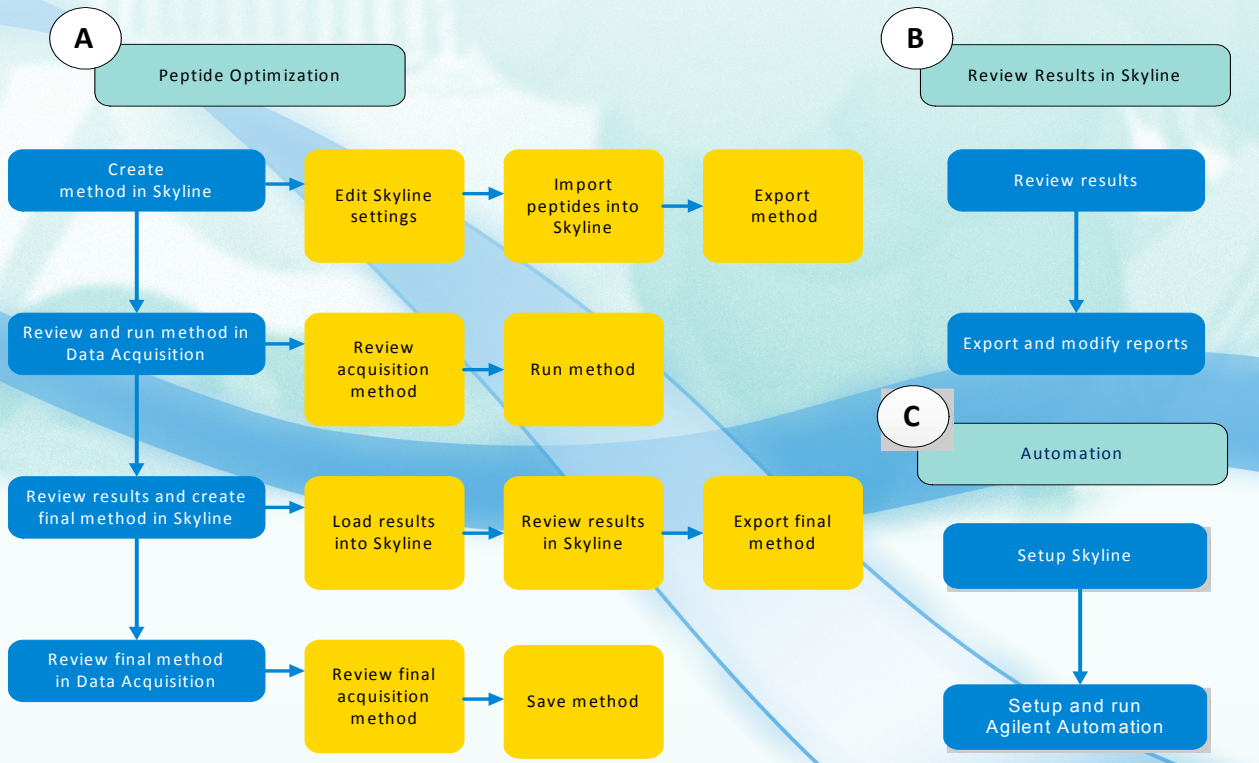
Agilent Triple Quadrupole LC/MS Peptide Quantitation with Skyline

Workflow Guide



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Notices

Manual Part Number

5990-9887EN

Edition

Revision B, February 2017

Printed in USA

Agilent Technologies, Inc.
5301 Stevens Creek Blvd.
Santa Clara, CA 95051

Acknowledgements

Skyline software is created by the MacCoss Lab in the Department of Genome Sciences at the University of Washington.

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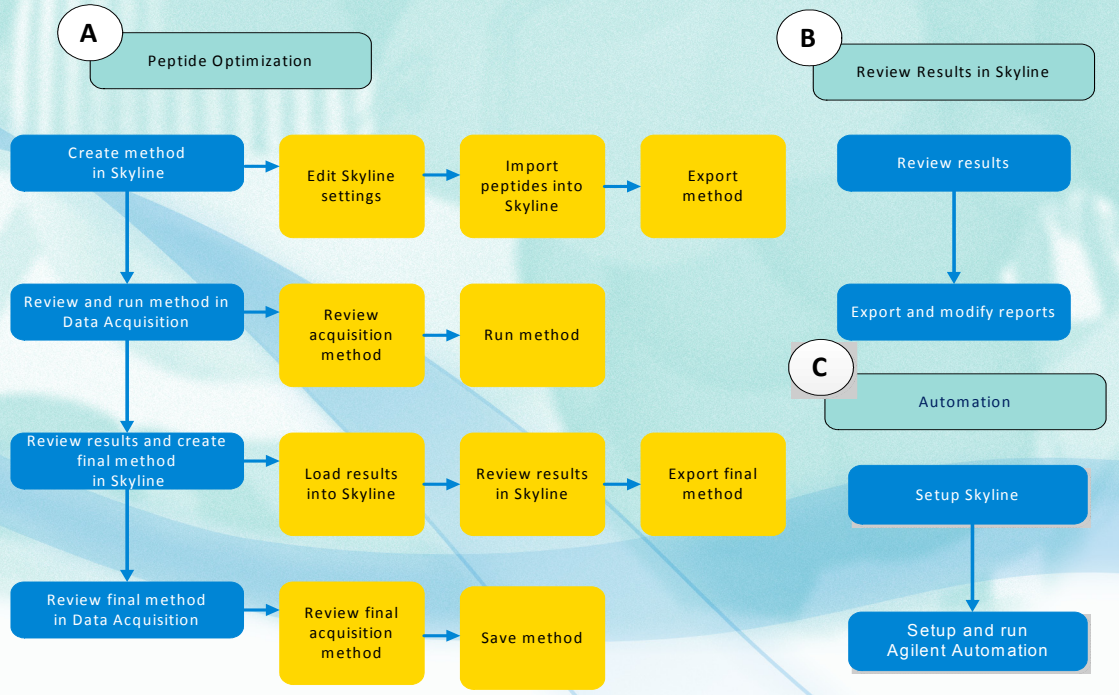
WARNING

A WARNING notice denotes a hazard. It calls attention to an operating procedure, practice, or the like that, if not correctly performed or adhered to, could result in personal injury or death. Do not proceed beyond a WARNING notice until the indicated conditions are fully understood and met.

Contents

Before You Begin

Make sure you read and understand the information in this chapter and have the necessary instrumentation, software, solvents, and lab supplies before you start the analysis.



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Introduction

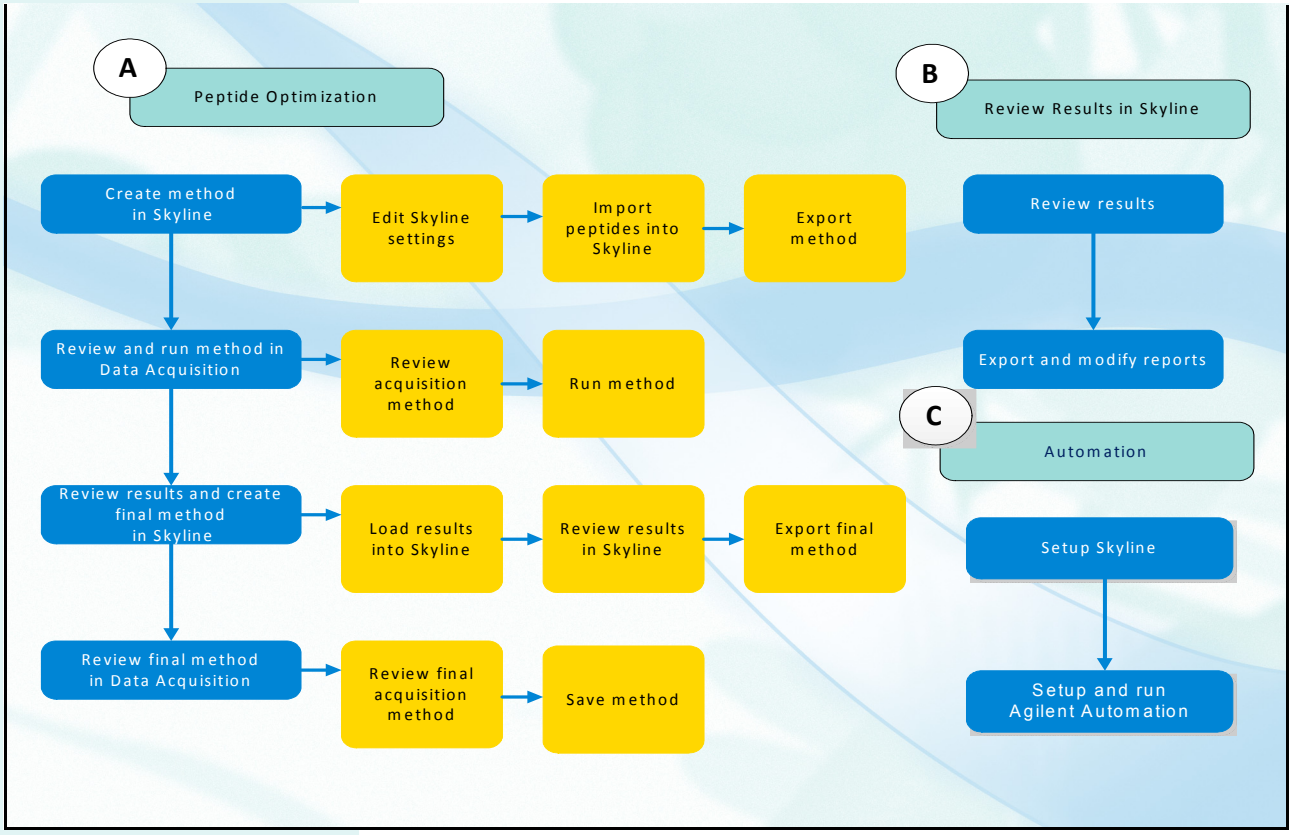
The MacCoss Lab at the University of Washington has developed the Skyline software package which provides an intuitive set of peptide-centric tools. Among its many features, Skyline can create Agilent TQ acquisition methods to run targeted proteomics experiments. Skyline can also create transition lists. This software is open source and is free for you to install on your computer.

This manual outlines how to use the Skyline software package to do the following tasks:

- Optimization of collision energies for peptides
- Review results
- Modify and export a report
- Use Agilent Automation to automatically optimize collision energies

Overview of the workflow

This guide describes the workflow to use the LC/MS Data Acquisition software with the Skyline software from the University of Washington to optimize the collision energy. This guide also describes how to use Skyline to analyze peptides and create reports that contain quantitative information. In the Automation chapter, you learn how to use the Agilent Automation process to automatically optimize collision energies.



More information

If you need a general introduction to triple quadrupole (TQ) mass spectrometry before you begin, see the *Agilent 6400 Series Triple Quadrupole LC/MS System Concepts Guide*. The following sections are especially useful:

- "How a triple quadruple mass spectrometer works"
- "How Dynamic MRM works"

You can also view an online video that describes how a triple quadrupole works.

For more information about Dynamic MRM, refer to the *Triple Quadrupole LC/MS System Concepts Guide* or the online Help for the MassHunter Data Acquisition software for the Triple Quadrupole instrument.

If you need a general introduction to Skyline software from the University of Washington's MacCoss lab, you can watch the videos that are available online on the Skyline software website.

Advantages of this workflow

The Skyline program is organized by proteins and then peptides and then transitions. The organization of this program is very intuitive to people working in proteomics.

What you cannot do with the workflow

The Skyline program does not have all of the quantitative analysis functionality that is available in the Agilent Quantitative Analysis program.

Safety Notes

WARNING **When you disconnect LC columns or fittings, solvents may leak. Use appropriate safety procedures (for example, goggles, safety gloves and protective clothing), especially when you use toxic or hazardous solvents. Read the material data safety sheets supplied by the solvent vendors.**

CAUTION Read, understand, and meet conditions of all cautions in the *Safety Guide* that you received with your Triple Quadrupole instrument.

Required items

Required hardware and software

Figure 1 *The workflow requires an Agilent LC and an Agilent 6400 Series Triple Quadrupole LC/MS System.*

To do this workflow, you need:

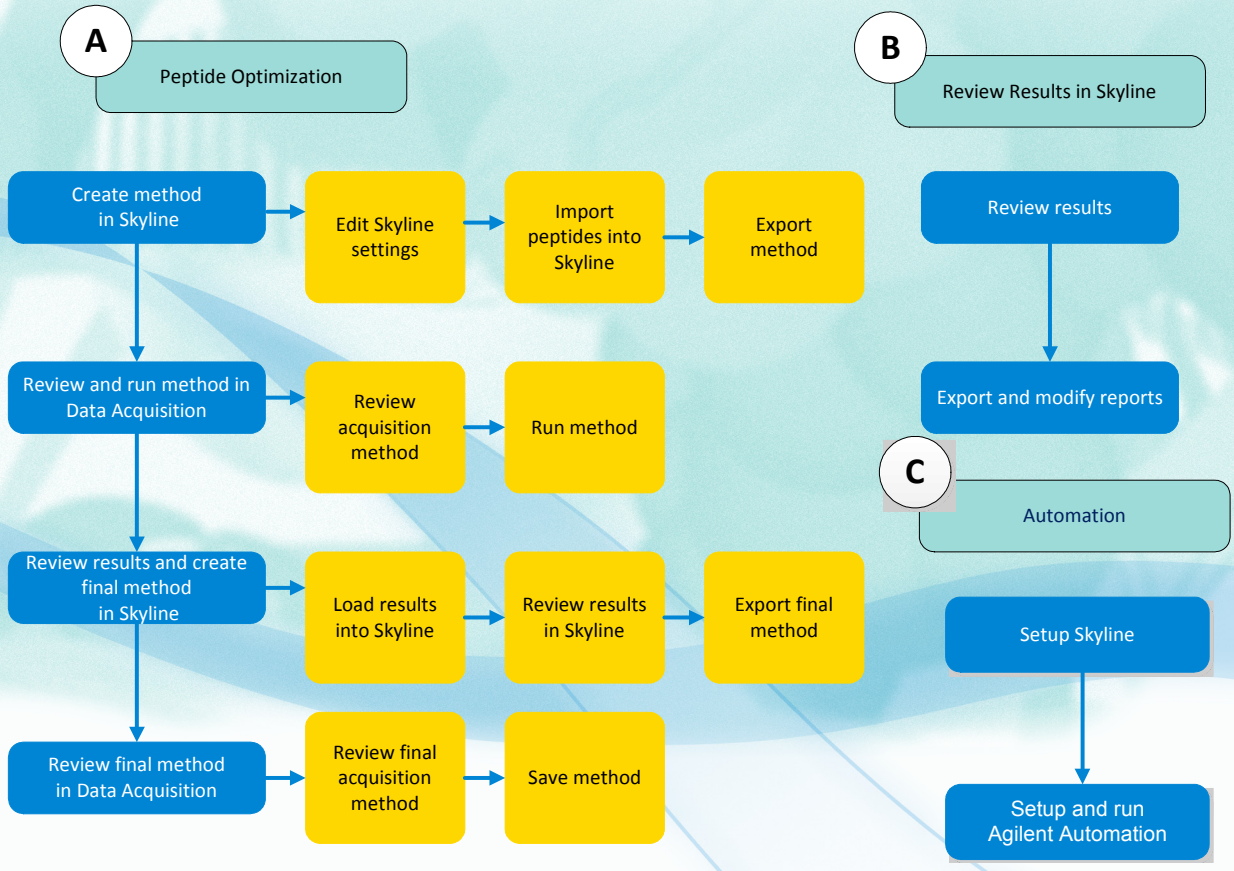
- One of the following LCs:
  - Agilent 1220 Infinity LC
  - Agilent 1260 Infinity LC
  - Agilent 1260 Infinity II LC
  - Agilent 1290 Infinity LC
  - Agilent 1200 Series LC system
  - Agilent 1200 Series Rapid Resolution LC system
- Agilent 6400 Series Triple Quadrupole LC/MS System
- Agilent MassHunter Data Acquisition for 6400 Series Triple Quadrupole Version B.08.00 or later
- Skyline software version 3.5 or greater from the MacCoss Lab at the University of Washington

The exercises in the next two chapters assume that:

- All instruments have already been installed and are working to specifications.
- You have been trained on the instrumentation and software. For example, you have taken an operator course at an Agilent training center or you have been trained on-site by an Agilent instructor (Application Engineer or consultant).
- That Skyline version 3.5 or later is installed.

Peptide Optimization

These exercises show you how to optimize the collision energy for the transitions that you are acquiring.



