

# Skyline DDA Search for MS1 Full-Scan Filtering

The Skyline Targeted Mass Spectrometry Environment provides informative visual displays of the raw mass spectrometer data you import into your Skyline documents. These displays allow you to manipulate the data by performing tasks such as refining the peptides and transitions you are measuring, and tuning integration boundaries. Originally developed to analyze quantitative assays from selected reaction monitoring (SRM – also referred to as multiple reaction monitoring or MRM) mass spectrometry, Skyline has been expanded to extract time-intensity chromatograms from MS1 spectra for use in peptide quantification experiments involving mass spec runs with data dependent MS/MS.

The Skyline MS1 Full-Scan Filtering supports importing data sets from discovery-type proteomics experiments where mass spectrometers were operated in data dependent acquisition (DDA) mode. After importing the raw data, new and previously existing Skyline features facilitate quantifying peptide precursor MS1 signal across many replicate acquisitions. This mode may also be used for visualizing and better understanding quantitative outputs from other “Label Free” quantitative tools, because of the exceptional data visualization plots in Skyline.

This tutorial will cover the following areas critical to making effective use of Skyline MS1 Filtering:

- Setting up a Skyline document for MS1 filtering
- Performing a DDA search on raw data to find potential quantitative targets

Skyline aims to provide a vendor-neutral platform for targeted mass spectrometry investigation. It can import raw data for MS1 filtering from the instrument vendors Agilent, Bruker, SCIEX, Shimadzu, Thermo-Scientific and Waters, making the expertise you gain here transferrable to any mass spectrometry lab with an instrument from one of these vendors.

## Getting Started

To start this tutorial, download the following ZIP file:

<https://skyline.ms/tutorials/DdaSearchMS1Filtering.zip>

Extract the files in it to a folder on your computer, like:

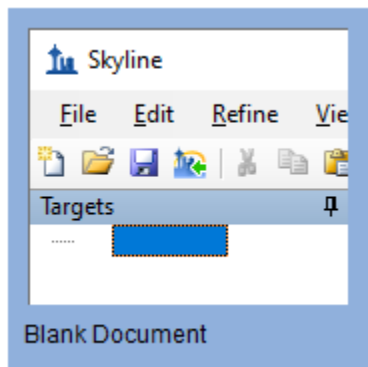
C:\Users\brendanx\Documents

This will create a new folder:

C:\Users\brendanx\Documents\DdaSearchMS1Filtering

If you have been using Skyline prior to starting this tutorial, it is a good idea to revert Skyline to its default settings. To do so:

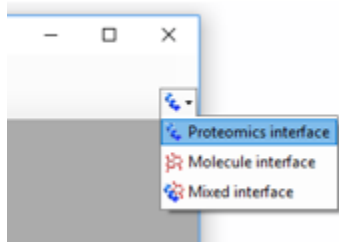
- Start Skyline.
- On the **Start Page**, click **Blank Document** which looks like this:




- On the **Settings** menu, click **Default**.
- Click **No** on the form asking if you want to save the current settings.

The document settings in this instance of Skyline have now been reset to the default. Since this tutorial covers a proteomics topic, you can choose the proteomics interface by doing the following:

- Click the user interface control in the upper right-hand corner of the Skyline window, and click **Proteomics interface** which looks like this:



Skyline is operating in proteomics mode which is displayed by the protein icon  in the upper right-hand corner of the Skyline window.

You could start editing this blank document in a number of ways, but for this tutorial you will use a sequential set of forms called a wizard that will walk you through the steps of searching mass spectrometer data dependent acquisition (DDA) data files, setting up targets, and importing chromatograms from those files.

Before starting the DDA search, you need to change the internal standard Skyline uses by default:

- On the **Settings** menu, click **Peptide Settings**.
- Click on the **Modifications** tab.
- Set the **Internal standard type** to “none”

The Peptide Settings form should now look like:

The screenshot shows the 'Peptide Settings' dialog box with the 'Modifications' tab selected. The 'Structural modifications' section contains a list with 'Carbamidomethyl (C)' checked and an 'Edit list...' button. Below this, 'Max variable mods' is set to 3 and 'Max losses' is set to 1. The 'Isotope label type' dropdown is set to 'heavy'. The 'Isotope modifications' section is empty with an 'Edit list...' button. The 'Internal standard type' dropdown is set to 'none'. 'OK' and 'Cancel' buttons are at the bottom right.

