non ACTG PID/ID1</li> <li>Non ACTG Prot/ID2</li> <li>OPID</li> <li>Other Specimen ID</li> <li>Primary</li> <li>Project</li> <li>Received Date</li> <li>Run ID</li> </ul>	<ul style="list-style-type: none"> <li>PID/ID1</li> <li>Specimen ID</li> <li>Global Specimen ID</li> <li>Assay Name</li> <li>Spec Date</li> <li>VID</li> <li>Spec Time</li> <li>Time/Unit</li> <li>Assay Date</li> <li>Run ID</li> <li>Pri</li> <li>Add</li> <li>Der</li> <li>Drug</li> <li>Conc</li> <li>Units</li> </ul>

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Specimen Time</li> <li>• Time</li> <li>• Time Unit</li> <li>• Visit Unit</li> <li>• Visit Value</li> </ul>	<ul style="list-style-type: none"> <li>• Cens</li> <li>• Reviewed</li> </ul>

### PK Summary with Assay Name (exportable)

Exportable version of PK Summary with Assay Name report

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Additive</li> <li>• Assay Date</li> <li>• Derivative</li> <li>• Drug</li> <li>• Global Spec ID</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• OPID</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Received Date</li> <li>• Run ID</li> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Specimen Time</li> <li>• Time</li> <li>• Time Unit</li> <li>• Visit Unit</li> <li>• Visit Value</li> </ul>	<ul style="list-style-type: none"> <li>• Group/Prot</li> <li>• Global Spec ID</li> <li>• Assay Name</li> <li>• Assay Date</li> <li>• Run ID</li> <li>• Drug</li> <li>• Conc</li> <li>• Units</li> <li>• Lower Limit</li> <li>• Upper Limit</li> <li>• Censors Reviewed</li> </ul>

## Quick Add Templates

### Quick Add Template List Report

This report provides a list of Quick Add templates available to your laboratory.

Sorting	Available filters	Information on report
Alphabetical by template name	<ul style="list-style-type: none"> <li>• ID2/protocol</li> <li>• project</li> <li>• Quick Add Template Name</li> <li>• Quick Add template Type</li> </ul>	<ul style="list-style-type: none"> <li>• Quick add template name</li> <li>• Type (local or preset by Frontier Science)</li> <li>• [list of enrollment and specimen data that will be</li> </ul>

Sorting	Available filters	Information on report
		populated by the template; this will vary by template]

## RPID Reports

### Random PID Report

Provides a link between the original ACTG/IMPAACT PID and the RPID ID assigned during shipment import. This report is sensitive and is only available to the RPID importing lab.

Sorting	Available filters	Information on report
-	<ul style="list-style-type: none"> <li>• Import Date</li> <li>• Original Specimen ID</li> <li>• Received Shipment Number</li> <li>• Shipment Number</li> <li>• Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>• PID</li> <li>• RPID</li> <li>• Other Specimen ID</li> <li>• Spec Date</li> <li>• Received Batch</li> <li>• Sending Lab</li> <li>• Contact</li> <li>• Phone</li> </ul>

### RPID Specimen Request Report

Report displaying the RPID values assigned to various request numbers in the RPID Requests module.

Sorting	Available filters	Information on report
-	<ul style="list-style-type: none"> <li>• Import Date</li> <li>• Received Shipment Number</li> <li>• Request Number</li> <li>• Shipment Number</li> </ul>	<ul style="list-style-type: none"> <li>• PID</li> <li>• RPID</li> <li>• Other Specimen ID</li> <li>• Shipment Number</li> <li>• Received Batch</li> <li>• Sending Lab</li> <li>• Contact</li> <li>• Phone</li> </ul>

## Shipping reports

### Daily imported specimen log report

Shows a list of specimens for a project-protocol combination that have been received from another laboratory in a shipping file.

Sorting	Filter criteria	Information displayed on report
This report is sorted by project-protocol combination, and then by specimen date	<ul style="list-style-type: none"> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Clinic ID</li> </ul>	<ul style="list-style-type: none"> <li>• Specimen ID</li> <li>• First global specimen ID</li> <li>• Second global specimen ID</li> </ul>

Sorting	Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>• Condition</li> <li>• Global specimen ID</li> <li>• Import date</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• project</li> <li>• SID/ID3</li> <li>• Sending lab ID</li> <li>• Specimen date</li> <li>• Specimen ID</li> <li>• Visit unit</li> <li>• Visit value</li> </ul>	<ul style="list-style-type: none"> <li>• Clinic</li> <li>• PID/ID1</li> <li>• SID/ID3</li> <li>• Visit</li> <li>• Specimen date</li> <li>• Import date</li> <li>• Sending laboratory</li> <li>• Specimen condition</li> </ul>

### Detailed imported specimen report

Shows specimens received through a shipping file from another laboratory, sorted by shipment number.

Sorting	Filter criteria	Information displayed on report
This report is sorted by shipment number, and then by specimen ID	<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Additive</li> <li>• Condition</li> <li>• Derivative</li> <li>• Import date</li> <li>• Laboratory ID</li> <li>• Non ACTG Prot/ID2</li> <li>• Other specimen ID</li> <li>• Primary</li> <li>• project</li> <li>• Shipment number</li> <li>• Specimen date</li> <li>• Specimen ID</li> <li>• Specimen time</li> <li>• Sub additive/derivative</li> <li>• Time</li> <li>• Time unit</li> <li>• Visit unit</li> <li>• Visit value</li> <li>• Volume</li> <li>• Volume unit</li> </ul>	<ul style="list-style-type: none"> <li>• Import batch no. (the shipment number)</li> <li>• Import date</li> <li>• Sending laboratory</li> <li>• Specimen ID</li> <li>• project/Prot</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Sub additive/derivative</li> <li>• PID/ID1</li> <li>• VID</li> <li>• Condition</li> <li>• Volume</li> <li>• Specimen date</li> <li>• Specimen time</li> <li>• Other specimen ID</li> <li>• Time/Time unit</li> </ul>

### Imported specimen report - summary

Shows the number of a specific type of specimen received as part of a shipment from another laboratory.

Sorting	Filter criteria	Information displayed on report
This report is sorted by shipment number	<ul style="list-style-type: none"> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Additive</li> <li>• Derivative</li> <li>• Import date</li> <li>• Non ACTG prod/ID2</li> <li>• Primary</li> <li>• project</li> <li>• Sending laboratory ID</li> <li>• Shipment number</li> <li>• Sub additive/derivative</li> </ul>	<ul style="list-style-type: none"> <li>• Sending laboratory</li> <li>• Batch number (shipment number)</li> <li>• project-protocol combination</li> <li>• Import date</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Sub additive/derivative</li> <li>• Count</li> </ul>

### Lab 263 Summary Detail of Shipped Specimens

Provides a summary of shipped specimens for lab 263.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• Additive</li> <li>• Derivative</li> <li>• Destination Lab</li> <li>• Primary</li> <li>• Project</li> <li>• Received Date</li> <li>• Shipment Date</li> <li>• Specimen Date</li> <li>• Sub Add/Der</li> </ul>	<ul style="list-style-type: none"> <li>• Project</li> <li>• Destination Lab</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Sub A/D</li> <li>• Tube count</li> <li>• Total Volume</li> </ul>

### Shipped specimen report - detail report

Lists the specimens within a shipment, organized by shipment number.

Sorting	Filter criteria	Information displayed on report
This report is sorted by shipment number, and then by global specimen ID	<ul style="list-style-type: none"> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Additive</li> <li>• Clinic ID</li> <li>• Condition</li> <li>• Derivative</li> <li>• Destination Lab</li> <li>• NON ACTG PID/ID1</li> <li>• NON ACTG PROT/ID2</li> <li>• Other Spec ID</li> <li>• Primary</li> <li>• project</li> <li>• Shipment Date</li> <li>• Shipment Number</li> <li>• Shipping Temp.</li> <li>• Spec Date</li> <li>• Spec ID</li> <li>• Specimen Time</li> </ul>	<ul style="list-style-type: none"> <li>• Shipment batch number</li> <li>• Shipment date</li> <li>• Laboratory shipped to</li> <li>• Clinic</li> <li>• Specimen ID</li> <li>• Other specimen ID</li> <li>• project/prot</li> <li>• Global specimen ID</li> <li>• PID/ID1</li> <li>• VID</li> <li>• Specimen Date</li> <li>• Specimen time</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Sub additive/derivative</li> <li>• Volume</li> </ul>

Sorting	Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>• Sub Add/Der</li> <li>• Visit Unit</li> <li>• Visit Value</li> <li>• Volume</li> <li>• Volume Unit</li> </ul>	<ul style="list-style-type: none"> <li>• Condition</li> </ul>

### Shipped specimen report - summary report

Shows the number of specimens of a specific derivative type on a shipment that was sent.

Sorting	Filter criteria	Information displayed on report
This report is sorted by shipment number, and then grouped by derivative	<ul style="list-style-type: none"> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Clinic ID</li> <li>• Derivative</li> <li>• Destination laboratory</li> <li>• Non ACTG prot/ID2 project</li> <li>• Shipment date</li> <li>• Shipment number</li> <li>• Shipping temperature</li> </ul>	<ul style="list-style-type: none"> <li>• Batch number</li> <li>• Ship date</li> <li>• Destination</li> <li>• project/protocol</li> <li>• Derivative</li> <li>• Number of specimens shipped</li> </ul>

### Shipping laboratory contact report

Shows contact information for a given laboratory.

Sorting	Filter criteria	Information displayed on report
This report is sorted by laboratory ID	<ul style="list-style-type: none"> <li>• Laboratory ID</li> </ul>	<ul style="list-style-type: none"> <li>• Laboratory ID</li> <li>• Laboratory name</li> <li>• Contact (with telephone number and email address)</li> <li>• Address</li> <li>• Room number</li> <li>• Country</li> <li>• Laboratory telephone number</li> <li>• Laboratory fax number</li> </ul>

### Specimens Marked for Shipping

Provides a list of specimens that are marked for shipping.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Additive</li> </ul>	<ul style="list-style-type: none"> <li>• PID/ID1</li> <li>• Specimen ID</li> <li>• Global Specimen ID</li> <li>• VID</li> </ul>



Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• Derivative</li> <li>• Intended Ship Date</li> <li>• Marked in Storage</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Primary</li> <li>• Project</li> <li>• Shipment Number</li> <li>• Specimen ID</li> <li>• Sub Add/Der</li> <li>• Visit Unit</li> <li>• Visit Value</li> </ul>	<ul style="list-style-type: none"> <li>• Pri</li> <li>• Add</li> <li>• Der</li> <li>• Sub A/D</li> <li>• Spec Date</li> <li>• Category</li> <li>• Intended Ship Date</li> <li>• Intended Destination</li> <li>• Batch Number</li> <li>• Overdue?</li> </ul>

## Specimen reports

### Cell yield QA/QC summary report

Provides a summary cell yield for viable PBMCs, along with a graph of cell yield by date, mean, standard deviation, and range.

Sorting	Filter criteria	Information displayed on report
<p>This report is sorted by collection date.</p>	<ul style="list-style-type: none"> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Non ACTG prot/ID2</li> <li>• project</li> <li>• Specimen date</li> <li>• Technician initials</li> </ul>	<ul style="list-style-type: none"> <li>• Patid</li> <li>• Collection date</li> <li>• Collection time</li> <li>• Tech</li> <li>• Additive</li> <li>• Total cell count (<math>\times 10^6</math>)</li> <li>• Total volume</li> <li>• Comments (from Specimen Management)</li> <li>• Cell yield (<math>\times 10^6</math>)</li> </ul>

### Lab 263 Processing Report

Provides processing information (processing date, amount aliquoted, etc.) for primaries and aliquots for lab 263.

Sorting	Filter Criteria	Information Displayed on Report
<p>This report is sorted by project-protocol combination, then by collection date, and then grouped by primary.</p>	<ul style="list-style-type: none"> <li>• ACTG Protocol</li> <li>• Additive</li> <li>• Available</li> <li>• Clinic ID</li> <li>• Condition</li> <li>• Derivative</li> <li>• Import Date</li> <li>• Non ACTG Prot/ID2</li> <li>• Primary</li> <li>• Project</li> </ul>	<ul style="list-style-type: none"> <li>• Global Spec ID</li> <li>• Add</li> <li>• Der</li> <li>• Other Spec ID</li> <li>• # of Tubes</li> <li>• Volume</li> <li>• # of Aliq.</li> <li>• Study</li> <li>• Visit</li> <li>• Processing Instructions</li> </ul>

Sorting	Filter Criteria	Information Displayed on Report
	<ul style="list-style-type: none"> <li>Received Date</li> <li>Shipment Date</li> <li>SID/ID3</li> <li>Specimen Date</li> <li>Specimen Type</li> <li>Stored</li> <li>Sub Add/Der</li> </ul>	<ul style="list-style-type: none"> <li>Cell Count</li> <li>Amt Aliq'd</li> <li>Processor's Initials</li> <li>Date/Time Processed</li> <li># of Unused Tubes</li> </ul>

### Lab 263 Summary of Specimens

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>ACTG PID</li> <li>ACTG Protocol</li> <li>Additive</li> <li>Available</li> <li>Clinic ID</li> <li>Condition</li> <li>Derivative</li> <li>Import Date</li> <li>Non ACTG PID/ID1</li> <li>Non-ACTG Prot/ID2</li> <li>Primary</li> <li>project</li> <li>Received Date</li> <li>Received Time</li> <li>Shipment Date</li> <li>SID/ID3</li> <li>Specimen Date</li> <li>Specimen Time</li> <li>Specimen Type</li> <li>Stored</li> <li>Sub additive/derivative</li> </ul>	<ul style="list-style-type: none"> <li>project</li> <li>Primary</li> <li>Additive</li> <li>Derivative</li> <li>Sub additive/derivative</li> <li>Participant count</li> <li>Tube count</li> <li>Total Volume</li> </ul>

### Primary specimens received report

Provides a summary of all primary specimens within a laboratory's database, and the total number of primaries.

Sorting	Filter criteria	Information displayed on report
<p>This report is sorted by project-protocol combination, and then by specimen ID</p>	<ul style="list-style-type: none"> <li>ACTG PID</li> <li>ACTG protocol</li> <li>ACTG protocol type</li> <li>Additive</li> <li>Clinic ID</li> <li>Condition</li> <li>Import date</li> <li>Non ACTG PID/ID1</li> <li>Non ACTG Prot/ID2</li> <li>OPID</li> </ul>	<ul style="list-style-type: none"> <li>Specimen ID</li> <li>project/protocol</li> <li>PID/ID1</li> <li>Clinic</li> <li>Global specimen ID</li> <li>Visit</li> <li>Specimen date</li> <li>Received date</li> <li>Primary</li> <li>Additive</li> </ul>

Sorting	Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>• Other specimen ID</li> <li>• Primary</li> <li>• project</li> <li>• Received date</li> <li>• SID/ID3</li> <li>• Specimen date</li> <li>• Specimen ID</li> <li>• Visit unit</li> <li>• Visit value</li> <li>• Volume</li> <li>• Volume unit</li> </ul>	<ul style="list-style-type: none"> <li>• Specimen condition</li> <li>• Volume</li> <li>• Other specimen ID</li> <li>• Comments (from the <b>Specimen Management</b> page)</li> </ul>

### Specimen count report

Should the number of aliquots entered, stored, and shipped by your laboratory by project-protocol combination, as well as the total across all projects and protocols.

Sorting	Filter criteria	Information displayed on report
This report is sorted by project-protocol combination	<ul style="list-style-type: none"> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Clinic ID</li> <li>• Derivative</li> <li>• project</li> <li>• Specimen date</li> </ul>	<ul style="list-style-type: none"> <li>• project/protocol combination</li> <li>• Number of aliquots entered into LDMS</li> <li>• Number of currently stored aliquots</li> <li>• Number of shipped aliquots</li> </ul>

### Specimen log report

Provides detailed information about every primary and aliquot within a laboratory's database.

Sorting	Filter criteria	Information displayed on report
This report is sorted by project-protocol combination, then by collection date, and then grouped by primary.	<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Additive</li> <li>• Clinic ID</li> <li>• Condition</li> <li>• Derivative</li> <li>• Global specimen ID</li> <li>• Import date</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• OPID</li> <li>• Other specimen ID</li> <li>• Primary</li> <li>• project</li> <li>• Received date</li> </ul>	<ul style="list-style-type: none"> <li>• PID/ID1</li> <li>• project/prot</li> <li>• SID/ID3</li> <li>• VID</li> <li>• Clinic</li> <li>• OPID</li> <li>• Primary specimen ID</li> <li>• Global specimen ID</li> <li>• Specimen time</li> <li>• Specimen date</li> <li>• Received date</li> <li>• Primary volume</li> <li>• Time/time unit</li> <li>• Other specimen ID</li> <li>• Comments [for primary specimen]</li> <li>• Aliquot specimen ID</li> </ul>

Sorting	Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>• SID/ID3</li> <li>• Shipped</li> <li>• Specimen date</li> <li>• Specimen ID</li> <li>• Specimen time</li> <li>• Sub add/der</li> <li>• System entry date</li> <li>• Test ordered</li> <li>• Time</li> <li>• Time unit</li> <li>• Visit unit</li> <li>• Visit value</li> <li>• Volume</li> <li>• Volume unit</li> </ul>	<ul style="list-style-type: none"> <li>• Global specimen ID</li> <li>• Other specimen ID</li> <li>• Primary/additive</li> <li>• Derivative/Sub-additive/derivative</li> <li>• Current volume</li> <li>• Condition</li> <li>• project/prot</li> <li>• Test(s) ordered</li> <li>• Shipped</li> <li>• Comments</li> </ul>

### Specimen processing report

Provides processing information (processing date, frozen date, etc.) for primaries and aliquots in a laboratory’s database.

Sorting	Filter criteria	Information displayed on report
<p>This report is sorted by project-protocol combination, then by collection date, and then grouped by primary.</p>	<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Additive</li> <li>• Derivative</li> <li>• Global specimen ID</li> <li>• Import date</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Other specimen ID</li> <li>• Primary</li> <li>• project</li> <li>• Received date</li> <li>• SID/ID3</li> <li>• Specimen date</li> <li>• Specimen ID</li> <li>• Visit unit</li> <li>• Visit value</li> </ul>	<ul style="list-style-type: none"> <li>• PID/ID1</li> <li>• project/Prot</li> <li>• SID/ID3</li> <li>• VID</li> <li>• Clinic</li> <li>• OPID</li> <li>• Primary specimen ID</li> <li>• Global specimen ID</li> <li>• Other specimen ID</li> <li>• Primary</li> <li>• Additive</li> <li>• Volume</li> <li>• Specimen date</li> <li>• Specimen time</li> <li>• Received date</li> <li>• Received time</li> <li>• Total cell count</li> <li>• Proc[essing] date</li> <li>• Proc[essing] time</li> <li>• Proc[essed] by</li> <li>• Aliquot specimen ID</li> <li>• Global specimen ID</li> <li>• Other specimen ID</li> <li>• Derivative</li> <li>• Sub-additive/derivative</li> <li>• Volume</li> <li>• project/prot</li> <li>• Frozen date</li> <li>• Frozen time</li> <li>• Proc[essing] date</li> </ul>

Sorting	Filter criteria	Information displayed on report
		<ul style="list-style-type: none"> <li>• Proc[essing] time</li> <li>• Proc[essing] by</li> </ul>

### Specimens for a given project report

Shows the aliquots for a given project-protocol combination.

Sorting	Filter criteria	Information displayed on report
<p>This report is grouped by project-protocol combination, and then sorted by ID1, and then by specimen ID.</p>	<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Additive</li> <li>• Clinic ID</li> <li>• Derivative</li> <li>• Import date</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG prot/ID2</li> <li>• OPID</li> <li>• Other specimen ID</li> <li>• Primary</li> <li>• project</li> <li>• Received date</li> <li>• SID/ID3</li> <li>• Specimen date</li> <li>• Specimen ID</li> <li>• Specimen time</li> <li>• Sub additive/derivative</li> <li>• Visit unit</li> <li>• Visit value</li> </ul>	<ul style="list-style-type: none"> <li>• Protocol (and project)</li> <li>• PID/ID1</li> <li>• OPID</li> <li>• Specimen ID</li> <li>• Global specimen ID</li> <li>• Specimen date</li> <li>• Specimen time</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Sub additive-derivative</li> <li>• Received date</li> <li>• Received time</li> <li>• Import date</li> <li>• VID (visit value and unit)</li> <li>• Other specimen ID</li> </ul>

### Specimens for a given project 2

Shows the aliquots for a given project-protocol combination in aggregate form, with the number of aliquots with a given specimen ID.

Sorting	Filter criteria	Information displayed on report
<p>This report is grouped by project-protocol combination, then grouped by Specimen ID, and then sorted by ID1, and then by specimen ID.</p>	<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Additive</li> <li>• Clinic ID</li> <li>• Derivative</li> <li>• Import date</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG prot/ID2</li> <li>• OPID</li> <li>• Other specimen ID</li> <li>• Primary</li> <li>• project</li> </ul>	<ul style="list-style-type: none"> <li>• Protocol (and project)</li> <li>• PID/ID1</li> <li>• OPID</li> <li>• Specimen ID</li> <li>• Count</li> <li>• Specimen date</li> <li>• Specimen time</li> <li>• SID/ID3</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Sub additive-derivative</li> <li>• Received date</li> </ul>

Sorting	Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>Received date</li> <li>SID/ID3</li> <li>Specimen date</li> <li>Specimen ID</li> <li>Specimen time</li> <li>Sub additive/derivative</li> <li>Visit unit</li> <li>Visit value</li> </ul>	<ul style="list-style-type: none"> <li>Received time</li> <li>Import date</li> <li>VID (visit value and unit)</li> <li>Other specimen ID</li> </ul>

### Time to freeze QA/QC summary report

Shows the time to freeze for aliquots, along with a graph and summary of overall time to freeze.

Sorting <sup>1</sup>	Filter criteria	Information displayed on report
-	<ul style="list-style-type: none"> <li>ACTG protocol</li> <li>ACTG protocol type</li> <li>Non ACTG prot/ID2</li> <li>project</li> <li>Specimen date</li> <li>Tech initials</li> </ul>	<ul style="list-style-type: none"> <li>Patid</li> <li>Collection date</li> <li>Collection time</li> <li>Frozen date</li> <li>Frozen time</li> <li>Time to freeze (in minutes)</li> <li>Tech</li> <li>Additive</li> <li>Derivative</li> <li>Comments</li> </ul>

### Time to process QA/QC summary report

Shows the time to process for aliquots, along with a graph and summary of overall time to process.

Sorting <sup>2</sup>	Filter criteria	Information displayed on report
-	<ul style="list-style-type: none"> <li>ACTG protocol</li> <li>ACTG protocol type</li> <li>Non ACTG prot/ID2</li> <li>project</li> <li>Specimen date</li> <li>Tech initials</li> </ul>	<ul style="list-style-type: none"> <li>Patid</li> <li>Collection date</li> <li>Collection time</li> <li>Process time</li> <li>Frozen time</li> <li>Time to process (in minutes)</li> <li>Tech</li> <li>Additive</li> <li>Derivative</li> <li>Comments</li> </ul>

<sup>1</sup> You must specify a sample type to report on to generate this report. You can generate the report for PBMCs, plasma, or both.

<sup>2</sup> You must specify a sample type to report on to generate this report. You can generate the report for PBMCs, plasma, or both.

## Storage reports

### Specimens in storage per PID report

Shows the number for a given project-participant combination that have a storage location assigned in a laboratory's database.

Sorting	Filter criteria	Information displayed on report
This report is sorted by project, and then by participant.	<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG prot/ID2</li> <li>• OPID</li> <li>• Primary</li> <li>• project</li> </ul>	<ul style="list-style-type: none"> <li>• project</li> <li>• PID</li> <li>• Count (number of aliquots)</li> </ul>

### Specimens not in storage report

Shows specimens that are available in a laboratory's database, but have not had a storage location assigned on the **Storage** page.

Sorting	Filter criteria	Information displayed on report
This report is grouped by project-protocol combination, and then by specimen ID, and then sorted by global specimen ID.	<ul style="list-style-type: none"> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Additive</li> <li>• Condition</li> <li>• Derivative</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG prot/ID2</li> <li>• Primary</li> <li>• project</li> <li>• Specimen ID</li> <li>• Sub additive/derivative</li> <li>• Visit unit</li> <li>• Visit value</li> <li>• Volume</li> <li>• Volume unit</li> </ul>	<ul style="list-style-type: none"> <li>• project/prot</li> <li>• Specimen ID</li> <li>• Global specimen ID</li> <li>• PID/ID1</li> <li>• Specimen date</li> <li>• Pri[mary]</li> <li>• Add[itive]</li> <li>• Der[ivative]</li> <li>• Sub a[dditive]/d[erivative]</li> <li>• VID (visit unit and value)</li> <li>• Volume</li> <li>• Condition</li> <li>• Status</li> </ul>

### Specimens remaining in storage report

Shows the number of aliquots for a given participant with a storage location assigned in a laboratory's database.

Sorting	Filter criteria	Information displayed on report
This report is grouped and sorted by project, ID1, and protocol.	<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Additive</li> </ul>	<ul style="list-style-type: none"> <li>• project</li> <li>• PID</li> <li>• Protocol</li> <li>• Volume</li> </ul>

Sorting	Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG prot/ID2</li> <li>• OPID</li> <li>• Primary</li> <li>• project</li> <li>• Specimen date</li> </ul>	<ul style="list-style-type: none"> <li>• Volume unit</li> <li>• Derivative</li> <li>• Aliquots remaining in storage</li> </ul>

### Storage container location report

Shows the storage location for all containers in a laboratory's database.

Sorting	Filter criteria	Information displayed on report
This report is sorted by storage unit name, and then by container position.	<ul style="list-style-type: none"> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Freezer name</li> <li>• Level name</li> <li>• Non ACTG prot/ID2</li> <li>• project</li> <li>• Sublevel name</li> </ul>	<ul style="list-style-type: none"> <li>• Storage location</li> <li>• Container name</li> <li>• Position</li> </ul>

### Storage count report by freezer

Shows the number of specimens stored in a given storage unit for a given project-protocol combination.