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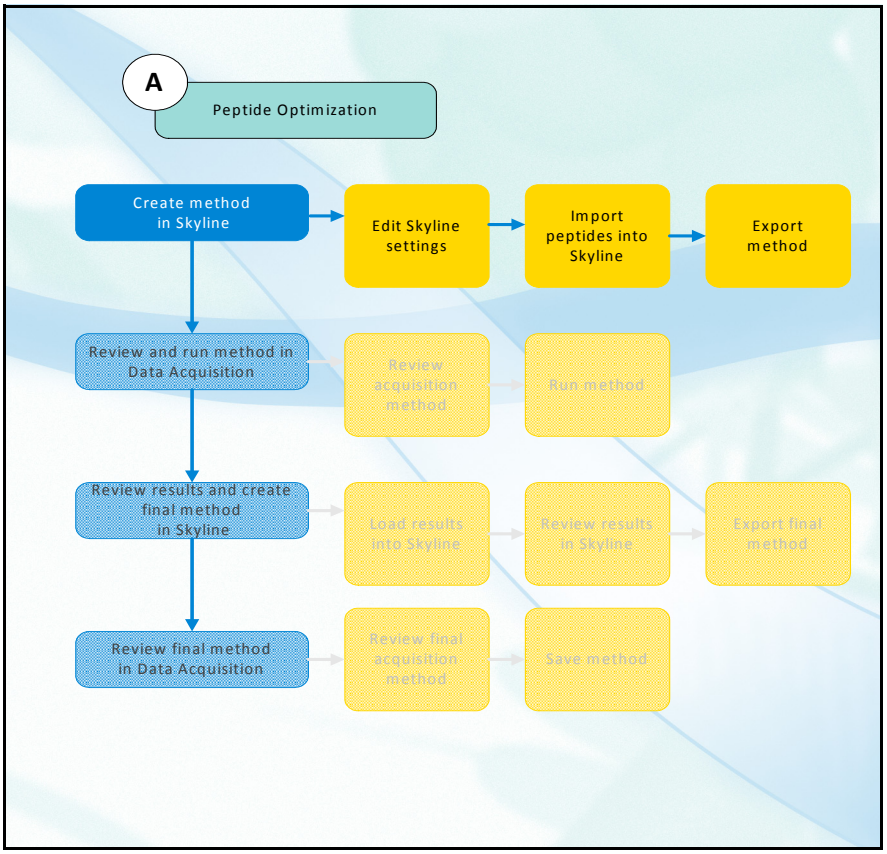
Create method in Skyline

In this exercise, you first enter your proteins or peptides into Skyline. Then, Skyline creates a list of precursor ions based on your settings and predicts the product ions. From this list, you can select which precursor ions and product ions to include. Then, you can create a Data Acquisition method. The LC parameters and the other MS parameters are copied from the template method that you select.

You can also export a transition list that you can use to optimize the collision energy for each transition. This transition list can be pasted into an existing Data Acquisition method in the Data Acquisition program.



Edit Skyline settings

Before you enter your protein or peptide information, you need to verify that the settings in Skyline are correct for your proteins or peptides. For more information on installing the software, see "Installing Skyline" on page 64.

1. Start the Skyline program.

   - From the Start button, click **All Programs** > **Skyline** > **Skyline**.
   - Click **File** > **New** to make sure that you are not starting from a previous project.

2. Edit Peptide Settings.

   a Click **Settings** > **Peptide Settings**.

   b On the Digestion tab, verify that the **Enzyme** is set correctly. In this example, the Enzyme is **Trypsin [KR | P]**. See Figure 2.

c Select **1** for **Max missed cleavages**. See Figure 2.

d Select **None** for **Background proteome**. This setting is useful if you are trying to have unique peptides associated with only one protein of a given organism.

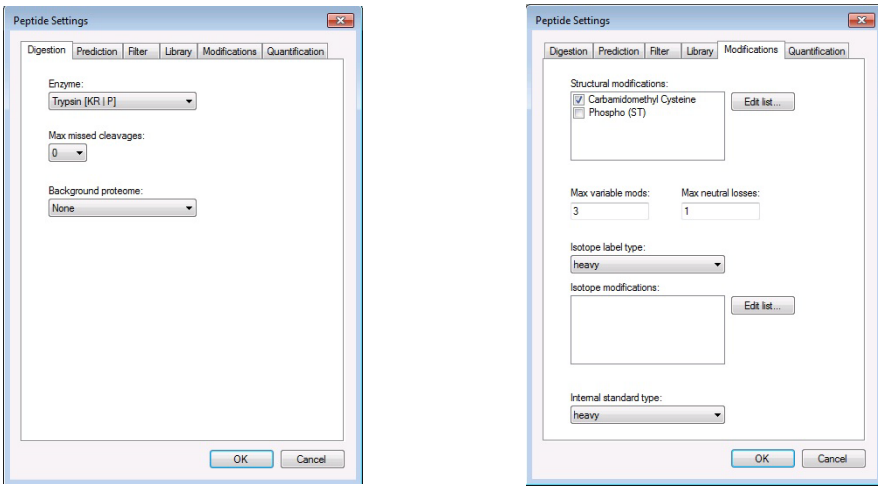


Figure 2 *The Digestion and Modification tabs in the Peptide Settings dialog box*

e Click the **Modifications** tab.

f On the Modifications tab, mark any **Structural modifications**. In this example, the **Carbamidomethyl Cysteine** check box is marked. See Figure 2 on page 13.

g Click the **Prediction** tab. See Figure 3 on page 14. In order to do retention time scheduling, Skyline needs to have a predictor in; the predictor is overwritten by the MRM results, so it does not need to be perfect. It is important that Skyline believes that it can make the prediction.

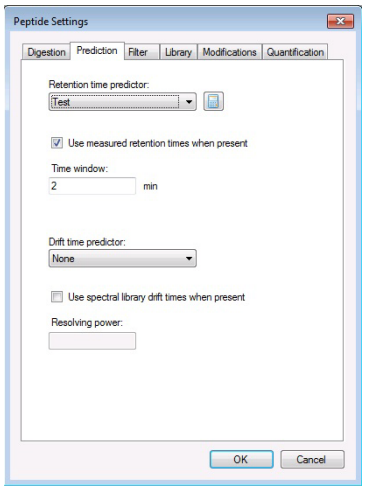
h Select **Add** for the **Retention time predictor**. The **Edit Retention Time Predictor** dialog box opens.

i Type a **Name**. In this example, the **Name** is `Test`.

j Type the **Slope** and **Intercept**. In this example, the **Slope** is 1; the **Intercept** is 0.

k Type the **Time window**. In this example, the **Time window** is `2.0`.

l Select the **Calculator**. For this example, the **SSRCalc 3.0 (100A)** calculator is selected.



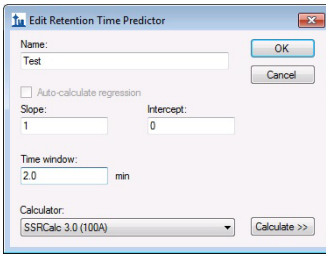


Figure 3 *The Prediction tab and the Edit Retention Time Predictor dialog box*

m Mark the **Use measured retention times when present** check box.

n Click the **OK** Button.

3. Edit the collision energy settings in the Transition Settings dialog box.

a Click **Settings > Transition Settings**.

b On the Prediction tab, select **<Edit list...>** in the **Collision energy box**. The **Edit Collision Energy Regressions** dialog box is opened.

c Select **Agilent QQQ** in the **Edit Collision Energy Regressions** dialog box and click the **Edit** button. If **Agilent QQQ** is not an option, then click **Add**.

The **Edit Collision Energy Equation** dialog box is opened.

d Type `Agilent QQQ` for the **Name**.

e Type `2` in the **Charge** column.

f Type `0.031` in the **Slope** column.

g Type `1` in the **Intercept column**.

h In the next row, type 3 in the **Charge** column.

i Type `0.036` in the **Slope** column.

j Type `-4.8` in the **Intercept column**.

k Type `3` for the **Step size**. This step size is the number of volts to change the collision energy for each step. For Agilent Triple Quadrupole, a value of 3 or 4 is fine because Agilent TQ have a relatively wide collision energy optimum.

l Type 3 for the **Step count**. A step size of 3 means that when you are optimizing, the collision energy is checked for 3 steps above and 3 steps below the specified collision energy. In this example, the step size is 3, so the collision energy is checked at +9, +6, +3, 0, -3, -6, and -9. This is a reasonable starting point.

A set of standard peptides was reviewed. Given that the response tends to be 90% of maximum over 5 to 10 V, a step size of 3 V can quickly determine the optimal value.

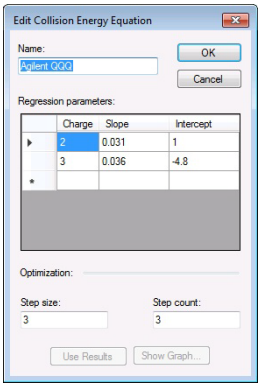


Figure 4 *Edit Collision Energy Equation dialog box*

m Click the **OK** button. The **Edit Collision Energy Equation** dialog box closes.

n Click the **OK** button. The **Edit Collision Energy Regressions** dialog box closes.

o Mark the **Use optimization values when present** check box.

p Select **Agilent QQQ** for the **Collision energy**.

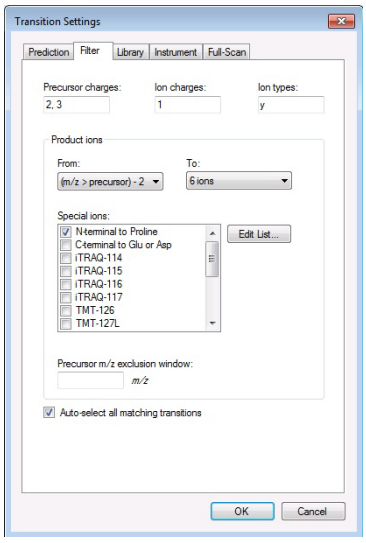
q Select either **Precursor** or **Transition** for the **Optimize by** value.

4. Edit the filter settings in the Transition Settings dialog box.

a If necessary, click **Settings > Transition Settings**.

b Click the **Filter** tab.

c Review the parameters. For this example, make the following changes:
- Type `2, 3` for the **Precursor charges**.
- Type `1` for the **Ion charges**.
- Type `y` for the **Ion Types**.
- Select **(m/z > precursor) - 2** under Product ions in the **From** list.
- Select **6 ions** under Product ions in the **To** list.



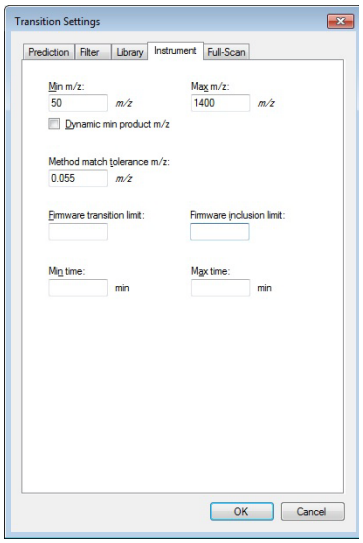


Figure 5 *Two tabs of the Transition Settings dialog box*

5. Edit the instrument settings in the Transition Settings dialog box.

a If necessary, click **Settings > Transition Settings**.

b Click the **Instrument** tab.

c Enter a value in the **Max m/z** box that is not greater than the maximum m/z value for the Agilent Triple Quadrupole model that you own. You can find the maximum *m/z* for your instrument in the Data Acquisition program in the Acquisition > QQQ tab in the Method Editor window. If you right-click a **Precursor Ion** or **Mass value** in the Scan segments table, the **Maximum value** is displayed in the shortcut menu. For a 6490, set this value to **1400**.

d Click the **OK** button.

6. Save the settings for future use.

a Click **Settings > Save Current**.

b Type a **Name** and click the **OK** button.

Import peptides into Skyline

1. Copy your peptide to the Clipboard.

In this example, a peptide from beta casein is typed into Notebook.
- Highlight the entire peptide and press **Ctrl** and **C**. You can also highlight the entire peptide and click **Edit > Copy**.
- The example peptide is **FQSEEQQQTEDELQDK**.

2. Paste the peptide from the Clipboard into Skyline.

a Click **Edit > Insert > Peptides**.

b Click the first cell in the Peptide Sequence column.

c Press **Ctrl** and **V** to paste the peptide into this cell.

d Type the **Protein Name**. In this example, the protein name is `beta casein`.

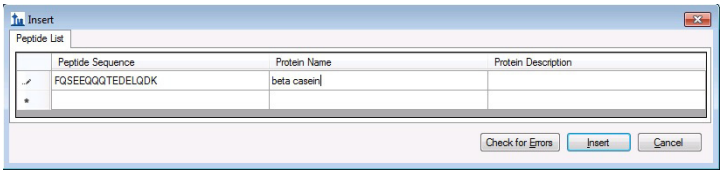


Figure 6 *Insert dialog box*

e Click the **Insert** button.
- You can also directly paste the peptide into the **Targets** list. Right-click the "..." in the list and click **Paste**.

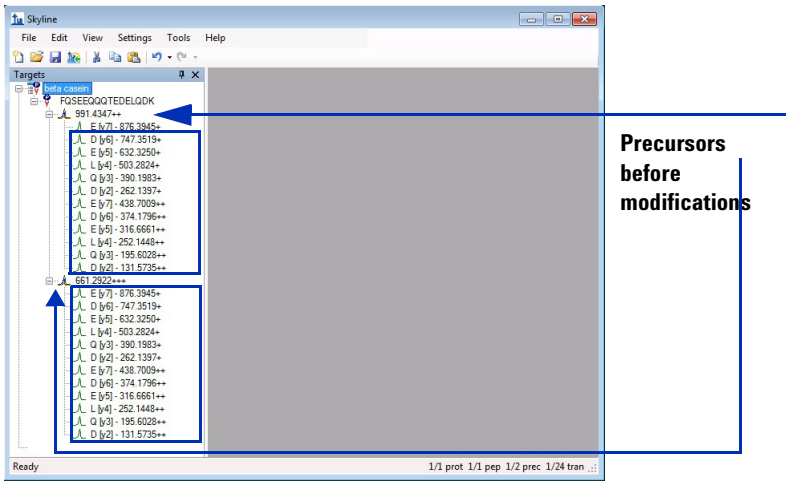


Figure 7 *Main window of the Skyline program before modifications*

3. Make modifications to the Peptide.

a Right-click the peptide and click **Modify**.

In this example, it is a phosphopeptide, so you have to modify the serine.

b Select **Edit list** from the serine (S) list. The **Edit Structural Modifications** dialog box opens.

c In the **Edit Structural Modifications** dialog box, select **Phospho (ST)** in the **Name** list. Click the **Edit** button. If **Phospho (ST)** is not available, click the **Add** button.

d Enter `HO3P` for the **Chemical formula**.

e Type `S,T` in the **Amino acid** box.

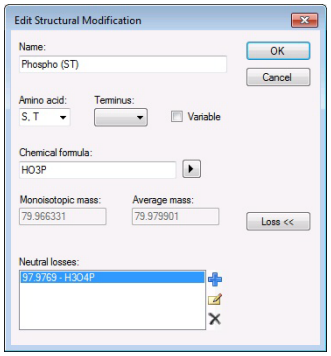
f Click the **Loss >>** button.

g Click the  button next to the **Neutral losses** list.

h Type `H3O4P` in the **Neutral loss chemical formula** box.

i Click the **OK** button in the **Edit Neutral Loss** dialog box.

j Click the **OK** button in the **Edit Structural Modification** dialog box.



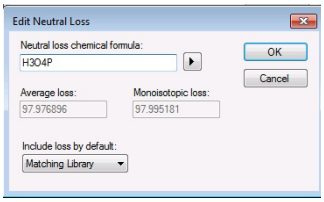


Figure 8 *Edit Structural Modification and Edit Neutral Loss dialog boxes*

k Select **Phospho (ST)** for the **S** modification.

l Click the **OK** button in the **Edit Modifications** dialog box.

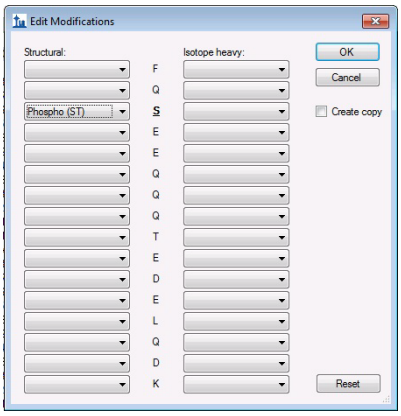


Figure 9 *Edit Modifications dialog box*

The protein name and the peptide are shown in the Skyline program. The Skyline program uses the Peptide Sequence and the values in the Filter tab of the Transition Settings to determine the precursors. Then, the Skyline program predicts the transitions.

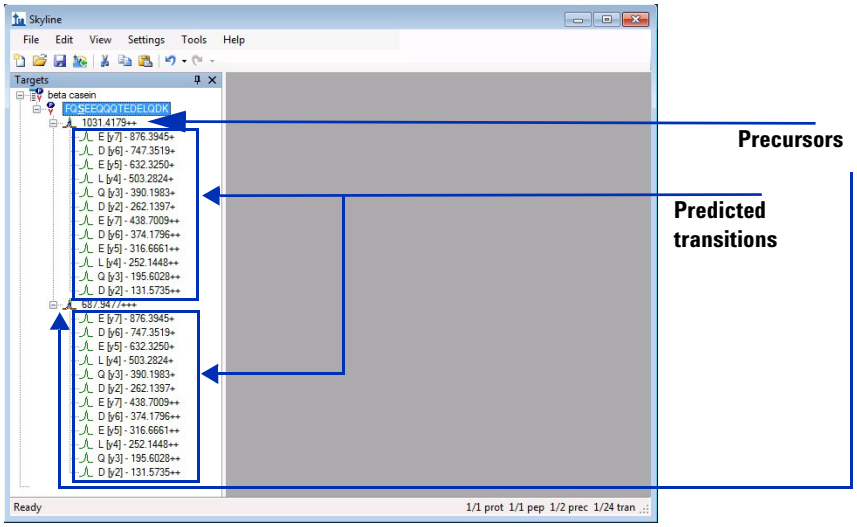


Figure 10 *Main window of the Skyline program*

Export method

You can either export a method directly from Skyline or you can export a transition list that you can import into the MassHunter Data Acquisition program. Exporting a method is the recommended option, but both options are documented here.

a Click **File > Export > Method**. The Export Method dialog box opens.

b Select **Agilent 6400 Series** as the **Instrument type**.

c Click the **Single method** button.

d Select **Collision Energy** for **Optimizing**.

e Select **Standard** for **Method type**.

f Click the **Browse** button. The Browse For Folder dialog box is opened.

g Select the method to use as a template in the **Template file** box. This method is an existing Data Acquisition method. All of the parameters in the existing Data Acquisition method are copied to the new method except for the Scan segments table. The Scan segments table is created from the information in Skyline. The Time segments table is taken from the template method's first Time segment row.

h Click **OK** in the Browse For Folder dialog box.

i Click **OK** in the **Export Method** dialog box.

j Click the **OK** button in the **Export Agilent 6400 Series Method** dialog box.

k Type a **File name** for the new method and click **Save**.

