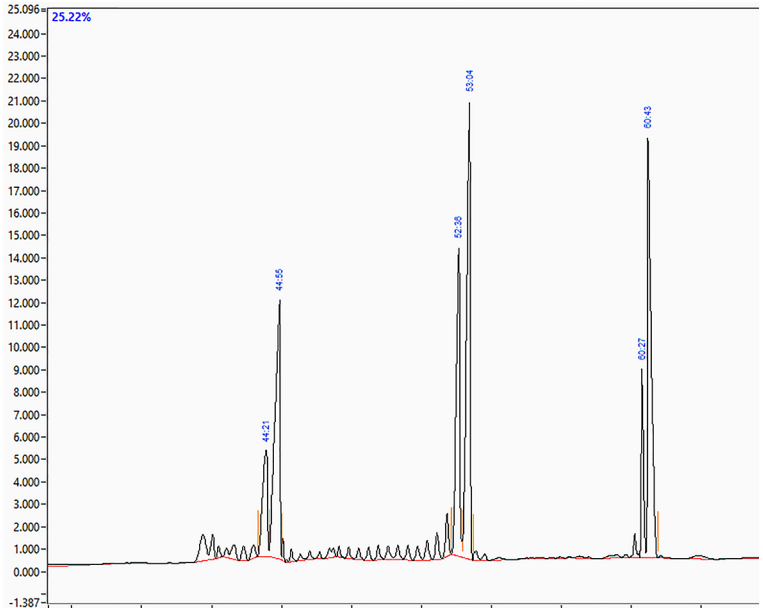
Agilent

Oligo Pro II Data Analysis Software

User Manual



Notices

Document Information

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In This Guide

Agilent has prepared this manual as a technical reference for the Oligo Pro II data analysis software for use with the Oligo Pro II parallel capillary electrophoresis system.

This document is intended for use by technical personnel that are proficient with analytical instrumentation operation. A certain level of training and expertise is assumed and fundamentals are not addressed herein. Information is presented in a section-by-section format using screen captures and written descriptions. If questions remain after reviewing a given topic, please contact your corresponding Agilent Sales/Service Representative.

1 Oligo Pro II Data Analysis System Overview

This chapter gives an overview of the Oligo Pro II data analysis software.

2 Oligo Pro II System Requirements and Installation

This chapter provides information on the requirements and installation instructions for the Oligo Pro II data analysis software.

3 Oligo Pro II Data Analysis – Main Screen

This chapter provides an overview of the Oligo Pro II data analysis software main screen.

4 Oligo Pro II Data Analysis Software – Settings Menu

This chapter provides an overview of the settings menu, which is available on the main screen of the Oligo Pro II data analysis software.

5 Oligo PRO II Data Analysis Software – Overlay Samples

This chapter provides an overview of the possible ways to compare samples in the Oligo PRO II data analysis software.

6 Oligo Pro II Data Analysis – View Capillary Positions

This chapter briefly covers the tools and functions of the View Capillary Positions window.

Content

1 Oligo Pro II Data Analysis System Overview

This chapter gives an overview of the Oligo Pro II data analysis software.

About the System

Oligo Pro II System

The Oligo Pro II system is an UV absorbance-based DNA/RNA oligomer analysis system for determining the purity of nucleic acid oligomers.

Dedicated Oligo Pro II instrument software is provided for system operation and data collection, employing a simple user interface for programming experiments from one to as many as three 96-well sample plates.

Oligo Pro II Data Analysis Software

Agilent's Oligo Pro II data analysis software is designed for analyzing the raw data from the Oligo Pro II instrument and reporting the purity of oligomers. The Oligo Pro II data analysis software performs the following general functions:

- Reads the raw data files generated from the Oligo Pro II instrument operational software.
- Provides quantitative measurements of DNA/RNA oligomer purity present in a sample.
- Exports purity data as well as raw Electropherogram trace data (time vs. absorbance) and digital Electropherogram traces in .jpg, .bmp or .png image formats.
- Generates PDF format sample reports containing user specified information.

This manual serves as a guide to the Oligo Pro II data analysis software and will assist the user in taking advantage of the many benefits of the Oligo Pro II system.

2 Oligo Pro II System Requirements and Installation

This chapter provides information on the requirements and installation instructions for the Oligo Pro II data analysis software.

System Requirements

General Software Requirements

Report Review

A PDF viewer is required to read Adobe PDF formatted reports.

Install the most recent version of Adobe Reader. The software is available free of charge for download at www.adobe.com.

Data File Export

- The Oligo Pro II data analysis software exports data in a generic comma-separated values (.csv) file format, which can be read by most spreadsheet and database management programs. Install a spreadsheet program (for example, Excel, OpenOffice) to open and read exported .csv files.
- Electropherogram images are exported in a .jpg, .bmp, or .png image format. A suitable program for viewing these file formats should be installed.

Operating System

The Oligo Pro II data analysis software must be installed on a computer running a Windows operating system to function properly.

Table 1 Supported operating systems

Operating System	Details
Windows	Windows 10, 32-bit or 64-bit

PC Recommendation

The table provides the recommended hardware configuration for the Oligo Pro II data analysis software.

Table 2 Recommended hardware configuration

Item	Details
Processor speed (CPU)	Intel Core 2, or faster
Physical memory (RAM)	4 GB
Hard disk	500 GB (for accommodation of raw data files)
Graphic resolution	1280 x 800 minimum screen resolution 1280 x 1024 recommended

Oligo Pro II Data Analysis Software Installation Instructions

To Install the Software

1 Download the appropriate installer from the Agilent website.

2 Run the installer and follow the instructions and prompts provided by the installation wizard.

3 Oligo Pro II Data Analysis – Main Screen

This chapter provides an overview of the Oligo Pro II data analysis software main screen.

Main Screen (No Data File Open)

The functions and menu items available from the main screen of the Oligo Pro II data analysis software prior to opening a *.raw data file are summarized in **Table 3**.

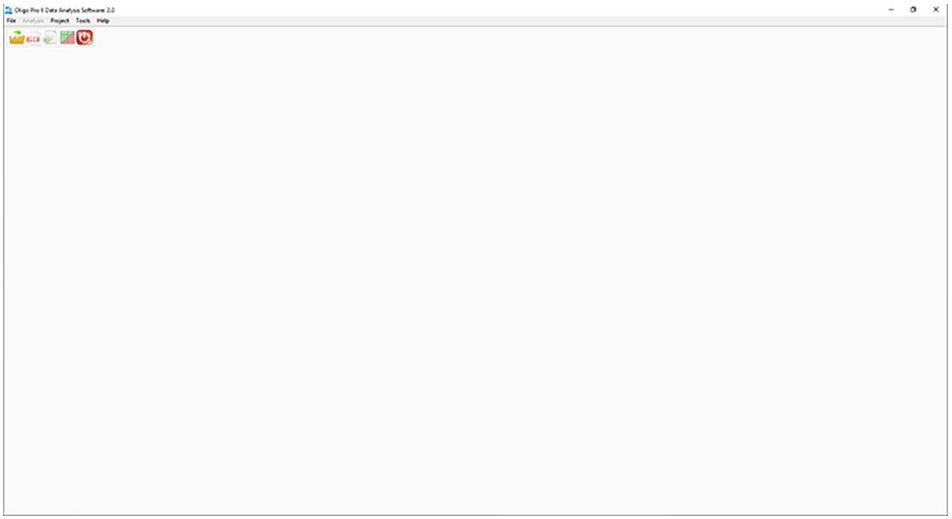


Figure 1 Main Menu screen of Oligo Pro II data analysis software (no data file open)

Table 3 Main menu screen menu items (active with no data file open)

Menu Option	Description
File	
Open File	Opens a file browser dialog for locating and opening a raw data file (*.raw extension) generated by the Oligo Pro II instrument control software, for subsequent data analysis.
Recent Files	Displays up to the last 10 data file locations opened in the Oligo Pro II data analysis software.
Exit	Closes the Oligo Pro II data analysis software. When closing, the data file, all settings and operations are automatically saved.

Table 3 Main menu screen menu items (active with no data file open)

Menu Option	Description
Project	
Load Project	Opens a file browser dialog for locating and opening a Project data file (*.proj extension) generated by the Oligo Pro II data analysis software. For further information on creation of project data files, see **Chapter 5**, "Oligo PRO II Data Analysis Software – Overlay Samples".
New Project	Allows you to open the Project screen and create a project by selecting different *.raw data files.
Tools	
Options	Allows you to set default file path, language, capillary data format (row or column), and default peak analysis parameters.
Help	
User Manual	Displays User manuals associated with the Oligo Pro II data analysis software.
About	Displays software information, version information, copyright information and Agilent technical support contact information.

Opening a Data File in the Oligo Pro II Data Analysis Software

To Open a Data File

1 From the main menu, select **File** > **Open File** (alternatively, select from the toolbar).

A file browser opens (**Figure 2**).

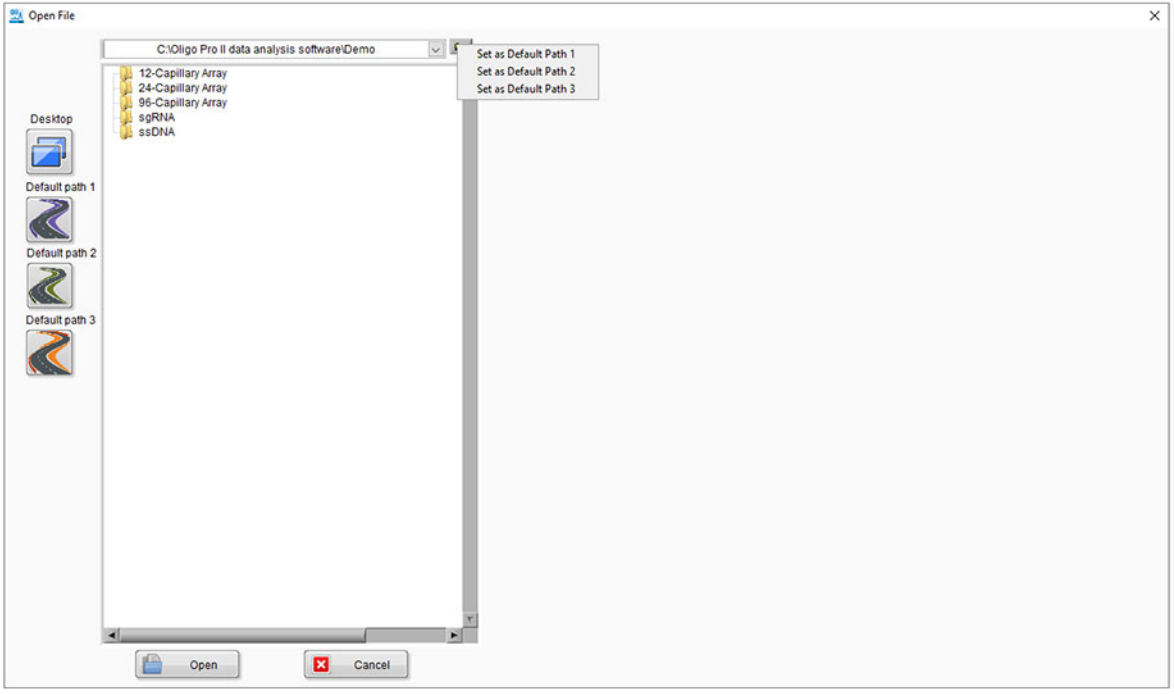


Figure 2 Main Menu screen of Oligo Pro II data analysis software (data file open)

2 Navigate to your raw data file (*.raw extension) generated by the Oligo Pro II instrument control software.

- To set a file location as default location: In the file browser, right-click either the folder or select the arrow , and from the menu, select **Set as Default Path**.
- To go to a default location: In the file browser, select one of the four default paths on the left side.

3 Select the .raw file (**Figure 3**).

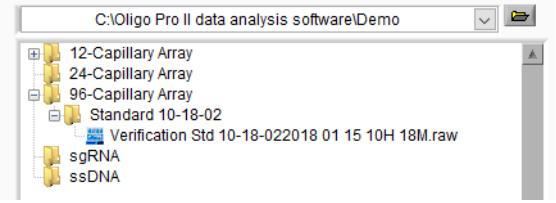


Figure 3 Data selection

Main Screen (Data File Open)

Once a data file is opened in the Oligo Pro II data analysis software, several additional functions are enabled as summarized in **Table 4**. The opened data is displayed in the main screen as shown in **Figure 4**.

