

# LabChip® GX Reviewer

## User Manual

## Preface

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### Contact Us

If you have a question about the LabChip GX Reviewer software that is not answered in this manual or online Help, or if you need assistance with this product, contact the PerkinElmer Technical Support Center:

Phone: (US Toll Free): **800-762-4000**  
(Worldwide): **+1 203-925-4602**

Fax: **+1 203-944-4904**

Email: [global.techsupport@perkinelmer.com](mailto:global.techsupport@perkinelmer.com)

Internet: [www.perkinelmer.com](http://www.perkinelmer.com)

For support outside the United States, contact your local PerkinElmer representative.

Before you call, you should have the following information available for the technical representative:

- Product serial number
- Software version (found by choosing About from the main Help menu)
- If applicable, the *error number* shown in the software or in the log file.

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## FCC

This device complies with part 15 of the FCC (United States Federal Communications Commission) Rules. Operation is subject to the following two conditions:

- This device may not cause harmful interference, and
- This device must accept any interference received, including interference that may cause undesired operation.

## CE

This device complies with all CE rules and requirements.

### NOTE



*Changes or modifications to this equipment not expressly approved by the party responsible for compliance could void the user's authority to operate the equipment.*

### REMARQUE



*Tout changement ou modification apporté à cet instrument non expressément approuvé par l'entité responsable de la conformité peut annuler l'autorisation d'opérer l'appareil accordée à l'utilisateur.*

## Table of Symbols

**Table 1** contains symbols that identify particularly important information and alert you to the presence of hazards. These symbols may appear in this manual and/or on the product it describes.

**Table 1. Important Symbols**

Symbol Symbole	Description Description
	<b>DANGER:</b> An imminently hazardous situation, which, if not avoided, will result in death or serious injury. <b>DANGER:</b> Situation présentant un danger imminent qui, s'il n'est pas éliminé, peut entraîner des blessures graves, voire la mort.
	<b>WARNING:</b> Caution, risk of danger. Refer to the user documentation. <b>AVERTISSEMENT:</b> Attention, danger potentiel. Se reporter à la documentation de l'utilisateur.
	<b>NOTE:</b> A cautionary statement; an operating tip or maintenance suggestion; may result in instrument damage if not followed. <b>REMARQUE:</b> Énoncé indiquant une précaution à prendre, un conseil de fonctionnement ou une suggestion d'entretien; son non-respect peut provoquer des dommages à l'instrument.
	CE compliance mark. Marque de conformité CE.
	Helpful hints, additional information Conseils utiles, informations supplémentaires

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# Introduction

This manual includes instructions for using the LabChip GX Reviewer software. It includes procedures for analyzing data from LabChip GX/GXII and GX Touch/GXII Touch instruments, using the optional LabChip GxP software to comply with 21 CFR Part 11 requirements, and software troubleshooting.

DNA, gDNA, RNA, Protein, Glycan, and Protein Charge Variant (CZE) Chip and Reagent Kits are available to run specific assays on the LabChip GX or GX Touch instruments. The Assay Kits include the reagents and consumables required to run the specific assay. Protein, Glycan, and Protein Charge Variant assays are only supported on LabChip GXII or GXII Touch instruments.

## Assay User Guides

Assay User Guides provide information about the assay. Instructions for preparing the chip, the plate, the ladder vial, and the buffer vial are included in the *LabChip GX Touch/GXII Touch Assay User Guide* you are running. Detailed information about the assays, including Specifications, Safety Warnings, Preparation Procedures, Expected Results, Troubleshooting, LabChip Kit Essential Practices, and Reordering Information is also located in the *LabChip GX Touch/GXII Touch Assay User Guide* for the specific assay that you are running.

The current version of the Assay User Guides can be accessed on the PerkinElmer web site at:

[www.perkinelmer.com](http://www.perkinelmer.com).

## Assay Quick Guides

Assay Quick Guides are included with each Assay Kit and include instructions for preparing the chip to run an assay.

The current version of the Assay Quick Guides can be accessed on the PerkinElmer web site at:

[www.perkinelmer.com](http://www.perkinelmer.com).

## Principles of Operation

The LabChip GX/GX Touch assays are based on traditional gel electrophoresis principles that have been transferred to a chip format. The chip format dramatically reduces separation time and provides automated sizing and quantitation information in a digital format.

The LabChip Reviewer software is used to analyze data generated by LabChip GX and GX Touch instruments. The LabChip Reviewer software should be installed on the computer that will be used to analyze the data. Note that the LabChip GX Reviewer software must be able to access the location where the LabChip GX or GX Touch data files are stored.

The LabChip GX Reviewer software can be set up to access the data files directly on the instrument, or can access copies of the data files that are copied to a network location.

If the LabChip GxP option is installed, the data files are stored in a secure folder that can only be accessed by the GX instruments, GX Touch instruments, and the LabChip GX Reviewer software. The folder can be located on the GX Touch instrument, on the GX Reviewer computer, or on a network server.

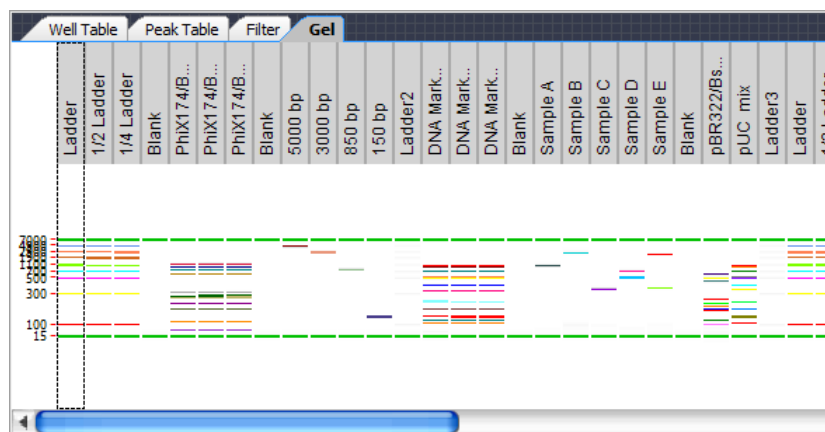
The LabChip GX Reviewer software plots fluorescence intensity versus time and produces electropherograms for each sample (see [Figure 1](#)).



Figure 1. Electropherogram

## Principles of Operation (Continued)

The data can be viewed in a gel-like format on the Gel Tab to achieve the appearance of a slab gel. (The colors of the gel can be changed.)



**Figure 2. Gel View**

For DNA, RNA, Protein, and Glycan assays, quantitating the concentration and accurately sizing each fragment are achieved by comparing against a sizing ladder and running internal standards or “markers” with each sample. Internal standards of known concentration are mixed with the sample to aid in quantitation.

The amount of sample sipped into the chip depends on pH, salt concentration, and buffer additives. The internal standards normalize these factors so that the software can use the ratio of the area of the curve of the standard to the unknown peak to determine concentration directly. The internal standards lie slightly outside the assay range so they do not interfere with analysis.

Capillary Zone Electrophoresis (CZE) is an electrophoretic separation technique used to evaluate the charge heterogeneity of proteins in a sample. For Protein Charge Variant assays, analytes are separated based on their net charges, with molecules with a higher net charge migrating faster than those with a lower net charge. The data is analyzed to calculate the % Relative Amount of the peaks.

## Operation

This section includes general instructions for using the LabChip GX Reviewer software.

This section contains the following information:

- [Setting Up the LabChip GX Reviewer Software](#)
- [Opening the LabChip GX Reviewer Software](#)
- [Saving Workspace Files](#)

## Setting Up the LabChip GX Reviewer Software

If the LabChip GxP option is installed, the LabChip GX Reviewer software must be connected to the CDR before it can be used to analyze data files or manage user accounts.

To set up the LabChip GX Reviewer software:

- 1 After the LabChip GX Reviewer software and the LabChip GxP option is installed, open the LabChip GX Reviewer software (see [Opening the LabChip GX Reviewer Software](#)). The [CDR / Database Server Mapping Window](#) opens.
- 2 Type the name or IP address of the server where the CDR is installed in the **Server Name/IP Address** text box and click the **Apply** button.

### NOTE



*If desired, the server can be remapped to a different address after setup. See [“Remapping the CDR Server” on page 125](#).*

- 3 Wait for the server connection to be established, and then click **OK** in the Connection Established window.
- 4 Log in to the LabChip GX Reviewer software as administrator with the password administrator.
- 5 Create the desired LabChip GX Touch user accounts for use in the GX Reviewer software and the GX Touch software (see [“Adding New Users” on page 111](#)).
- 6 To switch users, close and re-open the LabChip Reviewer software. Log in as the desired user.

## Opening the LabChip GX Reviewer Software

To open the LabChip GX Reviewer software:

- 1 Double-click on the **LabChip GX Reviewer** icon on the Windows desktop.
- 2 If the LabChip GxP option is installed, the [Login Window](#) opens. Type a valid LabChip GX Touch user name and password into the text boxes and click the **OK** button. (For instructions on creating LabChip GX Touch user names, see [“Adding New Users” on page 111.](#))

The [LabChip GX Reviewer Main Window](#) opens.

## Saving Workspace Files

When viewing plate data in the LabChip GX Reviewer main window, you view the selected [Data Files](#) in a [Workspace](#). The Data Files are not saved in the Workspace file. The workspace file contains links to the revision of the data file that was last open in the collection. If a Workspace file is moved to another folder or computer, the data files must be moved with the Workspace file. The data files must be in the same location relative to the Workspace file as they were, otherwise you are prompted to find the missing data files when you open the Workspace. It is a good practice to save the workspace files in the same location as the data files that are included in the workspace.

Saving a Workspace file automatically saves any changes to the data files that are open in the workspace, and the settings for each collection in the workspace.

If the LabChip GxP option is installed, saving Workspace files does not require permission to save data files unless the data files in the workspace have been modified.

## Data Analysis

After a run is complete, use the LabChip GX Reviewer software to view and analyze the plate data. The LabChip GX Reviewer software can open multiple data files in the same workspace to compare the data from different plates. Analysis settings can be changed for single wells, entire plates, or all plates in the workspace.

This section contains the following information:

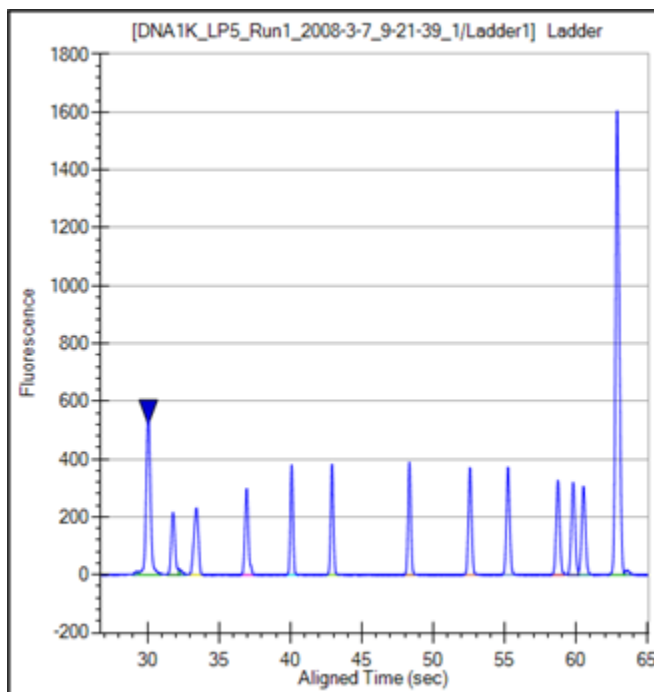
- [How the Software Analyzes DNA Data](#)
- [How the Software Analyzes Protein Data](#)
- [How the Software Analyzes RNA Data](#)
- [How the Software Analyzes Glycan Data](#)
- [How the Software Analyzes Protein Charge Variant Data](#)
- [How the Software Analyzes Genomic DNA Data](#)
- [Organizing, Retrieving, and Backing Up Data Files](#)
- [Opening a New Workspace](#)
- [Opening a Data File](#)
- [Adding a Collection to a Workspace](#)
- [Selecting the Wells in a Collection](#)
- [Using Sample Names Files](#)
- [Using Expected Fragments/ Expected Proteins/ Expected Glycans](#)
- [Using Filters](#)
- [Using Replicates](#)
- [Modifying Analysis Parameters](#)
- [Marker Peaks](#)
- [Saving and Exporting Assays](#)
- [Changing the View of the Data](#)
- [Copying Information](#)
- [Reanalyzing a Data File](#)
- [Printing Workspace Information](#)
- [Exporting Data](#)

## How the Software Analyzes DNA Data

The LabChip GX [DNA Assay Analysis](#) calculates the size and concentration of nucleic acid fragments.

The data analysis process for DNA assays consists of the following steps:

- 1 Raw data is stored by the system for each individual well.
- 2 The data is filtered (see [“Data Filtering” on page 261](#)) and the resulting electropherograms of all wells are plotted.
- 3 Peaks are identified (see [“Understanding Peak Finding” on page 101](#)) for all wells and are tabulated by migration time. The peak find settings can be changed for all wells or only for specific wells.
- 4 A sizing ladder (see [Figure 3](#)), which is a mixture of DNA fragments of different known sizes, is run first from the ladder vial. The concentrations and sizes of the individual base pairs in the ladder can be changed on the [Analysis Tab](#).



**Figure 3. Ladder Graph - DNA**



## How the Software Analyzes DNA Data (Continued)

- 5 The ladder is analyzed (see [“Ladder Analysis” on page 265](#)) and a standard curve of migration time versus DNA size is plotted from the DNA ladder by interpolation between the individual DNA fragment size/migration points. The standard curve derived from the data of the ladder well should resemble [Figure 4](#).

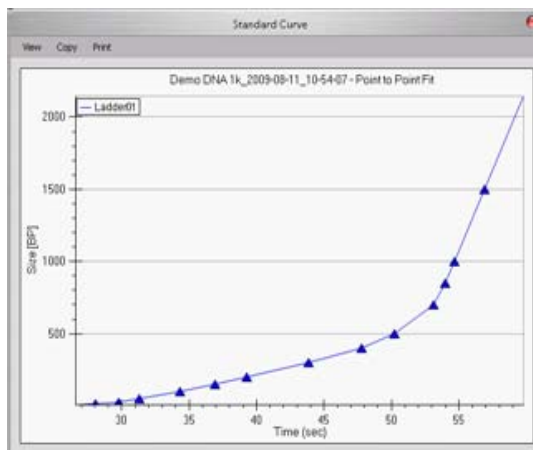


Figure 4. Standard Curve Window - DNA

- 6 Two DNA fragments, the **Lower Marker** and **Upper Marker**, are run with each of the samples, bracketing the DNA sizing range. The Lower Marker and Upper Marker are internal standards used to align the ladder data with data from the sample wells. [Figure 5](#) shows an example of assigned marker peaks in a sample well.

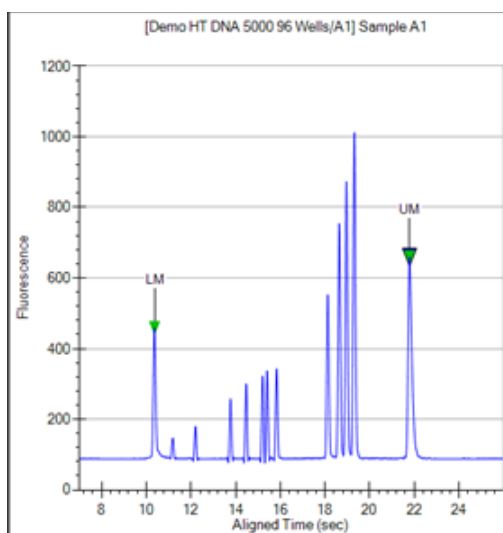


Figure 5. Markers - DNA

## How the Software Analyzes DNA Data (Continued)

- 7 The standard curve and the markers are used to calculate DNA fragment sizes for each well from the migration times measured.
- 8 To calculate the concentration of the individual DNA fragments in all sample wells, the upper marker, in conjunction with a calibration curve plotting assay-specific concentration against base-pair size, is applied to the individual sample peaks in all sample wells.
- 9 To calculate the concentration of a smear, the entire area under the curve defined by the smear is partitioned into sections corresponding to different base-pair sizes. The area of each section is evaluated against the area of the upper marker and the calibration curve. The total area of all the evaluated sections is given as the concentration of the smear.
- 10 If a titer is being used, the ladder is not used for quantization. Instead, peak sample areas or smear sample areas are normalized using the upper marker and then quantization is performed using the titer standard curve to convert normalized area to concentration; see [“Titer” on page 282](#).

### NOTE



*The software allows you to define upper and lower markers. Changing the markers causes quantitative changes in the calibration procedure, however, and therefore in the entire data evaluation.*

## How the Software Analyzes Protein Data

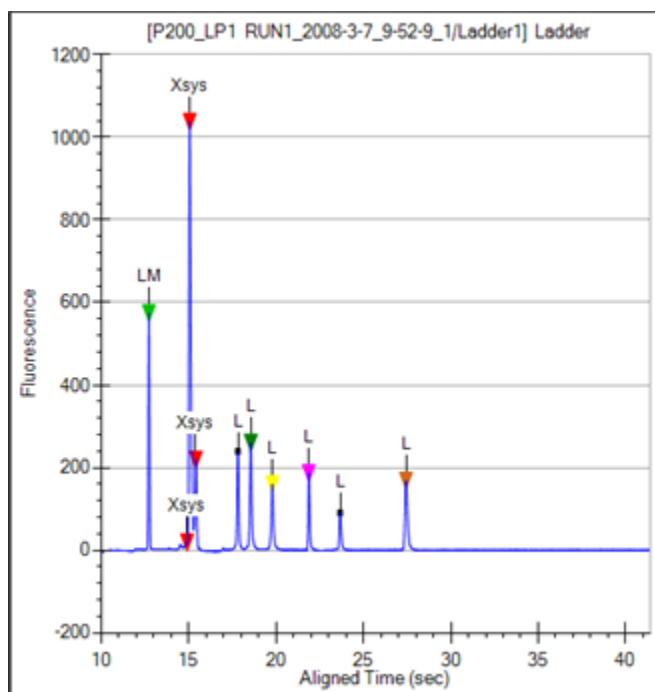
Protein assays are only supported on LabChip GXII or GXII Touch instruments.

The LabChip GX [Protein Assay Analysis](#) consists of the following steps:

- 1 Raw data is read and stored by the system for each individual well.
- 2 The data is filtered (see [“Data Filtering” on page 261](#)) and the resulting electropherograms of all wells are plotted.

## How the Software Analyzes Protein Data (Continued)

- 3 Peaks are identified (see [“Understanding Peak Finding” on page 101](#)) for all wells and are tabulated by migration time. The settings of the peak find algorithm can be changed and the data can be reanalyzed after the run has finished. (See [“Reanalyzing a Data File” on page 88](#).) The peak find settings can be changed for all or only certain wells.
- 4 A sizing ladder (see [Figure 6](#)), which is a mixture of protein fragments of different known sizes, is run from the ladder vial before and after every 12 samples. The concentration and sizes of the individual proteins (in kDa) in the ladder can be changed on the [Analysis Tab](#).



**Figure 6. Ladder Graph - Protein**

- 5 The ladder is analyzed (see [“Ladder Analysis” on page 265](#)) and a standard curve of migration time versus mobility is plotted from the ladder by interpolation between the individual protein size/migration points. The standard curve derived from the data of the ladder well should resemble [Figure 7](#).

## How the Software Analyzes Protein Data (Continued)

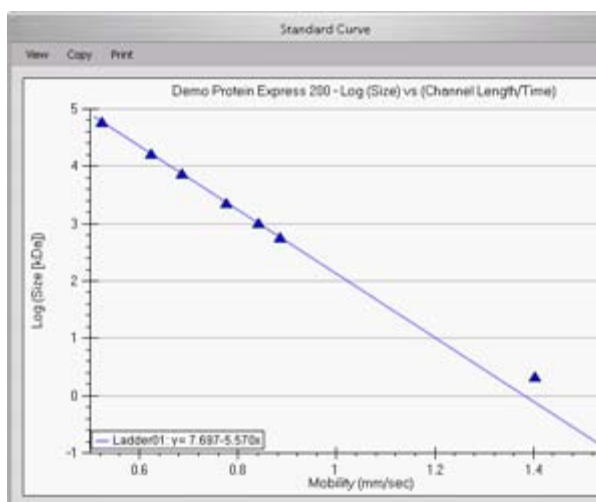


Figure 7. Standard Curve - Protein

- 6 A **Lower Marker** is the internal standard used to align the ladder data with data from the sample wells. Figure 8 shows an example of the assigned **Lower Marker** peak (marked LM) in a sample well.

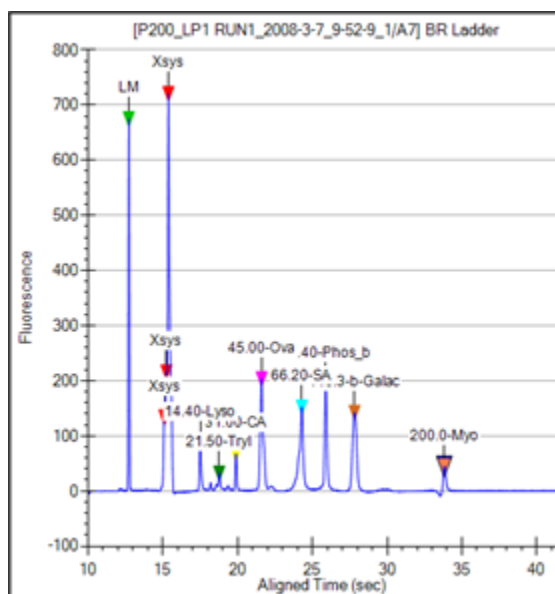


Figure 8. Markers - Protein

## How the Software Analyzes Protein Data (Continued)

- 7 Before calculating either the protein size or concentration, the sample data is processed relative to the two ladders that bracket every 12 samples. First, all of the data is aligned to the lower marker and then stretched, relative to the highest molecular weight protein in the ladder.
- 8 The concentration of the sample proteins is determined relative to the bracketed ladders. There are seven proteins in the ladder (not including the lower marker). The ladder concentration can be changed on the [Analysis Tab](#) (see [page 178](#)).
- 9 If a titer is being used, the ladder is not used for quantization. Instead, peak sample areas are normalized using the lower marker and then quantization is performed using the titer standard curve to convert normalized area to concentration; see [“Titer” on page 282](#).

### NOTES



- *The seven proteins are assumed to represent the average staining behavior of proteins and are used to determine an average peak area per  $\mu\text{g/mL}$  of protein. This factor is used to convert sample peak areas into relative concentration. The total relative concentration of all proteins is calculated by addition of the relative concentration of the individual proteins and is displayed in the Well Table View (see [page 161](#)).*
- *Since the conversion factor is determined for each ladder, the factor can be linearly interpolated for each sample and thus account for any assay drift.*
- *The software allows you to define the lower marker. Changing the selection of the marker will lead to quantitative changes in the calibration procedure, and therefore in the entire data evaluation.*

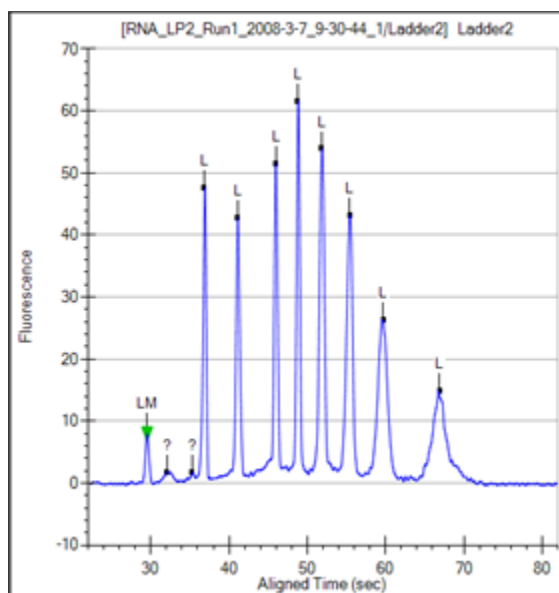
## How the Software Analyzes RNA Data

The LabChip GX [RNA Assay Analysis](#) determines the quality of the RNA sample by measuring the relative amounts of known RNA fragments relative to the total RNA present in the sample. Results for each well are calculated after all data for the well has been read.

The data analysis process for RNA assays consists of the following steps:

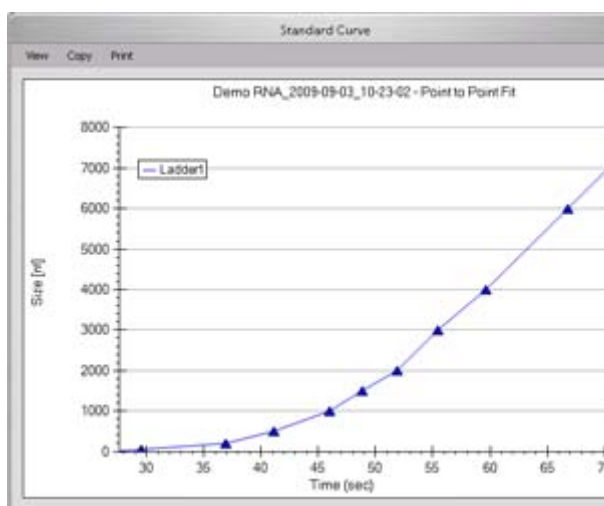
- 1 Raw data is read and stored by the system for each individual well.
- 2 The data is filtered (see [“Data Filtering” on page 261](#)) and the resulting electropherograms of all wells are plotted.
- 3 A curve spline fit to the data is performed to generate a baseline above which RNA fragment peaks are detected. This baseline is displayed as a blue line on the electropherogram when Show Peak Baselines is selected in the [Graph View Properties](#) (see [page 153](#)).
- 4 Peaks extending above the baseline are identified (see [“Understanding Peak Finding” on page 101](#)) for all wells and are tabulated by migration time. The settings of the peak find algorithm can be changed and the data can be reanalyzed after the run has finished. The peak find settings can be changed for all or only certain wells.
- 5 A sizing ladder (see [Figure 9](#)), which is a mixture of RNA fragments of different known sizes, is run first from the ladder vial. The concentrations and sizes of the individual nucleotides in the ladder can be changed on the [Analysis Tab](#).

## How the Software Analyzes RNA Data (Continued)



**Figure 9. Ladder Graph - RNA**

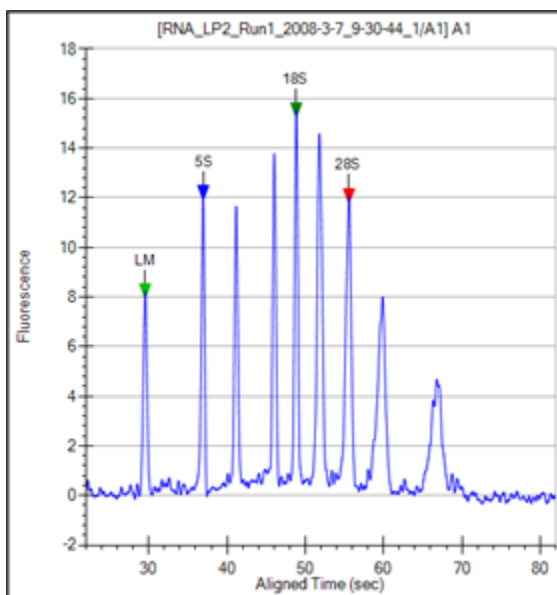
- 6 The ladder is analyzed (see [“Ladder Analysis” on page 265](#)) and a standard curve of migration time versus RNA size is plotted from the RNA ladder by interpolation between individual RNA fragment size/migration points. The standard curve derived from the data of the ladder well should resemble [Figure 10](#).



**Figure 10. Standard Curve - RNA**

## How the Software Analyzes RNA Data (Continued)

- 7 A dye matching the lowest peak in the ladder is run with each of the samples. This lower marker, labeled LM in the RNA sample (see [Figure 11](#)) is used to align the ladder data with data from the sample wells.



**Figure 11. Markers - RNA**

- 8 The standard curve and the markers are used to calculate RNA fragment sizes for each well from the migration times measured.



## How the Software Analyzes RNA Data (Continued)

- 9 The Total RNA present is computed by finding the area under the electropherogram trace. The baseline for this integration is a straight line starting at the end of the lower marker and ending at the baseline end time. The height of the baseline endpoints is computed from an average of a five second window around the baseline [Start Time](#) and [End Time](#) (shown on the [Peak Find Tab](#)). View the baseline by selecting Show Peak Baselines in the [Graph View Properties](#). Adjust the Start Time and End Time by dragging the left (Start) and right (End) vertical dashed lines to areas that more properly reflect the signal baseline. (Right-click in the graph, select Set Scale, and change the X axis Minimum and Maximum values if the start and end times are not shown in the graph.)

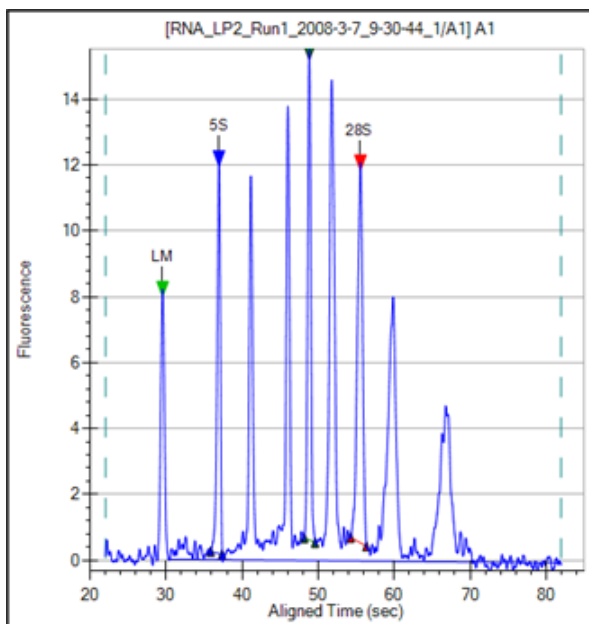


Figure 12. Peak Baseline - RNA

- 10 The **Total RNA concentration** in the sample is computed from the ratio of the RNA area in the sample to the RNA area in the ladder multiplied by the ladder concentration specified in the assay.

If a titer is being used, the ladder is not used for quantization. Instead, peak sample areas are normalized using the lower marker and then quantization is performed using the titer standard curve to convert normalized area to concentration; see [“Titer” on page 282](#).

## How the Software Analyzes RNA Data (Continued)

- 11 Assay-defined RNA fragments are identified from the peaks in the peak table. Fragments are located by finding the largest peak within a size range associated with the fragment. For Eukaryote RNA assays, 5S, 18S and 28S fragments are located. For Prokaryote assays, 5S, 16S and 23S fragments are identified.
- 12 The following values are calculated for RNA assays:
  - Fragment\_Area:** Area of each rRNA Fragment.
  - %\_of\_Total\_Area:** Each Fragment area as a percent of total area.
  - Corrected RNA Area:** Total RNA Area corrected with Lower Marker height.
  - RNA Concentration (ng/ul):** Estimated Total RNA Concentration in the sample.
  - rRNA Area Ratio [28S / 18S]:** 28S area divided by 18S area.
  - rRNA Height Ratio [28S / 18S]:** 28S height divided by 18S height or 23S height divided by 16S height.
  - rRNA Fast Area Ratio:** Region between 5S and 18S or 16S, percent of total area.
  - RNA quality metrics:** rRNA Area and Height Ratios (28S/18S or 23S/16S) and Fast/Total RNA area ratio are computed.

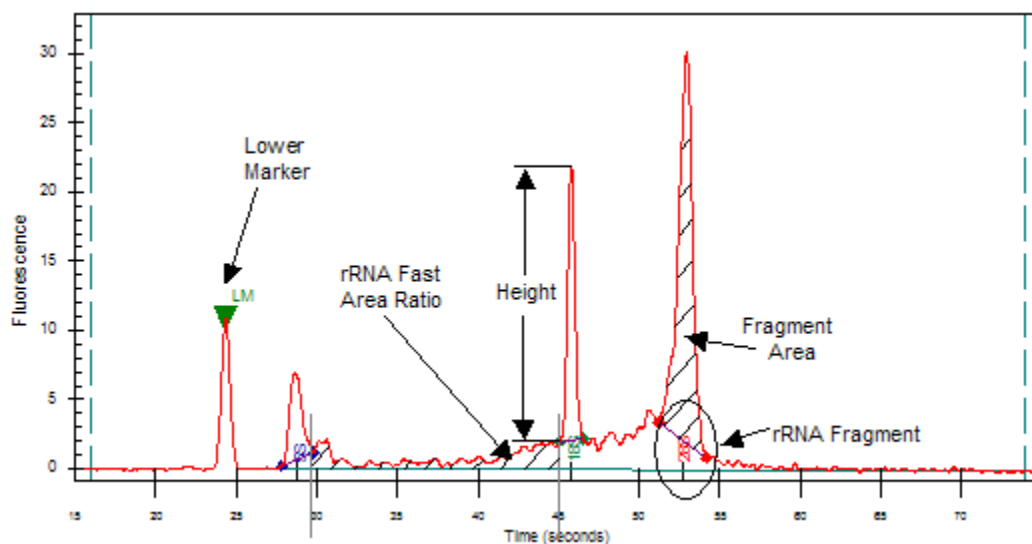


Figure 13. rRNA Graph Analysis

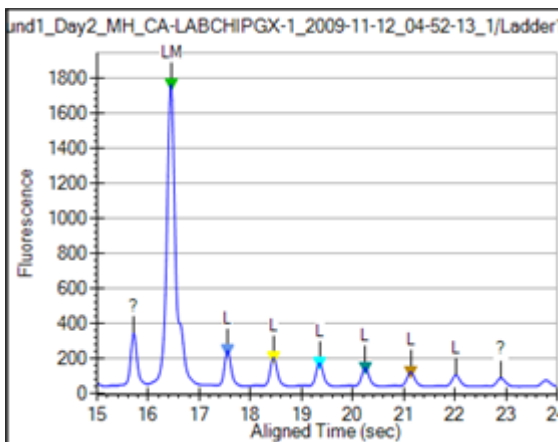
- 13 **Messenger RNA Assay:** The RNA contamination ratio is computed. This is the ratio of the area of all the fragments to total RNA area.

## How the Software Analyzes Glycan Data

Glycan assays are only supported on LabChip GXII or GXII Touch instruments.

The LabChip GX Glycan Assay Analysis consists of the following steps:

- 1 Raw data is read and stored by the system for each individual well.
- 2 The data is filtered (see [“Data Filtering” on page 261](#)) and the resulting electropherograms of all wells are plotted.
- 3 Peaks are identified (see [“Understanding Peak Finding” on page 101](#)) for all wells and are tabulated by migration time.
- 4 A sizing ladder (see [Figure 14](#)), which consists of multiples of a basic sugar molecule, is run from the ladder vial before and after every 12 samples. The simplest molecule is assigned a size unit of 1 CGU (Caliper Glucose Unit). The sequence of ladder peaks is assigned integer size values, providing a migration time to size ruler for sizing other sugar molecules.



**Figure 14. Ladder Graph - Glycan**

- 5 The ladder is analyzed (see [“Ladder Analysis” on page 265](#)) and a standard curve of migration time versus mobility is plotted from the ladder by interpolation between the individual glycan/migration points. The standard curve derived from the data of the ladder well should resemble [Figure 15](#).

## How the Software Analyzes Glycan Data (Continued)

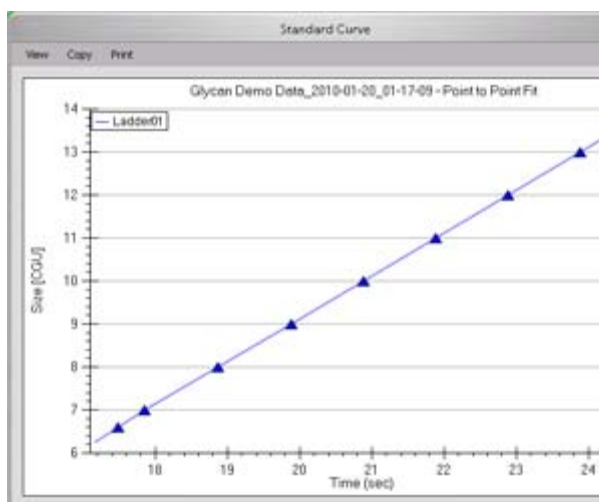


Figure 15. Standard Curve - Glycan

- 6 A **Lower Marker** is the internal standard used to align the ladder data with data from the sample wells. Figure 16 shows an example of the assigned **Lower Marker** peak (marked LM) in a sample well.

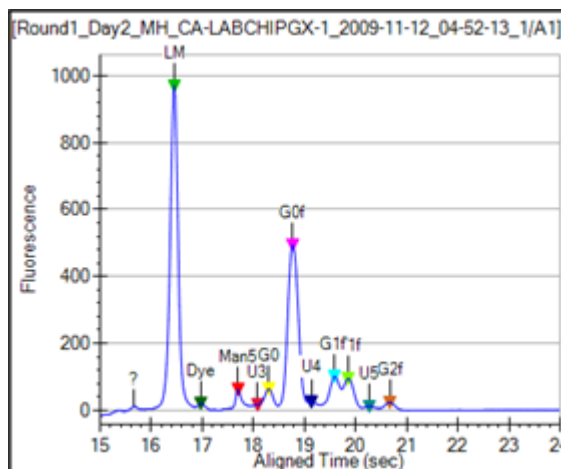


Figure 16. Markers - Glycan

## How the Software Analyzes Glycan Data (Continued)

- 7 The standard curve and the markers are used to calculate glycan sizes in each well from the migration times measured.
- 8 The area under each peak is calculated.
- 9 All the sample peak areas are added together and an area ratio is calculated for the %Area for each peak.

### NOTES



- *In Glycan assays, the lower marker does not precede all ladder peaks but appears between the 6th and 7th ladder peak. The concentration of the lower marker has been made sufficiently large to avoid confusion with ladder peaks. Since peaks before the lower marker are ignored, the ladder peaks used for the sizing ruler range from 7 to 13 CGU.*
- *The software allows you to define the lower marker. Changing the selection of the lower marker will lead to quantitative changes in the calibration, and therefore in the entire data evaluation.*

## How the Software Analyzes Protein Charge Variant Data

Protein Charge Variant assays are only supported on LabChip GXII or GXII Touch instruments.

The LabChip GX Protein Charge Variant Assay Analysis consists of the following steps:

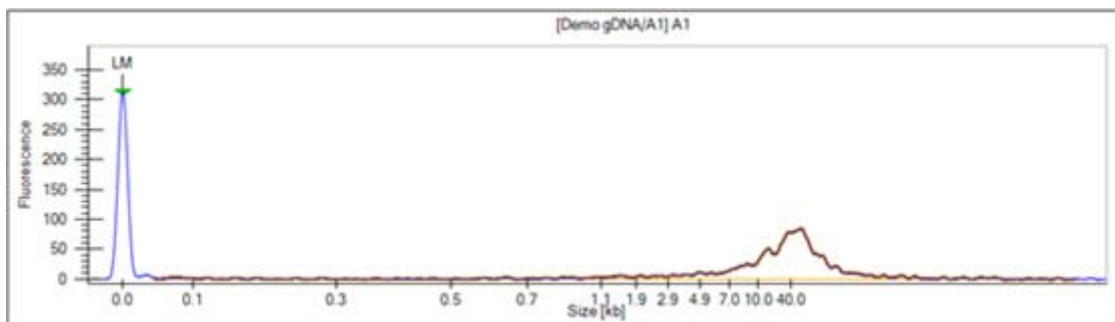
- 1 Raw data is read and stored by the system for each individual well.
- 2 The data is filtered (see [“Data Filtering” on page 261](#)) and the resulting electropherograms of all wells are plotted.
- 3 A baseline is generated for the data using the settings on the Peak Find tab on the [Assay Analysis Window](#). This baseline is displayed on the electropherogram when Show Peak Baselines is selected in the [Graph View Properties](#) (see [page 153](#)).
- 4 Peaks are identified (see [“Understanding Peak Finding” on page 101](#)) for all wells and are tabulated by migration time. The settings of the peak find algorithm can be changed and the data can be reanalyzed after the run has finished. (See [“Reanalyzing a Data File” on page 88](#).) The peak find settings can be changed for all or only certain wells.
- 5 The % Relative Amount for each peak is calculated as a percent of total area.

## How the Software Analyzes Genomic DNA Data

The Genomic DNA (gDNA) assay analyzes data similar to the other DNA assays, except that the alignment of the sample data with the ladder data is based solely on the Lower Marker. To improve the accuracy of the alignment of the 12 samples between ladders, gDNA assays use the bracketed alignment described in [“How the Software Analyzes Protein Data”](#) on page 18.

For calculating concentration, the Genomic DNA assay uses a GQS Smear, starting at 0.175 kb and extending to 300 kb, by default (see [Figure 17](#)). The start size of the gDNA smear can be changed on the [Advanced Tab](#) in the Assay Analysis window before the run starts or on the [Smear Analysis Tab](#) after the run. The calculation of concentration is similar to that used for individual peaks, as described in [How the Software Analyzes DNA Data](#); however, the GQS Smear is used in place of individual sample peaks, and the lower marker is used in place of the upper marker to normalize areas. The Total gDNA Concentration of each sample is reported in the Well Table.

The Genomic DNA assay also reports a Genomic Quality Score (GQS) for each sample in the Well Table. The GQS represents the degree of degradation of a sample, with 5 corresponding to intact gDNA and 0 corresponding to highly degraded gDNA. The GQS is calculated using the size distribution of the sample.



**Figure 17. Genomic DNA GQS Smear (in orange)**

## Organizing, Retrieving, and Backing Up Data Files

As you work in the LabChip GX Reviewer software, it's a good practice to organize the LabChip GX Reviewer files.

- Create a folder in which to save the data files. If desired, each person can save data files to their own subfolder to organize the data files.
- Save Workspace files in the same directory as the data files to prevent missing data files in the workspaces.
- Review the files periodically, even if only one person uses the LabChip GX Reviewer software. If you are not using the LabChip GxP option, archive files you are no longer using but want to save to a backup disk, and discard unneeded files. Verify there is enough free space on the hard drive to save new plate data files. If you are using the LabChip GxP option, see [“LabChip GxP Option” on page 107](#) for backup options.
- Each user in the laboratory can specify a particular data file name prefix to easily differentiate data files.

## Opening a New Workspace

A workspace displays data from one or more plate data files from the same type of assay. Each workspace can contain one or more [Collections](#) to display the data.

To open a new workspace:

- 1 On the menu bar, select **File → New Workspace**. If changes have been made to an open workspace, you are prompted to save any unsaved changes. A blank workspace opens in the [LabChip GX Reviewer Main Window](#).

To view data, see:

- [Opening a Data File](#)
- [Adding a Collection to a Workspace](#)
- [Selecting the Wells in a Collection](#)
- [Modifying Analysis Parameters](#)
- [Saving and Exporting Assays](#)



## Opening a Data File

Open a data file to view the data, to compare the data to other data files in the same workspace, or to change analysis setting and view the reanalyzed data. Data files generated by the LabChip GX or GX Touch software have a .gxd file extension.

To open a data file:

- 1 Open a new workspace (see [page 32](#)) or a workspace that already contains compatible data files.
- 2 On the menu bar, select **File → Import Data File**. If the LabChip GxP option is not installed, the [Select a Data File Window](#) opens. If the LabChip GxP option is installed, the [CDR Manager Window](#) opens.
- 3 Select the name of the data file to open and click the **Open** button. The selected data file is imported into the open workspace. Use Ctrl+click or Shift+click to select multiple files.
  - To select a .cla file, select CLA from the Files of Type drop-down list in the Select a Data File window. The selected .cla file is converted to a .gxd file, and the new .gxd file is imported into the open workspace. The new .gxd data file is saved in the same folder as the original .cla file. Any changes are saved to the .gxd file. The .cla file cannot be changed.

### NOTE



*After the .cla file is converted to a .gxd file, use the .gxd file in any workspaces. Re-importing the same .cla file will over-write the existing .gxd file and any analysis changes saved in the .gxd file will be lost.*

- 4 If desired, right-click on the data file name in the [Plate View or Plate List](#) and select **Rename Plate** to change the name of the plate in the display. (If desired, select the Rename File to Match check box to change the name of the data file.)
- 5 Select the desired wells to view in each collection in the workspace (see [page 35](#)).
- 6 See [“Modifying Analysis Parameters” on page 61](#) for information about changing analysis parameters.

## Adding a Collection to a Workspace

Collections are used to specify the wells selected for view in each plate data file, the layout of the views in the Collection tab, and the display properties for each view in each collection.

To add a new collection to an open workspace:

- 1 On the menu bar, select **Collection → New Collection**. The [New Collection Window](#) opens.
- 2 Select the desired option for creating the new collection:
  - **Template** - Opens a new collection with the same settings as a saved collection template file.
  - **Blank Collection** - Opens a new template using the default collection settings.
  - **Current Collection** - Opens a new template based on the current settings in the currently open collection.
- 3 If no plates are open in the collection, choose the desired Assay Type for the collection: DNA, Protein, RNA, Glycan, CZE, or gDNA. (Protein, Glycan, and CZE are only supported on LabChip GXII or GXII Touch instruments.) Only data files from the selected assay type can be imported into the workspace.
- 4 If desired, type a new name for the collection in the **Name** text box.
- 5 Click the **OK** button to open the new collection.

## Selecting the Wells in a Collection

Each collection can display different wells or the same wells in different orders. To select the wells to display in a collection:

- 1 Select the collection where the wells will be displayed.
- 2 In the plate diagram in the Plate View, select the wells to display:

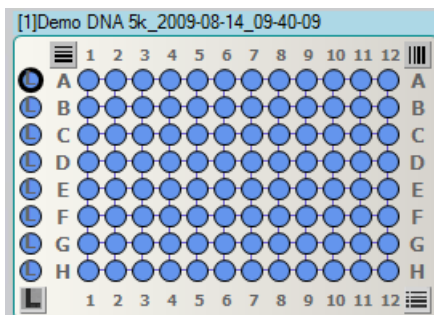


Figure 18. Selecting Wells

- **Select individual wells:** click on the well.
  - **Select a block of wells:** click on the well in one corner and drag to the opposite corner well.
  - **Select an entire row:** click the row letter at the left.
  - **Select an entire row and the corresponding ladder:** click the row letter at the right (if the plate sip order is row-wise).
  - **Select an entire column:** click the column number at the top.
  - **Select an entire column and any corresponding ladder:** click the column number at the bottom (if the plate sip order is column-wise).
  - **Select all the wells by rows:** click the button in the top left corner of the microplate.
  - **Select all the wells by columns:** click the button in the top right corner of the microplate.
  - **Select all ladder wells and microplate wells:** click the button at the bottom right corner of the microplate.
  - **Select individual ladders:** click on the ladder.
  - **Clear individual ladders:** right-click on the ladder and select **Remove Ladder**.
  - **Select all ladder wells:** click the “L” icon at the bottom left corner of the microplate.
  - **Clear individual wells:** right-click on the well and select **Remove Well**.
- 3 Save the workspace to save the wells selected in the collection.

## Using Sample Names Files

Sample Names files are used to import sample names into a data file in the LabChip GX Reviewer software. The Sample Name file can also contain expected peaks.

After the run is complete, you can use the [Sample Name Editor Window](#) to rename the samples or to import an existing sample name file. Sample name files are saved as .CSV files and can be edited with a spreadsheet program such as Microsoft Excel.

The Color, Name, and Display Property for an Expected Peak cannot be set in the Sample Name Editor window. When new Expected Peaks are created in the Sample Name Editor window, default values are assigned for these properties.

This section contains:

- [“Creating a Sample Names File” on page 37](#)
- [“Importing a Sample Names File into a Data File” on page 37](#)
- [“Sample Name File Format \(.CSV Format\)” on page 38](#)
- [“Applying Different Window Values to Expected Peaks of the Same Size in Different Wells” on page 39](#)
- [“Sample Name File Import Errors” on page 39](#)

## Creating a Sample Names File

To create a Sample Names file to specify the sample names, comments, and Expected Peaks:

- 1 Select **Tools** → **Sample Name Editor** on the [LabChip GX Reviewer Main Window](#). The [Sample Name Editor Window](#) opens.
- 2 Modify the **sample names** as desired in the Sample Name Editor window.
- 3 Enter any desired comments for the samples in the **Sample Comment** column.
- 4 For DNA, gDNA, Protein, or Glycan assays, if desired, click the Edit Expected Peaks check box and enter the desired Expected Peaks and Window (%) in the columns. Separate each peak size or window value with a semi-colon (;). If only one Window % value is entered, the same value applies to all expected peaks. If multiple values are entered, separated by semi-colons, each expected peak will use the corresponding Window value. If more expected peaks are entered than Window values, the last Window applies to all remaining expected peaks in the list.
- 5 Click the **Export** button, navigate to the desired location for the file, type the desired name for the file, and click the **Save** button.

## Importing a Sample Names File into a Data File

To import the sample names into a data file:

- 1 Open the data file in an open workspace in the [LabChip GX Reviewer Main Window](#).
- 2 Select **Tools** → **Sample Name Editor**. The [Sample Name Editor Window](#) opens.
- 3 Click the **Import** button, navigate to the file location, select the name of the .csv file that contains the sample names, and click the **Open** button.

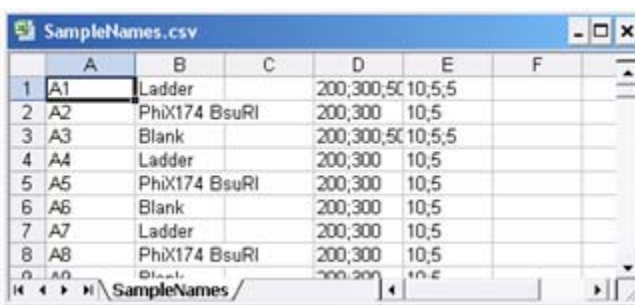
If a Sample Names file is imported into the Sample Name Editor window, rows are added for any wells that are not listed in the original Sample Names file. All wells are included in the new Sample Names file.

- 4 Click the **Apply** button in the Sample Name Editor window to apply the sample names to the active plate.

## Sample Name File Format (.CSV Format)

The Sample Names created in the [Sample Name Editor Window](#) can be exported to a .CSV file. A .CSV file can also be created in Microsoft Excel or generated automatically with a LIMS to import the Sample Names into the data file.

[Figure 19](#) shows a Sample Names file open in Microsoft Excel.



	A	B	C	D	E	F
1	A1	Ladder		200,300,500	10,5,5	
2	A2	PhiX174 BsuRI		200,300	10,5	
3	A3	Blank		200,300,500	10,5,5	
4	A4	Ladder		200,300	10,5	
5	A5	PhiX174 BsuRI		200,300	10,5	
6	A6	Blank		200,300	10,5	
7	A7	Ladder		200,300	10,5	
8	A8	PhiX174 BsuRI		200,300	10,5	

**Figure 19. Sample Name .CSV File**

A Sample Name .CSV file must use the following format:

**Column A:** The well label (A1 to P24). The wells labels can be entered in any order and do not need to cover the entire plate.

**Column B:** The desired sample name for each well.

**Column C:** A user comment to be added to the well properties.

**Column D:** A list of Expected Peak sizes for the well. This list is separated by semi-colons (;).

**Column E:** The search window size for each Expected Peak in column D as a % (10 = +/-10% of Expected Peak size). If all Expected Peaks use the same window size, enter a single value; otherwise enter unique values as a semicolon separated list. If fewer windows than EPs are entered, the last window applies to all remaining EPs in the list.

**Column F...** Any higher columns are ignored.

## **Applying Different Window Values to Expected Peaks of the Same Size in Different Wells**

Only one Expected Peak of a particular size can exist in the assay analysis settings. If the same Expected Peak size with a different Expected Peak window is entered in the Sample Name Editor window, only the first Expected Peak is created. All other Expected Peaks of the same size use the same window as the first Expected Peak. To overcome this restriction, use Expected Peaks of slightly different sizes; e.g. 200, 200.1, 200.2, etc. to apply different windows to the same Expected Peak in different wells.

## **Sample Name File Import Errors**

Any row in the .CSV file that does not match the expected format and cannot be interpreted is ignored. If none of the rows can be interpreted, usually because the first column does not contain the well label, the following error message displays: "No rows found matching format: label, name, comment, EP, window."

## Using Expected Fragments/ Expected Proteins/ Expected Glycans

You can track expected DNA fragments (EFs), proteins (EPs), Glycans (EGs), or peaks (EPs) for the samples in a DNA, gDNA, Protein, Glycan, or Protein Charge Variant assay, respectively. (Protein, Glycan, and Protein Charge Variant assays are only supported on LabChip GXII or GXII Touch instruments.) You enter the EFs, EPs, and EGs in the [Assay Analysis Window](#).