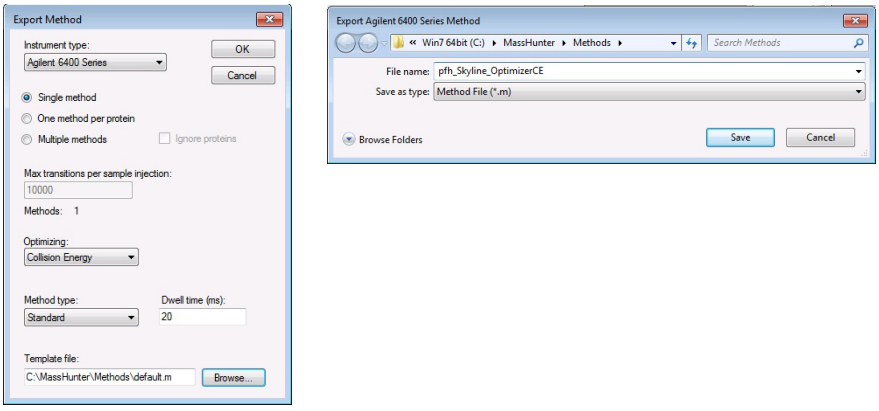


Figure 11 *Export Method and Export Agilent 6400 Series Method dialog boxes*

Export transition list

If you have not yet developed your template method, you can instead export a transition list. Then, when you create your method in the Data Acquisition program, you can paste this transition list into the Scan segments table.

a Click **File > Export > Transition List**. The Export Transition List dialog box is opened.

b Select **Agilent** as the **Instrument type**.

c Select **Collision Energy** for **Optimizing**.

d Select **Standard** for **Method type**.

e Click the **OK** button. The "Export Transition List" dialog box opens.

f Navigate to the folder where you want to save the list.

g Type a name for the transition list.

h Click the **Save** button.

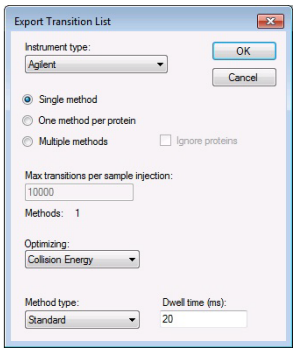


Figure 12 *Export Transition List dialog box*

i Select **Transition List (*.csv)** for the **Save as type**.

j Enter a **File name**. You can create a folder in MassHunter to store your CSV files.

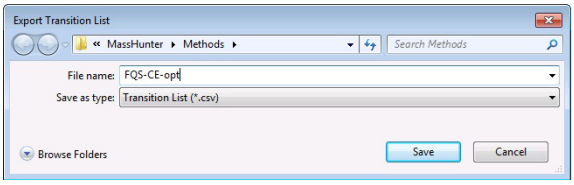


Figure 13 *Export Transition List dialog box*

k Click the **Save** button.

Save Skyline project

You can save this project; then, you can open this project at a future time.

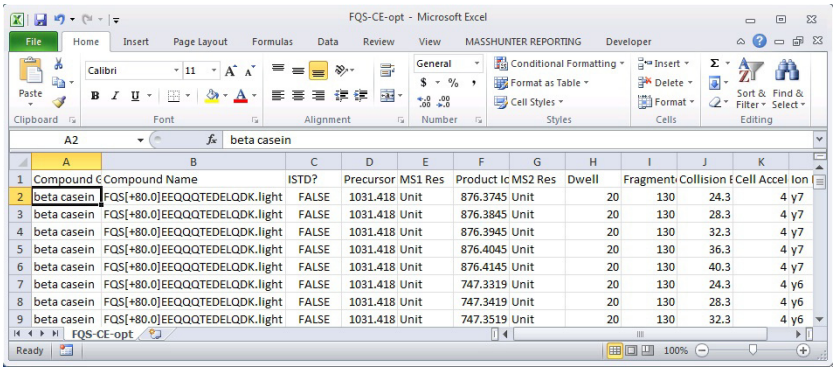
a Click **File > Save** or **File > Save As**.

b Type a name in the **Save As** dialog box.

c Click the **Save** button.

Format of CSV file

The format of the CSV file that contains the Transition List is:



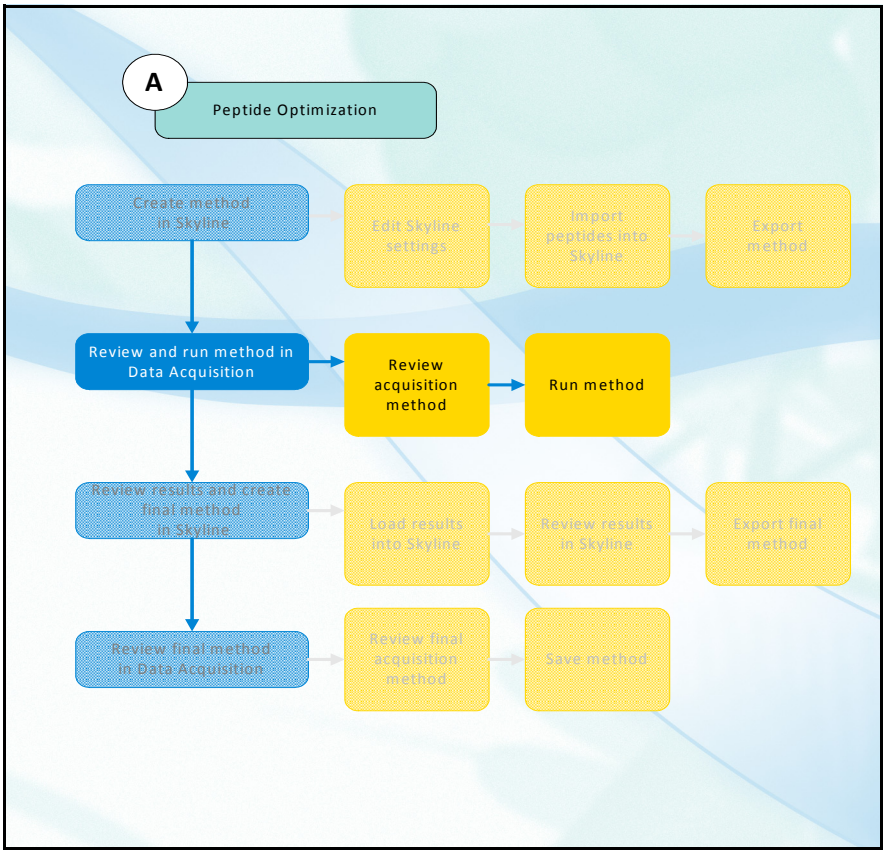
	A	B	C	D	E	F	G	H	I	J	K
1	Compound C	Compound Name	ISTD?	Precursor	MS1 Res	Product Ic	MS2 Res	Dwell	Fragmenti	Collision E	Cell Accel	Ion
2	beta casein	FQS[+80.0]EEQQQTEDELQDK.light	FALSE	1031.418	Unit	876.3745	Unit	20	130	24.3	4	y7
3	beta casein	FQS[+80.0]EEQQQTEDELQDK.light	FALSE	1031.418	Unit	876.3845	Unit	20	130	28.3	4	y7
4	beta casein	FQS[+80.0]EEQQQTEDELQDK.light	FALSE	1031.418	Unit	876.3945	Unit	20	130	32.3	4	y7
5	beta casein	FQS[+80.0]EEQQQTEDELQDK.light	FALSE	1031.418	Unit	876.4045	Unit	20	130	36.3	4	y7
6	beta casein	FQS[+80.0]EEQQQTEDELQDK.light	FALSE	1031.418	Unit	876.4145	Unit	20	130	40.3	4	y7
7	beta casein	FQS[+80.0]EEQQQTEDELQDK.light	FALSE	1031.418	Unit	747.3319	Unit	20	130	24.3	4	y6
8	beta casein	FQS[+80.0]EEQQQTEDELQDK.light	FALSE	1031.418	Unit	747.3419	Unit	20	130	28.3	4	y6
9	beta casein	FQS[+80.0]EEQQQTEDELQDK.light	FALSE	1031.418	Unit	747.3519	Unit	20	130	32.3	4	y6

Figure 14 *CSV file for the Transition List*

- Each transition has five rows in the transition list. There are two steps below the original collision energy and two steps above the original collision energy. Your file will contain (2 * Step Count + 1) rows for each transition.
- The collision energy increases by the step size that you set in "Edit the collision energy settings in the Transition Settings dialog box." on page 14.
- The Product Ion also changes slightly. The Skyline program uses those slight changes to keep track of which step it is on.
- Skyline always exports the transition list using **Unit** for the **MS1** and **MS2** resolution. You can modify the **MS1** and **MS2** resolution before or after you paste the transition list into the **Scan segments** table.

Create and run the method in Data Acquisition

In this exercise, you load the method created by Skyline and run it to optimize the collision energy. You could also import the transition list from Skyline and run a method that optimizes the collision energy. This task gives you the basic steps to set up an LC/MS method with the MassHunter Data Acquisition program. If you need more details and practice, see the *Agilent MassHunter Workstation Software – Data Acquisition for 6400 Series Triple Quadrupole LC/MS Familiarization Guide*.



Review acquisition method

1. Start the MassHunter Data Acquisition program.

   - Double-click the MassHunter Data Acquisition icon.

   If you need help, see Step 1 in the "Getting Started" section of the *Agilent 6400 Series Triple Quadrupole LC/MS System Quick Start Guide*.

2. Load the acquisition method from Skyline.

   a Click **Method > Open**. The "Open Method" dialog box is opened.

   b Navigate to the folder where you saved the method in Skyline.

c Select the method that you created in Skyline.

d Click the **Open** button.

3. (optional) Prepare the LC modules.

a Switch the LC stream to waste (or disconnect it from the MS).

b Purge the LC pump.

c Install the column and condition it as described in the column instructions included in the column package.

d Set up to view real-time parameter values (actuals).

e Set up to display real-time plots.

f Set the LC parameter values in the Method Editor window.

If you need help, see Step 2 in the "Getting Started" section of the *Agilent 6400 Series Triple Quadrupole LC/MS System Quick Start Guide*.

It is very important to purge solvent channels A and B because trapped air causes irreproducible retention times for analytes.

4. Prepare the Agilent 6400 Series Triple Quadrupole LC/MS System.

a Do a Checktune, or if necessary do an Autotune.

b Switch the LC stream to MS.

c Start the flow at initial method conditions.

d Monitor the MS baseline and spectral displays.

If you need help, see Step 3 in the "Getting Started" section of the *Agilent 6400 Series Triple Quadrupole LC/MS System Quick Start Guide*.

5. Review values for all the LC modules.

- In the MassHunter Data Acquisition program, review the parameters on each LC tab.

If you need help, see Step 4 in the "Getting Started" section of the *Agilent 6400 Series Triple Quadrupole LC/MS System Quick Start Guide*.

6. Review parameters on the QQQ tabs.

a Review parameters on the **Acquisition** tab.
   - Each transition has five rows in the Scan segments table. There are two steps below the original collision energy and two steps above the original collision energy.
   - The collision energy increases by the step size that you set in "Edit the collision energy settings in the Transition Settings dialog box." on page 14.
   - The Product Ion also changes slightly. The Skyline program uses those slight changes to keep track of which step it is on.

b Review parameters on the **Source** tab.

c Review parameters on the **Chromatogram** tab. You can specify which chromatograms to show in the Chromatogram Plot window during a run.

d Review parameters on the **Instrument** tab. You can specify which instrument curves to store on this tab.

7. Review the parameters on the DA tab.

You typically do not run Qualitative Analysis or Quantitative Analysis with this data file because the software doesn't know that these are the same compound since the product ions are different. Skyline changes the product ion to a slightly different value for each of the different collision energies as an internal way of keeping track of the collision energy optimization.

a Click the **DA** tab.

b Clear the **Qual Automation** check box on the Qual tab.

c Click the **Quant** tab.

d Clear the **Quant Automation** check box on the Quant tab.

8. Save the method.

a Click **Method > Save**.

Or, to save with a different name:

a Click **Method > Save As**.

b Enter a name for the method and click **OK**.

Import transition list

If you created a transition list, then the contents of the CSV file can be pasted directly into the Scan segments table using the shortcut command, **Paste from Clipboard**. You can follow the steps in the "Review acquisition method" on page 22 and then follow these steps to modify the Scan segments table.

1. Open the CSV file in Excel.

a Open the Excel program.

b Click the Microsoft Office button and then click **Open**.

c Navigate to the folder containing the CSV file and click **Open**. See Figure 14 on page 21.

2. Copy the transition list to the Clipboard.

a Select all of the cells in the transition list including the header.

b Click **Edit > Copy**. You can also press **Ctrl** and **C**.

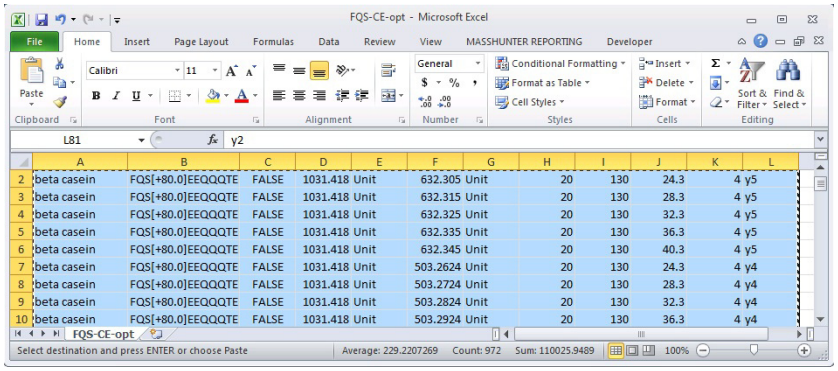


Figure 15 *After selecting all of the cells in the transition list*

3. Import the transition list.

a In the Data Acquisition program, click the **QQQ** tab in the Method Editor window.

b Make sure that you have saved your method before changing the **Scan Type**. The **Scan segments** table is reset to one, default line when the **Scan Type** is changed.

c Select **MRM** for the **Scan Type** in the first row of the **Time segments** table.

d Right-click the **Scan segments** table and click **Paste from Clipboard**.

e Select the first row in the **Scan segments** table. This row is the default row in the **Scan segments** table.

f Right-click the **Scan segments** table and click **Delete Row**.

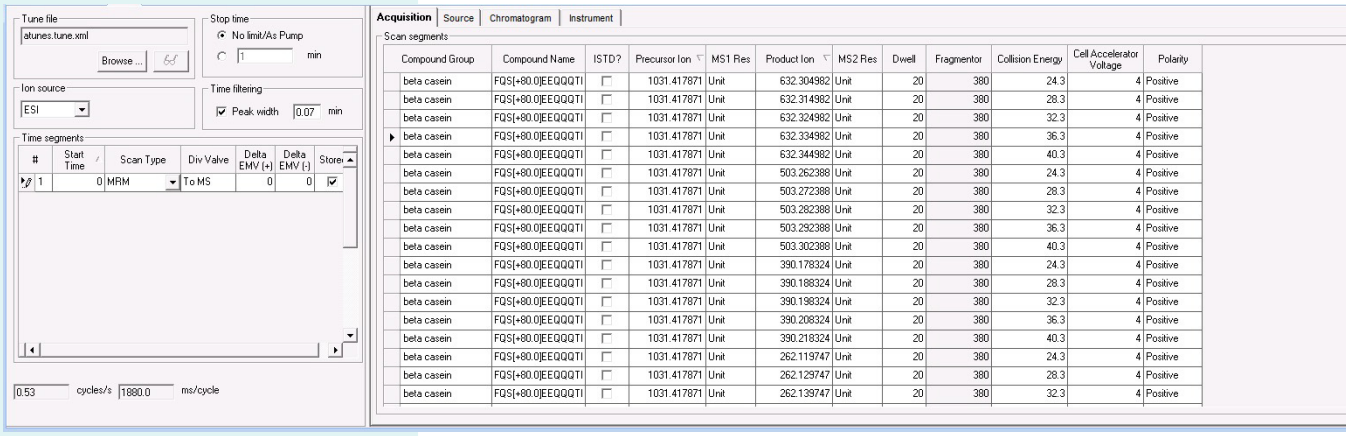


Figure 16 *The QQQ > Acquisition tab in the Method Editor window*

4. Save the method.

a Click **Method > Save**.

Or, to save with a different name:

a Click **Method > Save As**.

b Enter a name for the method and click **OK**.

Run the method

1. Start the MassHunter Data Acquisition program, if it is not currently running.

   - Double-click the MassHunter Data Acquisition icon.

   If you need help, see Step 1 in the "Getting Started" section of the *Agilent 6400 Series Triple Quadrupole LC/MS System Quick Start Guide.*

2. Load your method.

3. Edit the information in the Sample Run window.

   a Type a **Name** for the Sample.

   b Type a **Comment** for the Sample.

   c Type a **Name** for the Data File.