Table 4 Additional Main Menu screen menu items (active only with data file open)

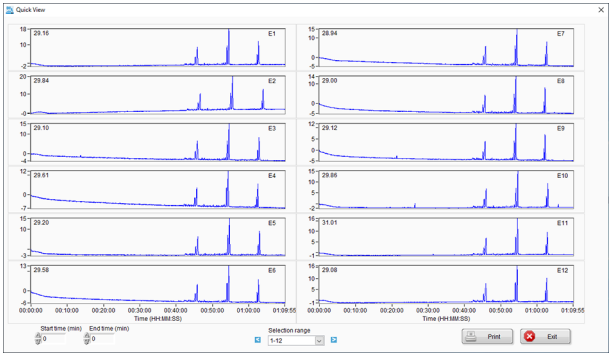
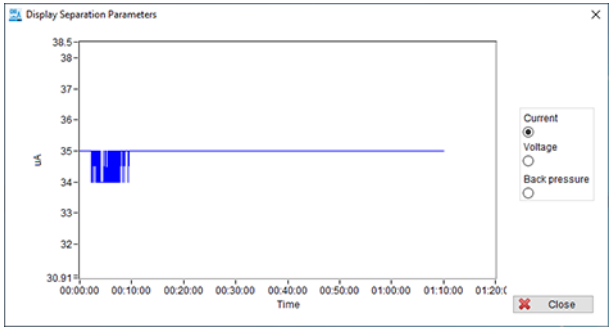
Menu Option	Description
Icons	
Generate PDF	Opens a menu for configuring and generating a .pdf report, containing user specified information (electropherograms, gel images, peak information, etc.). For more information, see **Chapter 8**, "Generating Reports from the Oligo Pro II Data Analysis Software".
Export Files	Opens a menu for configuring and exporting User specified data to a user specified folder. Types of data include gel images, electropherograms, peak tables, etc. For more information, see **Chapter 7**, "Exporting Data from the Oligo Pro II Data Analysis Software".
Purity Table	Allows you to generate a Purity Analysis table.
Analysis	
Quick View	Displays the **Quick View** window, which shows non-normalized electropherograms for all 12 capillaries (or windows of 12-capillaries each for a 96-capillary array format) enabling quick review of the data. 
View Capillary Positions	Opens the **View Capillary Positions** screen, which allows you to view and modify the alignment of the detector signal with the capillary positions. For more information, see **Chapter 6**, "Oligo Pro II Data Analysis – View Capillary Positions".

Table 4 Additional Main Menu screen menu items (active only with data file open)

Menu Option	Description
Display Separation Parameters	Opens the **Display Separation Parameters** window, which allows you to view the current, voltage, and back pressure that occurred during the separation. 
Project	
Create Project	Allows you to create a new project for overlaying data files (it uses the existing file for project creation).
Help	
Zip Open Data File	Allows you to ZIP currently opened data file. This is used primarily in preparing data files to send to Agilent in cases where troubleshooting is required.

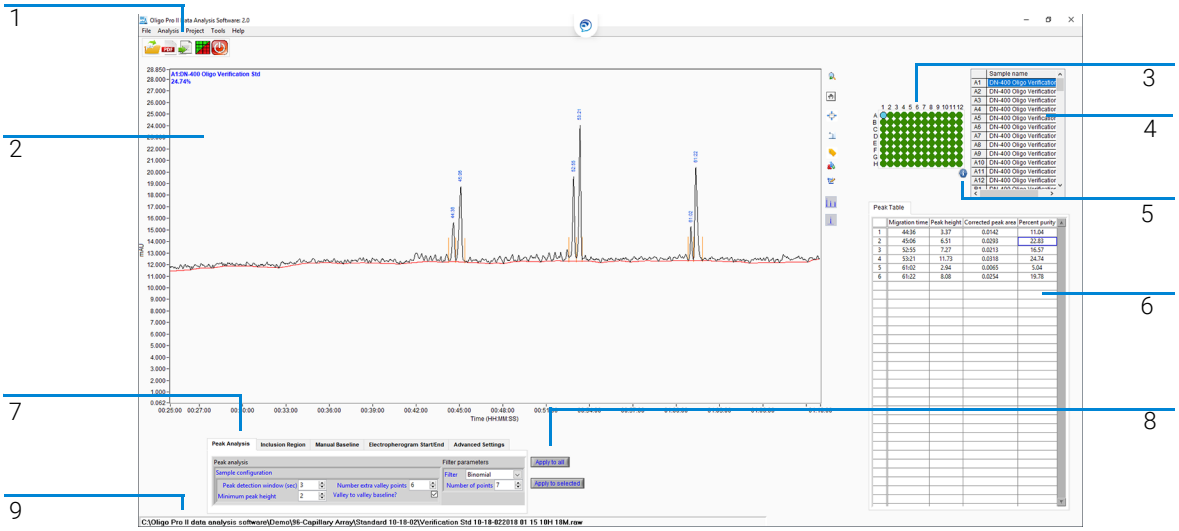


Figure 4 Main menu screen of Oligo Pro II data analysis software (96-capillary data file open)

The primary accessible functions from the main screen are shown in **Figure 4**, and are summarized in the legend table:

1	**Main screen toolbar**	
2	**Electropherogram trace**	An Electropherogram trace of the currently selected well. The well position and sample name (if imported) is displayed in the upper left corner of the trace. Use the Electropherogram trace toolbar and context menu to process or annotate the data (**Table 5** and **Table 6**).
3	**Plate map**	Shows the currently selected well highlighted in green (A1 is the default location on opening the file). Click on the appropriate well by using the keyboard arrows. You can select any well of the plate for individual viewing.
4	**Sample name table**	Displays the sample names as entered into the instrument software, or imported after post-run. Enables you to navigate to the samples (**Figure 9**). A brief summary is given in section **"Sample Name Table"** on page 27.
5	**Info**	Click to access experimental information regarding the method used to collect the data file (**Figure 5**).
6	**Peak table**	Displays information about the selected and integrated sample peaks (see also **Figure 8**). For more information, refer to section **"Peak Table"** on page 26.
7	**Settings tabs**	Configuration settings, for which most settings can be individually adjusted for each sample as desired. For more detailed information, refer to **Chapter 4**, "Oligo Pro II Data Analysis Software – Settings Menu".
8	**Apply settings**	Applies configuration settings individually to a selected sample, or to all samples.
9	**Filename**	Upon opening a data file, the currently selected filename/directory is displayed in the lower left toolbar.

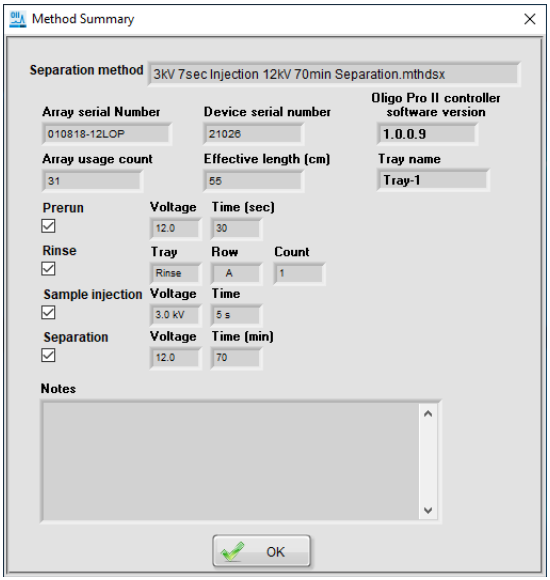


Figure 5 Experimental information (method summary) window

Electropherogram Trace Toolbar Menu

The options available in the Electropherogram trace toolbar are summarized in **Table 5**.

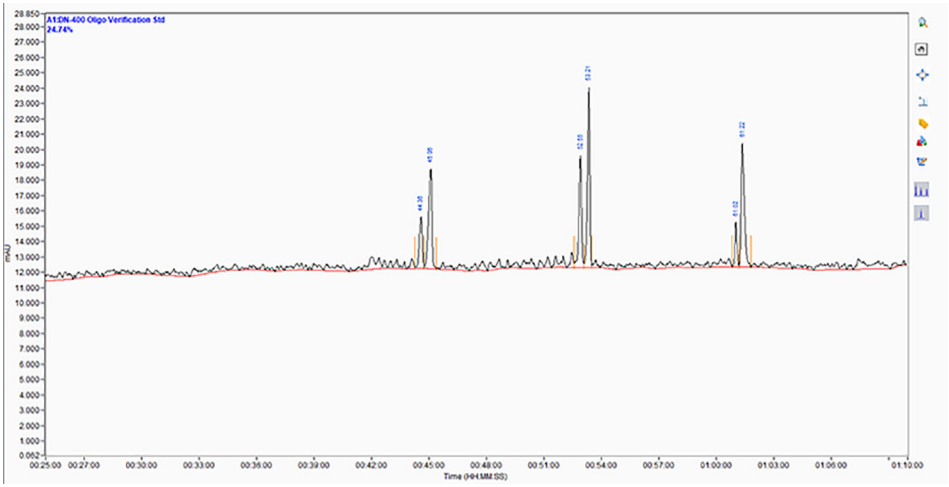


Figure 6 Electropherogram trace and toolbar menu

Table 5 **Electropherogram trace toolbar functions**

Toolbar Option	Description
Zoom	Enables zooming in the x- and y-axis of the Electropherogram trace. To zoom-in: Place the mouse over the trace, click and drag it outward to expand a box area to define the zoom region. Release the mouse button to apply. The zoomed image can be copied to the clipboard. The zoom region will be preserved when viewing other samples in the Plate map. To undo the zoom, use the **AutoFit** function.
Drag	Enables panning of the image. Move the image around with the mouse cursor, while holding the left mouse key.
AutoFit	To autoscale the Electropherogram trace x-/y-axis display.
Copy	Copies an image of the current view of the Electropherogram trace to the clipboard, for pasting in another program such as Microsoft PowerPoint. Any zoom, annotation, baseline and/or peak start/end point displayed will be copied in the image. The well ID and sample name will be copied in the top left of the trace, and the x-/y-axis will correspond to the currently selected view in the copied image

Table 5 Electropherogram trace toolbar functions

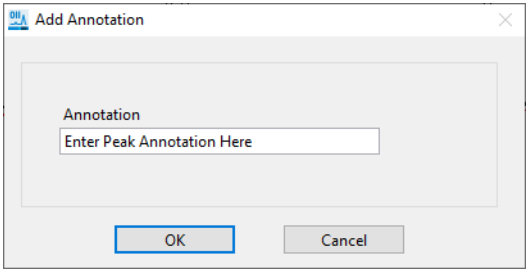
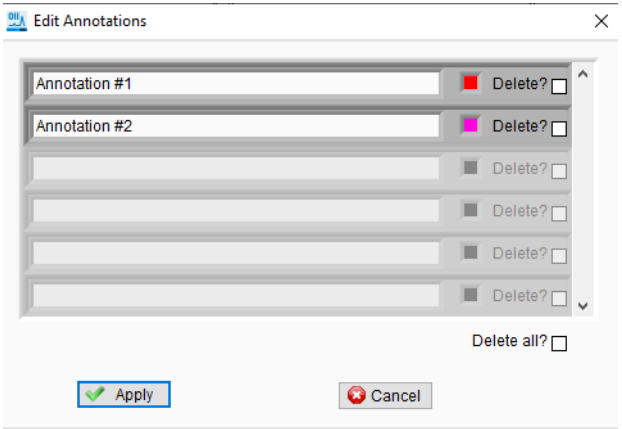
Toolbar Option	Description
Units	Displays a menu for changing the peak annotation of the Electropherogram trace. Only integrated peaks are annotated. Units for peak annotation: • None • Peak ID (labels in order as 1, 2, etc.) • Migration Time (min:sec): Raw migration time • Peak Height (in mAUs) • Corrected Peak Area (Peak Area/Migration Time)
Create Annotation	To create customized annotation in the Electropherogram trace display. In the **Add Annotation** dialog, the user can type desired annotation into the field. Click **OK** and the annotation will be displayed in the Electropherogram trace.  To move the annotation to the desired location on the trace: Click the annotation and drag it to the desired position. An arrow will appear at the opposite end of the annotation upon dragging. The arrow and/or annotation can be repositioned by selecting, holding and dragging the mouse. Multiple annotations can be created by repeatedly selecting **Create Annotation**. Any created annotations will be copied to the clipboard with the **Copy** function.