Sorting	Filter criteria	Information displayed on report
This report is sorted by storage unit, and then by project-protocol combination, and then by derivative.	<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Derivative</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG prot/ID2</li> <li>• project</li> </ul>	<ul style="list-style-type: none"> <li>• Freezer</li> <li>• project/protocol</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Sub a[dditive]/d[erivative]</li> <li>• Count</li> </ul>

### Storage detail report

Shows detailed information about the contents of containers in storage units.

Sorting	Filter criteria	Information displayed on report
This report is sorted by storage location, and then by storage position.	<ul style="list-style-type: none"> <li>• ACTG PID</li> <li>• ACTG protocol</li> <li>• ACTG protocol type</li> <li>• Additive</li> <li>• Derivative</li> <li>• Import date</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• OPID</li> </ul>	<ul style="list-style-type: none"> <li>• Storage location</li> <li>• Specimen ID</li> <li>• Global spec[imen] ID</li> <li>• project/prot</li> <li>• PID/ID1</li> <li>• VID/unit</li> <li>• Prim[ary]</li> <li>• Add[itive]</li> <li>• Der[ivative]</li> </ul>



Sorting	Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>• Other specimen ID</li> <li>• Primary</li> <li>• project</li> <li>• Received date</li> <li>• SID/ID3</li> <li>• Shipment number</li> <li>• Specimen date</li> <li>• Specimen ID</li> <li>• Specimen time</li> <li>• Stored date</li> <li>• Sub add[itive]/der[ivative]</li> <li>• Visit unit</li> <li>• Visit value</li> <li>• Volume</li> <li>• Volume unit</li> </ul>	<ul style="list-style-type: none"> <li>• Sub a[dditive]/d[erivative]</li> <li>• Volume</li> <li>• Ship</li> <li>• Storage date</li> <li>• Spec[imen] date</li> <li>• Time</li> <li>• Clinic</li> <li>• Pos[ition]</li> <li>• Other specimen ID</li> </ul>

## Test Result Reports

### Abbott Realtime HIV1 Assay Report

Filtering Criteria	Information Displayed on Report
<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG/Protocol</li> <li>• ACTG Protocol Type</li> <li>• Assay Date</li> <li>• Clinic ID</li> <li>• Global Spec ID</li> <li>• Non-ACTG PID/ID1</li> <li>• Non-ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>• Group/protocol</li> <li>• PID</li> <li>• SID</li> <li>• Visit</li> <li>• PRI</li> <li>• Specimen ID</li> <li>• Other Spec ID</li> <li>• Spec Date</li> <li>• Assay Date</li> <li>• RUN ID</li> <li>• Dilution</li> <li>• Result</li> <li>• System Censor</li> <li>• User Censor</li> <li>• Run System Censor</li> <li>• Run User Censor</li> <li>• Group/Pro Total</li> <li>• Grand Total</li> </ul>

### Abbott Realtime HIV1 Patient Report

An individualized report per specimen showing associated participant details along with detailed test results including censor codes, run limits, and a final calculated result.

Filtering Criteria	Information Displayed on Report
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<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG/Protocol</li> <li>• ACTG Protocol Type</li> <li>• Assay Date</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Non-ACTG PID/ID1</li> <li>• Non-ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Received Date</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>• Patient</li> <li>• SID</li> <li>• Group/Protocol</li> <li>• Specimen Date</li> <li>• Visit</li> <li>• Clinic Info</li> <li>• Fax</li> <li>• Testing Lab Info</li> <li>• Specimen ID</li> <li>• Received Date</li> <li>• Primary</li> <li>• Global Spec ID</li> <li>• Received Time</li> <li>• Additive</li> <li>• Other Spec ID</li> <li>• Sample Condition</li> <li>• Derivative</li> <li>• Type of Assay</li> <li>• Assay Date</li> <li>• Sample Prep Tech</li> <li>• Amplification Tech</li> <li>• Input Volume</li> <li>• Data Transfer Tech</li> <li>• Results: <ul style="list-style-type: none"> <li>• Run Comment</li> <li>• Sample Comment</li> <li>• Reportable Page</li> </ul> </li> </ul>
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### Abbott Repeat and Censored Run/Samples

Filtering Criteria	Information Displayed on Report
<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG/Protocol</li> <li>• ACTG Protocol Type</li> <li>• Assay Date</li> <li>• Global Spec ID</li> <li>• Non-ACTG PID/ID1</li> <li>• Non-ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Received Date</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>• Group/Prot</li> <li>• System Censor</li> <li>• Run System Censor</li> <li>• User Censor</li> <li>• Run User Censor</li> <li>• Specimen ID</li> <li>• Global Spec ID</li> <li>• PID</li> <li>• Spec Date</li> <li>• RUN ID</li> <li>• Run Valid/Invalid</li> <li>• Assay Date</li> <li>• Dilution</li> <li>• Result</li> </ul>

### Abbott SARS-COV-2 Quant Assay Report

Displays specimen details and results from Abbott SARS-COV-2 Quant runs in the Test Results module.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Assay Date</li> <li>• Clinic ID</li> <li>• Global Spec ID</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Specimen List</li> </ul>	<ul style="list-style-type: none"> <li>• Group/Prot</li> <li>• PID</li> <li>• SID</li> <li>• Visit</li> <li>• PRI</li> <li>• Specimen ID</li> <li>• Other Spec ID</li> <li>• Global Spec ID</li> <li>• Spec Date</li> <li>• Assay Date</li> <li>• RUN ID</li> <li>• Result</li> <li>• System Censor</li> <li>• User Censor</li> <li>• Run System Censor</li> <li>• Run user Censor</li> </ul>

### Abbott SARS-COV-2 Quant Patient Report

An individualized report per specimen showing associated participant details along with detailed test results including censor codes, run limits, and a final calculated result.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG Protocol</li> <li>• ACTG Protocol Type</li> <li>• Assay Date</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Non ACTG PID/ID1</li> <li>• Non ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Received Date</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Specimen List</li> </ul>	<ul style="list-style-type: none"> <li>• Participant</li> <li>• SID</li> <li>• Group/Protocol</li> <li>• Specimen Date</li> <li>• Visit</li> <li>• Clinic Info</li> <li>• Fax</li> <li>• Testing Lab Info</li> <li>• Specimen ID</li> <li>• Global Spec ID</li> <li>• Other Spec ID</li> <li>• Received Date</li> <li>• Received Time</li> <li>• Sample Condition</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Type of Assay</li> <li>• Assay Date</li> <li>• Input Volume</li> <li>• Sample Prep Tech</li> <li>• Amplification Tech</li> <li>• Data Transfer Tech</li> <li>• Results</li> <li>• Log copies/mL</li> <li>• Run Comment</li> <li>• Sample Comment</li> </ul>

Filter criteria	Information displayed on report
	<ul style="list-style-type: none"> <li>Assay Reportable Range and Dilution Information</li> </ul>

### **IQA Cryopreservation Patient Report**

An individualized report per specimen showing associated participant details along with detailed test results including censor codes, run limits, and a final calculated result.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>ACTG PID/ID1</li> <li>ACTG Protocol</li> <li>ACTG Protocol Type</li> <li>Assay Date</li> <li>Derivative</li> <li>Global Spec ID</li> <li>Non ACTG PID/ID1</li> <li>Non ACTG Prot/ID2</li> <li>On Cryopreservation Test Run</li> <li>Other Specimen ID</li> <li>Primary</li> <li>Project</li> <li>Received Date</li> <li>Run ID</li> <li>SID/ID3</li> <li>Specimen Date</li> <li>Specimen ID</li> <li>Specimen List</li> </ul>	<ul style="list-style-type: none"> <li>Group/Study</li> <li>Run ID</li> <li>Assay Tech</li> <li>PID</li> <li>Spec No</li> <li>GlobalSpec ID</li> <li>Spec Date</li> <li>VID</li> <li>Primary</li> <li>Additive</li> <li>Derivative</li> <li>Sub A/D</li> <li>Data Entered By</li> <li>Data Entry Date</li> </ul>

### **TaqMan HCV Repeat and Censored Run/Samples**

Filtering Criteria	Information Displayed on Report
<ul style="list-style-type: none"> <li>ACTG PID/ID1</li> <li>ACTG/Protocol</li> <li>ACTG Protocol Type</li> <li>Assay Date</li> <li>Global Spec ID</li> <li>Non-ACTG PID/ID1</li> <li>Non-ACTG Prot/ID2</li> <li>Project</li> <li>Run ID</li> <li>Specimen Date</li> <li>Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>Group/Prot</li> <li>System Censor</li> <li>Run System Censor</li> <li>User Censor</li> <li>Run User Censor</li> <li>Specimen ID</li> <li>Global Spec ID</li> <li>PID/ID1</li> <li>Spec Date</li> <li>RUN ID</li> <li>Run Valid/Invalid</li> <li>Result</li> <li>Assay Date</li> </ul>

### **TaqMan HIV-1 Repeat and Censored Run Samples**

Filtering Criteria	Information Displayed on Report
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<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG/Protocol</li> <li>• ACTG Protocol Type</li> <li>• Assay Date</li> <li>• Global Spec ID</li> <li>• Non-ACTG PID/ID1</li> <li>• Non-ACTG Prot/ID2</li> <li>• Project</li> <li>• Run ID</li> <li>• Specimen Date</li> <li>• Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>• Group/Prot</li> <li>• System Censor</li> <li>• Run System Censor</li> <li>• User Censor</li> <li>• Run User Censor</li> <li>• Specimen ID</li> <li>• Global Spec ID</li> <li>• PID/ID1</li> <li>• Spec Date</li> <li>• RUN ID</li> <li>• Run Valid/Invalid</li> <li>• Result</li> <li>• Assay Date</li> </ul>
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### TaqMan Realtime HCV Assay Report

Filtering Criteria	Information Displayed on Report
<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG/Protocol</li> <li>• ACTG Protocol Type</li> <li>• Assay Date</li> <li>• Clinic ID</li> <li>• Global Spec ID</li> <li>• Non-ACTG PID/ID1</li> <li>• Non-ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Version</li> </ul>	<ul style="list-style-type: none"> <li>• Group/Prot</li> <li>• SID/ID3</li> <li>• VID</li> <li>• PRI</li> <li>• Specimen ID</li> <li>• Other Spec ID</li> <li>• Global Spec ID</li> <li>• Spec Date</li> <li>• Assay Date</li> <li>• RUN ID</li> <li>• Ver</li> <li>• Result</li> <li>• System Censor</li> <li>• User Censor</li> <li>• Run System Censor</li> <li>• Run User Censor</li> </ul>

### TaqMan Realtime HCV Patient Report

An individualized report per specimen showing associated participant details along with detailed test results including censor codes, run limits, and a final calculated result.

Filtering Criteria	Information Displayed on Report
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<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG/Protocol</li> <li>• ACTG Protocol Type</li> <li>• Assay Date</li> <li>• Clinic ID</li> <li>• Global Spec ID</li> <li>• Non-ACTG PID/ID1</li> <li>• Non-ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Version</li> </ul>	<ul style="list-style-type: none"> <li>• Patient</li> <li>• SID</li> <li>• Group/Protocol</li> <li>• Specimen Date</li> <li>• Visit</li> <li>• Clinic Info</li> <li>• Fax</li> <li>• Testing Lab Info</li> <li>• Specimen ID</li> <li>• Global Spec ID</li> <li>• Other Spec ID</li> <li>• Received Date</li> <li>• Received Time</li> <li>• Sample Condition</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Type of Assay</li> <li>• Assay Date</li> <li>• Prep Method</li> <li>• Sample Prep Tech</li> <li>• Data Transfer Tech</li> <li>• Results</li> </ul>
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### TaqMan Realtime HIV-1 Assay Report

Filtering Criteria	Information Displayed on Report
<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG/Protocol</li> <li>• ACTG Protocol Type</li> <li>• Assay Date</li> <li>• Clinic ID</li> <li>• Global Spec ID</li> <li>• Non-ACTG PID/ID1</li> <li>• Non-ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Version</li> </ul>	<ul style="list-style-type: none"> <li>• PID/ID1</li> <li>• SID/ID3</li> <li>• VID</li> <li>• PRI</li> <li>• Specimen ID</li> <li>• Other Spec ID</li> <li>• Global Sec ID</li> <li>• Spec Date</li> <li>• Assay Date</li> <li>• RUN ID</li> <li>• Ver</li> <li>• Result</li> <li>• System Censor</li> <li>• Use Censor</li> <li>• Run System Censor</li> <li>• Run User Censor</li> </ul>

### TaqMan Realtime HIV-1 Patient Report

An individualized report per specimen showing associated participant details along with detailed test results including censor codes, run limits, and a final calculated result.

Filtering Criteria	Information Displayed on Report
--------------------	---------------------------------

<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG/Protocol</li> <li>• ACTG Protocol Type</li> <li>• Assay Date</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Non-ACTG PID/ID1</li> <li>• Non-ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Received Date</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Version</li> </ul>	<ul style="list-style-type: none"> <li>• Patient</li> <li>• SID</li> <li>• Group/Protocol</li> <li>• Specimen Date</li> <li>• Visit</li> <li>• Clinic Info</li> <li>• Fax</li> <li>• Testing Lab Info</li> <li>• Specimen ID</li> <li>• Global Spec ID</li> <li>• Other Spec ID</li> <li>• Received Date</li> <li>• Received Time</li> <li>• Sample Condition</li> <li>• Primary</li> <li>• Additive</li> <li>• Derivative</li> <li>• Type of Assay</li> <li>• Assay Date</li> <li>• Prep Method</li> <li>• Sample Prep Tech</li> <li>• Data Transfer Tech</li> <li>• Results</li> </ul>
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### Taqman Realtime Qual Assay Report

Filtering Criteria	Information Displayed on Report
<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG/Protocol</li> <li>• ACTG Protocol Type</li> <li>• Assay Date</li> <li>• Global Spec ID</li> <li>• Non-ACTG PID/ID1</li> <li>• Non-ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Version</li> </ul>	<ul style="list-style-type: none"> <li>• PID/ID1</li> <li>• SID/ID3</li> <li>• VID</li> <li>• PRI</li> <li>• Specimen ID</li> <li>• Other Spec ID</li> <li>• Global Spec ID</li> <li>• Spec Date</li> <li>• Assay Date</li> <li>• RUN ID</li> <li>• Ver</li> <li>• Result</li> <li>• System Censor</li> <li>• Run System Censor</li> <li>• User Censor</li> <li>• Run User Censor</li> </ul>

### TaqMan Realtime Qual Patient Report

An individualized report per specimen showing associated participant details along with detailed test results including censor codes, run limits, and a final calculated result.

Filtering Criteria	Information Displayed on Report
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<ul style="list-style-type: none"> <li>• ACTG PID/ID1</li> <li>• ACTG/Protocol</li> <li>• ACTG Protocol Type</li> <li>• Assay Date</li> <li>• Derivative</li> <li>• Global Spec ID</li> <li>• Non-ACTG PID/ID1</li> <li>• Non-ACTG Prot/ID2</li> <li>• Other Specimen ID</li> <li>• Primary</li> <li>• Project</li> <li>• Run ID</li> <li>• SID/ID3</li> <li>• Specimen Date</li> <li>• Specimen ID</li> <li>• Version</li> </ul>	<ul style="list-style-type: none"> <li>• PID/ID1</li> <li>• SID/ID3</li> <li>• VID</li> <li>• PRI</li> <li>• Specimen ID</li> <li>• Other Spec ID</li> <li>• Global Spec ID</li> <li>• Spec Date</li> <li>• Assay Date</li> <li>• RUN ID</li> <li>• Ver</li> <li>• Result</li> <li>• System Censor</li> <li>• Run System Censor</li> <li>• User Censor</li> <li>• Run User Censor</li> </ul>
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## WIHS

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### Processing Log - Lab 263

Displays specimen processing details and instructions based on WIHS processing codes.

Filter criteria	Information displayed on report
<ul style="list-style-type: none"> <li>• Non ACTG PID/ID1</li> <li>• Specimen Date</li> <li>• Specimen ID</li> </ul>	<ul style="list-style-type: none"> <li>• Global Spec ID</li> <li>• Der</li> <li>• Other Spec ID</li> <li>• Volume</li> <li>• Number of Aliquots</li> <li>• Study</li> <li>• Processing Instructions</li> <li>• Cell Count</li> <li>• Amt</li> <li>• Storage</li> <li>• Processor's Initials</li> <li>• Date/Time Processed/Frozen</li> <li>• Unused Tubes</li> </ul>

## Labels

### Label formats

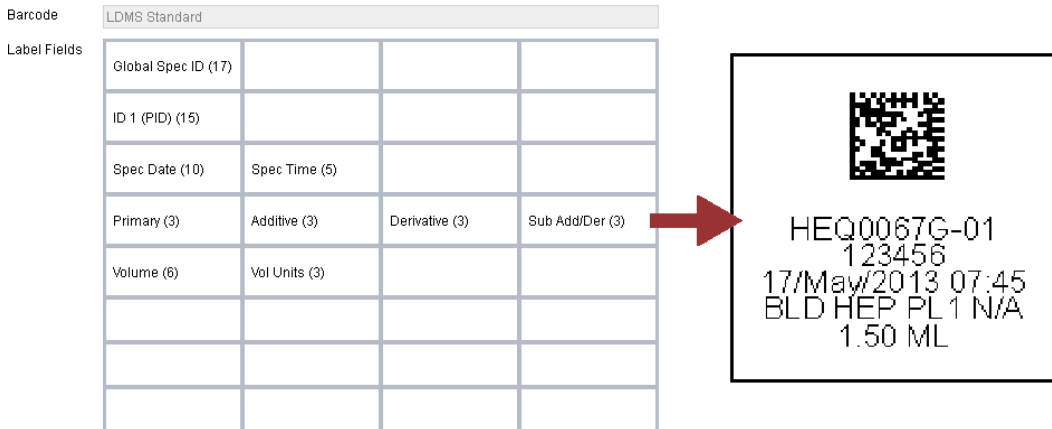
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Labels are setup like grids, with items that appear on the label occupying one cell.



Items that can appear are most of the information that can be found on the **Specimen Management** page, such as the primary type and the received date and time. Each row on a label can hold up to four items, and a label can have up to 8 rows.

**Figure 52: Label definition and corresponding output**



A label as it is set up in LDMS (left) compared to a generated label (right). The colored background shows how each item in the label definition matches up to the item on the label.

## Barcodes

LDMS supports generating 2D barcodes on labels

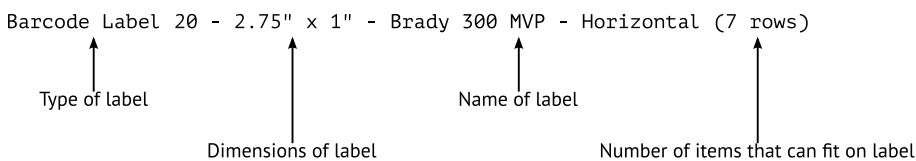
If a label has a barcode, it will appear as the first item on the label. The barcodes generated by LDMS contain the specimen's *global specimen ID*.

## Label sizes

Labels can be generated in a variety of common sizes.

The label's name in LDMS indicates information about its size, manufacturer, and use.

**Figure 53: Example label name**



There are three types of labels available:

- Laser labels** For printing using a desktop printer with special 8.5-by-11-inch paper
- Barcode labels** For printers specifically made for printing labels
- Dot matrix labels** For use with dot matrix printers



**Note:** If you choose a label format that has a barcode, only barcode labels can be selected.

For laser and dot matrix labels, the size of the label refers to the label itself, not the paper it will be printed on. These labels are generated in US letter size paper (8.5-by-11-inches), with the assumption that the user is using special label paper that can be peeled apart. Barcode labels, on the other hand, require special printers and label paper that are designed exclusively for printing labels.

## How to use a barcode reader with LDMS

LDMS supports using any Windows compatible barcode reader.

Barcode readers that are compatible with Windows will extract the global specimen ID from the 2D barcodes that are generated by LDMS. You can test this yourself by opening Notepad and scanning a barcode. Doing so will cause the global specimen ID from the barcode to appear in Notepad.

In any place in where you would need to type a global specimen ID, you can use a barcode reader to input the ID instead. Select the box where you want the global specimen ID to appear, and then scan the barcode. This can help avoid errors when trying to type out a global specimen ID using the keyboard.

## Printing labels anywhere

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Specimen labels can be printed in many places in LDMS, not just the Labels page.

Labels can be printed almost anywhere where you can interact with specimens.

- On the Specimen Management page, click the down arrow next to any of the **Edit** buttons, and then select **Print Labels**. This will print all labels associated with that item. For example, if you select **Edit Participant** > **Print labels**, you will print the labels for all specimens associated with that participant. Likewise, if you click **Edit [primary]** > **Print Labels**, you will print all labels associated with that primary.
- Also on the Specimen Management page, when adding a participant using Quick Add, after a record is added a success message appears at the top of the page. Below it, click the button that says **Print labels**.
- On the Storage page, click the down arrow next to **Edit** button next to any storage item, and then click **Print Labels**. This will allow you to print labels for all specimens stored at that location.
- On the Pending Shipments page, click the down arrow next to the **Edit/Ship** button next to a shipment, and then click **Print Labels**.

When creating labels, specimens that are not available will not be included.

## Support for LabelScape-generated Barcodes

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The LabelScape LDMS-supported barcode is a data matrix 2D barcode that includes the ID1/PID & specimen date in the barcode.

In LDMS, there are two ways of scanning LabelScape barcodes. One method is to scan a barcode in **Specimen Management** and search for primary records. Another method is to scan a label into **Quick Add** which will populate the PID and specimen date.

## Generating labels

---

While labels can be generated from many places, the **Print Labels** page allows you to generate labels from multiple sources.

### Background

If you want to generate labels, you generally want to do so on either the **Specimen Management, Storage, or Shipping** page. On these pages, you can create labels for a specific participant, a particular shipping or storage container, or an individual shipment. These are the most common scenarios for which you will need to generate labels. You can also choose to upload a list of unique specimen IDs, which will set a specimen criteria to locate any sample with a unique specimen ID appearing in the list.

There may be times where you need to generate labels from a variety of sources. For example, you may want to print labels for all specimens received on a specific day.

**Figure 54: The label generation page**

The screenshot displays the 'Print Labels' interface. At the top, there is a search icon and a 'Print Labels' title. Below this, a 'Remove All Filters' button is visible. The 'Participant Filters' section includes dropdown menus for 'Project' (set to 'ACTG/IMPACT'), 'ID1', and 'OPID'. Other filter sections for Enrollment, Visit, Specimen, and Shipment are present but collapsed. A table with 10 rows of specimen data is shown, with columns for 'Selected', 'Global Specimen Id', 'Specimen Id', 'Other Specimen Id', 'Primary Type', 'Additive', 'Derivative Type', 'Sub Add/Der Type', 'Available Volume', and 'ID1'. Below the table, there is a 'Sort Order' dropdown menu set to 'Primary/Aliquot Creation Order' and a 'Print Labels' button.



**Note:**

Labels can be generated for up to 500 specimens.

**Steps**

1. On the navigation bar, hover over **Labels**, and then click **Print Labels**.
2. Optional: At the top of the **Print Labels** page, use filters to narrow down the list of specimens displayed.
3. For each specimen you want to print a label, select the check box in the **Selected** column.
4. Optional: Use dropdown next to **Sort Order** to specify the order in which labels are generated. This option is also available in the **Print Labels** window.
5. Click **Print Labels**.
6. In the **Print Labels** window, select the following.

**Option**

**Project**

Only shown if specimens from different projects were selected.

<b>Option</b>	
<b>Use Defaults</b>	If the project has a default label format defined, selecting this check box will re-select that default
<b>Format</b>	The label format to use
<b>Size</b>	The size of your label stock
<b>Skip</b>	
<b>Sort Order</b>	Order in which labels are sorted

**7.** Click **Generate Labels**.

A PDF with the labels will be generated, which may open or you may be prompted to save it, depending on your browser's settings.

If generating labels for specimens from more than one project, a check will appear in the **Generated** column for that project. Repeat the previous steps with the next project.

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## Defining new label formats

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You can create new label formats.

### Steps

- 1.** In the menu bar, hover over **Labels**, and then click **Define Custom Labels**.
- 2.** Optional: Use the **Project** and **Format** lists to select a label as the basis for your new label.  
This is not needed if you want to create a new label from scratch.
- 3.** Click **Create Format**.
- 4.** In the **Name** box, enter a name for your new format.  
If your new label format is based on an existing format, you must also select the check box next to **Copy Fields**.
- 5.** Click **Create Format**.

### Result

Your new label format will be created and will be available for selection.

### After you are finished

You will want to customize your new label format and define the information that will appear on it.

## Customizing label formats

You can customize that information that appears on label formats created by your laboratory.

### Background

New label formats are blank when they are created. You must customize the format to show the information that you want displayed. New labels and existing labels are modified the same way. Only label formats that your laboratory created can be modified. Label formats that are pre-defined in LDMS cannot be changed.

**Figure 55: The label modification page**

Name FRONTIER

Barcode LDMS Standard

Fields

Global Spec ID (17)			
ID 1 (PID) (15)			
Spec Date (10)	Spec Time (5)		
Primary (3)	Additive (3)	Derivative (3)	Sub Add/Der (3)
Volume (6)	Vol Units (3)		

Row 6 Column 1

Ship Batch No. (8)

### Steps

1. In the menu bar, hover over **Labels**, and then click **Define Custom Labels**.
2. In the **Project** and **Format** lists, select a locally defined project and label format.
3. Click **Modify Format**.
4. Modify the label format as needed.
  - To change the barcode options, select from the **Barcode** dropdown. There are various 1D and 2D options for the user to define.
  - To add a field to a label, select a box from the **Fields** section where you want the information to appear. Select an item from the list below the **Fields** section, and then click **Set Field**.

- To remove a field, select it from the **Fields** section, and then click **Clear Field**.
5. Click **Modify Format**.