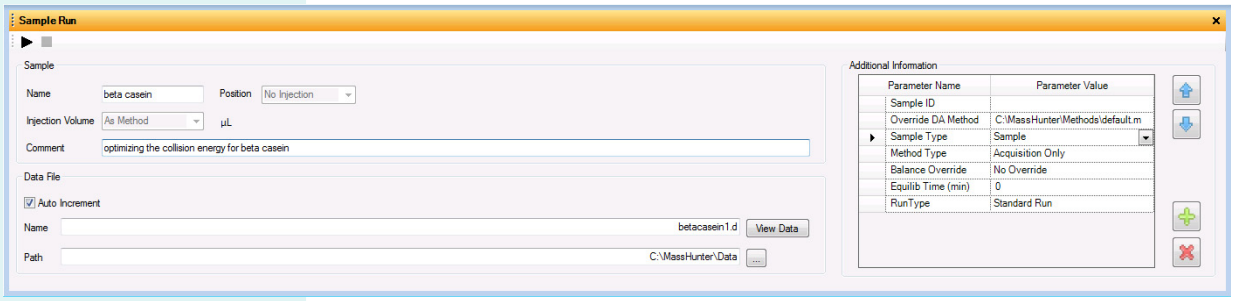


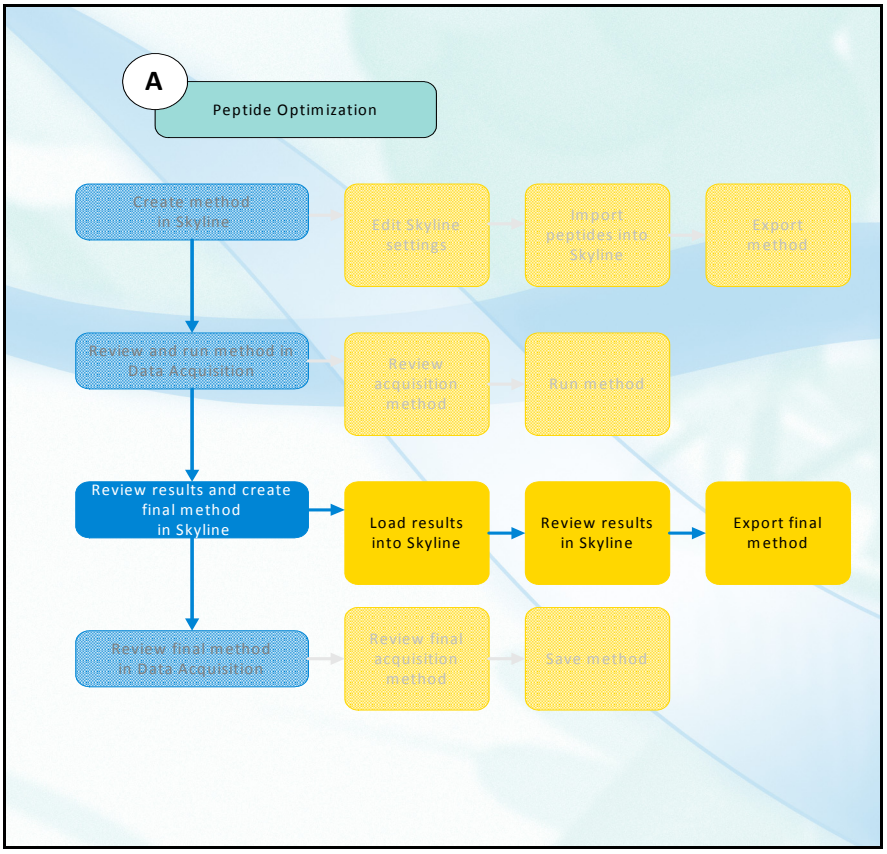
Figure 17 *The Sample Run window*

4. Run the method.

   - Click **Sample > Run**.
   - Click the icon in the toolbar in the Sample Run window.
   - Click the icon in the main toolbar.

Review results and export final method from Skyline

This section shows you how to create the final optimized method. You first need to import the results from the data file you created in "Create and run the method in Data Acquisition" on page 22. Then, you can graphically review the results and then export a Dynamic MRM method.



Load results into Skyline

1. Start Skyline program.

   - From the Start button in the All Programs list, click **Skyline > Skyline**.

2. Open the Skyline project.

   a Load the settings that you saved in "Save the settings for future use." on page 16. A menu item with the name you used to save the settings is added to the Settings menu when you saved the settings.

   b Click **File > Open**.

   c In the Open dialog box, select the project you saved in "Export method" on page 18.

3. Import results.

   a Click **File > Import > Results**.

   b Click the **Add one new replicate** button.

c Type a **Name** for the import. In this example, **Name** is set to `FQS opt`.

d Select **Collision Energy** from the **Optimizing** list.

e Click the **OK** button.

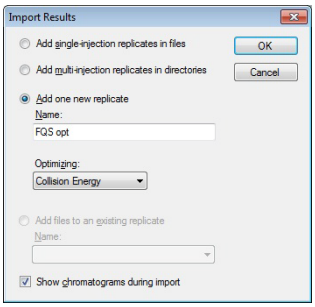


Figure 18 *The Import Results dialog box*

f In the **Import Results Files** dialog box, select the data file you created in "Create and run the method in Data Acquisition" on page 22.

g Select **Agilent Data** for the **Sources of type** box.

h Click the **Open** button.

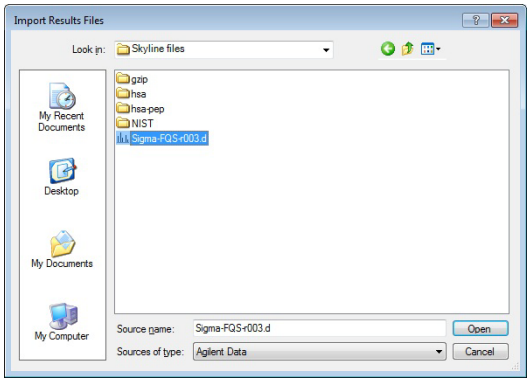


Figure 19 *The Import Results Files dialog box*

Review results in Skyline

The graphical user interface contains a lot of information.

- A green dot next to a product ion means that the transition was found in the data file.
- The numbers after the peptide represents the relative abundance of that transition compared to the other transitions for that peptide. This value helps when you have optimized more transitions than you will use in the final method which is the typical method development strategy.
- If you place the mouse over the items in the list, a tooltip is displayed which gives you more information.
- You can change the graphs that are displayed using the commands in the View menu.

- You can right-click each graph to change how the graph is displayed. For example, you can right-click the graph and click **Transitions > Single** to display the transitions as a bar graph or click **Transitions > Total** to display the transitions stacked together. You can also use the commands in the View menu.
- If a green dot is beside a precursor ion, then all of the selected transitions were found.
- If a yellow dot is beside a precursor, then at least one of the selected transitions was not found.
- If a red dot is beside a precursor, that means that over half of the selected transitions were not found.

Figure 20 *Skyline program after importing results file*

1. Select the transitions that were found.

a Click the down arrow next to the precursor ion. This arrow is visible when you move the mouse over the precursor in the list.

b In the list that is displayed, mark the transitions that have a green dot next to them. The transitions with a green dot next to them are found. Clear the check box for each transition that does not have a green dot next to it.

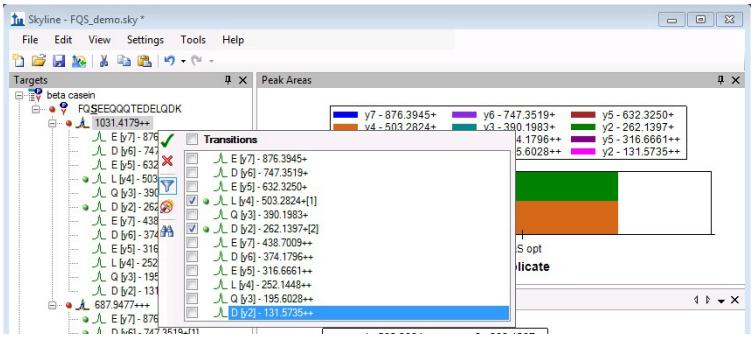


Figure 21 *Marking the transitions that were found*

c Click the green check mark icon to save the changes.

NOTE: In this example, only the transitions that were found are marked.

2. Examine each transition to see which collision energy created the greatest peak area.

a Right-click the Peak Areas graph and click **Selection** if it does not have a check next to it. When **Selection** is marked, then a line is drawn from the maximum collision energy to the y-axis.

b Click a transition in the list.

c Right-click the Peak Areas graph and click **Transitions > Single**.

d Examine the Peak Areas graph to determine the collision energy that produces the greatest peak area.

e Examine the FQS opt tab to see the overlay of the peaks. This graph is also color coded. You can customize this graph when you right-click and click **Properties**.

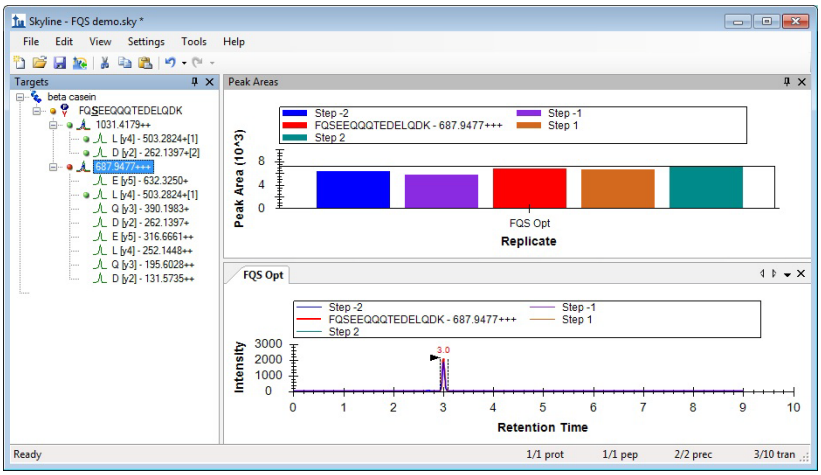


Figure 22 *Comparing collision energies for the same transition*

3. (optional) Edit the regression parameters to change the initial equation.

Typically, you only want to determine a new equation if you have a much bigger distribution of peptides. However, this example is included for demonstration purposes.

a Click **Settings > Transition Settings**.

b Click the **Prediction** tab.

c Select **Transition** for **Optimize by**.

d Select **Edit list** from the Collision energy list.

e Click **Agilent QQQ** in the Edit Collision Energy Regressions dialog box, and then click the **Edit** button.

f In the Edit Collision Energy Equation dialog box, click the **Show Graph** button.

g Examine the different graphs. The slope and the intercept are shown for each different charge state. Click **Close** to close the **Regression** dialog box.

h If you want to use the new information, click the **Use Results** option. Otherwise, click **Cancel** to close the **Edit Collision Energy Equation** dialog box. Then, click **Cancel** to close the **Edit Collision Energy Regressions** dialog box. Finally, click **Cancel** in the **Transition Settings** dialog box.

Export final method

You do the following steps to use the optimal collision energies for a peptide or set of peptides to create a final method. You can also export a final transition list. You can use this transition list to create a method in the Agilent Data Acquisition program.

a Click **File > Export > Method**.

b In the Export Method dialog box, select **Agilent 6400 Series** as the **Instrument type**.

c Click the **Single method** button.

d Select **None** for Optimizing.

e Select **Scheduled** as the **Method type**.

f Click the **Browse** button. The Browse For Folder dialog box is opened.

g Select the method to use as a template in the **Template file** box. This method is an existing Data Acquisition method. All of the parameters in the existing Data Acquisition method are copied to the new method except for the **Time segments** table and the **Scan segments** table. The **Time segments** table and the **Scan segments** table are created from the information in Skyline.

h Click **OK** in the Browse For Folder dialog box.

i Click the **OK** button in the Export Method dialog box.

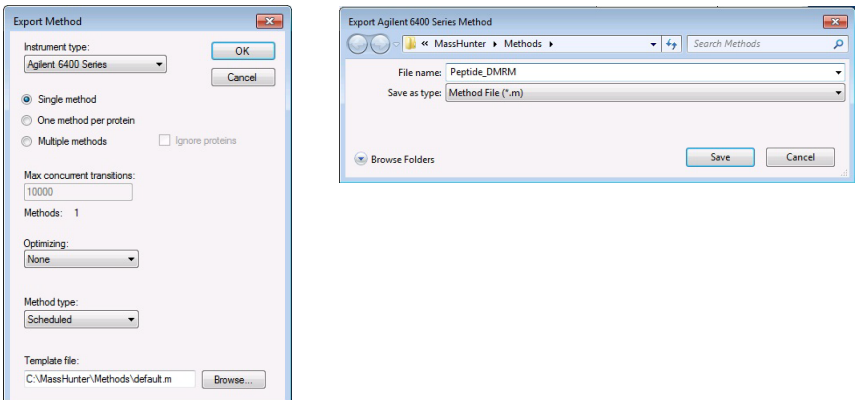


Figure 23 *Export Method and Export Agilent 6400 Series Method dialog boxes*

j In the Export Agilent 6400 Series Method dialog box, select **Method File (*.m)** as the **Save As type**.

k Enter a name for the method and click the **Save** button.

Export final transition list

If you do not have a method to use as the Template file, you can export a transition list instead of a method. You can paste this transition list into the Scan segments table in the MassHunter Data Acquisition program.

a Click **File > Export > Transition List**.

b In the Export Transition List dialog box, select **Agilent** as the Instrument type.

c Select **Scheduled** as the Method type.

d Click the **Single method** button.

e Select **None** for Optimizing.

f Click the **OK** button.

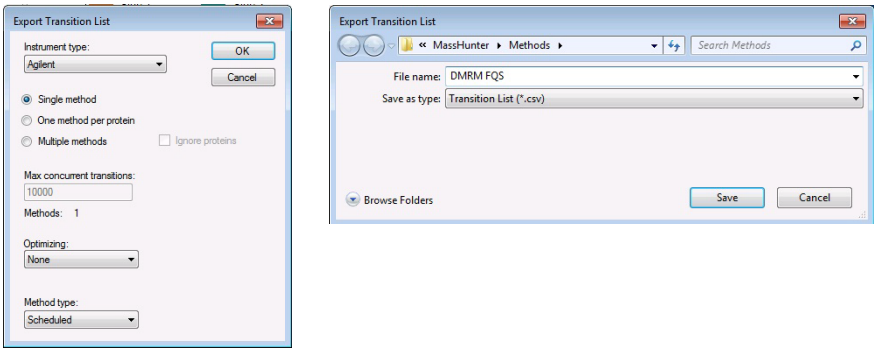


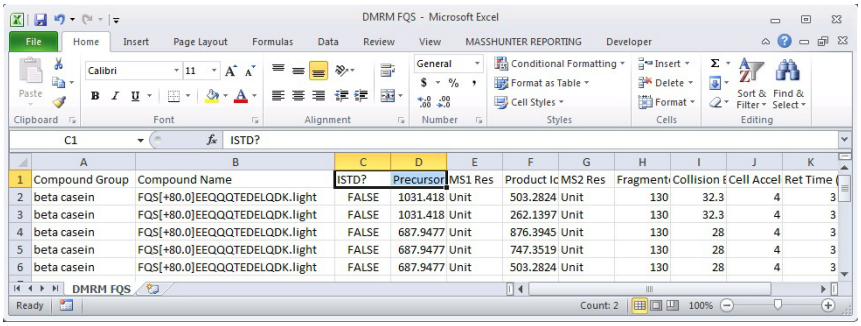
Figure 24 *Export Transition List - page 1 and page 2*

g In the next **Export Transition List** dialog box, select **Transition List (*.csv)** as the **Save as type**.

h Enter a name for the transition list and click the **Save** button.

Format of the final transition list file

The final Transition List contains only one line for each transition including the optimized collision energy:

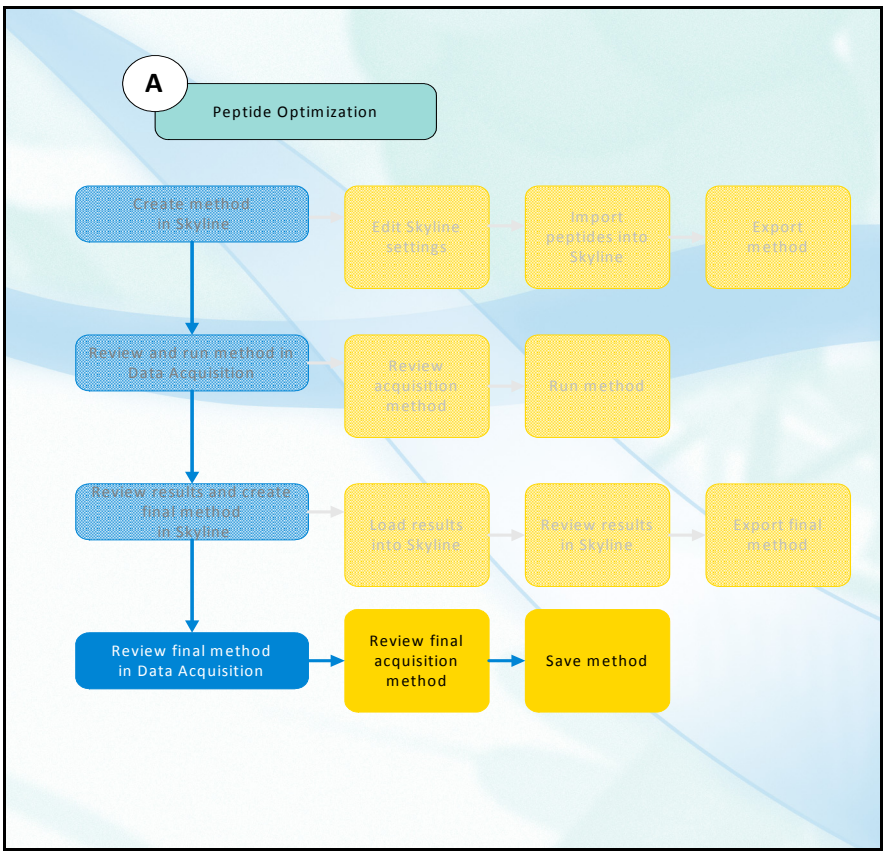


	A	B	C	D	E	F	G	H	I	J	K
1	Compound Group	Compound Name	ISTD?	Precursor	MS1 Res	Product Ic	MS2 Res	Fragment	Collision E	Cell Accel	Ret Time (
2	beta casein	FQS[+80.0]EEQQQTEDELQDK.light	FALSE	1031.418	Unit	503.2824	Unit	130	32.3	4	3
3	beta casein	FQS[+80.0]EEQQQTEDELQDK.light	FALSE	1031.418	Unit	262.1397	Unit	130	32.3	4	3
4	beta casein	FQS[+80.0]EEQQQTEDELQDK.light	FALSE	687.9477	Unit	876.3945	Unit	130	28	4	3
5	beta casein	FQS[+80.0]EEQQQTEDELQDK.light	FALSE	687.9477	Unit	747.3519	Unit	130	28	4	3
6	beta casein	FQS[+80.0]EEQQQTEDELQDK.light	FALSE	687.9477	Unit	503.2824	Unit	130	28	4	3

Figure 25 *CSV file for the Final Transition List*

Review final method in Data Acquisition

This exercise shows you reviewing the final method. You can also review importing the final transition list.