Table 5 Electropherogram trace toolbar functions

Toolbar Option	Description
Edit Annotations 	Opens the **Annotation Editor** window. Allows you to: • Edit the Annotation text by typing in the text field • Change the color of the annotation by selecting the annotation color • Delete one or all annotations by selecting **Delete** next to each annotation, or selecting **Delete All**.  Select **Apply** to confirm your settings.
Show/Hide Baseline 	Toggle to display and hide the baseline drawn for peak integration, shown as an orange line. Displaying the baseline helps if adjustments need to be made to the baseline to better define the actual peak area via the **Peak Width (sec)**, **Valley to Valley**, or **Manual Baseline Setpoints** tools. Note: It is highly recommended to enable the display of the baseline, to ensure the correct baseline is being drawn to the data.
Show Peak Start/End Edge 	Toggle to display or hide the start and end points used for peak integration, shown as vertical orange lines. Displaying the peak integration start/end points helps if adjustments need to be made to the peak integration to better define the actual peak area. The user can change the peak start/end points by adjusting the **Peak Width (sec)**, or by using the context menu tools in the Electropherogram trace, such as **Split Peak** or **Move Peak Start/End Points** (see Table 5). The user can change the baseline drawn (and subsequently the peak start/end points) via the **Peak Width (sec)**, **Valley to Valley**, or **Manual Baseline Setpoints** tools. Note: It is highly recommended to enable the display of the baseline, to ensure the correct integration is being drawn to each peak.

Electropherogram Trace Context Menu

The context menu of the Electropherogram trace, the y-axis, and the x-axis contains functions for adjusting peak assignment, peak integration, and scaling the x-axis (**Figure 7**). Functions are also provided for copying the trace and exporting the data, and are summarized in **Table 6**.

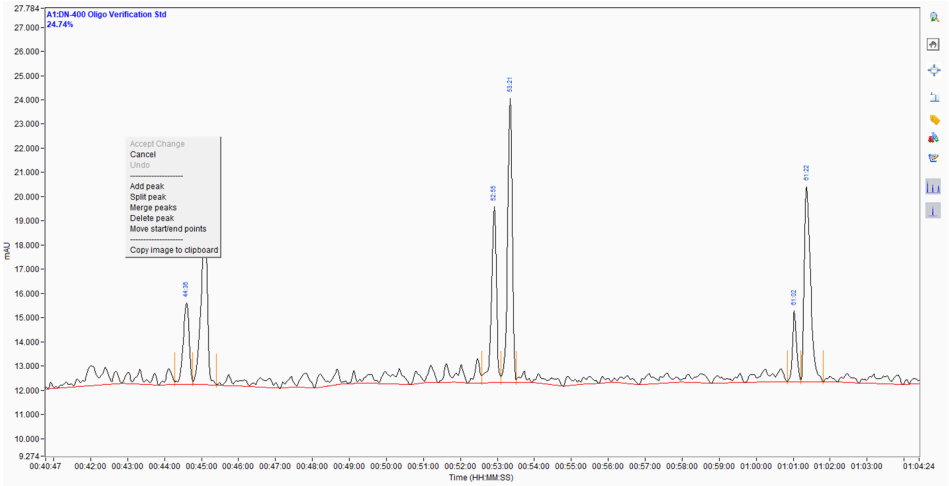


Figure 7 Main screen zoomed to the Electropherogram trace with context menu displayed

Table 6 Electropherogram trace context menu functions

Menu Option	Description
Accept Change	Accepts any manual modification to the performed peak integration (**Add Peak**, **Split Peak**, **Merge Peaks**, **Delete Peak**, **Move Peak Start/End Points**). After the manual modification has been made, select **Accept Change** to apply the changes to the trace.
Cancel	Cancels any manual modification to the peak integration (**Add Peak**, **Split Peak**, **Merge Peaks**, **Delete Peak**, **Move Peak Start/End Points**). Select **Cancel** to discard the changes applied to the trace.
Undo	To undo any manual modification applied to the peak integration (**Add Peak**, **Split Peak**, **Merge Peaks**, **Delete Peak**, **Move Peak Start/End Points**). Select **Undo** to revert back one step.

Table 6 Electropherogram trace context menu functions

Menu Option	Description
Add peak	To manually add a peak which has not been auto-integrated by the **Peak Analysis** settings, and to define the start and end point for integration. Zoom-in to the region where the peak is to be added. Right-click this region, and select **Add Peak**. Two red vertical cursors will appear; the left cursor defines the new peak start point and the right cursor the new peak end point. Drag each cursor to the desired position, then right-click, and select **Accept Change** to add the peak for integration.
Split peak	To manually split a peak which is currently integrated into two peaks, and to define where the split occurs. Zoom-in to the region where the peak is to be split. Right-click this region, and select **Split Peak**. A red vertical cursor will appear. Drag the cursor to the desired location, then right-click, and select **Accept Change** to split the peak into two peaks for integration.
Merge peaks	To merge any number of peaks and integrate as a single peak. Zoom-in to the region where the peak is to be split. Right-click this region, and select **Merge Peaks**. Two red vertical cursors will appear; the left cursor defines the left most peak to merge and right cursor defines the right most peak to merge. Drag the cursor within that peak's start/end point region to merge, then right click, and select **Accept Change** to merge the peaks into a single peak for integration.
Delete peak	To manually delete a peak which has been integrated. Zoom-in to the region where the peak is to be deleted. Right-click this region, and select **Delete Peak**. A red vertical cursor will appear. Drag the cursor to the desired peak location, then right-click, and select **Accept Change** to delete the peak from the integration.
Move peak start/end points	To change the currently positioned start/end integration points of a peak. Zoom-in to the region where the peak is located. Place the cursor between the start and end points of the integration. Right-click and select **Move Peak Start/End Points**. Two red vertical cursors will appear at the current start/end points. Drag the cursors to the desired locations, then right-click, and select **Accept Change** to apply the new start/end point positions to reintegrate the peak. Note: This function will not change the baseline; only the start and end points are affected. To change the baseline, the user must adjust the via the **Peak Width (sec)**, **Valley to Valley,** or **Manual Baseline Setpoints** tools.
Copy image to clipboard	Copies an image of the current view of the Electropherogram trace to the clipboard, for pasting in another program, such as Microsoft PowerPoint. Any zoom, annotation, baseline and/or peak start/end point displayed will be copied in the image. The well ID and sample name will be copied in the top left of the trace, and the x-/y-axis will correspond to the currently selected view in the copied image.

Peak Table

The **Peak Table** displays information about the selected and integrated sample peaks (**Figure 8**). The data in this table can be directly exported via its context menu. The fields of the **Peak Table** are summarized in **Table 7**.

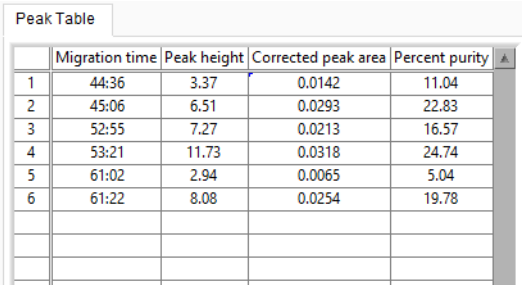


Figure 8 Peak Table form on main screen

Table 7 Peak Table functions

Item	Description
Migration time	Reports the migration time of the peak (in mm:ss).
Peak height	Reports the peak height, in milli absorbance units (mAU).
Corrected peak area	Reports the corrected peak area.
Percent purity	Reports the percent purity of the peak as a percentage of the total integrated peak area.
Export data to clipboard	Click in the peak table, and select this option from the context menu. Exports the peak table information to the clipboard for pasting directly into common spreadsheet programs such as Microsoft Excel. The full table is exported.

Sample Name Table

The **Sample name** table displays the well location and sample name for each sample.

To Import Sample Names

- When queuing samples in the Oligo Pro II instrument control software
- Post-run by selecting the **Import** function from the context menu of the sample name table (**Figure 9**):
  - Import .txt files: Depending on the number of samples, enter the names of the individual samples in the file in the order 1–12, 1–24, or 1–96
  - Import .csv files: Depending on the number of samples, enter the names of the individual samples in the file in the column A1, A2, A3, etc. from 1–12, 1–24, or 1–96

To Export Sample Names

Export the currently entered sample names to a .csv file via the context menu. Right-click on the **Sample name** table, and select **Export** (**Figure 9**).

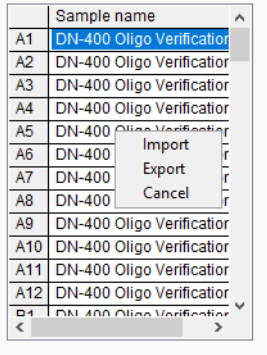


Figure 9 Sample name table form on main screen with context menu displayed

4 Oligo Pro II Data Analysis Software – Settings Menu

This chapter provides an overview of the settings menu, which is available on the main screen of the Oligo Pro II data analysis software.

About the Settings Menu

Use the settings menu of the main screen (**Figure 10**) to specify settings for processing the data file, including:

- Define peak width and peak height thresholds for peak integration
- Define how the baseline is drawn between peaks
- Define how and to what extent the raw data is filtered
- Define the **Inclusion Region** whereby peaks are to be integrated and analyzed
- Set a **Manual Baseline** between defined start and end points
- Enable or disable the **Purity Table** and establish **Flag Level %** for scoring purity results
- Define the viewable start and end points of each Electropherogram trace

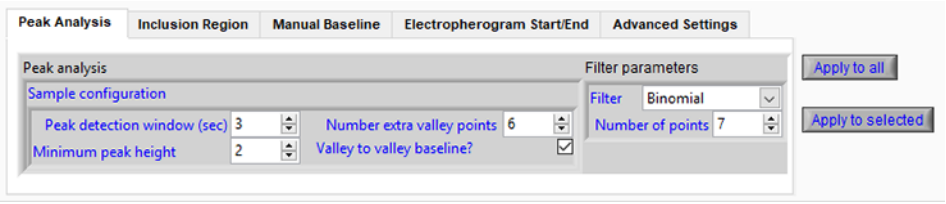


Figure 10 Settings menu (Peak Analysis tab shown)

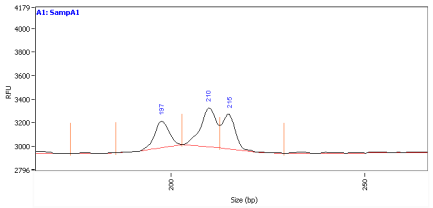
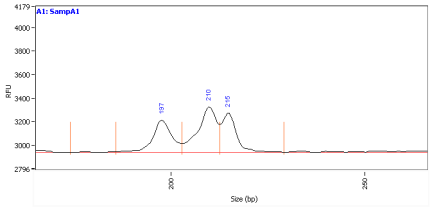
Peak Analysis Settings

On the **Peak Analysis** tab, you can assign width and height thresholds for peak selection and integration (**Figure 10**). The settings are described in **Table 8**.

Table 8 Peak analysis settings

Menu Item	Description
Peak Analysis	
Peak detection window (sec)	Defines the width threshold for peak detection in seconds. Higher values are better suited for wide peak start/end points; smaller values are better suited for sharp peak start/end points. For sharp peaks, typical values range from 3–5.
Minimum peak height (mAU)	Defines the minimum peak height threshold to select a peak for integration in mAUs. Peaks below the set value will not be selected for integration. Typical values for this setting are 0.2–1.0 mAU.
Number extra valley points	This setting influences the start/end point of baseline integration of peaks and the baseline drawn between peaks. This setting most affects the baseline between two peaks that are not baseline resolved. Higher values draw a straighter baseline between the first peak start point and second peak end point; lower values draw the baseline more to the "valley" between the two unresolved peaks. Note: To use this setting, you must enable **Valley to valley baseline?** setting.

Table 8 Peak analysis settings

Menu Item	Description
Valley to valley baseline?	This setting influences the start/end point of baseline integration of peaks and the baseline drawn between peaks. This setting most affects the baseline between two peaks that are not baseline resolved. Disable to draw a straighter baseline between the first peak start point and second peak end point:  Enable to draw the baseline more to the "valley" between the two unresolved peaks: 
Filter parameters	
Filter	Applies a **Binomial**, **Wavelets De-Noising**, or no filter to the data.
Number of points	Defines the number of points to use in the selected data filter.