This section contains:

- [“Entering EFs, EPs, or EGs in the Assay Analysis Window” on page 40](#)
- [“Exporting EFs, EPs, or EGs” on page 41](#)
- [“Importing EFs, EPs, or EGs” on page 42](#)
- [“Forcing Expected Peaks” on page 42](#)
- [“Viewing the EFs/EPs/EGs in the Graph View” on page 43](#)
- [“Viewing the EFs/EPs/EGs in the Gel View” on page 44](#)
- [“Viewing the EFs/EPs/EGs in the Well Table” on page 44](#)
- [“Viewing the EFs/EPs/EGs in the Peak Table” on page 45](#)

### Entering EFs, EPs, or EGs in the Assay Analysis Window

- 1 Select **Analysis** → **Analysis Settings** on the [Menu Bar](#). The [Assay Analysis Window](#) opens.
- 2 Click on the [Expected Fragments/Proteins/Glycans Tab](#).
- 3 Click in the bottom (empty) row in the table.
- 4 In the **Size** column, type the size of the expected fragment (bp for DNA or kb for gDNA), protein (kDa), or glycan (CGU).
- 5 For CZE assays, type the time of the expected peak, in seconds, in the **Time** Column.
- 6 In the **Window (%)** column, if desired, change the tolerance value to allow for variations in the expected fragment/protein/glycan size or peak time. This value is specified as a percent of the expected size for that fragment/protein/glycan or time for a peak. The default is 10% for DNA, protein, and CZE, and 2.5% for Glycan.  
**Note:** If there are multiple peaks in the tolerance range, the largest peak is labeled as the expected peak, even if it is not the exact size specified. To change the peak identified as an expected peak, see [“Forcing Expected Peaks” on page 42](#).



## Entering EFs, EPs, or EGs in the Assay Analysis Window (Continued)

- 7 A default color is automatically assigned. To change the color, click on the color block in the **Color** column and select the desired color in the Color window.
- 8 If desired, change the name shown in the **Name** column.
- 9 If desired, change the **Property Displayed in the Well Table**. This setting specifies the property that will be displayed in the Expected Peak column for each expected peak listed in the [Well Table View](#).
- 10 To align the data to one or more specific peaks, select the **For Aligning** check box. The data is realigned so the selected peaks match their aligned size. Note: Incorrect alignment settings can cause analysis errors.
- 11 To apply the expected peak only to specific wells, click in the **Apply to Wells** column. The Select Wells window opens. Click (or click and drag) to select the wells that you want to apply the expected peaks to, and then click the OK button.
- 12 To apply the EFs, EPs, or EGs to the active plate, click the **Apply** button.
- 13 To apply the EFs, EPs, or EGs to all plates in the workspace, click the **Apply Global** button.

## Exporting EFs, EPs, or EGs

- 1 After the EFs, EPs, or EGs are entered in the [Expected Fragments/Proteins/Glycans Tab](#), click the **Export** button at the bottom of the window. The Export Expected Fragments/Proteins/Glycans Window opens.
- 2 Navigate to the desired location for the file, type the desired name for the file in the File Name text box, and then click the **Save** button. A .GEP file is created to save the expected peak settings.

## Importing EFs, EPs, or EGs

After an Expected Peak file (\*.GEP) has been exported, you can import the settings into another plate or workspace.

- 1 With the plate open in a workspace, in the [Expected Fragments/Proteins/Glycans Tab](#), click the **Import** button at the bottom of the window. The Import Expected Fragments/Proteins/Glycan Table window opens.
- 2 Navigate to the location of the file, select the name of the file to import, and then click the **Open** button. The expected peak settings are imported into the tab.
- 3 To apply the EFs, EPs, or EGs to the active plate, click the **Apply** button.
- 4 To apply the EFs, EPs, or EGs to all plates in the workspace, click the **Apply Global** button.

## Forcing Expected Peaks

If there are multiple peaks in the tolerance range, the largest peak is labeled as the expected peak, even if it is not the exact size specified. If a different nearby peak should have been selected as the expected peak, you can specify which peak is labeled the expected peak.

- 1 In the [Graph View](#), right-click on the peak that should be labeled as the expected peak.
- 2 On the shortcut menu, select **Force Expected Fragment/Peak** and then select the desired fragment or peak from the menu.

To clear a forced peak and revert to the default expected peak, right-click on the forced expected peak and select **Clear Forced EP**.

## Viewing the EFs/EPs/EGs in the Graph View

**Expected Fragments, Expected Proteins, and Expected Glycans** are identified in the electropherogram by open triangles over the peaks. The triangles are the same color as specified in the [Expected Fragments/Proteins/Glycans Tab](#).

To display the expected peak indicators in the Graph view:

- 1 Click the **Properties** tab on the right side of the **Graph view** to open the [Graph View Properties](#).
- 2 To view the size of all expected peaks, select **Expected Fragments, Expected Proteins, or Expected Glycan** in one of the Annotation list boxes.

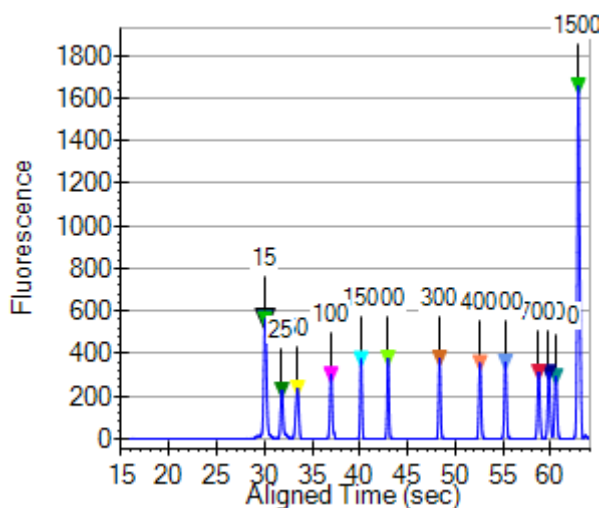


Figure 20. Expected Fragments

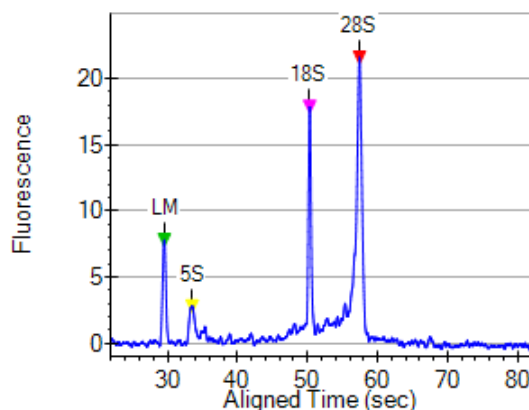


Figure 21. Expected Peaks

## Viewing the EFs/EPs/EGs in the Gel View

**Expected Fragments/Proteins/Glycans** are indicated in the [Gel View](#) by colored lines. The color of the line matches the color specified in the [Expected Fragments/Proteins/Glycans Tab](#).

To display the expected peaks in the Gel View:

- 1 Click the **Properties** tab on the right side of the [Gel View](#) to open the [Gel View Properties](#).

- 2 Select the **Show Expected Peaks** check box.

To display the legend that identifies the colors and sizes of the expected peaks:

- 1 Click the **Properties** tab on the right side of the [Gel View](#) to open the [Gel View Properties](#).

- 2 Select the **Show Expected Peaks Legend** check box.

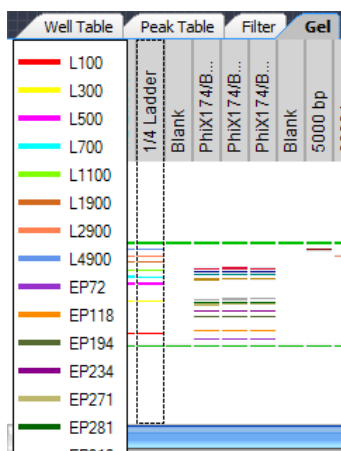


Figure 22. Expected Peaks Legend

## Viewing the EFs/EPs/EGs in the Well Table

A column is added to the Well Table for each Expected Peak entered in the [Expected Fragments/Proteins/Glycans Tab](#). The column displays the property selected in the **Property Displayed in Well Table** list in the [Assay Analysis Window](#).

## Viewing the EFs/EPs/EGs in the Peak Table

**Expected Fragments, Expected Proteins, and Expected Glycans** are identified in the Peak Table with the peak name displayed in the **Type** column.

Well Table	Peak Table	Filter
Plate Name	Sample Name	Type
DNA1K_LP5_Run1_2008-3-7_...	1XLad	LM
DNA1K_LP5_Run1_2008-3-7_...	1XLad	EP0025
DNA1K_LP5_Run1_2008-3-7_...	1XLad	EP0050
DNA1K_LP5_Run1_2008-3-7_...	1XLad	EP0100
DNA1K_LP5_Run1_2008-3-7_...	1XLad	EP0150
DNA1K_LP5_Run1_2008-3-7_...	1XLad	EP0200
DNA1K_LP5_Run1_2008-3-7_...	1XLad	EP0300
DNA1K_LP5_Run1_2008-3-7_...	1XLad	EP0400
DNA1K_LP5_Run1_2008-3-7_...	1XLad	EP0500
DNA1K_LP5_Run1_2008-3-7_...	1XLad	EP0700

**Figure 23. DNA Assay Peak Table**

## Using Filters

Filters are used to select the wells included in a collection based on specific criteria specified in each filter. The types of filters available depend on the type of data in the workspace. Each filter is available in all collections in the workspace. Each collection can contain unique combinations of filters. Well and filter selections are specific to each collection if the workspace contains multiple collections.

This section contains:

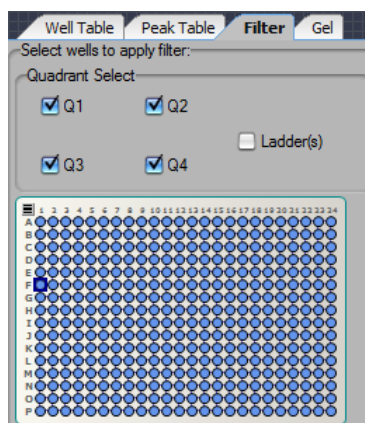
- [Creating a New Filter](#)
- [Selecting Filters in a Collection](#)
- [Well Colors in a Filtered Collection](#)
- [Searching Data Files using a Filter](#)

### Creating a New Filter

The filter specifies the criteria that determines whether a well is included in the current collection. Filters can be turned on and off to change the wells selected in a collection.

To create a new filter:

- 1 Open the data files that you want to filter.
- 2 Click the [Filter View](#) tab.
- 3 Select the desired wells to apply the filter to in the Filter Plate diagram. The Filter Plate diagram always displays a 384-well plate. For 96-well plates, any wells selected outside the 96-well plate boundaries are ignored.



**Figure 24. Selecting Wells to Apply Filter**

- a To select or clear quadrants, select or clear the **Quadrant Select** check boxes.

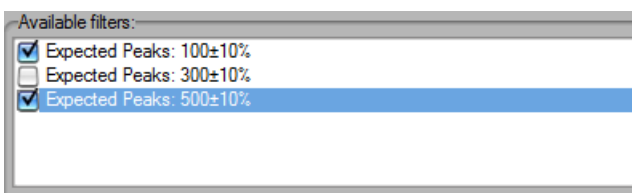
## Creating a New Filter (Continued)

- b** To include or exclude ladder wells, select or clear the **Ladder(s)** check box.
  - c** To select all wells in the plate, click the **Select All Rows** button in the upper right corner of the Filter Plate Diagram.
  - d** To select or clear specific wells or columns, click the row letter or column number in the Filter Plate diagram.
- 4** In the **Type** drop-down list, select the desired filter type. The filter types available depend on the assay that was used to create the data file.
- 5** If desired, click the Color button to the right of the Type drop-down list and select the desired color for the filter. Any wells selected by the filter display the filter color in the Plate View or List View. (See [“Well Colors in a Filtered Collection” on page 49](#) for more information.)
- 6** Select the desired filter criteria. Numeric value operators are equal to (with percent threshold), between, less than, or greater than. Text expressions can contain wild cards. Expected Peaks criteria specify expected peaks in a well.
- 7** Click the **Add** button. The filter is added to the Available Filters list box and is selected by default. The Plate View displays the selected wells.
- 8** If multiple filters are selected, select the desired Filter Options: OR, AND(Peak), or AND(Well). (See [Selecting Filters in a Collection](#) for more information.)

## Selecting Filters in a Collection

The **Available Filters** list box displays all of the filters that are part of the current workspace. The check box next to each filter in the list is used to include or exclude that filter from the analysis for the current collection. Each collection in a workspace can have a different filter selection.

- 1 If the workspace contains more than one collection, click a collection tab to select the desired collection.
- 2 Open the data files that you want to filter.
- 3 In the **Available Filters** list box, select or clear the check box next to a filter to enable or disable the desired filters.



**Figure 25. Selected Filters**

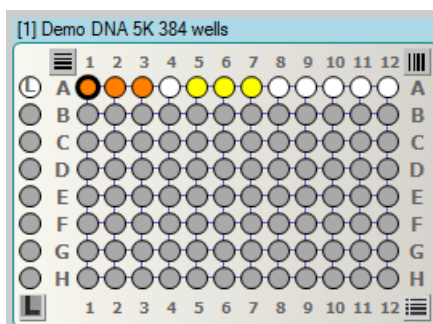
- 4 Select the desired **Filter Options** to determine how multiple filters are logically combined. The options available are OR, AND(Peak), and AND(Well). See [“Well Colors in a Filtered Collection” on page 49](#) for information about well colors.
  - **OR** - Selects any well that contains a peak that matches any of the filters selected in the Available Filters list.
  - **AND(Peak)** - Selects any well that contains a single peak that matches all of the filters selected in the Available Filters list.
  - **AND(Well)** - Selects any well that contains peaks that match all of the filters selected in the Available Filters list. Different peaks in the same well can match different filters, as long as all filter conditions are met in the same well.



## Well Colors in a Filtered Collection

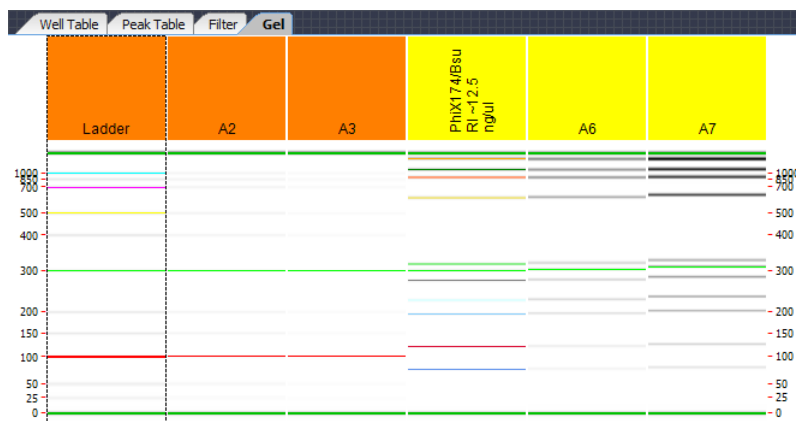
The wells selected in a collection by a filter are color-coded in the Plate View and the Gel View to indicate which wells are selected by each filter. By designating a different color for each filter when using the OR filter option, the color indicates which wells meet which filter criteria.

If a well is selected by more than one filter, the well color is a combination of the filter colors. If a well is selected by both a yellow filter and a red filter, the well is colored orange. In the Plate diagram in [Figure 26](#), the orange and yellow wells are the wells that meet the filter criteria. White wells are not selected. Gray wells were not run.



**Figure 26. Plate View with Filters**

The Gel View in [Figure 27](#) shows the expected peaks marked with colored lines on the Gel view. The well header is yellow if the well meets the filter criteria for the yellow filter, and orange if it meets the filter criteria for both the yellow and red filters. The filter option is OR so that any well meeting either or both of the filters are selected.



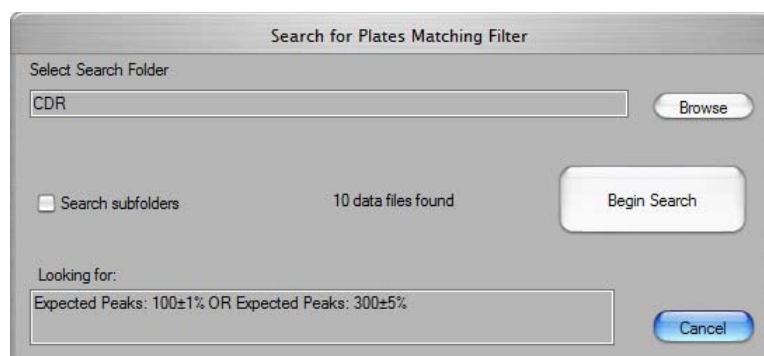
**Figure 27. Gel View with Filters**

## Searching Data Files using a Filter

When using filters, the normal process is to load all the desired data files, and then apply the filter to select the desired wells in the plates. If the exact data files that contain the wells are unknown, or if there is a large number of data files, you can use the Search Data Files feature to search a specified folder for plate data files that contain wells that match the filter criteria. As the matching wells are located, only the data files with matching wells are loaded into the workspace.

To search the data files using a filter:

- 1 Open at least one data file in the workspace.
- 2 Create the desired filters in the workspace (see [“Creating a New Filter” on page 46](#)).
- 3 Click the **Search Data Files** button in the [Filter View](#). The Search for Plates Matching Filter window opens as shown in [Figure 28](#).



**Figure 28. Search for Plates Matching Filter Window**

- 4 Either type the desired path to the data file folder in the **Select Search Folder** text box, or click the **Browse** button and select the desired data file folder. The number of data files in the selected folder and subfolders displays in the window.
- 5 To search data files in subfolders of the selected folder, select the **Search Subfolders** check box. If not selected, only data files saved in the specified folder are searched. Subfolders of the specified folder are not searched.
- 6 Click the **Begin Search** button. The Plate Search Progress window displays the progress of the search.
- 7 As plates with matching wells are found, the plates are added to the workspace. The wells that match the filter criteria are selected in the current collection.

## Filter Example for Expected Peaks

Figure 29 shows a single Expected Peaks filter that includes three expected peaks: 100 +/- 10%, 300 +/- 10%, and 500 +/- 10%, with each expected peak size identified by a different color. This filter will select any wells that contain **all three** expected peaks: 100, 300, AND 500. The wells selected by this filter are colored orange in the Plate View or the Gel View. Note that the filter is selected (checked) under Available Filters, indicating that the filter is being applied to the data.

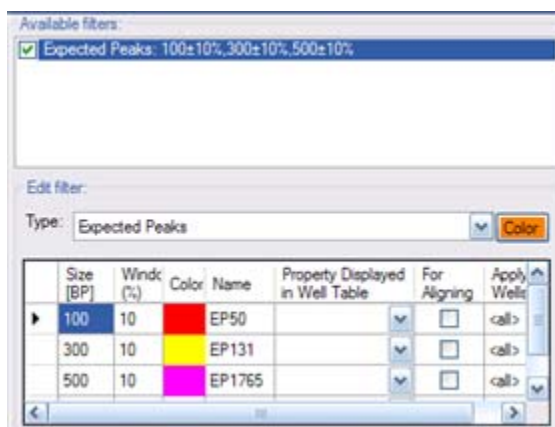


Figure 29. Expected Peaks Filter with Three Peaks

To select wells that contain **any of the three** peaks, create a separate filter for each peak as shown in Figure 30 and select the OR option.

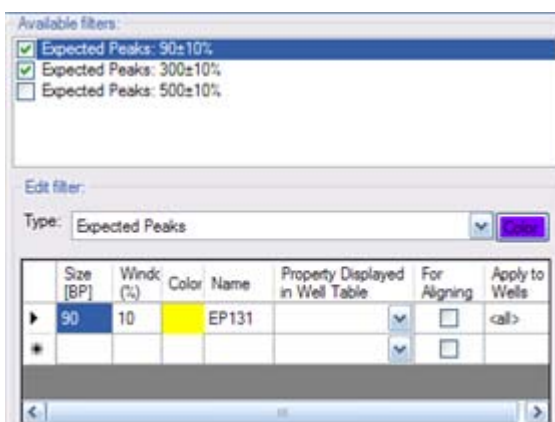


Figure 30. Three Separate Expected Peaks Filters

When using multiple filters that include peak properties, if AND(Peak) is selected, a single peak in the well must meet all selected filter properties. See the examples below, which each use two filters:

## Filter Example for Expected Peaks (Continued)

- Height > 100 AND(Peak) Conc > 50 selects any well that contains a single peak that meets both criteria.
- Height > 50 AND(Well) Conc > 50 selects any well that contains a peak with height greater than 50 and a peak with concentration greater than 50. (The peaks do not have to be the same peak.)
- Height >100 OR Conc > 50 selects any well that contains any peak that meets either (or both) criteria.
- Height >100 AND(Peak) Height <50 does not select any wells because no peak can have a height that is both less than 50 and greater than 100. Use OR to select wells that contain peaks that match either criteria. Use AND(Well) to select wells that contain peaks that each match a single criteria.

Expected Peak Filters can contain multiple size peaks in the same filter as shown in [Figure 29](#). Expected Peak filters with multiple peak sizes in the same filter always select only wells that contain all the peaks listed.

## Using Replicates

Replicates define wells on a plate that contain the same sample. Since all replicates should contain the same peaks, replicates can be used to identify erroneous peaks caused by signal noise over baseline fluctuations. The identified erroneous peaks can be excluded to remove them from the %Purity calculation.

Replicates can also be used to improve measurement accuracy and assess variability within a measurement. To use replicates:

- 1 Define the replicate wells (see [Defining Replicates](#)).
- 2 If automatic peak exclusion is desired, select the desired Exclude Peak when Missing in Replicate Option (see [page 56](#)).
- 3 If replicates are being used to improve measurement accuracy by averaging, print a replicate report (see [page 57](#)).

## Defining Replicates

Before excluding a peak from replicate wells using the [Excluded Peaks Tab](#), the replicate wells must be defined in the [Replicates Tab](#). Replicates can be defined as part of the assay or after the run in the assay analysis settings.

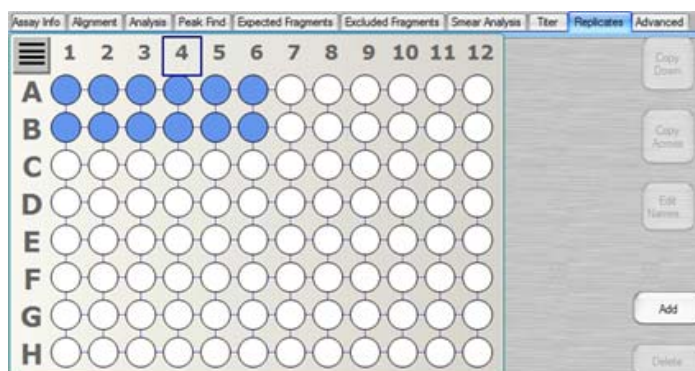
### To open the Replicates tab:

- For an existing data file, open the data file in a workspace. Select **Analysis** → **Analysis Settings**. The [Assay Analysis Window](#) opens. Click the [Replicates Tab](#).
- In an assay file, select **Tools** → **Assay Editor**. The Select Assay To Edit window (or CDR Manager window for GxP instruments) opens. Select the assay that you want to add the replicates to and click the Open or Import button. The Assay Analysis window opens. Click the [Replicates Tab](#).

### To define the replicates:

- 1 Select the wells that all contain the same sample. Click and drag to select contiguous wells. Shift + click or Shift + click and drag to add additional wells. To select the rows shown in [Figure 31 on page 54](#), click on well A1 and drag to well B6.

## Defining Replicates (Continued)



**Figure 31. Wells Selected for Replicate Set**

- 2 Click the **Add** button to create a replicate set. Each of the selected wells is marked with the same number to indicate that the wells contain the same sample as shown in [Figure 32](#).

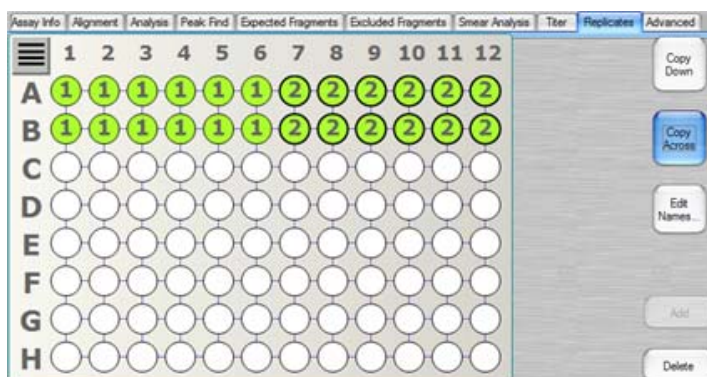


**Figure 32. Replicate Set Added**

- 3 If the replicates use a common pattern, click any well in a replicate set and then click the **Copy Down** or **Copy Across** buttons to copy the defined pattern across the rows or down the columns.

To create the pattern in [Figure 33 on page 55](#), click any well marked with the number “1” and then click the **Copy Across** button.

## Defining Replicates (Continued)



**Figure 33. Copy Across**

To create the pattern in [Figure 34](#), click any well marked with the number “1” and then click the **Copy Down** button.



**Figure 34. Copy Down**

- 4 To rename a default replicate name, click the **Edit Names** button. The Replicate Name Editor window opens. Type the desired replicate name over the default name and click the **OK** button.
- 5 To delete a single replicate set, click any well marked in the replicate set and then click the **Delete** button.
- 6 To clear all selections and replicate sets on the plate, click the **Clear** button below the plate diagram.



## Defining Replicates (Continued)

- 7 To copy a replicate definition to another plate:
  - Click the **Export** button. The Export Replicates Table window opens.
  - Type the desired replicate export file name and click the **Save** button.
  - Click the **OK** button or **Cancel** button on the [Replicates Tab](#) to exit the [Assay Analysis Window](#).
  - Select another plate in Workspace or select **File → Import Data File** to add another plate.
  - Select **Analysis → Analysis Settings** to open the [Assay Analysis Window](#), and then click the [Replicates Tab](#).
  - Click the **Import** button to import the saved exported file.

## Selecting the Exclude Peak when Missing in Replicate Option

After creating the desired replicates on the Replicates tab (see [“Defining Replicates” on page 53](#)):

- 1 Click the [Excluded Peaks Tab](#) on the Assay Analysis window.
- 2 Select the desired Excluded Peaks option:
  - **Disabled** - No peaks will be excluded based on the replicates.
  - **Any** - A peak is excluded if it is not found in ANY of the other wells in the replicate set.
  - **All** - A peak is excluded if it is not found in ALL of the other wells in the replicate set.

**Note:** If a replicate set only contains two wells, the Any and All options produce the same results.



## Printing Replicate Reports

After creating the desired replicates on the Replicates tab (see [page 53](#)), replicate reports can be printed to a printer or to a PDF file (if desired). See [“Print Replicate Report” on page 95](#) for an example of a replicate report.

To print a replicate report:

- 1 Select **File** → **Print** from the [Menu Bar](#). The [Print Window](#) opens.
- 2 Click the **Print Replicate Reports** button. The [Replicate Report Generator Window](#) opens.
- 3 For each desired Replicate Report, complete Step 4 to Step 8 below create a replicate report definition.
- 4 Type the desired title into the **Report Title** column.
- 5 Select a well property to be analyzed from the **Property** drop-down menu.

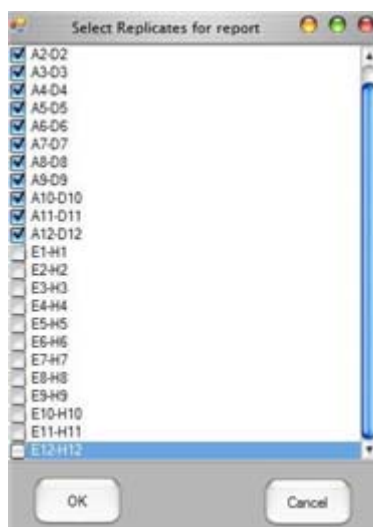
### NOTE



*The Property drop-down menu lists well properties only. To analyze peak properties, convert the peak properties into well properties using the existing Expected Peak mechanism (see [“Entering EFs, EPs, or EGs in the Assay Analysis Window” on page 40](#)).*

- 6 Double-click inside the **Replicates** column to select the replicate wells to be analyzed (see [Figure 35 on page 58](#)).

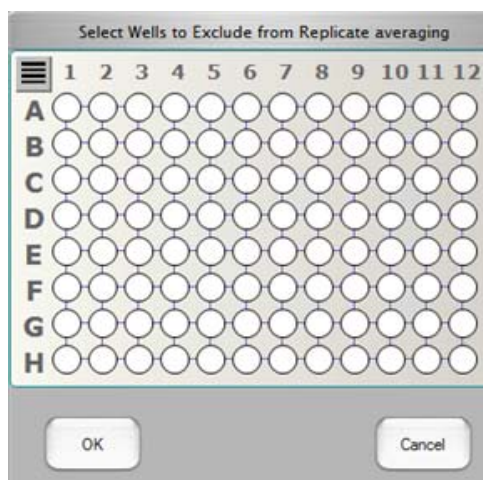
## Printing Replicate Reports (Continued)



**Figure 35. Select Replicates for Report**

Use the default “<all>” value in the **Replicates** column to analyze all replicate sets defined for the plate (as described in [“Defining Replicates” on page 53](#)).

- 7 To exclude a well from the replicate set due to an anomaly in the well, click the **Exclude Wells** button. The Select Wells to Exclude from Replicate averaging window opens (see [Figure 36](#)). Select the wells not to use in the statistical analysis. These wells appear in the report, but with strike-through values to indicate they are not included in the statistics.



**Figure 36. Select Wells to Exclude from the Replicate averaging**

## Printing Replicate Reports (Continued)

- 8 To add Custom Columns to enhance the Replicate Report (optional):
  - a Double-click inside the **Custom Columns** field of the report. The [Replicate Equation Editor Window](#) opens.
  - b Type the desired Custom Column title into the **Title** column.
  - c Select the **Check Box?** column to add a check box custom column. If the result of the equation set in the **Equation to Evaluate** column is true, the check box in the check box column is selected in the replicate report. If the result of the equation is false, the check box is not selected.
  - d Enter the annotations for the equation to evaluate in the Replicate Report manually or automatically:

### NOTE



*Separate multiple annotations for the equation with a semicolon [;].*

#### Manually

- Click the **Annotate Results** button on the [Replicate Report Generator Window](#). The replicate report displays in table format.
- Type the desired annotations into the empty field in the table.
- Edit any other fields as desired.

#### Automatically

- Double-click inside the Equation to Evaluate field in the [Replicate Equation Editor Window](#).
- Select the options above the table in the [Replicate Equation Editor Window](#) to add the desired annotations to apply to the equation to evaluate, including **Mean**, **StdDev**, **CV**, a specific replicate property from the **Replicate Selector Drop-Down List**, **+**, **-**, **\***, **/**, **<**, **>**, **<=**, **>=**, **And**, **Or**, **(**, **)**, and/or a specific number from the **Insert Number** text box.
- Click the **OK** button.
- If desired, click the **Annotate Results** button to preview the report in table format and edit any of the fields as desired.

## Printing Replicate Reports (Continued)

### NOTE



*Once you become familiar with the equation syntax, you may bypass the function buttons and type the desired equation directly into the Equation to Evaluate column, or use the manual method above.*

- 9 Select the **Select** check box on the [Replicate Report Generator Window](#) table to add the selected equation to the Replicate Report.
- 10 Click the **Print Preview** button to view a preview of the Replicate Report.
- 11 Click the **Print To PDF** button to print the Replicate Report as a PDF file.
- 12 Click the **Print** button to print the Replicate Report to a printer.

## Modifying Analysis Parameters

Some analysis parameters can be changed in the software to modify the data evaluation for sample analysis. The following procedures are included in this section:

- [“Changing the Peak Find Parameters” on page 62](#)
- [“Adding a Peak” on page 63](#)
- [“Splitting a Peak” on page 64](#)
- [“Manually Excluding a Peak” on page 63](#)
- [“Merging Two or More Peaks” on page 64](#)
- [“Removing a Peak Merge” on page 66](#)
- [“Adjusting the Peak Baseline” on page 66](#)
- [“Setting the Baseline for a Range of Peaks” on page 67](#)
- [“Selecting a Default Ladder” on page 68](#)
- [“Using the Default Ladder for Alignment” on page 69](#)
- [“Exporting the Default Ladder in an Assay” on page 69](#)

These settings can be changed after the run is complete or when reanalyzing a previously saved data file.

## Changing the Peak Find Parameters

After data filtering, the peak find algorithm locates the peaks and calculates the local peak baselines. The algorithm begins by finding all the peaks above the noise threshold to determine the baseline, after which any peaks below the noise threshold are rejected. A local baseline is calculated for each peak to allow for baseline drift.

The following Peak Find parameters can be changed:

- Min Peak Height
- Min Peak Width
- Slope Threshold
- Inflection Threshold
- Start Time
- End Time
- Filter Width
- Baseline Plateau

To change the Peak Find parameters for all wells:

- 1 Select **Analysis → Analysis Settings** to open the [Assay Analysis Window](#), and then click the [Peak Find Tab](#).
- 2 Change the parameters as necessary at the top of the window.
- 3 Click the **OK** button to save the setting, reanalyze the data, and close the window.  
Click the **Apply** button to apply the changes and reanalyze the data, but keep the Assay Analysis window open.  
Click the **Apply Global** button to apply the settings to all plates in the workspace and reanalyze the data, but keep the Assay Analysis window open.

To change peak find settings for individual wells:

- 1 Select **Analysis → Analysis Settings** to open the [Assay Analysis Window](#), and then click the **Peak Find Tab**.
- 2 In the Well drop-down list, select the well number that you want to change the settings for.
- 3 Change the settings at the bottom of the window under **Well Peak Find Settings** to change the settings for the selected well.
- 4 Click the **OK** button to save the setting, reanalyze the data, and close the window.  
Click the **Apply** button to apply the changes and reanalyze the data, but keep the Assay Analysis window open.

## Adding a Peak

You can manually add a peak in a region where a peak has not been identified.

- 1 In the [Graph View](#), right-click at the top of the area where the peak is to be added. The area must be outside any previously identified peak and the cursor must be an up arrow.
- 2 Select **Add Manual Peak** from the shortcut menu. A new peak centered at the selected location is created.
- 3 If necessary, adjust the [Peak Baseline](#).

## Manually Excluding a Peak

You can manually exclude any peak or fragment from being used in the analysis. (To exclude specific peaks sizes, use the [Excluded Peaks Tab](#).)

To manually exclude a peak:

- 1 In the [Peak Table View](#), right-click on the peak to be excluded.
- 2 Select **Exclude Peak** from the shortcut menu. The Type for the peak changes to X (excluded), and the value is not used in the analysis.
- 3 Right-click on an Excluded Peak in the peak table and select **Include Peak** to include the peak in the data analysis.

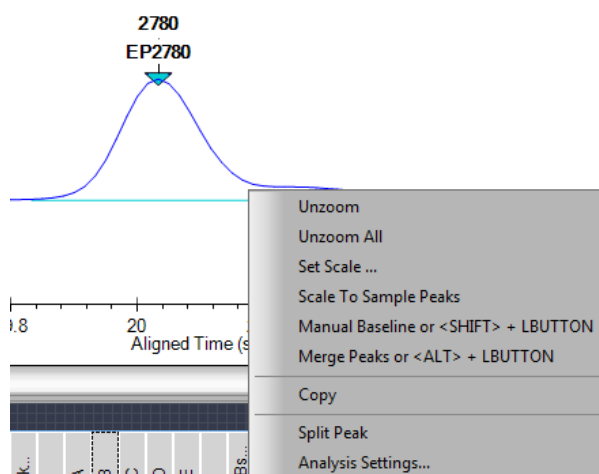
OR

- 1 In the [Graph View](#), right-click near the top of the peak to be excluded.
- 2 Select **Exclude Peak** from the shortcut menu. The Type for the peak changes to X (excluded), and the value is not used in the analysis.
- 3 Right-click on an Excluded Peak in the Graph view and select **Include Peak** to include the peak in the data analysis.

## Splitting a Peak

If two poorly resolved peaks have been identified as a single peak, you can split the single peak into two separate peaks.

- 1 In the [Graph View](#), zoom in as necessary to view the single peak. See [“Zoom In and Zoom Out” on page 81](#).
- 2 Position the cursor inside the peak at the horizontal location where you want to split the peak. (The Split Peak option is not available if the cursor is an up arrow. Move the cursor until the peak is not selected.)



**Figure 37. Splitting a Peak**

- 3 Right-click on the graph and select **Split Peak** on the shortcut menu. A new Manual Peak is created abutting the original peak.

## Merging Two or More Peaks

If the analysis has split a single peak into multiple peaks due to undulations in the shoulders or craters in the peak, these adjacent peaks can be merged into a single peak. The tallest of the selected peaks becomes the identified peak with its extends expanded to encompass the merged peaks. The tallest peak has the area, concentration, and %purity of the merged collective. The other peaks appear as excluded peaks in the peak table and no longer contribute to %purity.

To merge two or more adjacent peaks:

- 1 In the [Graph View](#), zoom in as necessary to view the peaks to be merged. See [“Zoom In and Zoom Out” on page 81](#).



## Merging Two or More Peaks (Continued)

- 2 Hold down the ALT key + Left Mouse button while performing the bullet steps below:

OR

Right-click on the graph and select **Merge Peaks** from the drop-down menu, and perform the bullet steps below:

- Click the Mouse inside the peak furthest to the left to be merged.
- Drag the Mouse to the peak further to the right to be merged. A green line displays on the graph tracking the start and end points.

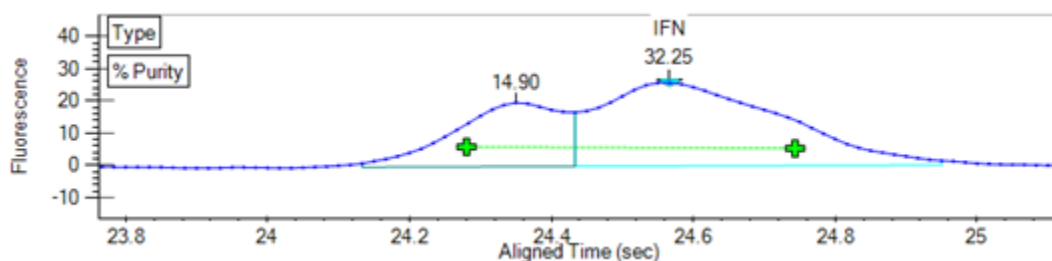


Figure 38. Start and End Points of Peak Merge

- Release the Mouse. All peaks within the start and end points are merged into a single peak. An X displays above the smaller peak indicating it has been excluded to allow the main peak to extend across it.

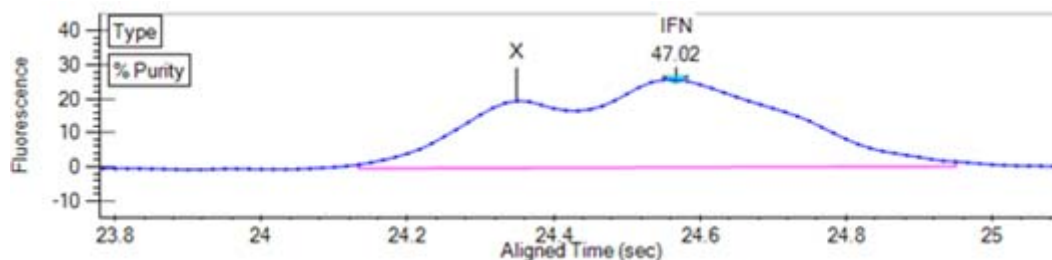


Figure 39. Resulting Merged Peak

### NOTE



*If Merge Peaks from the drop-down was used to merge the peaks, right-click on the graph and select Merge Peaks to exit Merge Peak mode. This step is not necessary if the ALT key + Left Mouse button was used to merge the peaks.*

## Removing a Peak Merge

To remove a peak merge:

- 1 Right-click on the baseline of the merged peak.
- 2 Select **Reset to Analyzed Base** from the shortcut menu.  
Excluded peaks inside the extended baseline of the merged peak will be included. Baseline adjustments made prior to the merge will also be undone.

### NOTES



*If multiple electropherograms overlaid in the graph view were merged, removing these merges requires the undo function on each electropherogram.*

## Adjusting the Peak Baseline

The Peak Baseline can be manually adjusted in the Graph View.

- 1 In the [Graph View](#), zoom in on the peak baseline as described in [“Zoom In and Zoom Out” on page 81](#). (If the peak baselines are not displayed, select **Show Peak Baselines** in the [Graph View Properties](#) to display the baseline for each peak.)
- 2 Click the triangle at one end of the peak baseline and drag to the desired location.

To reset the baseline to the original position, right-click near the baseline end point and choose **Reset to Defaults**.

## Setting the Baseline for a Range of Peaks

A straight line can be drawn under multiple peaks to create a single baseline for all peaks above the straight line.

To draw a single baseline:

- 1 In the [Graph View](#), zoom in on the peaks as described in [“Zoom In and Zoom Out” on page 81](#). (If the peak baselines are not displayed, select **Show Peak Baselines** in the [Graph View Properties](#) to display the baseline for each peak.)
- 2 Holding the SHIFT key, click at the point where the baseline will begin and drag to the desired end point of the baseline.
- 3 Release the mouse at the end of the baseline. The baselines for peaks that are entirely contained within the baseline span are adjusted to the new baseline.

To draw multiple baselines using Manual Baseline mode:

- 1 In the [Graph View](#), zoom in on the peaks as described in [“Zoom In and Zoom Out” on page 81](#). (If the peak baselines are not displayed, select **Show Peak Baselines** in the [Graph View Properties](#) to display the baseline for each peak.)
- 2 Right-click on the graph, away from a peak, and select **Manual Baseline** on the shortcut menu.
- 3 Click and drag in the graph to draw manual baselines.  
**Note:** Clicking and dragging in the graph does not zoom in while Manual Baseline mode is on. Clicking and dragging in the [Gel View](#) still zooms in when Manual Baseline mode is on.
- 4 To turn off Manual Baseline mode, right-click on the graph, away from a peak, and select **Manual Baseline** again.

## Removing a Manual Baseline

To reset a manual baseline back to the original analyzed baseline:

- 1 Right-click on one end of the manual baseline and select **Reset to Analyzed Base** from the shortcut menu.

To reset all manual baselines:

- 1 Right-click on one end of a manual baseline and select **Reset All Peak Bases**.
- 2 Click **OK** in the Reset All Peak Bases window.

## Selecting a Default Ladder

For DNA, gDNA, and RNA assays, a ladder in an assay can be defined as the default ladder. The default ladder can be used as the ladder for wells on the plate, can be applied to all of the plates in the open collection, or can be saved as the default ladder in a new assay.

To set a specific ladder on a plate as the default ladder for the plate:

- 1 With the plate data file open, select **Analysis → Analysis Settings** to open the [Assay Analysis Window](#), and then click the [Peak Find Tab](#).
- 2 Under **Well Peak Find Settings**, in the **Well** drop-down list, select the ladder that will be defined as the default ladder.
- 3 Click the **Save as Default Ladder** button. (The Save as Default Ladder button only displays when a ladder is selected.)
- 4 Click the **Apply** button to save the default ladder settings. The [Analysis Tab](#) displays the ladder data in the Default Ladder table and the Markers table (see [Figure 40](#)).

The screenshot shows the 'Assay Analysis' window with the 'Analysis' tab selected. The 'Default Ladder' section contains a table with the following data:

Size [BP]	Time (sec)	Area
100	13.57	26.97
300	16.33	25.78
500	17.78	26.53
700	18.35	24.58
1100	18.95	22.59
1900	19.60	21.35
2900	20.10	21.26
4900	20.67	17.29

Below the table is a 'Clear Default Ladder' button. To the right, the 'Ladder Concentration' is set to 1.00 ng/ul. The 'Standard Curve' section has 'Point to Point' selected. The 'Data Range' section shows 'Baseline' at 6.0 sec and 'Well End' at 28.0 sec. The 'Markers' section contains a table with the following data:

	Conc. ng/ul	Size [BP]	Time(sec)	Height	Area
Lower	5.00	15.0	12.53	1627.0	217.4
Upper	2.50	7000.0	21.2	372.6	62.6

**Figure 40. Default Ladder Settings**

- 5 The Ladder Peak Time and Area settings can be changed in the Default Ladder table, but default ladder peaks cannot be added or deleted and the ladder peak sizes cannot be changed.
- 6 The Marker Time, Height and Area can be changed in the Markers table.

## Selecting a Default Ladder (Continued)

- 7 Click the **Apply** button at the bottom of the window to save the changes to the active plate. Click the **Apply Global** button to apply the default ladder settings to all open data files in the collection. (This allows you to import the default ladder into a plate that does not include any good ladders on the plate.)
- 8 See [“Using the Default Ladder for Alignment” on page 69](#) to align wells in the plate using the default ladder.

## Using the Default Ladder for Alignment

For DNA, gDNA, and RNA assays, after the default ladder is selected for a data file, the default ladder must be assigned to the desired wells in the plate.

- 1 With the plate data file open, select **Analysis → Analysis Settings** to open the [Assay Analysis Window](#), and then click the [Alignment Tab](#).
- 2 Select the **Align Well Groups to Specified Ladder** option.
- 3 For each group of wells under Align Well Group, select **Default Ladder** in the **To Ladder** column.
- 4 Click the **Apply** button to apply the changes to the active data file or click the **Apply Global** button to apply the changes to all data files in the current collection.

## Exporting the Default Ladder in an Assay

The default ladder in a data file is included in the analysis settings for a new assay when the settings are exported as an assay. Exporting the assay enables you to use the default ladder in future runs.

- 1 After clicking the **Apply** or **Apply Global** button in the [Assay Analysis Window](#), the **Export as Assay** button displays.
- 2 Click the **Export as Assay** button. The Export Assay Settings from Plate to Assay File window opens.
- 3 Select the desired location for the assay file, type the desired name for the assay file, and click the **Save** button.
- 4 Select the new assay in the Run Tab on the Start Run Window when starting the next run. The new data file will include the default ladder.

## Clearing the Default Ladder in a Plate

To delete the default ladder for a plate and return the alignment to the ladder settings for the assay type:

- 1 With the plate data file open, select **Analysis → Analysis Settings** to open the [Assay Analysis Window](#), and then click the [Analysis Tab](#).
- 2 Click the **Clear Default Ladder** button at the bottom of the Default Ladder table.

## Changing the Time Window for Analysis

The **Start Time** and **End Time** parameters in the **Peak Find tab** define the time window within which peaks are found.

To change the Start Time and End Time parameters for all wells in the open assay:

- 1 Select **Analysis → Analysis Settings** to open the [Assay Analysis Window](#), and then click the **Peak Find Tab**.
- 2 Change the parameters as necessary.
- 3 Click the **OK** button to save the setting, reanalyze the data, and close the window.  
Click the **Apply** button to apply the changes and reanalyze the data, but keep the Assay Analysis window open.

## Marker Peaks

This section contains the following sections:

- [“Aligning or Unaligning the Marker Peaks” on page 71](#)
- [“Upper and Lower Marker Peaks for DNA Assays” on page 72](#)
- [“Lower Marker Peaks in Protein or RNA Assays” on page 73](#)
- [“Lower Marker Peaks in Glycan Assays” on page 74](#)

### Aligning or Unaligning the Marker Peaks

To perform data analysis for DNA, Protein, RNA, and Glycan assays, the LabChip GX Reviewer software aligns marker peaks included in the sample wells with markers from the ladder.

- To view the unaligned data (spike rejected, filtered and baseline corrected), choose **Analysis** → **Turn Off Analysis**.
- To re-enable analysis, choose **Analysis** → **Turn On Analysis**.

The default setting for this function is enabled. Turning off the analysis displays the data without aligning the markers in the wells and the ladders.

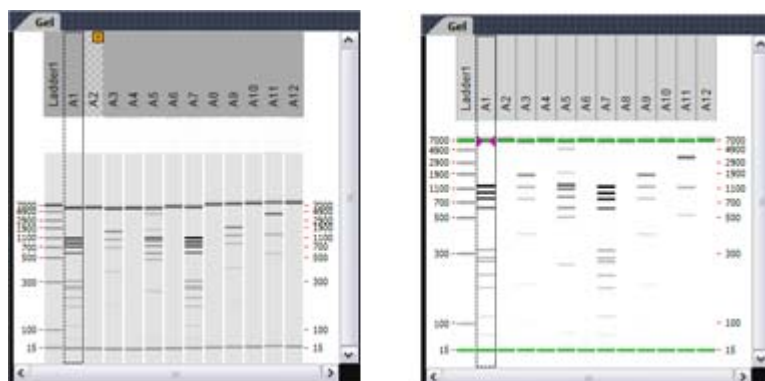


Figure 41. Data Before and After Alignment

## Upper and Lower Marker Peaks for DNA Assays

For each DNA sample, the upper and lower marker peaks are assigned first and then the data is aligned so that the well markers match the ladder markers in time, allowing the size and concentration of the sample peaks to be determined.

For DNA assays, the first peak is assigned to be the lower marker and is then offset to match the lower marker in the ladder. The upper marker is then assigned to the last peak in the sample well or to the peak nearest the ladder's upper marker. The **Upper Marker** and **Lower Marker** are *aligned* to the ladder markers by resampling the well data in a linear stretch or compression using a point-to-point fit.

If the sample marker peaks are either more than twice as far apart or less than half as far apart as the ladder markers, they are assumed to be the wrong peaks, and analysis of the well stops, producing the error **Marker peaks not detected**.

In DNA assays, the height of marker peaks is assay dependent. Ladder peaks are analyzed to calculate a marker peak threshold that is used to locate the marker peaks in the sample wells. If the marker peaks found using this calculated method fail to align with those of a sample, the LabChip GX Reviewer software will use the minimum peak height threshold setting instead (if this value is lower than the value for the marker peak). For example, the calculated threshold might be too high to find the sample's markers if they happen to be very small for some reason. Either no markers will be found or the wrong peaks will be assumed to be markers and these may not align with the ladder markers. Consequently, the software attempts to use the minimum peak height threshold that, if it is set low enough, will catch the real markers, allowing the sample to align.

If you get unexpected peaks in the ladder analysis or the markers have been set incorrectly, you can manually exclude peaks or set a peak to be used as a marker.

### NOTES



- *Excluding a peak or manually setting a peak to be an upper or lower marker for a DNA assay can cause errors with analysis.*
- *You can move the boundary between the **Peak Table** and the **Graph view** up or down to increase or decrease the size of the Peak Table, making it possible to see all of the results at once.*



## Upper and Lower Marker Peaks for DNA Assays (Continued)

Right-clicking in the [Peak Table View](#) of a well of a DNA assay opens a shortcut menu with the following commands:

- Include Peak (only for peak type “?”)
- Exclude Peak
- Force Lower Marker
- Force Upper Marker
- Add Expected Peak

### NOTE



*You can also right-click on a peak in the [Graph View](#) to view the same menu.*

## Lower Marker Peaks in Protein or RNA Assays

For each protein or RNA sample, the first peak in the sample is designated as the Lower Marker. After all lower markers are assigned, the data is aligned so that the well markers match the ladder markers in time, allowing the size and concentration of the sample peaks to be determined.

If there are unexpected peaks in the ladder analysis or if the marker has been set incorrectly, you can manually exclude peaks or set a peak to be used as a marker.

### NOTES



- *Excluding a peak or manually setting a peak to be the lower marker can cause analysis errors.*
- *You can move the boundary between the **Peak Table** and the **Graph** view up or down to increase or decrease the size of the Peak Table, making it possible to see all of the results at once.*

Right-clicking in the [Peak Table View](#) of a well of a Protein or RNA assay opens a shortcut menu with the following commands:

- Include Peak (only for peak type “Xsys” or “?”)
- Exclude Peak
- Force Lower Marker
- Force Expected Peak

## Lower Marker Peaks in Glycan Assays

For each Glycan sample, the lower marker is added to the samples and ladders. The lower marker is identified because the concentration is much higher than the sample or ladder. After all lower markers are assigned, the data is aligned so that the well markers match the ladder markers in time, allowing the size and corrected area of the sample peaks to be determined.

If there are unexpected peaks in the ladder analysis or if the marker has been set incorrectly, you can manually exclude peaks or set a peak to be used as a marker.

### NOTES



- *Excluding a peak or manually setting a peak to be the lower marker can cause analysis errors.*
- *You can move the boundary between the **Peak Table** and the **Graph** view up or down to increase or decrease the size of the Peak Table, making it possible to see all of the results at once.*

Right-clicking in the [Peak Table View](#) of a well of a Glycan assay opens a shortcut menu with the following commands:

- Include Peak (only for peak type “Xsys” or “?”)
- Exclude Peak
- Force Lower Marker
- Force Expected Peak

## Saving and Exporting Assays

Assays are created by PerkinElmer and are included with the LabChip GX or GX Touch software. The instrument and software settings used to run each plate and to analyze the plate are contained in an assay (.asy or .asyx) file. If the default analysis settings often need to be modified for more optimal analysis, a new assay file can be created with the modified settings to be used on subsequent runs.