Review acquisition method

1. Start the MassHunter Data Acquisition program.

- Double-click the MassHunter Data Acquisition icon.

If you need help, see Step 1 in the "Getting Started" section of the *Agilent 6400 Series Triple Quadrupole LC/MS System Quick Start Guide*.

2. Load the acquisition method from Skyline.

a Click **Method > Open**. The **Open Method** dialog box is opened.

b Navigate to the folder where you saved the final method in Skyline.

c Select the final method that you created in Skyline.

d Click the **Open** button.

3. Review values for all the LC modules.

- In the MassHunter Data Acquisition program, review the parameters on each LC tab.

If you need help, see Step 4 in the "Getting Started" section of the *Agilent 6400 Series Triple Quadrupole LC/MS System Quick Start Guide*.

4. Review parameters on the QQQ tabs.

a Review parameters on the **Acquisition** tab.

b Review parameters on the **Source** tab.

c Review parameters on the **Chromatogram** tab. You can specify which chromatograms to show in the Chromatogram Plot window during a run.

d Review parameters on the **Instrument** tab. You can specify which instrument curves to store on this tab.

5. Review the parameters on the DA tab.

a Click the **DA** tab.

b Review the parameters on the **Qual** tab.

c Click the **Quant** tab.

d Review the parameters on the **Quant** tab.

Import final transition list

If you created a final transition list, then you follow these instructions to create a final method.

1. Open the method.

- Click **Method > Open** or click the Open Method icon on the main toolbar. Open the method to which you want to add the **Scan segments**.

2. Open CSV file in Excel.

a Open the Excel program.

b Click the Microsoft Office button and then click **Open**.

c Navigate to the folder containing the CSV file and click **Open**. See Figure 25 on page 33.

3. Copy the transition list to the Clipboard.

a Select all of the cells in the transition list including the header.

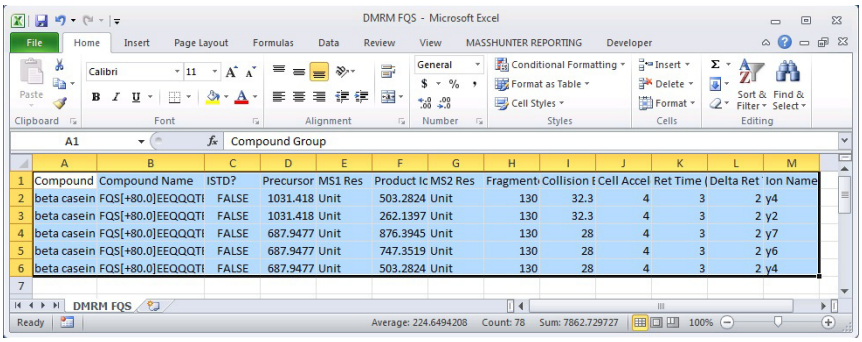


Figure 26 *After selecting all of the cells in the final transition list*

b Click **Edit > Copy**. You can also press **Ctrl** and **C**.

4. Import the transition list.

a In the Data Acquisition program, click the **QQQ** tab in the Method Editor window.

b Make sure that you have saved your method before changing the **Scan Type**. The **Scan segments** table is reset to one, default line when the **Scan Type** is changed.

c Select **Dynamic MRM** for the **Scan Type** in the first row of the **Time segments** table.

d Right-click the **Scan segments** table and click **Paste from Clipboard**.

e Select the first row in the **Scan segments** table. This row is the default row in the **Scan segments** table.

f Right-click the **Scan segments** table and click **Delete row**.

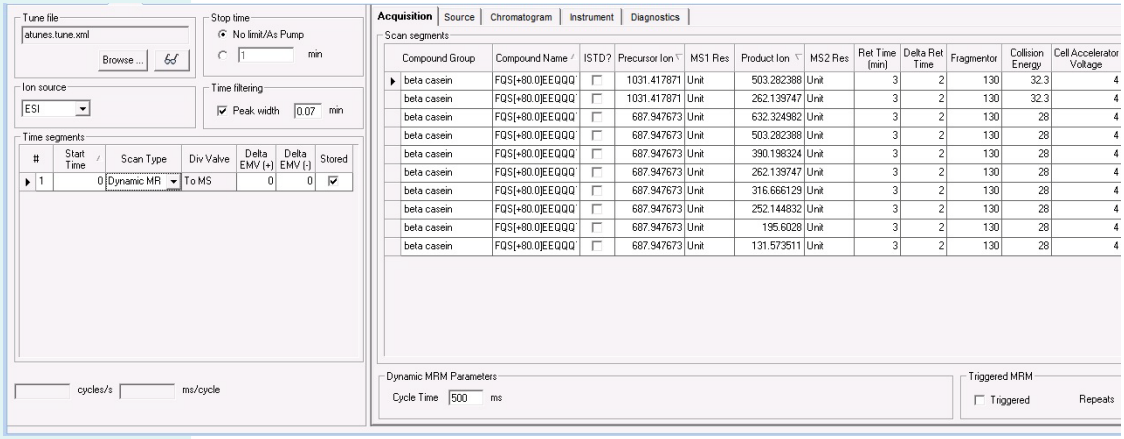


Figure 27 *The QQQ > Acquisition tab in the Method Editor window*

5. Review parameters on the other MS tabs.

a Review parameters on the **Source** tab.

b Review parameters on the **Chromatogram** tab. You can specify which chromatograms to show in the Chromatogram Plot window during a run.

c Review parameters on the **Instrument** tab. You can specify which instrument curves to store on this tab.

Save the method

a Click **Method > Save**.

Or, to save with a different name:

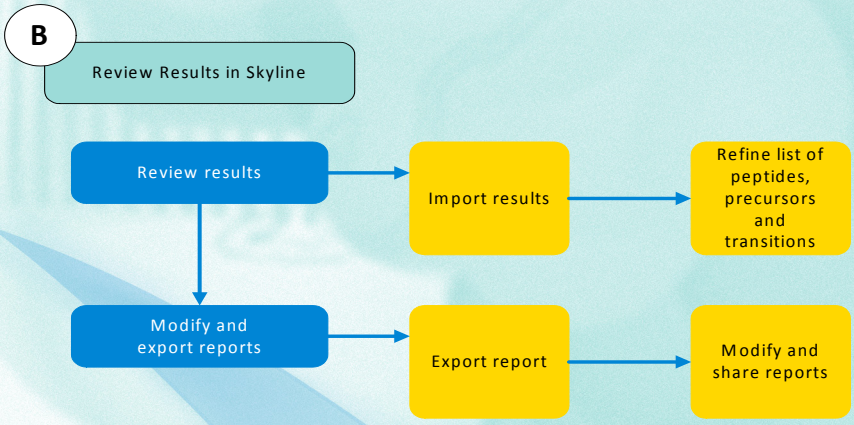
a Click **Method > Save As**.

b Enter a name for the method and click **OK**.

Review Results in Skyline

These exercises show you how to use Skyline to review the proteins, peptides and transitions. You can remove proteins, peptides and transitions, and you can also add other proteins, peptides, and transitions.

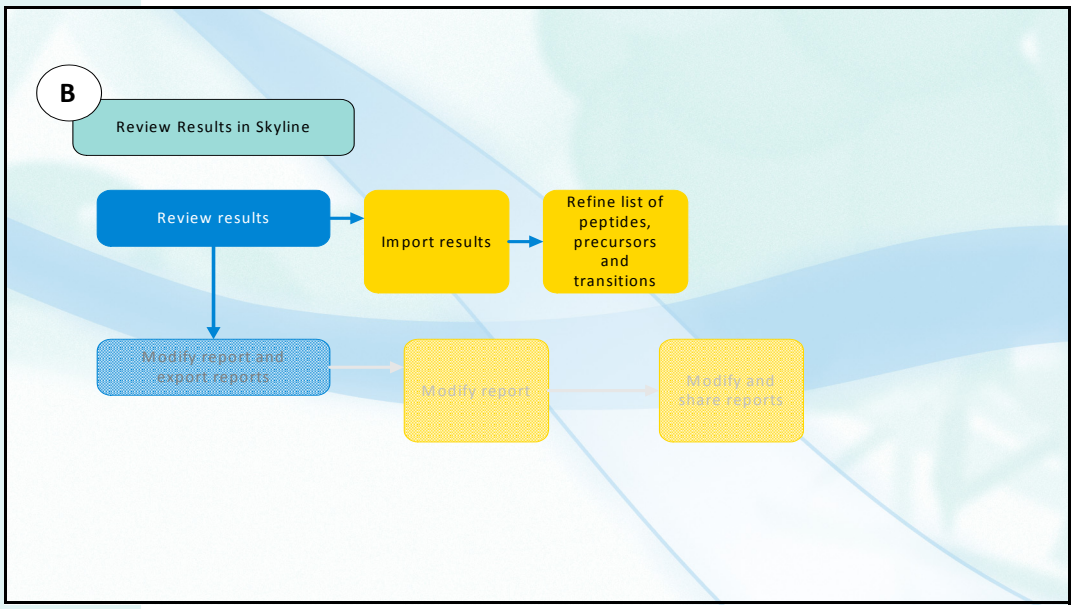
You can also export reports which are CSV files. The CSV file contains a table with quantitative information for each data file that is opened. You can load this CSV file into Excel or another program to do further analysis.



Agilent Technologies

Review results

In this exercise, you learn several different techniques for reviewing and refining your data in Skyline. When you refine your data, you change the proteins, peptides and transitions that are included. Your data files and knowledge of your experiment help you make changes to the proteins, peptides and transitions.



Import results

1. Start the Skyline program.

   - From the Start button in the All Programs list, click **Skyline > Skyline**.

2. Select previously saved settings.

   - In the **Settings** menu, click the name of the settings that you saved in "Save the settings for future use." on page 16.

3. Paste list of proteins or peptides.

   In this example, human serum albumin is loaded by opening an existing Skyline project.

   a Click **File > Open**.

   b Select **hsa-pep-demo.sky**.

   c Click the **OK** button.

   It is possible to import proteins and peptides in several different ways:
   - Open an existing project.
   - Copy the protein or peptides into the Clipboard and paste them into Skyline.
   - Click **Edit > Insert > FASTA** and select a FASTA file to import.
   - Click **Edit > Insert > Proteins** and specify the proteins to import.
   - Click **Edit > Insert > Peptides** and specify the peptides to import.

4. Modify the peptides.

If necessary, you can modify the peptides after loading the list.

a Right-click the name of the peptide and then click **Modify**.

b Click the arrow next to the amino acid that you want to modify. NOTE: If the amino acid appears multiple times in the peptide, you need to apply the modification to each amino acid.

c Click the modification if it is available. If not, do the following:
- Click **Add**.
- Enter the information for your modification.
- Click the **OK** button.

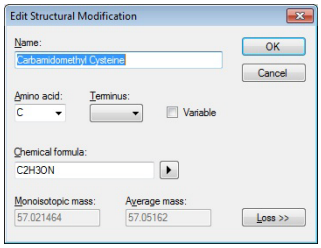
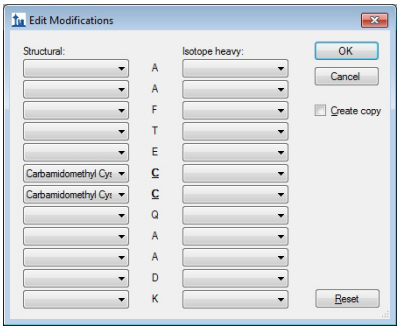


Figure 28 *Add or Edit Structural Modifications dialog box*

d Click the **OK** button.



Each amino acid in the peptide is listed in order, so you can modify any of the amino acids in the peptide. In this example, the first two amino acids are both alanine, and the last amino acid is lysine. This peptide contains two cysteines which are both modified.

Figure 29 *Edit Modifications dialog box*

5. (optional) Select a library.

a Click **Settings > Peptide Settings**. The **Peptide Settings** dialog box opens.

b Click the **Library** tab.

c Mark the library to use. If no libraries are listed, you can either click **Cancel** or see "Downloading a library" on page 65 for information on getting a library.

d Review the other parameters on this tab.

e Click **OK**.

6. Save the project.

- Save the document. Click **File > Save** or **File > Save As** to save the current proteins/peptides in a Skyline project. Type a **File name** and click the **Save** button.

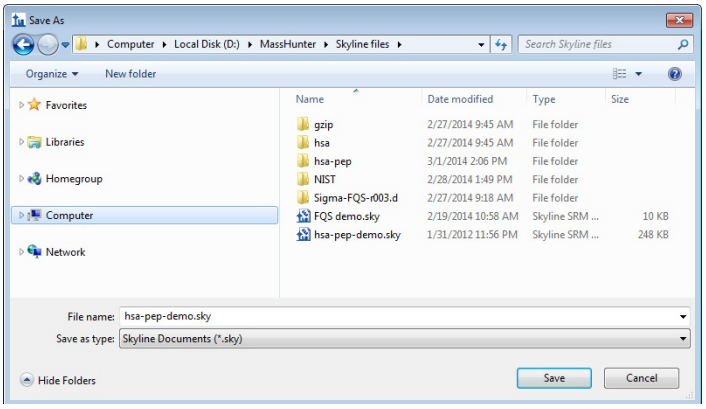


Figure 30 *Save As dialog box*

Import data file or data files

To start reviewing the list of predicted transitions, you first load a data file. After doing an initial review, you can import multiple replicates (see "Import replicate data files." on page 44).

7. Import one data file.

a Click **File > Import > Results.**

b Click the **Add one new replicate** button.

c Select **None** from the Optimizing list. See "Review results and export final method from Skyline" on page 27 for more information on using Skyline to optimize the collision energy.

d Click the **OK** button.

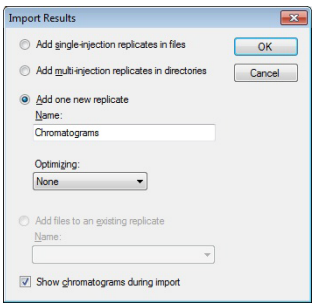


Figure 31 ***Import Results*** *dialog box*

e Select **Agilent Data** from the **Sources of type** list.

f Navigate to your data file. Select one of the data files.

g Click the **Open** button.

Refine list

Skyline has many tools to allow you refine the list of transitions. The following methods are described in this section:

- Remove peptides that are not present in the data file
- Change the transitions that are selected

Skyline can automatically refine proteins and peptides when you use the commands in the **Edit > Refine** menu.

1. Remove peptides that were not present in the data file.

a Select a precursor in the tree view.

b If you see a green dot next to the peptide, then the specified transitions were found in the data file. You probably will keep this peptide in the list. You can manually review the transitions to make a final decision.

c Expand the precursor to show the predicted transitions.

d If no dot is shown next to the precursor, then none of the selected transitions were found. Click the arrow next to the precursor and examine the list of transitions.

e If none of the transitions have a green dot next to them, then no transitions were found in the data file. Click the green check mark. You may decide to delete this precursor.

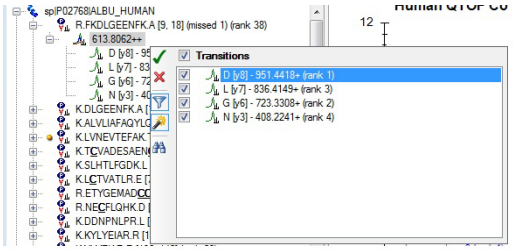


Figure 32 *No transitions were found for this precursor*

f If no precursors exist for a peptide, then delete the peptide. If you cannot expand the peptide, then no precursors exist.

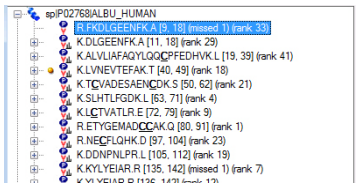


Figure 33 *No precursors were found for this peptide*

2. Change selected transitions for a peptide.

You can also change the transitions that are selected for a precursor. If the dot before the precursor is orange, then one or more selected transitions were not found.

a Select a precursor for a peptide in the tree view.