Inclusion Region Settings

On the **Inclusion Region** tab, you can set the start and end time in minutes at which you want to integrate and analyze the respective electropherogram (**Figure 11**). The settings of the tab are described in **Table 9**.

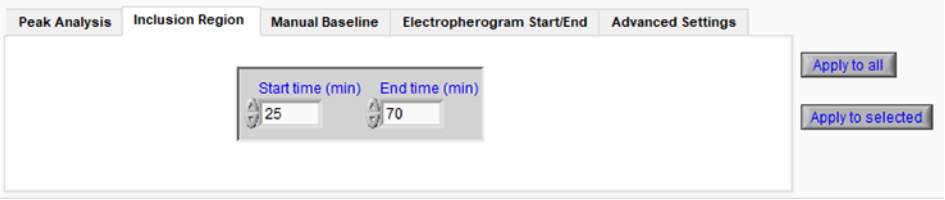


Figure 11 Settings menu (Inclusion Region tab shown)

Table 9 Inclusion region settings

Menu item	Description
Start time (min)	Defines the start time in minutes at which you want to integrate and analyze the electropherogram data. Note: If 0 is entered, data are analyzed from start of the electropherogram at 0 min.
End time (min)	Defines the end time in minutes at which you want to integrate and analyze the electropherogram data. Note: If 0 is entered, data are automatically analyzed to the full time range of the electropherogram.

Manual Baseline Settings

On the **Manual Baseline** tab, you can set the start and end time in minutes at which you want to start drawing the baseline (**Figure 12**). The settings of the tab are described in **Table 10**.

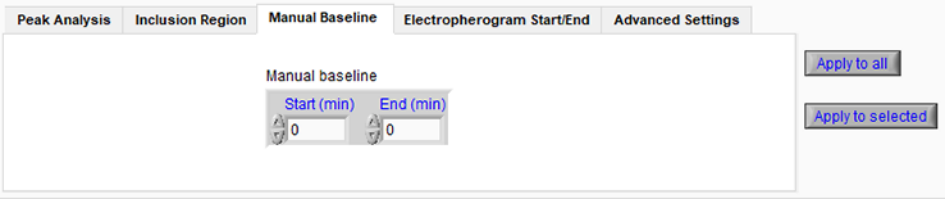


Figure 12 Settings menu (Manual Baseline tab shown)

Table 10 Manual Baseline settings

Menu item	Description
Start (min)	Defines the start time in minutes at which you want to start drawing the baseline. Note: If start and end points are set to 0, no manual baseline will be displayed.
End (min)	Defines the end time in minutes at which you want to end the baseline integration. Note: If start and end points are set to 0, no manual baseline will be displayed.

Electropherogram Start/End Settings

On the **Electropherogram Start/End** tab, you can define the region of the respective electropherogram to be displayed (**Figure 13**). The settings of the tab are described in **Table 11**.

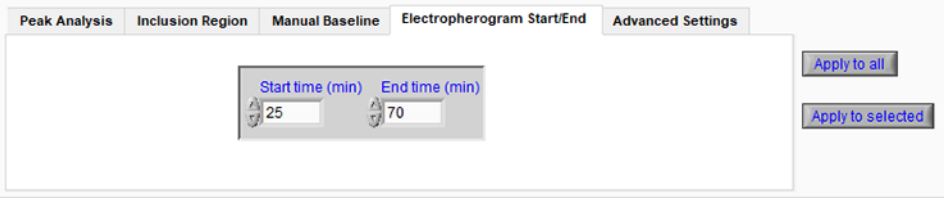


Figure 13 Settings menu (Electropherogram Start/End tab shown)

Table 11 Electropherogram Start/End settings

Menu item	Description
Start time (min)	Defines the start time in minutes to be displayed for the electropherogram. Note: If 0 is entered, the electropherogram starts at 0 min.
End time (min)	Defines the end time in minutes to be displayed for the electropherogram. Note: The default setting is to show the entire run time.

Advanced Settings

On the **Advanced Settings** tab, you can define the display of the Purity table, Flag Level %, and the scaling to the inclusion region (**Figure 14**). The settings are described in **Table 12**.

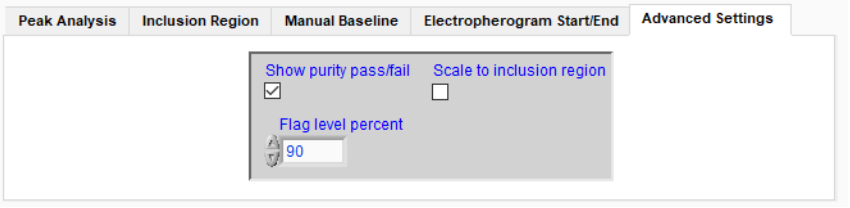


Figure 14 Settings menu (Advanced Settings tab shown)

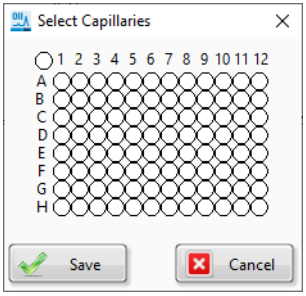
Table 12 Advanced settings

Menu item	Description
Show purity pass/fail	Shows a green or red well in the sample plate indicating a pass or fail percent purity status for the data, respectively.
Flag level percent	Determines the minimum percent purity value, which is used as the threshold for assigning the pass level for the purity analysis.
Scale to inclusion region	Scales the electropherogram to the largest peak in the defined inclusion region (you must define an inclusion region on the **Inclusion Region** tab).

Apply Settings

With exception of the **Advanced Settings** tab, you can apply the settings of the settings menu either to all capillaries or to selected capillaries (**Figure 10**, **Figure 11**, **Figure 12**, and **Figure 13**). For a description of the given Apply options, see **Table 13**.

Table 13 Apply settings

Menu item	Description
Apply to all	Applies the respective settings to all capillaries.
Apply to selected	Applies the settings to only the selected capillaries. Select this option, and a separate selection window appears that allows you to select the capillaries. 

5 Oligo PRO II Data Analysis Software – Overlay Samples

This chapter provides an overview of the possible ways to compare samples in the Oligo PRO II data analysis software.

Overlay Options

There are two methods for overlaying sample electropherogram traces in the Oligo Pro II data analysis software:

- Overlay multiple samples in the main screen
- Overlay multiple samples in the **Project Overlay** screen; here the overlay of samples from different data sets is possible

Overlay Samples in the Main Screen

1 In the Plate map of the main screen, right-click successive sample wells from which you want to overlay the Electropherogram trace.

2 Use the slider bar of the Electropherogram trace to adjust overlap spacing (**Figure 15**).

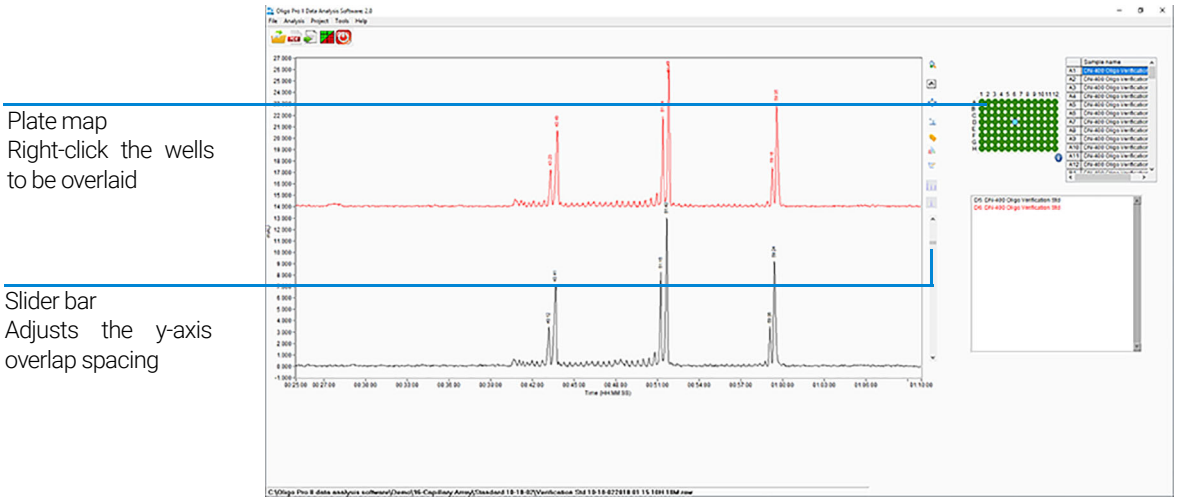


Figure 15 Overlay of multiple samples in the main screen

Overlay Samples in the Project Overlay Screen

In the **Project Overlay** screen, you can overlay samples from a single or multiple data files. Load the file(s) in the **Project Overlay** screen, and select the samples from which you want to compare the Electropherogram trace.

After saving your changes in the project, you can also export the results, or generate a PDF report.

1 In the main screen, navigate to **Project** > **Create Project**.

The **Project Overlay** screen opens.

2 From the **File** menu, select **Open File**.

Or select from the toolbar.

3 In the file browser, select as many files as desired.

In the **Project Overlay** screen, a separate Plate map is displayed for each of the data files (**Figure 16**).

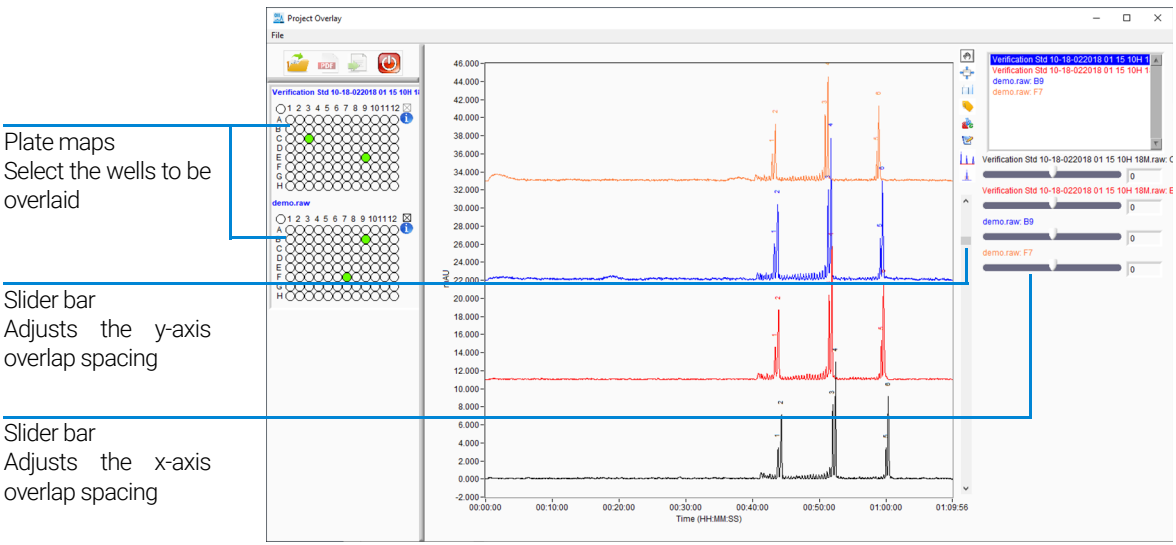


Figure 16 Overlay samples of multiple data files in the Project Overlay screen

4 In the Plate map(s), select the wells you want to overlay.

5 Use the slider bar to adjust the y-axis overlap spacing.

6 Use the slider bars in the upper right to adjust x-axis overlap spacing.

7 To save the data in the project, or start a new project, select the respective option from the **File** menu.

8 To create a PDF report, select  from the toolbar (the project must be saved in order to generate a PDF report).

9 To export the data, select  from the toolbar (the project must be saved in order to export the data).

For more information about exporting data files, refer to **Chapter 7**, “Exporting Data from the Oligo Pro II Data Analysis Software”. For more information about generating a PDF, refer to **Chapter 8**, “Generating Reports from the Oligo Pro II Data Analysis Software”.

6 Oligo Pro II Data Analysis – View Capillary Positions

This chapter briefly covers the tools and functions of the View Capillary Positions window.