## Setting the default label format for a project

The default label format and stock size can be set for individual projects.

### Background

This means that when you print labels for that project, the default format and size will automatically be selected. If you typically use the same format and size for a specific project's labels, then you can save time by defining these defaults.

### Steps

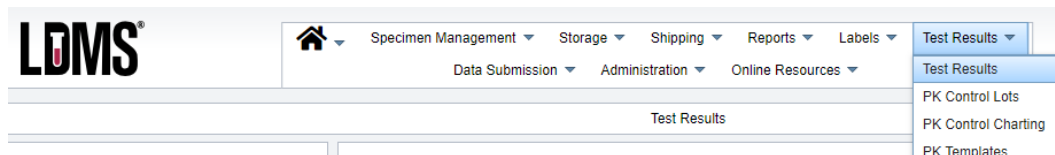
1. On the navigation menu, hover over **Labels**, and then click **Default Label Setup**.
2. In the **Project** box, select the project to set defaults.
3. In the **Format** box, select the applicable default label format.
4. In the **Label** box, select the applicable default label stock size.
5. Click **Add Default**.
6. Click **Save** to save the changes.

# Test Results

## Test Results

The **Test Results** page is where you can manage test results from the various available assays. The application captures the complete audit history of test runs. The **Test Results** page shows all test runs for the lab, users can access this history and view the run from each phase.

**Figure 56: Test Results Page**



Users can create, edit, and delete committed and uncommitted test results on the Test Results page.

When viewing the Test Results page, you'll notice two main features on the page. First is the Main Window, second is the filters window. There is a third, less noticeable yet incredibly useful feature, and that is the Add Pending Results bar. We'll examine these features one by one after a note on assays themselves.

## Test Supported in LDMS

Below is a list of all tests supported in LDMS:

- Abbott RealTime HIV-1 RNA
- Abbott SARS-COV-2
- COBAS TaqMan HCV
- COBAS TaqMan HIV-1
- COBAS TaqMan HIV-1 Qual
- PK Assay

## Running an assay means reading data

The method of getting assay data into LDMS will vary, depending on the assay and available equipment at your laboratory. There are two ways to get assay data into LDMS:

1. Read an output file that was created when the assay was run
2. Enter the assay results data by hand

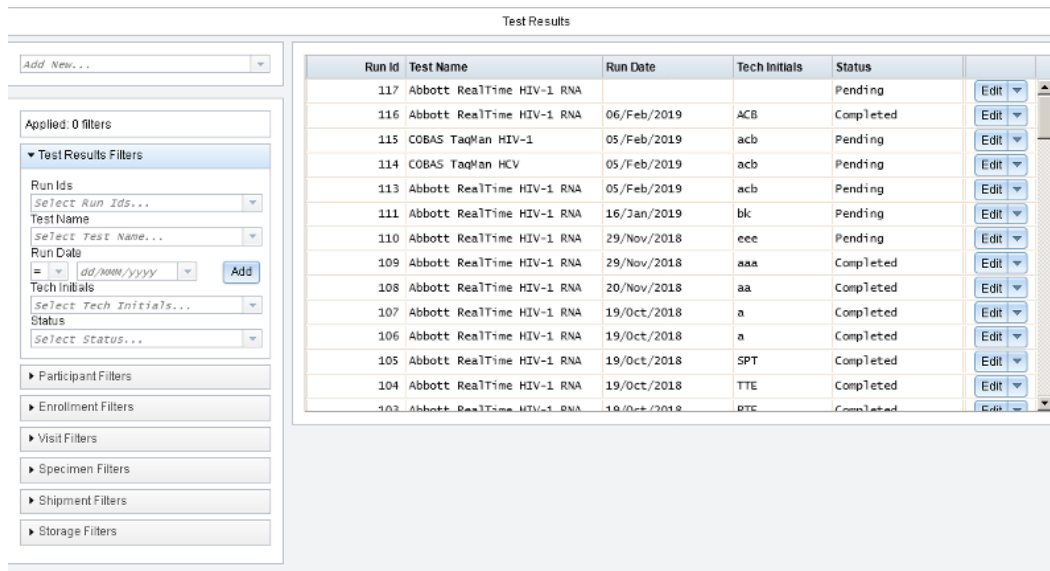
LDMS does not really run your assay; it is more accurate to say that LDMS *reads* assay data, and then stores it. Reading assay output using LDMS is also sometimes referred to as "resulting" an assay in LDMS, since the intent is to get assay results into LDMS's database for long-term storage.

## Test Results page

The **Test Results** page is where you can access all test result runs and create new runs.



**Figure 57: Test Results Main Window**




Column	Description
Run ID	ID number assigned automatically
Test name	Name of assay selected when run was created
Run date	Date that the assay was run (or is expected to be run)
Tech Initials	The assay technician who ran (or will run) the assay; not necessarily the data entry technician
Status	Current status of the run

### Locating assay runs

Additional filters are available for locating assays on the **Test Results** page.

In addition to the regular filters, **Test Results Filters** are available on the **Test Results** page. These provide additional filters specifically for assays, such as locating tests by assay name.

 **Note:** Deleted tests are not displayed by default. To see them, you must apply a **Status** filter set to Deleted.

### Censor Codes

Censor codes can be assigned to specimens, controls and assay runs to indicate an issue or special condition.

For example, a censor code might indicate a contaminated specimen or equipment failure. *User censors* are those that are added by a user. *System censors* are those that are added automatically by LDMS when certain conditions are met.

There are two types of user and system censors:

- specimen censurs** These censor a single specimen on a run; other specimens on the run are unaffected.
- run censurs** These censor the results of an entire assay run. They indicate that something went wrong with the entire test.

### Run Statuses

Each run has a status that indicates what state the run is at and what action is needed next.

Status	Meaning
Pending	The run has been created, but is awaiting data entry (or data entry is in progress)
Completed	Data entry is complete, but the run has not been reviewed
Reviewed	Data entry is complete and the run has been reviewed
Deleted	Run was created in error and has been removed. (Deleted runs are not displayed by default. You must apply a <b>Test Results Filter</b> for <b>Status</b> as Deleted to see them.)

### Creating New Test Result Runs


Adding assays results involves selecting specimens that were tested, uploading a results file, and then matching results to specimens.

#### Background

There are some differences between supposed assay, such as additional assay-specific fields.

You can create an assay run and then click **Save** without adding specimens or results. The run will be saved with the status of pending and can be updated later.

#### Steps

1. From the LDMS menu, click **Test Results**.
2. From the action menu, click **Add Pending Results**.
3. In the **Test Name** box, select an assay, and then click **Continue**
  -  **Warning:** The assay cannot be changed later. If the wrong assay was selected, the run must be deleted and a new run created.
4. On the **General** tab, complete the details of the run.

Field	Usage
Run Date	The date that the test was run in the laboratory

Field	Usage
Tech Initials	The initials of the laboratory technician who completed the test
Data Transfer Tech	The initials of the person entering this data into LDMS



**Note:** Additional fields specific to the selected assay may also be displayed.

5. Click the **Results** tab.
6. (If needed) To add controls to the run, click **Add Control**.
7. Click **Add Specimens**.

Use the filters to narrow down the list of specimens. You can also upload a list of unique specimen IDs.



**Tip:** Under **Specimen Filters**, there is a filter for **Assigned Test**. If you set the anticipate test for specimens when entering new specimens in LDMS, you can use this filter to quickly find and add specimens to test runs.

8. Optional: To add additional specimens to the run that have not been entered into LDMS click the arrow next to **Add Specimens**, and then click **Add non-logged specimens**.

You can enter any global specimen ID for non-logged specimens for the purposes of matching assay results, however non-logged specimens will *not* be available to view on the **Specimen Management** page; they are only found in this assay run.

9. Optional: Set Dilution. Some tests allow you to indicate if a specimen was diluted before being tested. The dilution will default to 1 for each specimen. If the specimen was diluted you can change this value as needed. For example, a dilution of 1:5 should be entered as dilution= 5. A dilution of 1:20 should be entered as dilution= 20.



**Note:** LDMS will adjust the final result according to the dilution and the adjusted final result will be reflected on any test result reports. This does not apply to the PK test.

10. Click **Upload File**, and then select your assay results file.

LDMS will attempt to match results in your file to specimens added to the run based on global specimen ID, other specimen ID, or ID1.



**Note:** If any results were matched incorrectly, you can drag and drop them to the correct specimen, or drag and drop them into the **Unmatched Results from File** section to remove them.

11. (If necessary) Match unmatched results to specimens. Click and drag unmatched results in the **Unmatched Results from file** section to appropriate specimens.
12. (If necessary) To manual change a result, select the result, and then click **Set Manual Result**.
13. Do one of the following:


- To save the run and change the status to *complete*, click **Complete**.
- To save the run and change the status to *pending*, click **Save**.

### **Adding Cryopreservation Test Results**


One of the test results is the Cryopreservation test. This feature allows the IQA lab to assign confirmatory post-thaw results to cryopreserved specimens and is only available at the IQA lab.

1. Under the **Test Results** dropdown, click **Test Results**.
2. From the action menu, select **Add Pending Results** The **Select Test** window will open.
3. From the **Test Name** dropdown, select **Cryopreservation** and click **Continue**.
4. On the **General** tab, define information about the test.
5. On the **Results** tab, add specimens that are already in LDMS by using the **Add Specimens** button. The user can also add specimens from a file using the **Upload File** button.
6. To save the test and complete it later, click **Save**.
7. To complete the test, click **Complete**.

### **Assigning Results to Blinded Controls (Pellets)**

 **Note:** The steps below apply only to the TaqMan Qual assay.

1. On the **Test Results** page, select **Add Pending Results** from the **Add New...** drop down.
2. Select the **COBAS TaqMan HIV-1 Qual** from the **Test Name** drop down.
3. Choose either the **24** or **48** radio button for the **Number of Items**.
4. Click **Continue**.
5. In the **Results** tab, choose pellets from the **Select Pellet** drop down.
6. Fill out the remaining field and click **Complete**.


 **Note:** Pellets can only be consumed once and will no longer be available once used.

### **Reviewing a Run**

Once a run has the status of completed, it must be reviewed for quality control purposes.

#### **Background**

Runs should typically be reviewed by someone other than the Data Transfer Tech who entered the results. The reviewer can check the calculated results, pass-fail status of specimens and the run, and apply censors as needed.

 **Note:** The review process should vary by project and assay. It is recommended that your laboratory have documentation or written procedures in place for this process.

### Steps

1. From the LDMS menubar, click **Test Results**.
2. Locate the completed run of interest.  
Use **Test Results Filters** to help locate the run.
3. Next to the run, click **Edit**.
4. Review the results.  
Consult any procedures or documentation applicable to your laboratory to complete this review.
5. (If applicable) Apply censor codes.  
To apply a censor to a specimen, locate the specimen, and then in the **User Censor** column, select the censor.  
To apply a censor to the entire run, on the **General** tab, in the **User Censor** box, select a censor.  
For details about a censor, hover over it with the mouse pointer.  
System censors are automatically applied and cannot be removed.
6. On the **General** tab, complete the **Review Date**, **Reviewer Initials**, and (optionally) **Reviewer Comments** boxes.
7. Click **Review**.

### Test History

Test results can be changed between completed and pending statuses. It is possible to view a snapshot of test results at the time the status changed.

To view the test result history, on the **Test Result** page, locate the run. Next to **Edit** for that run, click the arrow, and then click **View History**. Next to the even, click **View** to see the run at that point in time.

Only certain events are shown in the history. For example, making changes to a run while its status is *pending* will not be shown in the history.

### Deleting assay runs

Assay runs that were erroneously created can be deleted.

### Background

Deleted runs are not shown by default on the **Test Results** page. To display them, in the **Test Results Filters**, set the **Status** filter to *Deleted*.

### Steps

1. On the **Test Results** page, locate the run to be deleted.
2. Click the arrow next to the run's **Edit** button, and then click **Delete**.
3. Verify that the run you are about to delete is the correct run.
4. Complete the **History Date**, **History Tech Initials**, and **History Comments** boxes.  
The comments should indicate why the run is being deleted.

5. Click **Delete**.

### Restoring deleted runs

If an assay run is deleted in error, it can be changed back to pending without data loss.

#### Steps

1. On the **Test Results** page, in the **Test Results Filters**, set the **Status** filter to *Deleted*.
2. Locate the run to be restored.
3. Click the arrow next to the run's **Edit** button, and then click **Reset to Pending**.
4. Complete the **History Date**, **History Tech Initials**, and **History Comments** boxes.
5. Click **Reset**.

### Test result reports

Several tests can be run for assay result runs.

All reports are run by clicking the arrow next to the **Edit** button next to the run, and then clicking the desired reports.

Report	Purpose
Completed Test Run Report	Shows details of the specimens on a run, including plat positions, result filename, results for each specimen, and other result details.
Participant Report	Provides detailed results broken down by participant and specimen (one per page)
Pending Test Results Report	Shows details about specimens on the run and where they are located on testing plates (useful for setting up equipment to match a run already set up in LDMS).

### Entering PK Test Results

Users can enter PK test results by navigating to the **Test Results** tab, clicking the **Test Results** module, selecting a test, and then clicking **Edit**.

**Figure 58: Editing Test Results - General Tab**

Edit Pending Test Results

---

General
Results

Run Id: 13

Test Name: PK Assay

Status: Pending

Run Date:  1

Data Transfer Tech:

Assay Name:  2

Run Type:  3

Detect Platform:  4

Analytes

Analyte	Unit	Lower Limit	Upper Limit	Add Analyte
3TC	NG/ML	10	100	Edit

Control Lots

Lot Number	Calibrator	Creation Date	Expiration Date	Storage Temperature (C)	Derivative/Matrix Type	Add Control Lot
<           >						5

Comments

Complete
Save
Close

On the General Tab, the user must define some required information about the PK Test run, including (1) a Run Date, (2) Assay Name, (3) Run Type, and (4) Analytes. (5) The user may optionally add a Control Lot to a run.

**Assay Name:** The Assay Name is a free entry field that the user can define. This name will be used to group assays together on certain reports and in the PK Control Charting Module.

**Run Type:** Certain Run Types are used for different scenarios. For example, Routine and Routine/Proficiency are used to report network results whereas Calibration and Stability may be used when validating a new method.

**Add Analyte:** When adding an analyte the user may choose to add these individually for each run or they can select an Analyte Setup that was previously defined in the PK Templates module.



**Note:** The analyte setup can be modified for each run and for each item on the run. For example, a PK Template may have defined the analyte range as 10-1,000 but a special run today may need the range to be 100-100,000. The user can modify the range for any run as needed. Individual specimens and controls may also need range adjustments. For example a specimen analyte range may use ng/mL

but the controls may use a range in ng/sample. The LDMS will allow the user to change the limits for each individual item on the Results tab.

**Add Control Lot:** This will allow a user to add a Control Lot to this run. The user can either add a predefined set of controls created in the PK Control Lots module or, if a preset lot of controls have not previously been defined in the PK Control Lots module, the user can create it for this individual run. If the user chooses to not add or create the entire lot of controls here, they can add individual controls on the Results tab.

**Figure 59: Editing Test Results - Results Tab**

Create Pending Test Results

---

General
Results

**Controls** Add Control

Dilution	Control Name	Custom Name	Calibrator
1	HQC		

Edit

**Specimens** Add Specimens

Dilution	Project	ID1	Global Specimen ID	Other Specimen
1	ACTG/IMPAACT	0111111C	BEQ00002-00	
1	ACTG/IMPAACT	0111111C	-NO-GUSPEC-	CHANGE 1
1	ACTG/IMPAACT	0111111C	BEQ00002-00	
1	ACTG/IMPAACT	0111111C	-NO-GUSPEC-	CHANGE 1
1	ACTG/IMPAACT	0111111C	-NO-GUSPEC-	RES 2
1	ACTG/IMPAACT	0111111C	BEQ00002-03	NO082001

**Results** Clear Results For Analyte

Specify limits per specimen  Display Other Specimen ID

Name	Analyte	Unit	Target	+/-%	Lower Limit	Upper Limit	Result
HQC	10-1074	%	Percent				
BEQ00002-00	10-1074	%					
-NO-GUSPEC-	10-1074	%					

Complete Save Close

On the Results Tab the user can (1) add individual controls, (2) add specimens, (3) change the result grid to allow editing of the limits for each individual item, (4) review, define, or edit the limits, target, or range of each control and specimen

**Add Control:** The user can click Add Control to add additional controls to this run. Even if the user added a Control Lot on the general tab they can use this feature to include additional controls now.

**Add Specimens:** The user can choose to add specimens onto this run.


**Note:** Dilution will default to 1 for all specimens added to a PK Run. If the specimen was tested with a dilution the user can choose to change




the value here. Any result that has a dilution modified from 1 will be assigned a U censor.

**Specify Limits Per Specimen:** If any specimen on the run needs to use a limit range other than what was defined at the analyte level this option can be used to change the limit for each individual specimen.

**Setting Limits in the Result Grid:** The user can set the Target and +/- for each control or they can set a specific Lower and Upper limit. If the user has checked to Specify Limits per Specimen they can also set the lower and upper limit for each specimen.

 **Note:** If a specimen was diluted the LDMS will account for the dilution when comparing the input result to the limits. The user should not change the standard limits for a specimen to account for dilution as the LDMS will do this automatically.

 **Important:** If a result was not obtained for a specific specimen, leave the result field for that row Blank/Null. LDMS will allow the user to apply a User Censor to this result when Reviewing the run. Leaving a result Blank/Null may be necessary in scenarios such as a template including an analyte that was not tested for, a sample on the run having insufficient volume, or an issue in interpreting the final result.

**Figure 60: Editing Test Results - Results Tab (Continued)**

Edit Pending Test Results

---

General
Results

**Results**

Specify limits per specimen Clear Results For Analyte

Name	Analyte	Unit	Target	+/-%	Lower Limit	Upper Limit	Result
LQC	3TC	NG/ML			0	100	295
MQC	3TC	NG/ML	50	10	45	55	7980
HQC	3TC	NG/ML	1000	10	900	1100	11090
0500-002PQK00-001	3TC	NG/ML			10	100	25 <span style="color: red; font-weight: bold; border: 1px solid red; border-radius: 50%; padding: 2px;">3</span>
0500-002PSF00-001	3TC	NG/ML			10	100	25

**Unmatched Results from File** Upload File 1

{2}. 018\_PK Assay Test Result File.csv X

File Id	Item Name	Analyte	Unit	Lower Limit	Upper Limit	Result
{2}	SAMPLE 1 <span style="color: red; font-weight: bold; border: 1px solid red; border-radius: 50%; padding: 2px;">2</span>	3TC				24000
{2}	SAMPLE 1	EFV				22000
{2}	SAMPLE 2	3TC				240
{2}	SAMPLE 2	EFV				222
{2}	SAMPLE 3	3TC				950
{2}	SAMPLE 3	EFV				987
{2}	SAMPLE 4	3TC				1404
{2}	SAMPLE 4	EFV				1422
{2}	SAMPLE 5	3TC				8111
{2}	SAMPLE 5	EFV				7910
{2}	LQC	EFV				290

Complete
Save
Close

After the run setup is complete and results are available, the user can set these results on the Results tab by (1) uploading a file, (2) auto matching or drag and drop matching file results to the results grid, or (3) by skipping result file upload and manually setting results.

**Upload File:** An example PK assay test result file is shown below.


**Figure 61: Example PK Assay Test Result File**

	A	B	C	D
1	ID 1	3TC 4	EFV	
2	SAMPLE 1	24000	22000	
3	SAMPLE 2	240	222	
4	SAMPLE 3	950	987	
5	SAMPLE 4	1404	1422	
6	SAMPLE 5	8111	7910	
7	LQC 2	295	290	
8	LQC 2	310	315	
9	MQC	7980	7990	
10	MQC 2	8025	8055	
11	HQC	11090	11080	
12	HQC 2	12050	12060	
13	SAMPLE 6	24000	22000	
14	SAMPLE 7 3	240	222	
15	SAMPLE 8	950	987	
16	SAMPLE 9	1404	1422	
17	SAMPLE 10	8111	7910	
18				
19				

When uploading a result file the LDMS expects (1) a file that has a defined ID. The ID in the file will auto match to LDMS based on (2) the Control Name, (3) Global Specimen ID, Other specimen ID, or ID1 value. The LDMS also expects a result column named (4) as the Specific analyte being tested for.

**Unmatched Results From File:** Any result from the file that could not be automatically matched to an item on the run in LDMS will be available in this grid to drag-and-drop to match.

**Manually Setting Results:** If a file is not used or if the LDMS contains more results than are found in the result file, the user can manually enter results to LDMS by typing directly into the field.

 **Note:** Results from diluted specimens must be entered to LDMS pre-calculated to account for dilution. LDMS will not change the input result to account for dilution. LDMS will adjust the limits based on dilution for purposes of calculating the A and B censors but LDMS expects the user to input the final result pre-calculated to account for the dilution.

### Completing PK Test Results

After all required information has been defined for a run the user may click **Complete**. When clicking complete, the LDMS will calculate system censors such as A- above upper limit, B- below lower limit, and U- specimen diluted. The LDMS will also verify any controls on the run fall within the expected

range and may set a pass/fail censor for the run depending on the success of any defined controls.

## Reviewing a PK Test Run

When reporting PK Test results for certain network specimens, the networks expect the run to pass a Review. After completing the run, the application allows for the run to be reviewed from the main test results grid and set information such as Reviewer Initials, Reviewed Date, Review Comments, and define user censors.

## PK Control Lots

The PK Control Lot Module allows the user to pre-define the details of a control or calibrator lot in advance of using them on a run. Once a lot is added in the PK control lots module, it will be available in the Test Results module to quickly and easily place on any PK Assay runs for which it is used. When initially added to a specific run in the Test Result module, the lot will default to the details defined here.




**Figure 62: PK Control Lots**

(1) QC and Calibrator radio buttons, (2) choose existing PK lot, (3) add new PK lot, (4) make copy of PK lot, (5) add new calibrator/control, (6) list of calibrators/controls, (7) delete calibrator/control, (8) add new analyte, (9) list of analytes, (10) delete analyte, (11) save lot, (12) delete lot

The screenshot shows the 'PK Control Lots' interface. At the top, there are radio buttons for 'QC' (1) and 'Calibrator'. Below this is a dropdown menu for selecting an existing lot (2) and buttons for 'Add New...' (3) and 'Make Copy' (4). The form includes fields for Lot Number (ABC123), Creation Date (28/Jun/2021), Expiration Date (28/Jun/2021), Storage Temperature (C) (30), and Derivative/Matrix Type (AD4). Below the form is a table for 'Calibrators' with columns for Calibrator, Custom Name, and a Delete button (7). A '5' callout points to the 'Add New' button for calibrators. The 'Analytes' section has a table with columns for Analyte, Unit, Target, +/-%, Target Min, and Target Max, and a Delete button (10). A '8' callout points to the 'Add New' button for analytes. At the bottom, there are 'Save Lot' (11) and 'Delete Lot' (12) buttons.

## Adding a New Lot

1. Select **QC** or **Calibrator**.
2. Click **Add New**.
3. Enter the following information:

- 3.1. Lot Number
- 3.2. Creation Date
- 3.3. Expiration Date
- 3.4. Storage Temperature
- 3.5. Derivative/Matrix Type
4. To add a control/calibrator, do the following:
  -  **Note:** If the user selected **QC** in the first step, they will have the ability to add a control. If the user selected **Calibrator** in the first step, they will have the ability to add a calibrator.
  - 4.1. Click **Add New** in the **Controls/Calibrator** section.
  - 4.2. Select a control/calibrator from the dropdown.
  - 4.3. Enter a custom name for the control/calibrator.
    -  **Note:** When matching results from an uploaded file, the LDMS will first try to match using this Custom Name.
  - 4.4. Repeat step 4 as needed for additional controls/calibrators.
  - 4.5. To delete a control/calibrator, click the **Delete** button next to it.
5. To add an analyte, do the following:
  - 5.1. Click **Add New** in the **Analytes** section.
  - 5.2. Select an analyte from the dropdown.
  - 5.3. Enter a unit.
  - 5.4. Enter a target.
  - 5.5. Enter a **+/-%**.
    -  **Note:** LDMS will calculate the **Target Min** and **Target Max**. If necessary, these values can be modified for clarity during run set up when using this lot.
  - 5.6. Repeat step 5 as needed for additional analytes.
  - 5.7. To delete an analyte, click **Delete** next to the analyte.
6. Click **Save Lot**.

## Editing or Deleting a Lot

To Edit an existing lot, do the following:

1. Select **QC** or **Calibrator**
2. Select the lot from the dropdown.
3. **Optional:** a lot can be copied by clicking **Make Copy**.
4. Edit the lot information, controls/calibrators, and analytes as needed.
5. Click **Save Lot**.


To Delete a lot, select it and click **Delete Lot**.