To save a modified assay:

- 1 Right-click on the plate title in the [Plate View or Plate List](#), select **Export Assay**, specify a name and location for the assay file, and click the **Save** button.  
-- OR --  
On the [Assay Analysis Window](#), click the **Export as Assay** button, specify a name and location for the assay file, and click the **Save** button.

The procedure above can also be used to automatically include a set of expected peaks in the assay.

If the LabChip GxP option is installed, data files are saved in the Central Data Repository (CDR). The CDR is a secure folder that can only be accessed by the LabChip GX Touch software and the LabChip GX Reviewer software. The CDR can be located on the LabChip GX Touch instrument, the LabChip Reviewer computer, or a network server.

If the LabChip GxP option is installed and Require Signature on File Update is selected in the Set Policies tab on the [User Administration Window](#), the user must have signature rights to save an updated data file. If the data file is locked, a user with Unlock rights must unlock the data file before changes can be saved.

To save the data file when the LabChip GxP option is installed and Require Signature on File Update is selected:

- 1 The [Perform Electronic Signature Window](#) opens when you save a data file.
- 2 Select the name of the user who is signing the data file in the **Username** drop-down list.
- 3 Type a **Comment** that meets the requirements of the compliance policies.
- 4 If appropriate, select the desired **Approval State**.

## Saving and Exporting Assays (Continued)

- 5 If desired, select the **Lock** check box to lock the data file and prevent it from being changed.
- 6 Type the **User Password** for the signing user.
- 7 Click the **Sign** button. The Signature Performed window confirms that the signature has been performed.
- 8 Click the **OK** button. The signature is recorded in the data file.

### NOTE



*Changing the analysis settings and saving the plate data file does not change the raw data from the run. Only the display of the data is changed.*

If you change the analysis settings without saving the new settings, and then try to close the workspace, exit the software, or acquire new data, you are prompted to save the changes. Selecting Yes opens the [Save Workspace As Window](#).

## Changing the View of the Data

The views in the [LabChip GX Reviewer Main Window](#) can be customized to display data according to the preferences of the user. These options do not change the *raw* data but provide different means of displaying the data.

To change the view in the main window, see:

- [“Viewing Gels” on page 78](#)
- [“Viewing Zero Baselines” on page 79](#)
- [“Adjust Pane Widths” on page 80](#)
- [“Change Plate Order” on page 80](#)
- [“Show or Hide Views” on page 81](#)
- [“Zoom In and Zoom Out” on page 81](#)
- [“Viewing Graphs in the Overlay Electropherograms Tab” on page 82](#)
- [“Viewing Graphs in the Electropherograms Tab” on page 83](#)
- [“Viewing Analysis Errors and Warnings” on page 85](#)
- [“Viewing Multiple Properties in the Well Table View” on page 86](#)
- [“Exporting Data Manually” on page 99](#)

## Viewing Gels

To compare the gels generated by the instrument, view the gels in the [Gel View](#).



**Figure 42. Gel View**

The color, width, and contrast of the gels can be changed using the [Gel View Properties](#).

To rearrange gels, click on the column header (well name) and drag the well to the desired location. To hide a well, select the well and then click the (X) button on the column header, or right-click on the well in the [Plate View](#) or [Plate List](#) and select **Remove Well**.

## Viewing Zero Baselines

All electropherograms produced with the instrument show some amount of background fluorescence. By default, the LabChip GX Reviewer software enables the zero baseline function. To remove the zeroing, select **Analysis** → **Analysis Settings** to open the [Assay Analysis Window](#), click the **Peak Find Tab**, and select the **None** check box under Baseline Algorithm.

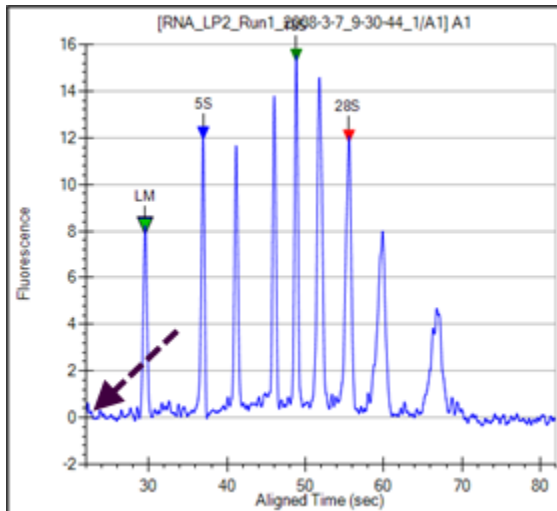


Figure 43. Zero Baseline On

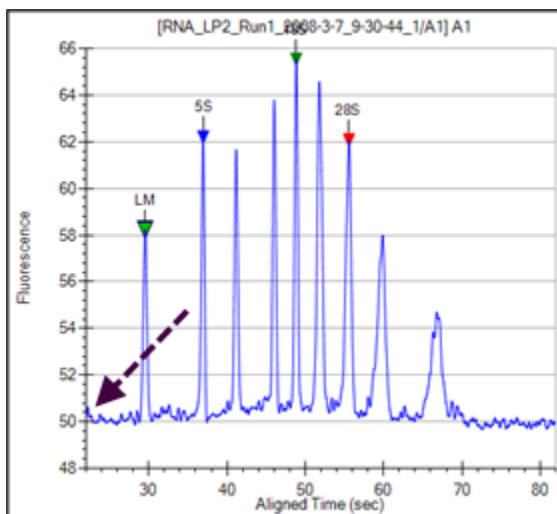


Figure 44. Zero Baseline Off

## Adjust Pane Widths

The [LabChip GX Reviewer Main Window](#) displays several different views of the data files open in the workspace. You can change the height and width of the views to make the views smaller or larger.

To adjust panes:

- 1 Place the cursor over the edge of the pane that you want to adjust. The cursor changes to a line with arrows on each end.
- 2 Click and drag up, down, left, or right. The pane is resized after you release the mouse button. The layout setting is saved as part of the collection.
- 3 To save the setting, save the workspace. To create new collections with the same settings, the collection can be saved as a collection template (see ["Collection Menu" on page 140](#)).

## Change Plate Order

The [Plate View or Plate List](#) displays the plates in the order they are imported into a collection. If desired, you can change the plate order.

To change the plate order:

- 1 Select the **List** tab at the bottom of the Workspace pane.
- 2 Place the cursor over the plate to be moved.
- 3 Click and drag up or down to the desired location. The new plate order displays on the [Plate View or Plate List](#) when you release the mouse button.



## Show or Hide Views

The views displayed in the [LabChip GX Reviewer Main Window](#) can be hidden to maximize other views in the main window.

To hide a view:

- 1 Select **Collection** → **Layout** on the LabChip GX Reviewer Main window. The [Layout Options Window](#) opens.
- 2 Click on the location that is selected for the view to clear the selection. The view is hidden.
- 3 If a location (Left, Right, or Bottom) does not contain any views, the pane closes and the remaining panes enlarge to fill the space.

Note: The [Gel View](#) is always displayed and cannot be hidden.

To display a hidden view:

- 1 Select **Collection** → **Layout** on the LabChip GX Reviewer Main window. The [Layout Options Window](#) opens.
- 2 Click on the desired location for the hidden view (Left, Right, or Bottom). If multiple views are displayed in the same location, use the tabs at the top of the location to switch between views.

## Zoom In and Zoom Out

You can zoom in and out on data displayed in the [Gel View](#) and the [Graph View](#). The Graph View and the Gel view both zoom to the same levels when either view is zoomed in.

To zoom in:

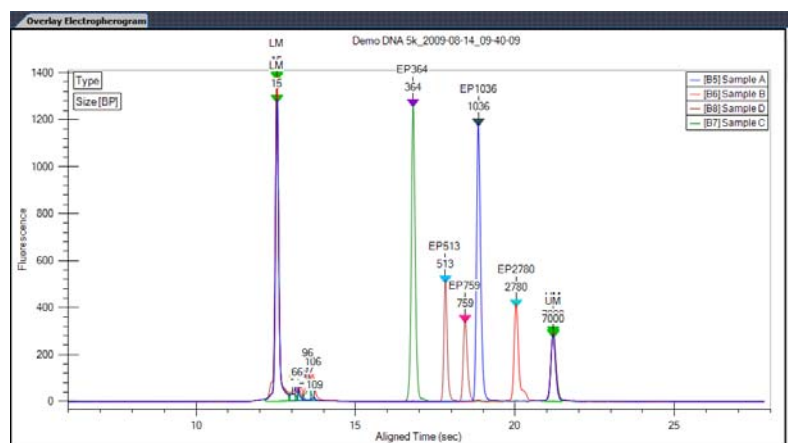
- Click and drag to enclose the region of interest. When you release the mouse button, the selected area enlarges to fill the view. In the Gel view, all lanes in the collection zoom to the same level.
- You can continue zooming in until you reach the maximum magnification (the graph will not zoom in any closer).
- Use the horizontal scroll bar under the graph to pan from left to right.

To zoom out:

- Right-click in the Graph view or Gel view and select **Unzoom** to go to the previous zoom setting or select **Unzoom All** to zoom out to the default view.

## Viewing Graphs in the Overlay Electropherograms Tab

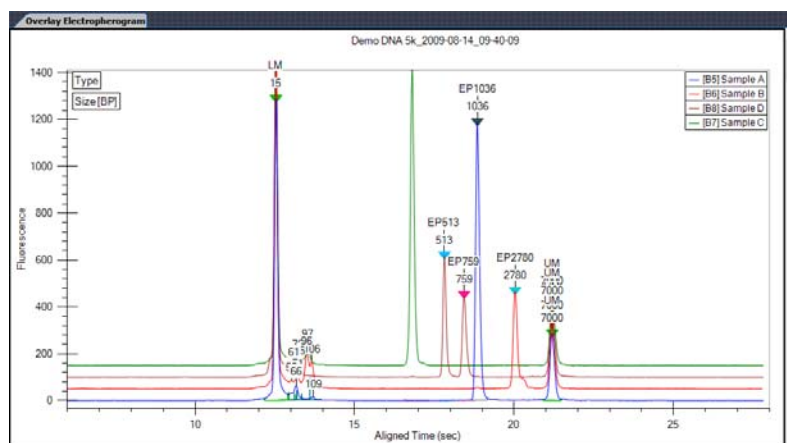
If the [Overlay Electropherograms Tab](#) is not open, select **Collection** → **Layout** on the [LabChip GX Reviewer Main Window](#), select the location where you want to display the Overlay Electropherograms tab, and click the **Apply** button. The Overlay Electropherograms tab opens.



**Figure 45. Overlay Electropherograms Tab with Multiple Graphs**

Data from multiple wells can be overlaid in the same graph for visual comparison. Click on one well, then hold down the CTRL key and click on the additional wells to view in the graph. Each peak graph is shown in a different color and line style with a legend at the top of the window. You can remove wells from the overlay by CTRL + clicking the corresponding wells (the bounding box disappears).

Use the Overlay Offset text box on the [Graph View Properties](#) to offset each of the graphs by the RFU value specified.



**Figure 46. Overlay Offset**

To add samples to the Overlay Electropherograms Tab, **Ctrl + click** on the sample that you want to add in the [Plate View or Plate List](#), [Gel View](#), [Well Table View](#), or [Peak Table View](#). Selected wells are identified by: dashed outlines around the selected gel lanes in the Gel view, light blue wells in the Plate view, and dark gray rows in the Well Table view and Peak Table view.

To remove a specific sample from the graph, **Ctrl + click** on the sample that you want to remove in the [Plate View or Plate List](#), [Gel View](#), [Well Table View](#), or [Peak Table View](#).

To display only one sample in the Overlay Electropherograms tab, click on one sample in the [Plate View or Plate List](#), [Gel View](#), [Well Table View](#), or [Peak Table View](#).

To view the point coordinates and size of the position of the cursor, hold down the **CTRL** or **Shift** key and move the cursor over the graph.

To view the point coordinates and slope of a point on the trace, hold down the **ALT** key and the **CTRL** key and move the cursor over the trace.

## Viewing Graphs in the Electropherograms Tab

If the [Electropherograms Tab](#) is not open, select **Collection** → **Layout** on the [LabChip GX Reviewer Main Window](#), select the location where you want to display the Electropherograms tab, and click the **Apply** button. The Electropherograms tab opens.

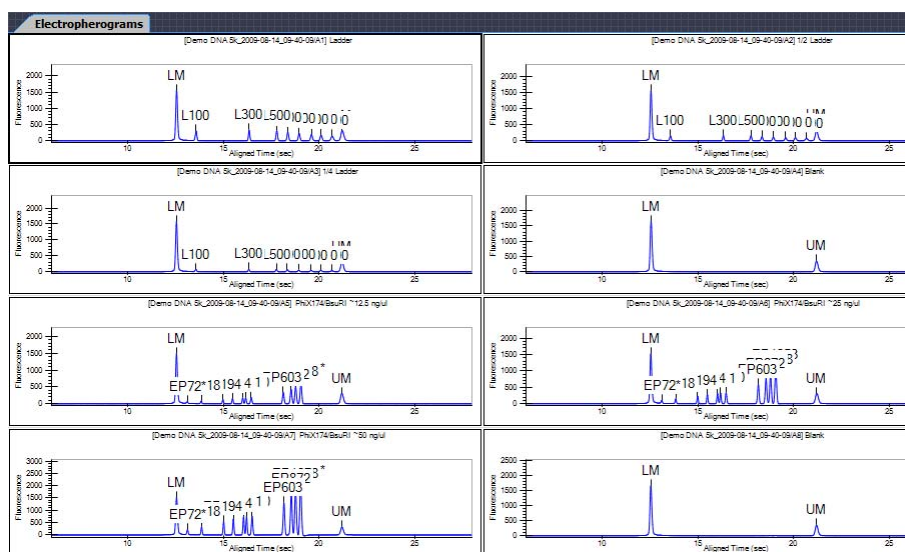


Figure 47. Electropherograms Tab with Multiple Graphs

Data from multiple wells can be displayed in the same tab for visual comparison. A separate graph for each well in the collection is displayed in the Electropherograms tab. The data file name and well name display at the top of each graph. If all of the wells are not visible, use the scroll bar on the tab to scroll through the wells in the collection.

**Zooming in or out** on one graph zooms all of the graphs in the tab to the same zoom level.

**To only display the wells selected in the [Gel View](#) or [Well Table View](#)**, select the **Graph Selected Gels Only** check box in the [Graph View Properties](#).

**To move the graphs in the tab**, in the [Gel View](#) click and drag the well to the desired position.

**To change the number of graphs displayed in the tab**, select the desired number of Rows and Columns of graphs to display in the [Graph View Properties](#). Selecting 8 Rows by 12 Columns displays an entire 96-well plate.

**To view the point coordinates and size of the position of the cursor**, hold down the **CTRL** or **Shift** key and move the cursor over the graph.

**To view the point coordinates and slope of a point on the trace**, hold down the **ALT** key and the **CTRL** key and move the cursor over the trace.

## Viewing Analysis Errors and Warnings

Analysis errors and warnings are indicated by red or yellow exclamation points in the wells in the Plate View or below the headers in the Gel View. The details of the error or warning can be displayed in the [Well Table View](#). After the Analysis Error column is added to the Well Table, the analysis error text can be displayed in the [Electropherograms Tab](#) or the [Overlay Electropherograms Tab](#).

### Viewing Analysis Errors and Warnings in the Well Table

To view the details of an analysis error or warning, display the Analysis Error in the [Well Table View](#).

- 1 Click the **Well Table** tab.
- 2 Right-click in the table header. The [Select Well Table Columns Window](#) opens.
- 3 In the **Available Columns** list, select **Analysis Error**.
- 4 Click the **Right Arrow** button to move Analysis Error to the Selected Columns list.
- 5 If desired, click and drag **Analysis Error** to the desired column location. (The top column in the list is the first column in the table.)
- 6 Click the **Save** button.

### Viewing Analysis Errors and Warnings on the Graphs

The text of analysis errors and warnings can be displayed on the graphs in the [Electropherograms Tab](#) or the [Overlay Electropherograms Tab](#). The Analysis Error columns must be displayed in the Well Table to be available for selection in the [Graph View Properties](#).

- 1 Click the [Electropherograms Tab](#) or the [Overlay Electropherograms Tab](#).
- 2 Click the Properties tab on the right side of the graph. The [Graph View Properties](#) tab opens.
- 3 Select **Analysis Error** in the Well Annotation drop-down list.
- 4 If desired, click the Well Annotation Location button to change the location.
- 5 Click off of the Graph View Properties tab to close the tab.

## Viewing Multiple Properties in the Well Table View

Properties for Expected Peaks and Smears display in the [Well Table View](#). When entering the settings in the [Expected Fragments/Proteins/Glycans Tab](#) or the [Smear Analysis Tab](#) on the [Assay Analysis Window](#), the property to display in the well table is specified in the Property Displayed in Well Table column.

To display multiple properties for the same Expected Peak or Smear in the Well Table:

- 1 In the Expected Fragments/Proteins/Glycans tab, or the Smear Analysis tab, enter the properties for the expected peak or smear, selecting one of the desired properties in the **Property Displayed in Well Table** column.
- 2 Click in the next row and type the same name as an existing EP or smear in the Name field of the table. The row will automatically update with the same entries as the original row. The only field that can be changed is the **Property Displayed in Well Table** column.
- 3 Change the **Property** to the desired selection.
- 4 Repeat until all desired properties have been added to the table.
- 5 Click the **Apply** button to display the new columns in the Well Table. Duplicate properties in the table will be removed when the settings are applied to the plate.

## Copying Information

The **Edit** menu and some of the right-click pop-up menus offer the following choices for copying information from the LabChip GX Reviewer software for use with other applications, depending on the selection:

- Copy Gel
- Copy Lane
- Copy Graph
- Copy Rows to Clipboard
- Copy Column to Clipboard

Choosing any of these commands places a copy of the selected item on the computer's clipboard. You can then paste the item into a word processing, graphics, or other program.

Choosing **Copy Gel** copies all of the wells displayed in the [Gel View](#) with the labels as part of the graphic. To copy a gel, right-click in the [Gel View](#) and choose **Copy Gel**.

Choosing **Copy Lane** copies the selected well in the [Gel View](#) with the labels as part of the graphic. To copy a gel, right-click in the [Gel View](#) and choose **Copy Lane**.

Choosing **Copy Graph** copies the graph displayed in the [Graph View](#). The size of the image that is placed on the clipboard when copying a graph is the same size as the graph displayed in the software.

Copying rows from the [Peak Table View](#) or the [Well Table View](#) places ASCII information from the selected row or rows on the clipboard. To copy a row or multiple rows, select the desired rows in the table, right-click on one of the selected rows, and select **Copy Rows to Clipboard**.

Copying columns from the [Well Table View](#) is only available for certain columns in the table. To copy a column, select a single cell in the column, right-click on the cell, and select **Copy Column to Clipboard**.

## Reanalyzing a Data File

Occasionally you may need to open and view or reanalyze a data file that was run and saved previously. The raw data values are saved in the plate data file, along with the original analysis settings that were chosen for the run and any changed analysis settings. This enables you to reanalyze the data with new settings or to view previously saved settings.

The following analysis parameters can be changed:

- Plate peak find settings and Well peak find settings (see [“Changing the Peak Find Parameters” on page 62](#))
- Sample names and comments (see [“Using Sample Names Files” on page 36](#))
- Add a Peak (see [“Adding a Peak” on page 63](#))
- Exclude peaks from analysis (see [“Manually Excluding a Peak” on page 63](#))
- Reassign upper/lower markers (see [“Upper and Lower Marker Peaks for DNA Assays” on page 72](#), [“Lower Marker Peaks in Protein or RNA Assays” on page 73](#), or [“Lower Marker Peaks in Glycan Assays” on page 74](#))
- Alignment or no alignment with ladder peaks (see [“Aligning or Unaligning the Marker Peaks” on page 71](#))
- Assay - you can save the changed settings under a new assay name, if desired (see [“Saving and Exporting Assays” on page 75](#))

To reanalyze a data file:

- 1 Open the workspace that contains the plate data (see [page 32](#)).
- 2 Change the analysis parameters (see list above) as needed.
- 3 When you click the **Apply**, **Apply Global**, or **OK** buttons in the [Assay Analysis Window](#), the data is automatically re-analyzed and the updated information is displayed.
- 4 To view previous analysis settings, click the **Restore Plate** button at the bottom of the Assay Analysis window and select the version to view.



## Printing Workspace Information

Choosing **File** → **Print** opens the [Print Window](#) to select the information to print from the open workspace. The selected information can be printed to a printer or to a PDF file. If the workspace contains multiple collections, information from the active (selected) collection is printed.

The header of each printout contains the workspace name, the collection name, and the page number. The footer of each printout contains information about the LabChip GX Reviewer software, data file, assay, and instrument. If the LabChip GxP option is installed, the footer also includes the data file version, signed state, and lock state.

The following information can be printed for the open workspace:

- [Print All](#)
- [“Gel” on page 90](#)
- [“Electropherogram” on page 90](#)
- [“Overlay Electropherogram” on page 91](#)
- [“Well Table” on page 92](#)
- [“Peak Table” on page 93](#)
- [“Multiple Electropherogram” on page 94](#)
- [“Print Replicate Report” on page 95](#)

See below for descriptions of each option.

### **Print All**

This option prints the results of the assay in all of the available formats. The page layout depends on the options selected in Print Settings.

## Gel

This option prints a gel image with the lanes marked by the sample name.

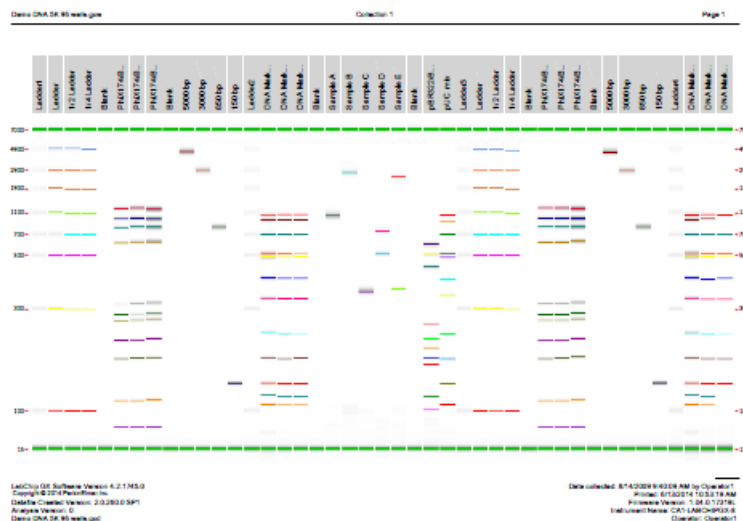


Figure 48. Printed Gel

## Electropherogram

Choosing this option prints an individual electropherogram of each of the selected wells.

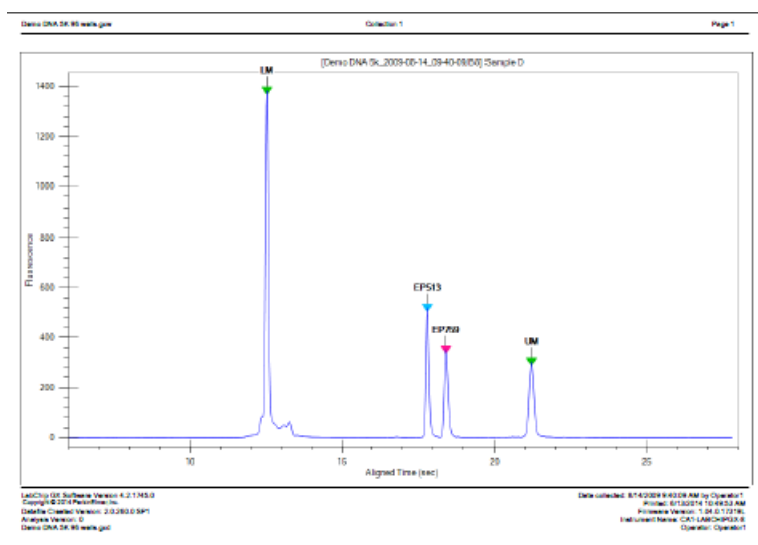


Figure 49. Printed Electropherogram

**Figure 50. Printed Overlay Electropherogram**



## Peak Table

Choosing this option prints the columns displayed in the [Peak Table View](#). To change the columns that are printed or the order of the columns, change the columns in the Peak Table View.

- Selecting the **Exclude Marker** check box removes all markers from the printout.
- Selecting the **Add Border** check box prints the table with a border around each cell in the table.
- Selecting the **Add Well Name as Header** check box prints a well header (plate name, well name, and sample name) before the peaks in each well.
- Selecting the **Per Page** or **Per Well** option for the Column Header specifies whether the Peak Table column headers are printed only at the top of each page (default), or if the headers are also printed at the beginning of each new well table.
- Selecting both the Well Table and the Peak Table prints each well on a separate page with the Well Table row at the top of the page and the Peak Table for the well below it.

Demo DNA 5k_90 wells.gal				Collection 1	Page 1
Well Label	Sample Name	Type	Size (bp)	Conc. (ng/μl)	% Purify
Demo DNA 5k_2009-05-14_09-40-09: # Ladder1: Ladder1					
Ladder1	Ladder1	LM	15	9.100	
Ladder1	Ladder1	L	15	9.100	
Ladder1	Ladder1	L	15	9.100	
Ladder1	Ladder1	L	15	9.100	
Ladder1	Ladder1	L	15	9.100	
Ladder1	Ladder1	L	15	9.100	
Ladder1	Ladder1	L	15	9.100	
Ladder1	Ladder1	L	15	9.100	
Ladder1	Ladder1	L	15	9.100	
Ladder1	Ladder1	L	15	9.100	
Demo DNA 5k_2009-05-14_09-40-09: # A1: Ladder					
A1	Ladder	LM	15	9.100	1.00
A1	Ladder	L	15	9.100	1.00
A1	Ladder	L	15	9.100	1.00
A1	Ladder	L	15	9.100	1.00
A1	Ladder	L	15	9.100	1.00
A1	Ladder	L	15	9.100	1.00
A1	Ladder	L	15	9.100	1.00
A1	Ladder	L	15	9.100	1.00
A1	Ladder	L	15	9.100	1.00
A1	Ladder	L	15	9.100	1.00
Demo DNA 5k_2009-05-14_09-40-09: # A2: 1/2 Ladder					
A2	1/2 Ladder	LM	15	9.100	2.00
A2	1/2 Ladder	L	15	9.100	2.00
A2	1/2 Ladder	L	15	9.100	2.00
A2	1/2 Ladder	L	15	9.100	2.00
A2	1/2 Ladder	L	15	9.100	2.00
A2	1/2 Ladder	L	15	9.100	2.00
A2	1/2 Ladder	L	15	9.100	2.00
A2	1/2 Ladder	L	15	9.100	2.00
A2	1/2 Ladder	L	15	9.100	2.00
A2	1/2 Ladder	L	15	9.100	2.00
Demo DNA 5k_2009-05-14_09-40-09: # A3: 1/4 Ladder					
A3	1/4 Ladder	LM	15	9.100	4.00
A3	1/4 Ladder	L	15	9.100	4.00
A3	1/4 Ladder	L	15	9.100	4.00
A3	1/4 Ladder	L	15	9.100	4.00
A3	1/4 Ladder	L	15	9.100	4.00
A3	1/4 Ladder	L	15	9.100	4.00
A3	1/4 Ladder	L	15	9.100	4.00
A3	1/4 Ladder	L	15	9.100	4.00
A3	1/4 Ladder	L	15	9.100	4.00
A3	1/4 Ladder	L	15	9.100	4.00

Figure 52. Printed Peak Table

### Figure 53. Printed Multiple Electropherograms

## Print Replicate Report

Choosing this option opens the [Replicate Report Generator Window](#) to setup and print report(s) of selected replicates by name, statistical mean, standard deviation, coefficient of variance (cv) for chosen well property/properties, and any desired custom settings. To set the properties of the Print Replicate Report, see [“Printing Replicate Reports” on page 57](#).

Demo Protein Express 200 Page 1

Replicate Report: Sample suitability: Purity with 1-2%									
#	Replicate	Well Name	66.20-5A % Purity	Mean Value	Std Dev	CV (%)	OK	Bad	Why
1	Control	BR Ladder	24.95	24.72	0.18	0.7%	<input type="checkbox"/>	<input checked="" type="checkbox"/>	
		BR Ladder	24.83						
		BR Ladder	24.55						
		BR Ladder	24.53						
2	A2-D2	BR Ladder	25.51	24.87	0.41	1.6%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
		BR Ladder	24.93						
		BR Ladder	24.58						
		BR Ladder	24.46						
3	A3-D3	BR Ladder	25.46	24.97	0.33	1.3%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
		BR Ladder	25.07						
		BR Ladder	24.73						
		BR Ladder	24.61						
4	A4-D4	HighConc	0.00	0.00	0.00	NaN%	<input type="checkbox"/>	<input checked="" type="checkbox"/>	
		HighConc	0.00						
		HighConc	0.00						
		HighConc	0.00						
5	A5-D5	CarryOver	0.00	0.00	0.00	NaN%	<input type="checkbox"/>	<input type="checkbox"/>	
		CarryOver	0.00						
		CarryOver	0.00						
		CarryOver	0.00						
6	A6-D6	BR Ladder	25.27	24.85	0.32	1.3%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
		BR Ladder	25.02						
		BR Ladder	24.70						
		BR Ladder	24.41						
7	A7-D7	BR Ladder	25.12	24.76	0.27	1.1%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
		BR Ladder	24.86						
		BR Ladder	24.67						
		BR Ladder	24.38						
8	A8-D8	BR Ladder	25.05	24.71	0.29	1.2%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
		BR Ladder	24.85						
		BR Ladder	24.70						
		BR Ladder	24.25						
9	A9-D9	LowConc	0.00	0.00	0.00	NaN%	<input type="checkbox"/>	<input checked="" type="checkbox"/>	
		LowConc	0.00						
		LowConc	0.00						
		LowConc	0.00						
10	A10-D10	BR Ladder	25.03	24.72	0.34	1.4%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
		BR Ladder	24.81						
		BR Ladder	24.90						
		BR Ladder	24.15						
11	A11-D11	BR Ladder	24.98	24.74	0.35	1.4%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
		BR Ladder	24.91						
		BR Ladder	24.94						
		BR Ladder	24.14						
12	A12-D12	BR Ladder	24.86	24.79	0.32	1.3%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
		BR Ladder	25.03						
		BR Ladder	25.03						
		BR Ladder	24.75						
13	E1-H1	BR Ladder	23.32	23.77	0.31	1.3%	<input type="checkbox"/>	<input type="checkbox"/>	
		BR Ladder	23.65						
		BR Ladder	23.94						
		BR Ladder	24.13						
14	E2-H2	BR Ladder	23.17	23.70	0.36	1.5%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	
		BR Ladder	23.62						
		BR Ladder	23.88						
		BR Ladder	24.15						

LabChip GX Software Version 5.0.1821.0  
Copyright © 2015 PerkinElmer, Inc.  
Datafile Created: 06/06/2008 5:43:58 PM with S/W Version: 1.0.66.0  
Analysis Version: 9  
Chip: C893A-0903N-06 (Expiry: 01/10/2008)  
Demo Protein Express 200.gcd

Modified: 11/06/2015 1:26:41 PM by PERKINELMER\NET\jcampresed  
Printed: 11/06/2015 3:58:39 PM  
Firmware Version: 1.03.0.110116  
Instrument: CA-LABCHIPGX-2 (SN: )  
Operator: HK

**Figure 54. Printed Replicate Report**

## Exporting Data

Data from a Peak Table, Well Table, Gel, or Graph can be exported automatically and/or manually.

- To manually export data, see [“Exporting Data Manually” on page 99](#).

Peak Tables, Well Tables, and Raw Data are exported to .CSV files, which can be imported into a spreadsheet program such as Microsoft Excel.

Gel and Graph data is exported to the selected image format.

This section shows export examples for the following:

- [Peak Table](#)
- [“Raw Data” on page 97](#)
- [“Gel” on page 98](#)

### Peak Table

ASCII text file that contains the data in all columns in the Peak Table. [Figure 55](#) is an example of part of a Peak Table file exported from a DNA assay (data truncated for this example):

	A	B	C	D	E	F	G	H	I
1	Plate Name	Sample Name	Size [BP]	Conc. (ng/	% Purity	Expected I	Type	Molarity (nmol/l)	
2	DNA1K_LP5_F1XLad						?		
3	DNA1K_LP5_F1XLad		15	5		15	LM	505.05	
4	DNA1K_LP5_F1XLad		25.14905	1.048493	9.919342	25	L0025	63.16838	
5	DNA1K_LP5_F1XLad		50.50482	0.987021	9.337781	50	L0050	29.61074	
6	DNA1K_LP5_F1XLad		100.0837	0.980348	9.274644	100	L0100	14.84132	
7	DNA1K_LP5_F1XLad		150.4032	0.968136	9.159115	150	L0150	9.752927	
8	DNA1K_LP5_F1XLad		200.0971	0.960094	9.083032	200	L0200	7.269901	
9	DNA1K_LP5_F1XLad		300.4446	0.953961	9.025009	300	L0300	4.810849	
10	DNA1K_LP5_F1XLad		400.3406	0.940726	8.899798	400	L0400	3.56032	
11	DNA1K_LP5_F1XLad		500.4173	0.947864	8.967327	500	L0500	2.869916	
12	DNA1K_LP5_F1XLad		699.6255	0.933113	8.82778	700	L0700	2.020805	
13	DNA1K_LP5_F1XLad		849.921	0.928357	8.782785	850	L0850	1.654978	
14	DNA1K_LP5_F1XLad		1004.273	0.922079	8.723387	1000	L1000	1.391143	
15	DNA1K_LP5_F1XLad		1500	5		1500	UM	5.0505	

**Figure 55. Exported Peak Table**

Peaks that are excluded are not exported and are missing in the exported file. For example, if peaks 3, 5, and 7 are excluded, when the data is exported into Microsoft Excel, peaks 3, 5, and 7 are not included.



## Raw Data

ASCII text file that contains the signal data from the run as one file per well or multiple wells in the same file. Note that data that is exported has been smoothed using the polynomial filter.

In addition to exporting time and value information, you can choose to export Size information. This information is determined based on aligned data and is used to correlate the peaks across different runs or from one row to another.

When **Include Size Data** is not checked and only time and values are exported, the state of the analysis function (peaks aligned or not aligned with the ladder data) determines whether or not data that is exported is or is not aligned. The same is true for the [Zero Baseline](#) function: if enabled, data that is exported is also zeroed to the baseline.

Below is an example of part of a raw data file exported from a DNA assay (header not included and data truncated in this example):

```
DATA
Time, Size, Value
0.000,-158.365,0.80
0.017,-158.269,0.86
0.033,-158.173,0.53
0.050,-158.077,0.63
0.067,-157.981,0.45
0.083,-157.885,0.28
0.100,-157.788,0.24
0.117,-157.692,-0.05
0.133,-157.596,-0.38
0.150,-157.500,-0.66
0.167,-157.404,-1.06
0.183,-157.308,-1.45
0.200,-157.212,-1.70
...
```

Raw data can also be exported in a **Chromatography Data Interchange Format** (formerly AIA format), which is used by some graphical analysis software tools. The Include Size Data and Export Single Table options are not available with Chromatography Data Interchange Format.

## Gel

Exports the selected gel(s) in the selected image format. Options are available to export the entire collection or only the selected gels. Gels can be exported into the same image file or into separate files for each gel.

Figure 56 shows multiple selected gels exported to the same image file.

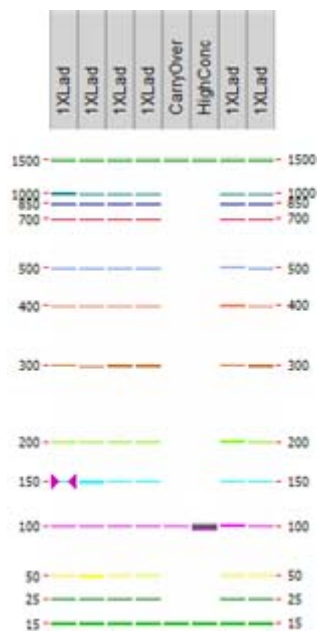


Figure 56. Exported Gel

## Exporting Data Manually

If the workspace contains multiple collections, the data exported is from the active/selected collection.

- 1 Open the file that you want to export the data from.
- 2 Select **Export** from the **File** menu. The [Export Window](#) opens.
- 3 Select the check boxes next to the views to export. Selecting **Export All** selects all check boxes.
- 4 For each selected view, to change the location for the files, click the **Browse (...)** button and select the desired location. If the path is the default path, the path displays in blue. If the path is not the default path, the path displays in purple. The default path is the location of the data file for the first well in the collection. To reset the path to the default, right-click on the path and select **Reset to Default**. (Changing the first well in the collection changes the default path to the location of the appropriate data file.)
- 5 If **Raw Data** is selected, choose the desired export options:
  - Select the **AIA Format** check box to export in Chromatography Data Interchange Format, which is used by some graphical analysis software tools. The **Include Size Data** and **Export Single Table** options are not available with AIA Format.
  - Select **Include Size Data** to align the data to the well's ladder (for one file per well) or to the first well (for a single data file) and include the size data in the exported data.
  - Select **Export Single Table** to export the data for all wells in the plate to one .CSV file. If not selected, the data from each well is exported to a separate .CSV file.
- 6 If **Electropherogram** is selected, select either **Entire Collection** to export a separate graph for each well in the collection or select **Selected Wells** to export a separate graph for only the selected wells.

## Exporting Data Manually (Continued)

- 7 If **Gel** is selected, choose the desired export options:
  - Select either **Entire Collection** to export all of the wells in the collection or select **Selected Wells** to export only the wells that are selected in the Gel view.
  - Select either **Single File** to include gels for all wells in the same image file, or select **Separate Files** to export each gel to a separate image file.
  - If desired, change the height of the exported graphic in the **Height** text box.
- 8 If either **Electropherogram** or **Gel** is selected, choose the desired format for the image files.
- 9 Click **OK** to export the data to the specified location.

## Understanding Peak Finding

Peak finding is the complex data analysis process of converting the raw data signal into a list of meaningful peaks. It involves smoothing the data signal, applying the selected baseline algorithm, identifying the peak baseline, detecting peaks within the smoothed signal, and discarding peaks failing to meet user specified thresholds. This process is controlled by the Peak Find analysis parameters selected in the [Assay Analysis Window](#) on the [Peak Find Tab](#).

## Data Smoothing

The raw data signal is initially smoothed using the Filter Width and Polynomial Order parameters. This filter removes high frequency noise from the data by performing a local weighted averaging of the data using a Savitzky-Golay convolution kernel. The filter width defines the range over which the averaging takes place; a 0.3 sec filter width averages over 0.3 seconds of data or more precisely, the data is convolved with a weight array that is 0.3 seconds wide. At the typical sampling rate of 60 HZ, this kernel is  $0.3 * 60 = 18 + 1 = 19$  points wide (forced to be odd by algorithm requirements).

Using a very large filter width to try and reduce signal noise will have an adverse effect on sharp peaks. Typically, the over-filtering of sharp peaks causes side-lobe artifacts to appear. The sample shown below has both sharp peaks and signal noise, particularly near the end of the trace. Removing the noise in the broad tail of the upper marker by setting the filter width to 1.0 sec causes the early sharp peaks to lose height and become distorted.

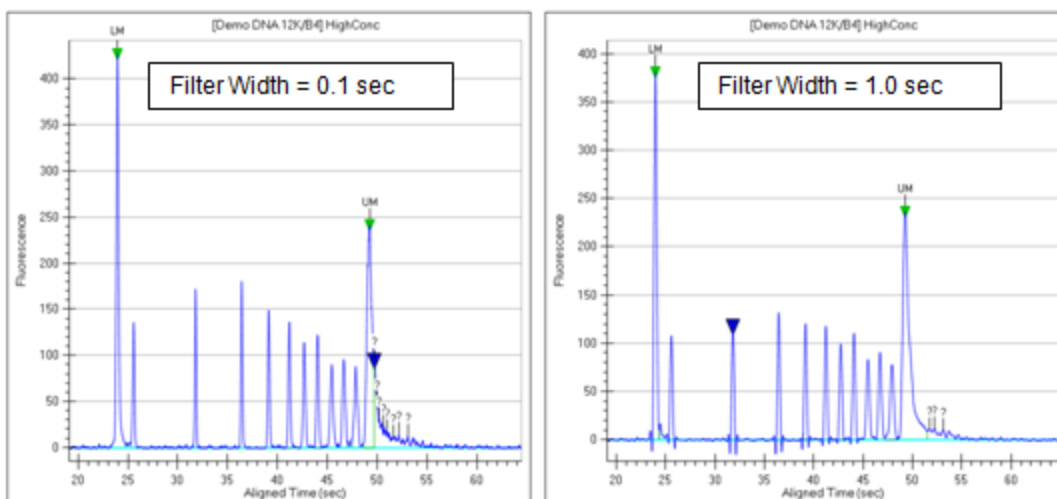


Figure 57. Filtering Examples

## Data Smoothing (Continued)

Because peaks tend to broaden as time progresses, use a short filter width initially and then switch to a wider filter near the end of the signal for this type of signal. The High Size filter on the [Peak Find Tab](#) can be used to smooth the tail of the upper marker without affecting the earlier peaks. Ultimately, some noise may have to be tolerated to avoid distorting the peak shape.

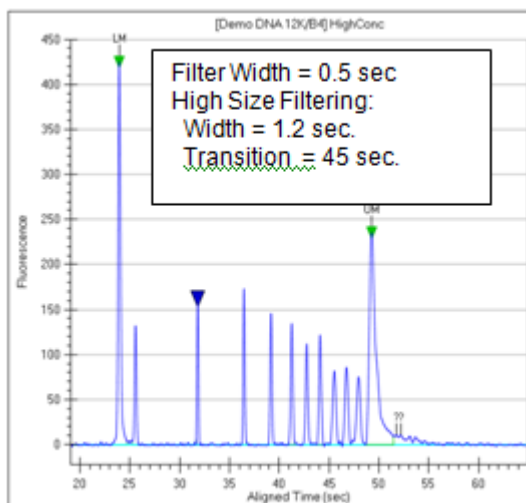


Figure 58. High Size Filtering

## Peak Detection - Slope Threshold

Peak baseline and Peak detection are controlled primarily through the Slope Threshold property on the [Peak Find Tab](#). The signal slope increases rapidly at the start of the peak, becomes negative after crossing the peak apex, and then returns to a small value at the end of the peak. The slope threshold is the slope value used to identify the start and end of the peak. The regions outside the zone where the absolute value of the slope exceeds the slope threshold are deemed baseline.

The slope threshold determines the peak start point and end point:

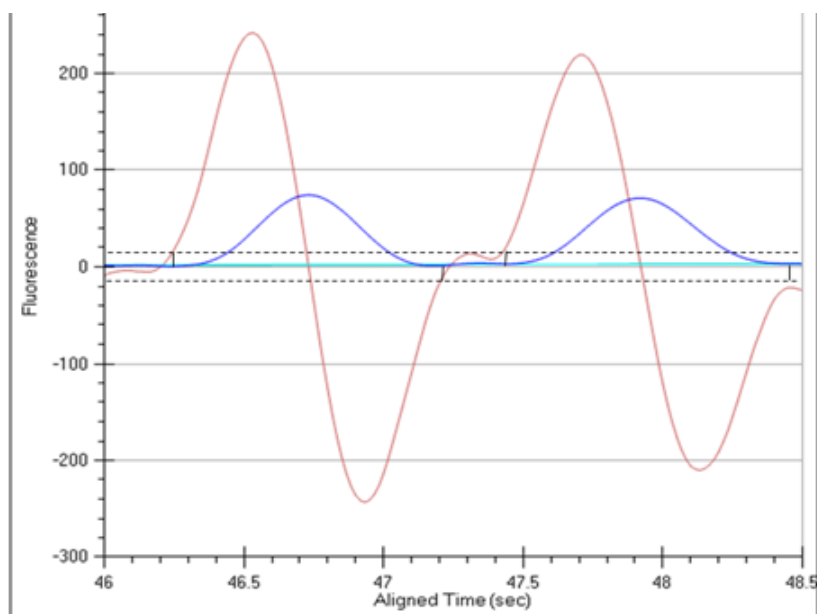
- The first point with local derivative above the slope threshold indicates the Start Point of a peak.
- The first point where the negative slope on the falling edge of the peak is below the slope threshold indicates the End Point of a peak.

A baseline is drawn under each peak region using a signal average in the baseline regions on each side of the peak.

## Peak Detection - Slope Threshold (Continued)

The Baseline Plateau property defines the minimum length of baseline region needed for computation of this average. Often, the region between peaks may not be long enough to qualify as baseline, in which case the baseline is drawn from the nearest qualifying baseline region on each side of the peaks.

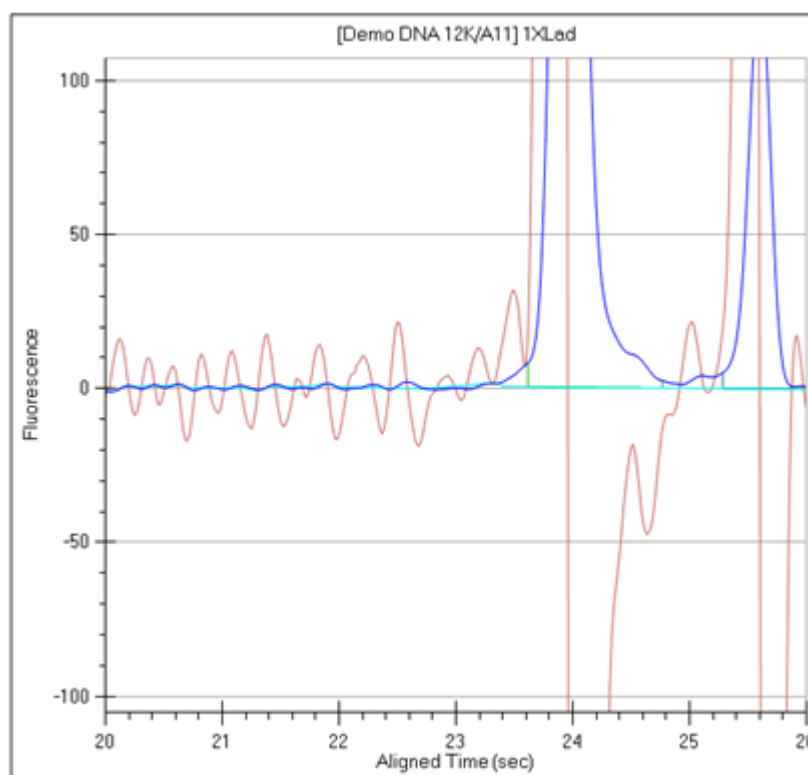
In [Figure 59](#), the orange trace shows the signal slope superimposed over the data. The light blue traces are the peak baseline. The scale for the slope is the same as for the data but with units of /sec. For these well defined peaks, a threshold of 15 /sec clearly extracts the full peak signal.



**Figure 59. Slope Threshold**

The Slope Threshold is used to distinguish between baseline and peak regions, so it should be set with care. A common mistake is to set the threshold too low, making it difficult for the analysis to find the baseline. On the same data signal, near the lower marker there is sufficient noise to create variation in the slope values as shown in [Figure 60 on page 104](#).

## Peak Detection - Slope Threshold (Continued)



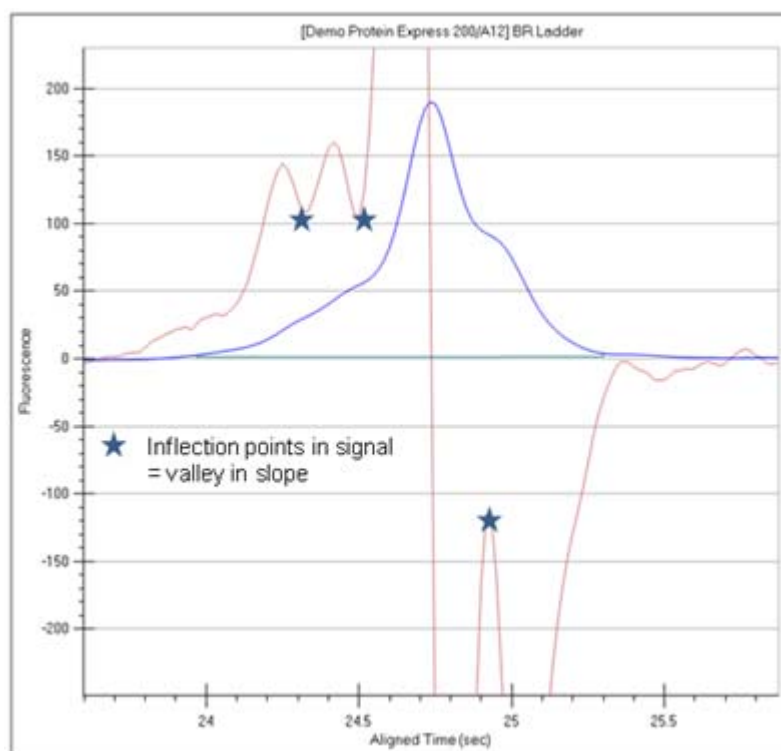
**Figure 60. Slope Values**

Although the region before 23 sec is baseline, the slope ranges between  $\pm 15$  /sec. Setting the slope threshold much below 15/sec causes the analysis to detect these noise bumps as peaks. The bumps will not be identified as peaks because they do not meet the Minimum Height and/or Minimum Width thresholds, but the analysis runs much slower as it carefully explores each bump. Also, the analysis will have difficulty finding baseline regions of qualifying width.



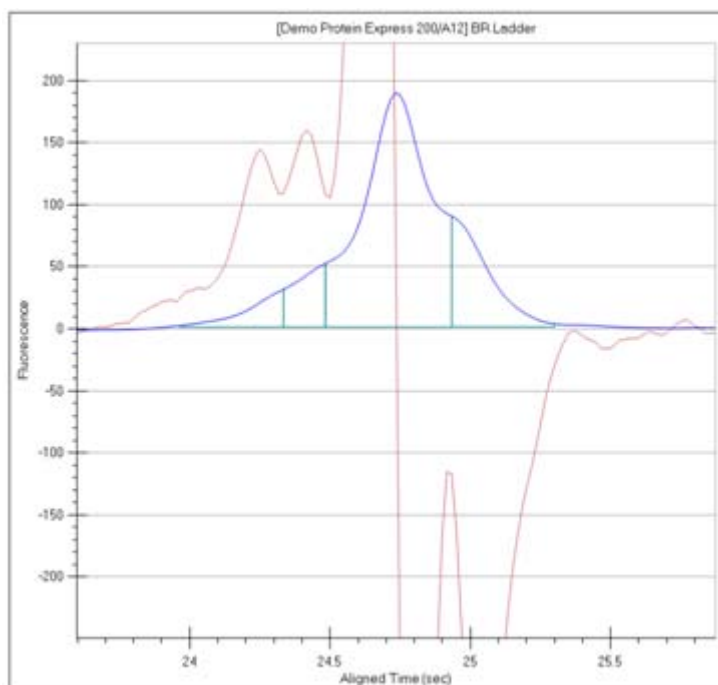
## Peak Splitting - Inflection Threshold

In situations where peaks overlap, the signal does not return to the baseline and the slope may or may not change sign, depending on how close the peaks are to each other. Two peaks with a valley in the middle is normally split into two peaks, but if a peak appears as a shoulder on another peak, splitting does not normally occur. A shoulder is recognized in the analysis as an inflection point. The slope reverses direction but does not change sign. The slope trace shows peaks and valleys - the valleys being the location of the inflection points. The peak in [Figure 61](#) is normally identified as a single peak although the orange slope trace shows three distinct inflection points.



**Figure 61. Single Peak**

Setting the inflection threshold above the value of the valleys in the slope splits the peak shoulders into separate peaks. The higher the inflection threshold, the more peak splitting occurs. In this example, a value of 150/sec splits off both shoulders. A value of 110/sec only splits off the left shoulder. (See [Figure 62 on page 106](#).)



**Figure 62. Inflection Threshold**

## Peak Identification

Peak identification involves generation of a peak baseline using the Slope Threshold and Baseline Plateau, detection of each peak using Slope and Inflection Thresholds, and then discarding peaks using the Minimum Height and Minimum Width thresholds. This process only occurs between the Start Time and End Time peak find properties. The Minimum Height threshold sets the minimum peak baseline-to-peak apex value needed for a peak to be identified by the analysis. The Minimum Width is the minimum left edge-to-right edge value needed for a peak to be identified.

## LabChip GxP Option

A LabChip GxP option is available for the LabChip GX Reviewer software. This option ensures that assays, output data, analysis settings, event data, and backup data files are not available for editing or tampering. Data is stored in a secure folder on either the LabChip GX Touch computer, the LabChip Reviewer computer, or a network server.

The LabChip GxP option utilizes two main components, the [Central Data Repository \(CDR\)](#) and the CFR database. The CDR is a secure folder that contains assay files and data files. The CFR database is a secure database that contains the GX Touch user accounts, Audit Trail, and data folder information. To create and maintain the CFR database, Microsoft SQL Server 2014 Express is provided with the LabChip GxP option.