About View Capillary Positions

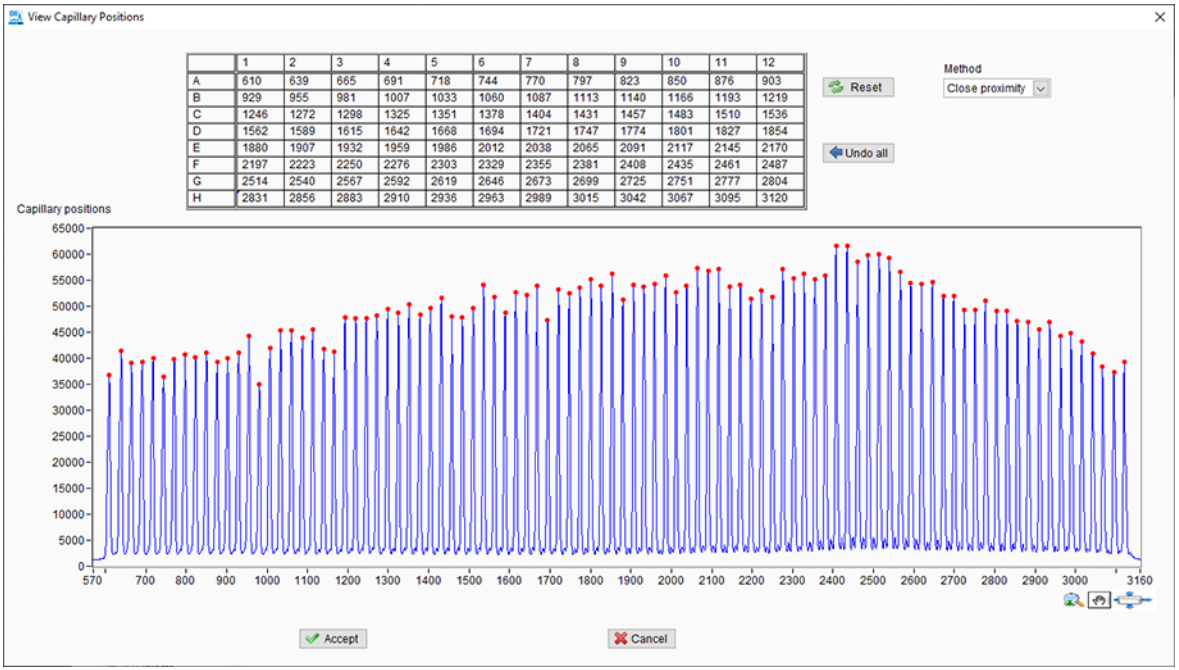
The Oligo Pro II data analysis software performs an automated capillary alignment procedure when reading in .raw data files generated by the Oligo Pro II instrument. This ensures that the capillary locations on the CCD detector selected for data analysis are of maximum absorbance intensity for providing the best possible signal to noise ratio.

View Capillary Positions is used to examine the capillary array alignment and the assigned locations used for data analysis. This option is typically not used in routine use since the locations are automatically assigned; it serves rather as a diagnostic/troubleshooting tool.

Open the View Capillary Positions Window

1 From the main screen of the Oligo Pro II data analysis software, select **Analysis** > **View Capillary Positions**.

The **View Capillary Positions** window opens (**Figure 17**). **Table 14** summarizes the available options in this window.



	1	2	3	4	5	6	7	8	9	10	11	12
A	610	639	665	691	718	744	770	797	823	850	876	903
B	929	955	981	1007	1033	1060	1087	1113	1140	1166	1193	1219
C	1246	1272	1298	1325	1351	1378	1404	1431	1457	1483	1510	1536
D	1562	1589	1615	1642	1668	1694	1721	1747	1774	1801	1827	1854
E	1880	1907	1932	1959	1986	2012	2038	2065	2091	2117	2145	2170
F	2197	2223	2250	2276	2303	2329	2355	2381	2408	2435	2461	2487
G	2514	2540	2567	2592	2619	2646	2673	2699	2725	2751	2777	2804
H	2831	2856	2883	2910	2936	2963	2989	3015	3042	3067	3095	3120

Figure 17 View Capillary Positions window

The View Capillary Positions window contains two sections:

- A plot of **Capillary Positions** (pixels) vs. Signal Distribution (intensity), which shows a summation of absorbance intensity for each capillary.
- The **Capillary Positions** table listing the pixel location for each of the 12, 24, or 96 capillaries in the 12-capillary, 24-capillary, or 96-capillary array, respectively.

In **Figure 17**, a proper alignment is shown where the red **Current Positions** symbols are centered on the peaks corresponding to each capillary. The algorithm automatically detects the peak locations and sets the capillary positions. If no absorbance is detected in a particular capillary, the algorithm will

fill the gap using the spacing between capillaries as a reference. In this way, the positions of all capillaries are indexed properly, even if no data was generated by some capillaries of the array.

During typical operation, no modifications should need to be made to the capillary positions. In rare occurrences, it may be necessary to adjust the positions slightly for one or two capillaries, or to manually adjust positions as described below. **Table 14** provides information on how to change a location and save the changes. Only changes necessary to center the red **Current Positions** symbols on any misaligned capillaries should be performed, to avoid introducing artifacts into the data.

View Capillary Positions Window Settings

The table summarizes the settings of **View Capillary Positions** window.

Table 14 View Capillary Positions window settings

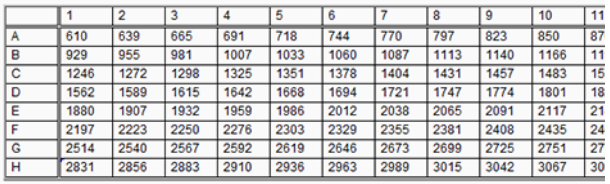
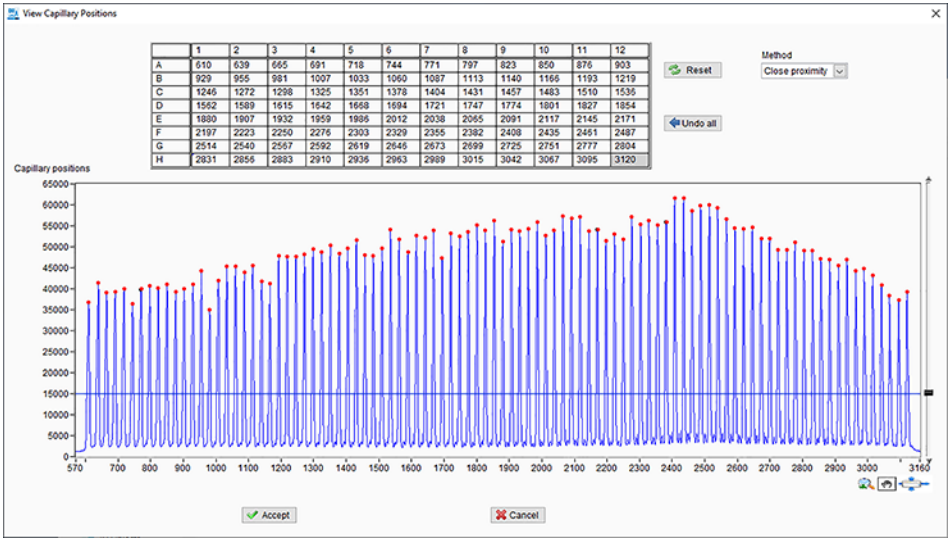
Menu Item	Description
Capillary Positions	The Capillary Positions table lists the pixel locations used on the CCD detector used for data analysis. There are either 12, 24, or 96 cells, each corresponding to a capillary of the array. The table is labeled by row and well position.  To view a particular capillary position, click the cell in the table, or click on a peak in the plot of Capillary Positions (Pixels) vs. Signal Distribution (Intensity) to view the corresponding assigned well. A red vertical cursor will be displayed on the plot to indicate the detector position.
Reset	Performs the automatic alignment algorithm to set the capillary locations. Any manual changes made to the pixel positions will be overwritten. A blue threshold line will appear (**Figure 18**). This line can be moved up or down to select an appropriate threshold for automatically determining capillary location.
Method	Two methods for determining capillary location can be used: • **Close Proximity** (default): This setting will use the original instrument alignment file to determine where to locate the capillary positions, filling any gaps in signal as needed. • **Ignore Original**: If the Close Proximity method fails to locate the correct capillary locations, this will attempt to assign capillary positions based on the signal positions; press **Reset** and use the threshold cursor and **Peak Width** settings to adjust assignments.

Table 14 View Capillary Positions window settings

Menu Item	Description
Peak Width	Provides a width threshold for selecting peaks in the plot of Capillary Positions (pixels) vs. Signal Distribution (intensity); a higher value selects wider peaks while a smaller value selects narrow peaks. The recommended value is 3.
Undo	To undo the last manual adjustment operation to the **Capillary Positions** table.
Zoom	Enables zooming in the x- and y-axis of the Capillary Positions (pixels) vs. Signal Distribution (intensity) plot. To zoom-in: Click the icon, and place the mouse over the plot. Click and drag it outward to expand a box area to define the zoom region. Release the mouse button to apply.
Autoscale	To autoscale the plot of Capillary Positions (Pixels) vs. Signal Distribution (Intensity).
Pan	Enables panning (shifting) the plot of Capillary Positions (pixels) vs. Signal Distribution (intensity). Click the icon, and place the mouse over the plot. Click and drag the cursor to shift the current view. This is most often used in combination with the **Zoom** function.
Accept	Accepts the current **Capillary Positions** table locations for the capillary array to use for data analysis and return to the main screen of the Oligo Pro II data analysis software.
Cancel	Cancels any changes made to the **Capillary Positions** table locations for the capillary array, close the **View Capillary Positions** window and return to the main screen of the Oligo Pro II data analysis software.



	1	2	3	4	5	6	7	8	9	10	11	12
A	610	639	665	691	718	744	771	797	823	850	876	903
B	929	955	981	1007	1033	1060	1087	1113	1140	1166	1193	1219
C	1246	1272	1298	1325	1351	1378	1404	1431	1457	1483	1510	1536
D	1562	1589	1615	1642	1668	1694	1721	1747	1774	1801	1827	1854
E	1880	1907	1932	1959	1986	2012	2038	2065	2091	2117	2145	2171
F	2197	2223	2250	2276	2303	2329	2355	2382	2408	2435	2461	2487
G	2514	2540	2567	2592	2619	2646	2673	2699	2725	2751	2777	2804
H	2831	2856	2883	2910	2936	2963	2989	3015	3042	3067	3095	3120

Figure 18 View Capillary Positions window after clicking **Reset**. A blue horizontal cursor can be used to select the threshold for locating capillary positions.

Manually Resetting Capillary Positions

In very few situations, it may be necessary to manually relocate the capillary positions in the **View Capillary Positions** window. This is usually the result of a combination of the two following conditions:

- The instrument optical alignment (i.e., capillary positioning) is not set properly. When the set capillary locations are far from the actual locations, the Oligo Pro II data analysis software will have difficulty locating them automatically, especially for 96-capillary data. Therefore, is it very important to ensure the capillary array locations have been reset and properly aligned after changing a capillary array.
- A capillary within the array has no detectable absorbance signal, either due to no sample or marker being loaded into the particular sample well, or because the capillary is plugged.

Ensuring the capillary array is properly aligned will in most all cases enable automatic detection of capillary locations, even if some capillaries do not generate signal. In this event, it is necessary to manually adjust or reset a capillary location, the user should follow the steps outlined below.

Figure 19 shows the **View Capillary Positions** window for a file where a capillary signal is missing (118 pixels). As a result of a slight misalignment of the instrument optical alignment, the software has mistakenly assigned a capillary to pixel 495 (red circle) and not assigned a location to the second capillary from the right (red circle). In this instance, it is not possible to adjust the threshold to successfully select the proper capillaries.

