

Quick Reference for ProteinArray Analysis

Use these Quick Reference instructions to get up and running with ProteinArray Analysis. Within minutes you can install the software and run an analysis using example files installed in the **ScanArray Express\Samples** directory. Or, you can use your own data if you have all of the necessary files ready. For a Tutorial and detailed instructions, see the User Manual.

Installing and Starting the Software

- First, install version 2.2 (required) of ScanArray Express: insert the ScanArray Express CD-ROM into the CD-ROM drive of your computer. The Install program starts automatically; follow the on-screen instructions.
- Next, install ProteinArray Analysis: insert the ProteinArray Analysis installation CD-ROM into the CD-ROM drive of your computer. The Install program starts automatically; follow the on-screen instructions.
- With your computer and monitor turned on, double click the ScanArray Express icon on the desktop.

The *Main Window* of ScanArray Express displays, with action buttons in the top left of the window.

Running an Analysis

Click the **Analyze** button in the upper left of the *Main Window* to start the Analysis Wizard.

1. Select **Start with manual settings – last used settings only**. This uses default settings out of the box.
2. Load a valid .CAL file (use the sample .CAL, installed in the ScanArray Express Samples directory).

A .CAL file specific to an analysis provides the concentration of the analytes in the standard samples (and optional thresholds for a normal range). You can use the example .CAL file to get started with the example standards and samples files. To create a new .CAL file for your own data, see Appendix A of the User Manual.

3. View and verify the Standards in the CAL file.
4. View and verify the Thresholds in the CAL file, if any.
5. Select the data column to use for the analysis (Mean intensity, Median intensity, Background-subtracted mean intensity, Background-subtracted median intensity). Optionally check one or more methods for detecting and removing outliers.
6. You can leave the default curve fitting method (linear regression), or select a different method for different analytes.
7. Add the standards files in ascending order (the number of standards files must equal the number of standard concentrations in the .CAL file).
8. Optionally add blank and reference data.
9. Add the experimental sample files.
10. Optionally save the files as a file set to use again, and optionally save the settings as a protocol to use again. Save the files first to “link” them to the protocol.
11. Click **Finish**.

Using a Protocol

Once a protocol is created, it's simple to run an analysis using the protocol and a file set.

1. Click **Analyze**.
2. Select **Start with a protocol**.
3. Select the protocol. If a file set is linked to the protocol, it is automatically loaded. If not, select a file set.
4. Click **Finish**.

Saving the Analysis Results

The results display in several tabs on the ScanArray Express *Main Window*.

1. In the Main Window, under the *Configure & File* menu, click **File**, then **Save All**.
2. At the dialog box prompt for each file, enter a file name and click **Save**.

The analysis results (Concentrations spreadsheet tab) can also be exported to Microsoft Excel by clicking the **View as Excel Spreadsheet** button in the spreadsheet tab. For more information on viewing and saving the plots and spreadsheets, see the User Manual.