### NOTE



*To perform the procedures in this section, log in to the LabChip GX Reviewer software as an administrator as described in [“Opening the LabChip GX Reviewer Software” on page 14](#).*

The following procedures are included in this section:

- [“Locking and Unlocking the Software” on page 109](#)
- [“Managing User Accounts” on page 110](#)
  - [“Adding New Users” on page 111](#)
  - [“Changing User Information” on page 112](#)
  - [“Printing User Information” on page 113](#)
  - [“Activating and Deactivating User Accounts” on page 113](#)
  - [“Changing Access Rights” on page 114](#)
  - [“Printing Access Rights” on page 115](#)
  - [“Setting Policies for User Accounts” on page 116](#)
  - [“Printing User Policies” on page 117](#)
- [“Electronic Signatures” on page 118](#)
- [“Reverting to a Specific Data File Revision” on page 119](#)
- [“Audit Trail” on page 120](#)
  - [“Viewing the Audit Trail” on page 121](#)
  - [“Exporting the Audit Trail” on page 122](#)

- “Central Data Repository (CDR)” on page 123
  - “CDR Security Suggestions” on page 124
  - “Remapping the CDR Server” on page 125
  - “Creating New Data Folders” on page 125
  - “Moving Data Files into Folders” on page 125
  - “Deleting Data Folders” on page 126
  - “Hiding Data Files in the CDR Manager Window” on page 126
  - “Showing Hidden Data Files in the CDR Manager Window” on page 127
  - “Setting CDR and Assay Folder Permissions” on page 128
  - “Loading Customized Assays into the CDR Folder” on page 129
- “Backing Up and Restoring Data” on page 130
  - “Backing Up the CDR Folder and CFR Database Manually” on page 130
  - “Setting Up the CFR Database for Automatic Backup” on page 131
  - “Restoring the CDR Folder and CFR Database” on page 135

## Locking and Unlocking the Software

The LabChip GX Reviewer software with the LabChip GxP option installed allows you to lock the LabChip GX Reviewer software. This prevents unauthorized users from accessing the software while you are away from the computer. After the software is locked, only the logged in user or a LabChip GX Touch Administrator can unlock the software.

To lock the LabChip GX Reviewer software:

- 1 On the [LabChip GX Reviewer Main Window](#), click **Security** → **Lock Application**. The [Unlock Application Window](#) opens on top of the LabChip GX Reviewer Main Window and displays the user name of the current user.



**Figure 63. Unlock Application Window**

To unlock the LabChip GX Reviewer software:

- 1 On the [Unlock Application Window](#), type the user password for the logged in user in the **Password** text box and click the **OK** button.
- 2 If the password for the current user is not available, type a LabChip GX Touch Administrator **Username** and **Password** in the [Unlock Application Window](#) and click the **OK** button. The Administrator is logged into the LabChip GX Reviewer software.
- 3 To change the user to a non-administrator user, close and restart the LabChip GX Reviewer software and then log in as the desired user.

## Managing User Accounts

Access to the LabChip GX Reviewer software is controlled by user names when the LabChip GxP option is installed. Each user must sign into the LabChip GX Reviewer software. The user's Access Level controls which options are available for each user name.

The following procedures are included in this section:

- [“Adding New Users” on page 111](#)
- [“Changing User Information” on page 112](#)
- [“Printing User Information” on page 113](#)
- [“Activating and Deactivating User Accounts” on page 113](#)
- [“Changing Access Rights” on page 114](#)
- [“Printing Access Rights” on page 115](#)
- [“Setting Policies for User Accounts” on page 116](#)
- [“Printing User Policies” on page 117](#)

## Adding New Users

Each person who uses the LabChip GX, LabChip GX Touch, or GX Reviewer software should have a unique LabChip GX Touch user account.

To add a new user:

- 1 Log into the LabChip GX Reviewer software using an account with Administrator access rights.
- 2 On the [LabChip GX Reviewer Main Window](#), select **Security** → **User and System Administration**. The [User Administration Window](#) opens.
- 3 Click the **Create User** button.
- 4 Type the desired **Username**.
- 5 Type the **First, Middle, and Last Name** for user.
- 6 Type the user's **Position** if desired.
- 7 Select the **Access Level** for the user. The Access Level controls which rights the user has. The following access levels are available:
  - Restricted User
  - Operator
  - Supervisor
  - Administrator
  - Service
- 8 Type the desired **User Password\***.
- 9 Type the **User Password** again.
- 10 Select whether the user can perform a signature.
- 11 Select whether the user can **Accept/Reject/Lock** data files.
- 12 Select whether the user can **Unlock** data files.
- 13 Click the **Save** button.

\* Passwords must be at least 5 characters long and must contain at least one uppercase letter and at least one number.

## Changing User Information

After a user account is created, the user details can be edited.

To change the user information:

- 1 On the [LabChip GX Reviewer Main Window](#), select **Security** → **User and System Administration**. The [User Administration Window](#) opens.
- 2 Click the **Edit Users** button.
- 3 Select the user to edit from the **User** drop-down list.
- 4 Change the User Information as necessary:
  - First Name
  - Middle Name
  - Last Name
  - Position
  - Access Level
  - User Can Perform Signature
  - Accept/Reject/Lock Data File
  - Unlock Data File
  - User Password
- 5 Click the **Save** button to save the updated user information.

### NOTE



*If changing the default administrator password, make sure to keep a copy of the password in a safe place. The default administrator password cannot be reset if forgotten.*



## Printing User Information

After editing a user account, the user details can be printed for record-keeping purposes.

To print the user information:

- 1 On the [LabChip GX Reviewer Main Window](#), select **Security** → **User and System Administration**. The [User Administration Window](#) opens.
- 2 Click the **Show User Info** button.
- 3 To print the information for a single user, select the user name in the **Select User to Display** list box.
- 4 To print the information for all users, select the **Print All Users** check box.
- 5 To preview the printout, click the **Print Preview** button.
- 6 To print the selected information, click the **Print** button.

## Activating and Deactivating User Accounts

If a user name is not going to be used, the user account can be deactivated. The user name is not removed from the system, but cannot be used to log into the LabChip GX Touch software or LabChip GX Reviewer software. User names cannot be deleted. A deactivated user name can be activated to continue to be used.

- 1 On the [LabChip GX Reviewer Main Window](#), select **Security** → **User and System Administration**. The [User Administration Window](#) opens.
- 2 Click the **De/Activate User** button.
- 3 Select the user name in the **Select User** drop-down list.
- 4 Click the **Deactivate** button.

To reactivate a user name, select the deactivated user and click the **Activate** button to return the user to active status. The user name can now log into the LabChip GX Reviewer software.

## Changing Access Rights

The rights assigned to each Access Level control the actions that a user is allowed to perform in the LabChip GX Touch software or LabChip GX Reviewer software. The rights apply to any user name assigned to the access level. Rights cannot be assigned to an individual user name.

To change the rights for an Access level:

- 1 On the [LabChip GX Reviewer Main Window](#), select **Security** → **User and System Administration**. The [User Administration Window](#) opens.
- 2 Click the **Define Access** button.
- 3 Select or clear the check boxes for the desired rights for each Access Level:
  - **User Administration** - Allows users to create, edit, activate and deactivate users, or to change policies.
  - **Run Assay** - Allows users to run assays and save the new data files that are created by the run. Users are not permitted to save changes to existing data files.
  - **Save Existing Data File** - Allows users to save changes to existing data files.
  - **Save Workspace** - Allows users to save new and existing workspaces. If Save Existing Data Files is not selected, users can only save workspaces where the data files have not changed.
  - **Plate Editor** - Allows users to add or edit plate dimensions in the Plate database.
  - **Hide/Show in CDR** - Allows users to hide and show data files in the CDR.
  - **Manage CDR Folders** - Allows users to create, rename, and delete folders in the CDR Manager window. This permission is not required for automatically creating daily subdirectories or to move data files in the CDR.
  - **Perform Validation** - Allows users to perform IQ (Installation Qualifications), OQ (Operation Qualifications), Teaching the robot, and Optics Calibration.
  - **Print/Export Analysis Results** - Allows users to print or export analysis results.
  - **Audit Trail Access** - Allows users to view the Audit Trail in the [Audit Trail Window](#).
  - **Assay Editor** - Allows users to edit and save assays.
- 4 Click the **Save** button.

## Printing Access Rights

After changing the user rights, the access rights can be printed for record-keeping purposes.

To print the access rights:

- 1 On the [LabChip GX Reviewer Main Window](#), select **Security** → **User and System Administration**. The [User Administration Window](#) opens.
- 2 Click the **Define Access** button.
- 3 To preview the printout, click the **Print Preview** button.
- 4 To print the selected information, click the **Print** button.

## Setting Policies for User Accounts

User Account Policies specify properties such as password options and whether to require a signature when updating data files.

- 1 On the [LabChip GX Reviewer Main Window](#), select **Security** → **User and System Administration**. The [User Administration Window](#) opens.
- 2 Click the **Set Policies** button.
- 3 Set the options as desired:
  - **Password Expires After** - The number of days until each password expires. Range is 1 to 1000 days.
  - **Number of Retired Passwords to Remember** - User cannot reuse the specified number of old passwords. Range is from 0 to 5.
  - **Minimum Password Length** - The minimum length of each password. Range is from 5 to 30 characters.
  - **Maximum Login Attempts** - The maximum number of times the user can attempt to log in before being locked out of the LabChip GX Touch software or LabChip GX Reviewer software. Range is from 3 to 20. This option can be disabled to allow unlimited retries without locking the user out.
  - **Minutes to Automatic Lock** - The number of minutes that the software is inactive until the LabChip GX Touch software or LabChip GX Reviewer software locks automatically. Range is from 5 to 4320 minutes (3 days). To disable this option, clear the check box. To unlock the software, see [“Locking and Unlocking the Software” on page 109](#).
  - **Require Signature on File Update** - If selected, an electronic signature is required to save modified data files. Signatures can be performed by any user who has the Perform Signature option selected in the [User Administration Window](#).
- 4 Click the **Save** button.

## Printing User Policies

After changing the user policies, the user policies can be printed for record-keeping purposes.

To print the user policies:

- 1 On the [LabChip GX Reviewer Main Window](#), select **Security** → **User and System Administration**. The [User Administration Window](#) opens.
- 2 Click the **Set Policies** button.
- 3 To preview the printout, click the **Print Preview** button.
- 4 To print the selected information, click the **Print** button.

## Electronic Signatures

Based on a company's procedural requirements, creating and saving data files may require a superior's signature. To sign a data file, a user with signature permissions must enter a valid user name, password, and comment to explain the purpose of the signature. When signing a data file, options are also available to set the file's approval state to Unreviewed, Accepted, or Rejected, and to lock or unlock the data file. (These options are only available if the signing user has the appropriate permissions.) A signature can be added to the data file any time, except while the assay is running.

### NOTE



*To change user signature permissions, see [“Changing User Information” on page 112](#).*

To electronically sign a data file:

- 1 On the [LabChip GX Reviewer Main Window](#), click **Security** → **Perform Signature**. The [Perform Electronic Signature Window](#) opens on top of the LabChip GX Reviewer Main Window.
- 2 Select the user name of the user that is signing the data file in the **Username** drop-down list.
- 3 Type a comment describing the reason for the signature, approval state, or lock state in the **Enter Comment** text box.
- 4 As required, set the **Approval State** by selecting the Unreviewed, Accept, or Reject option.
- 5 To lock the data file, select the **Lock** check box. Locking a data file prevents the data file from being saved until after it is unlocked.
- 6 Type the User Password for the signing user in the **User Password** text box.
- 7 Click the **Sign** button. The Signature Performed window opens to confirm the signature was performed.
- 8 Click the **OK** button in the Signature Performed window. The Perform Signature window closes. Signature information is embedded in the data file and the signature is logged in the Audit Trail.

## Reverting to a Specific Data File Revision

Each time a data file is changed, a new version of the data file is created and saved. The LabChip GX Reviewer software enables you to revert to a previous version of a data file.

To revert to a previous data file version:

- 1 On the [LabChip GX Reviewer Main Window](#), select **Analysis** → **Analysis Settings** on the main menu. The [Assay Analysis Window](#) opens.
- 2 Click the **Restore Plate** button at the bottom of the window. The Restore Plate Settings to Version window opens.
- 3 Select the data file version that you want to restore to.
- 4 Click the **OK** button. The Assay Analysis Window displays the settings for the selected data file version.
- 5 Click the **OK** button to display the data file with the selected settings.

## Audit Trail

LabChip GX Reviewer software uses secured, computer-generated, time-stamped audit trails to independently record the date and time of operator entries and actions that create, modify, or delete electronic records. The audit trails can be printed out for documentation purpose. The audit trail documents can be made available for agency review and copying.

The audit trail is a log of all of the following events that have occurred in the LabChip GX Reviewer software:

- Administration and user management (create/ edit / deactivate user, policy settings, access level modifications, login and lock events)
- Data file run events (prime, run started, run finished, run stopped, run aborted, wash started, wash finished)
- Data file signing events
- Data file hide/show events
- Instrument error events
- Data file version changes
- IQ events
- Application errors related to main database failures

In Windows 7 and 10, the “Computer User Role” records either User or Administrator, depending on how the LabChip GX software is started. If the LabChip GX software is started by right-clicking on the icon and selecting Run as Administrator, the Computer User Role is Administrator. If the software is started by double-clicking on the icon, the Computer User Role is User. The Computer User Role reflects the privilege that was used to start the LabChip GX software.

This section includes the following Audit Trail procedures:

- [Viewing the Audit Trail](#)
- [Exporting the Audit Trail](#)



## Viewing the Audit Trail

To view events in the Audit Trail Log:

- 1 On the [LabChip GX Reviewer Main Window](#), select **Security** → **Audit Trail Log**. The [Audit Trail Window](#) opens.
- 2 Select the desired data range:
  - Select whether to view most recent entries, entries between specific dates, or the entire database.
  - Select the number of entries or dates to search if Entire Database is not selected.
- 3 If desired, select a user name to view only events performed by a specific user.
- 4 To view events for a specific data file, select the name of the data file.
- 5 To search only specific types of events select the desired Event Category in the Event Category drop-down list. Default shows all events.
- 6 To change the columns that are displayed, click the green arrow button next to Event Category and select or hide the desired columns.
- 7 Click the **Search** button to search the database.

## Exporting the Audit Trail

The events displayed in the [Audit Trail Window](#) can be exported to a file. The following formats are available:

- Text
- XML
- Excel

To export the events:

- 1 On the [LabChip GX Reviewer Main Window](#), select **Security** → **Audit Trail Log**. The [Audit Trail Window](#) opens.
- 2 Click the **Export** button in the Audit Trail Window. The [Audit Trail Export Window](#) opens.
- 3 Select the desired export file format.
- 4 Click the **Export** button. The Save As window opens.
- 5 Choose the desired location for the file, type the desired file name, and click the **Save** button.

By default, the file name is *ATexport\_<date>\_<time>*, where <date> and <time> are the current date and time.

## Central Data Repository (CDR)

The Central Data Repository (CDR) is a protected folder located on either the LabChip GX Touch computer, the LabChip Reviewer computer, or a network server. The CDR is only used when the LabChip GxP option is installed.

The CDR contains assay files and data files. The folders and files in the CDR are protected from changes by unauthorized users.

The data files in the CDR can be organized into virtual folders. The folders are not actually created in the CDR folder, but are displayed in the CDR Manager Window to organize the data files.

The following procedures are included in this section:

- [“CDR Security Suggestions” on page 124](#)
- [“Remapping the CDR Server” on page 125](#)
- [“Creating New Data Folders” on page 125](#)
- [“Moving Data Files into Folders” on page 125](#)
- [“Deleting Data Folders” on page 126](#)
- [“Hiding Data Files in the CDR Manager Window” on page 126](#)
- [“Showing Hidden Data Files in the CDR Manager Window” on page 127](#)
- [“Setting CDR and Assay Folder Permissions” on page 128](#)
- [“Loading Customized Assays into the CDR Folder” on page 129](#)

## CDR Security Suggestions

To ensure proper security of data files, the LabChip GX Touch Administrator should change the Administrator password.

To change the administrator password:

- 1 Log into the LabChip GX Reviewer software as the administrator.
- 2 Select **Security** → **Change Password**.
- 3 Type the current password.
- 4 Type the new password in both the **New Password** and **Confirm Password** text boxes.

### NOTE



*Make sure to keep a copy of the password in a safe place. The administrator password cannot be reset if forgotten.*

- 5 Click the **OK** button.

The LabChip GX Reviewer software contains an option to copy the data files to an unsecured location on the local hard drive or on a mapped network drive. These data files do not meet 21 CFR Part 11 security requirements after they are copied out of the CDR. To copy data files to a non-secure location, use the Copy button on the [CDR Manager Window](#).

## Remapping the CDR Server

If desired, the administrator can reconfigure an existing CDR server with a new one.

To remap the server:

- 1 Log into the LabChip GX Reviewer software as the administrator.
- 2 Do NOT open a workspace or import data files.
- 3 Click the **Server Status** button at the top right of the [LabChip GX Reviewer Main Window](#). The [CDR / Database Server Mapping Window](#) opens.
- 4 Type the new server location into the **Server Name/IP Address** text box.
- 5 Click the **Apply** button. The server connects to the new location.
- 6 Click the **Done** button.

## Creating New Data Folders

To create a new CDR data folder:

- 1 Select **File** → **Import Data File**. The [CDR Manager Window](#) opens.
- 2 Click on the upper-level CDR folder.
- 3 Click the **New Folder** button on the left side of the window. A new folder named New Folder is created and the name is selected for update.
- 4 Type the desired name for the folder and then press the Enter key.
- 5 Close the CDR Manager Window.

## Moving Data Files into Folders

To move a data file into a CDR data folder:

- 1 Select **File** → **Import Data File**. The [CDR Manager Window](#) opens.
- 2 Click on the name of the data file.
- 3 Drag and drop the file into the desired folder.
- 4 Close the CDR Manager Window.

## Deleting Data Folders

To delete a CDR data folder:

- 1 Select **File** → **Import Data File**. The [CDR Manager Window](#) opens.
- 2 Verify the folder is empty.
- 3 Click on the folder name.
- 4 Click the **Delete** button on the left side of the window or at the top of the window.
- 5 Close the CDR Manager Window.

## Hiding Data Files in the CDR Manager Window

The CDR Manager window enables users to hide or show specific data files or folders in the CDR Manager window. This functionality can be used to reduce the number of data files displayed in the CDR Manager window when certain files or folders are not used. The user must have Hide/Show in CDR rights in the [Define Access](#) tab in the [User Administration Window](#).

Hiding data files or folders does not change the data file or folder, they are just not displayed in the CDR Manager Window.

To hide data files or folders:

- 1 Select **File** → **Import Data File**. The [CDR Manager Window](#) opens.
- 2 Select the name of the data file or folder that you want to hide. If you select a folder name, all data files and folders in the selected folder will also be hidden.
- 3 Click the Hide button on the left side of the CDR Manager Window.
- 4 Close the CDR Manager Window.

## Showing Hidden Data Files in the CDR Manager Window

To set hidden data files back to unhidden (show):

- 1 Click the **Show Hidden Files** button at the top right of the [CDR Manager Window](#). All hidden files and folders show in the CDR Manager window. The file or folder icon indicates if the file or folder is hidden.
- 2 Click the name of the file or folder that you want to show and click the **Show** button on the left side of the CDR Manager Window.

### NOTE



*Files and folders in a hidden folder do not show in the CDR Manager Window, even if the files are not set to hidden. To show files, the folder cannot be set to hidden.*

- 3 Click the **Hide Hidden Files** button at the top right of the [CDR Manager Window](#).
- 4 Close the CDR Manager Window.

## Setting CDR and Assay Folder Permissions

To set permissions to the CDR and Assay folder:

- 1 Log into the LabChip GX Reviewer software as an administrator.
- 2 Select **Security** → **Folder Permission**. The [Folder Permissions Window](#) opens.
- 3 Click the **Assay** radio button and select the user name for which permissions are being set from the **Select User** drop-down list.
- 4 Select the **CDR** radio button to set permissions for the CDR folder or its subfolders.
- 5 Select the **Assay** radio button to set permissions for the Assay folder or its subfolders.
- 6 Select the CDR, Assay, or subfolder to set permissions for.
- 7 Select the **Full Control** check box to give the user read/write access to the selected folder.
- 8 Select the **Read** check box to give the user read-only access to the selected folder.
- 9 Select the **Write** check box to give the user write-only access to the selected folder.
- 10 Select the **Apply permissions to subfolders** check box and click the **Save button** to implement the permissions.



## Loading Customized Assays into the CDR Folder

If desired, customized assays from PerkinElmer can be loaded into the CDR folder.

To load the customized assay into the assay CDR folder:

- 1 Select **Tools** → **Load Assay into CDR** on the [LabChip GX Reviewer Main Window](#). The [Load Assay into CDR Window](#) opens.
- 2 Click the **Browse** button next to the **Select CDR Assay Folder** text box. The **CDR Browser Window** opens.
- 3 Navigate to the **Assay** CDR folder.
- 4 Click the folder and click the **Select** button.
- 5 Click the **Browse** button next to the **Select Assay File to Load** text box.
- 6 Navigate to the folder containing the desired customized assay file. Click the **Select** button.
- 7 If desired, type applicable comments into the **Comment** text box.
- 8 If desired, type the source of the assay (e.g., PerkinElmer) into the **External Source** box.
- 9 Click the **Load Assay** button. The selected customized assay is added to the assay CDR folder.

## Backing Up and Restoring Data

The CDR folder and the CFR database can be backed up manually to a secure location. The CFR database can be set to back up automatically. The backup copies can be stored on another computer or on a removable storage drive. Backup completely replaces the previous backup files with new backup files. The CDR folder and CFR database can only be restored to the point when the files were backed up.

This section contains:

- [“Backing Up the CDR Folder and CFR Database Manually” on page 130](#)
- [“Setting Up the CFR Database for Automatic Backup” on page 131](#)
- [“Restoring the CDR Folder and CFR Database” on page 135](#)

### Backing Up the CDR Folder and CFR Database Manually

To back up the CDR Folder and CFR Database manually:

- 1 Log into the computer where the CDR is installed.
- 2 Open the application folder:  
**32-Bit Operating System:**  
**C:\Program Files\PerkinElmer\LabChip GX Reviewer**  
**64-Bit Operating System:**  
**C:\Program Files (x86)\PerkinElmer\LabChip GX Reviewer**
- 3 Right-click the **BackupDB.exe** file and select **Run as Administrator**. The Backup LabChip GX server CDR and Database window opens.
- 4 Click the **Backup** button. The backup script creates two files: **DBBack.bak** and **LabChipGXServerData.zip** in the \Backup folder in the application folder.
- 5 Click the **Done** button when the progress bar completes.
- 6 Move the two files to a backup or archive location or to a parallel folder on another Server PC to move the server instance.

## Setting Up the CFR Database for Automatic Backup

### NOTE



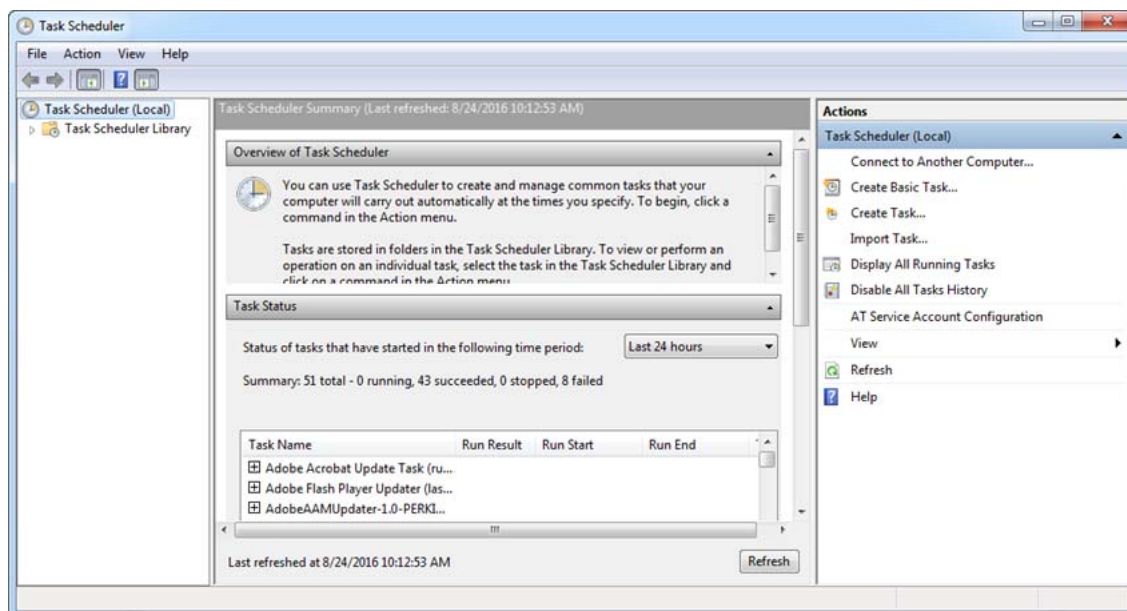
*Only the CFR database can be set for automatic backed up. The CDR Folder must be backed up manually (see [page 130](#)).*

If desired, the CFR database be set for automatic backup by using Windows Task Scheduler.

To set the CFR database for automatic backup:

- 1 Open the Task Scheduler using either of the following methods:
  - Click the **Windows key + R**, type **taskschd.msc** into the **Open** text box, and click the **OK** button.
  - OR
  - Go to **Control Panel** → **System and Security** → **Administrative Tools** → **Schedule Tasks**.

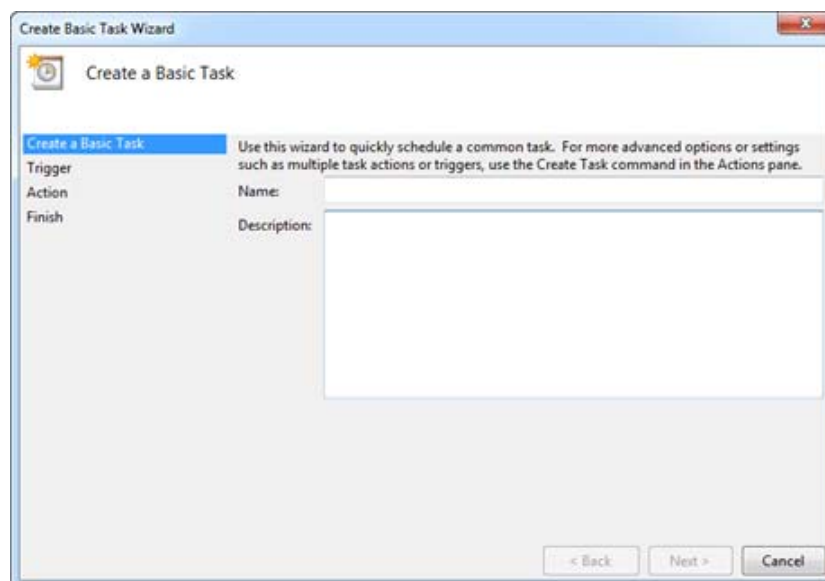
The **Task Scheduler Window** opens. See [Figure 64](#).



**Figure 64. Task Scheduler Window**

## Setting Up the CFR Database for Automatic Backup (Continued)

- 2 Click **Create Basic Task** on the Actions panel on the right side of the Task Scheduler window. The **Create Basic Task Wizard** window opens. See [Figure 65](#).



**Figure 65. Create Basic Task Window**

- 3 Type a name of for the backup into the **Name** text box.
- 4 If desired, type a description into the **Description** text box and click the **Next** button.

## Setting Up the CFR Database for Automatic Backup (Continued)

- 5 Select one of the radio buttons to indicate the desired frequency of the backup and click the **Next** button. See [Figure 66](#).

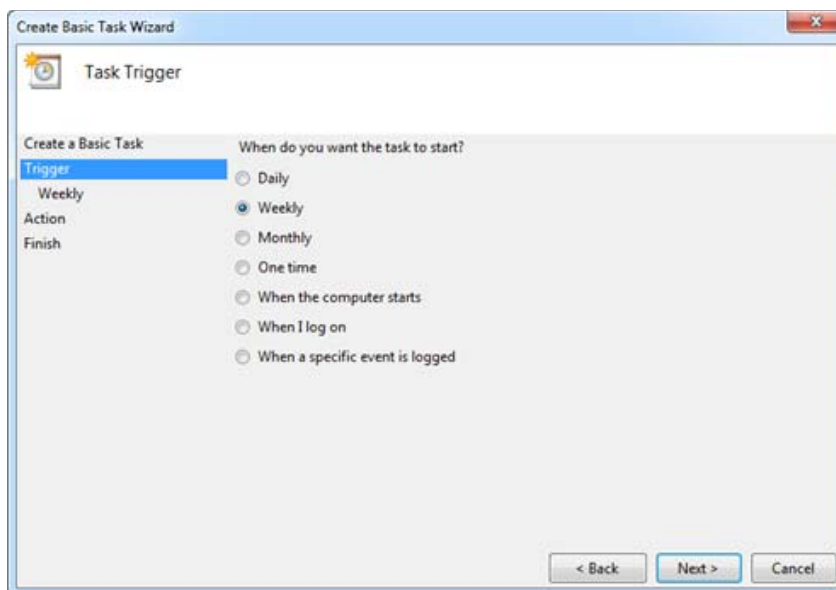


Figure 66. Task Trigger

### NOTE

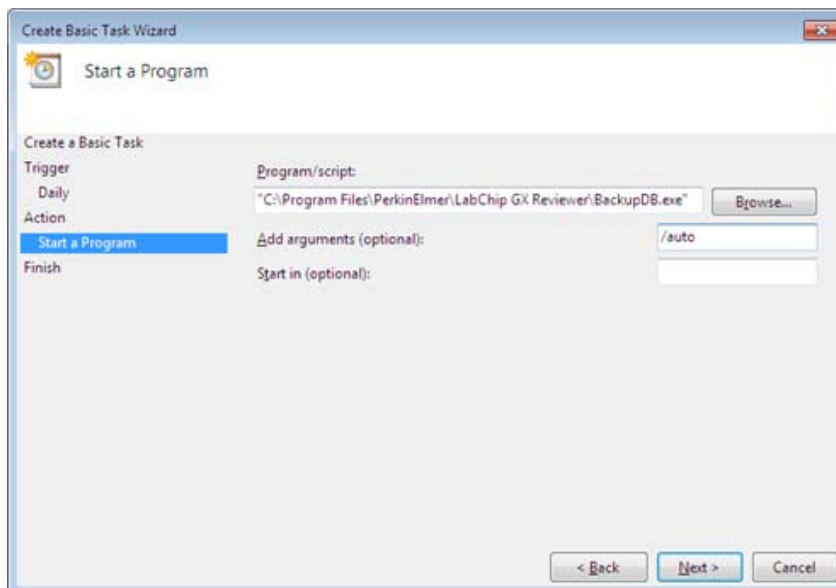


*Weekly or monthly is the recommended frequency of the backup.*

- 6 Specify the starting/timing parameters of the selected backup frequency and click the **Next** button.
- 7 Select the **Start a program** radio button and click the **Next** button.
- 8 Click the **Browse** button and navigate to the **BackupDB.exe** file (C:\Program Files\PerkinElmer\LabChip GX Reviewer\BackupDB.exe).

## Setting Up the CFR Database for Automatic Backup (Continued)

- 9 Type **/auto** into the **Add arguments** text box and click the **Next** button. See [Figure 67](#).



**Figure 67. Add Arguments**

- 10 Verify that the backup parameters displayed on the summary window are correct. If changes are needed, click the **Back** button until reaching the desired parameter to change and apply the changes.
- 11 Select the **Open the Properties dialog for this task when I click Finish** check box and click the **Finish** button. The backup task is added to the Windows schedule and the CFR database is set for automatic backup.
- 12 Periodically review the result (passed/failed) of backups by viewing the **CFR.log** file (**C:\Program Files\PerkinElmer\LabChip GX Reviewer\Log**).

## Restoring the CDR Folder and CFR Database

### NOTES



- *If restoring the CDR folder and CFR database to a new computer, install the LabChip GX Reviewer software with the LabChip GxP option and then restore the CDR folder and CFR database.*
- *The CDR folder and CFR database can only be restored to the point when the files were backed up.*

To restore the CDR folder and CFR database from a manual backup point:

- 1 Log into the computer where the CDR is installed.
- 2 Copy the two backup files **DBBack.bak** and **LabChipGXServerData.zip** to the \Backup folder in the application folder.

- 3 Return to the application folder:

**32-Bit Operating System:**

**C:\Program Files\PerkinElmer\LabChip GX Reviewer**

**64-Bit Operating System:**

**C:\Program Files (x86)\PerkinElmer\LabChip GX Reviewer**

- 4 Right-click the **RestoreDB.exe** file and select **Run as Administrator**. The **Restore LabChip GX server CDR and Database** window opens.
- 5 Click the **Restore** button.
- 6 Touch the **Done** button when the progress bar completes. The CDR folder and CFR database are restored.

### NOTE



*When the LabChip GX Touch or GX Reviewer software is restarted, a "Mapped Server is different. Do you want to remap?" message displays on a dialog box. Verify the server name/IP is correct on the dialog box and click the **Apply** button.*

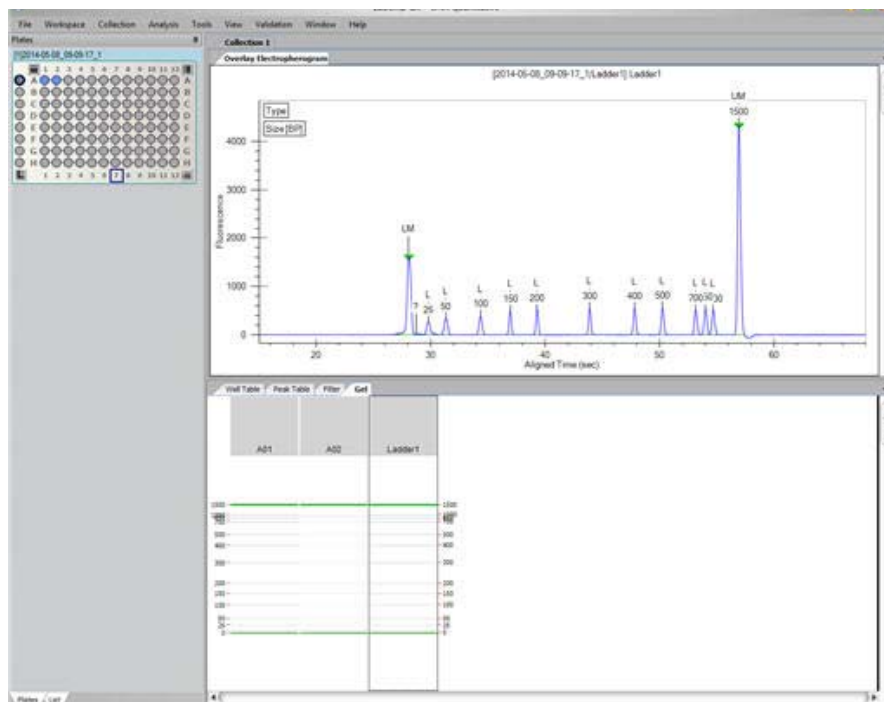
## Software Reference

This section describes the windows in the LabChip GX Reviewer software. Each topic describes the options and buttons on the window, and how to open the window. This section includes:

- [“LabChip GX Reviewer Main Window” on page 137](#)
- [“About LabChip GX Reviewer Window” on page 171](#)
- [“Add New Expected Peak Window” on page 172](#)
- [“Assay Analysis Window” on page 173](#)
- [“Audit Trail Window” on page 199](#)
- [“Audit Trail Export Window” on page 201](#)
- [“Audit Trail Manage Columns Window” on page 202](#)
- [“CDR / Database Server Mapping Window” on page 203](#)
- [“CDR Manager Window” on page 204](#)
- [“Change Password Window” on page 206](#)
- [“Data File Version Window” on page 207](#)
- [“Display Format Editor Window” on page 208](#)
- [“Event Viewer Window” on page 209](#)
- [“Export Window” on page 210](#)
- [“Folder Permissions Window” on page 213](#)
- [“Layout Options Window” on page 214](#)
- [“Load Assay into CDR Window” on page 216](#)
- [“Login Window” on page 217](#)
- [“New Collection Window” on page 218](#)
- [“Perform Electronic Signature Window” on page 219](#)
- [“Print Window” on page 220](#)
- [“Print Validation Reports Window” on page 226](#)
- [“Rename Collection Window” on page 227](#)
- [“Run Info Window” on page 228](#)
- [“Sample Name Editor Window” on page 230](#)
- [“Save Workspace As Window” on page 232](#)
- [“Select a Data File Window” on page 233](#)
- [“Software Installation Qualification Window” on page 234](#)
- [“Unlock Application Window” on page 236](#)
- [“Unlock Data File Window” on page 237](#)
- [“User Administration Window” on page 238](#)



## LabChip GX Reviewer Main Window



**Figure 68. LabChip GX Reviewer Main Window**

The main window of the LabChip GX Reviewer software includes:

- [“Menu Bar” on page 138](#)
- [“Plate View or Plate List” on page 143](#)
- [“Collection Pane” on page 147](#)
- [“Graph View” on page 148](#)
- [“Graph View Properties” on page 153](#)
- [“Gel View” on page 156](#)
- [“Gel View Properties” on page 159](#)
- [“Well Table View” on page 161](#)
- [“Peak Table View” on page 163](#)
- [“Peak Table Properties” on page 168](#)
- [“Filter View” on page 169](#)

Clicking and dragging the borders between the views changes the size of the views in the collection. To change the location of the views, see [“Changing the View of the Data” on page 77](#).

## Menu Bar

The menu bar is directly below the title bar on the [LabChip GX Reviewer Main Window](#). Clicking a menu name displays a list of commands to access software functions.

The LabChip GX Reviewer software contains the following menus:

- [“File Menu” on page 139](#)
- [“Workspace Menu” on page 140](#)
- [“Collection Menu” on page 140](#)
- [“Analysis Menu” on page 141](#)
- [“Tools Menu” on page 141](#)
- [“Security Menu” on page 142](#) (Only displays if the LabChip GxP option is installed)
- [“View Menu” on page 142](#)
- [“Validation Menu” on page 142](#)
- [“Window Menu” on page 143](#)
- [“Help Menu” on page 143](#)

## File Menu

The File menu contains the following commands:

**New Workspace** - Creates a new, blank workspace.

**Open Workspace** - Opens a saved workspace.

### NOTE



*You can open multiple data files, but you cannot mix DNA, Protein, RNA, Glycan, Protein Charge Variant, or gDNA data files in the same workspace.*

**Import Data File** - Opens a saved DNA, Protein, RNA, Glycan, Protein Charge Variant, or gDNA data file in the current workspace. If the LabChip GxP option is installed, opens the [CDR Manager Window](#). If the LabChip GxP option is not installed, opens the [Select a Data File Window](#). A graphical representation of the microplate displays in the workspace. Data files can be .GXD (LabChip GX or GX Touch) or .CLA (LabChip HT software). (Protein, Glycan, and Protein Charge Variant assays are only supported on LabChip GXII or GXII Touch instruments.)

**Export** - Opens the [Export Window](#) to choose the type of data to export. Exports a Peak Table, Well Table, Gel, Single Graph, or all open graphs in the current Collection to a file, depending on the options selected.

**Print** - Opens the [Print Window](#) to choose the data to print.

**Save Workspace** - Saves the current workspace.

**Save Workspace As** - Saves the current workspace with a new filename.

**Exit** - Closes the LabChip GX Reviewer software.

## Workspace Menu

The Workspace menu contains the following commands:

**Remove Plate** - Removes the selected plate data file from the workspace.

**Save Plate** - Saves the plate data file (\*.gxd). Changes to the analysis settings (in the [Assay Analysis Window](#)) are saved at the end of the plate data file. Previous analysis settings are not overwritten, enabling you to use the **Restore Plate** button on the [Assay Analysis Window](#) to go back to any previously saved settings. Plate data files are automatically saved when the Workspace is saved.

## Collection Menu

The Collection menu contains the following commands:

**Undo** - Undoes changes to the collection view settings and filter settings. Changes made in pop-up windows, such as analysis settings, export settings, etc, are not affected by this Undo.

**New Collection** - Opens the [New Collection Window](#) where you choose whether to create a new Collection from a saved Collection Template, a Blank Collection, or the Current Collection.

**Rename Collection** - Opens the [Rename Collection Window](#) to rename the currently selected Collection.

**Delete Collection** - Deletes the current Collection.

**Save As Template** - Opens the Save Template As window to save the display and filter settings currently displayed in the Collection tab as a collection template.

**Apply Template** - Opens the Apply Template window to open a saved collection template and apply it to the current Collection.

**Layout** - Opens the [Layout Options Window](#) to change where tabs are displayed by default on the main window.

## Analysis Menu

The Analysis menu contains the following commands:

**Turn On/Off Analysis** - Toggles analysis on and off. When analysis is on, the data displayed in the main window uses the analysis settings in the [Assay Analysis Window](#). When analysis is off, the unaligned data (spike rejected, filtered, and baseline corrected) displays.

**Scale to Sample Peaks** - Scales the view to the minimum and maximum X values of the current sample peaks. Marker and/or system peaks are ignored.

**Scale to All Peaks** - Scales the view to the minimum and maximum X values of the all peaks, including marker peaks and system peaks.

**Analysis Settings** - Opens the [Assay Analysis Window](#) to choose analysis parameters for the selected plate. These settings apply to all wells in the microplate. Use these settings to change the analysis and peak finding parameters to help resolve hard-to-decipher data.

**Standard Curve** - Opens the [Standard Curve](#) to view the ladder as a curve with a point-to-point fit. (Not available for Protein Charge Variant assays.)

## Tools Menu

The Tools menu contains the following commands:

**Sample Name Editor** - Opens the [Sample Name Editor Window](#) to change, import, or export the sample names assigned to the wells of the plate.

**Assay Editor** - Opens the Select Assay To Edit window or the CDR Manager window if the LabChip GxP option is installed. Selecting an assay opens the [Assay Analysis Window](#) to make changes to the selected assay.

**Load Assay into CDR** - Opens the [Load Assay into CDR Window](#) to add customized assays into the CDR assay folder from an external folder. This Tool menu command only displays if the LabChip GxP option is installed.

**Modify Data Presentation** - Opens the [Display Format Editor Window](#) to specify the number of decimal places to show for each numeric data type.

## Security Menu

The Security menu only displays if the LabChip GxP option is installed with the LabChip GX Reviewer software.

**User and System Administration** - Opens the [User Administration Window](#) to create, edit, and view user login information, activate or deactivate users, define user access, and set user policies.

**CDR Folder Permission** - Opens the [Folder Permissions Window](#) to set Full Control/Read/Write permissions for CDR folders for specific user accounts.

**Change Password** - Opens the [Change Password Window](#) to change the Login Password for the current user.

**Perform Signature** - Opens the [Perform Electronic Signature Window](#) to sign a data file.

**Unlock Data File** - Opens the [Unlock Data File Window](#) to unlock a locked data file.

**Audit Trail Log** - Opens the [Audit Trail Window](#) to view, search, export, and print the audit trail.

**Lock Application** - Opens the [Unlock Application Window](#) to lock the LabChip GX Reviewer software and prevent other users from using the software until the software is unlocked by the current user or an Administrator.

## View Menu

The View menu contains the following commands:

**Event Viewer** - Opens the [Event Viewer Window](#) to view events and errors that occur during the current run or during a previous run.

**Run Info** - Opens the [Run Info Window](#) to view information about the run.

**Version Change Details** - Displays the Data File Version Change Details window to view changed versions of the selected open data file.

## Validation Menu

The Validation menu contains the following commands:

**Software IQ** - Opens the [Software Installation Qualification Window](#) to perform the IQ.

**Reports** - Opens the [Print Validation Reports Window](#) to view or print IQ results.

## Window Menu

The Window menu contains the following commands:

**Cascade** - Displays each Collection in a separate, cascading window in the [Collection Pane](#).

**Tile Vertical** - Displays each Collection in separate side by side windows in the [Collection Pane](#).

**Tile Horizontal** - Displays each Collection in separate top to bottom windows in the [Collection Pane](#).

**Tabbed** - Displays each Collection in a separate tab in the [Collection Pane](#).

## Help Menu

The Help menu contains the following commands:

### **LabChip GX Reviewer Help**

Opens the Contents/Index page for the LabChip GX Reviewer Help file.

### **About LabChip GX Reviewer**

Opens the [About LabChip GX Reviewer Window](#), showing the software version number and firmware version number.

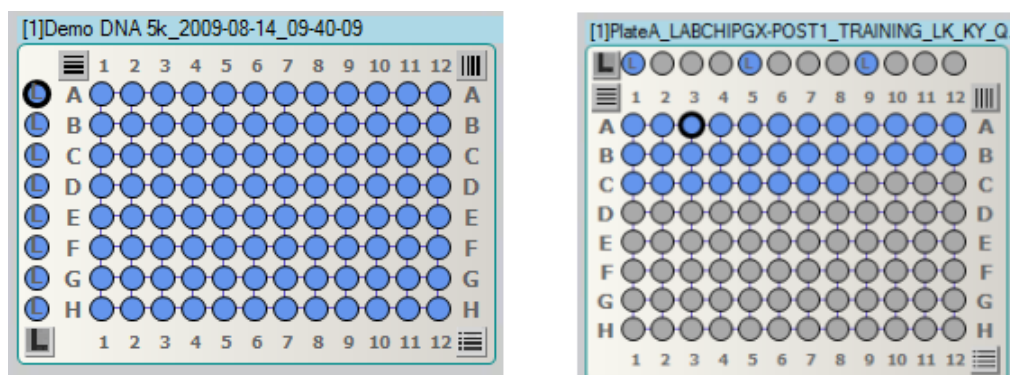
## Plate View or Plate List

The [Plate View](#) or [Plate List View](#) displays on the left side of the [LabChip GX Reviewer Main Window](#).

The Plate View or List View displays the data files in the open collection and enables you to select specific wells of microplate data. Click the tabs at the bottom of the view to switch between [Plate View](#) and [List View](#).

## Plate View

The Plate View displays a graphical representation of the microplates in the collection and indicates selected wells and ladders, filtered wells, and wells with errors. Wells included in the collection are colored blue. Ladder wells display on the left side of the plate if the sip order was row-wise, or along the top of the plate if the sip order was column-wise. The wells selected to view in the [Gel View](#) and [Well Table View](#) are outlined in black. Select the Plates tab at the bottom of the Workspace pane to see the Plates view.



**Figure 69. Plate View, Row-wise and Column-wise**

To select the wells to view in the [Collection Pane](#), see “[Selecting the Wells in a Collection](#)” on page 35.

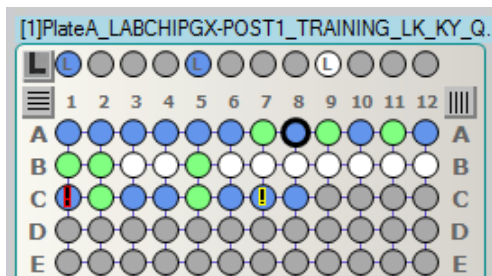
#### **Plate View Right-Click Menu**

Right-click on the plate name in the Plate view to display the following options in the shortcut menu:

- **Keep Gel in Sip Order** - Displays the gels in the sipped order.
- **Save Plate** - Saves the current data file.
- **Copy Plate** - Saves a copy of the plate data file (.gxd) to the selected folder.
- **Export Plate Datafile** - Displays the Export Plate as New Data File Window to save a copy of the plate data file (.gxd) without user specific names to the selected folder. Options to remove include Sample Names, Comments, EP Table, EP Names, Smear Table, and Smear Names.
- **Export Assay** - Saves a copy of the assay settings for the plate to an assay file (.asy for GX or .asyx for GX Touch) in the selected folder.
- **Rename Plate** - Renames the plate in the workspace. If desired, the original data file can be renamed by selecting the Rename File to Match check box.
- **Remove Plate** - Removes the plate data file from the workspace. The data file is not deleted, only the workspace view changes.
- **Analysis Settings** - Displays the [Assay Analysis Window](#) to change the analysis settings for the data file.
- **Version Change Details** - Displays the [Data File Version Window](#) to view a different version of the data file in the workspace.
- **Run Info** - Displays the [Run Info Window](#) to view the run information and Event Log.



## Plate Well Color Code



- **White** - Wells are not included in the open collection.
- **Gray** - Wells were not read.
- **Blue** - Wells are included in the open collection.
- **Any Other Color** - Wells are selected by a Filter. See the [Filter View](#) to determine which color represents each filter. If a well is selected by multiple filters, the colors are combined in the well. (In the figure above, light green wells are selected by a filter.)
- **Black Outline** - Wells are selected in the [Gel View](#) and [Well Table View](#).
- **Red Exclamation Point in Well** - An analysis error has occurred in the well, such as no lower marker detected (well C1 above).
- **Yellow Exclamation Point in Well** - An analysis warning has occurred in the well (well C7 above).

## List View

The List View displays a list of all the wells in the currently open data files. Select the **List** tab at the bottom of the Workspace pane to see the List view.

- **Dark Blue** well names are included in the open collection.
- **Black** well names are not included in the open collection.
- **Light Blue** well names are selected in the [Gel View](#) and [Well Table View](#).
- Well names outlined in **Yellow** have an analysis warning.
- Well names outlined in **Red** have an analysis error.

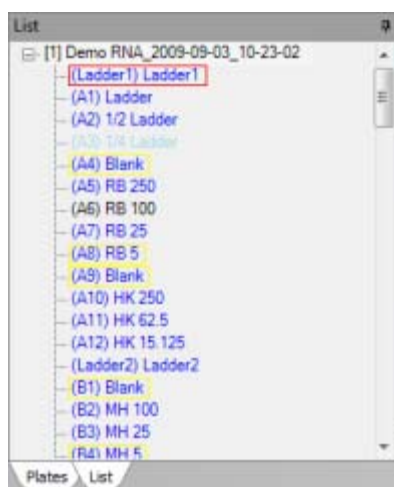


Figure 70. List View

## Collection Pane

The Collection Pane in the [LabChip GX Reviewer Main Window](#) displays a tab for each collection in the workspace. Each collection displays the information from the data files that are open in the [Plate View or Plate List](#).

The Collection Tabs each contain the following views:

- [Graph View](#)
- [Gel View](#)
- [Well Table View](#)
- [Peak Table View](#)
- [Filter View](#)

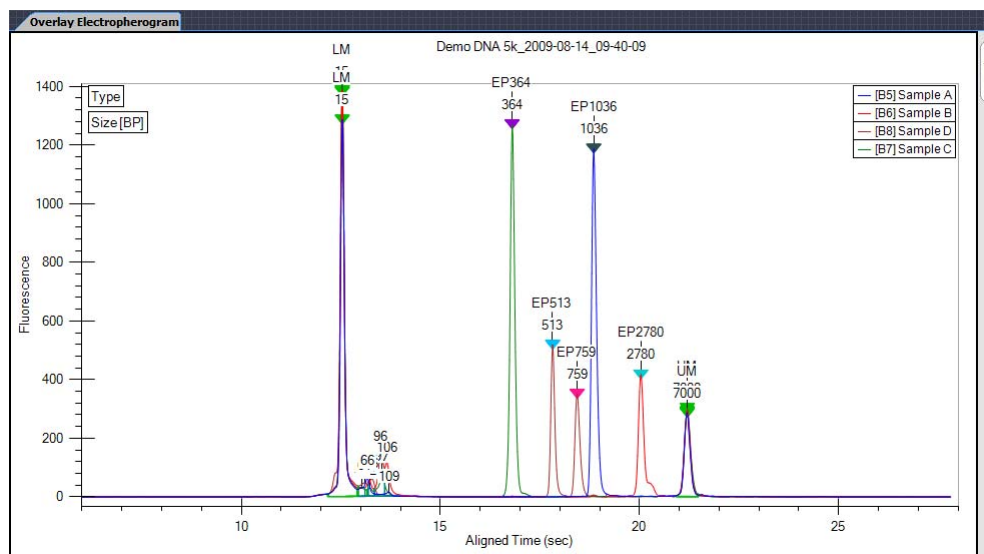
The views in the Collection pane are synchronized with each other.

- Selecting a graph on the Graph tab automatically selects the same well on the Gel tab.
- Selecting a peak in the Peak Table automatically selects the same peak in the Graph tab and the Gel tab.
- Closing a gel on the Gel tab closes the graph for the well and removes the well data from the Peak Table and Well Table tabs.

## Graph View

The Graph view in the [Collection Pane](#) is a visual representation of the data from each well as an electropherogram.

Use the [Overlay Electropherograms Tab](#) and the [Electropherograms Tab](#) to view data from completed wells. To change the view in the Overlay Electropherograms tab, see [“Viewing Graphs in the Overlay Electropherograms Tab” on page 82](#). To change the view in the Electropherograms tab, see [“Viewing Graphs in the Electropherograms Tab” on page 83](#).