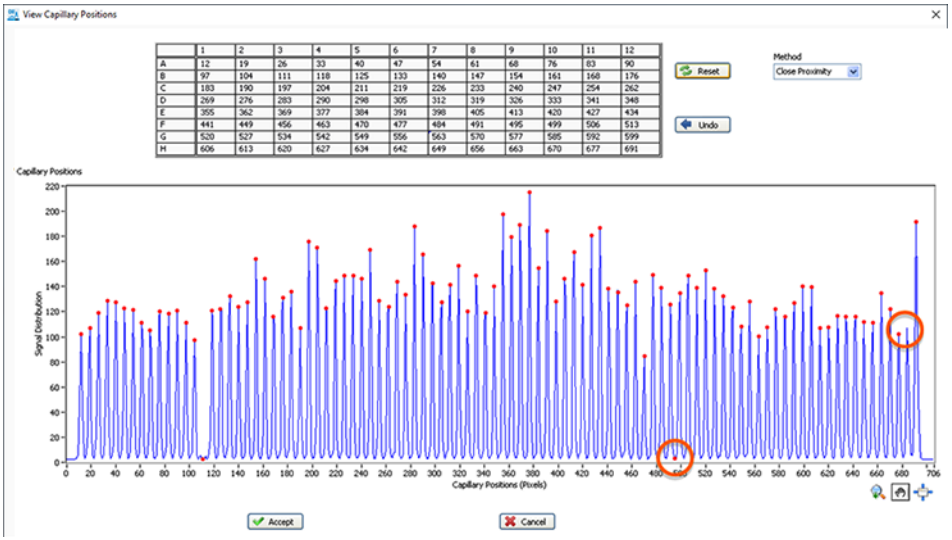


Figure 19 View Capillary Positions window where capillary is not assigned properly (circled)

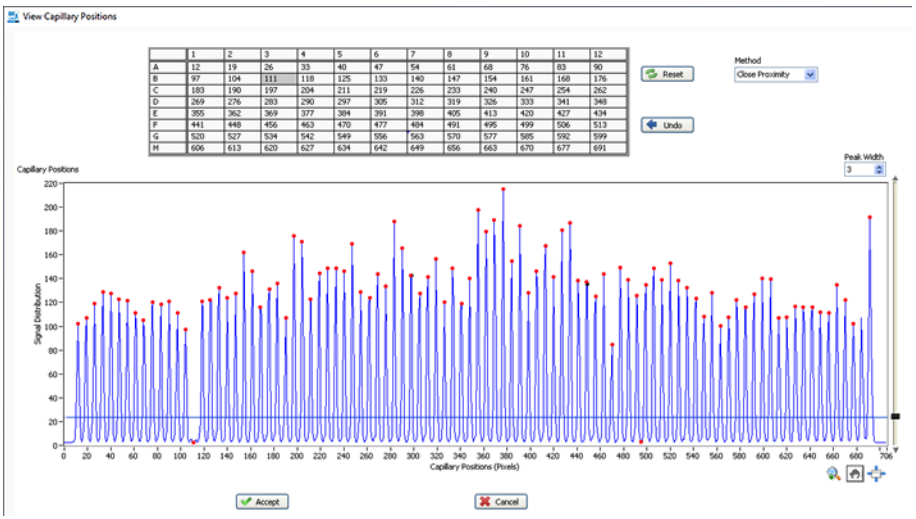


Figure 20 View Capillary Positions window showing misaligned capillary not reset by threshold

In **Figure 20**, it is shown that clicking **Reset** and using the threshold will not correctly reassign the capillaries due to the low signal from pixel 118.

To manually delete the improper capillary position, click the mouse over the location, and click **[Delete]** on the keyboard (**Figure 21**).

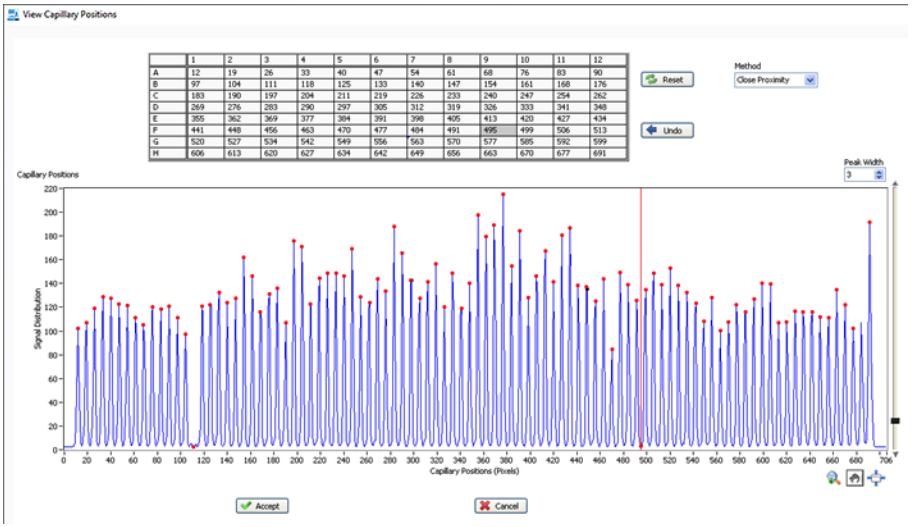


Figure 21 Manually deleting pixel 495 by selecting it and clicking [Delete] on the keyboard

Note that pixel 495 has now been removed from the **Capillary Positions** table and a blank cell is present in H12 (see **Figure 22**).

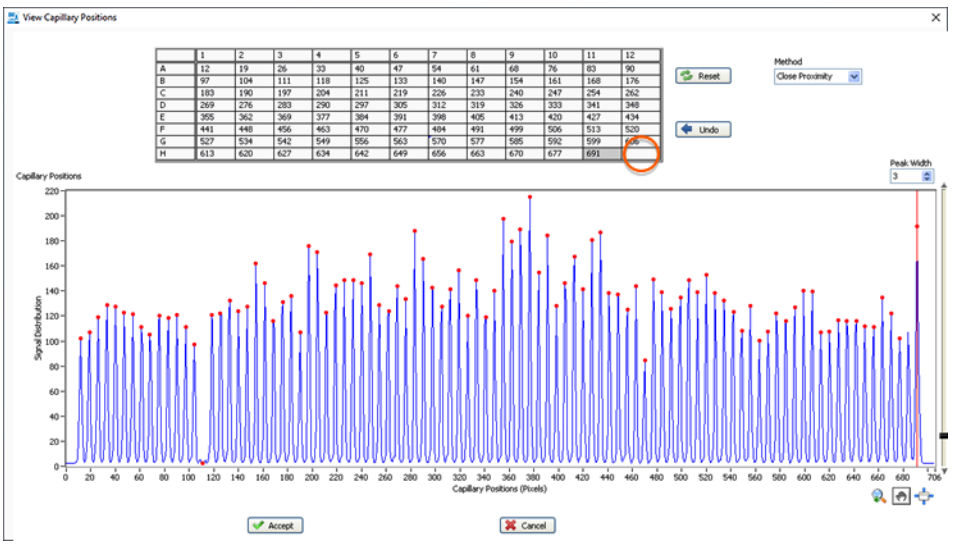


Figure 22 Alignment after manually deleting pixel 495

Next, to manually add a location, click on the adjacent capillary location to where you wish to add the capillary, and press **[Insert]** on the keyboard. Click the keyboard arrows to move the newly added vertical red cursor to the desired location, in this case pixel 684 (**Figure 23**).

Once the proper positions have been adjusted, click **Accept** to accept the current **Capillary Positions** table locations for the capillary array and return to the main screen of the Oligo Pro II data analysis software. All subsequent data analysis will use the newly saved capillary locations.

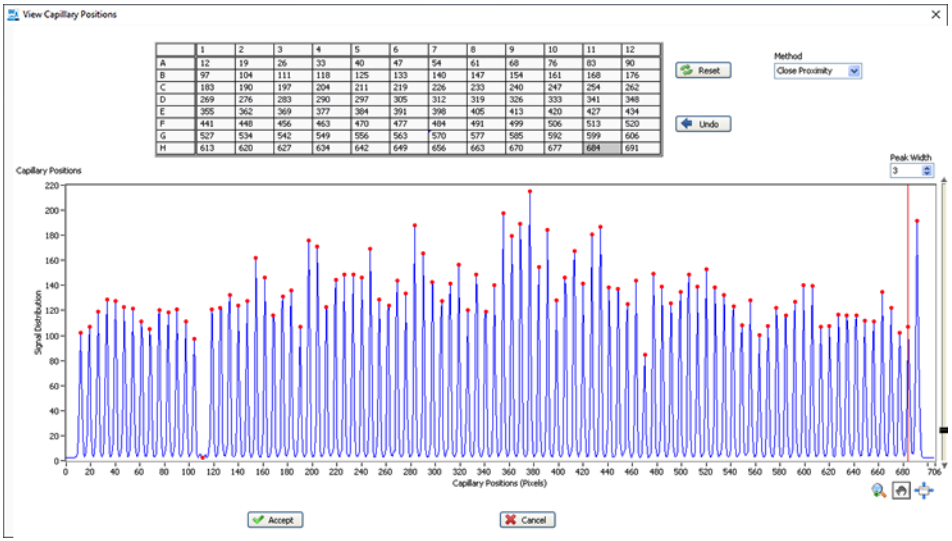


Figure 23 Alignment after clicking the **[Insert]** key at the rightmost position and using the keyboard arrow to move the vertical cursor to pixel 684. Capillary positions are now correctly located. Click **Accept** to save.

7 Exporting Data from the Oligo Pro II Data Analysis Software

This chapter provides an overview of the options available for exporting processed data from the Oligo Pro II data analysis software.

Export Data

Once data is opened and processed within the Oligo Pro II data analysis software, in many cases it is desirable to output the measured/calculated information in common formats for storage in a common database or for use in other programs.

The **Export** dialog is used to export information from the Oligo Pro II data analysis software.

Open the Export Dialog

To export sample results from the Oligo Pro II data analysis software:

1 From the main screen, select .

The **Export** dialog opens (**Figure 24**).

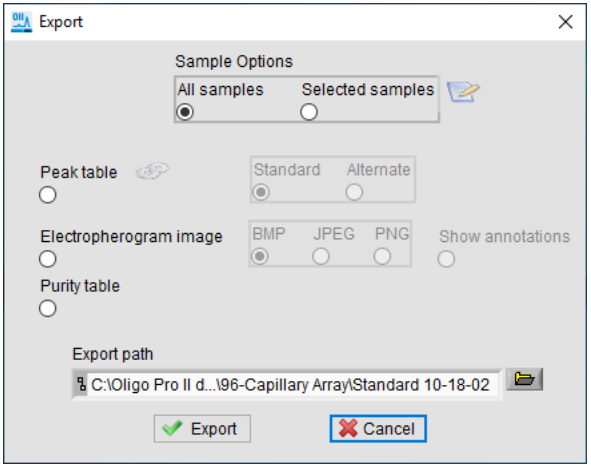


Figure 24 Export Data dialog

Table 15 summarizes the available options in this dialog.

Export Dialog Settings

Table 15 Export dialog settings

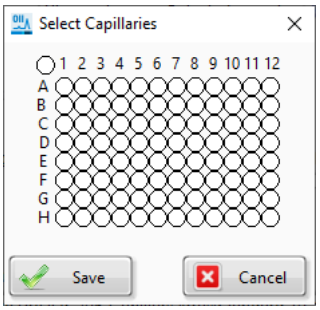
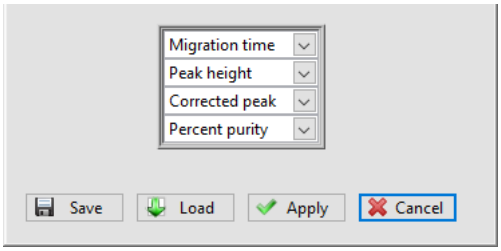
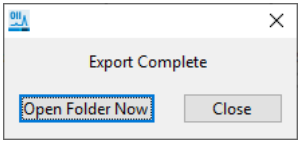
Menu Item	Description
Sample Options	Determines which samples of the data file will have information exported. There are two options: **All samples** (results for all samples of data file exported); and **Selected samples**. The Selected Samples option will open the **Select Capillaries** window (below).  Select the respective wells, columns and/or rows of the sample plate, and click **Save**. To abort the selection of the samples, click **Cancel**.
Peak table – Standard or Alternate	**Standard**: Exports the Peak table for all selected samples as a single .csv file, listed in order of the sample well (**Figure 26**). **Alternate**: Exports the Peak table for all selected samples as a single .csv file, listed in rows (**Figure 27**).  To define the report items and their order, click  . Make your entries in a separate dialog, and click **Apply**. Click **Save**, to save these settings for future use.
Electropherogram Image	Exports the electropherograms in the image format specified (.bmp, .jpg, or .png). Click **Show annotations** to include annotations.
Purity table	Exports the Purity table (**Figure 28**)

Table 15 Export dialog settings

Menu Item	Description
Export File Path	Determines the file path for saving exported data. The default directory is the same folder that contains the .raw data file (recommended). To select an alternative directory, click the folder icon. In the file browser menu, navigate to the desired directory.
Export	Exports the data file according to the settings made. In the dialog **Export Complete**, select **Open Folder Now** to open the directory. Click **Close** to close without opening the export folder. 
Cancel	Cancels the export operation and returns to the main screen of the Oligo Pro II data analysis software.