## PK Control Charting

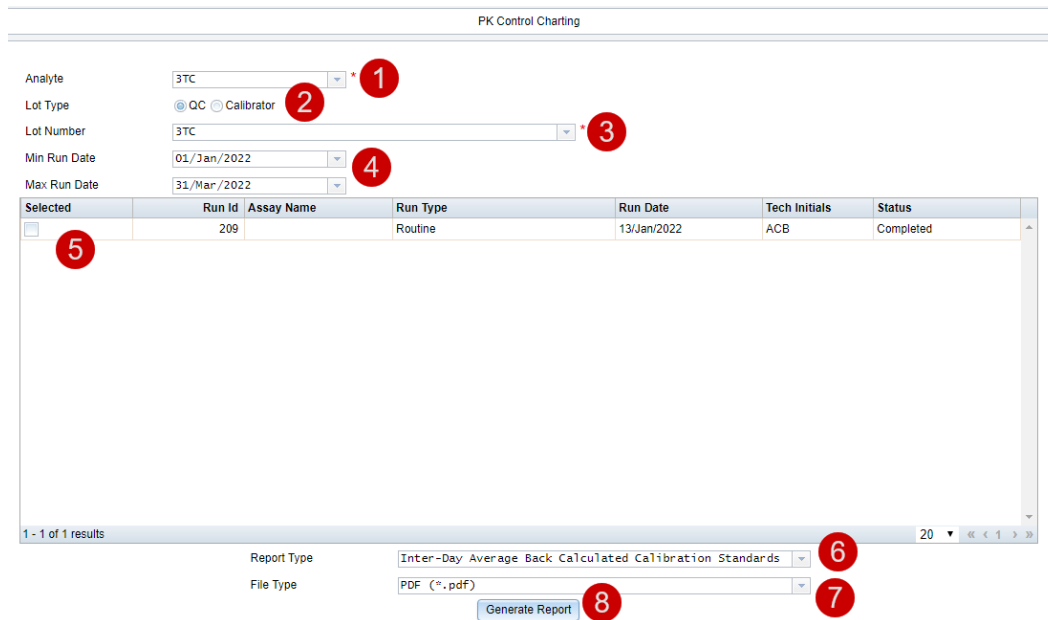
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The PK Control Charting module allows the user to report on specific PK Control or Calibrator lots to review their details over time. Various reports

are made available for the user to run, including Inter-Day Average Back Calculated Calibration Standards, Stability, Accuracy and Precision, and more. Generation of these reports requires a user to first define PK Control or Calibrator lots in the PK Control Charting Module and to then also make use of these lots on PK Assay runs in the Test Results Module.

 **Note:** In some scenarios the LDMS may be unable to generate PK Control Charting reports if the user chose to modify or manipulate certain lot details that result in mathematical queries and equations that cannot be properly executed.

**Figure 63: PK Control Charting**



The screenshot shows the 'PK Control Charting' interface. At the top, there are input fields for 'Analyte' (set to '3TC'), 'Lot Type' (with 'QC' selected and 'Calibrator' as an option), 'Lot Number' (set to '3TC'), 'Min Run Date' (set to '01/Jan/2022'), and 'Max Run Date' (set to '31/Mar/2022'). Below these is a table with columns: 'Selected', 'Run Id', 'Assay Name', 'Run Type', 'Run Date', 'Tech Initials', and 'Status'. One row is visible with 'Run Id' 209, 'Assay Name' blank, 'Run Type' 'Routine', 'Run Date' '13/Jan/2022', 'Tech Initials' 'ACB', and 'Status' 'Completed'. At the bottom, there are 'Report Type' and 'File Type' dropdowns, and a 'Generate Report' button.

(1) select Analyte, (2) QC and Calibrator radio buttons, (3) Lot Number, (4) Min Run Date and Max Run Date, (5) Selected runs, (6) report type to generate, (7) report file type, (8) Generate Report

## Generating a Report

1. Enter the following information:
  - 1.1. Select an analyte from the dropdown.
  - 1.2. Select **Lot Type (QC or Calibrator)**.
  - 1.3. Select **Lot Number** from the dropdown.
  - 1.4. Add **Min Run Date** and **Max Run Date**.
2. Tick boxes next to runs to include them in the report.
3. Choose the type of report to generate from the **Report Type** dropdown.
4. Select a file type for the report.
5. Click **Generate Report**.

## PK Templates

PK templates are predefined, specific analyte scenarios that can be used to help set up a Pending Test Results. Templates can be created for PK analyses that happen frequently for a specific set of analytes. Templates can be created and modified by users. User-created templates are only available at the laboratory where they were created; they are not sharable with other laboratories.

**Figure 64: PK Templates**

The screenshot shows the 'PK Templates' interface. At the top, there is a dropdown menu for selecting a template, currently showing '3TC\_FTC' (callout 1), and an 'Add New...' button (callout 2). Below this is a 'Name' field containing '3TC\_FTC' (callout 3). The main section is titled 'Analytes' and contains a table with columns for 'Analyte', 'Unit', 'Lower Limit', and 'Upper Limit'. The table has two rows: one for '3TC' with a lower limit of 10 and an upper limit of 200, and one for 'FTC' with a lower limit of 20 and an upper limit of 100. To the right of the table is an 'Add Analyte' button (callout 4) and two 'Delete' buttons (callout 5). At the bottom of the interface are 'Save Template' (callout 6) and 'Delete Template' (callout 7) buttons.

(1) Currently selected template, (2) add a new template, (3) template name, (4) add new analyte, (5) delete selected analyte, (6) save template, (7) delete template

### Adding a New Template

1. Name the template in the **Name** field.
2. Add analytes:
  - 2.1. Click **Add Analyte**.
  - 2.2. Select Analyte and Unit.
  - 2.3. **Optional:** Add **Upper Limit** and **Lower Limit**.
  - 2.4. To delete an analyte, click the **Delete** button.
3. Click **Save Template**.

### Updating an Existing Template

PK Templates can be modified at any time, even if they have previously been used on a live test run.




**Note:** PK Templates can be selected for use on a live test run and be further modified to meet the needs of that specific run. For example, additional analytes can be added or removed, the limit units can be changed, or the specified upper or lower limit can be updated as needed for the live run.

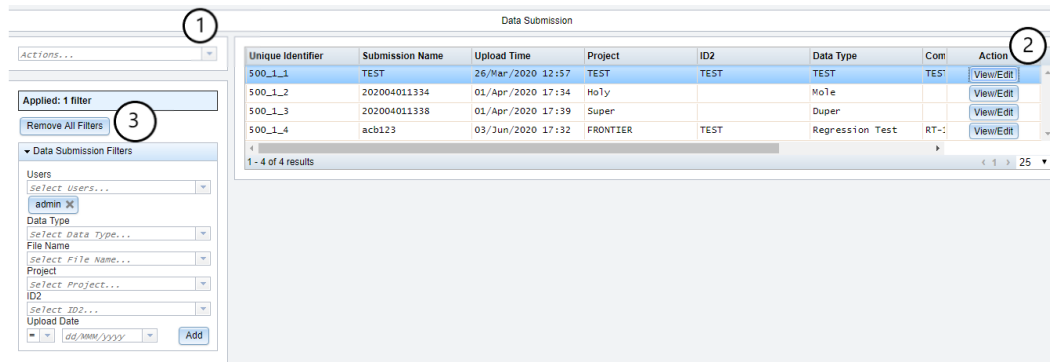
1. Select the template from the drop down menu.
2. Update the name or analyte information as needed.
3. Click **Save Template**.
4. To delete the template that is currently open, click **Delete Template**.

## Data Submission

The Data Submission Module is used to upload data files to Frontier Science within web LDMS without having to log into the Portal or other Frontier Science systems. This is accessed through the **Data Submission** menu.

 **Note:** Users must contact Frontier Science if access to this module is needed.

**Figure 65: The Data Submission Page**



(1) The dropdown list used to create new data submissions. (2) The View/Edit button used to edit data submissions. (3) Filters to narrow results.

## Adding Submissions

To add a data submission, follow the steps below.

### Steps

1. From the menu bar, click **Data Submission**, and then click **Data Submission**.
2. In the **Actions** dropdown menu on the left side of the screen, click **Upload Files**. The **Choose Files to Upload** window will appear.

Choose Files to Upload

---

Submission Name  \*

Project  \*

ID2  \*

Data Type  \*

Comments

#	Type	File Name	Size



3. Add the submission name to the **Submission Name** field.
4. Select the Project, ID2, and Data Type from the dropdown menus.
5. Add any comments as needed.
6. Below the **Comments** text box, click the **Select Files** button.
7. Select the necessary files.
8. To remove selected files, click **Remove Files**.
9. To complete the submission, click **Upload Files**.

## Editing Submissions

To edit a data submission, follow the steps below.

### Steps

1. From the menu bar, click **Data Submission**, and then click **Data Submission**.
2. To make changes to submissions, click **View/Edit** next to the submission in question. The **Edit Submission Group** window will appear.

Edit Submission Group

Unique Identifier	<input type="text" value="500_1_1"/>
Submission Name	<input type="text" value="TEST"/>
Project	<input type="text" value="TEST"/> *
ID2	<input type="text" value="TEST"/>
Data Type	<input type="text" value="TEST"/> *
Comments	<input type="text" value="TEST"/>

File Name	File Size	Action
1	1.9 KB	<input type="button" value="Download"/>

3. Make any changes to the project, ID2, Data Type, or Comments as needed by using the appropriate dropdown menus.
4. Files in the submission can also be downloaded individually by clicking the **Download** button next to the file in question at the bottom of the window.
5. Click **Save**.

## Data Submission Filters

---

Filters can be applied to narrow results in the **Data Submission** menu.

### Background

The following filters are available for the **Data Submission** module:

- Users
- Data Type
- File Name
- Project
- ID2 Upload Date

Select any filters as needed and click **Add**.

## Printers

This section will describe how to setup various printers that are known to work with LDMS.

### Setting up the Brady IP300 printer

---

These instructions will help ensure that your printer is set up to work correctly with LDMS.

#### Prerequisites

- Install the driver for your printer. For assistance obtaining and installing the driver, contact your laboratory's local IT department or the manufacturer's customer support.

#### Background

This printer is known to work with the following label and stock settings in LDMS:

<b>label stock</b>	THT-183-461
<b>LDMS label</b>	Barcode label 7

#### Steps

1. Open the printer settings from the Windows **Start** menu. These are typically found in **Start > Devices and Printers**.
2. Right-click the **IP300** icon, and then click **Printing preferences**.
3. Click **Advanced**.

4. Next to **Paper Size**, click **Properties**.
5. In the Paper Size box, select the appropriate paper size.
6. On the control panel in front of the printer, change the printer head to +1.0mm for the X axis and -3.0mm for the Y axis  
 These head adjustments have been tested with the THT-183-461 label stock. Other label stocks may require different printer head adjustments.

## Setting up the Brady® MVP 300 printer

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These instructions will help ensure that your printer is set up to work correctly with LDMS.

### Steps

1. Open the printer settings from the Windows **Start** menu.  
 These are typically found in **Start > Devices and Printers**.
2. Right click the icon for your printer, and click **Printing preferences**.
3. Set the stock size.
  - 3.1. Expand the **Paper/Output** settings
  - 3.2. In the **Paper Size** box, select **User Defined**.
  - 3.3. Click **Customize**.
  - 3.4. In the **Width** and **Height** boxes, entered the dimensions of your label stock.
  - 3.5. In the **Unit of Measure** box, select **Inches**.
  - 3.6. Click **OK**.
4. In the **Devices and Printers** window, right click the printer icon, and click **Properties**.
5. On the **Printer** tab, change the following settings:
  - 5.1. In the **Device Options > Head Settings > Print Darkness** section, change the **Print Darkness** setting to 22.
  - 5.2. In the **Speed Settings**, enter the following settings:
 


<b>Print speed</b>	2.00 in/sec
<b>Slew speed</b>	2.00 in/sec
<b>Back feed speed</b>	2.00 in/sec
6. On the **Ports** tab, click **Configure Port** and enter the following settings:
 


<b>Bits per second</b>	115200
<b>Data bits</b>	8
<b>Parity</b>	None

**Stop bits** 1

**Flow control** Xon/Xoff

7. Configure the printer hardware.
  - 7.1. Open the printer and remove the protective plate that is covering the ribbon sensor.
  - 7.2. Slide the transmissive sensor protector to the outside of the adjustable transmissive sensor.
  - 7.3. Place the ribbon on the ribbon supply spindle.

 **Note:** The shiny side of the ribbon must be facing up.
  - 7.4. Feed the ribbon through the ribbon sensor and around the print head assembly.
  - 7.5. Wrap the ribbon around the ribbon take-up spindle until it is tight.

 **Tip:** Attach a piece of tape to the end of the ribbon to help keep it tight during the loading process.
  - 7.6. Place the labels on the media supply spindle.

The printable side of the label must be face-up.
  - 7.7. Place the labels through the media guide and align the notch between labels with the tear-off plate of the printer.
  - 7.8. Adjust the ribbon sensor so that the notch of the label will cross the ribbon sensor.

The ribbon sensor is the red light under the label.
  - 7.9. Close the print head and ensure that the ribbon is aligned with the left side of the label.

This adjustment may require you to slide the ribbon across the print head assembly.
  - 7.10. Close the printer.
8. On the control pad on front of the printer, do the following:
  - 8.1. Press the **Setup/Exit** button.
  - 8.2. Press the **+** button until the printer displays **Manual Calibrate**.
  - 8.3. Press the **Select** button.
  - 8.4. Press the **+** button.

The printer will re-calibrate its label settings.
  - 8.5. Press the **Setup/Exit** button, and then press the **+** button to save the changes.

## Setting up the LabXpert printer

---

These instructions will help ensure that your printer is set up to work correctly with LDMS.

### Steps

1. Open the printer settings from the Windows **Start** menu.

These are typically found in **Start > Devices and Printers**.

2. Right click the icon for your printer, and click **Printing preferences**.
3. Expand the **Paper/Output** settings, and click **Properties** text to Paper Size.
4. In the Paper Size box, select the appropriate paper size.
5. In the **Devices and Printers** window, right click the LabXpert icon, and click **Properties**.
6. On the **Ports** tab, enter the following settings:

<b>Bits per second</b>	115200
<b>Data bits</b>	8
<b>Parity</b>	None
<b>Stop bits</b>	1
<b>Flow control</b>	Xon/Xoff

7. Configure the printer to accept input from your LDMS computer.



**Important:** This step must be completed every time the printer is turned on.

- 7.1. On the printer, press the Menu button.
- 7.2. Press the Next button three times.
- 7.3. Press the PC button.

#### After you are finished

After the printer is set up, you should print a set of test labels to ensure that it is working correctly.

---

## Setting up the Zebra® GX 430t printer

---

These instructions will help ensure that your printer is set up to work correctly with LDMS.

### Prerequisites

- Install the driver for your printer. For assistance obtaining and installing the driver, contact your laboratory's local IT department or the manufacturer's customer support.
- Load the printer with label stock and ribbon according to the printer's manual.

### Steps

1. Open the printer settings from the Windows **Start** menu.  
These are typically found in **Start > Devices and Printers**.
2. Right click the icon for your printer, and click **Printing preferences**.

3. On the **Options** tab, change the **Speed** to 2.
4. Change the **Print Darkness** to about 27.  
This setting should be adjusted up or down, depending on whether labels are too light or too dark.
5. In **Paper format**, select *inches*.
6. In **Paper Size**, set the **Width** to 4.00 and the **Height** to 1.75.
7. On the **Advanced Setup** tab, click **Calibrate**.
8. On the **Advanced Setup** tab, verify that the **Tracking Mode** is set to *Web Sensing*.

#### After you are finished

After the printer is set up, you should print a set of test labels to ensure that it is working correctly.

## Setting up the Brady BBP11-34L printer

---

These instructions will help ensure that your printer is set up to work correctly with LDMS.

#### Background

This printer is known to work with the following label and stock settings in LDMS:

<b>label stock</b>	THT-183-461-0.5-SC
<b>LDMS label</b>	Barcode Label 9

#### Steps

1. Open the printer settings from the Windows **Start** menu.  
These are typically found in **Start > Devices and Printers**.
2. Right click the icon for your printer, and click **Printing preferences**.
3. On the **Page Setup** tab, under **Stock** click **New**.
4. Enter the dimensions 1.75" × 1.00".  
These are the dimensions for the THT-183-461-0.5-SC label stock. If you are using a different stock, enter the appropriate dimensions.
5. Click **Advanced Options**, and verify that the horizontal and vertical offset options are set to 0".
6. On the **Stock** tab, enter the following into the **Media settings**:
 

<b>Method</b>	Thermal transfer
<b>Type</b>	Labels with marks
<b>Mark height</b>	0.08 in
<b>Mark offset</b>	0.00 in

**7.** On the **Options** tab, enter the following into the **Printer options**:

**Print speed**      2.00 in/sec  
**Darkness**        10

**8.** Click **OK**.

#### After you are finished

After the printer is set up, you should print a set of test labels to ensure that it is working correctly.

## Setting up the Brady® BBP33 printer

---

These instructions will help ensure that your printer is set up to work correctly with LDMS.

#### Prerequisites

- Install the driver for your printer. For assistance obtaining and installing the driver, contact your laboratory's local IT department or the manufacturer's customer support.

#### Background

This printer is known to work with the following label and stock settings in LDMS:

**label stock**            B33-179-482 (1"x1")  
**LDMS label**            Barcodelabel19

#### Steps

- 1.** Open the printer settings from the Windows **Start** menu. These are typically found in **Start > Devices and Printers**.
- 2.** Right click the icon for your printer, and click **Printing preferences**.
- 3.** Click **Advanced**.
- 4.** Next to **Paper Size**, click **Properties**.
- 5.** In the Paper Size box, select the appropriate paper size.
- 6.** In LDMS, set the printer as your label printer.

#### After you are finished

After the printer is set up, you should print a set of test labels to ensure that it is working correctly.

## Setting up the Brady BMP53 printer

---

These instructions will help ensure that your printer is set up to work correctly with LDMS.

### Prerequisites

- Install the driver for your printer. For assistance obtaining and installing the driver, contact your laboratory's local IT department or the manufacturer's customer support.

### Background

This printer is known to work with the following label and stock settings in LDMS:

<b>Cartridge</b>	M-156-492
<b>LDMS label</b>	Barcode Label 16

### Steps

1. Open the printer settings from the Windows **Start** menu. These are typically found in **Start > Devices and Printers**.
2. Right click the BMP51(53) icon, and click **Printing preferences**.
3. Click **Advanced**.
4. Next to **Paper Size**, click **Properties**.

### After you are finished

After the printer is set up, you should print a set of test labels to ensure that it is working correctly.

## Setting up the Brady BP-PR 300 printer

---

These instructions will help ensure that your printer is set up to work correctly with LDMS.

### Prerequisites

- Install the driver for your printer. For assistance obtaining and installing the driver, contact your laboratory's local IT department or the manufacturer's customer support.

### Steps

1. Open the printer settings from the Windows **Start** menu. These are typically found in **Start > Devices and Printers**.
2. Right click the Brady PR 300 PLUS icon, and click **Properties**.



3. In the **Size** section, change the **Width** and **Height** to the size of your label stock.

#### After you are finished

After the printer is set up, you should print a set of test labels to ensure that it is working correctly.

## Setting up the Zebra ZD620 Printer

---

These instructions will help ensure that your printer is set up to work correctly with LDMS.

### Prerequisites

- Install the driver for your printer. For assistance obtaining and installing the driver, contact your laboratory's local IT department or the manufacturer's customer support.
- Load the printer with label stock and ribbon according to the printer's manual.

### Steps

1. Open the printer settings from the Windows **Start** menu. These are typically found in **Start > Devices and Printers**.
2. Right click the icon for your printer and click **Printing Preferences**.
3. On the **Print Options** tab, change the **Speed** to 4. This setting should be adjusted accordingly.
4. Change the **Print Darkness** to about 20. This setting should be adjusted up or down, depending on whether labels are too light or too dark.
5. In the **Page Setup**, set the **Width** and **Height** according to labels used. Ex.: Width: 2.75" Height: 1"

#### After you are finished

After the printer is set up, you should print a set of test labels to ensure that it is working correctly.

## Setting up other printers

---

Label printers that do not have specific instructions provided in this manual may still work with LDMS, however they will not have been tested by LDMS User Support.

### Steps (completed in any order)

- Contact LDMS User Support for assistance.
- Consult the most current list of supported printers.

- If you are using a printer not listed in this manual, let LDMS User Support know so that it can be added.


## Preset projects

Preset projects are projects that are built into LDMS that have special rules and requirements.

Preset projects and their requirements cannot be modified or removed by users. These projects are designed based on the needs of a specific project working with Frontier Science. An example of a preset project is ACTG/IMPAACT. Specimens created until this project have specific requirements, which are defined by ACTG and IMPAACT. These requirements are implemented in LDMS to accommodate the needs of the project.

The rules for preset projects fall into two categories:

- Validation rules that can be enforced by LDMS, such as requiring that ID1 be formatted a certain way
- Requirements that cannot be enforced by LDMS, such as requiring specimens to be entered within a certain period of time after they are received by your laboratory.

 **Important:** The information for individual projects provided here are for convenience only. Always refer to guidance provided by the project for the most up-to-date instructions.

## ACTIV

---

The ACTIV (Accelerating COVID-19 Therapeutic Interventions and Vaccines) preset project must meet these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	Must be 9 numeric digits
ID2 (Study)	Required	"ACTIV2" in ID2 field; not editable
ID3 (ID3)	Optional	Warning generated if other spec ID is blank
Visit	Required	--
Clinic	Optional	--
Specimen Time	Required	--
Received Time	Required	--

## ACTG/IMPAACT

The ACTG/IMPAACT preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required*	8 characters long, 7 numbers and one letter between A and L; if the PID does not have 7 numbers, add leading zeros to the front of it. *This requirement can be disabled by Frontier Science for certain studies.
ID2 (Protocol)	Required	Select from the pre-defined list of protocols.
ID3	Optional	LDMS will remember previously entered ID3s and automatically populate ID3 when the same project-PID-protocol combination is entered.
Visit	Required	Select from pre-defined list of visit units.
OPID	Available	--
Clinic	Required	LDMS will automatically populate the clinic using one previously entered for the same PID, protocol, and SID combination.
Specimen Time	Depends	If you do not have a specimen time recorded on your CRF, contact the clinic that collected the specimen from the participant. This field is required for specimens with a specimen date of 01 January 2004 or later; it is optional for specimens prior to that date. This requirement can be overridden for specimens after this date, if necessary.
Received Time	Optional	--

### Notes

- ACTG/IMPAACT uses the standard LDMS Shipping File format to ship between ACTG and IMPAACT laboratories using LDMS.
- ACTG/IMPAACT requires specimens to be labeled with a 2D barcode and label from LDMS; LDMS comes with label formats for ACTG setup and ready to use.
- ACTG and IMPAACT are listed as a combined project throughout LDMS (ACTG/IMPAACT).
- Preloads are permitted for the ACTG/IMPAACT project, but users are not permitted to create their own. All ACTG preloads are created by Frontier Science in collaboration with network leadership.

## AERAS

The AERAS preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	11-digits of any combination of letters and numbers.
ID2 (Study)	Required	Selected from pre-populated list. Once selected, the LDMS will check that the PID is associated with the selected protocol.
ID3	Disabled	This field is not used by Aeras
Visit	Required	Select from pre-defined list of visit units.
OPID	Disabled	This field is not used by AERAS
Clinic	Required	AERAS clinics are in the format ARSXX, where XX are the 5th and 6th digits from the PID
Specimen Time	Required	--
Received Time	Optional	--

### Notes

Quick Add templates can be used for Aeras.

## AIEDRP

The AIEDRP preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	Must either pass the ACTG/IMPAACT or HPTN ID1 validation check, depending on the protocol
ID2 (Protocol)	Required	Will determine what ID1 format should be used
ID3 (SID)	Required	Must be NOSID or pass the ID1 validation
Visit	Required	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

### Protocol and ID1 check used

Protocol	ID1 validation used
I03005	ACTG/IMPAACT
I03006	ACTG/IMPAACT
I03007	ACTG/IMPAACT

Protocol	ID1 validation used
I03008	ACTG/IMPAACT
I03010	Either
I03011	Either
CORE01	Either
AIN501	Either
AIN502	Either
AIN503	Either
AIN504	Either

## AIS

The AIS (Nigeria State Level ART Impact Survey) preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PTID)	Required	Must be length 9. First 4 characters are letters only and last 5 characters are numeric only (e.g., ABCD12345)
ID2 (Country)	Required	"Nigeria" is the only available option
ID3 (HIVRT)	Required	Pick list of specific options
Collection Time	Required	--
Received Date and Received Time	Required	--
Clinic	Required	Must require the clinic be formatted like NG### where the first 2 characters are the letters NG and the next 3 characters are numbers. (e.g., NG000 or NG031)

## AMC

The AMC preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (ID1)	Required	--
ID2 (PROTOCOL)	Optional	--
ID3 (ID3)	Optional	--
Visit	Optional	--

Field	Required?	Note
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

## ATN

---

The ATN preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	A 6-digit number between 10001 and 999999. If the PID is less than 6 digits, leading zeros will automatically be added. LDMS will check that the PID is valid.
ID2 (Protocol)	Required	Must be a 3 digit number between 004 and 999
ID3 (SID)	Required	An 8-digit number between 40001 and 999999999. If the SID is less than 8-digits, leading zeros will automatically be added. 7-digit SIDs can still be imported by LDMS. If the same PID-protocol combination has been entered, LDMS will automatically default to the previously used SID. <i>NOSID</i> is a valid entry for ATN.
Visit	Required	Select from pre-defined list of visit units.
OPID	Available	--
Clinic	Optional	--
Specimen Time	Required	--
Received Time	Optional	--

### Notes

Quick Add templates can be used for ATN.

## BHP

---

The BHP preset project has these requirements.

**Data entry requirements**

Field	Required?	Note
ID1 (PID)	Required	8 characters long, 7 numbers and one letter between A and L; if the PID does not have 7 numbers, add leading zeros to the front of it.
ID2 (Study)	Required	The only available choice in the drop down menu is 'Tatelo'.
ID3 (Step)	Required	Available choices in drop down menu are 0, 1, 2, or 3.
Visit	Required	Select from pre-defined list of visit units.
OPID	Optional	--
Clinic	Required	Any clinic may be set.
Specimen Time	Required	--
Received Date	Required	--
Received Time	Required	--

**Notes**

- User Quick Add templates are not permitted for BHP.

**BM**

The BM preset project has these requirements.

**Data entry requirements**

Field	Required?	Note
ID1 (studyID)	Required	Must be in the BM studyID format
ID2 (ID2)	Optional	--
ID3 (ID3)	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

**BM ID1 format**

BM-XXX-Y

<b>BM</b>	Must be "BM"
<b>XXX</b>	Any 3 digits
<b>Y</b>	0 for mother; 1 to 9 for child

## Botswana MOH

---

The Botswana MOH preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	Requires 2 letters followed by 8 numbers.
ID2 (Study)	Required	Default option is IBBS3
ID3 (HIVRT)	Required	Select from a list of predefined HIV status value
Clinics	Optional	--

### Notes

- The application must allow FSTRF-defined preloads for this project.