**Figure 71. Graph View**

If Type is selected as an annotation, the lower (and upper for DNA) markers are displayed in the graph view with large green arrows labeled LM and UM respectively. The currently selected peak in the Gel view or Peak Table displays a small blue arrow above the peak.

You can zoom in and zoom out the Graph View of the wells. Zoom in by clicking and dragging over a region of an electropherogram. Zoom out by right clicking on a graph, and selecting either Unzoom or Unzoom All from the shortcut menu. Double-clicking in the graph will zoom out to the previous zoom level.

Graph data can be exported to a graphic file by choosing **Export** on the File menu. (See [“Exporting Data” on page 96](#) for details.) If the workspace contains multiple collections, the data exported is from the active/selected collection.

## Graph View (Continued)

To show or change the labels on the peaks in the graph, show the data points on the graph, show peak baselines, show smears, or change the graph colors, see [“Graph View Properties” on page 153](#).

To select a peak on the graph, move the cursor near the peak and click. A blue arrow above the peak shows that the peak is selected, and the cursor changes to an up arrow. The [Gel View](#) and [Peak Table View](#) also select the corresponding entry.

To adjust the peak baselines from the graph view, see [“Adjusting the Peak Baseline” on page 66](#).

### Graph View Shortcut Menus

#### Right-Click Menu (not near a peak)

Right-click away from a peak in the graph to display a shortcut menu containing the following commands:

**Unzoom** - Zooms out to the previous zoom level.

**Unzoom All** - Zooms out and returns to the standard view.

**Set Scale** - Opens the Set Graph Scales window to specify the X and Y ranges to show on the graph.

**Scale to Sample Peaks** - Scales the view to the minimum and maximum X values of the current sample peaks. Marker and/or system peaks are ignored.

**Scale to All Peaks** - Scales the view to the minimum and maximum X values of the all peaks, including marker peaks and system peaks.

**Manual Baseline or <SHIFT> + LBUTTON** - Turns Manual Baseline mode on or off. If selected, click and drag the mouse on the graph to create a new manual baseline for the peaks.

**Merge Peaks or <ALT> + LBUTTON** - Turns Peak Merge mode on or off. If selected, click and drag the mouse across two or more peaks to merge the peaks into one.

**Copy** - Copies the selected graph to the clipboard in a BMP format.

**Split Peak** - Splits a single peak into two separate peaks.

**Analysis Settings** - Opens the [Assay Analysis Window](#) to change the analysis settings.

## Graph View (Continued)

### Right-Click Menu (near a peak)

Right-click above or below a peak in the graph to display a shortcut menu containing the following commands:

**Exclude Peak** - Excludes the peak from the analysis. (The Peak Type label displays X.)

**Include Peak** - Includes an excluded peak in the analysis. Only available when the selected peak is already excluded or is type System Peak or "?". Including the peak will compute the peak properties, populate the peak table, and include the peak in the area total used for the %Purity calculation.

**Force Lower Marker** - Defines the selected peak as the Lower Marker. (The Peak Type label displays LM\*.)

**Clear Forced Lower Marker** - Allows the analysis to determine the lower marker. (The Peak Type label for the calculated lower marker displays LM.) Only available when the selected peak is a Forced Lower Marker.

**Force Upper Marker** - (DNA Assays only) Defines the selected peak as the Upper Marker. (The Peak Type label displays UM\*.)

**Clear Forced Upper Marker** - (DNA Assays only) Allows the analysis to determine the upper marker. (The Peak Type label for the calculated upper marker displays UM.) Only available when the selected peak is a Forced Upper Marker.

**Add Expected Peak** - Opens the [Add New Expected Peak Window](#) to add a new Expected Peak to the specified wells.

**Force Expected Peak** - Defines the selected peak as the specified Expected Fragment or Protein. A list of all of the defined Expected Peaks displays beside the shortcut menu. Select the desired Expected Peak from the list.

**Clear Forced EP** - Clears the forced peak and allows the analysis to determine the expected peak.

### Right-Click Menu (at the bottom of an RNA peak)

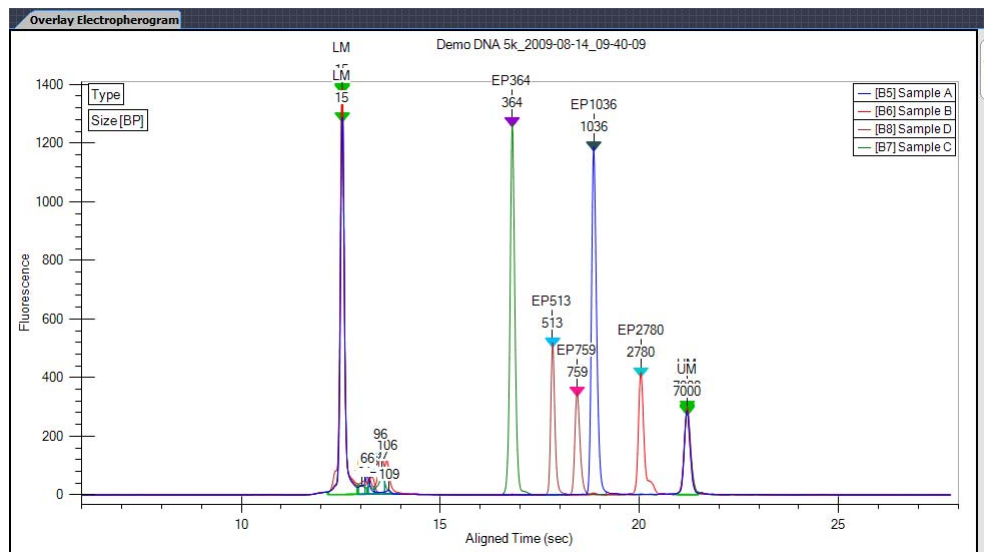
Right-click near the bottom of a peak in the graph for an RNA assay to display a shortcut menu containing the following commands:

**Reset to Defaults** - Sets the Peak Baseline endpoints back to the default values.

## Overlay Electropherograms Tab

Use the Overlay Electropherograms tab on the [Graph View](#) to view a single graph or multiple graphs overlaid on top of each other.

If the Overlay Electropherograms Tab is not open, select the **Collection** → **Layout** on the [LabChip GX Reviewer Main Window](#), select the location where you want to display the Overlay Electropherograms tab, and click the **Apply** button.



**Figure 72. Overlay Electropherograms Tab**

The sample list at the upper right displays the name of each sample and the color assigned to the graph for each sample. If only one graph is displayed, the [Gel View](#), [Well Table View](#), and [Plate View or Plate List](#) all show the same selected well.

The gel lanes selected in the [Gel View](#) are synchronized with the graphs displayed in the Overlay Electropherograms tab.

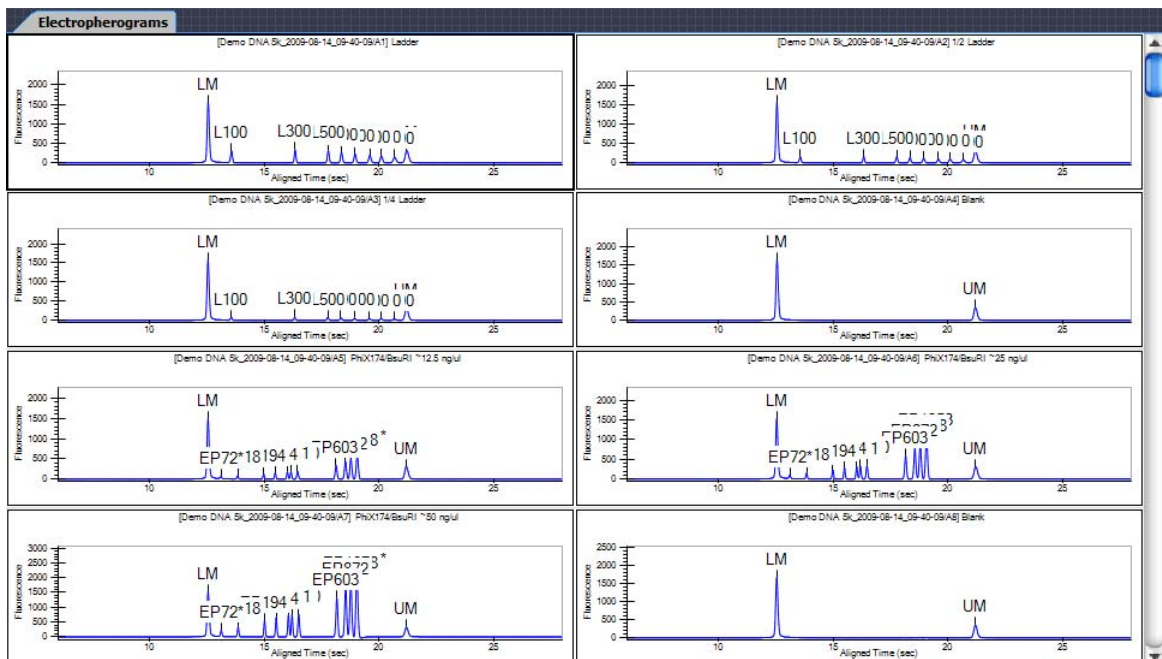
For information on changing the view in the Overlay Electropherograms tab, see [“Viewing Graphs in the Overlay Electropherograms Tab”](#) on page 82.

See [“Graph View Properties”](#) on page 153 for descriptions of the properties that can be set for the Overlay Electropherograms tab.

## Electropherograms Tab

Use the Electropherograms tab on the [Graph View](#) to view a single graph or multiple graphs in the same tab.

If the Electropherograms Tab is not open, select the **Collection** → **Layout** on the [LabChip GX Reviewer Main Window](#), select the location where you want to display the Electropherograms tab, and click the **Apply** button.



**Figure 73. Electropherograms Tab**

Each graph displays the data file name and well name at the top of the graph.

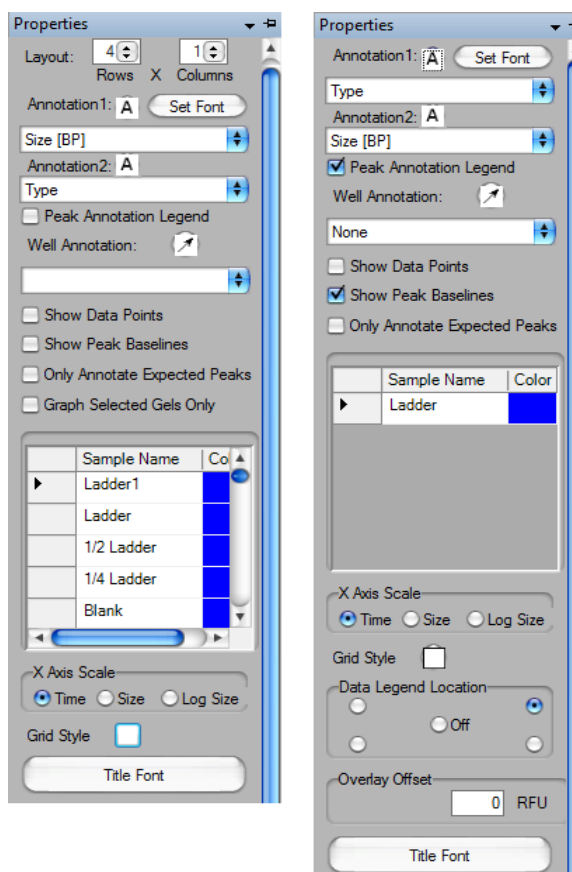
For information on changing the view properties in the Electropherograms tab, see [“Viewing Graphs in the Electropherograms Tab”](#) on page 83.

See [“Graph View Properties”](#) on page 153 for descriptions of the properties that can be set for the Electropherograms tab.



## Graph View Properties

To view the Properties for the [Electropherograms Tab](#) or the [Overlay Electropherograms Tab](#), click the **Properties** tab on the right side of the [Graph View](#).



**Figure 74. Electropherograms Properties and Overlay Electropherograms Properties**

This window contains the following options:

Option	Function
Layout	Specifies the number of rows and columns of graphs displayed on the <a href="#">Electropherograms Tab</a> . (Only displayed when the Electropherograms tab is selected.)
Annotation 1	Labels each peak in the graph with the peak property selected from the drop-down list. Default is Type. The Annotations available depend on the columns selected in the Peak Table View.
Text Orientation (A) button	Specifies the orientation of the text for the annotation: horizontal, vertical up, or vertical down.

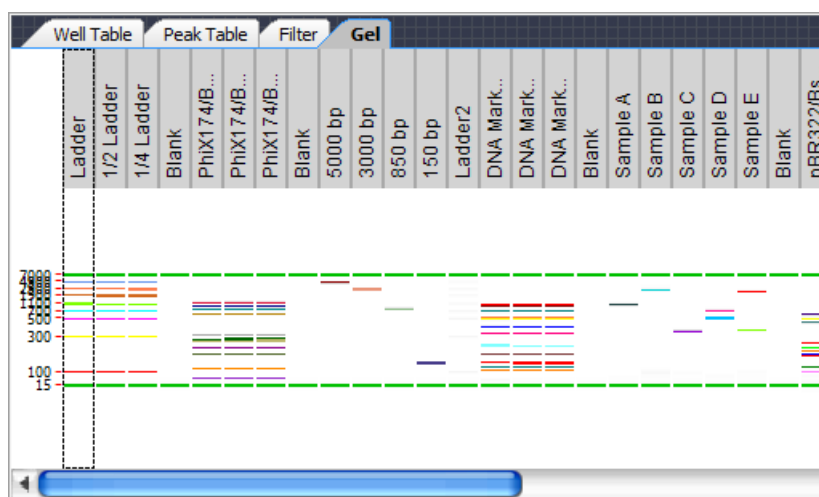
Option	Function
Set Font button	Opens the Font window to choose the font, style, and size of the text for all annotations.
Annotation 2	Labels each peak in the graph with a peak property selected from the drop-down list. Default is None.
Peak Annotation Legend	If selected, the types of the annotations display in the upper left corner of the graph.
Well Annotation	Displays the selected well property outside the graph. Only the columns displayed in the <a href="#">Well Table View</a> are available for selection.
Well Annotation Location Button (arrow)	The location of the well annotation. Click the button to change the location: upper right, upper left, lower left, or lower right.
Show Data Points	If selected, displays a dot on the graph at the location of each data point.
Show Peak Baselines	If selected, displays the baseline for each peak on the graph.
Show Smears	If selected, displays smears as a colored line on the trace and displays the smear baseline. This option only displays if smears are defined in the <a href="#">Assay Analysis Window</a> .
Only Annotate Expected Peaks	If selected, only the peaks that are labeled as Expected Fragments, Expected Proteins or Expected Glycans display the annotations. If not selected, all peaks display the annotations.
Graph Selected Gels Only	If selected, only the wells selected in the <a href="#">Gel View</a> or <a href="#">Well Table View</a> are displayed in the Electropherograms tab. If not selected, all wells in the collection are displayed. (Only displayed when the Electropherograms tab is selected.)
Sample Name/Color Table	Displays the names of the samples (well names) on the graph and the color associated with each sample (well). Click on the color to choose a different color for a sample.
X Axis Scale	Specifies the units displayed on the X Axis, either Time, Size, or Log Size. Log Size displays the size on a logarithmic scale.
Grid Style	Displays grid lines on the graph: vertical, horizontal, both, or none. Click the button to cycle through the grid options.
Data Legend Location	If multiple wells are displayed in the Overlay Electropherograms tab, specifies the location where the legend displays on the graph. The legend shows the color used for each well. (Only for the Overlay Electropherograms Tab.)
Overlay Offset	Offsets each of the graphs by the RFU value specified.

Option	Function
Title Font	Opens the Font window to select the Font, Font Style, Font Size, and Effects for the title above the graphs in the Electropherograms tab or the Overlay Electropherograms tab. The selected font is also used when exporting the graphs.
Pin icon	In the top right corner, this is used to lock in place or unlock the Properties tab. If locked in place, the Graph is resized to accommodate the tab.

## Gel View

The Gel view in the [Collection Pane](#) is a visual representation of the data formatted to look like the Gel slabs that were originally used to provide DNA, Protein, or RNA data. The data is shown in Time vs. Fluorescence (or digital form). (Protein, Glycan, and Protein Charge Variant assays are only supported on LabChip GXII or GXII Touch instruments.)

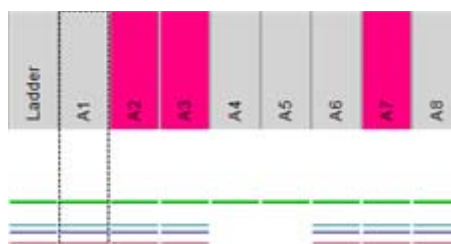
Click on a gel lane (well) to select the well. Ctrl + click to select multiple wells. Selected wells are outlined with a dotted gray line. Wells selected in the Gel view are also selected in the [Well Table View](#) and are displayed in the [Overlay Electropherograms Tab](#).



**Figure 75. Gel View**

Moving the cursor over a band in the Gel view displays a tool tip that includes the same information about the peak as the [Peak Table View](#). (Changing the columns displayed in the Peak Table will change the contents of the tool tip in the Gel view.)

For DNA assays, the upper and lower markers of all wells are aligned to the upper and lower markers of the first well in the gel view. For Protein and RNA assays, the lower markers of all wells are aligned to the markers of the first well in the gel view.



**Figure 76. Gel Headers**

## Gel View (Continued)

A colored column header indicates that the well is selected by a filter. Click the [Filter View](#) to view the color of each filter. A red exclamation point under the header indicates an analysis error occurred in the well. A yellow exclamation point under the header indicates an analysis warning occurred in the well. A gray header indicates a normal well. To change the size of the gel header, click on the border between the header and the well and drag the header to the desired size.

**Expected Peaks** are indicated on the gel by colored horizontal lines.

The graphs displayed in the [Graph View](#) are synchronized with the lanes selected in the Gel tab.

You can drag-and-drop the gel lanes to change the order of the wells for comparing two or more gel wells. To drag-and-drop a gel lane, click in the header of the lane to be moved and drag the gel lane to the desired location.

Double-click in the Gel view to zoom out to the previous zoom level.

Gel data can be exported to a graphic file by choosing **Export** on the [File Menu](#) (see “[Exporting Data](#)” on page 96 for details). If the workspace contains multiple collections, data is exported from the active/selected collection.

To change the Lane Width or Gel Contrast Range, see [Gel View Properties](#).

### Right-Click Menu

Right-click anywhere in a gel to display a shortcut menu containing the following commands:

**Unzoom** - Zooms out to the previous zoom level.

**Unzoom All** - Zooms out completely and returns to the standard view.

**Scale Gel Contrast to this Lane** - If selected for a lane, the minimum and maximum RFU values for all lanes in the collection are set to the minimum and maximum RFU values in the selected lane.

**Scale Gel Contrast to Collection** - Restores the minimum and maximum RFU values for all lanes in the collection to the default values. (Only available when Scale Gel Contrast to This Lane has been selected for a lane.)

## Gel View (Continued)

**Remove** - Removes the sample from the collection.

**Copy Gel** - Copies all of the open lanes (wells) to the clipboard in a .bmp format.

**Copy Lane** - Copies the selected lane (well) to the clipboard in a .bmp format.

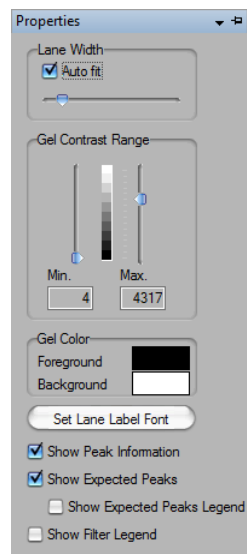
**Analysis Settings** - Opens the [Assay Analysis Window](#) to change the analysis settings.

**Edit Sample Name** - Opens the [Sample Name Editor Window](#) to change the well name or add a comment to the well. The comment displays in the [Well Table View](#) and in printed reports.

**Rename Plate** - Opens the **Rename Plate** window to specify a new name for the plate.

## Gel View Properties

To view the Gel View Properties, click the **Properties** tab on the right side of the [Gel View](#).



**Figure 77. Gel View Properties**

The following properties can be set for the Gel view:

Option	Function
Lane Width	Sets the width of the Collection column. Select <b>Auto Fit</b> to have the software automatically fit all the data, or use the slider to manually set the width.
Gel Contrast Range	Sets the minimum and maximum Gel Band Contrast for the bands in each well. Use the sliders to change the min and max values.
Gel Color	Click on the Foreground color or the Background color to open the Color window to choose the desired colors for the gel.
Set Lane Label Font button	Opens the Font window to change the font or size of the labels in the gel headers.
Show Peak Information	If selected, displays peak information in a tool tip when the cursor moves over a peak. If not selected, the tool tip does not display when the cursor is over a peak.
Show EPs and Smears	If selected, expected peaks are indicated in the gel by colored horizontal lines and smears are indicated by bands of translucent color.
Show EP/Smear Legend	Displays a legend of the band colors and expected peak sizes or smear sizes in the Gel view. Click and drag to move the legend. Only displays if Expected Peaks or Smears are defined in the <a href="#">Assay Analysis Window</a> .

Option	Function
Show Filter Legend	Displays a legend of the colors assigned to each filter. Click and drag to move the legend. Only displays if at least one filter is defined in the <a href="#">Filter View</a> .
Pin icon	In the top right corner, this is used to lock in place or unlock the Properties tab. If locked in place, the Gel display panel is resized to accommodate the tab.



## Well Table View

The Well Table view in the [Collection Pane](#) contains a summary of analysis results for the wells selected from the microplates in the collection.

Plate Name	Well Label	Sample Name	Peak Count	Ova Corr. Area	NG Ale HC Corr.	NG Inf HC Corr.	Ale HC Corr. Area	Inf HC Corr. Area	Rit Corr. Area	Ada Corr. Area
2016-05-12_14-33-36_dt c...	A01	NR CET/Ad...	5	N/A	N/A	N/A	N/A	N/A	N/A	34.00
2016-05-12_14-33-36_dt c...	A02	Blank 2	0	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2016-05-12_14-33-36_dt c...	A03	R Ale/NGHC...	4	N/A	47.47	N/A	1403.92	N/A	N/A	N/A
2016-05-12_14-33-36_dt c...	A04	NR CET/Ad...	5	N/A	N/A	N/A	N/A	N/A	N/A	28.06
2016-05-12_14-33-36_dt c...	A05	Blank 2	0	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2016-05-12_14-33-36_dt c...	A06	R Ale/NGHC...	4	N/A	45.62	N/A	1379.72	N/A	N/A	N/A
2016-05-12_14-33-36_dt c...	A07	NR CET/Ad...	5	N/A	N/A	N/A	N/A	N/A	N/A	29.48
2016-05-12_14-33-36_dt c...	A08	Blank 2	0	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2016-05-12_14-33-36_dt c...	C01	NR CET/Ad...	4	N/A	N/A	N/A	N/A	N/A	N/A	131.11
2016-05-12_14-33-36_dt c...	C02	NR Bev/Ova...	5	16.46	N/A	N/A	N/A	N/A	N/A	N/A
2016-05-12_14-33-36_dt c...	C03	R Ale/NGHC...	5	N/A	88.55	N/A	1478.42	N/A	N/A	N/A
2016-05-12_14-33-36_dt c...	C04	NR CET/Ad...	4	N/A	N/A	N/A	N/A	N/A	N/A	112.35
2016-05-12_14-33-36_dt c...	C05	NR Bev/Ova...	5	16.36	N/A	N/A	N/A	N/A	N/A	N/A
2016-05-12_14-33-36_dt c...	C06	R Ale/NGHC...	6	N/A	83.83	N/A	1417.91	N/A	N/A	N/A

**Figure 78. Well Table View**

To change the order of columns in the table, click on a column header and drag the column to the desired position in the table. Click a column header to sort the table in ascending/ descending/ original order.

Double-click on a **Plate Name** to open the **Rename Plate** window to rename the plate.

Double-click on a **Sample Name** to edit the well name.

Double-click on a **User Comment** to add or edit the User Comment (if applicable).

For gDNA assays, the Total gDNA Concentration in the Well Table is the concentration of the entire smear region from 0.175kb to 300kb. Use the [Smear Analysis Tab](#) to change settings or display columns in the Well Table.

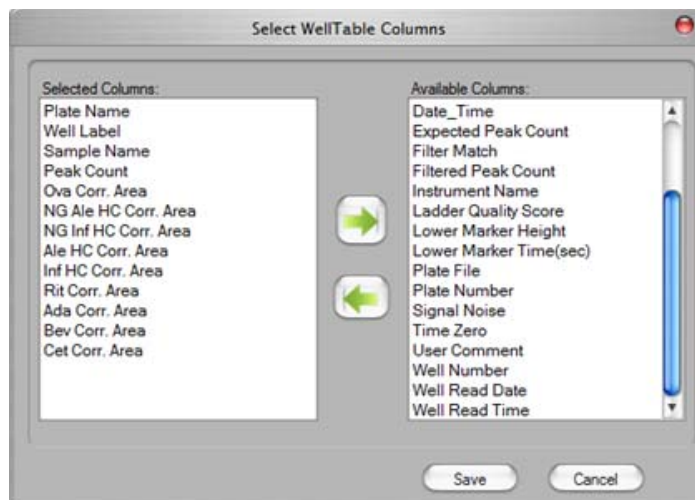
For HT Protein QC assays, the **Total Conc. (ng/ul)** column will not display.

The output of an exported Well Table includes the columns in the order displayed in the Well Table at export time. A Well Table is exported to a CSV format, which can be opened in a program such as Microsoft Excel. If the workspace contains multiple collections, the data is exported from the active/selected collection.

## Select Well Table Columns Window

Use the Select Well Table Columns window to show or hide columns in the [Well Table View](#). To open the Select Well Table window, right-click on a column header in the Well Table.

The Select Well Table Columns window displays all available columns with the current selections in the Selected Columns list. The columns available depend on the type of data file that is open and the selected analysis settings.



**Figure 79. Select Well Table Columns Window**

Show or hide columns in the well table by moving the column names between the **Available Columns** list and the **Selected Columns** list.

To change the order of the columns displayed in the Well Table, drag and drop the column names in the Selected Columns list. The columns display on the order listed in the Selected Columns list.

## Peak Table View

The Peak Table view in the [Collection Pane](#) is a text-based representation of all the information about each peak. The Peak Table View is hidden by default for gDNA assays.

Well Table Peak Table Filter Gel								
Well Label	Sample Name	Type	Size [kDa]	% Purity	Migration Time(sec) - Start	Migration Time(sec) - End	Corr. Area	
A03	Cet NR	?	0.72		12.25	12.47	18.10	
A03	Cet NR	LM	1.06		12.80	13.03	1224.54	
A03	Cet NR	Xsys	1.32		13.12	13.35	27.05	
A03	Cet NR	Xsys	7.61		16.53	16.68	320.12	
A03	Cet NR	Xsys	7.97		16.68	16.87	296.99	
A03	Cet NR	Xsys	8.50		16.87	17.13	121.11	
A03	Cet NR		140.21	0.59	30.47	31.30	23.72	
A03	Cet NR	Cet NG	172.08	1.93	32.32	33.34	78.33	
A03	Cet NR	EP200	190.72	96.94	33.34	35.80	3929.16	
A03	Cet NR		294.09	0.55	40.00	40.80	22.14	

**Figure 80. Peak Table View**

Change the order of columns in the table by clicking on a column header and dragging the column to the desired position in the table. Click a column header to sort the table in ascending/ descending/ original order.

To view or hide columns in the Peak Table view, right-click on the column headers in the table. The Select Peak Table Columns window displays all available columns in the Selected Columns list. Show or hide columns in the Peak Table by moving the column names between the Available Columns list and the Selected Columns list in the Select Peak Table Columns window. Drag and drop the column names in the Selected Columns list to change the order of the columns displayed in the Peak Table.

The analysis normally labels the upper marker (UM) (DNA Assays only) and lower marker (LM) in each sample and in the ladder. The labels display in the Type column of the table. If the analysis has misidentified the markers, the correct marker can be selected manually by right-clicking on the peak row to open a shortcut menu of possible peak types for the peak. This can also be used to label a peak as Excluded (X). The concentration of an excluded peak is forced to zero so that it does not affect the total well concentration and the %Purity calculation.

Expected Peaks are indicated by the Expected Peak Name in the Type column.

## Peak Table View (Continued)

The output of an exported Peak Table includes the columns in the order displayed in the Peak Table at export time. A Peak Table is exported to a CSV format, which can be imported into a program such as Microsoft Excel. If the workspace contains multiple collections, the data is exported from the active/selected collection.

To show only filtered peaks, sort within each well, or hide excluded peaks, see [Peak Table Properties](#).

Protein, Glycan, and Protein Charge Variant assays are only supported on LabChip GXII or GXII Touch instruments. DNA, RNA, and gDNA assays are supported on LabChip GX, GXII, GX Touch, and GXII Touch instruments.

### Peak Table Columns

The Peak Table can display the following columns:

**%Area** - (Glycan assay only) The peak's area as a percentage of the total area of peaks within the sample range (> 6.6 CGU).

**% of Total Area** - (RNA assays only) The area of the RNA fragment divided by the total area. The total RNA area is computed using trapezoidal integration of the electropherogram from the end of the lower marker to the baseline end time. The baseline for the total area is a straight line drawn from the baseline start time to the baseline end time. The height of the baseline at these points is the average signal value over a 5 second region around these points.

**% Purity** - (Protein assay only) The quantity of protein, expressed as a percentage of the total protein, found in a particular peak.

**Aligned Area** - If the sample has been aligned, the area of the aligned peaks is reported.

## Peak Table View (Continued)

**Area** - The peak area is calculated as the sum of the parallelograms of a point-to-point fit down to absolute zero minus the parallelogram of the local baseline down to absolute zero. Data points are 0.05 seconds apart.

**Barcode** - The barcode on the plate used in the run.

**Baseline** - The center average height of the peak baseline, measured in RFUs.

**Chip ID** - The ID number of the Chip used to run the plate.

**Comment** - Displays any comments associated with the well, either from the Sample Name File specified during the run or from the [Sample Name Editor Window](#).

**Conc. (ng/uL)** - (DNA and Protein assays *except* for HT Protein QC assay) - The concentration calculated relative to the ladder and marker peak concentrations. The ladder concentration is displayed in the [Analysis Tab](#) of the [Assay Analysis Window](#).

**Corr. Area** (Glycan assays) and **Time Corr. Area** (Protein assays) - Displays the mobility corrected area. The area of a peak should represent the total area of the compound responsible for the fluorescence. In the LabChip instruments, the fluorescence of the compound moving past the detector is sampled at constant time intervals unlike the conventional slab gel where the compound is spread out spatially and imaged at a single time. To convert from a peak area integrated in the time dimension to one integrated in the space dimension, we use the fact that  $x$  is proportional to  $\mu t$  so  $\Delta x \propto \mu \Delta t$  and the mobility  $\mu$  is proportional to  $1/T$  where  $T$  is the migration time of the peak. So the Time Corr Area =  $100 * \text{Area}/T$ . The 100 is an arbitrary constant designed to keep the corrected area in a range similar to the original area computed from the time series data.

**Date\_Time** - The date and time that the plate data file was created.

**Expected Fragment (BP or kb)/ Expected Protein (kDa)/ Expected Glycan (CGU)** - Displays the size of the Expected Fragments, Expected Proteins, or Expected Glycan.

**Fragment Area** - (RNA assays only) The sum of the trapezoids between the fragment start and end times. The trapezoid base is a line drawn across the fragment base from the start point to the end point.

## Peak Table View (Continued)

**Fragment End (sec)** - (RNA assays only) Amount of time from injection to the falling edge of the fragment in seconds.

**Fragment Start (sec)** - (RNA assays only) Amount of time from injection to the leading edge of the fragment in seconds.

**FWHM** - The width of the peak (Full Width at Half Maximum), measured in seconds.

**Height** - The value at the apex of the peak minus the local baseline start value.

**Instrument Name** - The name of the instrument that was used to run the plate and create the data file.

**Molarity (nmol/l)** - (DNA and gDNA assays only) Displays the molarity of the peak.

**Migration Time - Center** - The time from injection to the peak apex in seconds.

**Peak Index** - The index number of the peaks in the sample. Marker peaks, peaks before the lower marker, and peaks after the upper marker are not numbered.

**Peak Number** - The order in which the peaks were detected for each well. All peaks in each well are numbered, starting at 1.

**Plate File** - The name of the original plate data file. This name cannot be changed.

**Plate Name** - The name of the plate defined in the workspace.

**Plate Number** - The number of the plate in the same order as the plates are displayed in the [Plate View](#) or [Plate List](#).

**RNA Fragment** - (RNA assays only) The name of the fragment based on its size falling within a certain range set in the assay definition. (These definitions are visible only to assay developers).

**Sample Name** - The sample name defined in the Sample Name File specified during the run. The Sample name can also be changed in the [Well Table View](#) or the [Gel View](#).

**Signal Noise** - The statistical standard deviation of 1 second of data just before the Peak Find Start Time.

## Peak Table View (Continued)

**Size (BP for DNA assays, kb for gDNA assays, KDa for Protein assays, nt for RNA assays, CGU for Glycan assays)** - The size of the peak based on the ladder sizes specified in the assay.

**Type** - Displays the type of peak for markers or expected peaks.

**Well Label** - The row letter and column number of the well (A1 - H12 for 96-well plates, or A1 - P24 for 384-well plates).

**Well Number** - The number of the well in the same order as the wells were selected in the collection. See [Selecting the Wells in a Collection](#).

## Peak Table View Shortcut Menus

Right-click on a peak in the peak table to display a shortcut menu containing the following commands:

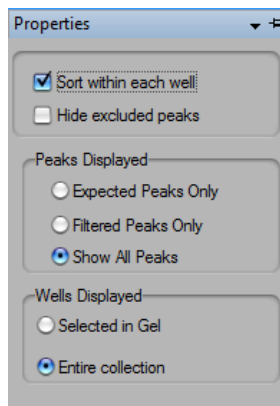
- Exclude Peak
- Include Peak (for excluded peaks, peaks of type "?", or System Peaks in Protein assays)
- Force Lower Marker
- Force Upper Marker (DNA assays only)
- Force Expected Peak

**NOTE:** *Excluding a peak or manually setting a peak to be an upper or lower marker can cause analysis errors.*



## Peak Table Properties

To view the Peak Table Properties, click the **Properties** tab on the right side of the [Peak Table View](#).



**Figure 81. Peak Table Properties**

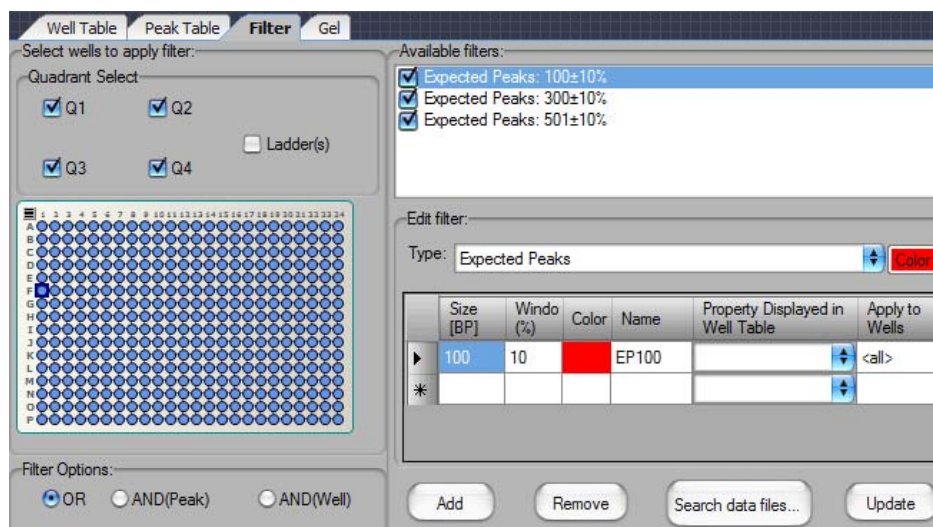
This window contains the following options:

Option	Function
Sort within each well	If selected (default), sorting occurs only within each well rather than across the entire table. Click a column header to sort the table rows by the column value. If cleared, uses conventional sorting, which mixes together peaks from all wells. Clicking the column header sorts in ascending/descending/original order.
Hide excluded peaks	If selected, excluded peaks and unknown peaks are hidden in the Peak Table view. In protein assays, the analysis excludes system peaks, which are compounds that are artifacts of the assay chemistry and not generally of interest.
Expected Peaks only	If selected, only peaks identified as Expected Peaks display in the Peak Table.
Filtered peaks only	If selected, the Peak Table displays only peaks that match the filter criteria. Useful when generating a collection based on a filter whose selection criteria are peak specific, such as Area, Concentration, %Purity, Expected Peaks, and Size.
Selected in Gel	If selected, only the gel lanes selected in the <a href="#">Gel View</a> display. To select multiple wells, Ctrl + click on the lanes in the Gel view.
Entire Collection	If selected, all wells in all plates that are included in the collection are displayed.
Pin icon	In the top right corner, used to lock in place or unlock the Properties tab. If locked in place, the Peak Table display panel is resized to accommodate the tab.



## Filter View

The Filter view in the [Collection Pane](#) is used to define criteria to select wells for a collection automatically. The filter types available depend on the type of assay that was used to create the data. Each filter can be assigned a different color to determine which filter applies to each well.



**Figure 82. Filter View**

**Quadrant check boxes**- The selected quadrants of all plates in the collection will have the specified filters applied to them. Selecting a quadrant check box applies the selected filters to that quadrant. Clearing a quadrant check box excludes that quadrant from all filters.

**Ladder(s) check boxes** - If selected, ladder wells are filtered. If cleared, ladders are not filtered.

**Filter Plate Diagram** - Only the wells selected in blue have the filter applied. Wells that are not selected (white) will not be selected by a filter.

**Filter Options** - determines how multiple filters are logically combined. The options available are OR, AND(Peak), and AND(Well).

- **OR** - Selects any well that contains a peak that matches any of the filters selected in the Available Filters list.
- **AND(Peak)** - Selects any well that contains a single peak that matches all of the filters selected in the Available Filters list.

- **AND(Well)** - Selects any well that contains peaks that match all of the filters selected in the Available Filters list. Different peaks in the same well can match different filters, as long as all filter conditions are met in the same well.

**Available Filters list box** - Displays all of the filters that are part of the current workspace. The check box next to each filter in the list is used to include or exclude that filter from the analysis in the collection.

**Filter Type drop-down list** - Specifies the Type of each filter. Available options depend on the assay used to create the data.

**Color button** - Displays the color selected for the filter. To select a different color, click the Color button to open the Color window.

**Filter Criteria** - The appropriate filter criteria options display based on the type of filter selected. Numeric value operators are Equal To (with percent threshold), Between, Less Than, or Greater Than. Text expressions can contain wild cards. Expected Peaks criteria specify expected peaks in a well.

**Add button** - Creates a new filter with the specified filter criteria and adds the new filter to the Available Filters list.

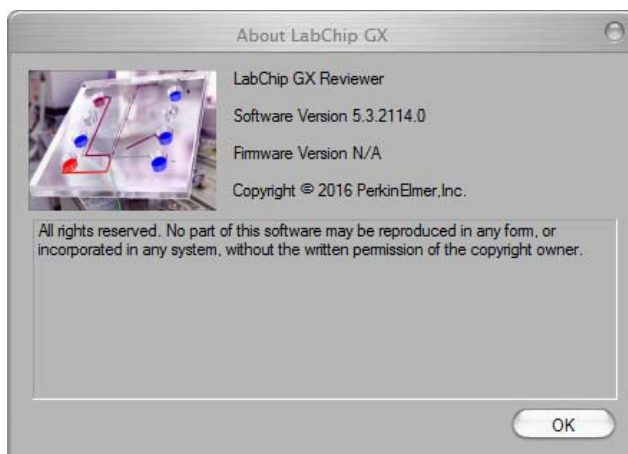
**Remove button** - Deletes the filter selected in the Available Filters list from the workspace.

**Search Data Files button** - Opens the Search for Plate Matching Filter window to search a specified folder for any plates that include wells matching the selected filters. See [“Searching Data Files using a Filter” on page 50](#) for more information.

**Update button** - Updates the filter selected in the Available Filters list with the specified filter criteria. Only available if the filter criteria has changed.

## About LabChip GX Reviewer Window

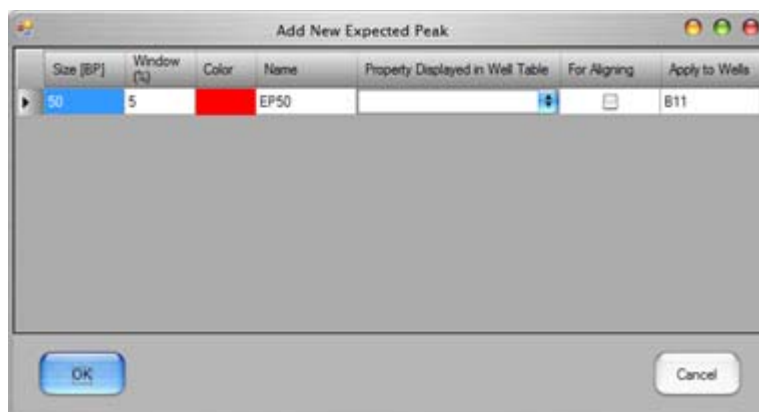
The About LabChip GX Reviewer window displays the software and firmware versions. Selecting **About LabChip GX Reviewer** on the [Help Menu](#) opens this window.



**Figure 83. About LabChip GX Reviewer Window**

## Add New Expected Peak Window

Use the Add New Expected Peak Window to add an expected peak to specific wells. To open this window, right-click near a peak in the [Graph View](#) and select **Add Expected Peak**.



**Figure 84. Add New Expected Peak Window**

Column	Function
Size	Specifies the expected size of the peak in BP for DNA assays, kb for gDNA assays, kDa for Protein assays, and CGU for Glycan assays. The default size is the size of the peak that was selected.
Time	Specifies the expected time of the peak in seconds. The default is the time of the peak that was selected. (Only for CZE assays.)
Window (%)	Specifies the tolerance window as a percent of the expected size for the fragment/protein/glycan to allow for small variations in expected peak size.
Color	Displays the color to use to mark the peak in the <a href="#">Graph View</a> or the <a href="#">Gel View</a> .
Name	Specifies a name to display in the Type description for the peak.
Property Displayed in Well Table	Specifies the content of a column added to the well table for each expected peak.
For Aligning	If selected, the data signal is realigned so the selected expected peaks match their aligned size. Note that incorrect alignment settings can cause analysis errors.
Apply to Wells	Specifies the wells that the expected peak is applied to. <All> specifies that the expected peak applies to all wells. Clicking on the column opens the Select Wells window to choose the specific wells to apply the expected peak to.

## Assay Analysis Window

The Assay Analysis window specifies the analysis parameters to use when analyzing the data from a completed run. Analysis parameters include alignment, peak find, expected/excluded peaks, smears, titers, and replicates. To open the Assay Analysis window, select **Analysis** → **Analysis Settings** on the main menu.

The Assay Editor window is used to create or edit assays that will be used to run the samples on the LabChip instruments and contains all of the same tabs except the Alignment tab. Alignment can only be performed after the data has been acquired.

The Assay Analysis window contains the following tabs:

- [Assay Information Tab](#)
- [Alignment Tab](#)
- [Analysis Tab](#)
- [Peak Find Tab](#)
- [Expected Fragments/Proteins/Glycans Tab](#)
- [Excluded Peaks Tab](#)
- [Smear Analysis Tab](#)
- [Titer Tab](#)
- [Replicates Tab](#)
- [Advanced Tab](#)

The **Assay Analysis window** contains the following buttons at the bottom of the window:

Button	Function
Apply	Apply setting changes and re-analyze the plate but keep the Assay Analysis window open.
Apply Global	Applies the selected analysis settings to all plates in the open workspace.
Export As Assay	Opens the Export Assay Settings from Plate to Assay file window to specify a name and location for a new assay file (*.asy or *.asyx). Clicking Save creates a new assay file with the settings in the Assay Analysis Window.
Restore Plate	Opens the Restore Plate Settings To Version window to restore the data file to the selected version.
OK	Apply changes in the Assay Analysis window and re-analyze the plate with these new settings.

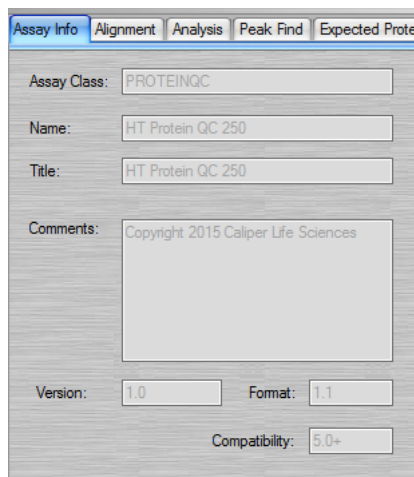
Button	Function
Print Preview	Opens the Print Preview window to view the analysis settings before printing.
Print	Opens the Print window to print the analysis settings.
Cancel	Restores the settings that were selected when the window was opened or when the last Apply was performed. No re-analysis is performed because the settings were used for the last analysis performed.

The **Assay Editor window** contains the following buttons at the bottom of the window:

Button	Function
Save Assay	Opens the Select Assay To Edit window or the CDR Manager window (LabChip GxP option) to specify the name and location of the saved assay file.
Restore Assay	Discards all changes to the assay and resets the window to the saved assay settings.
Close	Closes the Assay Editor window without saving changes to the assay. If there are unsaved changes, you are prompted to discard the changes.

## Assay Information Tab

The Assay Information tab on the [Assay Analysis Window](#) displays the header information for the current plate. The information displayed was specified when the assay was run and cannot be changed.



**Figure 85. Assay Analysis Window - Assay Info Tab**

The following read-only information displays:

Option	Function
Assay Class	Either DNA, gDNA, Protein, RNA, or Glycan. (Protein, Glycan, and Protein Charge Variant assays are only supported on LabChip GXII or GXII Touch instruments.)
Name	The name of the assay.
Title	The title of the assay.
Comments	Comments from the assay that was run.
Version	The version of the assay that was run.
Format	The format of the data file.
Compatibility	The version of LabChip GX or GX Touch software that supports the assay. LabChip GX Reviewer analyzes all assay versions including LabChip GX Touch assays (5.0+).
Plate	The name of the plate in the workspace. Usually the same as the name of the data file that was created when the plate was run, unless the name is changed after it is added to the workspace.

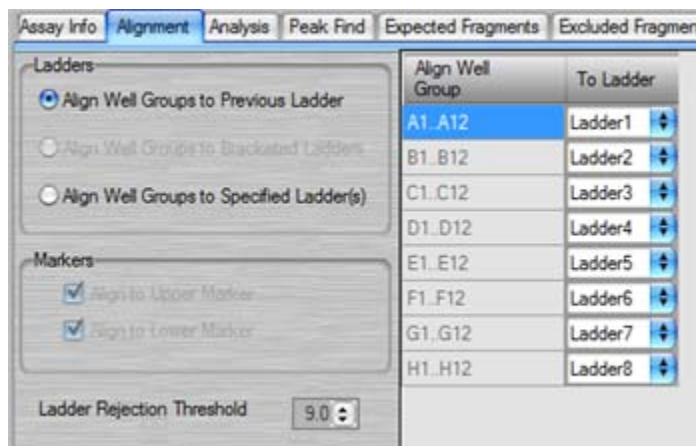
## Alignment Tab

The Alignment tab on the [Assay Analysis Window](#) is used to assign alternate ladders to a specified group of wells in the event of a faulty ladder result. The default assignment for full rows uses the ladder adjacent to the row where the sample is located. If this ladder cannot be analyzed, the software automatically looks for another nearby ladder to perform the analysis. The actual ladder used for the analysis is shown in the Well Peak Find Settings panel of the [Peak Find Tab](#). It can be changed by selecting the **“Align Well Groups to Specified Ladder”** option and then selecting a different ladder in the “To Ladder” column corresponding to the row to be changed.

For Protein, Glycan, and gDNA assays, which do not use an upper marker, alignment is normally performed with ladders on each end of the row to compensate for drift between start and end of each row. This feature can be disabled by selecting **“Align Well Groups to Previous Ladder”** or **“Align Well Groups to Specified Ladder”** instead of **“Align Well Groups to Bracketed Ladder”**.

Protein Charge Variant assays do not use ladders to align the data. The Alignment tab is not shown for Protein Charge Variant assays.

The Alignment tab is not displayed in the Assay Editor window. Alignment can only be changed after the data file is created.



**Figure 86. Assay Analysis Window - Alignment Tab**



## Alignment Tab (Continued)

The Alignment tab contains the following settings:

- **Align Well Groups to Previous Ladder** - If selected, each row is aligned to the ladder at the beginning of the row.
- **Align Well Groups to Bracketing Ladders** - (Protein, Glycan, and gDNA assays only.) If selected, each row is aligned with the ladder at the beginning of the row and a ladder at the end of the row. (Protein and Glycan assays are only supported on LabChip GXII or GXII Touch instruments.)
- **Align Well Groups to Specified Ladders** - If selected, each row is aligned with the ladder selected in the table.

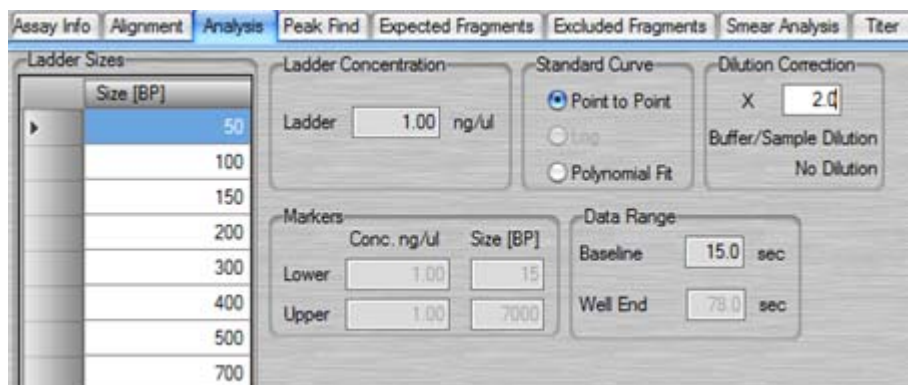
**Markers** - Displays the markers that are used for alignment. This setting is determined by the assay type and cannot be modified.

**Ladder Rejection Threshold** - Specifies the minimum Ladder Quality Score required to accept a ladder. If a ladder is below this threshold, the ladder is flagged as an error well and is not used for sizing or quantization. Set the value to 0 to turn off this feature.

To view the unaligned data (spike rejected, filtered, and baseline corrected), select **Turn Off Analysis** from the **Analysis** menu.

## Analysis Tab

Use the Analysis tab on the [Assay Analysis Window](#) to view the Upper and/or Lower marker peak designation (this setting cannot be changed) or to view or change the Ladder Sizes, Ladder Concentration, Standard Curve (not available for CZE assays), Data Range, Marker Concentration (DNA) Dilution Ratio (Protein), Dilution Correction (DNA and gDNA assays), and System Peak Exclusion (Protein). Protein Charge Variant assays only show the Data Range. (Protein, Glycan, and Protein Charge Variant assays are only supported on LabChip GXII or GXII Touch instruments.)



**Figure 87. Assay Analysis Window - Analysis Tab**

### Ladder Sizes

A table showing the sizes of the ladder peaks in bp (base pairs) for DNA, kDa (kiloDaltons) for protein, nt (nucleotides) for RNA, or kb (kilo base pairs) for gDNA assays. Click in the Size column and type the desired size to change the ladder size. (Not available for Protein Charge Variant assays.)

### Clear Default Ladder button

Displays at the bottom of the Ladder Sizes if a default ladder is defined for the plate. (Not available for Protein Charge Variant assays.)

### Ladder Concentration

The concentration (in ng/uL) for the ladder peaks. (Not available for Glycan or Protein Charge Variant assays.)

## Analysis Tab (Continued)

### Standard Curve

Determines whether the fit for the standard curve used to calibrate migration time to size will be done on a point-to-point, logarithmic, or Polynomial fit of the ladder. DNA, gDNA, and Glycan assays are set to point-to-point curve fits but can be changed to Polynomial. RNA assays are set to point-to-point curve fits but can be changed to Logarithmic. Protein assays are set to Log and cannot be changed. (Not available for Protein Charge Variant assays.)

### Dilution Correction (DNA and gDNA assays only)

Modifies the measured concentration/molarity reported in the peak table by compensating for sample dilution.

- **X** - Type the desired correction. The measured concentration/Molarity is multiplied by this number when reported.
- **Buffer/Sample Dilution** - Displays the dilution ratio that corresponds to the multiplier (X). For example, if X=1, the Buffer/Sample Dilution=No Dilution, and if X=2, the Buffer/Sample Dilution=1:1.

### Dilution Ratio (Protein assays only)

Used to compensate for differences between sample and ladder dilutions in the computation of the sample peak concentrations.