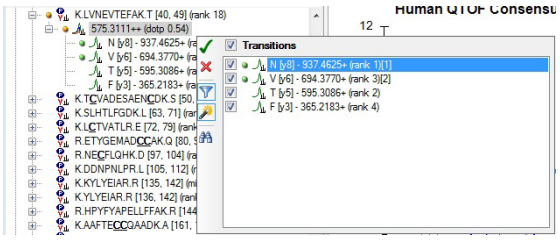


Figure 34 *This precursor is missing some of the selected transitions.*

b Mark the check boxes next to the transitions that have a green dot next to them.

c Clear the check boxes next to the transitions that do not have a green dot next to them.

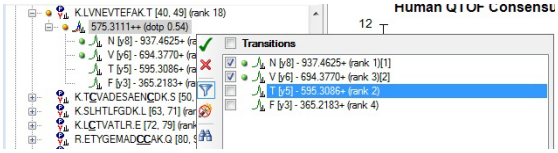


Figure 35 *Only the transitions that were found are marked.*

d Click the green check mark to keep changes in the **Transitions** list.

- A green dot is placed next to the precursor because all of the transitions are found. If all of the precursors have a green dot next to them, then the peptide also has a green dot next to it.
- The number in brackets at the end of the list of transitions shows the peak rank by area of the coeluting peaks for a precursor. In this example, the three most abundant peaks by peak area are found.
- If you selected a library in the Peptide Settings dialog box, then the rank of that peak in the library spectrum is also shown. The number in parentheses with the word "rank" shows you how large that peak is in the library spectrum. If the rank of the peak in the library spectrum is approximately the same as the peak rank of the spectrum, that is an indication that the peptide is correctly identified.

---

3. Import replicate data files.

If you have multiple replicates available, it may be useful to load the replicates before deleting more peptides. The deleted peptides may be available in one of the replicates.

a Click **File > Import > Results**.

b Click the **Add files to an existing replicate** button.

c Select the **Name** to which to add the replicates.

d Click the **OK** button.

e Select the replicate data files that you acquired. You can select a range of data files by pressing the **Ctrl** key while selecting a file. To select a range of data files, you select the first data file in the range. Then, you press the **Shift** key while selecting the last data file in the range.

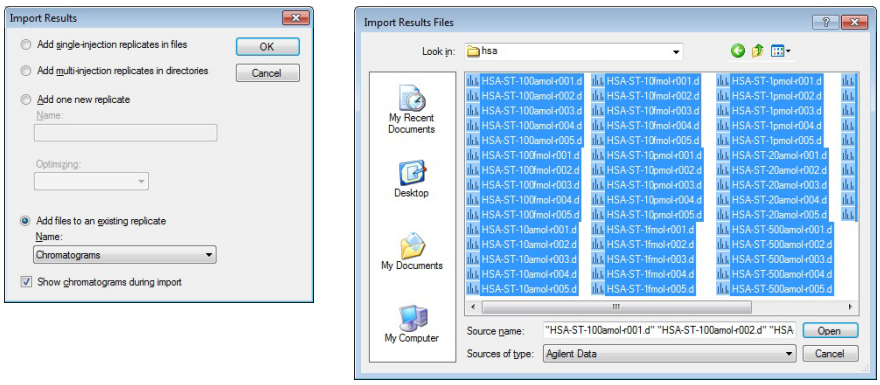


Figure 36 *Import replicates by clicking* ***Add files to an existing replicate***

f Click the **Open** button.

4. Display the retention time graph.

- Click **View > Retention Times > Replicate Comparison**.
- You can rearrange the windows to different positions if the window has a tab. You drag the window by the tab to reposition it.

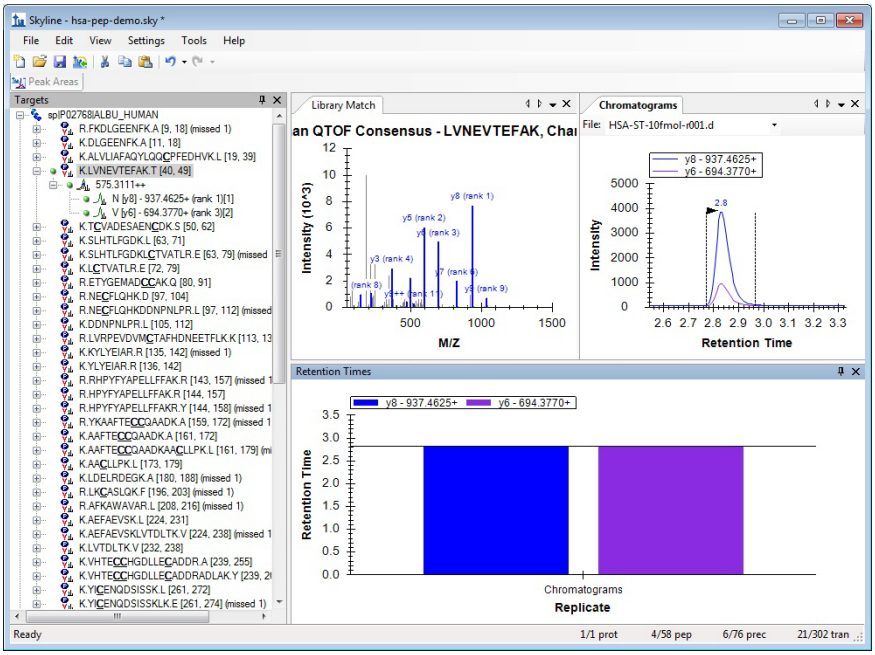


Figure 37 *The Library Match, Chromatograms and Retention Times windows*

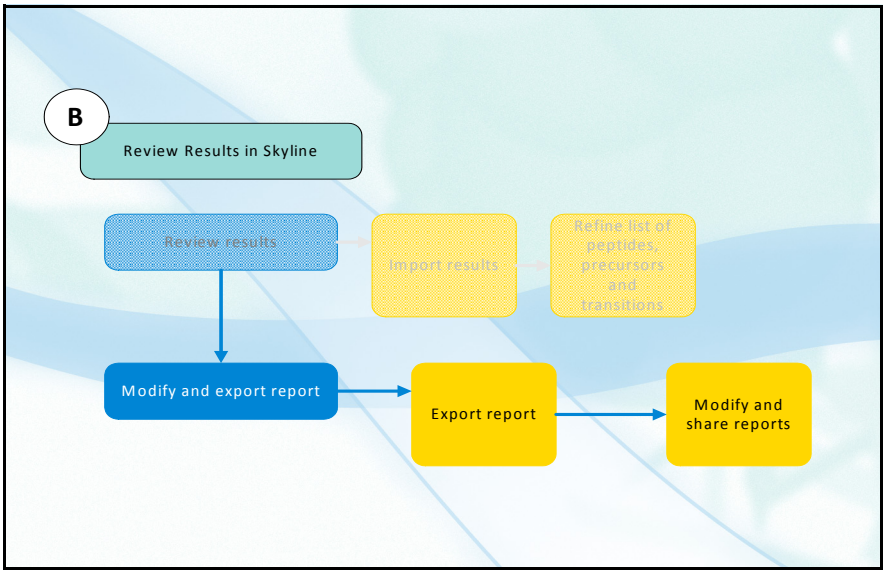
5. Remove additional peptides and transitions.

- In this example, these data files only contain one peptide, so all of the other peptides can be removed.

Modify and export reports

In this exercise, you learn how to modify and export a report. A report in Skyline is a CSV file. It contains a single table with many columns of information. Each row in the table is a different sample. You can load the report file into Excel to continue to review the data.

You can use the tools provided by Skyline to create and save new reports. You can add many new columns to the existing reports, and you can remove the columns that the report starts with. The output of a report is a CSV (comma separated variables) file.



Export report

When Skyline is installed, three report definitions are installed:

- Peptide Ratio Results definitions
- Peptide RT Results definitions
- Transition Results definitions

This exercise shows you how to export a report. The next exercise shows you how to modify and save a new report definition. You also learn how to import a report definition from a file.

1. Display the Export Report dialog box.

   - Click **File > Export > Report**.

2. Export a report.

   a Select the report that you want to export.

   b (optional) Click **Preview**. The Preview Report dialog box is opened, and you can review the report on the screen. You use this feature to make sure that the correct columns are included in the report and that all of the information is being displayed properly. Click the red **X** to close the Preview Report dialog box.

   c Click the **Export** button. The **Save As** dialog box opens.

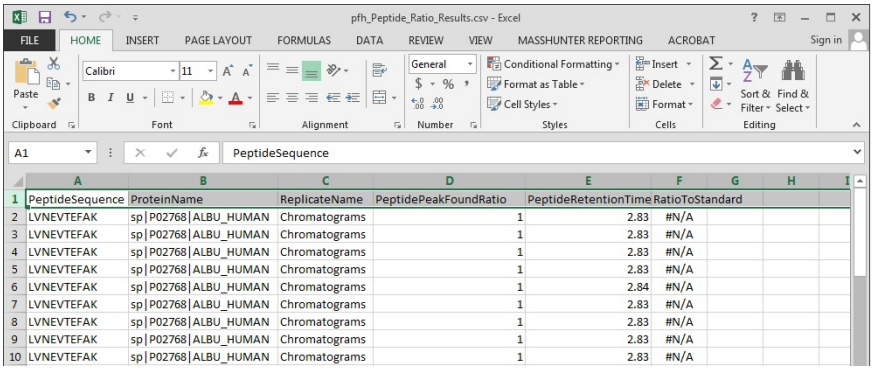
d Type a new **File name**. The default name of the File name is the name of the current project. If you do not type a unique name for the report, you are asked whether or not to replace the file.

e Click the **Save** button.

f Close the **Peptide Ratio Results** dialog box.

Open CSV file in Excel.

You can open this CSV file in Excel or another program. Then, you can use additional features in Excel to further process the data.



	A	B	C	D	E	F
1	PeptideSequence	ProteinName	ReplicateName	PeptidePeakFoundRatio	PeptideRetentionTime	RatioToStandard
2	LVNEVTEFAK	sp|P02768|ALBU_HUMAN	Chromatograms	1	2.83	#N/A
3	LVNEVTEFAK	sp|P02768|ALBU_HUMAN	Chromatograms	1	2.83	#N/A
4	LVNEVTEFAK	sp|P02768|ALBU_HUMAN	Chromatograms	1	2.83	#N/A
5	LVNEVTEFAK	sp|P02768|ALBU_HUMAN	Chromatograms	1	2.83	#N/A
6	LVNEVTEFAK	sp|P02768|ALBU_HUMAN	Chromatograms	1	2.84	#N/A
7	LVNEVTEFAK	sp|P02768|ALBU_HUMAN	Chromatograms	1	2.83	#N/A
8	LVNEVTEFAK	sp|P02768|ALBU_HUMAN	Chromatograms	1	2.83	#N/A
9	LVNEVTEFAK	sp|P02768|ALBU_HUMAN	Chromatograms	1	2.83	#N/A
10	LVNEVTEFAK	sp|P02768|ALBU_HUMAN	Chromatograms	1	2.83	#N/A

Figure 38 Excel Program with the CSV file from the Peptide Ratio Results default exported report

Modify and share reports

Skyline allows you to customize a report. You can remove columns from the report and add other columns. When you have created the report definitions, you can save the report definition to a file and move it to other computers in your lab.

1. Modify a report.

a Click **File > Export > Report**.

b Click the **Edit list** button.

c Select a report that closely matches the report that you want to create.

d Click the **Copy** button. The **Edit Report** dialog box is opened.

e Type a name for the **View Name**.

f Remove any columns that you do not want to include in your report. Click the item in the right column and then click the  button.

g Add values to the report. Select the value from the left column that you want in your report. Click the **Add >** button. You can only add a value to the report one time.

h Arrange the items in the report in the order that you want them to appear in the report. You click the  button to move an item up in the list, and you click the  button to move an item down in the list.

The first item in the list is the first item in the exported table.

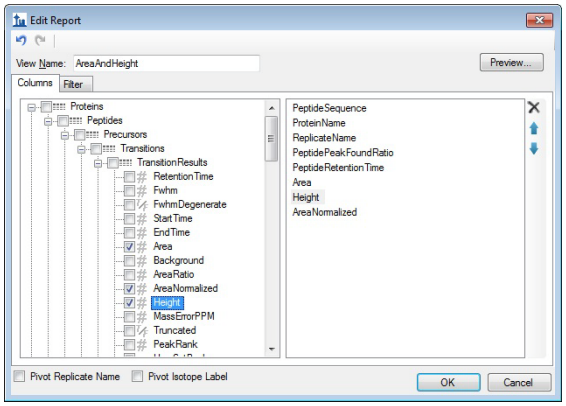


Figure 39 Edit Report dialog box

i Click the **Preview** button. Examine the report to see if all columns are included.

Click the  button to close the Preview Report dialog box.

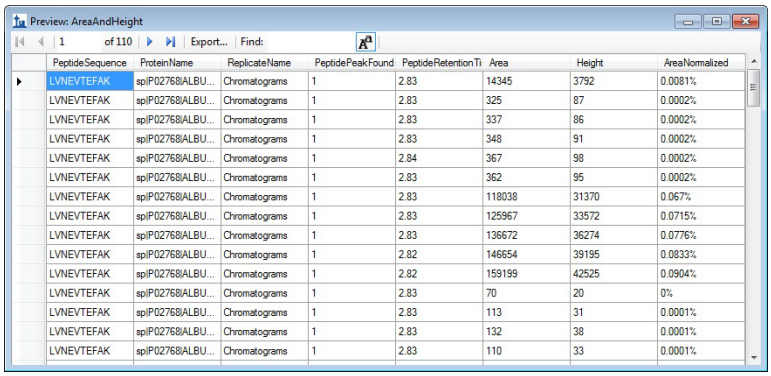


Figure 40 Preview Report dialog box

j Click the **OK** button in the Edit Report dialog box.

A report with the name you entered is added to the list of possible reports in the Edit Reports dialog box.

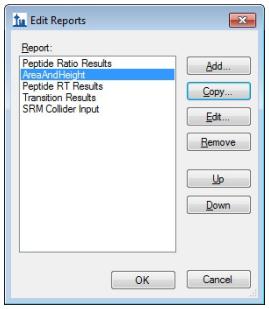


Figure 41 Edit Reports dialog box

k In the **Edit Reports** dialog box, click the **OK** button.

2. Save the report definitions (share a report).

l In the **Export Report** dialog box, click the **Cancel** button.

a Click **File > Export > Report**.

b In the Export Report dialog box, click the **Share** button.

c In the **Save Report Definitions** dialog box, mark the check box next to the Report Definitions that you want to save. Then, click the **OK** button.

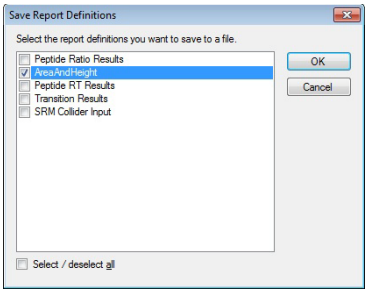


Figure 42 Save Report Definitions dialog box

d In the Save As dialog box, type the File name that you want to use to save the report definitions. Reports have the extension "skyr".

e Click the **Save** button.

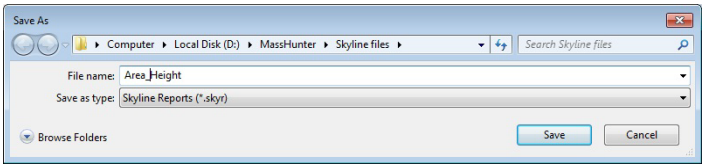


Figure 43 Save As dialog box

3. Import a report.

You can add a report to the list that you created and shared. Thus, you can move a report from one computer to another computer in your lab.

a Click **File > Export > Report**.

b Click the **Import** button. The **Open** dialog box is opened.

c Select the report that you want to be able to use in this program. Reports have the extension “skyr”.

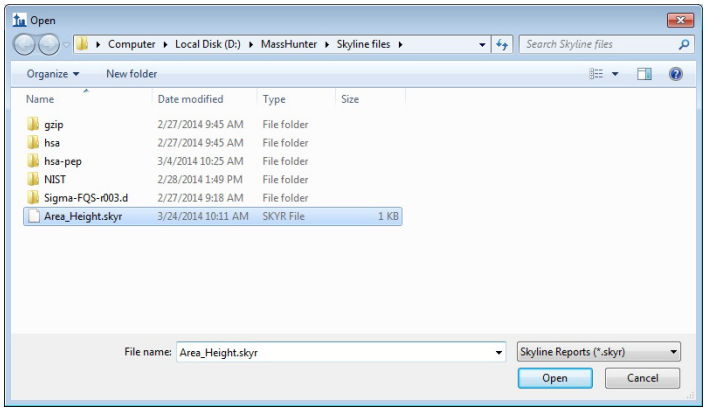


Figure 44 Open dialog box

d Click the **Open** button.

The name of the report is added to the list of reports in the Export Report dialog box.

