

PROTEINCHIP[®] SOFTWARE

VERSION 3.0.2

Release Notes

INSTALLATION

To install version 3.0.2 on a computer with a previous version of 3.0.x (alpha 1, alpha 2, or beta 1, beta 2, or release 3.0.1) installed, *the previous version must be uninstalled* before installing 3.0.2. To uninstall the previous version, select **Add/Remove Programs** from the **Control Panel** and select Ciphergen ProteinChip[®] Software 3.0. Choose **Change/Remove** from the options dialog, which will remove the previous version of the program. Uninstalling the software will not erase your data files or database.

During installation, the program will prompt for the model of your instrument (PBSI, PBSII, or PBSIIc). If you do not know which model is installed on your instrument, contact your Ciphergen field service engineer.

SUPPORT

If you encounter a problem installing or using this release, you may send an email to support@ciphergen.com or call Ciphergen Support at 1-888-864-3770.

NEW FEATURES IN RELEASE 3.0.2

Multi-User Database Access

The ProteinChip database is now multi-user accessible, allowing the same database to be accessed from multiple instances of the ProteinChip Software. For example, a user can open a database into which data will be acquired and saved. At the same time, another user can access the experiments in that same database to perform analysis on their desktop.

If an experiment file is open by an instance of ProteinChip Software, that experiment can only be opened in read-only mode by another instance of ProteinChip Software on another PC.

This feature is new to this 3.0.2 version. If a user opens a database with the 3.0.1 or earlier version of the software, they will lock others out from using that database, even if they are using version 3.0.2.

Note: Do not delete, rename or move files or folders under the database folder, or your data will be corrupted or lost! See the applicable sections of the *ProteinChip Software 3.0 Operation Manual* for details on how to import and export data into and out of the database, and how to backup and move databases.

Mass Deflector

ProteinChip Software, version 3.0.2 now allows the Mass Deflector to be set in acquisition protocols using mass units. Version 3.0.1 of the software only allowed the Mass Deflector to be set in the instrument configuration using arbitrary machine units rather than mass units.

Note: Only PBS IIc instruments support the Mass Deflector. Instruments that do not support the Mass Deflector do not show the Mass Deflector in the user interface.

There are four ways to configure the Mass Deflector: via the Spot Protocol Wizard, by editing a Spot Protocol, in the Manual Protocol Properties dialog, and in the Acquisition toolbar.

Setting the Mass Deflector in the Spot Protocol Wizard

The Mass Deflector can be set on the second page of the Spot Protocol Wizard as shown in Figure 1. The wizard provides a choice of **Auto** or **Mass**. **Auto** automatically sets the Mass Deflector to the minimum of the lower limit of the Optimization Range or at the maximum of 10,000 Daltons. In Figure 1, since **Auto** is selected, the Mass Deflector will be set to 3000 Daltons, the starting mass of the Optimization Range. The **Mass** option allows the user to set the Mass Deflector in Daltons, overriding the Optimization Range lower limit, again with a maximum of 10,000 Daltons.

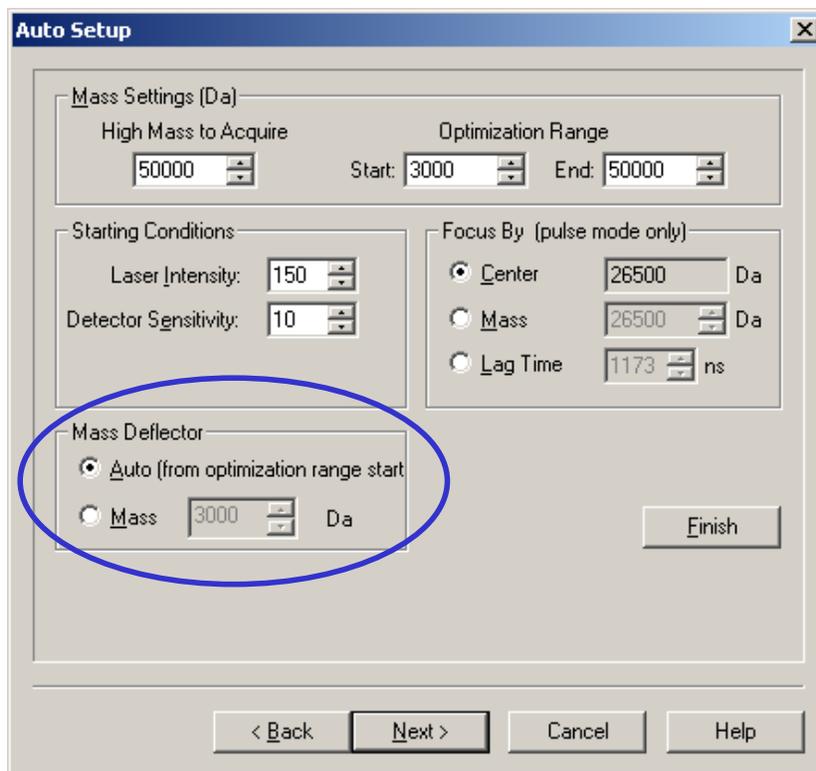


Figure 1. The second page of the Spot Protocol Wizard showing the new Mass Deflector settings