- **Ladder** - Reflects a dilution of ladder in a total volume of ladder and sample buffer according to the *LabChip GX Touch/GXII Touch Assay User Guide*.
- **Sample** - Reflects a dilution of sample in a total volume of sample, water, and sample buffer according to the *LabChip GX Touch/GXII Touch Assay User Guide*.

### Data Range

- **Baseline** - Specifies the time in seconds after the start of the run after which data is plotted and used for analysis. The data generated one second before the Baseline value is used to compute the initial baseline value and baseline noise.
- **Well End** - Specifies the time when analysis and data plotting ends.

## Analysis Tab (Continued)

### **System Peak Exclusion (Protein and Glycan assays only)**

Used to specify the region where System peaks are to be tagged and excluded from the analysis.

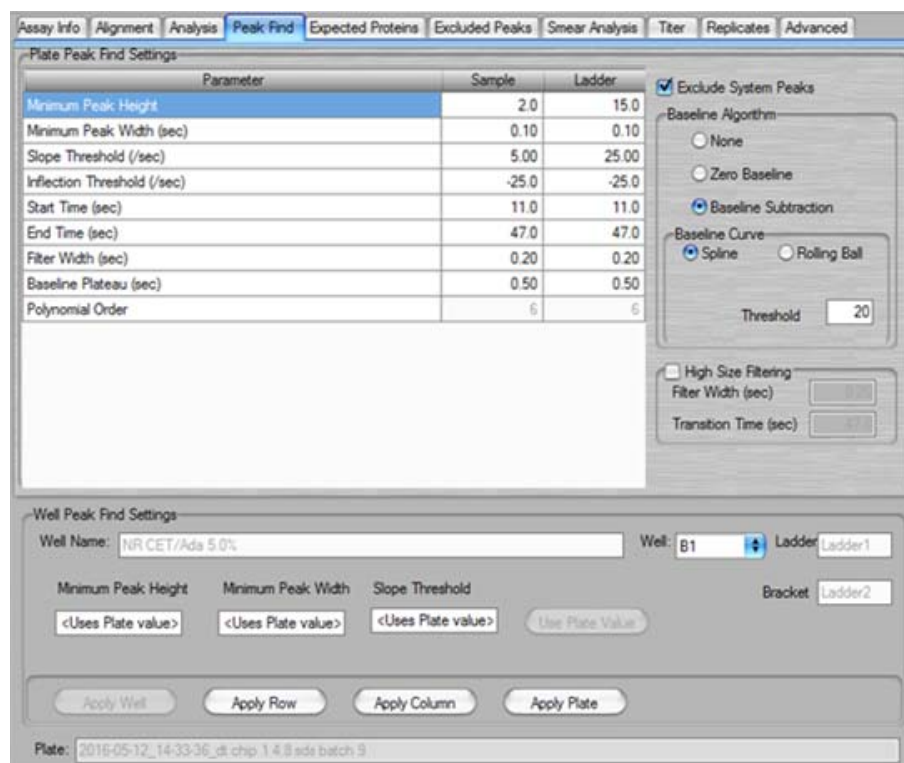
- **Ladder Ratio** - Time at which ladder peaks are detected as ladder peaks rather than system peaks. For example, if the ladder ratio is set to 1.5, the software multiplies the lower marker migration time x 1.5 and then begins ladder peak identification. In this example, if the lower marker elutes at six seconds, the ladder peak detection starts at 6x1.5 or 9 seconds.
- **Min. Sample Size (kDa or CGU)** - Size at which peaks are identified as sample peaks rather than system peaks (except the Lower Marker).

### **Markers (DNA, gDNA, and Glycan assays only)**

- DNA and gDNA assays: The concentration (ng/uL) and size for the upper and lower markers for the assay.
- Glycan assays: The size of the lower marker.
- If a default Ladder is defined for the plate, the Marker Migration Time, Height, and Area are available for editing.

## Peak Find Tab

Use the Peak Find tab on the [Assay Analysis Window](#) to adjust parameters to detect peaks for individual wells, rows, columns, a single plate, or the entire plate specified in the Plate field.



**Figure 88. Assay Analysis Window - Peak Find Tab**

Initial individual plate and well selections are made by right-clicking on a well in the [Gel View](#) or the graph in the [Graph View](#) and selecting the **Analysis Settings** option. The corresponding well settings are displayed in the Well Peak Find Settings fields. Subsequent well selections in a plate can be made using the Well down-down list. The well list includes all the wells on the current plate that are selected. The Plate and Well Name fields are read only, and cannot be changed from the Peak Find Tab. (Protein, Glycan, and Protein Charge Variant assays are only supported on LabChip GXII or GXII Touch instruments.)

## Peak Find Tab (Continued)

The Peak Find tab contains the following options:

**Table 1. Plate Peak Find Settings**

Plate Settings	Function
Minimum Peak Height	Specifies the height limit below which a peak is not detected. For each peak, the difference between the peak start time and the peak apex must be greater than the Min Peak Height value.
Minimum Peak Width	Specifies the limit (in seconds) for the peak width. Peaks narrower in time than this value are <b>not</b> detected.
Slope Threshold	Represents the amount of change in absorbance units over time required to indicate that a peak has occurred. This setting is used to detect the start and end of a peak. Increasing this setting may cause broad rolling bumps to be ignored or merge multiple bumps into a single peak. Decreasing this setting will broaden the peaks' width and potentially pick up broad bumps as peaks. See <a href="#">"Understanding Peak Finding" on page 101</a> for more information.
Inflection Threshold	Represents the value that the slope minimum must be below to trigger a splitting of the peak. As the threshold is increased, more peak splitting occurs. See <a href="#">"Understanding Peak Finding" on page 101</a> for more information.
Start Time	Specifies the time after the start of a run when the first peak will be detected (any peaks appearing before this time are ignored). The Gel and Graph views will not plot data earlier than this time.
End Time	Specifies the time after which peak detection stops. The Gel and Graph views will not plot data beyond this time.
Filter Width	Specifies the width, in seconds, of the low pass filter to be convolved with the data. The width of this filter should be about 6 samples wide (i.e. 0.1 sec for 60 Hz sampling). If this setting is too large, peaks will develop spurious side lobes (ringing) due to over-filtering.
Baseline Plateau	Specifies a baseline selection parameter for peak finding. The signal is at baseline whenever the slope of the data is less than the slope threshold setting (positive or negative) for longer than the Baseline Plateau. This rejects brief, low slope areas such as in between non-baseline-resolved peaks.
Polynomial Order	A filter algorithm is used to filter the data, increasing the signal-to-noise ratio. The data is convolved with a polynomial of this order to produce filter data and a filter slope and decrease the background or baseline noise and/or spikes in the signal. This value is read only.

Table 1. Plate Peak Find Settings (Continued)

Plate Settings	Function
Exclude System Peaks	(Protein and Glycan assays only) If selected, excludes the system peak (peak due to buffer constituent) from any changes to the peak find settings (the most recent custom ladder settings are used instead).
Baseline Curve	<ul style="list-style-type: none"> <li>• <b>None</b> - No correction.</li> <li>• <b>Zero Baseline</b> - Offsets all graphs to zero baseline but does not affect analysis.</li> <li>• <b>Baseline Subtraction</b> - A dynamic subtraction of the baseline that corrects for drifting Baseline. Select the desired method for generating the baseline curve: <ul style="list-style-type: none"> <li>— <b>Spline</b> - Creates a smooth line fit to the baseline data points and subtracts this smooth fit from the data. The Threshold determines how much the baseline fit follows changes in the data.</li> <li>— <b>Rolling Ball</b> - Generates a smooth baseline curve by mathematically rolling a ball under the sample signal, keeping it in contact with the closest signal point without crossing into the signal. Time Diameter and Signal Diameter determine the smoothness of the curve in the Time and Signal axes. (See <a href="#">“Rolling Ball Baseline Curve Example” on page 276</a> for more information.)</li> </ul> </li> </ul>
High Size Filtering	<p>If selected, a second, larger filter is applied to the data after the specified time. This is useful for assays where the peaks are narrow at the start of the assay and become broad and noisy for larger sizes of DNA, protein or Glycan. If not selected, the same size filter is used for all data.</p> <ul style="list-style-type: none"> <li>• <b>Filter Width (sec)</b> - The width of the second filter to be applied after the specified transition time. Filter Width must be greater than the Sample Well Filter width and less than or equal to 3.0 seconds.</li> <li>• <b>Transition Time (sec)</b> - The time at which to transition to the larger filter size. Transition time must be greater than the Baseline Time on the Analysis tab and less than the Well End time.</li> </ul>

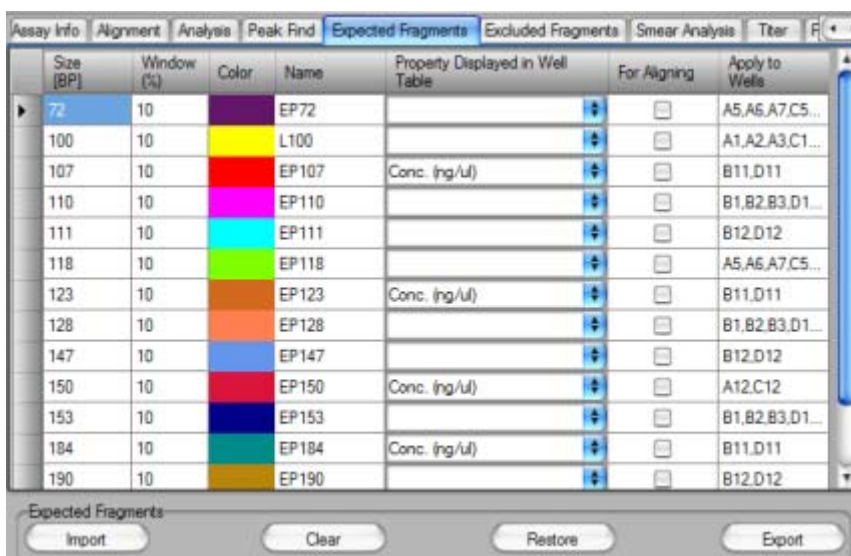
**Table 2. Well Peak Find Settings**

<b>Well Settings</b>	<b>Function</b>
Well	Displays the well being edited. Select any well or ladder on the plate belonging to the current collection.
Ladder	Read only. Displays the ladder used for aligning this well. Use the Alignment tab to edit. New value displays here after clicking Apply. (Not available for Protein Charge Variant assays.)
Bracket	Read only. Displays the bracket ladder used for aligning this well. Use the Alignment tab to edit. New selection displays here after clicking Apply. (Only for gDNA and Protein assays if Align Well Groups to Bracketed Ladders is selected on the Alignment tab.)
Minimum Peak Height	Specifies an override to the Peak Find Settings for Minimum Peak Height for the entire plate. Specify a valid numeric value to override, or clear the field to reset to the Global setting.
Minimum Peak Width	Specifies an override to the Peak Find Setting for Minimum Peak Width for the entire plate. Specify a valid numeric value to override, or clear the field to reset to the Global setting.
Slope Threshold	Specifies an override to the Peak Find Setting for Slope threshold for the entire plate. Specify a valid numeric value to override, or clear the field to reset to the Global setting.
Use Plate Value button	Sets Min Peak Height, Min Peak Width, and Slope Threshold text boxes to <Uses plate value> settings.
Save as Default Ladder	Sets the selected ladder to the default ladder for the plate. Does not align any wells to the default ladder. (Only available for DNA and RNA assays.)
Apply Well/Ladder	Apply well-specific peak find settings only to the well or ladder showing in the Well field.
Apply Row	Apply well-specific peak find settings to all wells in the same row as the selected well.
Apply Column	Apply well-specific peak find settings to all wells in the same column as the selected well.
Apply All Ladders	(Displays only if a ladder is selected in the Well field.) Applies peak find settings to all ladders in the plate.
Apply Plate	Apply well-specific peak find settings to all wells on the same plate.



## Expected Fragments/Proteins/Glycans Tab

Use the Expected Fragments/ Proteins/Glycans tab on the [Assay Analysis Window](#) to enter Expected Fragments for DNA or gDNA assays, Expected Proteins for Protein assays, Expected Glycans for Glycan assays, or Expected Peaks for Protein Charge Variant assays. (See [“Using Expected Fragments/ Expected Proteins/ Expected Glycans” on page 40](#) for more information.) After the data is analyzed, any peaks matching the expected fragments, proteins, or glycans are shown in the [Peak Table View](#), [Well Table View](#), [Gel View](#), and [Graph View](#) (if Type is selected as an Annotation in the [Graph View Properties](#)). (Protein, Glycan, and Protein Charge Variant assays are only supported on LabChip GXII or GXII Touch instruments.)



**Figure 89. Assay Analysis Window - Expected Fragments Tab**

The Expected Fragments/Proteins/Glycan tab contains the following options and buttons:

**Expected Peak Table** - Lists the expected peaks for the assay analysis.

- **Size** - Specifies the expected size of the peak in BP (DNA), kb (gDNA), kDa (Protein), or CGU (Glycan).
- **Time** - Specifies the expected time of the peak (Protein Charge Variant only).
- **Window (%)** - Specifies the tolerance window as a percent of the expected size for the peak to allow for small variations in expected peak size.

## Expected Fragments/Proteins/Glycans Tab (Continued)

- **Color** - Displays the color to use to mark the peak in the [Graph View](#) or the [Gel View](#).
- **Name** - Specifies a name to display in the Type description for the peak.
- **Property Displayed in Well Table** - Specifies the content of a column added to the well table for each expected peak.
- **For Aligning check box** - If selected, the data signal is realigned so the selected expected peaks match the specified size or time. Note that incorrect alignment settings can cause analysis errors.
- **Apply to Wells** - Specifies the wells that the expected peak is applied to. <All> specifies that the expected peak applies to all wells. Clicking on the column opens the Select Wells window to choose the specific wells to apply the expected peak to.

**Import button** - Opens the Import Expected Fragments/ Proteins/ Glycan Table window to select an Expected Peak File (.gep) to import. The .gep file is created by exporting expected peaks from another assay.

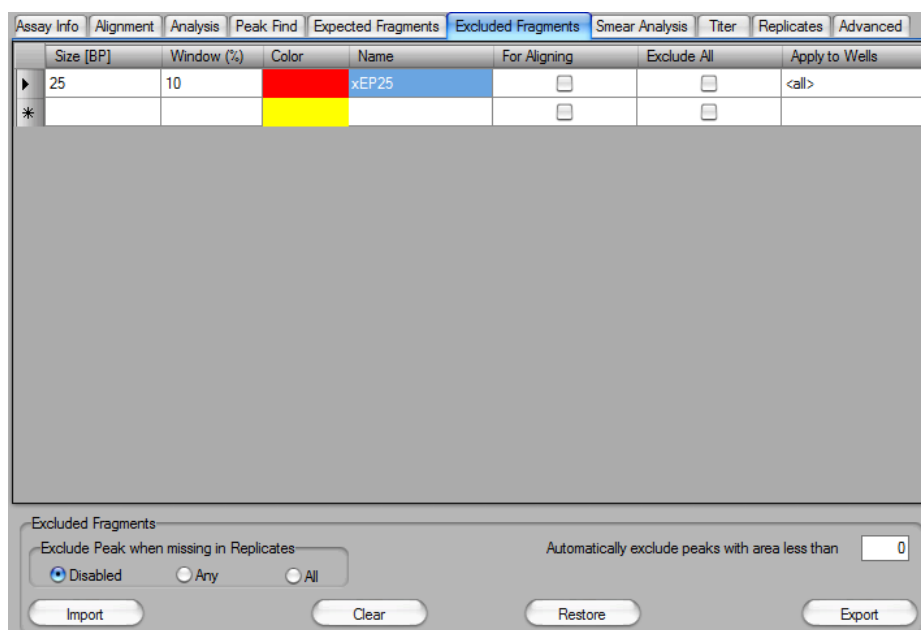
**Clear button** - Deletes all Expected Peaks from the table.

**Restore button** - Restores the settings to the last saved settings for expected peaks.

**Export button** - Opens the Export Expected Fragments/ Proteins/ Glycans window to create an Expected Peak File (.gep) from the current settings in the tab. Import the .gep file into another assay to use the same expected peaks in another assay.

## Excluded Peaks Tab

Use the Excluded Peaks tab on the [Assay Analysis Window](#) to enter Excluded Fragments for DNA or gDNA assays, Excluded Proteins for Protein assays, Excluded Glycans for Glycan assays, or Excluded Peaks for Protein Charge Variant assays. After the data is analyzed, any peaks matching the excluded peaks are excluded from the analysis. (Protein, Glycan, and Protein Charge Variant assays are only supported on LabChip GXII or GXII Touch instruments.)



**Figure 90. Assay Analysis Window - Excluded Peaks Tab**

The Excluded Peaks tab contains the following options and buttons:

**Excluded Peak Table** - Lists the excluded peaks for the assay analysis.

- **Size** - Specifies the size of the excluded peaks in BP(DNA), kb (gDNA), kDa (Protein), or CGU (Glycan).
- **Time** - Specifies the expected time of the peak (Protein Charge Variant only).
- **Window (%)** - Specifies the tolerance window as a percent of the size of the peak to allow for small variations in peak size.
- **Color** - Displays the color to use to mark the peak in the [Graph View](#) or the [Gel View](#).
- **Name** - Specifies a name to display in the Type description for the peak.

## Excluded Peaks Tab (Continued)

- **For Aligning check box** - If selected, the data signal is realigned so the selected excluded peaks match the specified size or time. Note that incorrect alignment settings can cause analysis errors.
- **Exclude All** - If selected, all peaks in the specified range are excluded from analysis.
- **Apply to Wells** - Specifies the wells that the excluded peak is applied to. <All> specifies that the excluded peak applies to all wells. Clicking on the column opens the Select Wells window to choose the specific wells to apply the excluded peak to.

**Exclude Peaks when Missing in Replicates options** - Specifies the desired option to automatically exclude a peak based on peaks in defined replicate wells. Only displays if at least one replicate set is defined on the [Replicates Tab](#).

- **Disabled** - No peaks will be excluded based on the replicates.
- **Any** - A peak is excluded if it is not found in ANY of the other wells in the replicate set.
- **All** - A peak is excluded if it is not found in ALL of the other wells in the replicate set.

**Automatically exclude peaks with area less than text box** - Specifies a peak area. Any peaks with an area (corrected or aligned) below the specified threshold are automatically excluded. Default value is 0.

**Import button** - Opens the Import Excluded Peaks window to select an Excluded Peak File (.gep) to import. The .gep file is created by exporting excluded peaks from another assay.

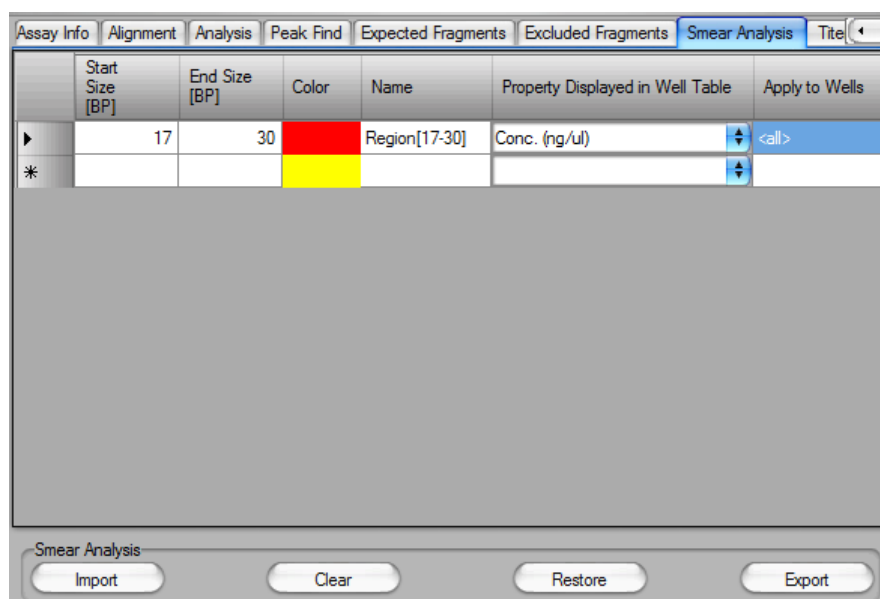
**Clear button** - Deletes all Excluded Peaks from the table.

**Restore button** - Restores the settings to the last saved settings for excluded peaks.

**Export button** - Opens the Export Excluded Peaks window to create an Excluded Peaks File (.gep) from the current settings in the tab. Import the .gep file into another assay to use the same excluded peaks in another assay.

## Smear Analysis Tab

Use the Smear Analysis tab on the [Assay Analysis Window](#) to define [Smears](#). After the data is analyzed, the area matching the smear is shown in the [Well Table View](#), [Gel View](#) (if Show EPs and Smears is selected in the [Gel View Properties](#)), and [Graph View](#) (if Show Smears is selected in the [Graph View Properties](#)).



**Figure 91. Assay Analysis Window - Smear Tab**

The Smear Analysis tab contains the following options and buttons:

**Smear Table** - Lists the smears for the assay analysis.

- **Start Size/Time** - Specifies the starting size (time for Protein Charge Variant) of the area to be included in the smear.
- **End Size/Time** - Specifies the ending size (time for Protein Charge Variant) of the area to be included in the smear.
- **Color** - Displays the color to use to mark the smear in the [Graph View](#) or the [Gel View](#).
- **Name** - Specifies a name to display in the [Well Table View](#).
- **Property Displayed in Well Table** - Specifies the content of a column added to the Well Table for each smear.

For gDNA assays, the Total gDNA Concentration in the Well Table is the concentration of the entire smear region from 0.175kb (or the specified smear start size) to 300kb.

## Smear Analysis Tab (Continued)

- **Apply to Wells** - Specifies the wells that the smear is applied to. <All> specifies that the smear applies to all wells. Clicking on the column opens the Select Wells window to choose the specific wells to apply the smear to.

**Import button** - Opens the Import Smear Analysis Table window to select an Smear Analysis Import File (.sma) to import. The .sma file is created by exporting smears from another assay.

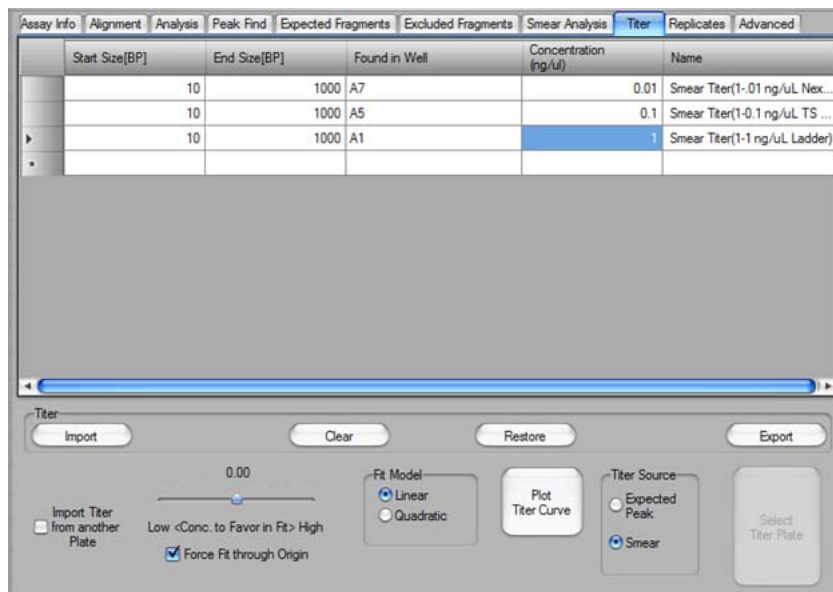
**Clear button** - Deletes all smears from the table.

**Restore button** - Restores the settings to the last saved settings for smears.

**Export button** - Opens the Export Smear Analysis Table window to create a Smear Analysis Export File (.sma) from the current settings in the tab. Import the .sma file into another assay to use the same smear in another assay.

## Titer Tab

Use the Titer tab on the [Assay Analysis Window](#) to specify the wells in the plate that contains the standard to be used as the calibration standard. The [Titer](#) is used for calibration instead of the ladder. (Titer is not available for Glycan or Protein Charge Variant assays.)



**Figure 92. Assay Analysis Window - Titer Tab**

The Titer tab contains the following options and buttons:

**Titer Table** - Lists the size, well locations, and concentrations for the titer on the plate.

- **Standard Size** - If **Expected Peak** is selected as the Titer Source, specifies the size of the standard peak in BP for DNA assays, kb for gDNA assays, nt for RNA assays, and kDa for Protein assays.
- **Window (%)** - If **Expected Peak** is selected as the Titer Source, specifies the tolerance window as a percent of the size for the standard peak to allow for small variations in size.
- **Start Size** - If **Smear** is selected as the Titer Source, specifies the start size of the standard smear in BP for DNA assays, kb for gDNA assays, and nt for RNA assays.
- **End Size** - If **Smear** is selected as the Titer Source, specifies the end size of the standard smear in BP for DNA assays, kb for gDNA assays, and nt for RNA assays.
- **Found in Well** - Specifies the location of the standard in the plate. Type the well number or double-click to select the well in the plate diagram. (Not displayed for imported titers.)

## Titer Tab (Continued)

- **Normalized Area** - Specifies the titer peak normalized area for imported titers. The table for imported titers is Read Only and cannot be edited. (Not displayed for manually entered titers.)
- **Concentration** - Specifies the concentration of the standard in the specified well.
- **Name** - Specifies a name to display in the Type description for the peak.

**Import Titer from Another Plate** - Selecting the check box opens the Select Plate For Titer Import window to select the desired titer from another plate. The plate must be open in the collection, the titer curve must be analyzed, and the normalization peak must match. The normalization peak is set in the Analysis tab: Lower Marker, Upper Marker (DNA only), or Sample Peak. If the Sample Peak option is used, the peak size specified must also match. If no compatible plate is found in the workspace, a message displays and the Import is canceled. Clearing the check box returns to the manually entered titer.

**Concentration to Favor in Fit** - Adjusts the weight of the points in the linear fit for the Titer Standard Curve. The points are weighted by raising the concentration to a power depending on the slider position. Each line on the slider represents a  $\frac{1}{2}$  power increment, with the center position equal to 0. The left most position raises the concentration to the power -2.5. The right most position raises the concentration to the power of 2.5 to weight each point.

**Force Fit through Origin check box** - If selected, the Titer Standard Curve is forced to include the origin (0,0). This prevents very small peaks from generating negative concentrations.

**Average Replicates check box** - If selected, replicate points are averaged before fitting the titer curve to the data points. If not selected, each replicate point contributes equally when fitting the titer curve to the data points. Used when multiple wells of the same concentration are used to improve accuracy.

**Fit Model** - Choose **Linear** or **Quadratic** to fit the Standard Curve to the Titer. Linear:  $y = a + bx$ . Quadratic:  $y = a + bx + cx^2$ .

**Plot Titer Curve button** - Plots the Titer Standard Curve using linear regression to fit the data to a straight line and displays the User Titer Window. Printing the Titer from the User Titer Window prints a report that contains the Titer graph, the fit parameters (fit model, concentration weight, origin option), fit coefficients, fit quality ( $R^2$ ), and the data table (normalized area vs concentration).



## Titer Tab (Continued)

**Titer Source** - Choose **Expected Peak** or **Smear** as the titer source (DNA, gDNA, and RNA assays only).

**Select Titer Plate button** - Opens the Select Plate For Titer Import window to select a different plate from which to import a titer. The plate must be open in the collection, the titer curve must be analyzed, and the normalization peak must match. The normalization peak is set in the Analysis tab: Lower Marker, Upper Marker (DNA only), or Sample Peak. If the Sample Peak option is used, the peak size specified must also match. Only displays after a titer has been imported.

**Import button** - Opens the Import Titer Table window to select a Titer Import File (.ttr) to import. The .ttr file is created by exporting a titer from another assay.

**Clear button** - Deletes all entries from the table. Clear the entries to use the default Standard Curve instead of the Titer Standard Curve.

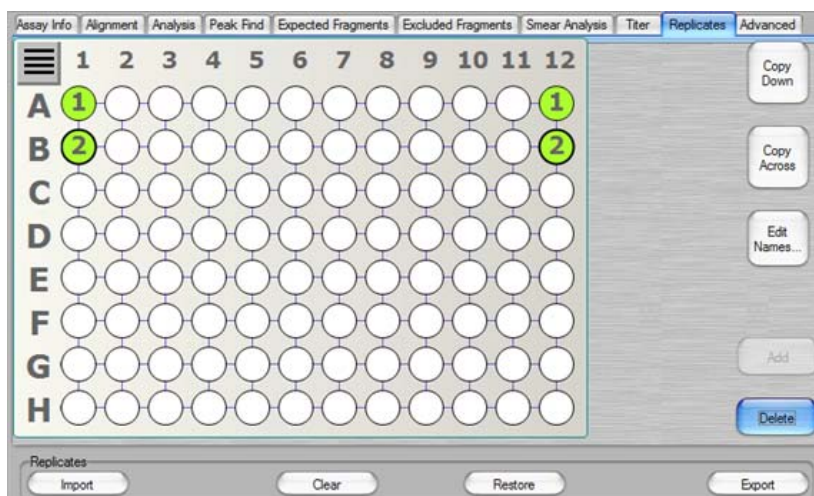
**Restore button** - Restores the settings to the last saved titer settings.

**Export button** - Opens the Export Titer Table window to create a Titer Export File (.ttr) from the current settings in the tab. The exported titer contains the entries in the titer table, Concentration to Favor in Fit, Force Fit through Origin, and Fit Model. Import the .ttr file into another assay to use the same titer in another assay.

## Replicates Tab

Use the Replicates tab on the [Assay Analysis Window](#) to identify wells that include the same samples. Each set of wells that contain the same sample or titer are referred to as a replicate set. [Figure 93](#) shows two replicate sets. Replicate set 1 contains A1 and A12. Replicate set 2 contains B1 and B12.

If replicate wells are identified in the Replicates tab, use the Exclude Peak when Missing in Replicates options on the [Excluded Peaks Tab](#) to exclude peaks that are missing in any or all of the replicate wells.



**Figure 93. Assay Analysis Window - Replicates Tab**

The Replicates tab contains the following options and buttons:

**Plate Diagram** - Displays the replicates defined for the plate. Click a well to select or deselect the well. Click a replicate well to select the replicate set.

**Copy Down button** - The pattern of the selected replicate set is repeated to the bottom of the plate.

**Copy Across button** - The pattern of the selected replicate set is repeated across the plate.

**Edit Names button** - If selected, opens the Replicate Name Editor window to change the name of the default replicate name.

**Add button** - Adds the selected wells to a replicate set. All wells in the same set display the same replicate set number.

**Delete button** - Deletes the selected replicate set.

## Replicates Tab (Continued)

**Import button** - Opens the Import Replicates Table window to select a Replicates Import File (.rep) to import. The .rep file is created by exporting a replicates file from another assay.

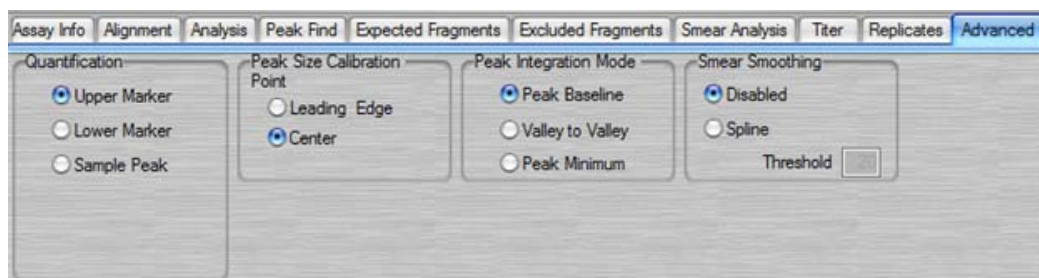
**Clear button** - Deletes all replicates from the plate diagram.

**Restore button** - Restores the settings to the last saved replicates settings.

**Export button** - Opens the Export Replicates Table window to create a Replicates Export File (.rep) from the current settings in the tab. The exported Replicates file contains the entries in the plate diagram. Import the .rep file into another assay to use the same replicates in another assay.

## Advanced Tab

Use the Advanced tab on the [Assay Analysis Window](#) to select the Quantification, Peak Size Calibration point, Concentration Size Correction, Peak Integration Mode, and Marker Find settings.



**Figure 94. Assay Analysis Window - Advanced Tab**

**Quantification** - Determines whether the upper marker, lower marker, or a sample peak is used in the calculations to convert the peak area to concentration. The selected peak is used to normalize the signal response between the ladder and the sample. The **Sample Peak** option is normally used with a user-supplied titer. The DNA fragment or protein that generates the Sample Peak must be included in both the titer and sample wells at the specified concentration. Protein, RNA, and gDNA assays use the lower marker. DNA assays use the upper marker. DNA and RNA settings cannot be changed. For Protein and gDNA assays, selecting **Sample Peak** uses the Peak Size and **Concentration** of the User Standard instead of the default ladder settings. Not available for Glycan or Protein Charge Variant assays.

**Peak Size Calibration Point** - Specifies which part of the peak is used as the size calibration point.

- **Leading Edge** - If selected, uses the start of the peak. (May be better when sample peaks are broader than ladder peaks.)
- **Center** - If selected, uses the top of the peak. (May be better when the leading edge is not well-defined.)

**Concentration Size Correction** (Protein assays only) - Protein concentration is size-corrected to account for differences in the amount of protein injected into the separation channel based on its size. The correction is obtained using the formula:

- $\text{Conc}(\text{Size Corrected}) = \text{Conc}(\text{Time Corrected Area}) * \text{Amplitude} * (\text{Size})^{\text{Power}}$

## Advanced Tab (Continued)

The default values for the Concentration Size Correction were determined empirically by measuring a wide range of proteins of known size and concentration. This correction can be bypassed by setting Amplitude = 1.0, Power = 0.0.

**Peak Integration Mode** - Specifies the mode for determining the baseline.

- **Peak Baseline** - A global peak baseline is used as the baseline for all peaks. This baseline is determined by stitching together regions of low variance across the data signal.
- **Valley to Valley** - Each peak is assigned a baseline by drawing a line under the peak joining the start and end of the peak at the data signal values.
- **Peak Minimum** - The peak baseline is extended to the bottom of the peak instead of starting and stopping where the signal slope crosses the slope threshold.

**Smear Baseline** - Specifies the method for determining the Smear Baseline. This option only displays after a smear has been added in the Smear Analysis tab. Not available for Protein Charge Variant assays.

- **Two Point** - The baseline is a single straight line between the flat baseline areas at the beginning and end of the trace. This option is preferred for very shallow smears where the signal slope does not rise above the Peak Slope Threshold.
- **Peak Baseline** - The Smear baseline uses the local peak baseline for the start and end points of the smear baseline. If the signal slope is below the peak slope threshold, the local peak baseline follows the signal.

**High Conc Size Corr** - Specifies the method of correction for the ladder migration time when the sample concentration is significantly higher than the ladder concentration. The ladder migration time is corrected independently for each well to compensate for the increased migration speed of high concentration samples. The desired option can be selected in the when editing an assay before the sample is run, and cannot be changed after the sample is run.

- **Disabled** - The ladder migration time is not corrected
- **Linear** - The ladder migration time correction is proportional to the sample to ladder concentration ratio.
- **Nonlinear** - The ladder migration time correction is a function of the ratio of sample and ladder concentrations and saturates at very high sample concentrations. (Default)

## Advanced Tab (Continued)

**Smear Smoothing** - Fits a smooth spline curve to the smear and replaces the actual data signal with the spline curve. Smear smoothing smooths out rough smears that can be generated by the DNA High Sensitivity assay when evaluating very low concentration samples. If the smear is very rough and a minor peak or noise spike is significantly higher than the smear, the Size at Maximum property may be the height of the spike, instead of the height of the smear. Use Smear Smoothing and adjust the Threshold until the smear is smooth.

- **Disabled** - The actual data signal is used to calculate the smear properties. (Default)
- **Spline** - A spline curve is fit to the data and replaces the actual data signal for analysis.
  - **Threshold** - Specifies how closely the spline curve follows the data signal in the smear. The higher the Threshold, the more closely the curve follows the data.

**Marker Find** - The Migration Time Drift specifies a percent of migration time to use when determining the correct marker peak. See (["Migration Time Drift" on page 267](#)) for details. Not available for Protein Charge Variant assays.

**Smear Molarity Integration** - The Integration Step Size specifies the time, in seconds at which to divide a smear into segments. The size at the center of each segment and the concentration of each segment is used to calculate the smear molarity.

**GQS Smear Start Size (gDNA Assays only)** - Specifies the start size of the GQS Smear used to calculate Total gDNA Concentration and Genomic Quality Score (GQS). Only editable when creating an assay before a run. After the sample is run, edit the start time in the [Smear Analysis Tab](#) on the Assay Analysis window or by dragging the start of the smear in the Graph View.

## Audit Trail Window

The Audit Trail Window enables you to search the Audit Trail Log for specific events, to export the events, or to print events.

To open the Audit Trail window, select **Security** → **Audit Trail Log** on the [LabChip GX Reviewer Main Window](#).



**Figure 95. Audit Trail Window**

The Audit Trail Window contains the following options:

Option	Function
Search most recent entries check box	If selected, the specified most recent number of entries is searched for entries matching the selected criteria.
Number of entries text box	Specifies the number of most recent entries to search.
Search by dates check box	If selected, entries between the specified dates are searched for entries matching the selected criteria.
From and To text boxes	Select the dates that contain the events that you want to view.
Search entire database check box	If selected, all entries in the database are searched.
Username text drop-down list	Select a specific user name to view only events performed under the specified user name. Select All Users to view events performed by any user.
Filename text box	Clicking the Browse (...) button opens the CDR Browser Window to open the audit trail for a different data file.
Event Category drop-down list	Specifies the Event Category of events to search for. Default selects all event categories.

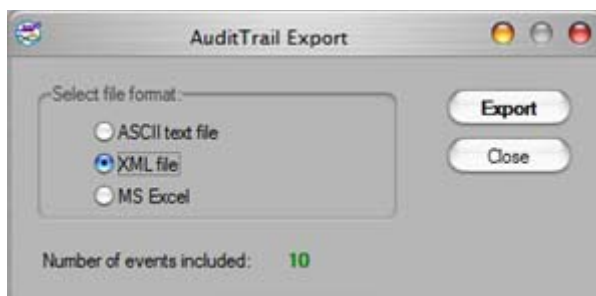
Option	Function
Green Arrow button	Displays the <a href="#">Audit Trail Manage Columns Window</a> to select the columns to view in the Audit Trail window.
Search button	Searches for events matching the search criteria specified.
Export button	Opens the <a href="#">Audit Trail Export Window</a> to export a copy of the selected events out of the audit trail log.
Print View button	Displays a preview for printing the Audit Trail Report.
Close button	Closes the Audit Trail Window.



## Audit Trail Export Window

Use the Audit Trail Export Window to export the contents of the [Audit Trail Window](#) to either an ASCII text file, and XML file, or a Microsoft Excel file. Only the events displayed in the Audit Trail Window are exported. Events filtered out of the view are not exported.

To open the Audit Trail Export Window, click the **Export** button in the [Audit Trail Window](#).



**Figure 96. Audit Trail Export Window**

The Audit Trail Export Window contains the following options:

**File Formats** - Select the desired format for the exported file:

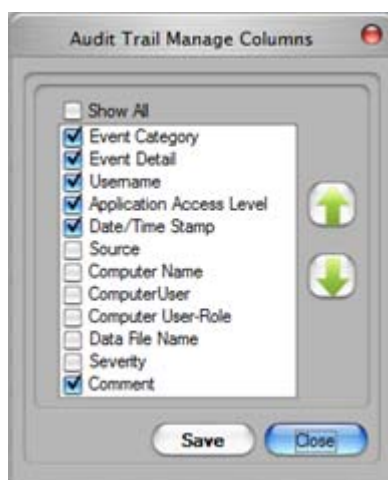
- **ASCII Text File** - If selected, the file is saved as a .txt file.
- **XML File** - If selected, the file is saved as a .xml file.
- **MS Excel** - If selected, the file is saved as a .xls file.

**Number of Events Included** - Displays the number of events that will be exported.

## Audit Trail Manage Columns Window

Use the Audit Trail Manage Columns Window to select the columns to view at the bottom of the [Audit Trail Window](#).

To open the Audit Trail Manage Columns Window, click the Green Arrow button next to the Event Category text box in the [Audit Trail Window](#).



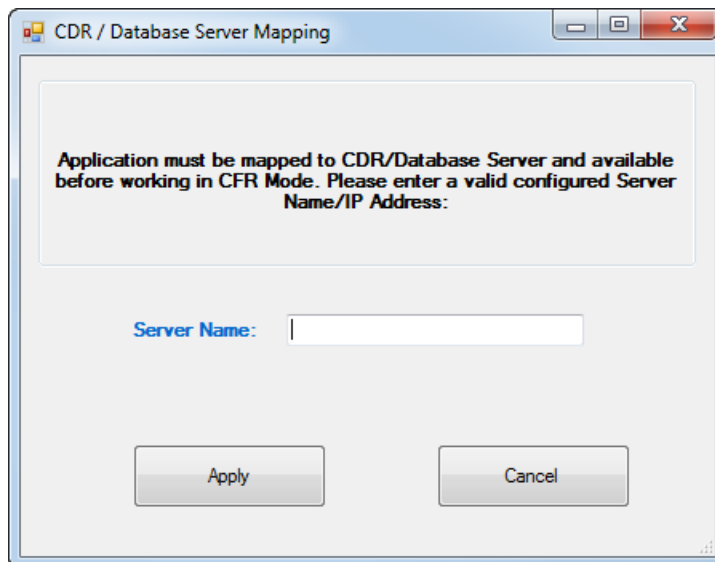
**Figure 97. Audit Trail Manage Columns Window**

The Audit Trail Manage Columns window contains the following parts:

Option	Function
Show All check box	Selecting the check box selects all of the listed columns to display at the bottom of the Audit Trail window. Clearing the check box clears all of the column check boxes.
Column list	Only the selected columns display at the bottom of the Audit Trail window. Cleared (unselected) columns are hidden.
Green Up and Down Arrows	Moves the selected column up or down in the list. The columns display in the Audit Trail window in order from the top column on the left to the bottom column on the right.
Save button	Saves the selections and applies the current column view to the Audit Trails window.
Close button	Closes the window without saving changes to the selections.

## CDR / Database Server Mapping Window

Use the CDR / Database Server Mapping Window to specify the location of the CDR folder.



**Figure 98. CDR / Database Server Mapping Window**

The CDR / Database Server Mapping window contains the following options:

**Server Name/IP Address text box** - Specifies the name or IP address of the server where the CDR folder is located.

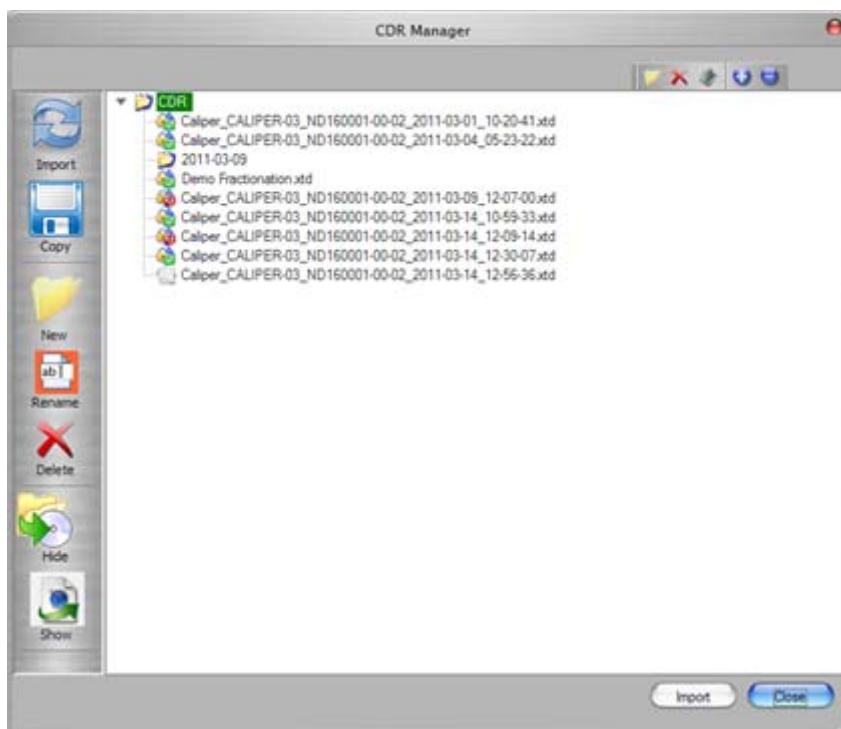
**Apply button** - Connects to the CDR on the specified computer or server. If the CDR cannot be contacted due to network problems or because the CDR is not installed yet, an error message displays.

**Cancel button** - Closes the window without connecting to the remote CDR Server. If the LabChip GX Reviewer software is not connected to the CDR, data in the CDR is not accessible.

## CDR Manager Window

Use the CDR Manager Window to select a data file to open, to create, rename, or delete CDR data folders, and to show or hide data files from view in the CDR Manager Window.

To open the CDR Manager Window, select **File → Import Data File** on the [LabChip GX Reviewer Main Window](#). The CDR Manager window only opens if the LabChip GxP option is installed. If the LabChip GxP option is not installed, see [“Select a Data File Window” on page 233](#).





**Figure 99. CDR Manager Window**

The CDR Manager Window contains the following options

Left Side Buttons	
Import Button	Imports a CDR data file into the open workspace.
Copy Button	Copies the selected data file to another location. The copy of the data file will not be part of the CDR and will not be change-controlled.
New Button	Creates a new folder in the CDR.
Rename Button	Renames the selected folder in the CDR. (Data files in the CDR cannot be renamed.)

Delete Button	Deletes an empty folder in the CDR. If the folder is not empty, you cannot delete the folder.
Hide Button	Hides the selected folder or data files from view in the CDR Manager window. If a folder is selected, all files and subfolders in the selected folder are hidden.
Show Button	Displays all hidden data files and folders in the selected folder.
<b>Top Right Buttons</b>	
New Button	Creates a new folder in the CDR.
Delete Button	Deletes an empty folder in the CDR. If the folder is not empty, you cannot delete the folder.
Show/Hide Hidden Files Button	Shows or hides the filenames of all files that have been hidden in the CDR Manager window.
Expand All Button	Expands all folders in the CDR to show all data files and folders.
Collapse All Button	Closes all folders in the CDR folder.

The icon next to the data file name indicates whether the data file is Accepted/Rejected and Locked as shown in the table below:

File Status	Icon
Locked	
Accepted	
Accepted and Locked	
Rejected	
Rejected and Locked	

## Change Password Window

Use the Change Password Window to change the password for the current user. (To change passwords for other users, see [User Administration Window](#).) This window is only available if the LabChip GxP option is installed with the LabChip GX Reviewer software.

To open the Change Password Window, select **Security** → **Change Password** on the [LabChip GX Reviewer Main Window](#).



**Figure 100. Change Password Window**

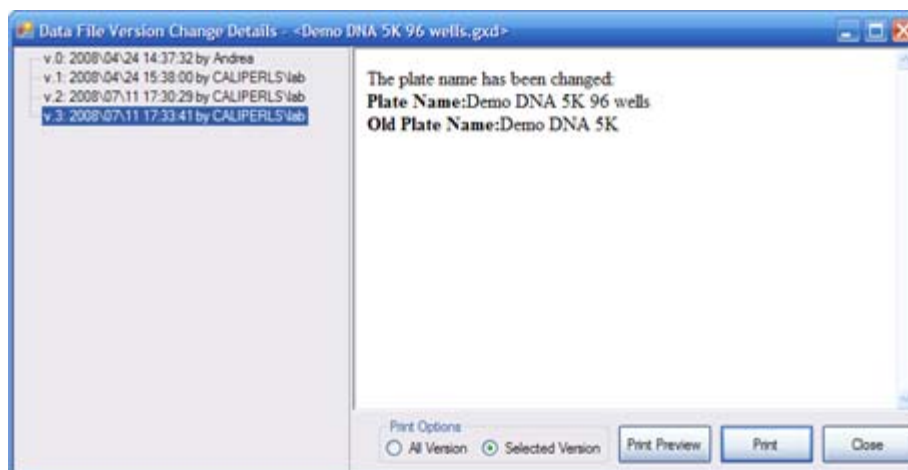
The Change Password Window contains the following options:

Option	Function
Username	Displays the user name for the current user.
Current Password	Type the current password for the current user.
New Password	Type the new password for the current user.
Confirm Password	Retype the new password for the current user.
OK button	Saves the new password and closes the window.
Cancel button	Closes the window without saving changes to the password.

## Data File Version Window

Use the Data File Version Window to view the saved versions of the data file. Also displays when the data file was signed.

To open the Data File Version Window, select **View → Version Change Details** on the main menu.



**Figure 101. Data File Version Window**

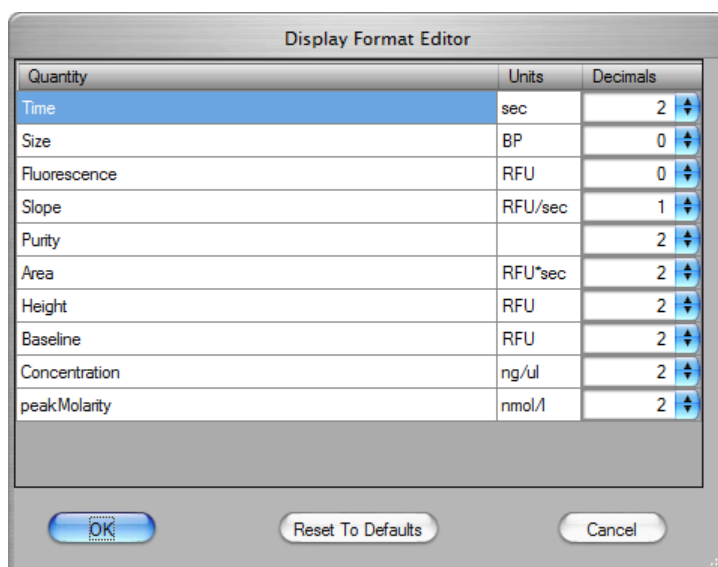
The Data File Version Window lists each version of the plate data file and describes the changes that were performed for each version change. Each time the data file is signed, the Data File Version Window lists the details of the signature. (To open a different version of the data file, click the **Restore Plate** button in the [Assay Analysis Window](#).)

The Data File Version Window contains the following options:

Option	Function
List of Versions	Displays the list of all saved data file versions and electronic signatures.
Details	Displays the details of the changes or signature.
Print Options	All Versions: If selected, version information and details for all data versions is printed. Selected Version: If selected, version information and details for only the selected version is printed.
Print Preview	Opens the Print Preview window to preview the printed version information.
Print	Opens the Print window to print the data file version information.
Close	Closes the Data File Version window.

## Display Format Editor Window

Use the Display Format Editor Window to specify the number of decimal places to display for each type of data. To open the Display Format Editor window, select **Tools** → **Modify Data Presentation**.



**Figure 102. Display Format Editor Window**

**Quantity Column** - Lists the data types that are displayed in or generated by the LabChip GX Reviewer software.

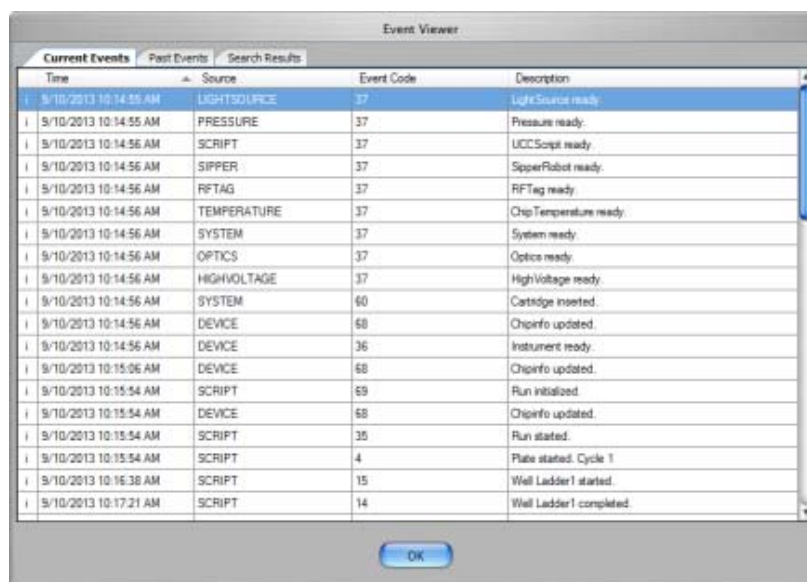
**Units Column** - Lists the units for each data type.

**Decimals Column** - Specifies the number of decimal places to display for each data type. All calculations are performed with full resolution double precision data. The decimal places properties are only used for formatting the computed results for display.



## Event Viewer Window

Use the Event Viewer window to view events and errors that occur during the current run or during a previous run. To open the Event Viewer window, select **View** → **Event Viewer** on the [LabChip GX Reviewer Main Window](#).