Examples of Exported Data

When exporting data from Oligo Pro II data analysis software, the exported files will be named by the .raw filename followed by an extension dependent upon the information exported (**Table 16**; **Figure 25**).

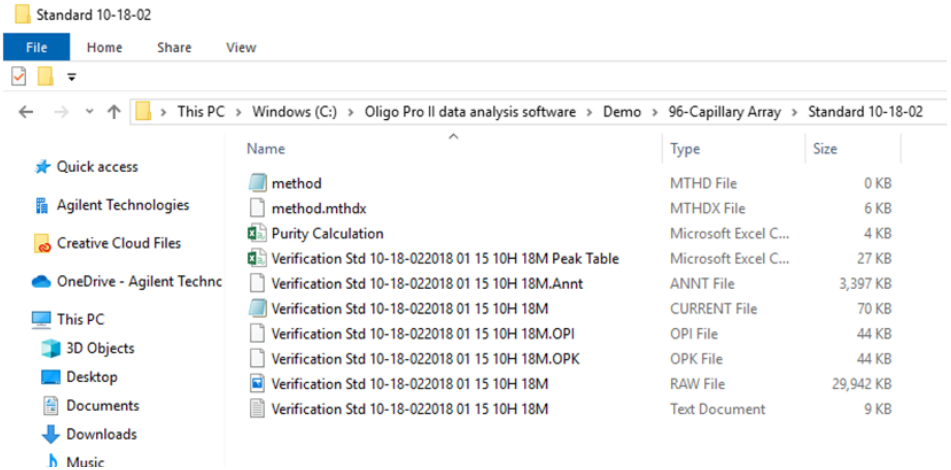


Figure 25 Exported data showing file name conventions

Table 16 Exported data naming conventions

Exported Item	Description
Peak Table	Filename Peak Table Example: *2013 07 15 18H 29M Peak Table*
Individual Electropherogram Gel Image	Filename Well ID Sample Name Example: *2013 07 15 18H 29M H1 SampH1*
Purity Table	Purity Calculation

The following figures show examples of typical exported data formats:

- Peak Table

	A	B	C	D	E	F
1	A1	DN-400 Oligo Verification Std				
2	Peak ID	Migration Time	Peak Height	Corr. Peak Area	% Purity	
3	1	44:36	3.37	0.0142	11.04	
4	2	45:06	6.51	0.0293	22.83	
5	3	52:55	7.27	0.0213	16.57	
6	4	53:21	11.73	0.0318	24.74	
7	5	61:02	2.94	0.0065	5.04	
8						
9	6	61:22	8.08	0.0254	19.78	
10	A2	DN-400 Oligo Verification Std				
11	Peak ID	Migration Time	Peak Height	Corr. Peak Area	% Purity	
12	1	44:30	3.46	0.0142	10.29	
13	2	45:01	7.14	0.032	23.21	
14	3	52:49	8.13	0.0232	16.79	
15	4	53:15	12.66	0.0348	25.23	
16	5	60:54	3.34	0.0073	5.3	
17						
18	6	61:14	8.9	0.0265	19.18	
19	A3	DN-400 Oligo Verification Std				
20	Peak ID	Migration Time	Peak Height	Corr. Peak Area	% Purity	
21	1	44:37	4.33	0.0205	10.66	
22	2	45:08	8.63	0.0432	22.43	
23	3	52:55	10.39	0.0321	16.66	
24	4	53:21	16.43	0.049	25.42	
25	5	60:58	4.44	0.0098	5.09	
26						
27	6	61:17	11.34	0.038	19.74	
28	A4	DN-400 Oligo Verification Std				
29	Peak ID	Migration Time	Peak Height	Corr. Peak Area	% Purity	
30	1	44:35	3.83	0.0176	11.39	
31	2	45:05	7.62	0.037	23.96	
32	3	52:52	8.47	0.0249	16.1	
33	4	53:18	13.24	0.0376	24.35	

OQ Std 10-18-022018 01 15 10H 1

Figure 26 Exported Peak Table - Standard file format

	A	B	C	D	E	F	G	H	I	J
1	Well	Sample ID	Peak ID	Migration	Peak Heig	Corr. Peak Area	% Purity			
2	A1	DN-400 Oligo Verification Std	1	44:36	3.37	0.0142	11.04			
3	A1	DN-400 Oligo Verification Std	2	45:06	6.51	0.0293	22.83			
4	A1	DN-400 Oligo Verification Std	3	52:55	7.27	0.0213	16.57			
5	A1	DN-400 Oligo Verification Std	4	53:21	11.73	0.0318	24.74			
6	A1	DN-400 Oligo Verification Std	5	61:02	2.94	0.0065	5.04			
7	A1	DN-400 Oligo Verification Std	6	61:22	8.08	0.0254	19.78			
8	A2	DN-400 Oligo Verification Std	1	44:30	3.46	0.0142	10.29			
9	A2	DN-400 Oligo Verification Std	2	45:01	7.14	0.032	23.21			
10	A2	DN-400 Oligo Verification Std	3	52:49	8.13	0.0232	16.79			
11	A2	DN-400 Oligo Verification Std	4	53:15	12.66	0.0348	25.23			
12	A2	DN-400 Oligo Verification Std	5	60:54	3.34	0.0073	5.3			
13	A2	DN-400 Oligo Verification Std	6	61:14	8.9	0.0265	19.18			
14	A3	DN-400 Oligo Verification Std	1	44:37	4.33	0.0205	10.66			
15	A3	DN-400 Oligo Verification Std	2	45:08	8.63	0.0432	22.43			
16	A3	DN-400 Oligo Verification Std	3	52:55	10.39	0.0321	16.66			
17	A3	DN-400 Oligo Verification Std	4	53:21	16.43	0.049	25.42			

Figure 27 Exported Peak Table - Alternate file format

- Purity Analysis

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	C:\Oligo Pro II data analysis software\Demo\96-Capillary Array\OQ Std 10-18-02\OQ Std 10-18-022018 01 15 10H 18M.raw													
2														
3		1	2	3	4	5	6	7	8	9	10	11	12	
4	A	24.74	25.23	25.42	24.35	25.44	25.5	25.93	24.7	25.23	26.23	25.3	26.18	
5	B	25.72	25.11	25.8	26.37	25.6	25.8	25.37	25.74	25.73	25.87	25.97	26.11	
6	C	24.49	25.45	25.78	25.32	25.4	25.27	25.83	25.4	25.85	26.18	25.41	25.49	
7	D	25.36	26	25.86	25.85	26.13	25.51	26.12	25.9	25.95	25.94	26.11	25.97	
8	E	25.85	26.22	25.64	25.54	25.48	26.2	25.94	26.97	25.96	26.15	25.78	24.87	
9	F	25.81	25.62	25.23	25.55	25.46	24.82	26.22	25.77	25.62	26.97	25.48	24.75	
10	G	25.5	25.66	25.52	25.19	25.85	25.58	25.57	25.06	25.19	26.06	24.82	25.45	
11	H	25.92	25.66	25.47	25.24	25.31	25.38	24.52	24.75	24.8	24.88	25.54	25.87	
12														
13														
14		1	2	3	4	5	6	7	8	9	10	11	12	
15	A	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	ligo Verifica	ligo Verifica	ligo Verifica	00 Oligo Verificatio	DN-400 Oligo Verification Std	
16	B	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	ligo Verifica	ligo Verifica	ligo Verifica	00 Oligo Verificatio	DN-400 Oligo Verification Std	
17	C	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	ligo Verifica	ligo Verifica	ligo Verifica	00 Oligo Verificatio	DN-400 Oligo Verification Std	
18	D	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	ligo Verifica	ligo Verifica	ligo Verifica	00 Oligo Verificatio	DN-400 Oligo Verification Std	
19	E	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	ligo Verifica	ligo Verifica	ligo Verifica	00 Oligo Verificatio	DN-400 Oligo Verification Std	
20	F	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	ligo Verifica	ligo Verifica	ligo Verifica	00 Oligo Verificatio	DN-400 Oligo Verification Std	
21	G	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	ligo Verifica	ligo Verifica	ligo Verifica	00 Oligo Verificatio	DN-400 Oligo Verification Std	
22	H	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	Oligo Verifica	ligo Verifica	ligo Verifica	ligo Verifica	00 Oligo Verificatio	DN-400 Oligo Verification Std	
23														
24														
25														
26														
27														

Figure 28 Purity Analysis

8 Generating Reports from the Oligo Pro II Data Analysis Software

This chapter provides an overview of the options available for generating reports from the Oligo Pro II data analysis software.

Generate Reports

The Oligo Pro II data analysis software can generate Adobe PDF formatted reports for convenient viewing of processed data, reporting detailed information for each sample analysis.

Open the Generate PDF Dialog

1 From the main screen, select .

The **Generate PDF** dialog opens (Figure 29).

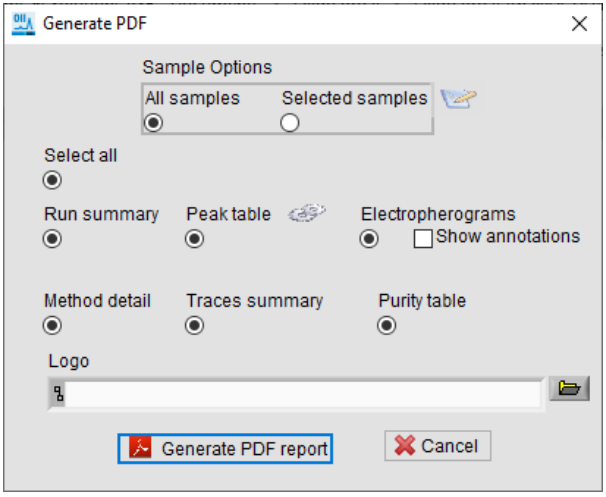


Figure 29 Generate PDF dialog

Table 17 summarizes the available options in this dialog.

Generate PDF Dialog Settings

Table 17 Generate PDF dialog settings

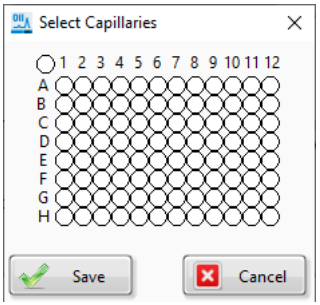
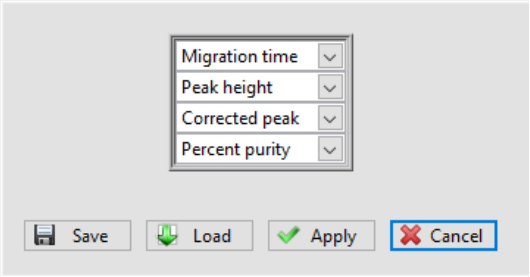
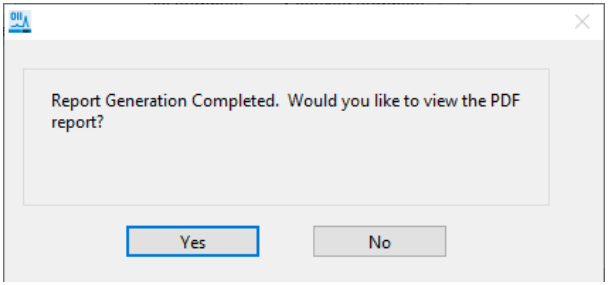
Menu Item	Description
Sample Option	Determines which samples of the data file will be included in the report. All selected samples will be saved in a single PDF report file; each sample will be printed on a separate page of the report. There are two options: **All samples** (results for all samples of data file exported); and **Selected samples**. The Selected Samples option will open the **Select Capillaries** window.  Select the respective wells, columns and/or rows of the sample plate, and click **Save**. To cancel the selection of the samples, click **Cancel**.
Run summary	A summary of run information is printed on the first page of the PDF report including **Filename** and **Data Path**; date **Created**; **# of Capillaries**; **Array Serial #** if entered; capillary **Effective Length**; **Array Usage Count**; **Version #** of software; **Device Serial #** (Figure 30). If this is not selected, these fields will be blank.
Method detail	Details of the experimental method of the Oligo Pro II instrument is printed on the first page of the PDF report.
Traces summary	The **Trace Summary** page is printed with up to 12 electropherograms per page (Figure 31). Traces will show the **Sample ID** information for each trace. If not selected, this field will be blank.