### Botswana MOH PID format

XXYYNNNNNN

<b>XX</b>	District (alphabet, length 2)
<b>YY</b>	KP type (numeric, length 2)
<b>NNNNNN</b>	Participant (numeric, length 6)

## CEMALB

---

The CEMALB preset project must meet these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	Must be 5 characters
ID2 (Protocol)	Required	--
ID3 (Visit)	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--



## CHAVI

---

The CHAVI preset project must meet these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	Must pass HPTN ID1 validation and must be 9 characters in length
ID2 (Protocol)	Required	Validated using ID1, where ID2 is embedded into ID1 as either the 4th or 4th and 5th digits, depending on the protocol
ID3 (ID3)	Optional	--
Visit	Required	--
OPID	Optional	Must be empty until the protocol is 008A
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Required	--

## CIPRA-HT

---

The CIPRA-HT preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	Must pass HPTN ID1 validation
ID2 (Protocol)	Required	--
ID3 (SID)	Required	Must pass the historical ACTG/IMPACT ID3 validation
Visit	Optional	--
OPID	Optional	--
Clinic	Required	--
Draw Time	Optional	--
Received Time	Optional	--

## CIPRA-ZA

---

The CIPRA-ZA project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	--
ID2 (CP#)	Optional	--
ID3 (SID)	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

## CIPRA

---

The CIPRA preset project must meet these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	Must be 9 characters in the CIPRA ID1 format
ID2 (Protocol)	Required	In the format P[0-10]
ID3 (ID3)	Optional	--
Visit	Required	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

### CIPRA ID1 format

AABBCCCD

<b>AA</b>	01 to 99
<b>BB</b>	01 to 99
<b>CCCC</b>	0001 to 9999
<b>D</b>	0 to 9

## CONTROL

---

The CONTROL preset project must meet these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (CONTROLNAME)	Required	--
ID2 (PROTOCOL)	Optional	--
ID3 (ID3)	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

## CoVPN

---

The CoVPN (COVID-19 Vaccine and Prevention Network) preset project must meet these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PATID)	Required	Study 3008 has a predefined ID1/PATID check.
ID2 (Study)	Required	--
ID3 (ID3)	Optional	--
Visit	Required	--
Clinic	Required	--
Specimen Time	Required	--
Received Time	Required	--

### Notes

- Information for study CoVPN 5001 should be logged under VTN study 5001.
- Labels are restricted to all supported VTN formats.
- CoVPN has a checkbox for **Collected Outside Protocol Requirements**.

## CPCRA

---

The CPCRA preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	--

Field	Required?	Note
ID2 (Study)	Optional	--
ID3 (Bth/Sex)	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

## CPQA

---

The CPQA preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PanelID)	Required	Must be five characters in length in the format <i>[Round_#][Panel_alpha_ID][2_numbers]</i> , such as 22A00
ID2 (RoundNo)	Required	This is the same as the first 2 digits of the PanelID. This field will automatically be populated by LDMS.
ID3 (ExpDate)	Optional	--
Visit	Optional	Select from pre-defined list of visit units.
OPID	Optional	--
Clinic	Optional	--
Specimen Time	Optional	--
Received Time	Optional	--

### Notes

- CPQA use the LDMS shipping file format
- There are CPQA barcode options available in LDMS.
- Quick Add templates can be used for CPQA, however users are not expected to use this feature.
- The *Pharmacology Proficiency Results* report can be generated from LDMS for Clinical Laboratory Improvement Amendments (CLIA). This is sometimes referred to as the "CLIA Report".

## CP-CTNET

---

The CP-CTNET (Cancer Prevention Clinical Trials Network) preset project must meet these requirements.

### Data Entry Requirements

Field	Required?	Note
ID1 (PID)	Required	--
ID2 (Study)	Required	--
ID3 (ID3)	Optional	--

## FACTS

---

The FACTS preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	A 7-digit number. LDMS will verify that the PID is valid.
ID2 (Study)	Required	Select from pre-populated list
ID3	Disabled	This field is not used by FACTS
Visit	Required	Select from pre-defined list of visit units.
OPID	Disabled	This field is not used by FACTS
Clinic	Disabled	This field is not used by FACTS
Specimen Time	Required	--
Received Time	Optional	--

### Notes

- Quick Add templates can be used for FACTS.

## HN

---

The HN preset project must meet these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (studyID)	Required	--
ID2 (ID2)	Optional	--
ID3 (ID3)	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--

Field	Required?	Note
Received Time	Optional	--

## HPTN

The HPTN preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	LDMS performs a checks to make sure the PID is valid. Based on the protocol, LDMS will determine whether a 9-digit or 10-digit PID must be used.
ID2 (Protocol)	Required	Special PID checks are enforced if the protocol is 043.0. For 043.0, the visit will also be set to 2.0 VST, and the user will not be able to modify it. This field allows dashes (e.g., 084-01)
ID3	Optional	Special ID3 checks are enforced if the protocol is 043.0. For 043.0, this field allows up to 12 characters, and should be scanned from the blood ID number.
Visit	Required	Defaults to the visit unit of VST. Interim, unscheduled visits should be entered by incrementing the visit value (e.g. 1.10 for the first unscheduled visit, 1.20 for the second, etc.). If the protocol is 043.0, the visit will also be set to 2.0 VST, and the user will not be able to modify it.
OPID	Disabled	--
Clinic	Optional	Any clinic may be set.
Specimen Time	Required	--
Received Time	Optional	--

### Notes

- There are several HPTN label formats available.
- Primary and aliquot volumes with default to ML.
- Quick Add templates are not permitted for HPTN.
- Old records may have a clinic set retroactively if not set at the time of entry

## IDCRC

The IDCRC (Infectious Diseases Clinical Research Consortium) preset project must meet these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PTID)	Required	LDMS checks that the PID is valid. Must be 9 or 10 characters. A PID cannot be changed without approval from VTN Laboratory Leadership.
ID2 (Study)	Required	Drop down menu
ID3 (ID3)	Optional	--
Visit	Required	--
Clinic	Required	The clinic is automatically populated based on the PID; the same clinical location can be associated with multiple clinic IDs (e.g. for Phase I/II or Phase II/III). IDCRC clinics start with the letter V (such as V101 instead of 101). LDMS will verify that an IDCRC clinic was selected.
Specimen Time	Required	--
Received Time	Required	--

## IPREX

The IPREX preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	Must be 5 to 7 characters long and a valid IPREX PID; NOPID is a valid PID, unless the SID is NOSID.
ID2 (Protocol)	Required	--
ID3 (SID)	Required	Must be 11 characters long, with the first 2 digits being the clinic and the last five being the screening number in the range 80001-99999
Visit	Required	--
OPID	Optional	--
Clinic	Required	Must be 3 characters long in the format I[86 to 97] (such as I92)
Draw Time	Optional	--
Received Time	Optional	--

### Notes

- IPREX using the LDMS Shipping File format.
- When entering sero-conversion visits, use the visit unit *sc*. The visit value should be the same as the originally scheduled visit.

- When entering sero-positive visits, use the visit unit *SP*. The visit value should be the number of weeks after the seroconversion visit.

## **IQA**

---

The IQA preset project has these requirements.

### **Data entry requirements**

<b>Field</b>	<b>Required?</b>	<b>Note</b>
ID1 (PID)	Required	--
ID2 (ID2)	Optional	--
ID3 (ID3)	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

## **IRC**

---

The IRC preset project has these requirements

### **Data entry requirements**

<b>Field</b>	<b>Required?</b>	<b>Note</b>
ID1 (PID)	Required	--
ID2 (Protocol)	Required	--
ID3 (SID)	Required	--
Visit	Required	--
OPID	Optional	--
Clinic	Required	--
Collection Time	Required	Only required if the collection date is after 01-Jan-2004
Received Time	Optional	--

## **KENPHIA2**

---

The KENPHIA2 preset project has these requirements.



### Data entry requirements

Field	Required?	Note
ID1 (PTID)	Required	Must be length 8. First 2 characters are letters only (KE) and last 6 characters are numeric only (e.g., KE123456)
ID2 (Country)	Required	"KENYA" is the only available option
ID3 (HIVRT)	Required	Pick list of specific options
Collection Time	Required	--
Received Date and Received Time	Required	--
Clinic	Required	Must be formatted like XX### where the first 2 characters are the letters KE and the next 3 characters are numeric (e.g., KE101)

## MACS

---

The MACS preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (MACSID)	Required	MACS Identifier
ID2 (Study)	Required	--
ID3	Optional	Previously entered ID3s will be automatically populated by LDMS for the MACSID and study combination
Visit	Optional	Select from pre-defined list of visit units.
OPID	Optional	--
Clinic	Optional	Previously entered clinics will be automatically populated by LDMS for the MACSID and study combination
Specimen Time	Optional	--
Received Time	Optional	--

### Notes

- Quick Add templates are permitted for MACS.
- MACS shipments being sent to Precision Bioservices (formally SeraCare) use the SeraCare shipping file format.

## MATRIX

---

The MATRIX preset project has these requirements.

**Data entry requirements**

Field	Required?	Note
ID1 (PTID)	Required	--
ID2 (Study)	Required	--
ID3	Optional	--
Collection Time	Required	--

**MAVRC**

---

The MAVRC preset project must meet these requirements.

**Data entry requirements**

Field	Required?	Note
ID1 (PID)	Required	--
ID2 (Protocol)	Optional	--
ID3 (ID3)	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

**MOSAIC**

---

The MOSAIC preset project has these requirements.

**Data entry requirements**

Field	Required?	Note
ID1 (PTID)	Required	--
ID2 (Study)	Required	--
ID3	Optional	--
Collection Time	Required	--

**mStudy**

---

The mStudy preset project must meet these requirements.

**Data entry requirements**

Field	Required?	Note
ID1 (PID)	Required	6 digit numeric format
ID2 (Study)	Required	Pre-populated with value = <code>MSTUDY</code>
ID3 (ID3)	Optional	--
Visit	Required	--
OPID	Optional	--
Clinic	Required	--
Draw Time	Required	--
Received Time	Required	--

**MTCT**

The MTCT preset project has these requirements

**Data entry requirements**

Field	Required?	Note
ID1 (PID)	Required	--
ID2 (Protocol)	Optional	--
ID3 (ID3)	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

**MTN**

The MTN preset project has these requirements.

**Data entry requirements**

Field	Required?	Note
ID1 (PID)	Required	9 characters long
ID2 (Protocol)	Required	Select from a pre-populated list
ID3	Disabled	Not used for MTN
Visit	Required	Visit unit defaults to VST, but this can be overridden
OPID	Disabled	Not used for MTN

Field	Required?	Note
Clinic	Optional	--
Specimen Time	Optional	This field is not required, but recommended
Received Time	Optional	This field is not required, but recommended

**Notes**

- Primary and aliquot volume will default to ML for MTN specimens.
- There are two label options available for MTN, one with a barcode and one without.
- Quick Add templates are permitted for MTN.

**MWCCS**

---

The MWCCS preset project has these requirements.

**Data entry requirements**

Field	Required?	Note
ID1 (PID)	Required	8 digits long
ID2 (Study)	Required	Select from a pre-populated list (e.g., MWCCS)
ID3	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Required	Select from pre-populated list. Correct options defined as XNNN (e.g., X206)
Specimen Time	Optional	This field is not required, but recommended
Received Time	Optional	This field is not required, but recommended

**Notes**

- The cross-LIMS shipping file format should be used for all shipments going to Precision Biosciences (lab 512).

**NICHD-Westat**

---

The NICHD-Westat has the same requirements the ACTG/IMPAACT project.

**PHACS**

---

The PHACS preset project has these requirements

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	8 characters long, 7 numbers with a letter at the end
ID2 (Protocol)	Required	Select from a pre-populated list; all protocols are in the format PHXXX (e.g. PH200).
ID3	N/A	Not used by PHACS
Visit	Required	Select from pre-defined list of visit units.
OPID	Optional	--
Clinic	Required	Will automatically populate using the previous clinic for the project, PID, and protocol combination entered; PHACS clinics range between 1 and 24. LDMS will check that a valid clinic was selected.
Specimen Time	Required*	*Required for HOPE, PH700, and all future PHACS studies. Optional but recommended for all previous or historical studies.
Received Time	Optional	This field is optional, but recommended

### Notes

- PHACS uses the standard LDMS shipping file format.
- There are two label options for PHACS specimens, one with a barcode and one without.
- Quick Add templates can be applied for PHACS, but users are not permitted to create their own templates. All PHACS templates are created by Frontier Science in collaboration with PHACS leadership.

## PHIA

---

The PHIA preset project has these requirements

### Data entry requirements

Field	Required?	Note
ID1 (PTID)	Required	[Country_Code][6_digits] (Example: ZW123456)
ID2 (Country)	Required	Automatically populated based on country code in PTID; <i>SW</i> (Swaziland) differs from the ISO 3166 country code (SZ)
ID3 (HIVRT)	Required	Testing result (POS, NEG, or IND)
Visit	Required	--
OPID	Optional	--
Clinic	Required	A warning will appear if the country codes in the PTID and clinic do not match

Field	Required?	Note
Specimen Time	Required	--
Received Time	Required	--

**Notes**

- Quick Add templates *cannot* be created for this project.
- Quick Add templates *can* be used for this project.

**REPRIEVE**

---

The REPRIEVE preset project has the same requirements as the ACTG/IMPACCT project.

**SHIMS**

---

The SHIMS preset project must meet these requirements.

**Data entry requirements**

Field	Required?	Note
ID1 (PID)	Required	Nine characters long that meets the SHIMS ID1 requirements
ID2 (Study)	Required	--
ID3 (Rapid Test)	Required	--
Visit	Required	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Required	--
Received Time	Required	--

**SHIMS ID1 format**

RAAAhhcpp

- R**                    1 to 4
- AAA**                001 to 599
- hh**                    01 to 26
- c**                     Check digit
- pp**                    01 to 99

## SNRP

---

The SNRP preset project has these requirements

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	--
ID2 (Study)	Optional	--
ID3 (SID)	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

## TIES

---

The TIES preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	8 characters long, 7 numbers and one letter between A and L; if the PID does not have 7 numbers, add leading zeros to the front of it.
ID2 (Protocol)	Required	Select from the pre-defined list of protocols.
ID3 (ID3)	Available	ID3 is not used by this project
Visit	Required	Select from pre-defined list of visit units.
OPID	Available	--
Clinic	Required	In the format T[ <i>Clinic_Number</i> ]
Specimen Date	Required	--
Specimen Time	Required	--
Received Date	Required	--
Received Time	Optional	--

## VQA

---

The VQA preset project has these requirements.

**Data entry requirements**

Field	Required?	Note
ID1 (PanelID)	Required	LDMS will determine if this field is valid. Specimens entered or received in a shipping file prior to 01-July-2007 will not be validated.
ID2	N/A	This field is not used by VQA
ID3	N/A	This field is not used by VQA
Visit	N/A	This field is not used by VQA
OPID	N/A	This field is not used by VQA
Clinic	N/A	This field is not used by VQA
Specimen Time	N/A	This field is not used by VQA
Received Time	N/A	This field is not used by VQA

**PanelID format**

*[Assay\_Category][Panel\_Number][Panel\_Subtype].[Num]Panel\_Configuration*

**Assay\_Category** RNA, DNA, or CUL

**Panel\_Number** A number between 000 and 999

**Panel\_Subtype**

UM	Ultrasensitive RNA
SM	Standard RNA
RT	DNA proficiency panel
PQ	DNA pre-qualification panel
CC	Culture panel

**Num** A number between 01 and 99

**Panel\_Configuration** A, B, or C

**VTN**

The VTN preset project has these requirements.

**Data entry requirements**

Field	Required?	Note
ID1 (PID)	Required	LDMS checks that the PID is valid. Must be 9 or 10 characters. A PID cannot be changed without approval from VTN Laboratory Leadership.
ID2 (Protocol)	Required	LDMS checks that the PID and protocol combination are valid.
ID3	Disabled	--



Field	Required?	Note
Visit	Required	Use VST for routine HIV diagnostic visits, otherwise use the appropriate visit unit. This visit unit is used by certain laboratories for driving testing algorithms.
OPID	Disabled	--
Clinic	Required	The clinic is automatically populated based on the PID; the same clinical location can be associated with multiple clinic IDs (e.g. for Phase I/II or Phase II/III). VTN clinics start with the letter V (such as V101 instead of 101). LDMS will verify that a VTN clinic was selected.
Specimen Time	Required	--
Received Time	Required	--

### Notes

- Throughout LDMS, HVTN is listed as VTN.
- The volume for VTN specimens will default to ML.
- Within VTN, LDMS Shipping files are sometimes called "e-manifests".
- Barcodes must be printed on labels for VTN specimens.
- Quick Add templates are not permitted for VTN specimens.
- Information for study CoVPN 5001 should be logged under VTN study 5001.

## WHIN

---

The WHIN preset project must meet these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (ParticipantID)	Required	--
ID2 (Protocol)	Optional	--
ID3 (ID3)	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

## WIHS

---

The WIHS preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	Must meet WIHS PID format requirements
ID2 (Protocol)	Required	Select from pre-populated list
ID3 (SID)	Optional	--
Visit	Required	The visit unit will default to VST, and the visit number will be automatically populated based on an algorithm that uses the current date
OPID	Optional	--
Clinic	Optional	--
Specimen Time	Optional	--
Received Time	Optional	--

### WIHS PID format

*[Site\_Number][Recruitment\_Number][Participant\_Number][Check\_Digit]*

#### Site\_Number

1	NYC (Bronx)
2	Brooklyn
3	Washington, D.C.
4	Los Angeles
5	San Francisco
6	Chicago

#### Recruitment\_Number

2B	New recruit
0B	Original recruit
1B	Original recruit

#### Check\_Digit

Any character; an algorithm will determine if the character is valid based on the read of the PID.

### Notes

- WIHS shipments being sent to Precision Bioservices (formally SeraCare) use the SeraCare shipping file format.
- Quick Add templates are permitted for WIHS, and users are expected to create and use template for WIHS data entry.
- Collection Date and Received Date will automatically be set to your local date.

### WITS

The WITS preset project has these requirements

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	--
ID2 (ID2)	Optional	--
ID3 (ID3)	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

## WITSRepos

---

The WITSRepos preset project must meet these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (Subject ID)	Required	--
ID2 (Study ID)	Optional	--
ID3	Optional	--
Visit	Optional	--
OPID	Optional	--
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

## ZEBS

---

The ZEBS preset project has these requirements

### Data entry requirements

Field	Required?	Note
ID1 (STUDYID)	Required	--
ID2 (ID2)	Optional	--
ID3 (ID3)	Optional	--
Visit	Optional	--
OPID	Optional	--

Field	Required?	Note
Clinic	Optional	--
Draw Time	Optional	--
Received Time	Optional	--

## ZIP

The ZIP preset project has these requirements.

### Data entry requirements

Field	Required?	Note
ID1 (PID)	Required	Must be a 6-digit (for ID2=ZIP) or 7-digit (for other ID2 values). Following the digits, there must be a letter. A hard check should run to ensure the first two digits match to a corresponding ZIP clinic code ZXX.
ID2 (Study)	Required	Use allowed studies (ZIP, Z1.0, or Z2.0)
ID3 (Screening ID)	Required	It must be in the format SAAXXX, where AA is a valid clinic number (i.e., ZAA) and XXXX is any numeric number.
Visit Value and Vist Unit	Required	--
Clinic	Required	The LDMS will automatically populate the correct, corresponding clinic ID based off of the entered PID. If a corresponding clinic ID is not found, leave the clinic field blank and select a value.
Specimen Date	Required	--
Specimen Time	Required	--
Received Date	Required	--
Received Time	Required	--

### Notes

- The application must allow FSTRF and user defined preloads for this project.
- The application must not restrict the user from co-enrolling specimens for this project.

## Administration

The **Administration** page is where you can manage various settings in LDMS

## Projects

Projects are the collaborative project, organization, or network that conduct studies.

There are two types of projects: *local projects* and *government projects*.

**Figure 66: The Projects page.**

Name	Description	<sup>1</sup> ID1	<sup>2</sup> ID2	<sup>3</sup> ID3	Export	Local	In Use	
PHIA	Population-Based HIV Impact Assessments	PTID	Country	HIVRT	✓		✓	View
CONTROL	CONTROL	CONTROLNAME	PROTOCOL	ID3	✓		✓	View
UNKNOWN	Unknown Group	ID1	ID2	ID3				View
FRONTIER	Frontier Science-Internal Study	PID	Study			✓	✓	Edit
cadmus	cadmus	pid	prot	sid		✓		Edit
XLOCAL	XLOCAL	ID1	ID2	ID3		✓	✓	Edit

(1) Whether data is copied into Frontier Science’s central database (2) Whether the project is a government or local project (3) Whether there are specimens currently using the projects.

### Local projects

Local projects are *projects* that only exist at your laboratory.

A local project is one that has been defined by your laboratory. These are general used for internal studies that only your laboratory will utilize, although they can be sent to other laboratories through shipments.

Defining a new local project requires you to specify what you are going to call *ID1*, *ID2*, and *ID3*.

**Table 16: Identifiers**

Identifier	Description	Example
ID1	Uniquely identifies a participant or specimen source	Participant ID
ID2	Identifies the study in which the participant is enrolled	Study number
ID3	Used to further identify a branch or sub-unit in a study	Sub-study number

While there are no rules for what you can name each identifier, they must be used for these purposes. For some projects, it may be more appropriate to think of ID1 as identifying the source from which specimens were collected, such as a testing solution that you received, rather than a participant.

### Creating a new project

New projects can be created on the **Project Administration** page.

## Steps

1. Click **Administration > Projects** from the LDMS menu bar.
2. From the LDMS action menu, select **Create Project**.  
The **Create Project** window will open.

**Figure 67: The Create Project Window**

3. Enter the name of the project as you would like it to appear in menus throughout LDMS into the **Name** box.
4. Enter a brief description of the project into the **Description** box.  
The description is generally used to provide the full name of the project, especially when the project is an acronym.
5. Enter the name that you want to use for *ID1* for the project into the **ID1 Name** box, and a brief description into the **ID1 Description** box.  
The format and acceptable values for *ID1* may also be set.  
*ID1* is typically used as an identifier for a participant. For other types of work, such as quality control testing, *ID1* could also be something else, like a testing panel number.

**Figure 68: Enrollment Configuration**

6. Enter the name that you want to use for *ID2* into the **ID2 Name** box, and a brief description into the **ID2 Description** box. The format and acceptable values for *ID2* may also be set. *ID2* is typically used for a study or protocol identifying number.

**Figure 69: Visit Configuration**

7. Enter the name that you want to use for *ID3* into the **ID3 Name** box, and a brief description into the **ID3 Description** box. The format and acceptable values for *ID3* may also be set. *ID3* is typically used as a sub-study or sub-protocol identifying number.
8. Click the **Save** button.

**Result**

The new project will be added to the list of groups that you specified.

## Modifying and removing a project

Local project can be modified or removed after they are created

### Prerequisites

A local project can only be removed if it is not currently in use. Government projects cannot be modified or removed.

### Background

This might be needed if there was a mistake with the way the project was initially entered or if you need to update the descriptions for the participant fields. Changes made to a project will automatically update existing participant records in LDMS.

### Steps

1. Click **Administration > Projects** from the LDMS menu bar.
2. Locate the project to be modified or removed from the list of projects.
3. Do one of the following:
  - To modify the project, click the **Edit** button to the right of the project. The **Edit Project** window will open, where you can make your changes. When you are done, click the **Save** button.
  - To remove the project, select **Delete** from the **Edit** menu to the right of the project.

## Government projects

Government projects are those that are defined by Frontier Science.

Frontier Science works with government-funded projects to define the rules and specifications for their project. These projects cannot be modified or removed by users. Even though they cannot be modified, they will still be visible on the **Projects** page.

## Adding a Reagent

---

The Reagent Logging feature is used to track reagents used at a laboratory and uses a defined set of reagent codes.

You can use this feature to record information about reagents, such as the lot number and whether the reagent is still in use.

Once entered, the lot number for the reagent will be available on the **Specimen Management** page to assign to specimens that contain the reagent.



**Figure 70: The reagent logging module**

Reagent Logging

[Add Reagent](#)

Reagent Name	Lot Number	Expiration Date	Manufacturer	Start Date	End Date	Active	In Use	Action
FOR	aa2018	22/Jan/2019	f5	21/Jan/2018	21/Jan/2019		✓	Delete
FOR	aaEXPIRED	08/Jan/2017	fstrf	21/Jan/2018	21/Jan/2019	✓	✓	Delete
FOR	aaINACTIVE	13/Jan/2019	fstrf	21/Jan/2018	31/Jan/2019			Delete

Selected Reagent

Reagent Name  \*

Lot Number  \*

Expiration Date  \*

Manufacturer  \*

Start Date  \*

End Date  \*

Active

[Update Reagent](#)

[Save](#)

## Adding Reagent Information

Reagents can be added through the **Administration** menu.

### Steps

1. From the menu bar, click **Administration** and then click **Reagent Logging**
2. Click **Add Reagent**  
A new blank row will be added to the bottom of the name. You may need to scroll down to see it.
3. Complete the information for the new reagent.

Field	Usage
Reagent Name	This field contains the three letter code for the reagent that is being tracked.
Lot Number	This is a free text field. Enter the lot number from the container
Expiration Date	Manufacturer set date of expiration
Manufacturer	This is a free text field. Enter the manufacturer name from the container.
Start/End Date	These fields record the date the reagent was first used and the date use was discontinued.
Active	New entries default to active.

4. At the bottom of the page, click **Save**.

## Linking Reagent to Sample in Specimen Management

Users can assign reagent lots to primary and aliquot samples in Specimen Management or via Quick Add. Options are limited to the lots that have been defined in the reagent logging module.

### Background

After the lot is entered in the Reagent Logging module, the lot number is available in the Edit Aliquot menu to be applied to any sample using the sub-additive.