- Click the **OK** button in the **Peptide Settings** form.

## Searching DDA Files to Load Peptides into a Skyline Document

Skyline runs peptide searches on DDA MS/MS files via the **Import Peptide Search** wizard. Do the following to save your new document:

- Click the **Save** button on the toolbar (Ctrl-S).
- Navigate to the DdaSearchMS1Filtering folder you created for this tutorial.
- In the **File name** field, enter 'DdaSearchMS1FilteringTutorial.sky'.
- Click the **Save** button.

Now, initiate the **Import Peptide Search** wizard as follows:

- On the **File** menu, choose **Import** and click **Peptide Search**.

Skyline should present a form that looks like this:

The screenshot shows the 'Import Peptide Search' dialog box. It has a title bar with a Skyline icon and a close button. The main area is titled 'Spectral Library'. Below the title, there are three radio buttons: 'Build' (selected), 'Use existing', and 'Perform DDA Search'. Below these is a 'Cut-off score:' label and a text box containing '0.95'. Underneath is a 'Search files:' label and a large empty text box. To the right of this box are two buttons: 'Add Files...' and 'Remove Files'. Below the search files section is a label 'iRT standard peptides:' and a dropdown menu showing 'None'. Below the dropdown is a checkbox labeled 'Include ambiguous matches' which is currently unchecked. At the bottom, there is a 'Workflow' section with three radio buttons: 'DDA with MS1 filtering' (selected), 'DIA', and 'PRM'. At the very bottom of the dialog are three buttons: 'Finish', 'Next >', and 'Cancel'.

Note that the Build mode works on the output from DDA search engines (e.g. pepXML files from Comet, .dat from Mascot) and the DDA search mode works on the raw data (e.g. RAW, WIFF, \*.d, mzML, mzXML). The mz5 files for this tutorial are centroided to make them faster to download than the profile Thermo RAW files.

Add the included DDA mz5 files to the search by doing the following:

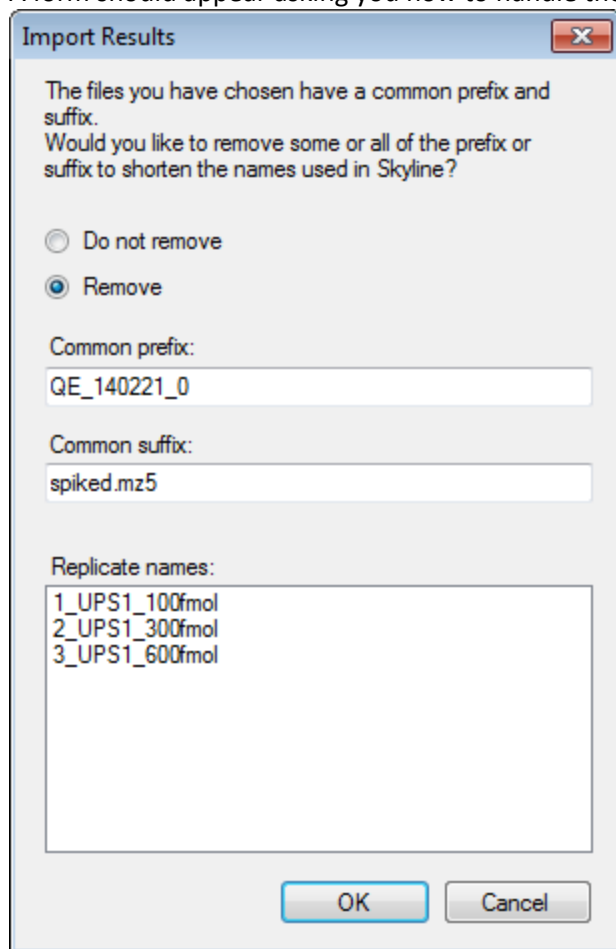
- Click the **Perform DDA Search** radio option.
- Click the **Add Files** button.
- Select all the mz5 files in the DdaSearchMS1Filtering folder you created for this tutorial.
- Click the **Open** button.