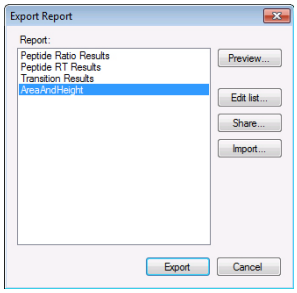
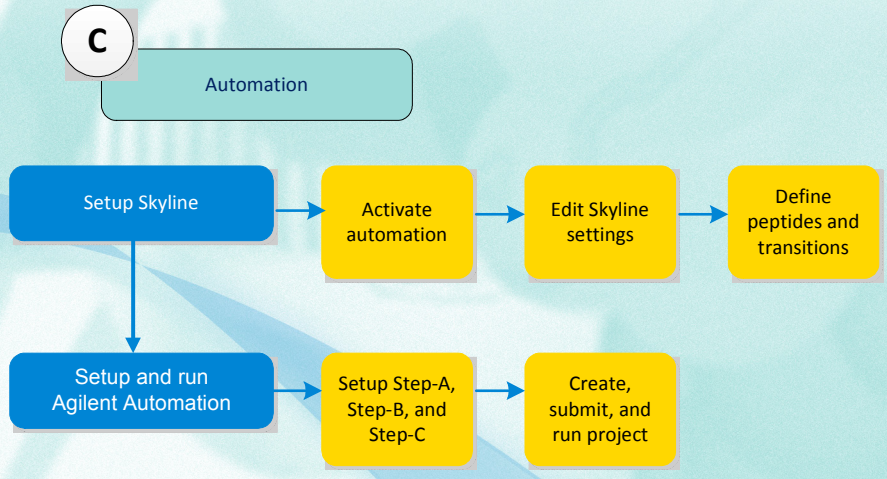


Figure 45 Export Report dialog box

e Click **Cancel** if you do not want to print a report at this time.

Run Skyline Automation

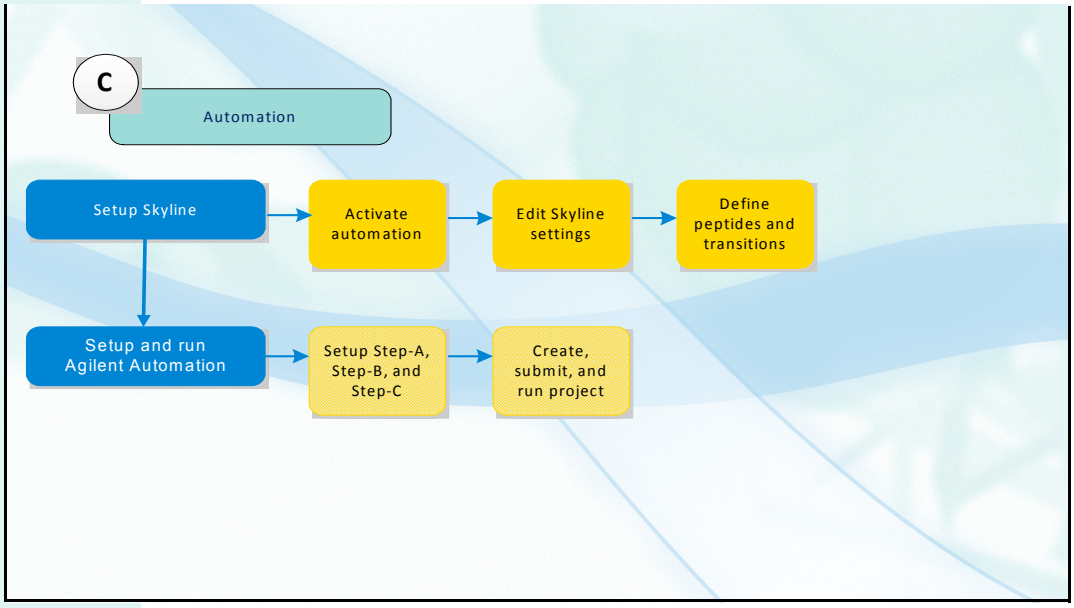
In this exercise, you learn how to activate the Agilent Automation tool, modify the Skyline settings, and save a method in Skyline. For Agilent Automation to work, Skyline must be installed on the same computer as the Agilent Data Acquisition software.



Agilent Technologies

Setup Skyline

In this exercise, you learn how to activate the Agilent Automation tool, modify the Skyline settings, and save a method in Skyline.



Run Skyline Automation Enabler

1. Open the Acq Tools folder.

- Double-click the Agilent MassHunter Workstation icon.

2. Run the Skyline Automation Enabler.

a Double-click the **Acq Tools** folder.

b Double-click the **Skyline Automation Enabler** tool.

You can instead click **All Programs > Agilent > MassHunter Workstation > Acq Tools > Skyline Automation Enabler** command.

The program runs automatically. A message appears when it is enabled.

Edit Skyline settings

Before you enter your protein or peptide information, you need to verify that the settings in Skyline are correct for your proteins or peptides. For more information on installing the software, see "Installing Skyline" on page 64.

1. Start the Skyline program.

- From the Start button, click **All Programs** > **Skyline > Skyline**.
- Click **File > New** to make sure that you are not starting from a previous project.

2. Edit Peptide Settings.

a Click **Settings > Peptide Settings**.

b On the Digestion tab, verify that the **Enzyme** is set correctly. In this example, the Enzyme is **Trypsin [KR | P]**. See Figure 46.

c Select **1** for **Max missed cleavages**. See Figure 46. For other target peptides, you may need to enter a higher value.

d Select **None** for **Background proteome**. This setting is useful if you are trying to have unique peptides associated with only one protein of a given organism.

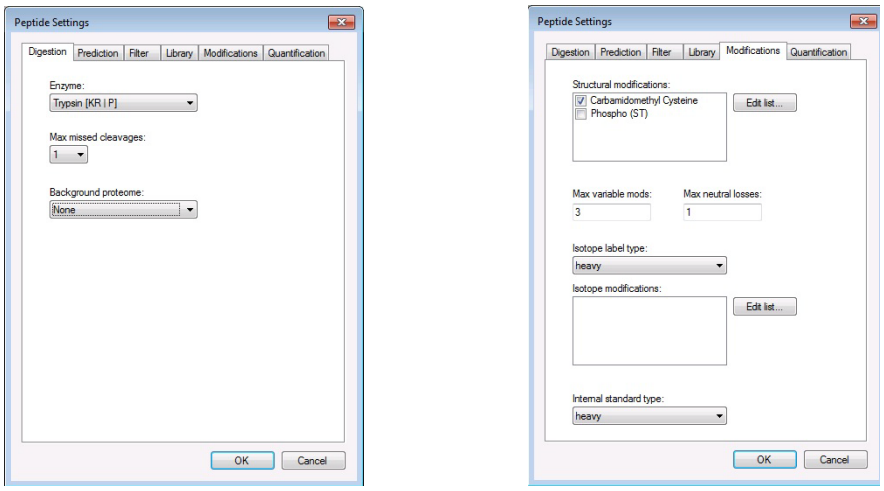


Figure 46 *The Digestion and Modification tabs in the Peptide Settings dialog box*

e Click the **Modifications** tab.

f On the Modifications tab, mark any **Structural modifications**. In this example, the **Carbamidomethyl Cysteine** check box is marked. See Figure 46 on page 53.

g Click the **Prediction** tab. See Figure 47 on page 54. In order to do retention time scheduling, Skyline needs to have a predictor in; the predictor is overwritten by the MRM results, so it does not need to be perfect. It is important that Skyline believes that it can make the prediction.

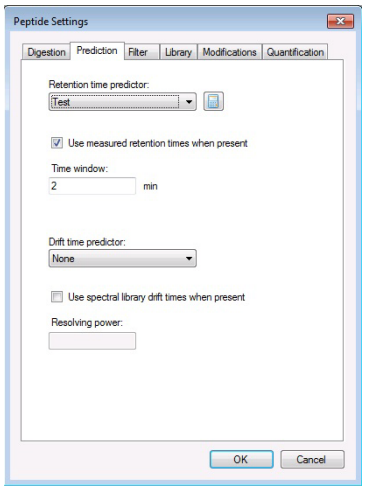
h Select **Add** for the **Retention time predictor**. The **Edit Retention Time Predictor** dialog box opens.

i Type a **Name**. In this example, the **Name** is `Test`.

j Type the **Slope** and **Intercept**. In this example, the **Slope** is 1; the **Intercept** is 0.

k Type the **Time window**. In this example, the **Time window** is `2.0`.

l Select the **Calculator**. For this example, the **SSRCalc 3.0 (100A)** calculator is selected.



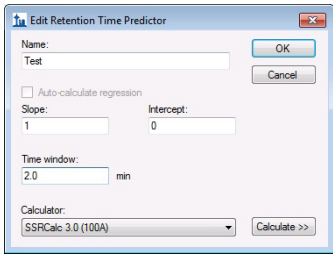


Figure 47 *The Prediction tab and the Edit Retention Time Predictor dialog box*

m Mark the **Use measured retention times when present** check box on the Prediction tab.

n Click the **OK** Button.

3. Edit the collision energy settings in the Transition Settings dialog box.

a Click **Settings > Transition Settings**.

b On the Prediction tab, mark the **Use optimization values when present** check box.

c Select **<Edit list...>** in the **Collision energy** box. The **Edit Collision Energy Regressions** dialog box is opened.

d Select **Agilent** in the **Edit Collision Energy Regressions** dialog box and click the **Edit** button. If **Agilent** is not an option, then click **Add**.

The **Edit Collision Energy Equation** dialog box is opened.

e Type `Agilent` for the **Name**.

f Type `2` in the **Charge** column.

g Type `0.03` in the **Slope** column.

h Type `1` in the **Intercept column**.

i In the next row, type 3 in the **Charge** column.

j Type `0.036` in the **Slope** column.

k Type `-4.8` in the **Intercept column**.

l Type `2` for the **Step size**. This step size is the number of volts to change the collision energy for each step. For Agilent, a value of 2, 3, or 4 is fine because Agilent TQ have a relatively wide collision energy optimum.

m Type 4 for the **Step count**. A step size of 4 means that when you are optimizing, the collision energy is checked for 4 steps above and 4 steps below the specified collision energy. In this example, the step size is 4, so the collision energy is checked at +8, +6, +4, +2, 0, -2, -4, -6, and -8. This is a reasonable starting point.

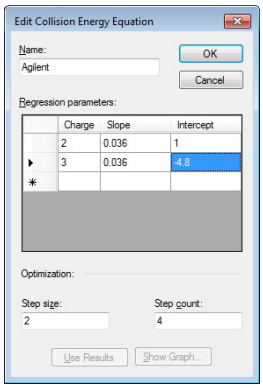


Figure 48 *Edit Collision Energy Equation dialog box*

n Click the **OK** button. The **Edit Collision Energy Equation** dialog box closes.

o Click the **OK** button. The **Edit Collision Energy Regressions** dialog box closes.

p Select **Agilent** for the **Collision energy**.

q Select either **Precursor** or **Transition** for the **Optimize by** value. For this example, select **Transition**.

4. Edit the filter settings in the Transition Settings dialog box.

a If necessary, click **Settings > Transition Settings**.

b Click the **Filter** tab.

c Review the parameters. For this example, make the following changes:
- Type `2, 3` for the **Precursor charges**.
- Type `1` for the **Ion charges**.
- Type `y` for the **Ion Types**.
- Select **(m/z > precursor) - 2** under Product ions in the **From** list.
- Select **6 ions** under Product ions in the **To** list.
- Mark the **N-terminal to Proline** check box.

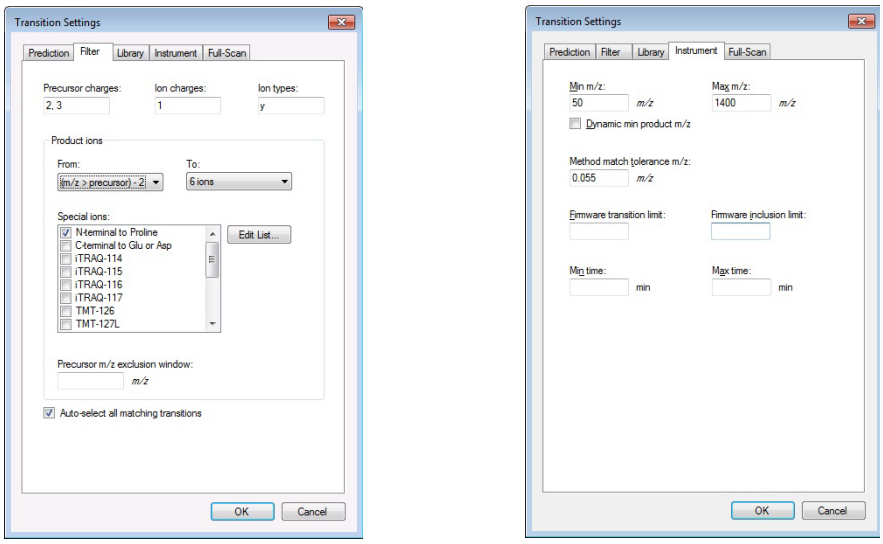


Figure 49 *Two tabs of the Transition Settings dialog box*

5. Edit the instrument settings in the Transition Settings dialog box.

a If necessary, click **Settings > Transition Settings**.

b Click the **Instrument** tab.

c Enter a value in the **Max m/z** box that is not greater than the maximum m/z value for the Agilent Triple Quadrupole model that you own. You can find the maximum m/z for your instrument in the Data Acquisition program in the Acquisition > QQQ tab in the Method Editor window. If you right-click a **Precursor Ion** or **Mass value** in the Scan segments table, the **Maximum value** is displayed in the shortcut menu. For an Agilent 6490, set this value to **1400**.

d Click the **OK** button.

6. Save the settings for future use.

a Click **Settings > Save Current**.

b Type a **Name** and click the **OK** button.

Define peptides and transitions

In this example, several peptide sequences are used.

1. Copy your peptide to the Clipboard.

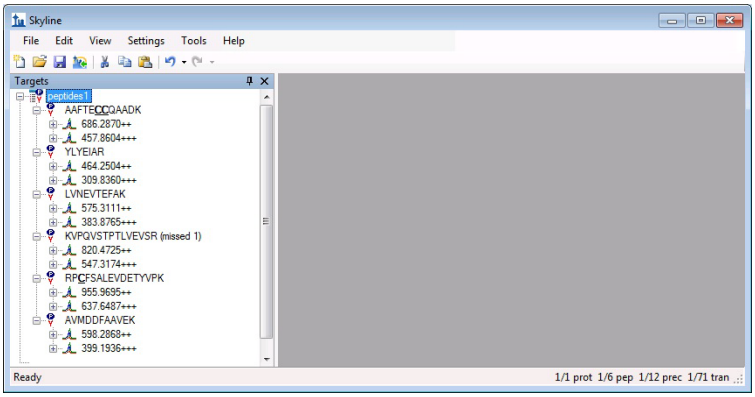
In this example, a peptide from beta casein is typed into Notebook.

- Type the following peptides into Notepad:
  - AAFTECCQAADK
  - YLYEIAR
  - LVNEVTEFAK
  - KVPQVSTPTLVEVSR
  - RPCFSALEVDETYVPK
  - AVMDDFAAVEK
- Highlight all of the peptides and press **Ctrl** and **C**. You can also click **Edit > Copy**.

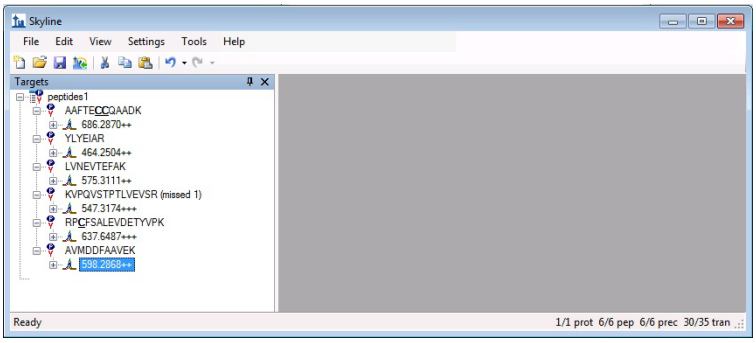
2. Paste the peptide from the Clipboard into Skyline.

a Right-click the gray bar in the **Targets** pane. Click **Paste**.

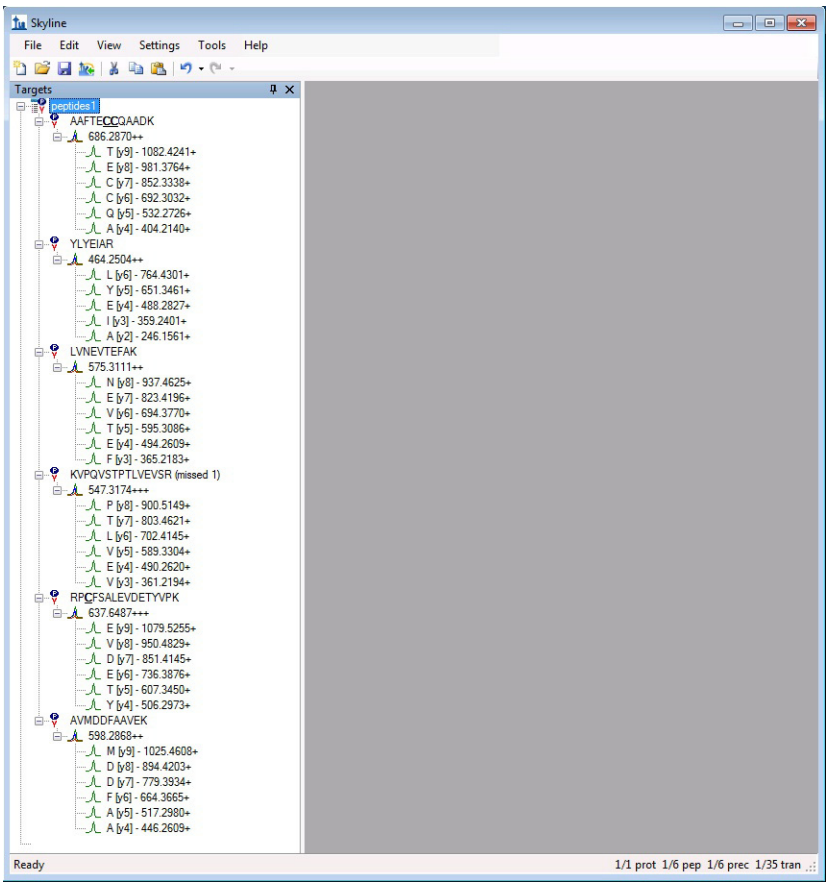
b Press **Ctrl** and **D** to expand all of the peptides.



c Remove unwanted precursors. Select the value, and then right-click and click **Delete**. The final precursor list should look like the following for this example.