### Steps

**Figure 71: Linking Reagent to Sample via the Specimen Management Menu**

Aliquots for 0500-001ZLC00-000

Global Specimen ID	Status	Derivative Type	Sub Add/Der Type	Specimen Condition	Available Volume	Other Specimen ID	Action
0500-001ZLC00-001	✓	PL2	N/A	SAT	1 ML		Edit
0500-001ZLC00-002	✓	PL2	N/A	SAT	1 ML		Edit
0500-001ZLC00-003	✓	PL2	N/A	SAT	1 ML		Edit
0500-001ZLC00-004	✓	CEL	DMS	SAT	3000000 CEL		Edit
0500-001ZLC00-005	✓	CEL	DMS	SAT	3000000 CEL		Edit
0500-001ZLC00-006	✓	CEL	DMS	SAT	3000000 CEL		Edit

Edit Aliquot

FRONTIER.0111111  
 TEST  
 6 Wk 01/Oct/2015  
 0500-001ZLC00-000  
 0500-001ZLC00-004

Global Specimen ID: 0500-001ZLC00-004  
 Specimen ID:  
 Other Specimen ID:  
 Enrollment: FRONTIER/TEST  
 Derivative Type: CEL  
 Sub Add/Der Type: DMS  
 Sub Add/Der Reagent: 123456  
 Is Available:

1. In Specimen Management, use the filters to navigate to the specimen's page.
2. In the Aliquot grid, locate the specimens utilizing the logged reagent
3. Click the **Edit** button, the Edit Aliquot menu will open in a pop up window
4. Select the appropriate lot number in the Sub Add/Der Reagent menu
5. Click **Save**

## Linking Reagent to Sample in Quick Add

### Background

If known, the reagent lot number can be applied in `Quick Add` at the time of accessing.

### Steps

1. In the `Aliquot` grid, locate entry with the `Sub Additive/Derivative`.
2. Click the `Edit` button
3. Select the lot number in the `Sub Add/Der Reagent` menu.

## Linking Additive to Reagent Lot

### Steps

**Figure 72: Linking Additive to Reagent Lot**

Additive	Additive Type	Additive Reagent
	EDT	*

1. In `Specimen Management`, click the `Edit` button for the `Primary` containing the logged `Additive`
2. In the `Edit Primary Specimen` window, select the lot number in the `Additive Reagent` menu

## Reagent Lot Sample Details Report

The `Reagent Lot Sample Details Report` provides a list of which specimens contain a reagent.

This report include information about the reagent at the top, and then lists all specimens and details about the specimens (such as specimen type, collection date and time, and specimen identifiers).

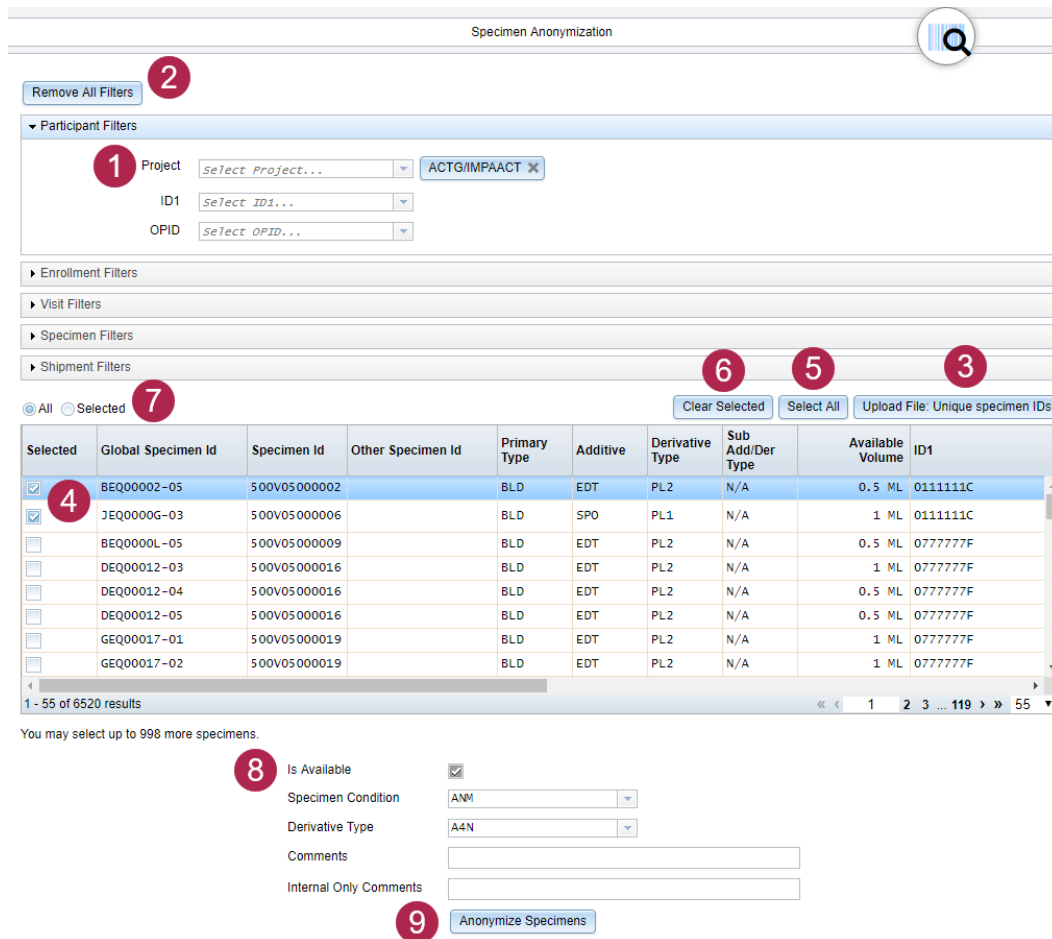
To generate this report, click **Administration** and then click **Reagent Logging**. Next to the reagent of interest, click **Report**.

## Specimen Anonymization

---


The specimen anonymization module is used to anonymize specimens. This module is disabled by default and must be enabled by LDMS User Support in order to be used.

**Figure 73: Specimen Anonymization Screen**



(1) Various filters that can be applied to the list of specimens, (2) remove all specimens filters, (3) upload a unique specimen IDs file, (4) manually select specimens from filtered list, (5) select all specimens in filtered list, (6) clear selected specimens in filtered list, (7) filter list of specimens by selected only, (8) mark specimen(s) as available or non-available, set condition and derivative type, and add comments, (9) anonymize selected specimens

1. To access the specimen anonymization module after it has been activated by LDMS User Support, navigate to the **Administration** dropdown and select **Specimen Anonymization**.
2. Use the various filters to locate the specimens that need to be anonymized. The list of filtered specimens will appear below.
3. If not all specimens in the filtered list are intended to be anonymized, select the specimens that are to be anonymized and click the **Selected** radio button.
4. A global specimen IDs file can also be added to the list of filtered specimens by clicking **Upload File: Unique specimen IDs**.
5. Check the **Is Available** checkbox to have the selected specimens remain available.
6. Change the **Specimen Condition** of the selected specimens from the dropdown.

 **Note:** Certain specimen conditions automatically change the specimen availability checkbox.

7. Change the **Derivative Type** and add **Comments** and **Internal Only Comments** to the selected specimens as necessary.

8. Click **Anonymize Specimens**.

After specimens have been anonymized, the original specimen records will become unavailable to store, ship, or test. LDMS will create new anonymized records for these specimens with scrambled/anonymized IDs. New barcode labels can be generated to apply to the specimen vials that display the anonymized IDs. Reports can be generated to review the link between the original IDs and newly assigned anonymized IDs.

## Lab Settings

Some laboratory-specific settings can be controlled by users by clicking **Administration** and then clicking **Lab Settings**.

Setting	Usage
Number of samples shown by default in sample picker	Set the default number of samples shown in sample picker
Processing Tech Initials defaults to current user	Currently signed-in user will automatically be set as the Processing Technician when creating aliquots.
Require a comment when modifying primaries and aliquots	If activated, the user must enter or modify the comment in order to be able to save the Edit Primary and Edit Aliquot popups.
Auto-set frozen date/time to the current date/time when storing specimens	When storing a specimen, its frozen date and time will automatically be set.
Include unavailable primary samples by default when printing labels	Unavailable primary samples will be included by default when printing labels.
Auto-assign next available fill-order position when adding and moving specimens, containers, and levels in storage	The next available fill-order will automatically be assigned when specimens are added to storage containers
Import shipments into storage by default	Shipments will be imported into storage by default
Mark to Ship reminds users when overdue by default	Users will be notified on login if they have overdue shipments
Override shipping container configurations when importing into storage?	Override various attributes for shipping container configurations when importing into storage, such as alphabetic columns, fill order, etc.

## User Settings

Users are able to change a limited number of settings for how their account works by clicking **Administration** and then clicking **User Settings**.

Setting	Usage
Default Module	Select the initial page that will be loaded when you sign into LDMS.
Default Lab ID	Select the lab ID that will be selected when you sign into LDMS.
Show ID1/PID and Specimen Number in Storage Tree	Select to display ID1/PID and Specimen Number in the Storage Tree

## User management

User accounts are managed by Frontier Science.

Accounts for individual users are created and maintained by LDMS User Support. To perform the following tasks, you would need to contact LDMS User Support for assistance:

- Create a new user
- Reset a user’s password
- Manage what features in LDMS a user can access

Users can modify their own passwords from within LDMS.

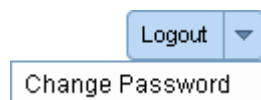
## Changing your password

While the creation and management of user accounts is handled by LDMS User Support, users can change their own passwords.

### Steps

1. From the logout menu in the upper-right corner of the page, click **Change Password**

**Figure 74: The Logout menu**



The **Change password** window will open.

2. Enter your current password into the **Password** box.
3. Enter your new password into the **New Password** box.
4. Re-enter your new password into the **Confirm Password** box.
5. Click the **Change Password** button.

## Password requirements

This section explains the requirements for user passwords.

- Passwords must contain at least one upper case letter, one lower case letter, one number, and one special character

- A password must not be the same as one of the your previous passwords
- A password must be between 10 and 50 characters
- Must not be similar to your current password, user ID, or display name

Temporary passwords expire within 24 hours. If you do not sign into LDMS using the temporary password before it expires, you must have a new temporary password generated.

## Dropdown Customization

---

The **Dropdown Customization** tab allows users to hide items from dropdown lists. This is accessed through the **Administration** menu.

### Steps

1. From the menu bar, click **Administration** and then click **Dropdown Customization**.

Dropdown Customization

Dropdown List: ID2

Project: IPREX \*

Active	Name	Description
<input checked="" type="checkbox"/>	IPREXOL	
<input checked="" type="checkbox"/>	iPrEx	
<input checked="" type="checkbox"/>	ESN	

Save

2. Select a value from **Dropdown List**.
3. Select a project from the **Project** dropdown list.
4. A table with items to hide will appear. Uncheck the boxes in the **Active** column to hide items.
5. At the bottom of the page, click **Save**.

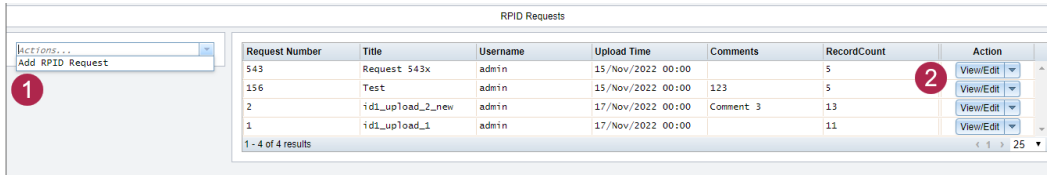
To unhide any items previously hidden, return to this page and re-check the applicable boxes, then click **Save**. The items will then return as options in dropdown lists.

## RPID Requests

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In the RPID Requests module, users can create new RPID requests, edit/delete existing requests, and download a list of ID1s associated with the request.

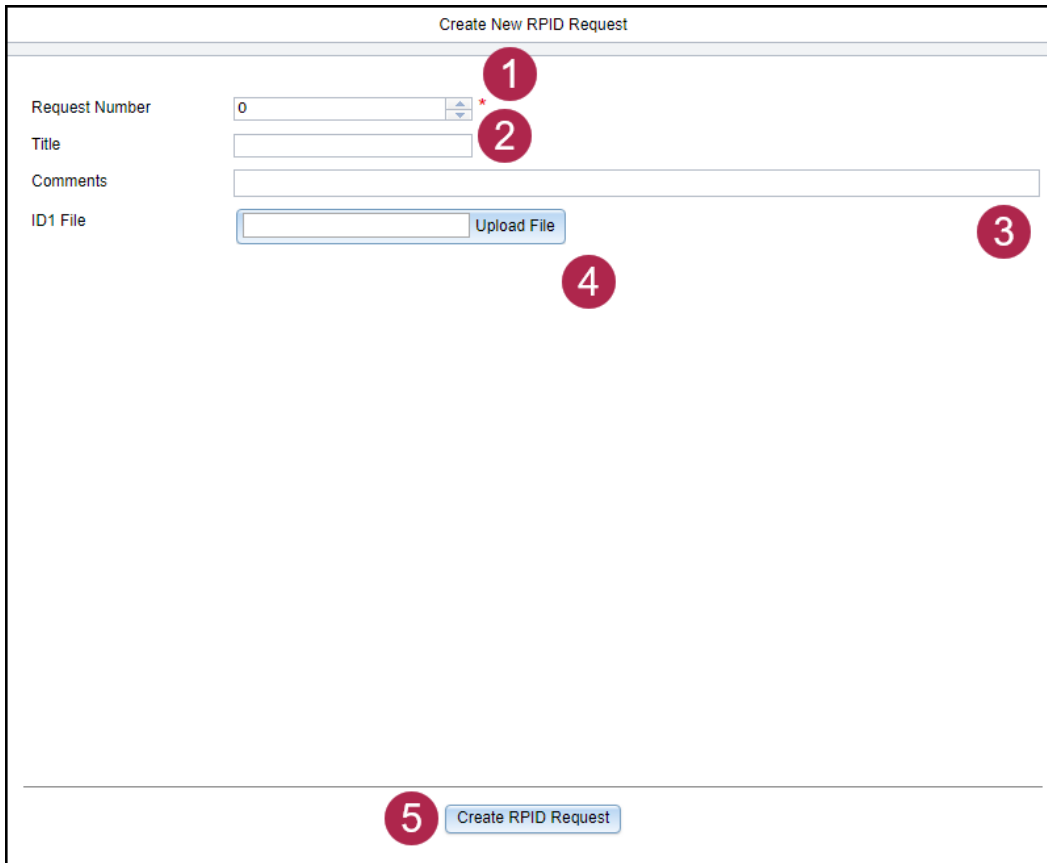
**Figure 75: RPID Requests - Main Screen**



(1) Add a new RPID request, (2) View, edit, delete existing RPID requests

## Adding a New RPID Request

**Figure 76: Create New RPID Request Window**



(1) RPID Request Number, (2) title of the request, (3) comments about the request, (4) upload ID1 file, (5) create the RPID request

- 1.** Navigate to **RPID Requests** from the **Administration** dropdown.
- 2.** Click **Add RPID Request** from the **Actions** dropdown.
- 3.** In the **Create New RPID Request** window, add the request number, title, comments, and ID1 file as needed, and click **Create RPID Request**.



## Editing an RPID Request

1. Navigate to **RPID Requests** from the **Administration** dropdown.
2. Click **View/Edit** next an existing RPID request.
3. Update the request information as needed.
4. Click **Save**.
5. To delete an RPID request, return to the main RPID Request screen, click the dropdown next to the **View/Edit** button of an existing request and click **Delete**. On the confirmation screen, click **Delete**.

A list of ID1s associated with an RPID request can be downloaded. To do this, click the dropdown next to an existing RPID request and click **Download ID1s**.

## Clear Filters

The Clear Filters page is used to clear filters across all modules.

**Figure 77: Clear Filters Screen**

Clear Filters

Select the filters to clear

Specimen	<input checked="" type="checkbox"/>
Storage	<input type="checkbox"/>
Filtering Sample Chooser	<input checked="" type="checkbox"/>
Pending Shipment	<input type="checkbox"/>
Shipment History	<input type="checkbox"/>
Test Results	<input type="checkbox"/>
Pending Shipment Storage Container	<input type="checkbox"/>
Data Submission	<input type="checkbox"/>
PK Control Charting	<input type="checkbox"/>

Clear Clear All

To access the Clear Filters module, navigate to the **Administration** dropdown and select **Clear Filters**.

To clear filters, do one of the following:

- To clear specific filters, check the boxes next to each applicable filter and then click **Clear**.
- To clear filters in all categories, click **Clear All**.

## Online Resources

The Online Resources menu option contains links to relevant web resources.

- **LDMS Validation Resources** - A link to a page on the LDMS website where users can request validation documentation.
- **Frontier Science Website** - A link to the main Frontier Science website.
- **Frontier Science Portal** - A link to the Frontier Science Portal.
- **Specimen Repository Website** - A link to the specimen repository website, a site that can be used to search for specimens located at a number of repositories.

## Codes, units, and abbreviations

This section lists the codes, units and abbreviations that are used in LDMS for various entry fields, such as visits and specimen types. These codes are used by both LDMS and LDMS for Windows.

### Specimen type codes

---

These are the codes use for primary, additive, and derivative types.

#### Primary codes

This section lists all of the available primary codes in LDMS

Code	Description
ADG	Adrenal Glands
ADP	Adipose
AHR	Non-Occipital scalp hair
AMN	Amniotic Fluid
ANL	Anal
AOR	Aorta
APP	Air Pollution Particles
ARB	Rectal Biopsy by Anoscopy
ARL	Breast Areola
ART	Arterial Blood Draw
ASC	Ascending Colon
BAL	Bronchoalveolar Lavage
BHR	Hair, Body
BLA	Bladder
BLC	Blood Clots
BLD	Blood (Whole - Venous)
BMA	Bone Marrow Aspirate
BMC	Bone Marrow Core Biopsy

<b>Code</b>	<b>Description</b>
BMK	Human Milk
BML	Human Milk - Left
BMR	Human Milk - Right
BNE	Bone
BNM	Bone Marrow
BRB	Bronchoscopy Brush
BRN	Brain Tissue
BRS	Breast Tissue
BSG	Basal Ganglia
BUC	Buccal
BUG	bulbourethral glands
CAT	Coronary Artery
CCD	Common Carotid
CDE	Caudate
CER	Cervix
CLL	Colon (left)
CLR	Colon (right)
CLS	Sigmoid Colon
CRB	Cerebellum
CRD	Cord Blood
CRN	Colorectal Neoplasm
CSC	Cervical Secretion
CSF	Cerebro-Spinal Fluid
CVB	Cervical Biopsy/Aspirate
CVF	Cervicovaginal Fluid
CVL	Cervical Vaginal Lavage
CVM	Cervical Mucous
CXC	Cervical Culturette
CXS	Cervical Swab
DDM	Duodenum
DIA	Dialysate
DMM	DMEM
DPL	Dried Plasma
DRG	Dorsal Root Ganglia
DSC	Descending Colon

<b>Code</b>	<b>Description</b>
DTC	Distal Colon
DWB	Dried Whole Blood
DWM	Deep White Matter
EBC	Exhaled Breath Condensate
END	Endometrium
ENV	Environmental
EPI	Epididymus
EPS	Expressed Prostatic Secretions
ESO	Esophagus
EVX	Endocervix
EYE	Corneal Tissue
FAT	Femoral Artery
FCM	Frontal Cortex (motor)
FCP	Frontal Cortex (pre-motor)
FGN	Finger Nails
FHR	Hair, Facial
FLT	Fallopian Tubes
FSC	Sigmoid Colon Biopsy by Flexible Sigmoidoscopy
FSI	Penis Foreskin, Inner Tissue
FSK	Penis Foreskin, Whole Tissue
FSO	Penis Foreskin, Outer Tissue
FSR	Rectal Biopsy by Flexible Sigmoidoscopy
FST	Blood from Fingertick (capillary)
GAS	Gastric Secretions
GCF	Gingival Crevicular Fluid
GLN	Glans
GLS	Glycerol Stock
GLU	Genital Lesion/Ulcer
GMI	Gastro Intestinal Mucosa
HAR	Hair
HPC	Hippocampus
HRT	Heart
HST	Blood from Heelstick (capillary)
ICD	Internal Carotid
ILM	Ileum

<b>Code</b>	<b>Description</b>
INT	Intestinal Biopsy/Aspirate
INW	Induction Waste
IVR	Intra-vaginal Ring
IVS	Intraventricular Septum
JJM	Jejunum
KDY	Kidney
KID	Kidney Biopsy
LAL	Lymph Node Axillary-left
LAR	Lymph Node Axillary-right
LAT	Left Atrium
LBL	Large Bowel
LBT	Lateral Border of the Tongue
LIL	Lymph Node Inguinal-left
LIR	Lymph Node Inguinal-right
LIV	Liver Tissue
LNA	Lymph Node (aortic)
LNC	Lymph Node (cervical)
LNE	Pre-auricular Lymph Node
LNF	Infraclavicular Lymph Node
LNG	Lung
LNI	Inguinal Lymph Node
LNK	Popliteal Lymph Node
LNM	Lymph Node (mediastinal)
LNO	Lymph Node (other)
LNP	Lymph Node (per-hilar)
LNR	Para-aortic Lymph Node
LNS	Supraclavicular Lymph Node
LNT	Mesenteric Lymph Node
LNX	Lymph Node (axillary)
LPK	Leukopak
LSG	Labial Salivary Gland
LUE	Lung, Excised
LUF	Lung, Filter Paper
LVE	Left Ventricle
LYM	Lymph Node Biopsy/Aspirate

<b>Code</b>	<b>Description</b>
MBR	Midbrain Consists of Cerebral Penduncles and Tectum
MCP	Prefrontal Medial Cortex
MEC	Meconium
MED	Medulla
MEN	Dura Mater – Meninges
MES	Mesentery
MFP	Placenta Membranes
MSB	Main Stem Bronchus Wash
MTC	Motor Cortex
NAS	Nasal
NPH	Nasopharyngeal
NPW	Nasopharyngeal Wash
NRH	Naso-oropharyngeal
NSB	Nasal brush
OCC	Occip Cortex
OCL	Ocular
OHR	Occipital scalp hair
OPW	Oropharyngeal Wash
ORH	Oropharyngeal
ORL	Oral
OTH	Other
OVR	Ovaries
PAD	Adipose (pericardial)
PAN	Perianal
PCF	Pericardial Fluid
PCT	Parietal Cortex
PEN	Penis
PFL	Pleural Fluid
PFR	Parotid Flow
PHR	Hair, Pubic
PHX	Pharynx
PLC	Placental Tissue
PLM	Placenta - Membrane Slice
PLN	Peritrach Lymph Nodes
PLP	Polyp

<b>Code</b>	<b>Description</b>
PLQ	Plaque
PMD	Plasmids
PNC	Pancreas
PON	Pons
PPK	Plasmapak
PRC	Premotor Cortex
PRO	Prostate
PRT	Prostate Tissue Biopsy
PTF	Peritoneal Fluid
PTY	Parathyroid
RAT	Right Atrium
RCT	Rectum
REC	Rectal
RSC	Rectosigmoid Colon
RVE	Right Ventricle
SAD	Subcutaneous Adipose
SAL	Saliva
SCC	Spinal Cord Cervical
SCL	Spinal Cord Lumbosacral
SCR	Scrotum
SCT	Spinal Cord Thoracic
SEM	Semen
SHR	Hair, Scalp
SIN	Sputum, Induced Non-Select
SIS	Sputum, Induced Select
SKN	Skin
SLU	Skin Lesion
SMD	Skeletal Muscle (distal)
SMP	Skeletal Muscle (proximal)
SMV	Seminal Vesicle
SPI	Sputum, Induced
SPL	Spleen
SPS	Sputum, Spontaneous
SPT	Sputum
SSN	Sputum, Spontaneous Non-Select

<b>Code</b>	<b>Description</b>
SSS	Sputum, Spontaneous Select
STL	Stool
STM	Stomach
SVG	Salivary Glands
TBD	Specimen type to be defined
TCA	Tracheal Aspirate
TCX	Temporal Cortex
TER	Tears
THD	Thoracic Duct
THL	Thalamus
THR	Throat Swab
THW	Throat Wash
THY	Thymus
TIL	Terminal Ileum
TNA	Toe Nails
TNG	Tongue
TON	Tonsillar Biopsy/Aspirate
TRN	Transverse
TST	Testes
TTH	Tooth
TUM	Tumor
TVC	Transverse colon
TYD	Thyroid
UMB	Placenta - Cord Slice
UNK	Unknown Primary
URN	Urine
UTH	Urethra
UTS	Uterus
VAG	Vaginal Swab
VCS	Cervicovaginal Secretions
VGL	Vaginal
VGN	Vagina
VSC	Vaginal Secretions
VUL	Vulva
WAR	Warts



## Additive codes

This section lists all of the additive codes available in LDMS.