The wizard form should now look like this:

The screenshot shows a software window titled "Import Peptide Search". Inside, there is a section titled "Spectral Library" with three radio buttons: "Build", "Use existing", and "Perform DDA Search". The "Perform DDA Search" option is selected. Below this, there is a "Cut-off score:" label and a text box containing "0.95". A "Files to search:" label is followed by a list box containing three file names: "QE\_140221\_01\_UPS1\_100fmolspiked.mz5", "QE\_140221\_02\_UPS1\_300fmolspiked.mz5", and "QE\_140221\_03\_UPS1\_600fmolspiked.mz5". To the right of the list box are two buttons: "Add Files..." and "Remove Files". Below the list box, there is a label "iRT standard peptides:" and a dropdown menu currently showing "None". Underneath the dropdown is a checkbox labeled "Include ambiguous matches" which is currently unchecked. A "Workflow" section contains three radio buttons: "DDA with MS1 filtering" (selected), "DIA", and "PRM". At the bottom of the window are three buttons: "Finish", "Next >", and "Cancel".

- Click the **Next** button.

A form should appear asking you how to handle the prefix shared by the three mz5 files:

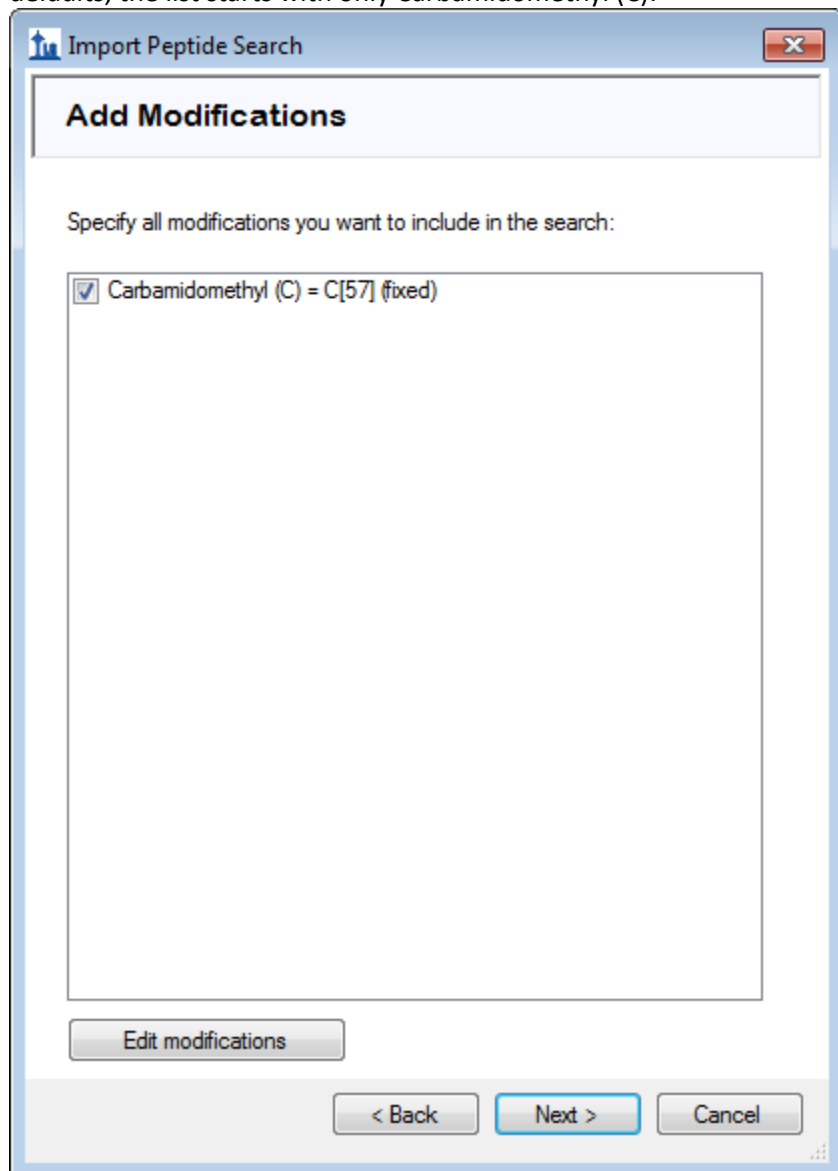


The dialog box is titled "Import Results" and contains the following text: "The files you have chosen have a common prefix and suffix. Would you like to remove some or all of the prefix or suffix to shorten the names used in Skyline?". There are two radio buttons: "Do not remove" (unselected) and "Remove" (selected). Below the radio buttons are two text input fields. The first is labeled "Common prefix:" and contains the text "QE\_140221\_0". The second is labeled "Common suffix:" and contains the text "spiked.mz5". Below these fields is a text area labeled "Replicate names:" containing the following text: "1\_UPS1\_100fmol", "2\_UPS1\_300fmol", and "3\_UPS1\_600fmol". At the bottom of the dialog are two buttons: "OK" and "Cancel".

- Click the **OK** button.

The wizard will advance to the **Add Modifications** page, where it lists all of the amino acid modifications in the document that you might want to include in the DDA search. It is important to distinguish here between fixed and variable modifications: fixed (sometimes called static) modifications are always applied to the specified amino acids. For example, Carbamidomethyl C is usually treated as a fixed modification because all cysteines in the data are expected to be alkylated. Oxidation M is almost always treated as a variable modification because oxidation is hit-or-miss depending on sample handling. Skyline's search always treats isotopic labels as variable, but you can change whether other modifications are treated as fixed or variable by clicking on the **Edit modifications** button.