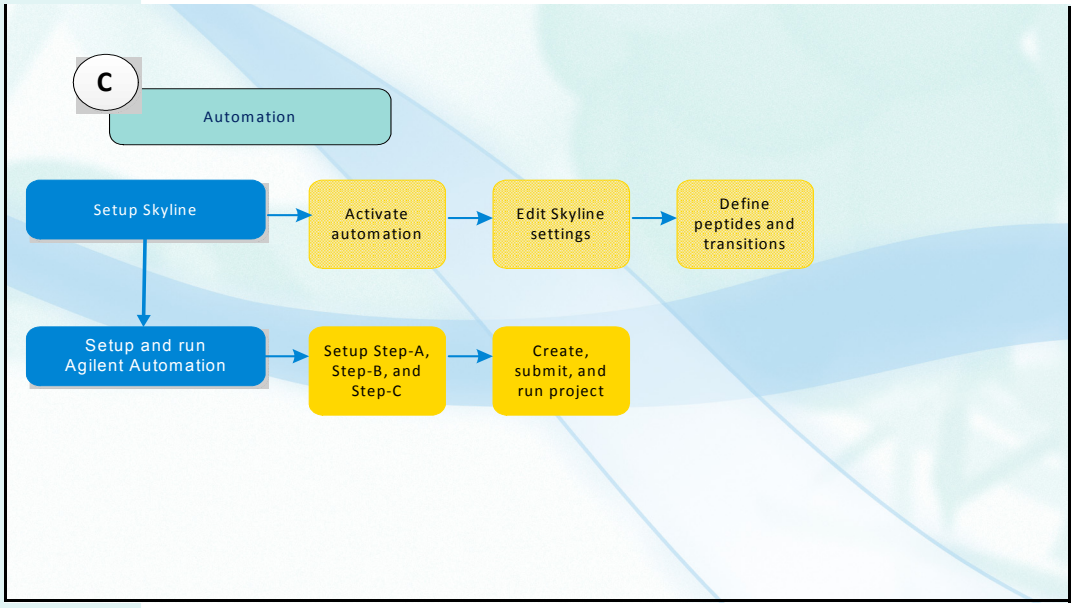
d Press **Ctrl** and **W** to expand all transitions. The final list for transitions should look like the following:



e Save the Skyline document. Click **File > Save As**.

Setup and run Agilent Automation

In this exercise, you use the Skyline Automation tool to create methods and work-lists to optimize collision energy for your peptides.



Setup Step A, Step B, and Step C

1. Start the Skyline Automation program.

   a If necessary, start Skyline.

   b Click **Tools > Agilent Automation**.

   If you see the message "This tool requires a Document Path to run", save your list of peptides. The Document Path is set when you save the current list of peptides.

2. Set the Project settings and the Action selections.

   a Select the Template method. You can click Browse to change the method.

   b Select the Study folder. All data files are saved to this folder.

   c Type the **Study name**.

   d Under Action selections, mark **Step-A (Update Retention Times)**.

   e Mark **Step-B (Optimize Collision Energy)**.

   f Mark **Step-C (Export method, create worklist)**.

   g Mark **Execute worklist**.

3. Set parameters in the **Step-A** tab.

a Click **Multiple methods**.

b Type `50` for the **Max transitions per sample injection** value.

c Select **None** for **Optimizing**.

d Select **Standard** for **Method type**.

e Type `5` for the **Dwell time (ms)** value.

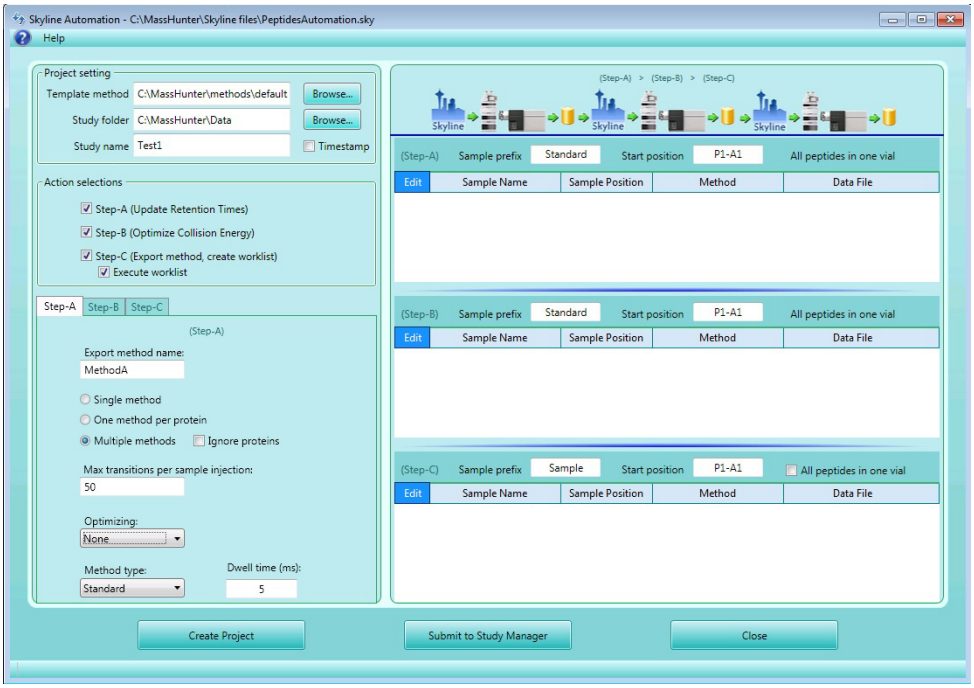


Figure 50 *Tab A in Skyline Automation*

4. Set parameters in the Step B tab.

a Click the **Step-B** tab.

b Click **Multiple methods**.

c Type `70` for **Max concurrent transitions**.

d Select **Collision Energy** for **Optimizing**.

e Select **Scheduled** for **Method type**. See Figure 51.

Figure 51 *Step B and Step C in Skyline Automation*

5. Set parameters in the **Step C** tab.

a Click the **Step-C** tab.

b Click **Single method**.

c Select **None** for **Optimizing**.

d Select **Scheduled** for **Method type**. See Figure 51 on page 60.

6. Select vial positions for standards.

- Select vial position for Step-A and Step-B (the standards).

All peptides in the project must be in a single vial for the standard. If your standard peptides are in more than 1 vial, make a separate Skyline project (document) for each vial. You can submit multiple projects to the Study Manager and queue the analyses. After method development is completed, you can combine documents in Skyline.

Create, submit, and run project

1. Create the project.

a Click the **Create Project** button.

b (optional) Edit the Step-C worklist to add vials and samples. The worklist editor is similar to the Worklist window in the MassHunter Data Acquisition program.

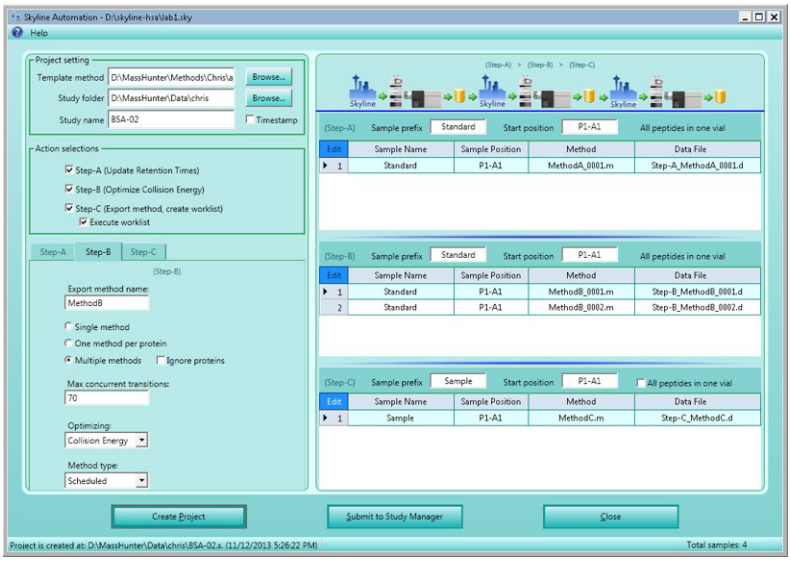


Figure 52 *After creating the project*

2. Submit the project to Study Manager.

- Click **Submit to Study Manager**.

You will get a message indicating that you should not open the Skyline project during the automation process. The Skyline Automation will be importing data into

Skyline and exporting new methods dynamically. After you click OK on this message, Study Manager will automatically launch.

3. Start the MassHunter Study Manager.

a Double-click the **Agilent MassHunter Workstation** folder.

b Double-click the **Study Manager** icon.

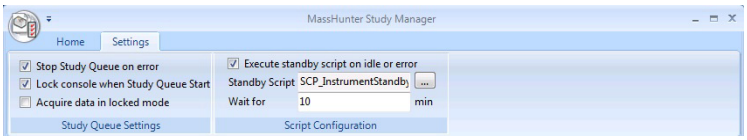
You can instead click **All Programs > Agilent > MassHunter Workstation > Study Manager**.

4. Set options in Study Manager.

a Click the **Settings** tab in the Ribbon.

b Mark the **Enable standby script execution on idle** check box.

c Select the **Standby Script**. For example, you can select **SCP_InstrumentStandby**.



5. Start running the automation.

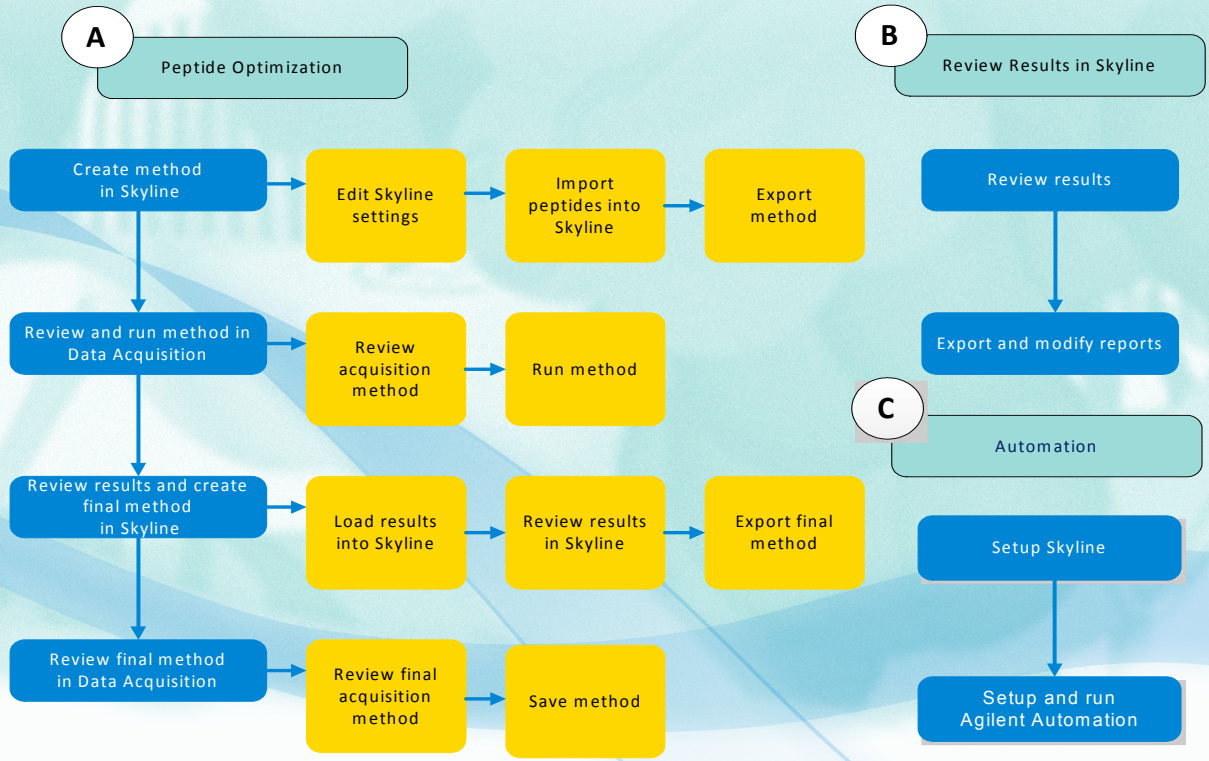
a Click the **Home** tab in the Ribbon.

b Click the **Start** icon to start the Automation.
- During the Automation process, the MassHunter Worklist editor is locked by the Study Manager.

c When the automation is complete, click **Stop > Stop Immediately**. When you click **Stop**, the Skyline project is released.

Reference Information

This chapter includes the instructions on how to install the MacCoss Skyline software. A list of reference manuals is also included.



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Installing Skyline

1. Find the location of the software online.

Skyline software is developed at the University of Washington in the MacCoss lab. You can download it from the internet for free.

a Start your internet browser.

b Start a search engine, such as *Google*.

c Type `Skyline Peptide` in the search box.

d Find the link to the proteome.gs.washington.edu site.

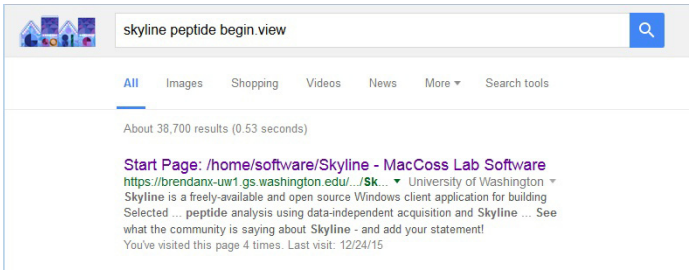

Figure 53 *Searching for Skyline Peptide using Google.*

e Connect to that site.

2. Download and install the software.

a Find the **Download & Install** buttons. This button also shows the version number. This guide is written using version 2.5.

b Click either the **Skyline 3.5 - 32 bit** button or the **Skyline 3.5 - 64 bit** button.

c Sign in or register for the Skyline software.

d Click the **I agree** button to agree to the license terms.

The **Name**, **Version** and **Publisher** information is displayed.

e Click the **Install Skyline** button.

f The "Opening setup.exe" message box appears. Click the **Save File** button.

g In the Downloads dialog box, double-click the setup.exe program. Then, follow the instructions to install the program. You may need to click **OK** in the "**Open Executable File?**" message box and click **Run** in the "**Open File - Security Warning**" message box.

When the installation program finishes installing the software, the Skyline program is started automatically.

Downloading a library

You can download a library from the internet. The Skyline web site contains links to allow you to download the following files:

- PeptideAtlas
- NIST - peptide.nist.gov
- GPM

You can use the WinZip program to unzip files with the extension "tar.gz". You can also build a library using the Skyline software.

1. Find the location of the Skyline software online.

You can use the links within the Skyline software to download a library, or you can search for the download page manually.

Using link in software

At the bottom of the **Edit Library** dialog box, you can click one of the Spectral Library Links to connect to the correct web site to download the library.

a Click **Settings > Peptide Settings**.

b Click the **Library** tab.

c Click the **Edit list** button.

d Click the **Add** or **Edit** button. The **Edit Library** dialog box is opened.

Search for the download site

a Start your internet browser.

b Start a search engine, such as *Google*.

c Type `Skyline Peptide begin.view` in the search box.

d Find the link to the proteome.gs.washington.edu site.

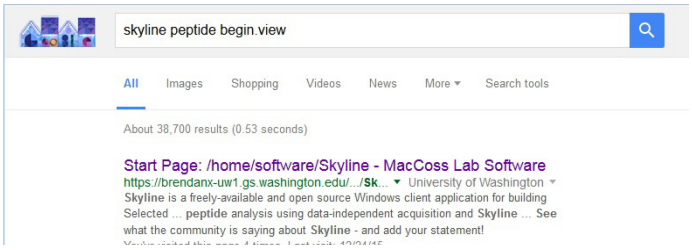

Figure 54 *Searching for Skyline Peptide using Google.*

e Connect to that site.

f Scroll to the bottom of the home page.

g In the Spectral Library Links section in the right column, click one of the links.

2. Download a library using the links to the libraries at the bottom of the home page for Skyline.

- Follow the instructions on the page that is opened to download the library.

References

The references in this list give valuable information that help you use Skyline software with the Agilent 6400 Series Triple Quadrupole LC/MS System.

Manuals

Agilent 6400 Series Triple Quadrupole LC/MS System Concepts Guide

Agilent 6400 Series Triple Quadrupole LC/MS System Quick Start Guide

Agilent 6000 Series LC/MS Safety Guide

Agilent 6000 Series LC/MS Maintenance Guide (animated)

Agilent MassHunter Workstation Software – Data Acquisition for 6400 Series Triple Quadrupole LC/MS Familiarization Guide

Agilent TQ Data Acquisition eFamiliarization Guide

Note: The MassHunter software includes online Help, in addition to manuals. See the online Help for details about the software.

www.agilent.com

For Research Use Only. Not for use in diagnostic procedures.

Revision B, February 2017

5990-9887EN

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