Code	Description
ACD	Acid Citrate Dextrose
AG1	ESAT 6-free cocktail 1
AG2	ESAT 6-free Cherry pick
AHP	Ammonium Heparin
APT	Allprotect
ATM	Abbott Transport Medium
BBL	CultureSwab Kit
BFM	Bacterial Freezing Media
BOR	Boric Acid
BSA	Bovine Serum Albumin
BTM	Biopsy Transport Media
CPD	Citrate Phosphate Dextrose
CPH	Cell Preparation Tube Heparin
CPS	Cell Preparation Tube SCI
CTK	Culture Transport Kit
DFA	Desferoxamine
DHP	Double dosage of Heparin
DPE	Spray Dried EDTA
DSE	Spray Dried Sodium EDTA
EDT	EDTA
ELB	elution buffer
END	Endometrial Tissue
ETH	Ethanol
FFN	Fetal Fibronectin Buffer
FFP	Formalin-Fixed, Paraffin Embedded
FMD	Formaldehyde
FOR	Formalin
GEN	GenAptima Media
GIT	Guanidine Isothiocyanate (GITC)
GLT	Glutaraldehyde
GRB	Guanidine Reduction Buffer
H2O	Water
HEP	Heparin

<b>Code</b>	<b>Description</b>
HPV	Human Papilloma Virus
HVS	High Virginal Swab
ISO	Isohelix kit
IST	Internal Standard
LHG	Lithium Heparin and Gel for Plasma
LHP	Lithium Heparin
LIN	LoBind tube lined with 5% BSA
LOB	LoBind Tube
LPE	Liquid Potassium EDTA
LSE	Liquid Sodium EDTA
LYB	Lysis Buffer
MBK	Microbank tube
MPA	Metaphosphoric Acid
MSA	Mannitol Salt Agar
NOH	Sodium Hydroxide
NON	None
NOR	Normasol
NSL	Normal Saline
NUC	NUNC Tube
OCT	Optimum Cutting Temperature Medium
OMN	Omnigen Collection Tube
ORA	OraSure Collection Container
ORG	Oragene Collection Container
OTH	Other
PAC	Port-a-cul Transport Tube
PAX	PAXgene Blood RNA tube
PBS	Phosphate Buffered Saline
PCT	PreservCyt: ThinPrep collection media
PED	Potassium EDTA
PFM	Paraformaldehyde
PI1	S8820 Sigma SIGMAFAST? Protease Inhibitor Tablets
PIA	Pseudomonas Isolation Agar
PLP	PLP Fixative
PPT	Plasma Preparation Tube
PRO	ProbeTec Media

<b>Code</b>	<b>Description</b>
PXD	Paxgene tube DNA Extraction
QAG	QFT-TB Ag Red Cap
QMT	QFT-Mitogen Purple Cap
QNL	QFT-Nil Grey Cap
QTF	QuantiFERON-TB Gold Assay
QTG	QFT-TB1 Ag Green Cap
QTY	QFT-TB2 Ag Yellow Cap
RBE	Royal blue - EDTA
RBN	Royal blue - no anticoagulant
RLS	Ringer's Lactate Solution
RNL	RNALater
RNP	RNAprotect
ROC	Roche Media
RPM	RPMI 1640 Medium
RPS	RNA Preservation Solution
SBC	Sodium Bicarbonate
SCC	Steck Cyto-Chex tubes - stabilized
SCI	Sodium Citrate
SED	Sodium EDTA
SFE	Sodium Fluoride/Na <sub>2</sub> EDTA
SFL	Sodium Fluoride
SIA	Sulfite Iron Agar
SKM	Skim Milk
SNP	Snap/Flash Freeze
SPH	Sucrose Phosphate
SPO	Sodium Fluoride/Potassium Oxalate
SPS	Sodium Polyanetholesulfonate
SST	Serum Separator
STG	Skim milk-Tryptone-Glucose-Glycerin Medium (STGG)
TAL	Blood Bag Tail
TBD	Specimen type to be defined
TBS	Tris-Buffered Saline
TCD	tween chlorhexidine digluconate
TEM	Tempus Tube
TFM	Tissue Freezing Medium

<b>Code</b>	<b>Description</b>
TFX	Tissue Fix
THM	Thrombin
TMS	Transport Medium-Stuarts
TRC	TruCulture Tube
TVT	TransFix Vacuum Blood Collection Tube
UNK	Unknown Additive
URM	Urine Transport Media
UTM	Universal Transport Media
VTM	Viral Transport Media
ZRD	Zymo RNA/DNA shield

### Derivative codes

This section lists the derivative codes available in LDMS.

<b>Code</b>	<b>Description</b>
A4N	Activated CD4+ without Tregs
AD4	Activated CD4
AD8	Activated CD8 Derivative
ADG	Adrenal Glands
ADL	Adipose Tissue Layer
ADP	Adipose (abdominal)
AHR	Non-Occipital scalp hair
AMN	Amniotic Fluid
AOR	Aorta
APL	Applicator Tip
ASP	Aspirate
BAC	Bacterial Isolate
BAL	Bronchoalveolar Lavage
BCL	B-cell Lymphoblastoid Cell Line
BHR	Hair, Body
BLA	Bladder
BLC	Blood Clots
BLD	Blood (Whole - Venous)
BLK	Tissue Block
BMA	Bone Marrow Aspirate
BMC	Bone Marrow Core Biopsy
BMK	Human Milk

<b>Code</b>	<b>Description</b>
BML	Human Milk - Left
BMR	Human Milk - Right
BMS	Human Milk - Spun
BMW	Human Milk - Whole
BNM	Bone Marrow
BPS	Biopsy
BRN	Brain Tissue
BRS	Breast Tissue
BSG	Basal Ganglia
BUC	Buccal
BUF	Unficolled Cryopreserved Buffy Coat, Viable
BUG	Bulbourethral Glands
CAN	Candida
CCC	Cryopreserved Cells from a Culture, Viable
CD4	CD4 Positive T-Cells
CD8	CD8 cells
CDE	Caudate
CDN	Copy DNA
CDP	Dry Pellet from a Culture, Non Viable
CEL	PBMC Cells, Viable
CEN	Fresh Cells from a Non-Blood Spec. Type
CER	Cervix
CGN	Cells in GITC
CIO	Cells in Other (Solution), Non-Viable
CLI	Cell Lines
CLL	Colon (left)
CLN	Cryopreserved primary cells from Non-Blood Spec Type, Viable
CLR	Colon (right)
CLS	Sigmoid Colon
CMV	CytoMegalovirus Isolate
CRB	Cerebellum
CRY	Generic Cryptococcus
CSF	Cerebro-Spinal Fluid
CSR	Serum - Chilled
CTB	Cytobrush

<b>Code</b>	<b>Description</b>
CTC	Cells from a CTL Assay
CTS	Supernatant generated from a CTL Assay
CUP	Cup
CVL	Cervical Vaginal Lavage
CVS	CVL Supernatant
CXS	Cervical Swab
DBE	Dried Blood Extract
DBS	Dried Blood Spot
DDM	Duodenum
DPE	Plasma, Dried Extract
DPL	Plasma, Dried
DPS	Dried Plasma Spot
DSP	Digested Sputum
DUR	Dried Urine
DWB	Dried Whole Blood
ED4	Effector Memory CD4 T-cells
END	Endometrial Tissue
EPI	Epididymus
EPP	Endodontic Paper Point
ESO	Esophagus
EYE	Eye
FCM	Frontal Cortex (motor)
FCP	Frontal Cortex (pre-motor)
FGN	Finger Nails
FHR	Hair, Facial
FLD	Fluid Portion from a Non-Blood Specimen Type
FLS	Flocked Swab
FLT	Fallopian Tubes
FPL	Plasma, Filtered
FSI	Penis Foreskin, Inner Tissue
FSO	Penis Foreskin, Outer Tissue
FSR	Rectal Biopsy by Flexible Sigmoidoscopy
FTP	Filter Paper
GLS	Glycerol Stock
GMI	Gastro Intestinal Mucosa

<b>Code</b>	<b>Description</b>
GRN	Granulocytes
HAR	Hair
HPC	Hippocampus
HRT	Heart
ICK	Supernatant generated from Inducible Cytokines
ILM	Ileum
IPK	Methanol Extract Supernatant
IPT	Immunophenotyping
IVR	Intra vaginal Ring
IVS	Intraventricular Septum
JJM	Jejunum
KDY	Kidney
LAT	Left Atrium
LAV	Lavage
LDB	Leukodepleted blood
LIV	Liver Tissue
LNA	Lymph Node (aortic)
LNC	Lymph Node (cervical)
LNE	Pre-auricular Lymph Node
LNF	Infraclavicular Lymph Node
LNG	Lung
LNI	Inguinal Lymph Node
LNK	Popliteal Lymph Node
LNM	Lymph Node (mediastinal)
LNO	Lymph Node (other)
LNP	Lymph Node (per-hilar)
LNR	Para-aortic Lymph Node
LNS	Supraclavicular Lymph Node
LNT	Mesenteric Lymph Node
LNX	Lymph Node (axillary)
LPD	Lipid Layer
LPK	Leukopak
LVE	Left Ventricle
LYM	Lymph Node Biopsy/Aspirate
LYS	Lysed whole blood

<b>Code</b>	<b>Description</b>
MBR	Midbrain Consists of Cerebral Penduncles and Tectum
MCL	Macrophage Cells - Viable
MCS	Microbiology Culture Slant
MD4	Central Memory CD4 T-cells
MDC	Myeloid Dendritic Cells
MEC	Meconium
MED	Medulla
MNO	Monocytes
MPE	Macrophage Dried Cell Pellet, Non Viable
MTB	MTB Isolates
MUC	Mucins
MUS	Mucous
N/A	Not Applicable - Same as Primary Specimen Type
NA4	Non-activated CD4
NA8	Non-activated CD8
NCL	Neutrophil (PMN) - Viable cells
ND4	Naive CD4 T-cells
NKC	Natural Killer Cells
NON	None
NPE	Neutrophil (PMN) Dried Cell Pellet, Non Viable
NPW	Nasopharyngeal Wash
NTM	Nontuberculous mycobacteria
NXD	Non-extracted DNA
OCC	Occipital Cortex
OHR	Occipital scalp hair
OPC	Ova & Parasite Concentrate
OTH	Other
OVR	Ovaries
PAD	Adipose (pericardial)
PCC	Culture Supernatant and Cells
PCF	Pericardial Fluid
PCT	Parietal Cortex
PDC	Plasmacytoid Dendritic Cells
PED	Dried Pellet - Digene
PEL	Non-viable PBMC s



<b>Code</b>	<b>Description</b>
PEN	Non-viable cells from non-blood specimen type
PEO	Wet Pellet Prep - Organon Teknika
PER	Dried Pellet - Roche
PFR	Parotid Flow
PHR	Hair, Pubic
PL*	Plasma, All
PL1	Plasma, Single-Spun
PL2	Plasma, Double-Spun
PLA	Plasma, Unspecified/Other
PLC	Placental Tissue
PLH	Plasma High Spin
PLM	Placenta - Membrane Slice
PLP	Supernatant & Cells from a Quantitative Culture
PLQ	Plaque
PLT	Placenta - Placenta Slice
PMD	Plasmids
PMN	polymorphnuclear leukocytes
PON	Pons
PNC	Pancreas
PPK	Plasmapak
PPS	Periopaper Strip
PRO	Prostate
PTF	Peritoneal Fluid
PTY	Parathyroid
RAT	Right Atrium
RBC	Red Blood Cells
RCT	Rectum
RD4	Resting CD4 T-cells
REC	Rectal
RVE	Right Ventricle
SAL	Saliva
SCC	Spinal Cord Cervical
SCL	Spinal Cord Lumbosacral
SCP	Scraping
SCT	Spinal Cord Thoracic

<b>Code</b>	<b>Description</b>
SDI	Supernatant Dermis, Inner
SDO	Supernatant Dermis, Outer
SEC	Secretions
SEI	Supernatant Epidermis, Inner
SEM	Semen
SEO	Supernatant Epidermis, Outer
SER	Serum
SHR	Hair, Scalp
SKN	Skin
SLD	Slide from a primary sample
SMD	Skeletal Muscle (distal)
SMP	Skeletal Muscle (proximal)
SMR	Smear
SMV	Seminal Vesicle
SNO	SNO - Strip
SPG	Sponge
SPI	Unfractionated Sputum, Induced
SPL	Spleen
SPQ	Supernatant from a Quantitative Culture
SPT	Unfractionated Sputum
SRH	Serum - High Speed Spun
STK	Quantitative Culture Held beyond 14 Days
STL	Stool
STM	Stomach
STP	Sterile Tooth Pick
SUP	Culture Supernatant
SVG	salivary glands
SWB	Swab
SWS	Stimulated Whole Saliva
TBD	Specimen type to be defined
TCX	Temporal Cortex
TD4	Transitional Memory CD4 T-cells
TFS	Tear-Flo Strips
THL	Thalamus
THW	Throat Wash

<b>Code</b>	<b>Description</b>
THY	Thymus
TIS	Tissue
TNA	Toe Nails
TON	Tonsillar Biopsy/Aspirate
TR4	T regs CD4+
TRC	Trucount
TRN	Transverse
TST	Testes
TTH	Tooth
TUM	Tumor
TYD	Thyroid
UMB	Placenta - Cord Slice
UNK	Unknown Derivative
URN	Urine
UTS	Uterus
UWS	Unstimulated Whole Saliva
VAG	Vaginal
VCP	Vaginal Cup
VGN	Vagina
VTM	Viral Transport Media
W/D	Wet/Dry
WBP	Whole Blood Pellet, Specify Methodology
WEK	Wick/Wek Cell Sponge
WFC	Unstimulated whole blood cell, lysed , fixed, frozen (with DMSO) for flow
WFS	Stimulated whole blood cells, lysed, fixed, frozen (with DMSO) for flow
WPK	Whole Blood Packed
XDA	Extracted DNA
XFL	Extracted Fluid from RNA RT PCR for Sequencing
XPA	Extracted RNA
XPD	Extracted Pellet from DNA PCR for Sequencing
XPR	Extracted Pellet from RNA RT PCR for Sequencing
XTN	Extracted total nucleic acid

### **Sub additive/derivative codes**

This section lists the sub additive/derivative codes available in LDMS.

<b>Code</b>	<b>Description</b>
01C	1 o'clock biopsy position
02C	2 o'clock biopsy position
03C	3 o'clock biopsy position
04C	4 o'clock biopsy position
05C	5 o'clock biopsy position
06C	6 o'clock biopsy position
07C	7 o'clock biopsy position
08C	8 o'clock biopsy position
09C	9 o'clock biopsy position
10C	10 o'clock biopsy position
11C	11 o'clock biopsy position
12C	12 o'clock biopsy position
14D	Tooth #14 Distal Buccal
14M	Tooth #14 Mesial Buccal
19D	Tooth #19 Distal Buccal
19M	Tooth #19 Mesial Buccal
24M	Tooth #24 Mesial Buccal
25D	Tooth #25 Distal Buccal
30D	Tooth #30 Distal Buccal
30M	Tooth #30Mesial Buccal
3DB	Tooth #3 Distal Buccal
3MB	Tooth #3 Mesial Buccal
562	K562 Cell Line
8MB	Tooth #8 Mesial Buccal
9DB	Tooth #9 Distal Buccal
ACD	Acid Citrate Dextrose
ADA	Adenosine Deaminase
ADJ	Adjuvant
AEB	Qiagen AE Buffer
AFS	Alsever's Freezing Solution
AG1	ESAT 6-free cocktail 1
AG2	ESAT 6-free Cherry pick
AMB	Amber Vial
ANT	Antigen
APR	Aprotinin

<b>Code</b>	<b>Description</b>
ASC	Ascorbate (Vit C)
ATC	Animal Tumor Cell Line
ATG	TB Antigen
AUO	Auramine O
AVE	Qiagen Buffer AVE
BCG	Bacille Calmette-Guiz 1/2rin
BCL	B-cell Lymphoblastoid Cell Line
BFM	Bacterial Freezing Media
BHT	Butylated hydroxytoluene
BLK	Tissue Block
BML	Breast - Left
BMR	Breast - Right
BSA	Bovine Serum Albumin
BSS	Blood Stabilizing Solution
BTM	Biopsy Transfer Media
CAN	Candida (CASTA)
CBS	Cellbanker Solution
CCM	CareHPV Collection Medium
CD4	CD4 cells
CD8	CD8 cells
CDN	cDNA
CFM	Cell Freezing Media
CME	Culture Media
CMV	CytoMegalovirus
CON	Control
CSC	Cervical secretions
CSP	Cytospin Slides
CVA	Complete Vaccine
CYT	Cytokines
DCF	2 - deoxycoformycin.
DEA	DEACTIVATED
DMS	DMSO used in cryopreservation solution (CPS)
DOD	Day of Donation
DOT	Day of Tail
DPH	Wyeth Ayerst Diphtheria Antigen

<b>Code</b>	<b>Description</b>
DPL	Depleted Cell Populations
DTM	Digene/Qiagen Specimen Transport Medium
DTT	Dithiothreitol
EDT	EDTA
ETH	Ethanol
FBS	Fetal Bovine Serum
FMA	Formic Acid
FMD	Formaldehyde
FOR	Formalin
FPR	Filter Paper
FRS	First Spin
FRZ	Frozen
FUN	Fungal Broth
GAG	HIV GAG envelope peptide
GIT	Guanidine Isothiocyanate (GITC)
GLM	Glycerol Media
GLT	Glutaraldehyde
GLY	20% Glycerol
GMS	Giemsa Staining
GRS	Gram Stain
H&E	Hematoxylin and Eosin stain
H2O	Water
HBS	Hank's Balanced Salt Solution
HCl	Hydrochloric Acid
HPA	Hep A
HPS	Human Pappilloma Virus Serology
HPV	Human Pappilloma Virus
HTC	Human Tumor Cell Line
I18	IL-18
I1b	IL-1b
IAP	Iodoacetic Acid/Phenanthroline
IgG	Immunoglobulin G
IL2	IL-2, Interleukin 2
IL6	Interleukin6
ILA	IL-12/IL-15, Interleukin-12/Interleukin-15

<b>Code</b>	<b>Description</b>
INK	India Ink
IPD	PBMCs for Intact Proviral DNA testing
LAA	L-ascorbic Acid
LES	Lesion
LFT	Left
LPS	Lipopolysaccharide
LSM	Lymphocyte Separation Media
LVT	L-var Target
LYB	Lysis Buffer
M2V	M2VP
MA1	MAC 101
MAC	MAC Antigen
MAF	MAC LR114F Culture Filtrate
MAS	M. Avium Sensitin
MCH	Mechanical Homogenization
MDB	Middlebrook broth
MET	Methanol
MFS	Malaria Freezing Solution
MIF	Merthiolate Formalin/Merthiolate-Iodine Formalin (MF/MIF)
MIT	Quantiferon Gold and/or Quantiferon Gold Plus Mitogen tube
MPP	For a mega peptide pool
MRN	Messenger RNA
MT2	MT2 Cell Line
MTV	For an MTB vaccine
MUC	Mucins
N/A	Not Applicable
NAS	Nucleic Acid Stabilization Solution
NAT	Sodium thioglycolate
NCL	N-acetyl-L-cysteine
NDN	NDVNS1, Newcastle disease virus with NS1 influenza protein
NDV	NDVB1, Newcastle disease virus wild type
NDW	Newcastle disease virus with W influenza protein
NIL	Quantiferon Gold and/or Quantiferon Gold Plus Nil tube
NKC	Natural Killer cells
NOH	Sodium Hydroxide

<b>Code</b>	<b>Description</b>
NON	None
NPI	Neuropepsidase Inhibitor
NSK	New Skin Lesion
NSL	Normal Saline
NUC	Nucleotides
OCT	Optimum Cutting Temperature Medium
OKT	OKT3 Treated
ORI	Oricol
OTH	Other
P24	P24
PAE	Pseudomonas aeruginosa
PAR	Parrafin
PBS	Phosphate Buffered Saline
PCS	PreserveCytSolution
PEI	Pre-Infusion
PFM	Paraformaldehyde
PHA	PHA-Treated
PI1	S8820 Sigma SIGMAFAST Protease Inhibitor Tablets
PIC	Protease Inhibitor Cocktail
PLC	Placenta Tissue
PLD	Plasma, Depleted
PLM	Placenta Membrane
PMI	Phorbol Myristate Acetate-Ionomycin
PPA	Phosphoric Acid
PRS	Protamine Sulfate
PTI	Post-Infusion
PTK	Proteinase-K
PTY	Parathyroid
PVA	Polyvinyl alcohol
PWM	Pokeweed Mitogen
QAG	QFT-TB Ag Red Cap
QMT	QFT-Mitogen Purple Cap
QNL	QFT-Nil Grey Cap
QTG	QFT-TB1 Ag Green Cap
QTY	QFT-TB2 Ag Yellow Cap



<b>Code</b>	<b>Description</b>
RDS	RNA/DNA shield
RFW	RNAse free water
RGT	Right
RLT	Buffer RLT Plus
RNL	RNAlater
RNP	RNA Protect
RPM	RPMI 1640 Medium
RTB	Reverse Transcriptase buffer
S52	Sendai 52 virus with defective infectious particules
SAU	Staph aureus
SBC	Sodium Bicarbonate
SCB	Sodium Carbonate
SDS	Second Spin
SEB	Sigma Staphylococcus Enterotoxin B
SLD	Slide from a primary sample
SNP	Snap/Flash Freeze
SPG	Sponge
SPN	Streptococcus pneumoniae
SPS	SMART TUBE INC Proteomic Stabilizer
STG	Skim milk-Tryptone-Glucose-Glycerin Medium (STGG)
STM	Stimulated by Multiple Antigens
SUB	Sub Gingival Plaque
SUG	Supragingival Plaque
SUP	Cultural Supernatant
TB4	Quantiferon Gold and/or Quantiferon Gold Plus CD4 tube
TB8	Quantiferon Gold Plus (only) CD8 tube
TBD	Specimen type to be defined
TBS	Tris-Buffered Saline
TCA	1% Thimersol/ 6.6% EACA (Epsilon Amino Caproic Acid)
TCL	T-cell Lymphoblastoid Cell Line
TCM	Trichrome stain
TEB	Tris-EDTA Buffer
TEM	Tempus Tube
TFM	Tissue Freezing Medium
TMD	Myeloid dendritic cell non infected and treated with TSST

<b>Code</b>	<b>Description</b>
TMS	Transport Medium-Stuarts
TND	Myeloid dendritic cell infected with NDVW and treated with TSST
TNN	TSST with NDVNS1
TNV	TSST with NDVB1
TOC	Tocopherol (Vit E)
TPB	Trypan Blue
TRI	TriReagent
TRX	Triton X
TRZ	Trizol
TSC	Myeloid dendritic cell infect w/ Sendai Cantell & treat w/ TSST
TSS	TSST, Toxic-Shock Syndrome Toxin
TTX	Tetanus Toxoid treated
UCT	Urine cartridge
ULQ	Upper Left Quadrant
UMB	Placenta cord slice
UNK	Unknown Sub A/D
UNT	Untreated / Unstimulated
URE	Urea
URQ	Upper Right Quadrant
VCS	Cervicovaginal Secretions
VIB	Veal Infusion Broth
VIR	Virus
VPS	VP Stimulator
VPT	VP Target
VTM	Viral Transport Media
ZLN	Ziehl Neelsen

## Condition codes

This section lists the specimen condition codes available in LDMS.

<b>Code</b>	<b>Description</b>
ANM	Sample Anonymized
ANP	Aliquot not prepared
BKV	Broken or cracked vial
BLD	Bloody
CDT	Consumed During Testing

<b>Code</b>	<b>Description</b>
CLT	Clotted
CMB	Combined Aliquots
COC	Combination of Conditions (Explain)
CTM	Contaminated
DCF	Data Clarification Form
DCG	Discharge present
DFB	Difficult Bleed
DIM	Dry Ice Melted
DMG	Damaged container
DSH	Delayed Shipment
DSR	Destroyed
EQF	Equipment Failure
EXP	Expired
FRO	Frozen
HEM	Hemolyzed
HUM	Exposed to high humidity
ICT	Icteric (Excess Bilirubin)
INT	Incorrect Tube
INV	Invalid Specimen
LBE	Lab Error
LIP	Lipemic
LKD	Leaked
LLT	Local Lab Testing
LSH	Lost Shipment
LYS	Lysed
NOT	No Test Performed
NQA	RT QA for viability and recovery NOT done due to low volume
NST	Did Not Consent to Storage
OPR	Sample drawn outside protocol requirements
OSW	Specimen drawn outside of protocol-defined visit window
OTH	Other (Explain)
PST	Processed after Specified Time
QNS	Quantity Not Sufficient
REF	Refrigerated
RLB	Re-labeled

Code	Description
SAT	Satisfactory
SHV	Short volume
SNC	Sample not collected
SNP	Specimen not processed
SNR	Sample Not Received,CRF Received
TNO	Shipping/storage temperature not optimal/warmed
TRM	Testing Remnant
TWD	Thawed
UNK	Unknown condition
VPL	Viability percent may be less than the expected parameter
VRU	Viable recovery may be outside expected parameters (higher or lower)
YST	Did Consent to Storage

## Unit codes

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Unit codes, such as visits, measurements, and time units.

## Measurement codes

This section lists the measurement codes available for specimen units available in LDMS.

Code	Description
CEL	CEL Cells
CM	CM Centimeters
CRD	Cards
CTN	CTN Container
EA	EA Each
GR	GR Grams
MG	MG Milligrams
ML	ML Milliliters
MM	MM Millimeter
N/A	N/A Not Applicable
PG	PG Picograms
pg/10 <sup>6</sup> cells	picogram per 10 <sup>6</sup> cells
UG	UG Micrograms
UL	UL Microliters
UNK	UNK Unknown Units

## Time unit codes

This section lists the time unit codes available in LDMS.

Code	Description
Day	Day
Fst	Fasting
Hrs	Hours
Min	Minutes
Mo	Months
MRN	Morning
Nft	Non-Fasting
Pol	Pooled
Prd	Predialyzer
PRI	Pre-Infusion
Pre	Pre-Dose
Psd	Postdialyzer
Pst	Post-Fasting
PTC	Post-Challenge
PTI	Post-Infusion
PTV	Post-Vaccination
Ran	Random
RPD	Random Post-Dose
Sec	Seconds
SRL	Serial
Tr	Trough
UNK	Unknown time unit

## Visit codes

This section lists the visit unit codes available in LDMS.