You can also add modifications to the document from this page. Since the document was reset to defaults, the list starts with only Carbamidomethyl (C):



The screenshot shows a software window titled "Import Peptide Search" with a standard Windows-style title bar (minimize, maximize, close buttons). The window has a tab labeled "Add Modifications". Below the tab, the text "Specify all modifications you want to include in the search:" is displayed. A list box contains a single entry: ☒ Carbamidomethyl (C) = C[57] (fixed). Below the list box is a button labeled "Edit modifications". At the bottom of the window are three buttons: "< Back", "Next >" (which is highlighted with a blue border), and "Cancel".

These data are SILAC labelled, so you will need to add heavy label modifications here. To add them, do the following:

- Click the **Edit modifications** button.
- Click the **Edit heavy modifications** menu option.
- Click the **Edit List** button beside the **Isotope modifications** list.
- Click the **Add** button in the **Edit Isotope Modifications** form.
- In the **Name** field of the **Edit Isotope Modification** form, enter "Label:13C(6)15N(2) (C-term K)".
- Click the down arrow at the right side of the **Name** field and click the item with the same name. This will populate the specificity and composition fields from Unimod.

The **Edit Isotope Modification** form should now look like this:

The screenshot shows the 'Edit Isotope Modification' dialog box. The 'Name' field is populated with 'Label:13C(6)15N(2) (C-term K)'. The 'Amino acid' dropdown is set to 'K' and the 'Terminus' dropdown is set to 'C'. The 'Chemical formula' checkbox is unchecked. The '13C' and '15N' checkboxes are checked, while '18O' and '2H' are unchecked. The 'Monoisotopic mass' is 8.014199 and the 'Average mass' is 7.941847. The 'Relative retention time' dropdown is set to 'Matching'. 'OK' and 'Cancel' buttons are visible.

- Click the **OK** button

Add a second isotope modification by doing the following:

- Click the **Add** button on the **Edit Isotope Modifications** form.
- From the **Name** dropdown list of the **Edit Isotope Modification** form, choose "Label:13C(6)15N(4) (C-term R)".

The **13C** and **15N** checkboxes are checked automatically to tell Skyline to use  $^{13}\text{C}$  for all carbon atoms and  $^{15}\text{N}$  for all nitrogen atoms present in an Arginine molecule, for a total mass shift of 10 Daltons ( $6 \times ^{13}\text{C} + 4 \times ^{15}\text{N}$ ).