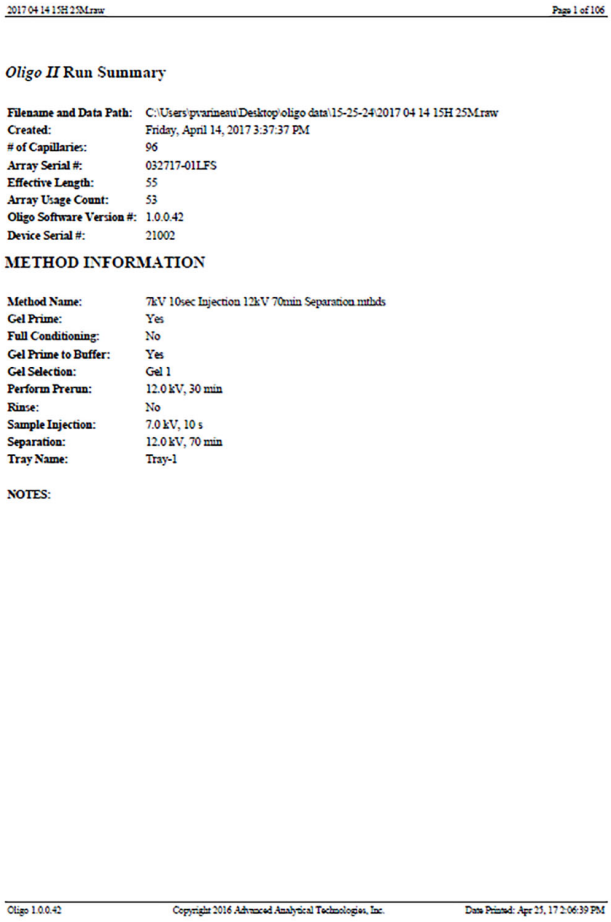
Table 17 Generate PDF dialog settings

Menu Item	Description
Peak table	For all selected samples, the Peak table is printed on each sample result page in the PDF report (**Figure 32**). If not selected, this field will be blank.  To define the report items and their order, click . Make your entries in a separate dialog, and click **Apply**. Click **Save**, to save these settings for future use.
Electropherograms	For all selected samples, the Electropherogram trace is printed on each sample result page in the PDF report. In the report, the peaks are annotated with the currently selected annotation. The x-axis scale is shown as displayed Oligo Pro II data analysis software at the time of printing (**Figure 32**). If not selected, this field will be blank.
Show annotation	Shows the annotation(s) made to the individual sample electropherograms. If not selected, no annotation for samples will be shown.
Purity table	Prints a Purity table (**Figure 33**).
Logo	Allows to import a company logo at the top of the report (any image can be imported).
Generate PDF report	Generates the configured report. In the file browser menu, navigate to the desired directory, and enter the desired report filename. The default directory is that containing the .raw data file.  In the Message dialog, click **OK** to open the report, or click **Cancel** to close without opening the report.
Cancel	Cancels the report generation operation and returns the main screen of the software.

Examples of Generated Reports

Figure 30 through **Figure 33** below show examples of the PDF report pages generated by the Oligo Pro II data analysis software.

The header of each page displays the .raw data file name and the page number; the footer contains software version and copyright information as well the date and time of report generation.



2017 04 14 15H 25M.raw Page 1 of 106

Oligo II Run Summary

Filename and Data Path:	C:\Users\pvarineau\Desktop\oligo data\15-25-24\2017 04 14 15H 25M.raw
Created:	Friday, April 14, 2017 3:37:37 PM
# of Capillaries:	96
Array Serial #:	032717-01LFS
Effective Length:	55
Array Usage Count:	53
Oligo Software Version #:	1.0.0.42
Device Serial #:	21002

METHOD INFORMATION

Method Name:	7kV 10sec Injection 12kV 70min Separation.mthds
Gel Prime:	Yes
Full Conditioning:	No
Gel Prime to Buffer:	Yes
Gel Selection:	Gel 1
Perform Prerun:	12.0 kV, 30 min
Rinse:	No
Sample Injection:	7.0 kV, 10 s
Separation:	12.0 kV, 70 min
Tray Name:	Tray-1

NOTES:

Oligo 1.0.0.42 Copyright 2016 Advanced Analytical Technologies, Inc. Date Printed: Apr 25, 17 2:06:39 PM

Figure 30 Page 1 of PDF report (all fields shown; 12 samples were selected)

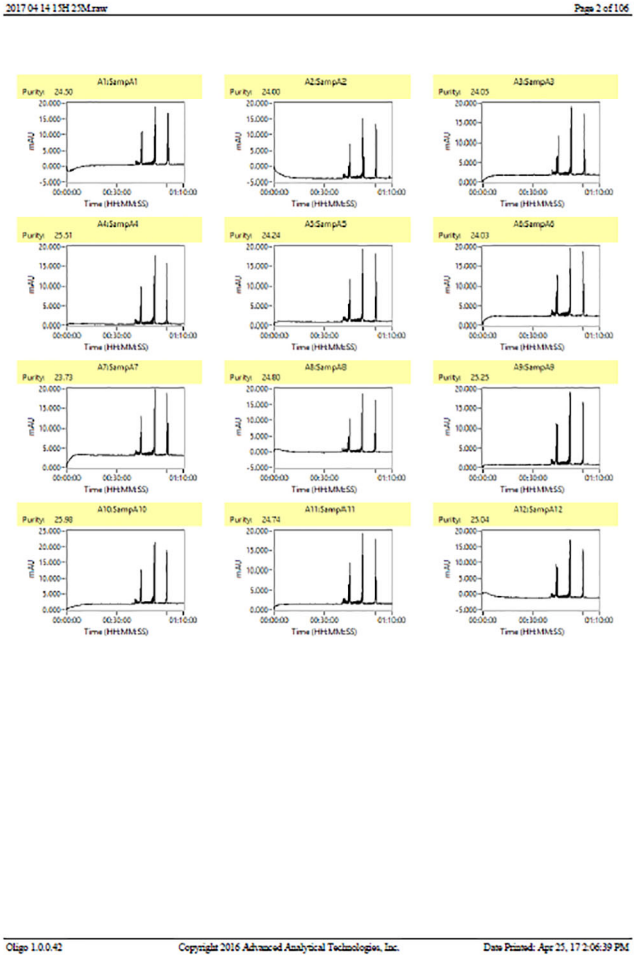
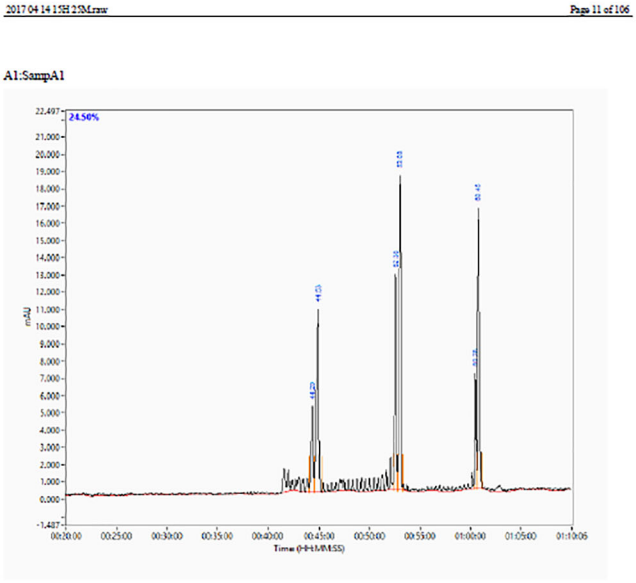
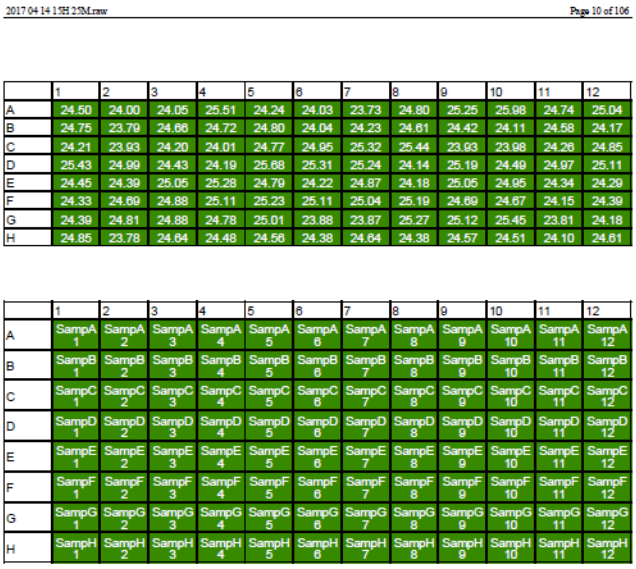


Figure 31 Trace summary of PDF report (all fields shown; 12 samples were selected)



Peak ID	Migration Time	Peak Height	Corr. Peak Area	% Corr. Peak Area
1	44:20	4.95	0.0300	10.23
2	44:53	10.57	0.0693	23.59
3	52:35	12.45	0.0479	16.32
4	53:03	18.20	0.0719	24.50
5	60:28	6.67	0.0160	5.45
6	60:45	16.21	0.0584	19.91

Figure 32 Individual result page of a PDF report (all fields shown)



2017 04 14 15H 25M.raw Page 10 of 106

	1	2	3	4	5	6	7	8	9	10	11	12
A	24.50	24.00	24.05	25.51	24.24	24.03	23.73	24.80	25.25	25.98	24.74	25.04
B	24.75	23.79	24.66	24.72	24.80	24.04	24.23	24.61	24.42	24.11	24.58	24.17
C	24.21	23.93	24.20	24.01	24.77	24.95	25.32	25.44	23.93	23.98	24.26	24.85
D	25.43	24.99	24.43	24.19	25.68	25.31	25.24	24.14	25.19	24.49	24.97	25.11
E	24.45	24.39	25.05	25.28	24.79	24.22	24.87	24.18	25.05	24.95	24.34	24.29
F	24.33	24.69	24.88	25.11	25.23	25.11	25.04	25.19	24.69	24.67	24.15	24.39
G	24.39	24.81	24.88	24.78	25.01	23.88	23.87	25.27	25.12	25.45	23.81	24.18
H	24.85	23.78	24.64	24.48	24.56	24.38	24.64	24.38	24.57	24.51	24.10	24.61

	1	2	3	4	5	6	7	8	9	10	11	12
A	SampA 1	SampA 2	SampA 3	SampA 4	SampA 5	SampA 6	SampA 7	SampA 8	SampA 9	SampA 10	SampA 11	SampA 12
B	SampB 1	SampB 2	SampB 3	SampB 4	SampB 5	SampB 6	SampB 7	SampB 8	SampB 9	SampB 10	SampB 11	SampB 12
C	SampC 1	SampC 2	SampC 3	SampC 4	SampC 5	SampC 6	SampC 7	SampC 8	SampC 9	SampC 10	SampC 11	SampC 12
D	SampD 1	SampD 2	SampD 3	SampD 4	SampD 5	SampD 6	SampD 7	SampD 8	SampD 9	SampD 10	SampD 11	SampD 12
E	SampE 1	SampE 2	SampE 3	SampE 4	SampE 5	SampE 6	SampE 7	SampE 8	SampE 9	SampE 10	SampE 11	SampE 12
F	SampF 1	SampF 2	SampF 3	SampF 4	SampF 5	SampF 6	SampF 7	SampF 8	SampF 9	SampF 10	SampF 11	SampF 12
G	SampG 1	SampG 2	SampG 3	SampG 4	SampG 5	SampG 6	SampG 7	SampG 8	SampG 9	SampG 10	SampG 11	SampG 12
H	SampH 1	SampH 2	SampH 3	SampH 4	SampH 5	SampH 6	SampH 7	SampH 8	SampH 9	SampH 10	SampH 11	SampH 12

Figure 33 Example Purity Analysis table in the PDF report

In This Book

This user manual contains information about the Oligo Pro II data analysis software.

The user manual describes the following:

- system overview,
- requirements and installation instructions,
- software main screen and menus,
- settings for data processing,
- comparing sample electropherogram traces,
- view capillary positions,
- data export,
- report generation.

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