Sequence Scanner and Peak Scanner

Recommended Software for Viewing Your DNA Data

Free from Applied Biosystems

Sequence Scanner Overview: Applied Biosystems Sequence Scanner^{TM} v1.0 is comprehensive software designed to display, edit, and trim, print, generate and export reports for sequencing sample files from Applied Biosystems genetic analysis instruments. This software is very user friendly and has an excellent user's manual in the help file.

To obtain Sequence Scanner:

Visit Applied Biosystems web site at:
https://products.appliedbiosystems.com/ab/en/US/adirect/ab?cmd=catNavigate2&catID=600583&tab=Overview
Click on Download Now and follow directions.

Quick Procedure for viewing DNA sequencing results with Sequence Scanner

1. Open "Sequence Scanner".
2. Click "Import Traces".
3. Go to the folder where you have your sequencing results (.ab1 files). Highlight the files you want to import (shift + click to get multiple files once or ctrl + click to get alternative files) and then click "Add selected trace" to import.
4. In the Trace Manger tab: Click on a file(s) to highlight, under File Tasks on the left hand side, select "Open Traces". This will open the trace window at the bottom. The view defaults to the analyzed data. Select "Raw" tab to view the actual fluorescence over time, select "Annotation" tab to view the signal strength along with other details of the data. Select the "Sequence" tab to view the results in text format.
5. In the Reports Tab: Click on a report type to view information about all the sequencing files. Double click on a file to open the trace window at the bottom and inspect the sequence data.
6. To print the trace file on a single page: In the Trace Manager tab click on a file(s) to highlight, click "File" "Print Setup". Set the parameters as: Panels per page to 6; set Points per page to at least 1800; can change "Set Y-Scale for Analyzed data" to change the peak height; select "Print QV information" if you want the quality bars present on the graph; click "Apply". Click "File" "Print preview" to make sure the whole trace file will be printed on one page (if it is more than a page, increase "Points Per Panel"). Click "Print". In the printer preferences, set Layout Orientation to "Landscape". Then "Print".
7. To export traces in different file formats: In the Trace Manager tab click on a file(s) to highlight. Under Trace Manager tab, select "Export Traces". Choose the desired file format and the directory in which to save the file.

Peak Scanner Overview: Peak Scanner™ Software is nucleic-acid-sizing software that identifies peaks and fragment sizes for application-specific capillary electrophoresis assays. This software allows you to annotate data with functions such as labeling, merging, and splitting peaks. The software stores all editing and analysis data in the original .fsa data files generated on Applied Biosystems genetic analysis instruments. This software is very user friendly and has an excellent user's manual in the help file.

To obtain Peak Scanner:

Visit Applied Biosystems web site at:
https://products.appliedbiosystems.com/ab/en/US/adirect/ab?cmd=catNavigate2&catID=603624
Click Begin the Peak Scanner™ Software v1.0 download process.

Quick Procedure for viewing DNA fragment analysis results with Peak Scanner

1. Open "Peak Scanner".
2. Select "Start New Project" button or in the upper left hand corner select "New" and "Project".
3. To Add Samples, click on the Add Files button. Go to the folder where you have your fragment analysis results (.fsa files). Highlight the files you want to import (shift + click to get multiple files once or ctrl + click to get alternative files) and click "OK". Or drag and drop .fsa files into the application window.
4. Select a size standard: If using G5 filter set, select either GS500(-250)LIZ or GS1200LIZ (depending on the size of your fragments). If using D or F filter set, select GS500(-250). If you are unsure of the size standard used, please contact the lab.
5. Select an analysis method: Select "Sizing default – NPP" if your samples do not contain the large primer peak at the start of the data or select "Sizing default – PP" if your samples do contain the large primer peak.
6. Click "Analyze" – green button on the left hand side.
7. Check the plot view and sizing view panels to evaluate the size quality. To zoom in to peaks in the plot view, hold the cursor over the top X axis or the side Y axis for the magnifying glass to appear. Click and drag to zoom in. Click on a peak to select it and view its height, area, size and data point.
8. Perform additional tasks (if needed): Edit peaks by merging, splitting, labeling, adding, and/or removing. Compare plots through the overlay function. Generate sizing tables with labeled peaks. Please see the user's manual for further instructions of these tasks.
9. Print data by clicking on "Print" from top menu. Highlight either the Samples View tab, Plot View tab or the Sizing Table tab before selecting print.
10. To export data: Select the Sizing Table tab and click " Export" from the top menu. Save as type: Tab Delimited (*.txt). This type of table then can be opened in Excel.