The **Edit Isotope Modification** form should now look like this:

**Edit Isotope Modification**

Name:

Amino acid:  Terminus:

☐ Chemical formula

☒ 13C ☒ 15N ☐ 18O ☐ 2H

Monoisotopic mass:  Average mass:

Relative retention time:

Skyline automatically calculates both the monoisotopic and average masses, approximately 8 Daltons for Lysine (K) and 10 Daltons for Arginine (R) that will result from using  $^{13}\text{C}$  and  $^{15}\text{N}$  in these amino acid residues. To finish adding the heavy modifications:

- Click the **OK** button in the **Edit Isotope Modification** form.
- Click the **OK** button in the **Edit Isotope Modifications** form.
- Check the checkboxes in the **Add Modifications** list for the “Label:13C(6)15N(2) (C-term K)” and “Label:13C(6)15N(4) (C-term R)” modifications you just created.

Now you will add Oxidation (M) as a structural modification:

- Click the **Edit modifications** button.
- Click the **Edit structural modifications** menu option.
- Click the **Edit List** button beside the **Isotope modifications** list.
- Click the **Add** button in the **Edit Structural Modifications** form.
- In the **Name** field of the **Edit Structural Modification** form, enter “Oxidation (M)”.
- Click the down arrow at the right side of the **Name** field and click the item with the same name. This will populate the specificity and composition fields from Unimod.
- Click the **OK** button in the **Edit Structural Modification** form.
- Click the **OK** button in the **Edit Structural Modifications** form.
- Check the checkbox in the **Add Modifications** list for the “Oxidation (M)” modification you just created.
- Also make sure the checkbox for “Carbamidomethyl (C)” is checked, as it should be because you chose the default settings.

At this point the **Add Modifications** page should look like:

The screenshot shows a dialog box titled 'Import Peptide Search' with a sub-header 'Add Modifications'. Below the sub-header, it says 'Specify all modifications you want to include in the search:'. There is a list of four modifications, each with a checked checkbox:

- ☒ Carbamidomethyl (C) = C[57] (fixed)
- ☒ Label: 13C(6)15N(2) (C-term K) = K[8] (isotopic label)
- ☒ Label: 13C(6)15N(4) (C-term R) = R[10] (isotopic label)
- ☒ Oxidation (M) = M[16] (variable)

Below the list, there is a checkbox for 'Select / deselect all' which is currently unchecked. Below that is a button labeled 'Edit modifications'. At the bottom of the dialog, there are three buttons: '< Back', 'Next >' (which is highlighted with a blue border), and 'Cancel'.

- Click the **Next** button.

The wizard will advance to the **Configure MS1 Full-Scan Settings** page. Set the **Mass Accuracy** to “20”. The other fields on this page should default to values you can use for this tutorial, and the wizard should look like this:

The screenshot shows a software window titled 'Import Peptide Search' with a sub-header 'Configure Full-Scan Settings'. The window contains the following settings:

- Precursor charges:** A text box containing the value '2'.
- MS1 filtering** (grouped in a box):
  - Isotope peaks included:** A dropdown menu set to 'Count'.
  - Precursor mass analyzer:** A dropdown menu set to 'Centroided'.
  - Peaks:** A text box containing the value '3'.
  - Mass Accuracy:** A text box containing '20' followed by 'ppm'.
- Use high-selectivity extraction:** An unchecked checkbox.
- Retention time filtering** (grouped in a box):
  - Use only scans within 5 minutes of MS/MS IDs:** A radio button that is selected.
  - Include all matching scans:** An unselected radio button.