Code	Description
-2	-2
A	A
Aut	Autopsy
B	B
B/L	Baseline
Bth	Birth
Cb	Cord Blood
CFM	Post Study Confirmation Test

<b>Code</b>	<b>Description</b>
CFU	Core Follow Up
Ch	Challenge
CRW	Crosswalk
DAV	Dose Adjustment Visit
Day	Days
DEL	Delivery
DVL	DBS Viral Load
EDV	Event Driven Visit
EID	Early Infant Diagnosis
EIT	End of Intensive Treatment
Ent	Entry/Baseline
EOR	End of Study & redraw
Eos	End-Of-Study
EOT	End of Treatment
EOX	Evaluation of Seroreactivity and Recent Exposure
EPH	Extension Phase
EWD	Early Withdrawal
Exp	Recent Exposure
Ext	Exit/Discontinuation
FCF	Failure Confirmation
FUP	Follow-up Test
Gel	On study without gel
Inf	Infected Participant Testing
IOT	Initiation of Treatment
LSF	Long-term Safety and Followup
L&D	Labor & Delivery
Mo	Months
NDL	New Delivery
NON	Not Pregnant
NPG	New Pregnancy
OFP	Off PrEP
OMB	Oral MB
ONP	On PrEP
PDT	Product Discontinuation
PE	Pre-entry

<b>Code</b>	<b>Description</b>
PFT	PFT
PK	PK
POR	Post study & redraw
Pos	Post-Study
POX	Post study & possible recent exposure
PPT	Post Partum
Prf	Proficiency
PRG	Pregnancy
Pri	Pre-Infusion
Pst	Post-Infusion
PTD	Premature Treatment Discontinuation
PVL	Plasma Viral Load
Qul	Qualification
Rdw	Redraw
RRV	Retrospective
RWK	R+ Week
SC	Seroconversion
SCK	Sick
Scr	Screening
SD	Study Day
SHR	Short
SP	Sero Positive
Sps	Special Studies
SRV	Post Study Service Test
TRI	Trimester
UnK	Unknown
Uns	Unscheduled
V	V
Vst	Visit
Wk	Weeks
Yr	Years

## **Assay Codes**

Codes used for assays, such as system and user censors.

## Reasons for not running an assay censor codes

This section lists the censor codes that can be used on an assigned test when the test will not be performed.

Code	Description	Numeric Value
COR	COR Controls Out of Range	10431
CTM	Contaminated	10430
EQF	Equipment Failure	10432
LBA	Laboratory Accident	10434
LBE	Lab Error	10433
MSW	Missing Well	10435
NPA	Sample Drawn Without Participant Adherence to Regimen	10440
OUT	Resulted outside LDMS	10439
PSW	Sample not Drawn Within Protocol Specified Window	10441
QNS	Quantity Not Sufficient	10436
STO	Specimen too old to run on test	10442
WCT	Wrong Controls	10437

## Immunology assay codes

Codes for immunology assays.

### Reasons why results were not obtained for immunology assays

This section lists the censor codes that can be applied to immunology assays tests when a result was not obtained.

Code	Description	Numeric Value
A	Wrong Anticoagulant	65804
C	Contamination	65800
E	Tech Error/Lab Error	65801
K	Kit/Reagent Problem	65806
P	Results Reported Under A Different Protocol	65807
S	Quantity Not Sufficient	65802
U	Unsatisfactory Sample	65803
V	Poor Viability	65805

## Virology assay codes

Codes for virology assays.

### Virology user censor codes

This section lists the virology assay user censor codes available in LDMS.



Code	Description	Validity	Numeric Value
B1	BOOM extraction used	Valid	100
C	Control re-run and valid - assay is valid	Valid	1,000
D	Contamination	Invalid	10,000
E	Poor viability	Invalid	1,000,000
K	Kit/Reagent Problem	Invalid	1
O	Lab error/Lab accident	Invalid	100,000,000
P	Equipment failure	Invalid	0.1
Q	Kit QC out of range - repeat	Invalid	10
R	Re-detected	Valid	1,000,000,000,000
V	Over amplified	Invalid	10,000,000
W	Inhibitory/Material didn't amplify	Invalid	100,000
Z	Per lab - Do not use	Invalid	0.001

### Roche COBAS Ampliprep/COBAS TaqMan HIV-1 assay censor codes

This section lists the Roche COBAS Ampliprep/COBAS TaqMan HIV-1 assay censor codes available in LDMS.

Code	Description	Validity	Numeric Value
F	Invalid control	Invalid	1000000.000000
G	Result less than lower limit of quantification	Valid	0.000100
H	No Result	Invalid	10000000.000000
I	No QS wells in range	Invalid	100000.000000
J	Undetectable	Valid	1.000000
X4	Results greater than upper limit of quantification	Valid, but needs repeat	10000.000000

### COBAS TaqMan HCV assay censor codes

This section lists the COBAS TaqMan HCV assay system censor codes available in LDMS

Code	Description	Validity	Numeric Value
F	Invalid Control	Invalid	1000000
G	Result less than lower limit of quantification	Valid	0.0001
H	No Result	Invalid	10000000
I	QS Invalid	Invalid	100000
J	Undetectable	Valid	1
X4	Results greater than upper limit of quantification	Valid	10000

**COBAS TaqMan HIV-1 Qual assay censor codes**

This section lists the COBAS TaqMan HIV-1 Qual assay system censor codes available in LDMS.

Code	Description	Validity	Numeric Value
A	0 control not negative	Invalid	1
B	10 control not positive	Invalid	10
C	20 control not positive	Invalid	100
E	VQA blinded control fails validation	Invalid	10000
F	Assay locked	Na	100000
H	No result	Invalid	10000000000
K	Invalid control	Invalid	1000000
L	Low positive control out of range or invalid	Invalid	1E+14
N	Negative control out of range or invalid	Invalid	10000000
O	Run based validity override	Valid	1E+12
P	Insufficient VQA blinded controls assigned to rack	Invalid	1000000000
Q	Insufficient VQA controls assigned to rack	Invalid	1E+13
R	Re-read	Valid	100000000
S	5 control invalid	Invalid	1E+11

**Abbott Realtime HIV-1 and Abbott SARS-COV-2 Quant assay censor codes**

This section lists the Abbott Realtime HIV-1 and Abbott SARS-COV-2 assay censor codes available in LDMS.

Code	Description	Validity	Numeric Value
F	Invalid Control	Invalid	1000000.000000
G	Detected - Result less than lower limit of quantification	Valid	0.000100
H	No Result	Invalid	10000000.000000
J	Undetectable	Valid	1.000000
X4	Results greater than upper limit of quantification	Valid, but needs repeat	10000.000000

**Pharmacology assay codes**

Codes for pharmacology assays.

**Pharmacology analyte codes**

This section lists the codes for pharmacology (PK) drug analyte codes available in LDMS.

Code	Description
3TC	Lamivudine

<b>Code</b>	<b>Description</b>
3TCDP	3TC diphosphate
3TCDP-PC	3TC diphosphate choline
3TCDP-PE	3TC diphosphate ethanolamine
3TCMP	3TC monophosphate
3TCTP	3TC triphosphate
4B-OHC	4 $\beta$ -hydroxycholesterol
6BHC	6 Beta Hydroxycortisol
7-COOH-CBD	7-Carboxoy Cannabidiol
7-OH-CBD	7-Hydroxy-Cannabidiol
10-1074LS	10-1074LS
AAG	Alpha-1 Acid Glycoprotein
ABC	Abacavir
ABC-CARB	Abacavir carboxylate
ABC-GLU	Abacavir glucuronide
ABC-MP	Abacavir Monophosphate
ACL	Acetyl-Isoniazid
ADF	Adefovir
AL	Artemether-lumefantrine
ALB	Albumin
AML	Amlodipine
AMP/DXAMP	Amphetamine/Dextroamphetamine
APV	Amprenavir
ARM	Artemether
ASV	Asunaprevir
Atorvast	Atorvastatin
Atorvast-2OH	2-hydroxy Atorvastatin
Atorvast-4OH	4-hydroxy Atorvastatin
Atorvast-LAC2OH	2-hydroxy Atorvastatin Lactone
Atorvast-LAC4OH	4-hydroxy Atorvastatin Lactone
ATV	Atazanavir
AZM	Azithromycin
BCV	Beclabuvir
BDCQ	Bisdesethylchloroquine
BDQ	Bedaquiline
BDQ-M2	N-monodesmethyl metabolite of Bedaquiline

<b>Code</b>	<b>Description</b>
BICUF	Bictegravir Unbound
BLM	Bleomycin Sulfate
BMS-936559	BMS-936559
Boc3004	SCH783004
Boc3005	SCH783005
Boc3006	SCH783006
Boc3007	SCH783007
Boc4128	SCH534128
Boc4129	SCH534129
Boceprvr	Boceprevir
BZD	Benznidazole
CAB	Cabotegravir
CBD	Cannabidiol
CBV-MP	Carbovir Monophosphate
CBVTP	carbovir triphosphate
CEM-ADA	Cemiplimab ADA
CIT	Citalopram
CLF	Clofazimine
CLQ	Chloroquine
CMS	Colistin Methane Sulfonate
CMS - CoA	CoA metabolite of Colistin Methane Sulfonate
CMS - CoB	CoB metabolite of Colistin Methane Sulfonate
COBI	Cobicistat
COP1	Coproporphyrin 1
CORT	Cortisol
CPM	Capreomycin
CPM1A	Capreomycin Compound 1A
CPM1B	Capreomycin Compound 1B
CS	Cycloserine
CTH	Cethromycin
CVC	Cenicriviroc
D4T	Stavudine
d4TTP	d4T triphosphate
DCB	Daclatasvir
DCV	Daclatasvir

<b>Code</b>	<b>Description</b>
ddATP	dideoxyadenosine triphosphate
DDC	Zalcitabine
ddI	Didanosine
DES	Desogestrel
des RBT	des rifabutin
des RFP	des rifapentine
des RMP	des rifampicin
DEX	Dexamethasone
DHA	Dihydroartemisinin
DHCQ	Desethylhydroxychloroquine
DHPG	Ganciclovir
DLM	Delamanid
DLM-DM6705	DM6705
DLT	Diltiazem
DLT- AL	Desacetyldiltiazem metabolite of DLT
DLT- MT	Desmethyldiltiazem metabolite of DLT
DLV	Delavirdine
DMPA	Medroxyprogesterone Acetate
DOR	Doravirine
DOX	Doxorubicin (liposomal-encapsulated and free)
DOXOL	Doxorubicinol
DPV	Dapivirine
DRV	Darunavir
DSI	Desipramine
DSV	Dasabuvir (previously <small>ABT-333</small> )
DSV-m1	Dasabuvir m1
DTG	Dolutegravir
DXAMPS	Dextroamphetamine sulfate
DXM	Dextromethorphan
DXM-3HM	3-Hydroxy Morphinan
DXM - DXO	Dextrorphan metabolite of Dextromethorphan
DXMPH	Dexmethylphenidate
E7OH	7-Hydroxy Efavirenz
E8OH	8-hydroxy efavirenz
EBR>	Elbasvir

<b>Code</b>	<b>Description</b>
EE	Ethinyl Estradiol
EFV	Efavirenz
EMB	Ethambutol HCL
ENF	Enfuvirtide
ENG	Etonogestrel
ESCIT	Escitalopram
ET	Etoposide
ETR	Etravirine
EVG	Elvitegravir
FCZ	Fluconazole
FLX	Fluoxetine
FOS	Foscarnet
FTC	Emtricitabine
FTC-TP	Emtricitabine Tri-phosphate
GES	Gestodene
GS-441524	Remdesivir Metabolite
HCQ	Hydroxychloroquine
HDP-THV	Hexadecyloxypropyl Tenofovir
HU	Hydroxyurea
HYC	Hydrocodone
Ibalzb	Ibalizumab
IDV	Indinavir
INH	Isoniazid
IQP-0528	IQP-0528
ISO	Isotretinoin
ISO-4OXO	4-OXO-Isotretinoin Metabolite
ISO-ATRA	All-Trans Retinoic Acid
ITX 5061	ITX 5061
KAN	Kanamycin
KYN	Kynurenine
LDV	Lepipasvir
LEN	Lenacapavir
LF	Lumefantrine
LF-DBL	Desbutyl Lumefantrine
LPV	Lopinavir

<b>Code</b>	<b>Description</b>
LPVF	Free or unbound lopinavir concentrations
LVF	Levofloxacin
LY-CoV555	LY3819253
LZD	Linezolid
M3	N-didesmethyl metabolite of bedaquiline (TMC207)
M8	NFV Metabolite
METF	Metformin
Minocyclene/Placebo	Minocyclene/Placebo
MK-3475	MK-3475
MOR	Morphine
MPA	Mycophenolic Acid
MPAF	Free Mycophenolic Acid
MPAG	Mycophenolic Acid Metabolite
MPH	Methylphenidate
MTD	Methadone HCl
MTX	Methotrexate
MVC	Maraviroc
MXF	Moxifloxacin
N-803	N-803 IL-15 Superagonist
N-DLV	Delavirdine's Metabolite
NET	Norethisteron
NFV	Nelfinavir
NFX	Nifurtimox
NGM	Norgestimate
NHC	$\beta$ -D-N4-hydroxycytidine
NIM	Nimodipine
NVP	Nevirapine
OBV	Ombitasvir (previously ABT-267)
OFX	Ofloxacin
OXT	Oxytocin
OXY	Oxycodone
P4	Progesterone
PA	Pretomanid
PAS	aminosalicylic acid
PEG-IFN	Pegylated-Interferon alfa 2b

<b>Code</b>	<b>Description</b>
PF-332	PF-07321332
PGT121-414-LS	PGT121-414-LS
PLD	Pegylated Liposomal Doxorubicin
PMPA	(9 - [2 - (R) - (phosphonomethoxy)propyl] adenine)
PNU -101603	PNU -101603 metabolite of Sutezolid
PPX	Pramipexole
PTV	Paritaprevir (previously ABT-450)
PTX	Paclitaxel
PXT	Paroxetine
PZA	Pyrazinamide
PZQ	Praziquantel
PZQ-4OH	4-Hydroxy metabolite of Praziquante
R-AMPH	Dextro-amphetamine
RBT	rifabutin
RDV-GS704277	Remdesivir alanine metabolite
RDV-GS441524	Remdesivir
RFP	rifapentine
RGV	Raltegravir
RIS	Risperidone
RMD	Romidepsin
RMP	Rifampicin
RPV	Rilpivirine
RTV	Ritonavir
RUX	Ruxolitinib
RV	Ribavirin
RV-TP	Ribavirin Triphosphate
S-AMPH	Levo-amphetamine
SERT	Sertraline
SERT - DMS	Desmethylsertraline
SLGN	Selgantolimod
SOF	Sofosbuvir
SOF-GS-331007	GS-331007 metabolite of SOF
SOF-GS-566500	GS-566500 metabolite of SOF
SQ109	SQ109
SQV	Saquinavir



Code	Description
STZ	Sutezolid
TAF	Tenofovir Alafenamide Fumarate
TEC	Tecovirimat
TFV	Tenofovir
TFVDP	Tenofovir Diphosphate
THA	Thalidomide
THC	Delta9-tetrahydrocannabinol
TPV	Tipranavir
TRP	Tryptophan
VCR	Vincristine Sulfate
VCV	Vicriviroc
VEL	Velpatasvir
VRC01	VRC-HIVMAB060-00-AB
VRC01LS	VRC-HIVMAB080-00-AB
ZDV	Zidovudine
ZDVDP	Zidovudine diphosphate
ZDVMP	Zidovudine monophosphate
ZDVTP	Zidovudine triphosphate

**Pharmacology system censor codes**

This section lists the pharmacology (PK) system censor codes available in LDMS.

Code	Description	Validity	Numeric Value
A	Invalid. Greater than the upper limit, dilute and repeat	Invalid	16
B	Below quantifiable limit	Valid	8
F	Failed	Invalid	32
H	Unacceptable HQC	Invalid	64
I	Unacceptable HOQ	Invalid	512
L <sup>3</sup>	Lower limit adjusted up for this run	Valid	1
M	Unacceptable MQC	Invalid	128
Q	Unacceptable LQC/ LQC1/LQC2	Invalid	256
R <sup>4</sup>	Repeat (with L system censor only)	Invalid	4
U	Sample Diluted	Valid	1,000,000,000,000

<sup>3</sup> No longer available, Windows LDMS specific

<sup>4</sup> No longer available, Windows LDMS specific

**Pharmacology assay user censor codes**

This section lists the pharmacology assay user censor codes available in LDMS.

Code	Description	Validity	Numeric Value
A <sup>5</sup>	Greater than the upper limit, dilute and repeat	Invalid	
B	Below Quantifiable Limit or No Peak	Valid	2048
D	Drug not required to be assayed	Valid <sup>6</sup>	512
F <sup>7</sup>	Failed	Invalid	
N	Not Detected	Valid	8
O	QC out of range, dilute and repeat	Invalid	4
P	Not Able to Interpret Result	Invalid	8192
S <sup>8</sup>	Quantity not sufficient	Invalid	
X	Per lab, sample must be repeated	Invalid	1024
Z	No Result, Lab Issue	Invalid	4096

**Pharmacology concentration units**

These unit codes are used for PK specimen concentration values.

Code	Description
%	percentage
FMOL/10 <sup>6</sup> CELLS	femtomol per 10 <sup>6</sup> cells
FMOL/ML	femtomol per milliliter
FMOLE	femtomol
FMOLE/MG	FMOLE/MG
FMOLE/SAMPLE	FMOLE/SAMPLE
NG/MG	NG/MG
NG/ML	nanogram per milliliter
NG/SAMPLE	nanogram per sample
NMOL	nanomol
pg/injection	picograms per injection
pg/mL	picogram per milliliter
PMOL/10 <sup>6</sup> CELLS	picomol per 10 <sup>6</sup> cells
PMOLE	picomol
UG/ML	microgram per milliliter

<sup>5</sup> No longer available, Windows LDMS specific

<sup>6</sup> Results removed from final views

<sup>7</sup> No longer available, Windows LDMS specific

<sup>8</sup> No longer available, Windows LDMS specific

<b>Code</b>	<b>Description</b>
UMOL	micromol

# Index

## Special Characters

<> [163](#)

## Numerics

21 CFR Part 11 [11](#)

## A

account management [230](#)  
additional time [37](#), [53](#)  
additive type [37](#), [53](#)  
additives  
    color icons [68](#)  
Adobe Reader [13](#)  
aliquot specimen  
    adding [41](#)  
    assigning storage location [75](#)  
    sequence number in global specimen ID [35](#)  
ANM [62](#)  
ANP [52](#), [58](#)  
assay runs [170](#)  
assays [63](#)  
assigning tests to specimens [63](#)  
audit trail [173](#)  
availability [37](#), [41](#), [52](#), [84](#)  
available [25](#), [53](#)  
available volume [53](#)

## B

barcode [25](#), [163](#)  
barcode labels [161](#)  
barcode scanner [13](#)  
barcodes  
    scanning [162](#)  
BKV [59](#)  
browse [18](#), [20](#)  
browser tabs [16](#)  
bulk specimen modification [85](#)

## C

cascading changes [40](#), [41](#)  
CEL [43](#)  
changing participant information [29](#)  
Chrome [13](#)  
clinic [33](#), [53](#)  
CLT [61](#)

co-enrolled [41](#), [53](#)  
co-enrollment [31](#)  
co-enrollments [38](#)  
COC [62](#)  
code [20](#)  
coenrollment [25](#)  
comments [37](#), [41](#), [53](#), [85](#)  
compatibility with LDMS [36](#)  
Completed Test Run Report [174](#)  
conditions [52](#)  
container  
    adding [73](#)  
    moving [80](#)  
containers  
    removing [84](#)  
corrections [38](#), [85](#)  
creating shipments [89](#)  
cryopreservation [43](#)  
CTM [61](#)

## D

database [14](#)  
deleting tests [63](#)  
derivative type [41](#), [53](#)  
destroying a specimen [58](#)  
DIM [60](#)  
DMG [59](#)  
dot matrix labels [161](#)  
downloads [17](#)  
draw date [33](#), [38](#), [53](#)  
draw time [37](#), [53](#)  
DSH [60](#)  
DSR [52](#), [58](#), [62](#)

## E

Edit Participant button [29](#)  
empty structure [70](#)  
enrollment  
    adding [30](#)  
    modifying [31](#)  
    removing [31](#)  
Enrollments [29](#)  
EQF [58](#)  
Evince [13](#)  
excluded position [66](#), [70](#), [72](#)  
EXP [59](#)  
extended search [18](#), [20](#)

## F

filters  
    applying [18, 20](#)  
    removing [18, 20](#)  
Firefox [13](#)  
FISMA [11](#)  
FRO [60](#)  
frozen date [37, 41, 53](#)

## G

global specimen ID [35, 36, 53, 161, 162](#)

## H

harvest date [53](#)  
HEM [61](#)  
HUM [61](#)

## I

icons [68](#)  
ICT [61](#)  
ID1  
    validation [27](#)  
ID2 [30, 30, 33, 221](#)  
ID3 [53, 221](#)  
identifiers [35](#)  
import date [53](#)  
INT [59](#)  
internal-only comments [37, 41, 53, 85](#)  
Internet Explorer [13](#)  
INV [58](#)

## L

label size [161](#)  
labels [160, 161, 161, 163, 165, 166](#)  
laboratory ID [35](#)  
laser labels [161](#)  
LBE [58](#)  
LDMS [65, 78](#)  
LDMS User Support [230](#)  
level  
    creating [72](#)  
    moving [80](#)  
levels  
    removing [84](#)  
LibreOffice Calc [13](#)  
LIP [61](#)  
LKD [59](#)  
local time [37](#)  
log on [14](#)  
logic [117](#)

LSH [52, 60](#)  
LYS [61](#)

## M

manage enrollments [38](#)  
marked to ship [25](#)  
menu bar [17, 64](#)  
Microsoft Excel [13](#)

## N

navigation [25](#)  
NIST [11](#)  
not available [52](#)  
not performed [63](#)

## O

Opera (web browser) [13](#)  
OPR [58](#)  
original volume [53](#)  
OSW [58](#)  
OTH [62](#)  
other specimen ID [35, 37, 53](#)

## P

paper size [161](#)  
participant  
    adding more than one [26](#)  
    creating [27, 27](#)  
    modifying [29](#)  
    multiple projects [27](#)  
    OPID [27](#)  
    project [27](#)  
    search for [25](#)  
    view different [25](#)  
participant identifier [29](#)  
Participant Report (test results) [174](#)  
password [230](#)  
passwords [230, 230](#)  
PBMC [43](#)  
PDF files [17](#)  
PDF viewer [13](#)  
pending shipment [25](#)  
Pending Test Results Report [174](#)  
permissions [230](#)  
positioning (in storage) [70, 72, 73](#)  
positions only [66](#)  
primary specimen  
    assigning storage location [75](#)  
    co-enrolling [38](#)  
    entering new [37](#)  
    modifying [40](#)

- move to different visit [31](#)
- moving between enrollments [38](#)
- sequence number in global specimen ID [35](#)
- primary type [37, 53](#)
- processing date [37, 53](#)
- processing information [41](#)
- processing tech initials [37, 53](#)
- project
  - validation rules [27](#)
- projects
  - creating [105, 221](#)
  - modifying [224](#)
  - removing [224](#)
  - shipping [105](#)
- protocol [30, 30, 31](#)
- PST [58](#)

## Q

- QA/QC [105, 107](#)
- QA/QC status [105](#)
- QNS [52, 61](#)
- quality control [172](#)

## R

- reason sample not collected [41](#)
- reason specimen not collected [53, 58](#)
- received date [37, 53](#)
- REF [60](#)
- removing tests [63](#)
- reports [17, 117](#)
- resolution [13](#)
- reviewing run results [172](#)
- run statuses [170](#)
- running assays [170](#)
- running tests [63](#)

## S

- Safari [13](#)
- sample condition [37](#)
- SAT [62](#)
- search [18, 20](#)
- searching [25](#)
- setting up assay runs [170](#)
- Shipment History page [110](#)
- shipment workflow [105](#)
- shipments
  - checking for issues [105](#)
  - creating [89](#)
  - marked to ship icon [68](#)
  - pending icon [68](#)
  - projects [105](#)

- receiving [105, 105](#)
- sending [105](#)
- unship [110](#)
- shipped [25, 53](#)
- shipping
  - QA/QC [107](#)
  - receiving [103](#)
- shipping file
  - modifying after sending [110](#)
  - re-downloading [110](#)
- shipping files [17](#)
- SHV [61](#)
- sign in [14](#)
- sign out [17](#)
- SNC [52, 61](#)
- SNP [52, 61](#)
- SNR [60](#)
- specimen
  - assigning storage location [75](#)
  - store [80](#)
- specimen condition [37, 41, 53, 58, 59, 60, 60, 61, 61, 62, 85](#)
- specimen entry [26](#)
- specimen ID [35, 36, 53](#)
- specimen management [18, 20, 23, 37](#)
- Specimen Management [25](#)
- spreadsheet viewer [13](#)
- status indicators [25](#)
- storage [18, 20, 64, 65, 66, 72, 73, 78, 78, 80, 80, 83, 85](#)
- storage hierarchy [65](#)
- storage items
  - icons [68](#)
  - removing [84](#)
- Storage Move Report [83](#)
- storage position [66](#)
- storage tree [65, 70](#)
- storage unit
  - creating [70](#)
  - moving [80](#)
- storage units
  - removing [84](#)
- stored [25, 53](#)
- stored specimens page [64](#)
- studies [30](#)
- sub add/der type [41](#)
- sub-additive/derivative [53](#)
- system requirements [13](#)

## T

- tabs [16](#)
- templates (for storage items) [64, 78, 78, 80](#)
- templates (in storage) [70, 72](#)
- Test Results [168](#)

Test Results Filters Window [169](#)

tests

- assigning [63](#)
- creating runs [170](#)
- history [173](#)
- not performed [63](#)
- remove [63](#)
- reports [174](#)
- reviewing [172](#)
- statuses [170](#)

thaw count [37](#), [41](#), [53](#)

TNO [60](#)

total cell count [37](#), [53](#)

TWD [60](#)

## U

UNK [62](#)

unshipping shipments [110](#)

user interface [17](#)

users

- changing [16](#)
- creating [230](#)
- manage permissions [230](#)
- reset password [230](#)

## V

visit

- adding [33](#)

visit value [53](#)

volume [37](#)

## W

web browser [13](#), [16](#), [17](#)

workflow [26](#)