Editing the Mass Deflector settings in a Spot Protocol

After a Spot Protocol has been created, the Mass Deflector settings can be edited. In the Spot Protocol view, double click the line with the Mass Deflector command. In Figure 2, this is line 5 in the Spot Protocol. After double clicking, the **Modify Command** dialog will be shown where the user can edit the Mass Deflector settings (Figure 2). As in the Spot Protocol Wizard, the user can select **Auto** or **By Mass**. **Auto** uses the minimum of the lower limit of the Optimization Range or 10,000 Daltons. **By Mass** allows the user to override the Optimization Range and enter a mass between 0 and 10,000 Daltons.

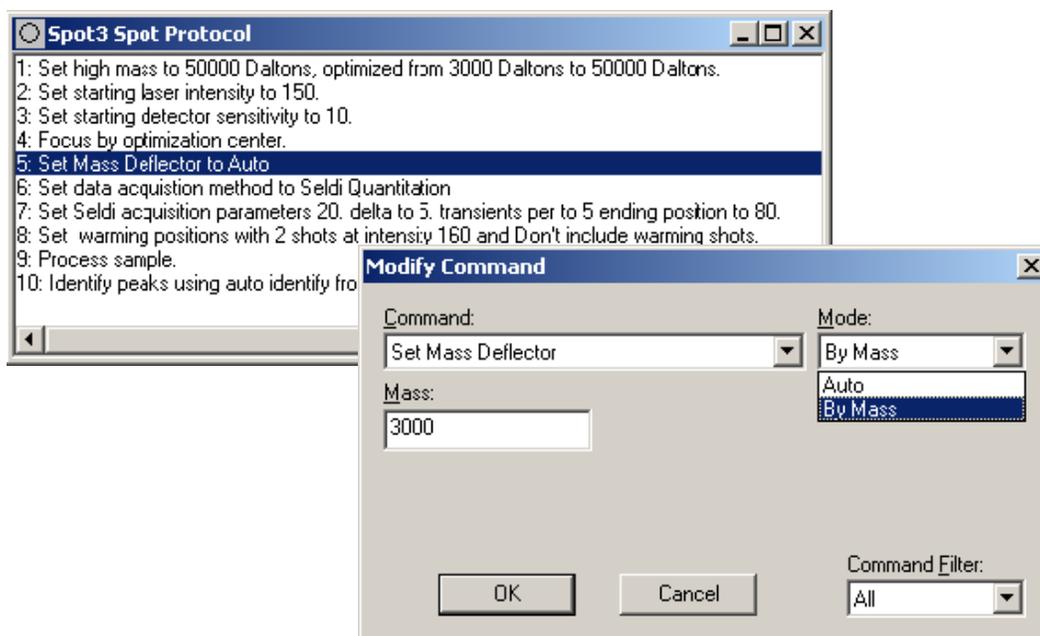


Figure 2. Editing the Mass Deflector settings in the Spot Protocol.

Setting the Mass Deflector in the Manual Protocol Properties Dialog

For manual acquisition, the Mass Deflector can be set in the Manual Protocol Properties dialog as shown in Figure 3. Similar to the settings in the Spot Protocol, the Mass Deflector can be set to **Automatic** or **Mass**. **Automatic** mode sets the Mass Deflector to the minimum of the lower limit of the Optimization Range or 10,000 Daltons. **Mass** mode allows the user to override the Optimization Range and set the Mass Deflector in Daltons with a limit of 10,000 Daltons.