**Figure 103. Event Viewer Window**

The Event Viewer window contains the following tabs:

**Current Events tab** - Displays the events that occurred during the current session.

**Past Events tab** - Displays all events from previous sessions.

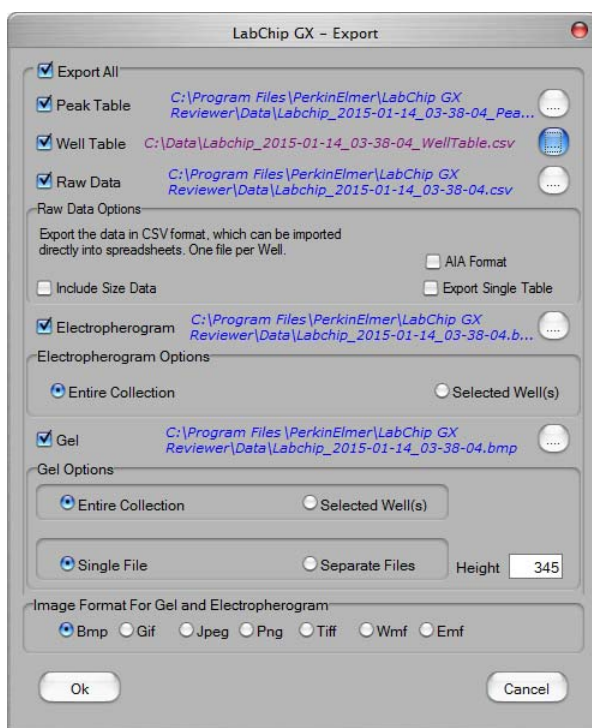
**Search Results tab** - Enables you to search for specified text in past events, current events, or all events.

lick the **OK** button to close the Event Viewer window.

## Export Window

Use the Export window to export data manually. To open the Export window, select **File** → **Export** on the main [Menu Bar](#).

Peak Tables and Well Tables are exported to .CSV files, which can be imported into a spreadsheet program such as Microsoft Excel. Raw Data can be exported to either a .CSV file or to a Chromatography Data Interchange Format file (formerly AIA), which is used by some graphical analysis software tools. Electropherogram and Gel data are exported to the selected image format. See [“Exporting Data” on page 96](#) for instructions.



**Figure 104. Export Window**

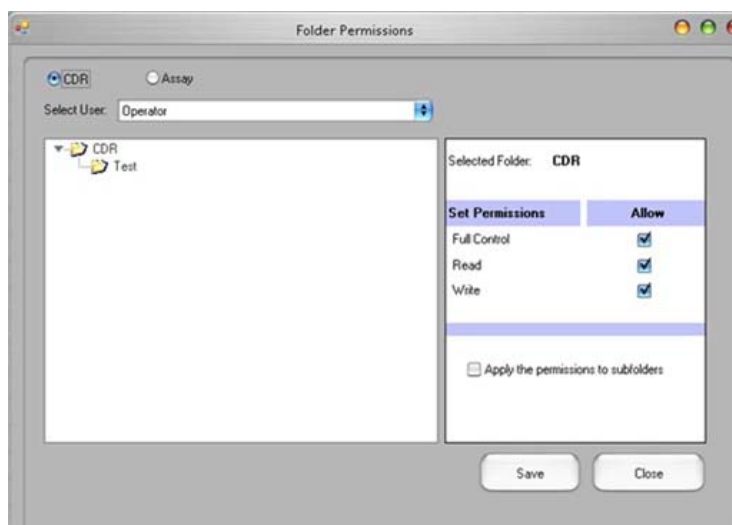
Option	Function
<b>Peak Table</b>	If selected, the data in the <a href="#">Peak Table View</a> is exported to a .CSV file. Click the Browse (...) button to specify the desired path and file name for the .CSV file.
<b>Well Table</b>	If selected, the data in the <a href="#">Well Table View</a> is exported to a .CSV file. Click the Browse (...) button to specify the desired path and file name for the .CSV file.

Option	Function
<b>Raw Data</b>	<p>If selected, the raw (unanalyzed) data from the run is exported.</p> <ul style="list-style-type: none"> <li>• If the <b>AIA Format</b> check box is selected, the raw data is exported to a file in the Chromatography Data Interchange Format (formerly AIA). (Include Size Data and Export Single Table are not available.)</li> <li>• If the AIA Format check box is NOT selected, the raw data is exported to a .CSV file. Click the Browse (...) button to specify the desired path and file name for the .CSV file. The following options are available: <ul style="list-style-type: none"> <li>— <b>Include Size Data:</b> If selected, the data is aligned to the well's ladder (for one file per well) or to the first well (for a single data file) and the size data is included in the exported data. If not selected, the data is not aligned to a ladder. (Not available for CZE assays.)</li> <li>— <b>Export Single Table:</b> If selected, the data for all wells in the plate is exported to one .CSV file. If not selected, the data from each well is exported to a separate .CSV file.</li> </ul> </li> </ul>
<b>Electropherogram</b>	<p>If selected, the graph displayed in the <a href="#">Graph View</a> is exported to the specified folder in the selected image format. Click the Browse (...) button to specify the desired path for the image file. The file names are &lt;plate name&gt;_Egram_&lt;well number&gt;. The following options are available on the Export window. (These options are not available on the Auto Export window.)</p> <ul style="list-style-type: none"> <li>• <b>Entire Collection:</b> If selected, a separate graph is exported for each well in the collection.</li> <li>• <b>Selected Wells:</b> If selected, a separate graph is exported for each of the wells selected in the <a href="#">Gel View</a> or <a href="#">Plate View or Plate List</a>.</li> </ul>

Option	Function
<b>Gel</b>	<p>If selected, the gels selected in the <a href="#">Gel View</a> are exported to the specified folder in the selected image format. Click the Browse (...) button to specify the desired path for the image file. The file names are &lt;plate name&gt;_Gel_&lt;well number&gt;. The following options are available on the Export window.</p> <ul style="list-style-type: none"> <li>• <b>Entire Collection:</b> If selected, a gel is exported for each well in the collection. (Not available on the Auto Export window.)</li> <li>• <b>Selected Wells:</b> If selected, a gel is exported for each of the wells selected in the <a href="#">Gel View</a> or <a href="#">Plate View or Plate List</a>. (Not available on the Auto Export window.)</li> <li>• <b>Single File:</b> If selected, the selected gels are all included in the same image file.</li> <li>• <b>Separate Files:</b> If selected, the selected gels are each exported to a separate image file.</li> <li>• <b>Contrast Lane:</b> Specifies the gel lane to use to set the minimum and maximum RFU values for all lanes in the collection or selected wells before exporting the gels. All exported gels are set to the minimum and maximum RFU values in the selected lane. The contrast lane option only displays in the Auto Export window after the sample wells have been selected. (Not available on the Auto Export window.)</li> <li>• <b>Height:</b> Specifies the desired height, in pixels, of the gel graphic.</li> </ul>
<b>Image Format for Gel and Electropherogram</b>	Select the desired format for the exported image files.

## Folder Permissions Window

Use the Folder Permissions window to set access rights to folders in the CDR for specific users. Each LabChip GX Touch user name can be assigned Full Control, Read, and/or Write access to each folder in the CDR. Permissions can be propagated to subfolders, if desired. To open the Folder Permissions window, select **Security** → **Folder Permissions**.



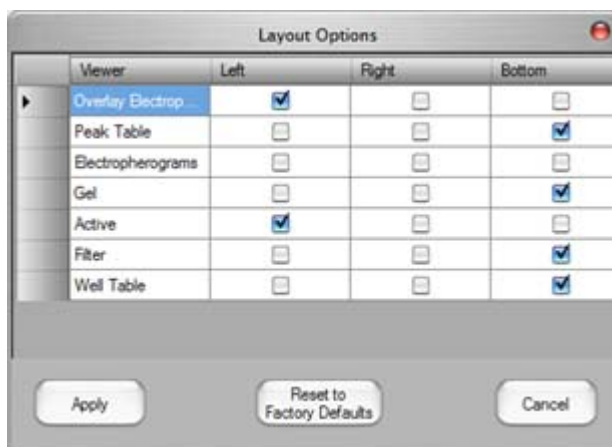
**Figure 105. Folder Permissions**

The Folder Permissions Window contains the following options:

Options	Description
<b>CDR radio button</b>	If selected, the CDR folder and its subfolders display in the Folder List.
<b>Assay radio button</b>	If selected, the ASSAY folder and its subfolders display in the Folder List.
<b>Select User drop-down list</b>	Displays the user name for which permissions are being set.
<b>Folder List</b>	Select the name of the folder to apply the settings for the specified user. The folder name displays next to <b>Selected Folder</b> .
<b>Set Permissions</b>	Select or clear the <b>Full Control</b> , <b>Read</b> , and <b>Write</b> check boxes to assign the desired permissions to the selected user name. Full Control gives read and write permissions to the selected user for the selected folder.
<b>Apply permissions to subfolders check box</b>	If selected, the permissions set for a folder are applied to any subfolder in the selected folder. If not selected, the settings are only applied to the selected folder.

## Layout Options Window

Use the Layout Options window to change the location of the views in a collection. To open the Layout Options window, select **Collection** → **Layout** on the [LabChip GX Reviewer Main Window](#).



**Figure 106. Layout Options Window**

The Layout Options window contains the following options and buttons:

**Viewer column** - Lists the viewers available to display in the [Collection Pane](#).

**Left check box** - If selected, the view displays on the right side of the Collection pane. (The view displays at the top if any view is selected to display at the bottom of the pane.)

**Right check box** - If selected, the view displays on the left side of the Collection pane. (The view displays at the top if any view is selected to display at the bottom of the pane.)

**Bottom check box** - If selected, the view displays at the bottom of the Collection pane. (The view displays at the top if there are no views displayed at the top left or right in the pane.)

**Apply button** - Applies the selections to the active collection and closes the Layout Options window.

**Restore to Factory Defaults button** - Restores the active collection to the default Layout options, table views, table columns, and viewer properties.

**Cancel button** - Closes the Layout Properties window without changing the collection layout.

## Layout Options Window (Continued)

### NOTES

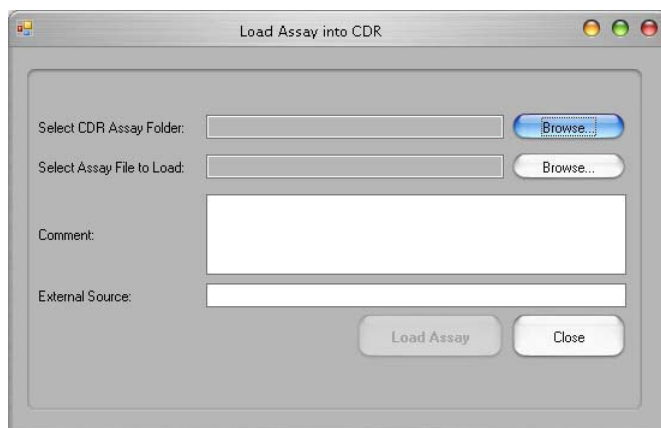


- *A view can only be displayed in one location. Selecting a location automatically clears any other selected location.*
- *To hide a view, click on the selected location to clear the selection.*
- *A location is hidden if it contains no views.*
- *The **Gel View** is always displayed and cannot be hidden.*

## Load Assay into CDR Window

Use the Load Assay into CDR Window to add customized assays to the CDR folder from a folder located outside of the CDR folder. This window only displays if the LabChip GxP option is installed.

To open the Load Assay into CDR Window, select **Tools** → **Load Assay into CDR** on the [LabChip GX Reviewer Main Window](#).



**Figure 107. Load Assay into CDR Window**

The Load Assay into CDR window contains the following options:

**Select CDR Assay Folder text box** - Click the **Browse (...)** button to open the **CDR Browser Window** to specify the path to the CDR assay folder.

**Select Assay File to Load text box** - Click the **Browse (...)** button to the path to the desired customized assay file.

**Comment text box** - Type any applicable comments (if desired).

**External Source text box** - Type the source (e.g., PerkinElmer) of the customized assay (if desired).

**Load Assay button** - Loads the selected customized assay file into the CDR assay folder.

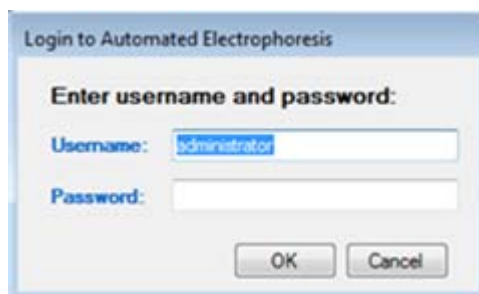
**Close button** - Closes the Load Assay into CDR window without loading an assay to the CDR assay folder.



## Login Window

Use the Login Window to log into the LabChip GX Reviewer software when the LabChip GxP option is installed. The LabChip GX Reviewer software will not open until a valid user name and password are entered.

The Login Window opens when you start the LabChip GX Reviewer software with the LabChip GxP option installed.



**Figure 108. Login Window**

The Login Window contains the following options:

Option	Function
Username text box	Type the user name to log into the LabChip GX Reviewer software. Each user should have a unique user name.
Password text box	Type the password assigned to the Username. All passwords must be at least 5 characters long and must contain at least one uppercase letter and at least one number. The User Account Policies specify additional password requirements.

## New Collection Window

The New Collection window is used to create a new collection using either a Blank Collection (default) or a Template. To open the New Collection window, select **Collection → New Collection** on the [LabChip GX Reviewer Main Window](#).



**Figure 109. New Collection Window**

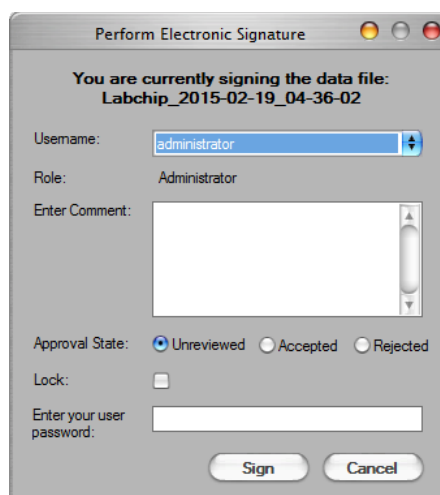
The following options are available:

Option	Function
<b>Template</b>	If selected, opens a blank collection and then applies the selected collection template.
<b>Blank Collection</b>	If selected, opens a blank collection that does not contain any data. The new collection will use the same settings as the last saved collection of the same assay type. <i>The current collection settings are automatically saved in a blank collection template in the current user's "Documents and Settings" folder on the local computer. These preferences are applied when a blank collection is created. User preferences are saved by assay type, with separate settings saved for DNA, RNA, Protein and Glycan assays.</i>
<b>Current Collection</b>	Only enabled if a collection is currently opened. If selected, opens a blank collection and applies the settings from the currently open collection as a template.
<b>Assay Type</b>	Select the type of data files (DNA, Protein, RNA, Glycan, CZE, or gDNA) that can be imported into the collection. Only enabled if this is the first collection and no plates have been imported into the workspace. If a workspace already contains a collection, all new collections are the same type as the existing collections. (Protein, Glycan, and Protein Charge Variant assays are only supported on LabChip GXII or GXII Touch instruments.)
<b>Name</b>	Specifies the name of the new collection.

## Perform Electronic Signature Window

Use the Perform Electronic Signature Window to add an electronic signature to a data file. Add signatures as required by the company's standard operating procedures. (Data files cannot be signed while the assay is running.) If multiple data files are open in the workspace, only one data file can be signed at a time.

To open the Perform Electronic Signature Window, select **Security** → **Perform Signature** on the [LabChip GX Reviewer Main Window](#).



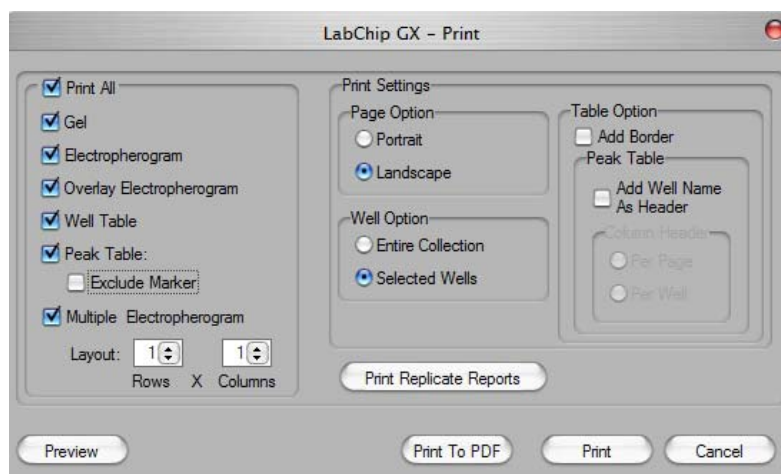
**Figure 110. Perform Electronic Signature Window**

The Perform Electronic Signature Window contains the following options:

Data File Name	Displays the name of the data file being signed.
Username	Select the user name of the user that is signing the data file.
Role	Displays the Access Level of the selected LabChip GX Touch user.
Comment	Details on why the signature is being performed and what actions have taken place. It is the signer's responsibility to ensure all details required by the company's procedures are included.
Approval State	Select the desired option: Unreviewed, Accepted, or Rejected. The icons in the <a href="#">CDR Manager Window</a> indicate the Approval State of the data file. All new data files are set to Unreviewed by default.
Lock	If selected, the data file cannot be saved and the Approval State cannot be changed. Only users with the Unlock permission can unlock data files.
User Password	The password for the user.
Sign button	Signs the data file and closes the window.
Cancel button	Closes the window without signing the data file.

## Print Window

Use the Print window to print information from the currently open workspace. If the workspace contains multiple collections, information from the active (selected) collection is printed. To open the Print window, select **File** → **Print** on the [LabChip GX Reviewer Main Window](#).



**Figure 111. Print Window**

The Print window contains the following options:

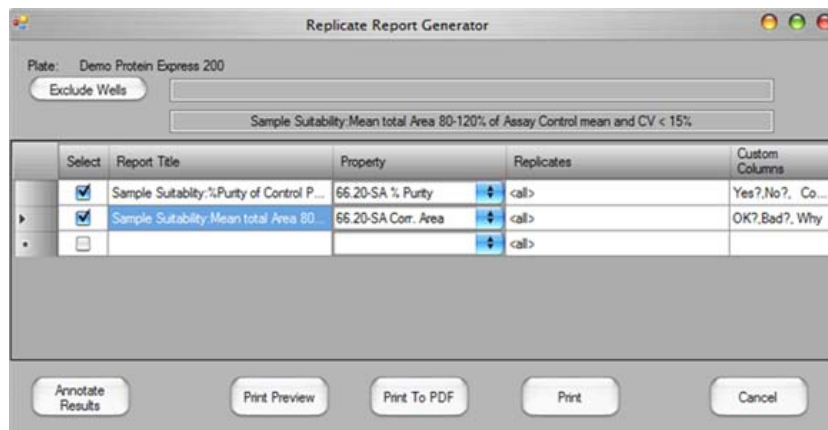
Option	Function
<b>Print All</b>	Selects all of the options.
<b>Gel</b>	Prints a graphic of the gel for either all wells in the collection or all selected wells.
<b>Electropherogram</b>	Prints a graph of either all wells in the collection or all selected wells.
<b>Overlay Electropherogram</b>	Prints a graphic of all electropherograms (either all selected or all in the collection) over-laid onto the same graph.
<b>Well Table</b>	Prints the well table for either all wells in the collection or all selected wells. The columns selected for view in the well table are printed. Changing the columns selected to view in the Well Table View changes the columns that are printed.

Option	Function
<b>Peak Table</b>	<p>Prints the peak table for all wells in the collection or all selected wells. The columns selected for view in the peak table are printed. Changing the columns selected to view in the <a href="#">Peak Table View</a> changes the columns that are printed.</p> <ul style="list-style-type: none"> <li>• <b>Exclude Marker</b> - If selected, markers are not printed.</li> <li>• <b>Multiple Electropherogram</b> - Prints a graph of either all wells in the collection or all selected wells in the specified format, rows by columns.</li> </ul>
<b>Page Option</b>	Select the page orientation, either Portrait or Landscape.
<b>Well Option</b>	Select the wells to be included in the printout, either Entire Collection or Selected Wells.
<b>Print Replicate Reports</b>	If selected, opens the <a href="#">Replicate Report Generator Window</a> to type the settings for the <a href="#">Print Replicate Report</a> if replicates have been defined in the <a href="#">Replicates Tab</a> .
<b>Add Border Option</b>	If selected, the Well Table and Peak Table will print with a border between each column and a border below the column header.
<b>Add Well Name as Header</b>	If selected, a well header, containing the plate, well, and sample name for the well, is printed before each set of peaks in a well. (This option is only available if Peak Table is selected.)
<b>Column Header</b>	<p>Specifies where to print the column headers, which identify each column in the Peak Table. (This option is only available if Peak Table is selected and Well Table is not selected.)</p> <ul style="list-style-type: none"> <li>• If <b>Per Page</b> is selected, the column header is printed only at the top of each page.</li> <li>• If <b>Per Well</b> is selected, the column header is printed at the top of each page and at the start of each new well.</li> </ul>
<b>Preview button</b>	Displays a preview of the selected options.
<b>Print to PDF button</b>	Prints the selected information from the active collection to a pdf file.
<b>Print button</b>	Prints the selected information from the active collection to the default Windows printer.
<b>Cancel button</b>	Closes the Print window without printing.

## Replicate Report Generator Window

Use the Replicate Report Generator window to define the [Print Replicate Report](#) settings.

To open the Replicate Report Generator window, click the **Print Replicate Reports** button on the [Print Window](#).



**Figure 112. Replicates Report Generator Window**

The following buttons display in the Replicate Report Generator window:

Button	Function
<b>Exclude Wells</b>	Opens a plate map to select wells to exclude from the replicate averaging. The excluded wells appear in the replicate report as strike-through values to indicate that they are not included in the statistics.
<b>Annotate Results</b>	Displays the Replicate Report in a table format, including the Replicate set number, replicate set name, well name, Mean, StdDev., CV%, and user defined columns.
<b>Setup Reports</b>	Returns the window to the original view after selecting Annotate Results.
<b>Print Preview</b>	Displays a preview of the report and allows you to print or export the results.
<b>Print to PDF</b>	Prints the selected information from the active collection to a pdf file.
<b>Print</b>	Opens the Print window to print the report.
<b>Cancel</b>	Closes the window without applying the replicate report settings.

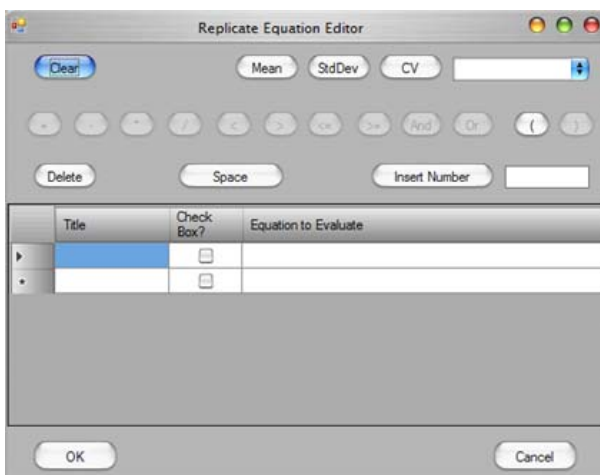
The following columns display in the Replicate Report Generator window:

Column	Description
<b>Select check box</b>	Adds the selected report title to the Replicate Report.
<b>Report Title</b>	Type the desired report title.
<b>Property</b>	Select a well property to be measured from the drop-down menu.
<b>Replicates</b>	If <all> displays, all replicate wells are included in the Replicate Report. Double-click the row to select individual replicates for the report.
<b>Custom Columns</b>	Double-click to open the <a href="#">Replicate Equation Editor Window</a> to. Type custom settings to include in the replicate report.

## Replicate Equation Editor Window

Use the Replicate Equation Editor Window to create custom columns to add to the [Print Replicate Report](#).

To open the Replicate Equation Editor Window, double-click inside the **Custom Columns** on the [Replicate Report Generator Window](#).



**Figure 113. Replicate Equation Editor Window**

The following options display on the Replicate Equation Editor window:

Option	Function
<b>Clear button</b>	Removes all current selections from window.
<b>Mean button</b>	Adds the mean value to the equation to evaluate.
<b>StdDev button</b>	Adds the standard deviation value to the equation to evaluate.
<b>CV button</b>	Adds the CV value to the equation to evaluate.
<b>Replicate Selector Drop-Down List</b>	Selects the specific replicate property to be added to the equation to evaluate.
<b>+, -, *, /, &lt;, &gt;, &lt;=, &gt;=, And, Or, (, )</b>	Operator values added to the equation to evaluate.
<b>Delete button</b>	Removes the last item added to the equation to evaluate.
<b>Space button</b>	Adds a space between operate values in the equation to evaluate.
<b>Insert Number</b>	Adds the numbered typed in to Insert Number text box into the equation to evaluate.
<b>Insert Number text box</b>	Type the desired number to be added to the equation to evaluate.



Option	Function
<b>OK button</b>	Applies the changes set in the Replicate Equation Editor window.
<b>Cancel</b>	Closes the window without applying the changes set in the Replicate Equation Editor window.

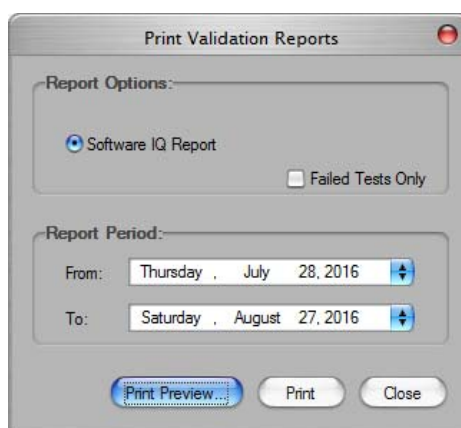
The following columns display in the Replicate Report Generator window:

Column	Description
<b>Title</b>	Displays the preferred custom column heading title to be added to the report.
<b>Check box?</b>	If selected, adds a check box to the rows in the custom column. If the result of the equation set in the Equation to Evaluate column is true, the check box is selected in the replicate report. If the result of the equation is false, the check box is not selected.
<b>Equation to Evaluate</b>	Displays the equation to be evaluated in the custom column of the Replicate Report. For example, Mean > 100 & Mean < 150.

## Print Validation Reports Window

Use the Print Validation Reports Window to print the results after performing Installation Qualification (IQ).

To open the Print Validation Reports Window, select **Validation** → **Reports** on the [LabChip GX Reviewer Main Window](#).



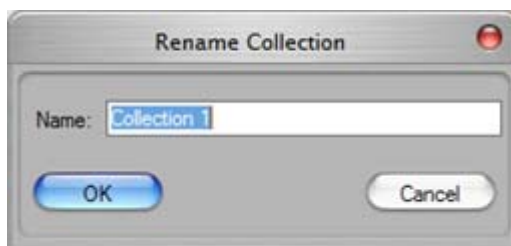
**Figure 114. Print Validation Reports Window**

The Print Validation Reports Window contains:

Option/Button	Function
Software IQ Report	If selected, the results of Software IQ tests are printed.
Failed Tests Only	If selected, only tests that have failed are printed. If not selected, both passed and failed tests are printed.
Report Period	Specifies the dates when the tests were run. Tests performed between the From and To dates (inclusive) are printed.
Print Preview button	Displays a preview of the report and enables you to print or export the results.
Print button	Opens the Print window to print the report.
Close button	Closes the window.

## Rename Collection Window

Use the Rename Collection window to rename the currently selected collection. The collection name displays on the Collection tab at the top of the [LabChip GX Reviewer Main Window](#). To open the Rename Collection window, select **Collection** → **Rename Collection** on the [LabChip GX Reviewer Main Window](#).



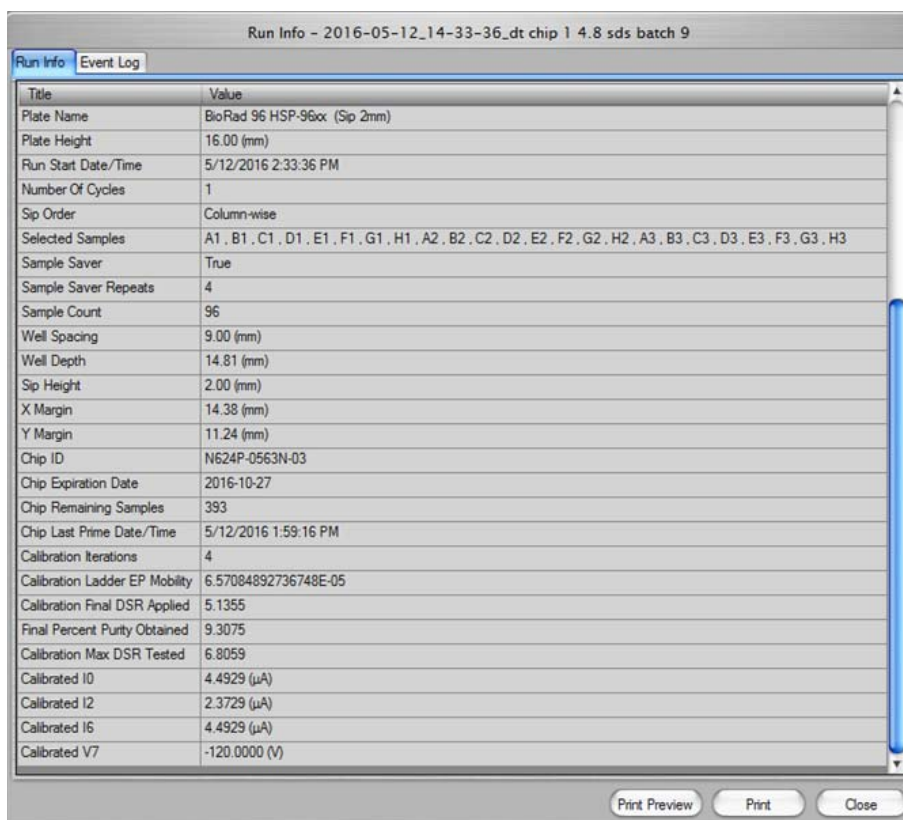
**Figure 115. Rename Collection Window**

**Name** - Type the desired name for the selected collection.

## Run Info Window

Use the Run Info window to view information about the run options for the selected plate data file. The Run Info window also displays the calibration options for the selected well containing the VeriMAb sample (for HT Protein QC assays only).

To open the Run Info window, select **View → Run Info** on the [LabChip GX Reviewer Main Window](#), or right-click on the name of the data file above the plate diagram and select **Run Info**.



**Figure 116. Run Info Window**

The information in this window is view-only and cannot be changed.

The **Run Info** tab displays assay information and run/calibration information.

The **Event Log** tab displays the events that occurred during the run/calibration.

## Run Info Window (Continued)

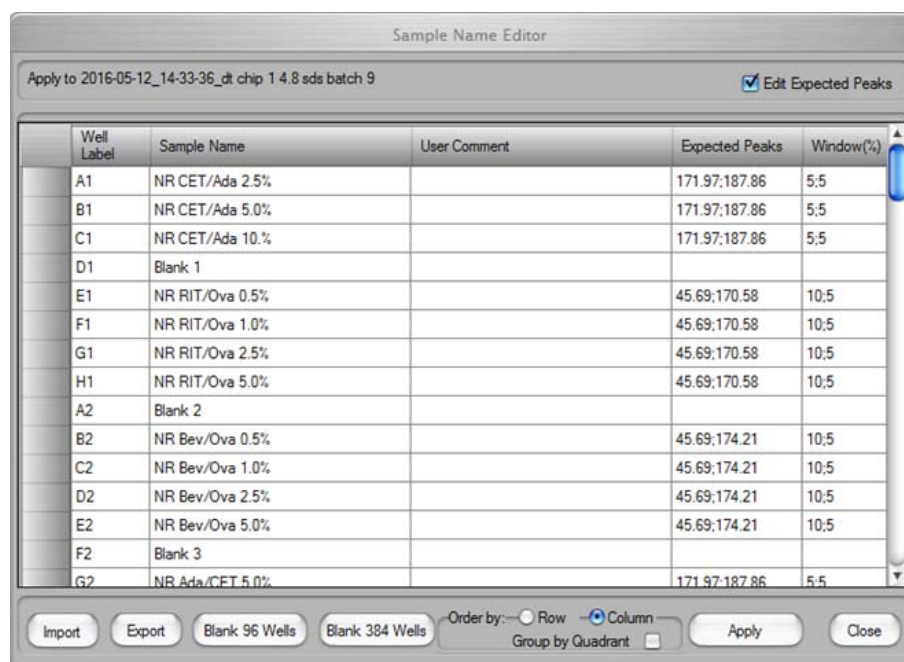
The Run Info window contains the following buttons:

Button	Function
<b>Print Preview</b>	Opens the Print Preview window to view the run information before printing.
<b>Print</b>	Opens the Print window to print the run information.
<b>Cancel</b>	Closes the Run Info window.

## Sample Name Editor Window

Use the Sample Name Editor window to specify names for the samples in the plate. For DNA, Protein, Glycan, CZE, and gDNA assays, also can be used to view, add, edit, or delete expected peaks. Sample Names can be exported to a .CSV file to be re-used in other workspaces or for other plates.

To open the Sample Name Editor window, choose **Tools** → **Sample Name Editor** on the [LabChip GX Reviewer Main Window](#).



**Figure 117. Sample Name Editor Window**

**Edit Expected Peaks check box** - If selected, displays the Expected Peaks and Window (%) columns for DNA, Protein, Glycan, CZE, and gDNA assays. This option is not available for RNA assays.

The following columns display in the Sample Name Editor window:

Column	Description
Well Label	Displays the row letter and column number of each well. Wells are ordered by column if the Order by Column check box is selected. If the window is opened from the Start Run Window, the wells display by column or well depending on the selection on the Run tab. If a plate is running when the window is opened, the wells display by column or well based on the sip order of the currently running plate.

Column	Description
Sample Name	The sample name for the sample in the specified well. Type a new name to change the sample name.
Sample Comment	Any comment to be associated with each well of the plate. Displays in the <a href="#">Well Table View</a> .
Expected Peaks	Displays the Expected Peaks for DNA, Protein, Glycan, or Protein Charge Variant assays. (The Expected Peaks are also displayed in the <a href="#">Expected Fragments/Proteins/Glycans Tab</a> on the <a href="#">Assay Analysis Window</a> .) Only displays if the Edit Expected Peaks check box is selected.
Window (%)	Specifies the tolerance window as a percent of the expected size for the peak to allow for small variations in expected peak size. Only displays if the Edit Expected Peaks check box is selected.

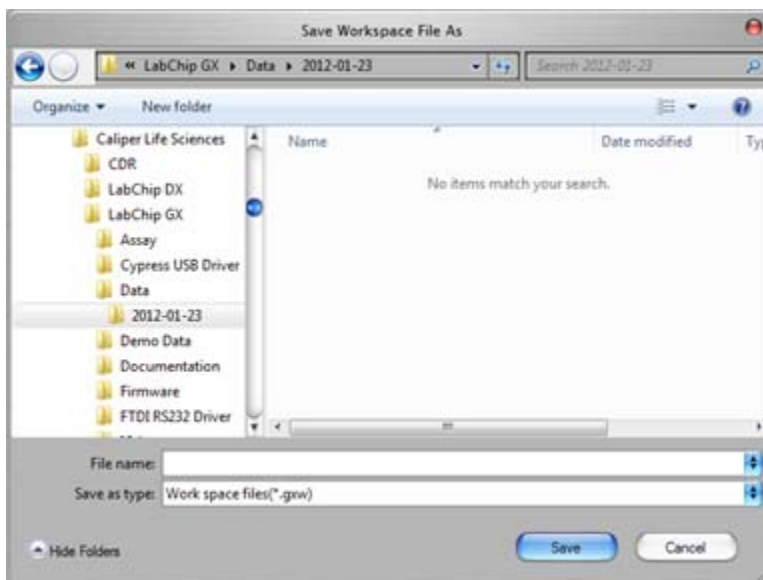
The following buttons and options are located at the bottom of the Sample Name Editor window:

Button	Description
Import	Imports a sample name file (*.csv) into the Edit Sample Names window.
Export	Exports the current sample names and comments into a Sample Names (*.csv) file. See <a href="#">“Using Sample Names Files” on page 36</a> .
Blank 96 Wells	Clears the sample names in the window and creates a new sample name that is the same as the well label for each well in a 96 well plate.
Blank 384 Wells	Clears the sample names in the window and creates a new sample name that is the same as the well label for each well in a 384 well plate.
Order by	<b>Row</b> - The sample names are ordered by row (A1, A2, A3, etc.). <b>Column</b> - The sample names are ordered by column (A1, B1, C1, etc.).
Group By Quadrant	If selected, the sample names are grouped by quadrant, as well as by rows or columns.
Apply	Applies the sample name changes to the plate. Sample names cannot be applied during a run.
Close	Closes the Edit Sample Names window. If changes have not been applied to the plate, prompts you to discard the changes. To save the changes, click the Apply button before clicking the Close button.

## Save Workspace As Window

The Save Workspace File As window saves the currently open workspace with the specified name in the specified location.

To open this window, choose **File → Save Workspace As**. This window also opens the first time you save a new workspace.



**Figure 118. Save Workspace As Window**

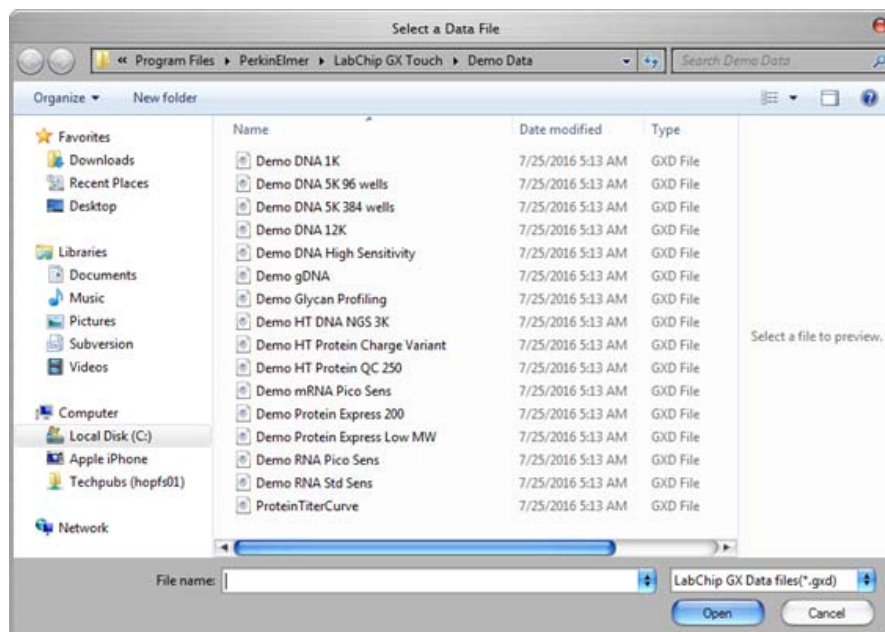
Tip: You may want to save the workspace file in the same location as the plate data files to prevent missing plate data files when moving workspace files.

If the LabChip GxP option is installed, the data files are saved in the CDR. Workspace files are saved outside the CDR.



## Select a Data File Window

When you choose **Import Data File** from the **File Menu**, the Select a Data File window opens as shown in [Figure 119](#). (If the LabChip GxP option is installed, the [CDR Manager Window](#) opens.) Data files generated by the LabChip GX or GX Touch software have a .gxd file extension. Data files generated by the LabChip HT software have a .cla file extension; change the File Type to display .cla files.



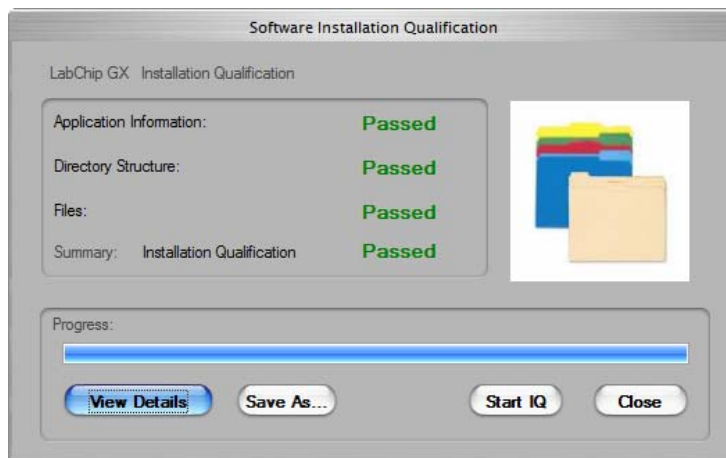
**Figure 119. Select A Data File Window**

Select a data file name in the list box and click the **Open** button or double-click a file name to open the data file.

To select multiple files, press and hold CTRL then click each file name. To select a continuous block of files, click the first file, press and hold SHIFT, and then click the last file. To select all files, press CTRL+A.

## Software Installation Qualification Window

Use the Software Installation Qualification Window to perform the IQ test. The IQ test verifies proper installation of the LabChip GX Reviewer software and verifies no unauthorized changes have been made to the software. To open the Software Installation Qualification Window, select **Validation** → **Software IQ** on the [LabChip GX Reviewer Main Window](#).



**Figure 120. Software Installation Qualification Window**

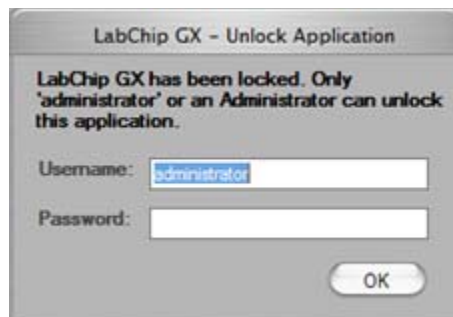
The Software Installation Qualification Window contains the following information:

Option	Function
Application Information	Verifies that the LabChip GX Reviewer registry entries exist. If all expected registry entries are found, displays Passed. If any problems are found, displays Failed.
Directory Structure	Verifies that all folders exist. If all expected folders exist, displays Passed. If any folders are not found, displays Failed.
Files	Verifies that all files that were installed by the LabChip GX Reviewer software still exist. If all file exist, displays Passed. If any files are not found, displays Failed.
Summary	Displays Passed if all tests passed. Displays Failed if any of the IQ tests failed.
Progress	Displays a progress bar while the IQ test is running.
View Details Button	Displays the detailed results of the current IQ. (Only displays after the IQ has been completed.)
Previous Result button	Displays the results of the last IQ that was completed. (Only available before another IQ test is run.)
Save As button	Saves the results of the IQ in an .xml file.

Option	Function
Start IQ button	Begins running the IQ.
Close button	Closes the Software Installation Qualification Window.

## Unlock Application Window

Use the Unlock Application Window to access the LabChip GX Reviewer software after it automatically locks. This window displays on top of the LabChip GX Reviewer software when the software is locked. The automatic lock option is set in the [Set Policies](#) tab on the [User Administration Window](#). This window only displays if the LabChip GxP option is installed.



**Figure 121. Unlock Application Window**

The Unlock Application Window contains:

Option/Button	Function
Username	Type the user name of the current user or a LabChip GX Touch administrator's user name.
Password	Type the password for the specified user name.
OK button	Verifies the Username and Password and opens the LabChip GX Reviewer software if the Username and Password are valid.

## Unlock Data File Window

Use the Unlock Data File Window to unlock a data file to enable the data file to be saved or to change the Approval State of the data file. Only users with the Unlock Data Files permission are permitted to access this window. Administrators can change this setting in the [Edit Users](#) tab on the [User Administration Window](#). The Unlock Data File option is only available if the LabChip GxP option is installed.

To open the Unlock Data File Window, select **Security** → **Unlock Data File**.



**Figure 122. Unlock Data File Window**

The Unlock Data File window contains:

**Username** - Select the user name of the LabChip GX Touch user that is unlocking the data file.

**Reason** - Type the reason why the data file is being unlocked.

**User Password** - The password of the selected LabChip GX Touch user.

**Unlock button** - Unlocks the data file specified at the top of the window if the Username and Password are correct.

**Cancel** - Closes the Unlock Data File window without unlocking the data file.

To lock a data file, use the [Perform Electronic Signature Window](#).

## User Administration Window

Use the User Administration window to create new LabChip GX Touch users, to edit existing users, to view user information, to activate or deactivate users, to set rights for each access level, and to set policies for LabChip GX Touch software and LabChip GX Reviewer software. The User Administration Window only displays if the LabChip GxP option is installed.

If multiple GX or GX Touch instruments are connected to the CDR, all user accounts are available on all instruments and each user name has the same access rights on all instruments.

To open the User Administration window, choose **Security → User and System Administration**.

**Figure 123. User Administration window**

The User Administration window contains the following tabs:

- “Create New User” on page 239
- “Edit Users” on page 241
- “Show User Info” on page 242
- “De/Activate User” on page 244
- “Define Access” on page 245
- “Set Policies” on page 247

**Close button** - Closes the User Administration window without saving changes. Save the changes on each tab before closing the window.

## Create New User

Use the Create New User tab to add a new user name to the LabChip GX Touch software and LabChip GX Reviewer software. This window creates the LabChip GX Touch user account, it does not create a Windows user account.

**Figure 124. User Administration Window - Create New User**

The Create New User tab contains:

Option/Button	Function
Username	Type the user name that the new user will use to log into the LabChip GX Touch software or the LabChip GX Reviewer software.
First Name	Type the first name of the user.
Middle Name	Type the middle name or initial of the user.
Last Name	Type the last name of the user.
Position	If desired, type the job title of the user.

Option/Button	Function
Access Level	<p>Choose the access level for the user. The access level controls the user's rights in the LabChip GX Touch and GX Reviewer software. The following access levels are available:</p> <ul style="list-style-type: none"><li>• Restricted User - Can only access Audit Trail.</li><li>• Operator - Operates the LabChip GX Touch instrument.</li><li>• Supervisor - Can save existing data files.</li><li>• Administrator - Run assays, analyze data files, edit assays, and manage user accounts and CDR for LabChip GxP option.</li><li>• Service - Run Assays and perform system validation.</li></ul> <p>The default permissions described above can be changed by an administrator.</p>
Password	Type the desired password for the user. The password must meet the password policies selected on the <a href="#">Set Policies</a> tab.
Confirm Password	Repeat the desired password for the user.
User Can Perform Signature	If selected, the user can sign data files using the <a href="#">Perform Electronic Signature Window</a> .
Accept/Reject/Lock Data File	If selected, the user can Accept, Reject, and/or Lock data files in the <a href="#">Perform Electronic Signature Window</a> .
Unlock Data File	If selected, the user can unlock data files using the <a href="#">Unlock Data File Window</a> .



## Edit Users

Use the Edit Users tab to edit an existing user account.

**Figure 125. User Administration Window - Edit Users**

The Edit Users tab contains:

Option/Button	Function
Select User to Edit	Select the Username for the account to edit.
First Name	The first name of the user.
Middle Name	The middle name or initial of the user.
Last Name	The last name of the user.
Position	If desired, the job title of the user.
Access Level	The Access Level of the user.
User Can Perform Signature	If selected, the user can sign data files using the <a href="#">Perform Electronic Signature Window</a> .
Accept/Reject/Lock Data File	If selected, the user can Accept, Reject, and/or Lock data files in the <a href="#">Perform Electronic Signature Window</a> .
Unlock Data File	If selected, the user can unlock data files using the <a href="#">Unlock Data File Window</a> .
Edit User Password	If selected, the user's password can be changed.
Password	Type the desired password for the user. The password must meet the password policies selected on the <a href="#">Set Policies</a> tab.
Confirm Password	Repeat the desired password for the user.

## Show User Info

Use the Show User Information tab to view the account information for an existing Username.

The screenshot shows the 'LabChip GX - User Administration' window. On the left, under 'Select Task:', there are buttons for 'Create New User', 'Edit Users', 'Show User Info' (highlighted in blue), 'De/Activate User', 'Define Access', 'Set Policies', and 'Close'. The main area, 'User Information:', has a 'Select User to Display:' dropdown menu with 'administrator' selected. Below this, the following information is displayed:

- Username: administrator
- Full Name: Default Administrator
- Position: administrator
- Access Level: Administrator
- Can Perform Signature: YES
- Can Accept/Reject/Lock data file: YES
- Can Unlock data file: YES
- Account Created On: Monday, January 30, 2012 at 12:54:45 PM
- Account Last Changed On: Monday, January 30, 2012 at 12:54:45 PM
- Status: Active

At the bottom left, there is a checkbox for 'Print All Users'. At the bottom right, there are buttons for 'Print Preview...' and 'Print'.

**Figure 126. User Administration Window - Show User Info**

The Show User Info tab contains:

Option/Button	Function
Select User to Display	Select the Username for the account to view.
Username	The user name for the displayed information.
Full Name	The first, middle, and last name of the user.
Position	The job title of the user.
Access Level	Displays the Access Level of the user.
Can Perform Signature	Displays Yes if the user has rights to perform signatures. Displays No if the user does not have rights.
Can Accept/Reject/Lock Data File	Displays Yes if the user has rights to Accept, Reject, and Lock data files. Displays No if the user does not have rights.
Can Unlock Data File	Displays Yes if the user has rights to unlock data files. Displays No if the user does not have rights.
Account Created On	Displays the date and time when the account was created.
Account Last Changed On	Displays the date and time when the account was last changed.

Option/Button	Function
Status	Displays Active if the user account is activated. Displays Deactivated if the account has been deactivated.
Print All Users check box	If selected, information for all user accounts will be printed.
Print Preview button	Displays a preview of the printed report. The report can be exported to a .rpt file from the Print Preview window.
Print button	Opens the Print window to print the report.

## De/Activate User

Use the De/Activate User tab to Deactivate an active user or to Activate a deactivated user. Users cannot be deleted from the database. User names that will not be used should be deactivated to prevent unauthorized access to the LabChip GX Touch or LabChip GX Reviewer software.



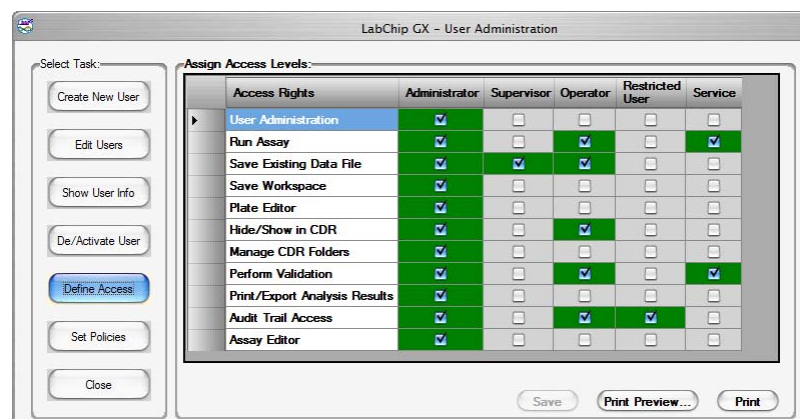
**Figure 127. User Administration Window - De/Activate User**

The De/Activate User Info tab contains:

Option/Button	Function
Select User	Select the Username to be activated or deactivated.
User Info	Displays the information associated with the selected Username.
Activate button	Click to activate a deactivated Username.
Deactivate button	Click to deactivate an active Username.

## Define Access

Use the Define Access Tab to assign the desired rights to each access level. These rights control the actions each user is permitted to perform in the LabChip GX Touch software and the LabChip GX Reviewer software.



**Figure 128. User Administration Window - Define Access**

The Define Access tab displays a column for each access level (Administrator, Supervisor, Operator, Restricted User, and Service). Select the check box for each right to be allowed for an access level, or clear the check box for each right not allowed for an access level.

The table below describes the function of each Access Right.

Access Right	Function
User Administration	If selected, allows access to the <a href="#">User Administration Window</a> to add and edit users, set access rights, and set policies.
Run Assay	If selected, allows users to run assays and save the new data files that are created by the run. Users are not permitted to save changes to existing data files.
Save Existing Data File	If selected, allows users to save changes to existing data files.
Save Workspace	If selected, allows users to save new and existing workspaces. If Save Existing Data Files is not selected, users can only save workspaces where the data files have not changed.
Plate Editor	If selected, allows users to add plates or edit plate dimensions in the Plate database.
Hide/Show in CDR	If selected, allows users to hide and show data files in the <a href="#">CDR Manager Window</a> .

Access Right	Function
Manage CDR Folders	If selected, allows users to create, rename, and delete folders in the CDR Manager window. This permission is not required for automatically creating daily subdirectories or to move data files in the CDR.
Perform Validation	If selected, allows users to perform IQ (Installation Qualifications), OQ (Operation Qualifications), Teaching the robot, and Optics Calibration/Normalization.
Print/Export Analysis Results	If selected, allows users to print or export analysis results.
Audit Trail Access	If selected, allows users to view the Audit Trail in the <a href="#">Audit Trail Window</a> .
Assay Editor	If selected, allows users to edit and save assays.