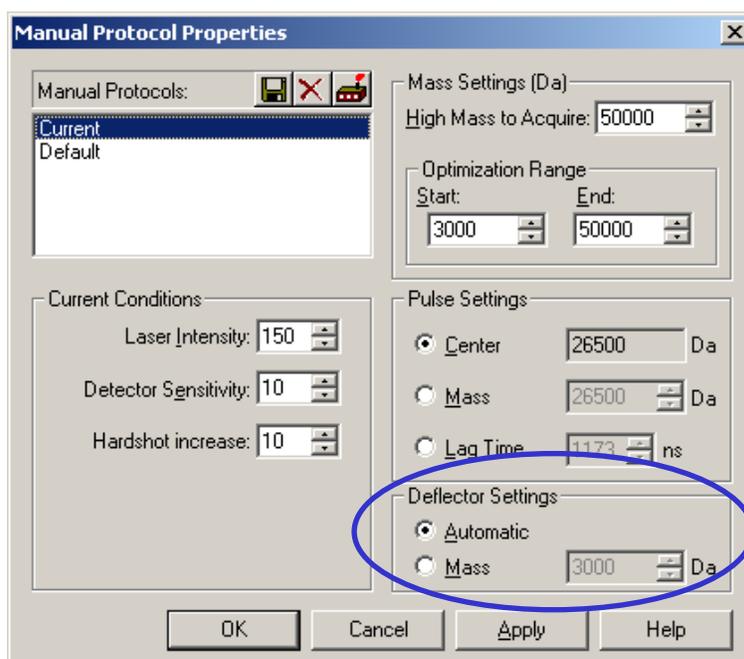


Figure 3. Manual Protocol Properties dialog highlighting Mass Deflector settings.

Setting the Mass Deflector settings in the acquisition toolbar

The Mass Deflector can also be set in the acquisition toolbar. If it is in Auto mode, the Mass Deflector will be tied to the Optimization Range and will be grayed out. If not, as shown in Figure 4, the user can set the mass in the toolbar. Again, the valid range is between 0 and 10,000 Daltons.



Figure 4. The acquisition toolbar highlighting the Mass Deflector setting.

255 Shot Limit

The limit of 255 shots per spectrum has been lifted (Problem ID 1640 below). However, spectra that are collected with more than 255 shots using ProteinChip Software version 3.0.2 will not be displayed properly if viewed using version 3.0.1.

SUMMARY OF PROBLEMS RESOLVED

The table below provides a summary of the problems and issues resolved in ProteinChip Software version 3.0.2.

Problem ID	Description
1616	The serial number was not getting recorded for first spectrum during acquisition due to sample exchange dialog being left open.
1617	Fields added to the sample properties weren't being saved when the file was exported and then imported into a different database.
1640	Eliminate limit of 255 transients.
1651	Some instruments intermittently gave an error message on initialization because the NDF filter can't be zeroed. This operation now retries three times before giving an error message.
1671	Exporting directly from the Data Average window did not save the acquisition information.
1697	ProteinChip Software crashed after running Biomarker Wizard, deleting a spectrum, re-running Biomarker Wizard, and zooming in the Biomarker Wizard view.
1709	Commas were converted to spaces in the Biomarker Patterns Software output file from Biomarker Wizard (.csv) in the spectrum tag and group columns.
1733	High Voltage Recondition Watch Dog Time Out errors were appearing in the ProteinChip Software log file (they are not true errors).
1753	In some conditions, the software didn't correctly reset the high voltage devices (e.g. when the cabinet/interlock was removed).
1765	Applying clusters from a cluster list file (.ccl) picked peaks off to the side of the clusters.
1784	Sometimes the instrument would be in a state where it would hang with a "motor moving" status.
1794	The software no longer allows opening read-only databases.

MAJOR KNOWN ISSUES

The table below lists known issues with ProteinChip Software version 3.0.2 and provides workaround solutions if applicable.

Problem ID	Description	Workaround
1770	A user cannot delete an experiment if someone else has it open in read-only mode. Attempting to delete and then reopen opens in read-only mode. Having all users close experiment will restore it to normal behavior.	You can only delete an experiment if no other users have it open.
1698	Deleting the Biomarker Wizard view while all spectra are selected causes the first spectra to be deleted as well	Don't clear out Biomarker Wizard in this manner. Use Experiment → Biomarker Wizard → Clear clusters
1645	Need horizontal scroll bar, especially when viewing lots of spectra vertically	None
1639	The software doesn't recover well from a network failure.	Export the experiment to a file (.xpt) and re-import after connecting to another database.
1620	The offset overlay view does not work properly. Pushing the offset overlay toolbar button works fine as does the right-click menu. However, selecting offset overlay in the Options → Presentation Protocol Properties → Experiment dialog does not remove the display properties, so the axis lines and grid are still visible.	Use the toolbar buttons to get offset overlay.
1619	The signal enhancer exaggerates the baseline, especially in the higher mass range.	None
1584	Launching software by double clicking an xpt file results in a Windows error message; however, the application still starts up and loads the desired xpt file.	Launch the ProteinChip Software first, then open the file.
1573	Spectra exported from the Data Average window have "Data Average" as their spectrum tag after import	Rename the spectrum when you save it to the database after importing.
1547	The default calibration is off for PBSIIC instruments. This is an issue when a new user is added as the default calibration becomes part of the new user's profile.	Create an individual calibration profile after the new user is added (PBSIIC instruments only).
1381	Performing mass normalization can result in a software crash when multiple instances of the same mass are added.	Don't run mass normalization on spectra that have already been normalized for mass. Don't run mass normalization on copies of the same spectra with the same calibration.