## Set Policies

Use the Set Policies tab to specify password, login, automatic lock, and signature policies for the LabChip GX Touch software and LabChip GX Reviewer software.

**Figure 129. User Administration Window - Set Policies**

The Set Policies tab contains:

Access Right	Function
Password Expires After	Specifies the number of days until each password expires. Range is 1 to 1000 days.
Number of Retired Passwords to Remember	User cannot reuse the specified number of old passwords.
Minimum Password Length	Specifies the minimum length of each password.
Maximum Login Attempts	Specifies the number of times the user can attempt to log in before being locked out of the software. Range is from 3 to 20. This option can be disabled to allow unlimited retries without locking the user out.
Minutes to Automatic Lock	Specifies the number of minutes that the software is inactive until the LabChip GX Touch software or LabChip GX Reviewer software locks automatically. Range is from 5 to 4320 minutes (3 days). To disable this option, clear the check box.

Access Right	Function
Require Signature on File Update	If selected, an electronic signature is required to save modified data files. Signatures can be performed by any user with the Perform Signature option selected in the <a href="#">Set Policies</a> tab.



## Troubleshooting and Diagnostics

This section contains the following topics to help troubleshoot problems with the LabChip GX Reviewer software:

- [“Searching for Events in the Events Tab” on page 249](#)
- [“Viewing Current Events in the Events Tab” on page 250](#)
- [“Viewing Past Events in the Events Tab” on page 250](#)
- [“Running Installation Qualification \(IQ\)” on page 251](#)
- [“Software Troubleshooting” on page 252](#)
  - [“Cannot Save a File” on page 252](#)
  - [“Computer Software Lock-Ups” on page 253](#)
  - [“Cannot Connect to Remote CDR Server” on page 253](#)
- [“Zipping the Log Files” on page 254](#)

### Searching for Events in the Events Tab

Events and errors that occurred during the screening of previous jobs are displayed in the **Past Events** tab in the [Event Viewer Window](#).

To search for a specific event:

- 1 On the Event Viewer window, click the **Search Result** tab.
- 2 In the **Events** list, select **Current**, **Past**, or **All**.
- 3 In the **Search Text** box, type a search query and click the **Search** button. The Source, Event Code, and Description fields are searched. The search results appear in the **Search Result** fields.

The Search Result tab contains the following fields:

**Time** - The time the event or error occurred.

**Source** - The source of the event or error.

**Event Code** - The event/error ID number used by PerkinElmer to troubleshoot problems.

**Description** - A detailed description of the event or error that occurred.

## Viewing Current Events in the Events Tab

While a job or batch is running, the events and errors that occur during the screening display in the **Current Events** tab in the [Event Viewer Window](#).

- On the Event Viewer window, click the **Current Events** tab. The **Current Events** fields display. (These fields are read only.)

The Current Events tab contains the following fields:

**Time** - the time the event or error occurred.

**Source** - The source of the event or error.

**Event Code** - The event/error ID number used by PerkinElmer to troubleshoot problems.

**Description** - A detailed description of the event or error that occurred.

## Viewing Past Events in the Events Tab

All events and errors that have occurred during the screening of previous jobs or batches display in fields on the **Past Events** tab in the [Event Viewer Window](#).

- On the Event Viewer window, click the **Past Events** tab. The **Past Events** fields display. (These fields are read only.)

The Past Events tab contains the following fields:

**Time** - The time the event or error occurred.

**Source** - The source of the event or error.

**Event Code** - The event/error ID number used by PerkinElmer to troubleshoot problems.

**Description** - A detailed description of the event or error that occurred.

## Running Installation Qualification (IQ)

The Installation Qualification (IQ) verifies proper installation of the LabChip GX Reviewer software and verifies no unauthorized changes have been made to the software. The IQ can be run whenever required by your laboratory procedures.

The Installation Qualification can be used to check software installation qualification after routine computer maintenance, such as disk cleanup, after installing antivirus software, or after installing Microsoft service packs. The Installation Qualification checks LabChip GX Reviewer software registry settings, the directory structure, and the integrity of each file specified for the software application.

To run the IQ:

- 1 On the [LabChip GX Reviewer Main Window](#), select **Validation** → **Software IQ**. The [Software Installation Qualification Window](#) opens.
- 2 To view the results of the previous IQ before running a new IQ, click the **Previous Result** button. The View Installation Qualification Results Window displays the results of the last IQ that was run.
- 3 To start the IQ, click the **Start IQ** button. The Software Installation Qualification window displays the tests that are run for the IQ, the progress of each test, and the Pass/Fail status of each test as it is completed.
- 4 To save the results of the IQ, click the **Save As** button, specify the desired location and name of the file, and click the **Save** button. IQ results are saved as .XML files.

## Software Troubleshooting

If any of the following software problems occur, follow the suggestions to correct the problem:

- [Cannot Save a File](#)
- [“Computer Software Lock-Ups” on page 253](#)
- [“Cannot Connect to Remote CDR Server” on page 253](#)

### Cannot Save a File

#### **File has been saved as a Read Only file.**

If you editing an existing file, verify the file is not Read Only. If it is, the title bar shows Read Only after the file name. Read-only files can be edited and saved with a new name or in a new location with the same name, but cannot be saved over the original file.

#### **Hard drive is full.**

Verify there is sufficient free space on the drive to save the file. If not, clear some space on the hard drive. On systems that do not have the LabChip GxP option installed, you can archive files that you are not using to another location.

If you do have sufficient space, try closing all open applications and then turning off the power to the computer. After a few seconds, restart the computer, open another file, and try re-saving it to verify the Save function is working properly.

#### **LabChip GX Reviewer software is corrupted.**

Reinstall the software. If the problem persists, contact PerkinElmer Technical Support (see [page 2](#)).

## Computer Software Lock-Ups

If a computer or software lock-up occurs:

- 1 Try to exit and then re-launch the LabChip GX Reviewer software.
- 2 If this is not successful, exit the application using the **Task Manager**:
  - a Right-click in the desktop menu bar and select **Task Manager**.
  - b Click the **Applications** tab.
  - c While holding down the **Shift** key, select all running applications.
  - d Hold the **Ctrl** key and click **End Task**.
- 3 If the **Task Manager** cannot be accessed, try one or all of the following:
  - Press the **Ctrl**, **Alt**, and **Delete** keys on the keyboard simultaneously.
  - Perform a hard reboot by turning off the computer and then restarting it.
- 4 Contact PerkinElmer Technical Support (see [page 2](#)).

## Cannot Connect to Remote CDR Server

If experiencing trouble connecting to the CDR server computer:

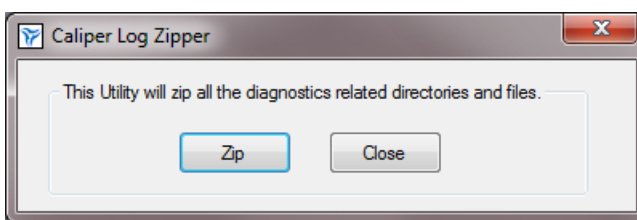
- If using a firewall other than Windows Firewall, open Port TCP/3690 for incoming traffic on the server computer.
- Ensure that the server computer is reachable from the GX Reviewer client by pinging the CDR server from the DOS Command window on the client computer.
- Verify that the network provides a DNS for name to IP mapping.
  - The Windows Name Service will not work for name mapping the SVN connection.
  - If the server computer does not have an entry in the DNS, the server IP address must be used for mapping and the IP address must be assigned statically.

## Zippping the Log Files

The Caliper Log Zipper is a software utility that zips the LabChip GX Reviewer log files and system info files and places the resulting DiagnosticsLog.zip file on the computer desktop. This utility can be used to package all of the log and diagnostic files together if the files need to be emailed to PerkinElmer Technical Support.

To zip the LabChip GX Reviewer diagnostics logs:

- 1 On the Windows desktop, select **Start** → **All Programs** → **PerkinElmer** → **LabChip GX Reviewer** → **Caliper Log Zipper**. The Caliper Log Zipper window opens.



**Figure 130. Caliper Log Zipper Window**

- 2 Click the **Zip** button. The DiagnosticsLog.zip file is saved to the computer desktop. Any existing older file with the same name is over-written.
- 3 To save a copy of the file, either rename the file or move the file to a different location.

## Tips and Shortcuts

This section describes the shortcuts and actions that can be performed in the LabChip GX Reviewer software by clicking, right-clicking, etc.

### Single Click

- **In Plate View** - Selects or de-selects a well.
- **In Gel View** - Selects a well and displays the graph in the Graph view.
- **In Well Table View** - Selects a well, displays the graph in the Graph view, and selects the well in the Gel view.
- **In Peak Table View** - Selects a peak, displays the graph in the Graph view, and selects the well in the Gel view.

### Ctrl + Click

- **In Gel View** - Overlays second and subsequent well data over original well data in the Graph view (for each Ctrl + click on a lane in the gel). Each well in the graph is shown in a different color.
- **In Well Table view** - Overlays second and subsequent well data over original well data in the Graph view (for each Ctrl + click on a row in the Well Table). Each well in the graph is shown in a different color.

### Ctrl + Shift + Click

- **In Gel View** - Highlights corresponding well data trace in Overlay Electropherogram view (adds trace to overlay if not already included). This trace becomes the foreground trace for peak selection. Repeat click to undo highlighting.

### Right-Click

- Right-click in any view to display a shortcut menu with available options. In the [Graph View](#), different shortcut menus display depending on whether the cursor is near a peak or not near a peak.

## Glossary of Terms

This Glossary includes explanations and examples of the following terms:

- [Apex](#)
- [Assay File](#)
- [Baseline](#)
- [CLA](#)
- [Clipboard](#)
- [Collection](#)
- [Collection Template](#)
- [Data Files](#)
- [Data Points](#)
- [Data Filtering](#)
- [DNA Assay Analysis](#)
- [Electrokinetic Forces](#)
- [Electroosmotic Flow](#)
- [Electrophoresis](#)
- [End Point](#)
- [End Time](#)
- [Filter Width](#)
- [Genomics Quality Score \[0-5\]](#)
- [GXD Files](#)
- [Inflection Threshold](#)
- [Lab-on-a-Chip](#)
- [Ladder](#)
- [Ladder Analysis](#)
- [Lower Marker](#)
- [Log Files](#)
- [Microfluidics](#)
- [Migration Time Drift](#)
- [Minimum Peak Height](#)
- [Minimum Peak Width](#)
- [Molarity](#)
- [Molecular Separation Techniques](#)
- [Optical Calibration](#)



- [Peak Baseline](#)
- [Peak Height](#)
- [Peak Identification](#)
- [Point-to-Point Fit](#)
- [Polynomial Filter](#)
- [Polynomial Order](#)
- [Protein Assay Analysis](#)
- [Protein Charge Variant Assay](#)
- [RNA Assay Analysis](#)
- [RNA Degrade Factor](#)
- [Rolling Ball Baseline Curve Example](#)
- [Slope Threshold](#)
- [Slope Threshold](#)
- [Smear](#)
- [Standard Curve](#)
- [Start Point](#)
- [Start Time](#)
- [Titer](#)
- [Tool Tip](#)
- [Upper Marker](#)
- [Workspace](#)
- [Zero Baseline](#)

## Apex

After locating a start point, the peak find algorithm looks for the first negative slope value and saves the previous point as the apex. If the value of the apex is less than the minimum peak height limit, the algorithm starts looking for a new peak.

## Assay File

File used by the LabChip GX or GX Touch software to specify assay and default analysis settings, such as Ladder and marker sizes and concentrations, peak find settings, expected peaks, and excluded peaks.

Create assay files and modify analysis settings in the LabChip GX Reviewer software.

## Baseline

A baseline is established just after the start time setting. (For DNA and RNA assays, you can change the Baseline Start time on the [Analysis Tab](#).) After the overall baseline is established, a local baseline is calculated for each peak to compensate for baseline drift.

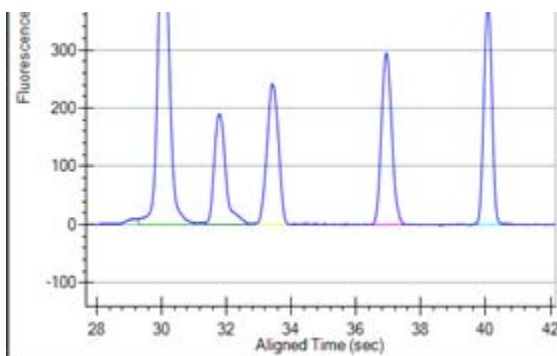
To select the desired baseline algorithm for all of the samples in the plate, choose the desired option on the [Peak Find Tab](#): No Baseline, Zero Baseline, or Baseline Subtraction. See [“Zero Baseline” on page 283](#) for more information about the Zero Baseline option.

Baseline Subtraction can use either Spline fit or Rolling Ball fit for the baseline curve algorithm.

- **Spline** - Creates a smooth line fit to the baseline data points and subtracts this smooth fit from the data. The Threshold determines how much the baseline fit follows changes in the data. Lowering the Threshold below the default value of 20 allows the baseline fit to ignore regions that are slow changes of real signal peaks and not baseline drift. This spline curve is not constrained to remain below the signal and may produce negative signal values when subtracted from the signal.
- **Rolling Ball** - Generates a smooth baseline curve by mathematically rolling a ball under the sample signal, keeping it in contact with the closest signal point without crossing into the signal. Time Diameter and Signal Diameter determine the smoothness of the curve in the Time and Signal axes and determine how closely the curve follows the signal. The ball is constrained to never cross into the signal, therefore the baseline curve is never greater than the signal and will not produce negative signal values when subtracted from the signal. See [“Rolling Ball Baseline Curve Example” on page 276](#) for more information.

For isolated peaks, the local peak baseline is a straight line connecting the start point of the peak with the end point. For peaks that are very close together, an average baseline is used when the value between the peaks does not drop to the actual baseline.

[Figure 131 on page 259](#) shows baselines established for DNA assay peaks (based on the settings in the [Peak Find Tab](#)). DNA peaks are determined on a peak-by-peak basis (the overall baseline is shown).



**Figure 131. Baselines**

## CLA

The file extension for data files created by the LabChip HT software. CLA files can be opened in the LabChip GX or GX Reviewer software only if the LabChip GxP option is not installed. Opening a .CLA file (see [page 33](#)) creates a .GXD file with the same name.

## Clipboard

A temporary storage area that contains information you have cut or copied. You can paste the contents of the clipboard into other programs (provided that program supports that type of information). Information remains on the clipboard until you replace it with the information from another cut or copy command.

## Collection

Use a collection to view the plate data. A workspace can contain multiple collections to supply different views of the same data.

Each collection specifies:

- the wells selected for view in each plate data file,
- the layout of each Collection tab, and
- the display properties for each view in each collection.

## Collection Template

A collection template saves the display options for a collection and any defined filters in the collection. Collection templates are used to create new collections using the saved display settings and filters. Collection templates do not save the list of plates or the wells selected in the plates.

To save a collection template based on the settings in the open collection, select **Collection → Save As Template** on the main [Menu Bar](#).

To apply a collection template to a new collection, select the **Template** option in the [New Collection Window](#).

To apply a collection template to an existing collection, select the tab for the desired collection and then select **Collection → Apply Template** on the main [Menu Bar](#).

## Data Files

While running an assay, the raw data received from the instrument is automatically saved to the plate data file (\*.gxd). As the data from each single well is received, it is saved to the data file. The name of the data file is specified during the run. If a run is stopped before the run is complete, the data file contains the data for the completed wells.

After a run is complete, the data is analyzed using the analysis settings in the assay. The analysis settings are saved in the data file (.gxd).

After the run, you can change the analysis settings using the [Assay Analysis Window](#). When the new settings are applied, the data is reanalyzed and the updated results are displayed. Changes to the analysis settings are not saved until the workspace is saved. To save analysis settings without saving the workspace, select **Workspace → Save Plate** or right-click on the plate name above the plate diagram on the left side of the window and choose Save Plate.

Changes to the analysis settings are saved at the end of the plate data file without overwriting previous settings in the file. The Restore Plate option can be used to return to previous analysis settings.

## Data Points

Data points are determined by the data collection rate set in the assay properties.

**Show Data Points** is an option in the [Graph View Properties](#) that displays the data points used to generate the graph.

## Data Filtering

Before identification of peaks in the fluorescence data can proceed, the raw data is smoothed to prevent the detection of signal noise as peaks. For details on the data filtering process, see [“Data Smoothing” on page 101](#).

## DNA Assay Analysis

DNA samples contain two marker peaks outside the limits of the DNA fragment sizes the assay is designed to detect. The ladders contain the same two marker peaks. The sample data is aligned to the ladder data by matching the peak times of the two markers in the sample data with the same two markers in the ladder data. The size of each sample peak is calculated by linear interpolation between the known ladder peak migration time and size using the peak aligned migration time. The analysis settings can be changed to perform the interpolation using a local third order polynomial fit to the time instead of the size relationship provided by the ladder.

The concentration of the sample peaks is calculated using the known area and concentration of the ladder peaks. The molarity of each sample peak is calculated using the sample concentration, the DNA fragment size (in base pairs) attributed to the peak, and the known molecular weight of the DNA base pair.

## Electrokinetic Forces

Electrokinetic forces are used to move, switch, mix, and separate the nucleic acid samples. Active control over voltage gradients directs the movement of materials using the phenomenon of electroosmotic flow or electromigration.

## Electroosmotic Flow

A phenomenon that results from an electrical double layer formed by ions in the fluid and surface electrical charges immobilized on the capillary walls. When an electric field is applied, the bulk solution moves towards one of the electrodes. This phenomenon can be used to move fluids through microfabricated channels

## Electrophoresis

A technique of separating molecules on the basis of their mobility. An electrical potential is applied across a capillary containing a sample in a fluid medium. Positive molecules migrate towards the cathode and negative molecules migrate towards the anode at different speeds depending on their electrophoretic mobility.

## End Point

The peak find algorithm looks for a leveling off when the value of the slope is less than the value set for the slope threshold. This is marked as the end point of the peak.

## End Time

This setting determines the time after the start of a run before which the last peak or fragment will be located (any peaks appearing after this time are ignored).

## Filter Width

This setting on the [Peak Find Tab](#) determines the width of the polynomial (in seconds) to be applied to the data for filtering (noise reduction). The default depends on the assay selected.

## Genomics Quality Score [0-5]

Calculated in gDNA assays to measure the quality (relative intactness) of the gDNA. The Genomics Quality Score ranges from 0 to 5, where 5 represents the highest quality of gDNA. The Genomics Quality Score can be used to measure the quality of gDNA before proceeding with further analysis of the sample. The Genomics Quality Score displays in the [Well Table View](#).

## GXD Files

The file extension for data files created in the LabChip GX and GX Touch software. The data file contains the data from the read, assay information, analysis settings, and Run Information for the run.

Data is saved to the file as each well is read. If a run is stopped before the run is complete, the data for any completed wells is saved in the data file.

The file name is specified during the run.

## Inflection Threshold

Peaks that are very close together are identified as a single peak if the peaks do not have a clear valley between them. The Inflection Threshold property splits peaks based on the slope. The inflection threshold defines the value that the slope minimum must be below to trigger a splitting of the peak. As the threshold is increased, more peak splitting occurs. For details, see [“Understanding Peak Finding” on page 101](#).

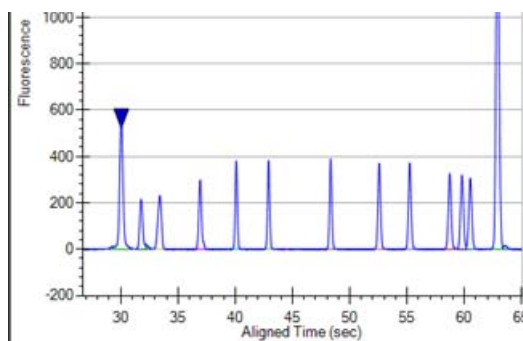
## Lab-on-a-Chip

The generic term for a microfluidic product, signifying a chemical process or material movement taking place on a microchip. In contrast to analysis in a standard laboratory that relies on human intervention at several stages to manipulate or observe samples and record results, the self-contained lab-on-a-chip represents an almost hands-free technology.

## Ladder

Ladders are used to align the data and calculate the size of data peaks. (Protein Charge Variant assays do not use ladders or markers.) The Ladder vial is located in the front right corner of the microplate carrier, next to the buffer vial. The Ladder is sipped before the first well and then after every 12 wells. The ladder is analyzed before sample analysis starts.

The peak sizes and markers defined for the ladder in the assay are assigned consecutively, starting with the first peak detected in the ladder. If too few peaks are detected in the ladder well, analysis stops and an error is generated. Peaks appearing above the upper marker do not have to be detected. The [Peak Table View](#) for the ladder well shows the peak size and concentration set in the [Assay Analysis Window](#).



**Figure 132. Ladder Graph**



## Ladder Analysis

A ladder is a mix of compounds of known sizes that is used to create a size ruler for the samples. Ladder data is used to convert the migration time of each sample peak into a size for the compound responsible for that peak. The known sizes of the ladder compounds are supplied in the assay file and can be viewed in the [Analysis Tab](#) on the [Assay Analysis Window](#).

The initial step in ladder analysis is to identify the most prominent peaks in the ladder well and associate each peak with the known ladder sizes. The analyzed ladders provide a table of values relating size to migration time. Typically the migration time uses the center of the peak in the ladder and the sample.

Failure to find the correct number of ladder peaks prevents further analysis of the sample wells using the faulty ladder. The software automatically attempts to use the nearest good ladder before generating an analysis error.

A **Ladder Quality Score** is computed for each Ladder well. The Ladder Quality Score is the  $R^2$  value for the fit of the peak migration times to size curve multiplied by 10. If the Ladder Quality Score is less than the **Ladder Rejection Threshold** specified on the [Alignment Tab](#) in the [Assay Analysis Window](#), the ladder well generates an error and is not used for sizing or quantization. The software will use the nearest good ladder to analyze the samples.

The analysis settings can specify which ladder is used to size any particular sample row. If more accurate sizing can be obtained by measuring migration times at the start of each peak, this option can be selected in the [Assay Analysis Window](#).

## Lower Marker

An internal standard that is added to a sample in a well to assist in determining size and concentration of the sample. For DNA assays, the marker is the same as the first peak in the DNA ladder. DNA ladders and samples also contain an [Upper Marker](#). For Protein and RNA assays, the marker is the same as the first peak in the ladder. Protein Charge Variant assays do not use ladders or markers.

## Log Files

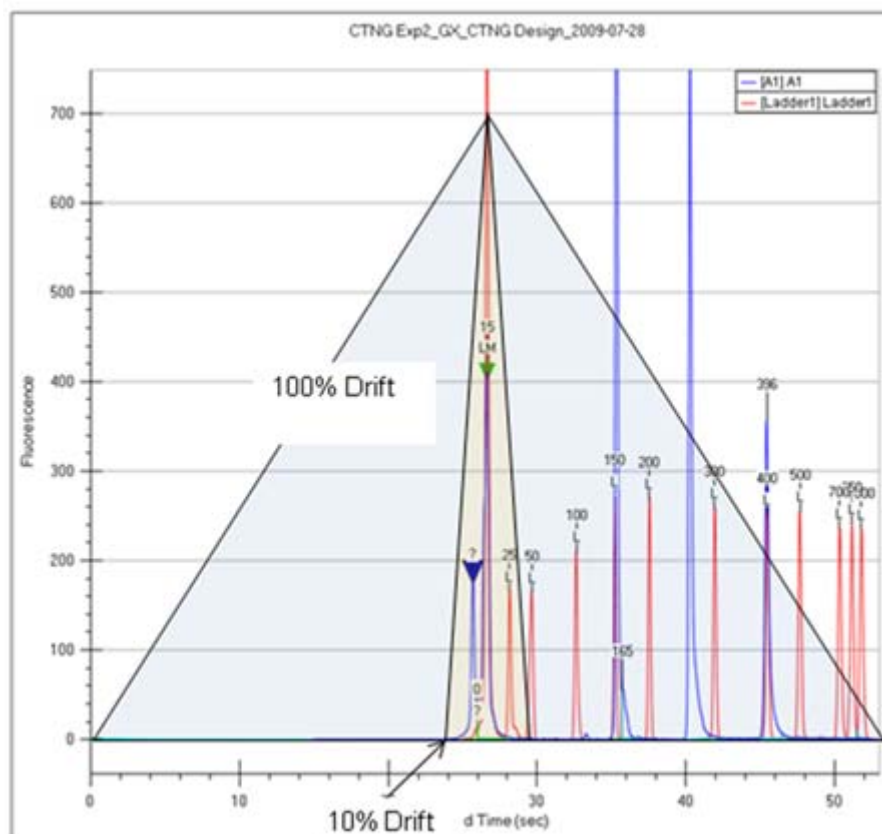
The LabChip GX Reviewer software log file displays in the [Event Viewer Window](#). The log file maintains a running record of all events that occur in the LabChip Reviewer software. Each event specifies the date and time of the event, source of the event, the event code, and a description of the event.

## Microfluidics

The miniaturization of chemical processes generally pertaining to systems involved in the control of fluid flow. This includes pumps, valves, jets, and microchannels.

## Migration Time Drift

Isolating the markers in the sample is key to alignment and sizing. The markers in the sample appear similar in size and migration time to the markers in the ladder. Markers are discriminated from nearby peaks through a weighing scheme which attributes a numerical value to the migration time similarity and area similarity. This approach is usually successful as long as the first peak is the marker, but when there is a peak of similar size arriving just before the true marker, the first marker is likely to be confused with the marker. When the primary differentiator between the two peaks is the migration time, the migration time drift can be used to narrow the acceptable range for the migration time by increasing the importance of the similarity between the sample and ladder marker peak times. The migration time drift specifies the accepted range as a percentage of the ladder migration time. The blue and yellow triangles shown in the figure below represent the weight assigned to a peaks migration time for a tolerance of 100% and 10% respectively.



**Figure 133. Migration Time Drift**

As the migration time drift is reduced, the acceptable deviation from the ladder marker migration time is reduced, causing the analysis to reject nearby peaks preceding the true marker.

The migration time drift is specified on the [Advanced Tab](#) of the [Assay Analysis Window](#) (see [page 196](#)).

## Minimum Peak Height

The Minimum Peak Height value determines the height limit below which a peak will not be detected. For each peak, the difference between the peak start time and the peak apex must be greater than the **Minimum Peak Height** value.

The Minimum Peak Height is specified on the [Peak Find Tab](#) of the [Assay Analysis Window](#).

## Minimum Peak Width

The **Min Peak Width** value determines the width (in seconds) under which a peak will not be detected. For each peak, the difference between the peak start time and the peak end time must be greater than the **Minimum Peak Width** value.

The Minimum Peak Width is specified on the [Peak Find Tab](#) of the [Assay Analysis Window](#).

## Molarity

$$\text{Molarity} = (\text{Concentration} * 10^6) / (660 * \text{Size}) [\text{nmol/l}]$$

where molarity is measured in nanomoles per liter (nmol/l),

Concentration is measured in nanograms per microliter (ng/μL),

Size is measured in base pairs (bp), and

$660 * [\text{g}/(\text{mol} * \text{bp})]$  is the molecular weight of a single base pair

## Molecular Separation Techniques

Processes such as gel electrophoresis, liquid chromatography, and capillary electrophoresis, which can separate biomolecular organic substances from other compounds.

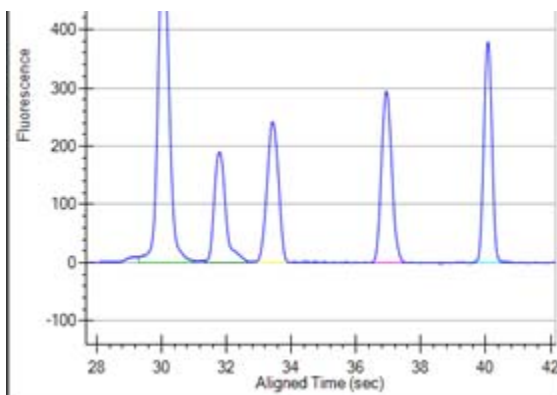
## Optical Calibration

The LabChip GX and GX Touch instruments read fluorescence of a laser illuminated dye attached to compounds present in a sample. The absolute value of this fluorescence has little meaning as all computed quantizations, such as concentration, are derived from ratios of fluorescence to known standards found in the supplied ladder. Due to component variations in the optical subsystem, the same sample delivers different absolute fluorescence on different instruments, making it somewhat disconcerting to the user when comparing the e-grams of similar samples run on different instruments. In order to provide a more consistent absolute fluorescence for visual comparisons, an optical calibration process is included in the LabChip GX and GX Touch software.

The Optical Calibration uses a calibrated test chip (Test Chip C), which has a stable, dry fluorescent material embedded in the channel. Test Chip C is provided with all new instruments. Test Chip C is factory-calibrated with a reference contrast value written in the chip RF tag. Each instrument uses this test chip to determine an optical gain correction factor, which will scale its optical response to a common standard.

## Peak Baseline

A local peak baseline is calculated for each peak. For isolated peaks, the local peak baseline is a straight line connecting the start point with the end point. For peaks that are very close together, an average baseline is used when the value between the peaks does not peak to the actual baseline. The peak baseline for each peak in [Figure 134](#) is shown in a different color.



**Figure 134. Peak Baselines**

The peak baseline algorithm starts at the earliest peak and checks whether the end point is within a certain distance from the start of the next peak. When a cluster of peaks is detected, the peak baseline is the line joining the first peak's start to the last peak's end. The start and end points of adjacent peaks in the cluster are averaged to the same point so that no gaps exist between peaks.

The peak baseline [Start Point](#) and [End Point](#) can be moved in the [Overlay Electropherograms Tab](#) if **Show Peak Baselines** is selected in the [Graph View Properties](#).

## Peak Height

The value at the apex of the peak minus the local baseline start value.

## Peak Identification

From the smoothed data, peaks are identified using a hill-climbing algorithm running along the smoothed data and its first derivative.

The peak baseline is drawn across the peak bottom by taking local averages just outside the peak start and end points and connecting the two points. The peak height, measured from the apex down to the peak baseline, must exceed the minimum peak height specified in the [Assay Analysis Window](#) for the bump to be identified as a peak. For details, see [“Understanding Peak Finding” on page 101](#).

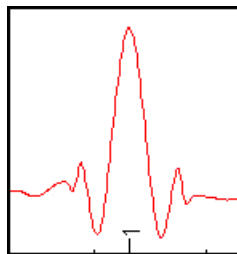
The peak start, end, and baseline can be viewed in the [Graph View](#) by selecting the **Show Peak Baselines** option in the [Graph View Properties](#). The area of each peak is determined by trapezoidal integration of the peak signal between peak boundaries and above the peak baseline.

## Point-to-Point Fit

This curve fit is composed of line segments between each pair of data points that are used to interpolate data between the points.

## Polynomial Filter

The first step the software takes in analyzing the raw data is to apply [Data Filtering](#). Data filtering is performed by means of a polynomial “filter” that is applied to the raw data. The figure below approximates the shape of the filter and shows what peaks may resemble if the filter application is too strong.



## Polynomial Order

This setting on the [Peak Find Tab](#) determines the order of the polynomial filter used to convolve with the data. A polynomial filter is used to filter the data to increase the signal-to-noise ratio and calculate filter slope information for peak detection. The default setting is 6 (for 6th order). A setting of 4 produces a straighter baseline, preventing quick changes in the signal.

## Protein Assay Analysis

Protein assays utilize a chemistry that generates an extra set of peaks (system peaks) just above the lower marker that should not be included in the analysis. These system peaks must be identified and excluded from further quantitative analysis. For ladder analysis, peaks occurring after the lower marker less than the “Ladder Ratio” analysis setting, are tagged system peaks to avoid confusion with legitimate ladder peaks.

Protein samples contain a single lower marker. Alignment to a single marker does not provide enough constraints to align large proteins, so data is aligned to two ladders, one sipped just before the sample wells and another sipped just after the sample wells. The second ladder is called the bracket ladder. Samples are scaled so the sample's lower marker is nearly aligned with both ladder lower markers. The scaling is weighted by the proximity in sip time to each ladder. The sample sipped closest to the primary ladder is scaled to align more closely to the primary ladder and the sample sipped just before the bracket ladder is scaled to align most closely to the bracket ladder. Then each sample is shifted in time so the sample's lower marker aligns exactly with the primary ladder lower marker.

After alignment, the size of the protein producing each peak is calculated from the aligned peak time using a  $\log(\text{size})$  versus  $1/(\text{Time}-T_0)$  fit to the primary ladder peaks of known size and measured migration time.  $T_0$  is determined empirically as the time offset which delivers the best straight line fit to the ladder data. The value of  $T_0$  used for the fit can be viewed in the [Well Table View](#).

This fit to the ladder peak data can be viewed by selecting Standard Curve from the Analysis menu. After sample peaks have been sized, the system peaks are identified and excluded based on their size. Any peak of size greater than the lower marker but less than the Min. Sample Size specified in the [Assay Analysis Window](#) is labeled a system peak and excluded from concentration and purity analysis.

To determine sample peak concentration, the peak areas are first corrected to compensate for the fact that the fluorescence intensities are sampled at a constant time interval so slower moving proteins spend more time under the detector than fast moving proteins. The peak concentration is then calculated using the ladder peak areas and concentration for the ladder supplied in the [Assay Analysis Window](#). The concentration is adjusted for the differing peak ratios of sample and ladder.



To quantitize the sample peak concentration based on a different standard, the new standard must be added into each sample well at a known concentration. The analysis settings provide a Sample Peak Quantitation option using the peak area and concentration of the User Standard instead of the ladder concentrations.

## Protein Charge Variant Assay

Capillary Zone Electrophoresis (CZE) is an electrophoretic separation technique used to evaluate the charge heterogeneity of proteins in a sample. The LabChip GXII or GXII Touch performs a microfluidic adaptation of this technique for the Protein Charge Variant Assay. For Protein Charge Variant assays, the separation channel does not contain a polymer gel because the analytes are not separated by size.

Protein Charge Variant assays separate analytes based on differences in their net charge: molecules with a higher net charge migrate faster than those with a lower net charge. The relative difference in migration speeds (and therefore the resolution) between molecules of different pI is higher when the pH of the running buffer is closer to the pIs of the molecules.

For the HT Protein Charge Variant assay, the pH of the running buffer is less than the pIs of the variants, so molecules have a net positive charge. Variants that are more basic (have a higher pI) than others appear earlier in electropherogram. The software can be used to track expected variants, based on migration time, and to determine the relative amount of each variant, based on peak area.

Protein Charge Variant assays do not use ladders or markers to align the data. The size of a peak is not calculated, only the % Rel amount of each peak. Protein Charge Variant assays and data files do not include any ladder or marker parameters or options.

## RNA Assay Analysis

RNA analysis initially progresses similarly to DNA analysis except that the baseline for RNA peaks is calculated using a spline-fit, much like the baseline used for the Baseline Subtraction option. However, this computed fit is not subtracted from the data; instead it is used to determine the peak height and to limit the peak extends.

The RNA ladder is similar to the DNA ladder but does not contain an upper marker. RNA sample data is aligned with the lower marker and then the sample peaks are sized using point-to-point interpolation between ladder peaks. The most prominent peaks found within predefined size windows are identified as ribosomal rRNA genes 5S, 18S and 28S (for eukaryote RNA), 16S and 23S (for prokaryote RNA).

For the purpose of quantizing the full RNA content in the sample, a straight-line baseline is drawn across the bottom of the sample by finding the local averages about its endpoint. The area baseline endpoints can be moved on the [Graph View](#) after the “Show Peak Baselines” option is selected in the [Graph View Properties](#). Trapezoidal integration from the straight-line baseline to the data signal is used to calculate the total RNA area. Integration is performed from the end of the lower marker to the endpoint of the area baseline. The range from the end of the 5S to the start of the 18S peak is termed the Fast Area. This area is calculated in the same way as the total RNA area.

For the purpose of quantizing the rRNA peaks, a two-point baseline is drawn across the bottom of each peak identified as rRNA and the area is computed. These areas and rRNA peak heights and some relevant ratios are available for display in the [Well Table View](#). A combination of the quantities is used to assess the quality of the RNA sample.

## RNA Degrade Factor

This value quantifies the degradation of the ribosomal peaks, which typically leads to an increase in the fast area region between the 5S and the 16S (prokaryote) or 18S (eukaryote) ribosomal peaks. The quantity is computed as follows:

For prokaryote:

$$200 * \text{Fast Area} / (\text{Fast Area Time Span}) / (\text{Height of 16S} + \text{Height of 23S})$$

For eukaryote:

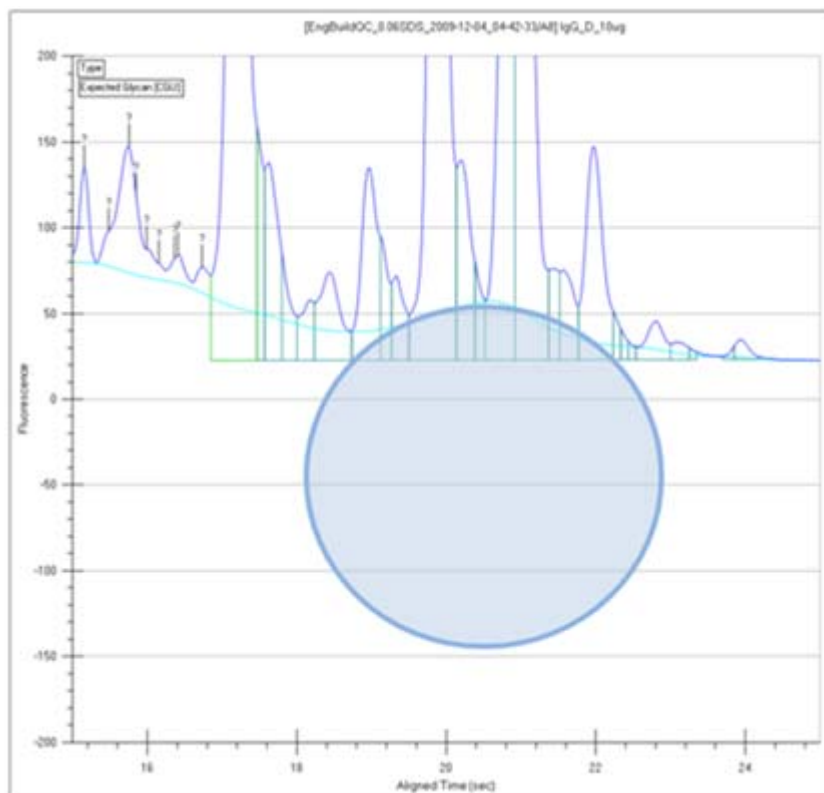
$$200 * \text{Fast Area} / (\text{Fast Area Time Span}) / (\text{Height of 18S} + \text{Height of 28S})$$

As the sample RNA degradation increases, this factor will increase. A value below 10 is obtained with high quality RNA but the user should determine their own threshold for discriminating between good and bad RNA. This quantity can be viewed and reported in the [Well Table View](#).

## Rolling Ball Baseline Curve Example

The figures below show the effect of changing the size of the ball when using the Rolling Ball Baseline Curve.

Figure 135 shows a baseline (the light blue line) generated by a ball with settings of Time Diameter = 5 sec and Signal Diameter = 100 RFU.



**Figure 135. Rolling Ball - 5 Sec x 200 RFU**

Figure 136 on page 277 shows a baseline (the light blue line) generated by a ball with settings of Time Diameter = 10 sec and Signal Diameter = 200 RFU. The baseline curve does not follow the signal as closely because the ball is larger. Increasing the ball size generates a smoother baseline.

Either ball dimension can be used to increase the smoothness of the curve, but increasing the Time Diameter increases the computation time required to compute the curve, while increasing the RFU Diameter does not.

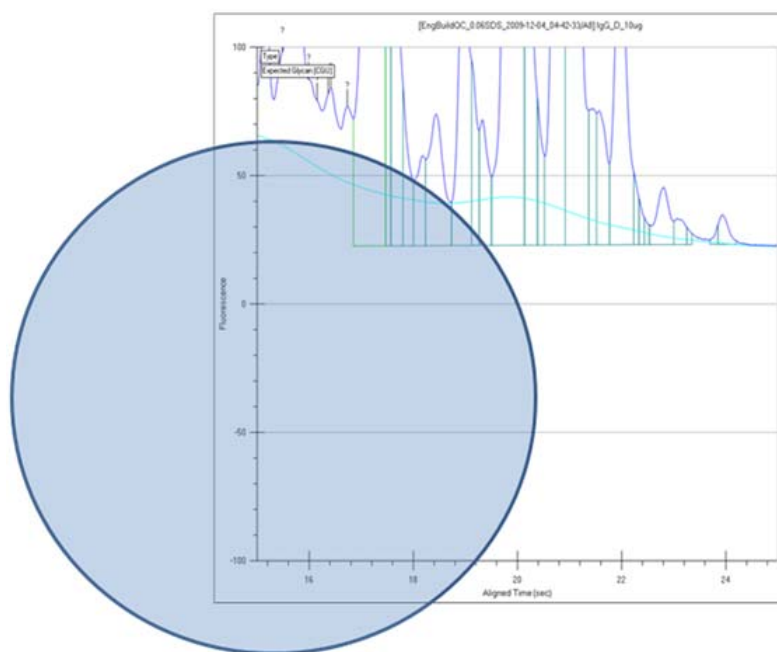


Figure 136. Rolling Ball - 10 Sec x 200 RFU

## Slope Threshold

The **Slope Threshold** setting represents the amount of change in response over time required to differentiate between a peak and baseline noise. Changing this setting may cause certain peaks that were previously detected to be ignored or to interpret noise as peaks. For details, see [“Understanding Peak Finding” on page 101](#).

The **Slope Threshold** setting can be changed in the [Peak Find Tab](#).

## Smear

Specifies a size range in which to detect the region of the fluorescence signal instead of specifying a specific size for a peak. Use a smear to detect a broad mix of molecules of similar but distinct sizes in a sample. The concentration or fractional presence within a specified range of molecule sizes is measured. Specify the Start Size and End Size of a smear in the [Assay Analysis Window](#) on the [Smear Analysis Tab](#).

The Smear Properties can be viewed in table form in the [Well Table View](#). To view the Smear Properties in the table, add the desired property to the [Well Table View](#). The properties extracted from the smear match those of a peak, having start and end points, area, concentration, etc. % Purity is the ratio of smear concentration to total sample peak concentration, exclusive of markers, system peaks, and excluded peaks. Excluded peaks are not excluded from analysis calculations such as concentration or area within the smear region, so the limits must avoid excluded peaks. An additional Peak Count property is available for smears. Peak Count is the number of non-excluded sample peaks in the region, where the center of the peak is inside the smear limits.

In the [Graph View](#), the smear regions display with the start and end points drawn at the base of the smear in the chosen color and the trace highlighted with the smear color. Override the smear baseline by dragging with the mouse in the Graph view. The baseline start and end points can be adjusted in the graph to change the height of the baseline or the size range of the smear. Smears can overlap to include the same region in multiple smears.

In the [Gel View](#), the smear region is shown on the gel as a colorized region. The color is a transparent version of the color selected for the region, so that the fluorescence intensity shows through.

## Standard Curve

The Standard Curve window shows the Standard curve used for the selected plate data. Each window displays the following menus:

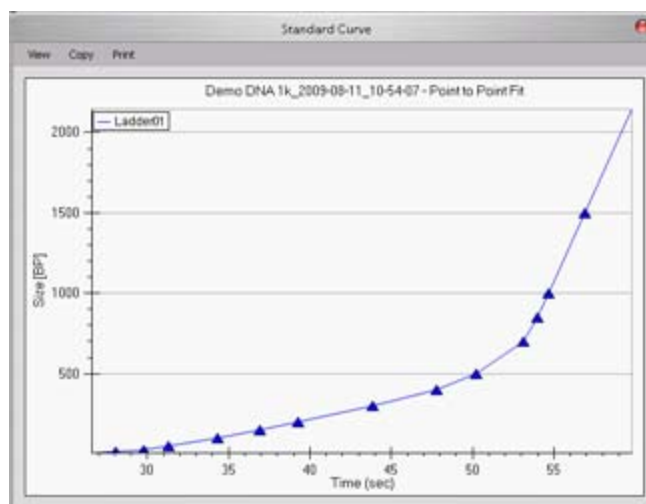
**View menu** - Select or clear the ladders to display in the window.

**Copy menu** - Copies the current view to the clipboard.

**Print menu** - Displays the Print Preview or prints the Standard Curve.

### DNA Assays

When you choose **Standard Curve** from the **Analysis** menu for a DNA assay, a window similar to [Figure 137](#) opens. The standard curve is drawn from the values obtained for the DNA ladder. It is a plot of the size of the ladder peaks vs. time with a point-to-point fit. For each sample peak, the apex is interpolated from the Standard Curve to determine the peak size in bp (base pairs).

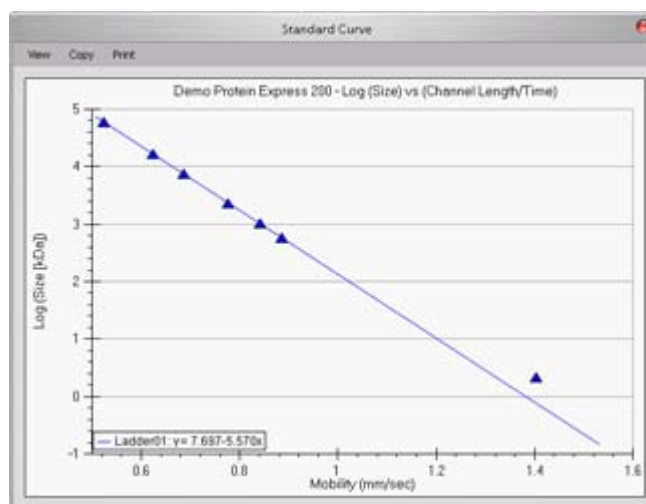


**Figure 137. DNA Assay Standard Curve**

For more information about the use of the standard curve during analysis, see [“How the Software Analyzes DNA Data” on page 16](#).

### Protein Assays

When you choose **Standard Curve** from the **Analysis** menu for a Protein assay, a window similar to [Figure 138](#) opens. The standard curve is drawn from the values obtained for the protein ladder. It is a plot of the size of the ladder peaks vs. time with a Log fit. For each sample peak, the apex is interpolated from the Standard Curve to determine the peak size in kDa (kiloDaltons).

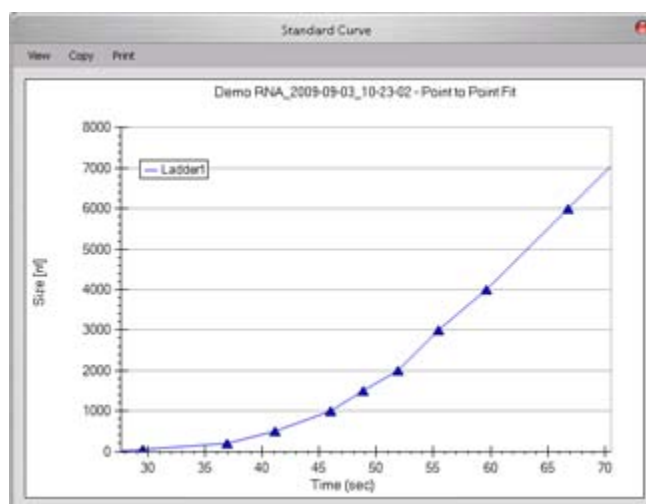


**Figure 138. Protein Assay Standard Curve**

For more information about the use of the standard curve during analysis, see [“How the Software Analyzes Protein Data” on page 18.](#)

### RNA Assays

When you choose **Standard Curve** from the **Analysis** menu for an RNA assay, a window similar to [Figure 139](#) opens. The standard curve is drawn from the values obtained for the RNA ladder. It is a plot of the size of the ladder peaks vs. time with a point-to-point fit. For each sample peak, the apex is interpolated from the Standard Curve to determine the peak size in nt.



**Figure 139. RNA Assay Standard Curve**

For more information about the use of the standard curve during analysis, see [“How the Software Analyzes RNA Data” on page 22.](#)



## gDNA Assays

When you choose **Standard Curve** from the **Analysis** menu for a gDNA assay, a window similar to [Figure 140](#) opens. The standard curve is drawn from the values obtained for the gDNA ladder. It is a plot of the size of the ladder peaks vs. time with a point-to-point fit. For each sample peak, the apex is interpolated from the Standard Curve to determine the peak size in kb (kilo base pairs).

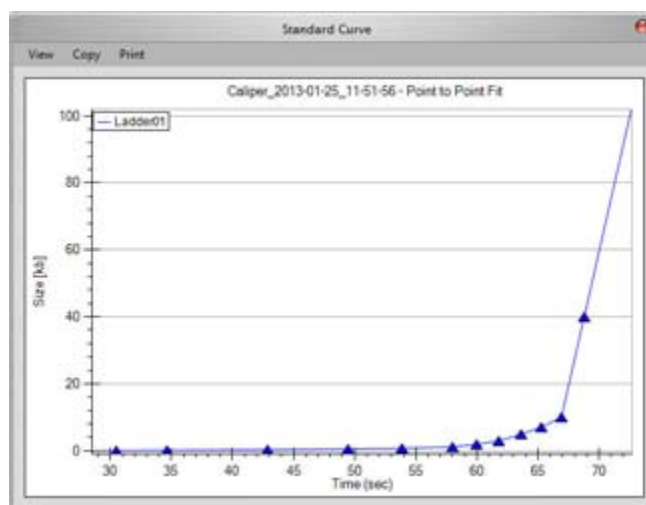


Figure 140. gDNA Assay Standard Curve

## Start Point

The peak find algorithm analyzes the data from time zero looking for a slope greater than the **Slope Threshold**. The point where the slope is greater than the slope threshold specified in the [Peak Find Tab](#) is marked as the start point of a peak.

## Start Time

This setting determines the time after the start of a run when peaks will be detected. Any peaks appearing before this time are ignored.

## Titer

Allows the use of a standard with a known concentration to be used as a calibration standard instead of using a ladder. The well location and known concentrations of the standard are specified in the [Assay Analysis Window](#) on the [Titer Tab](#).

The Titer Standard Curve used for calibration is normalized against the lower marker (protein and RNA) or upper marker (DNA) to adjust for slight variations in each well. A normalization standard can be added to each well to be used only for normalization. (Normalization standards must be the same concentration in each well.) Specify the normalization standard in the [Assay Analysis Window](#) on the [Advanced Tab](#). Titters can also be imported from another plate if the Normalization Standard is the same. If Sample Peaks is selected, the Sample Peaks must be the same size.

The Concentration to Favor in Fit adjustment on the Titer tab enables you to choose whether to weight either the higher or lower concentrations more heavily when calculating the Titer Standard Curve.

## Tool Tip

A small box containing text that describes the item indicated by the mouse pointer. To view a Tool Tip, position the cursor over an item on the window. Leave the cursor stationary for a moment and a **Tool Tip** (if one exists for that item) displays.

## Upper Marker

An internal standard that is added to a DNA sample in a well to assist in determining size and concentration of the sample. The marker is the same as the last peak in the DNA ladder.

## Workspace

Use a workspace file to view the plate data from a run. Multiple plate data files can be opened in the same workspace to enable comparison between data from different plates or different runs.

Each workspace can contain multiple [Collections](#) for viewing the same data in different layouts.

A Workspace file includes:

- the links to the plate data files in each collection
- the selected wells and arrangement of the wells in the views
- the layout selected for each collection

## Zero Baseline

Selecting this setting in the [Peak Find Tab](#) offsets the graphs shown for the individual wells but does not affect analysis. The mean of 100 points before the baseline time (derived when calculating well noise) is used as the zero baseline value.

All electropherograms produced with the instrument show some amount of background fluorescence. By default, the LabChip GX Reviewer software enables the Zero Baseline function. To change the Baseline Algorithm, select None, Zero Baseline, or Baseline Subtraction on the [Peak Find Tab](#).

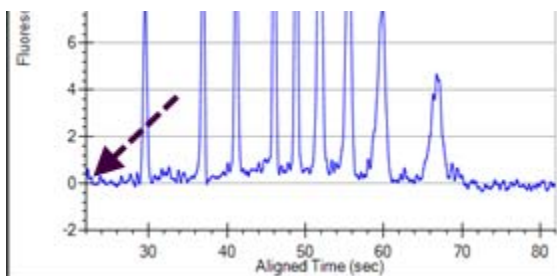


Figure 141. Zero Baseline On

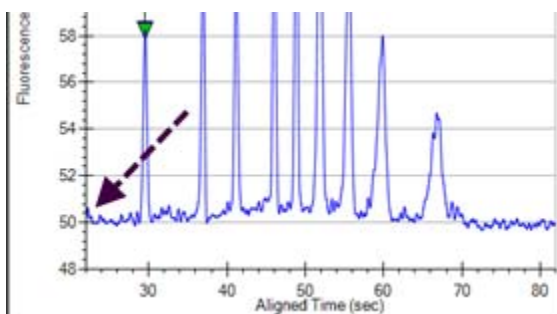


Figure 142. Zero Baseline Off

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