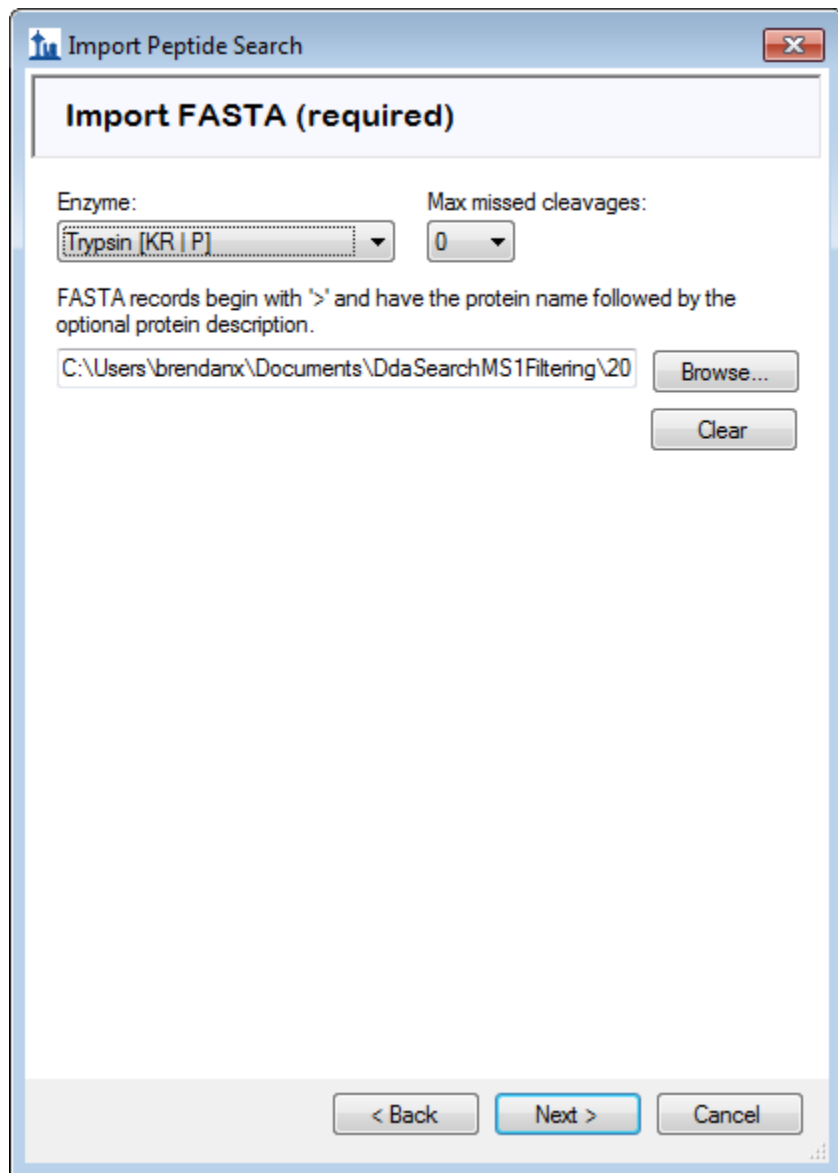
At the bottom of the window are three buttons: '< Back', 'Next >', and 'Cancel'. The 'Next >' button is highlighted with a blue border.

- See the [MS1 Full Scan Filtering tutorial](#) (page 9) to learn more about these settings.
- Click the **Next** button.

This should bring you to the **Import FASTA** page in the wizard. For this tutorial you will use a human protein FASTA with the sequences from Sigma-Aldrich's Universal Proteomics Standard (UPS) prepended at the top (so that Skyline uses those accessions for any peptides that are shared between UPS and non-UPS proteins). To select the FASTA:

- Click the **Browse** button.
- Select the '2014\_01\_HUMAN\_UPS.fasta' file in the folder you created for this tutorial.
- Click the **Open** button in the **Open FASTA** form.

The wizard should now look like this:



The screenshot shows a Windows-style dialog box titled "Import Peptide Search". Inside, there is a section titled "Import FASTA (required)". Below this, there are two dropdown menus: "Enzyme:" with "Trypsin [KR | P]" selected, and "Max missed cleavages:" with "0" selected. Below these is a text box containing the path "C:\Users\brendanx\Documents\DdaSearchMS1Filtering\20", followed by "Browse..." and "Clear" buttons. At the bottom of the dialog are three buttons: "< Back", "Next >" (which is highlighted with a blue border), and "Cancel".

- Click the **Next** button.

The wizard will advance to the **Adjust Search Settings** page. Here you can set the most important parameters for the DDA search. For this tutorial, do the following:

- Set MS1 tolerance to 5. Note that when you leave the text box the form will assume you mean ppm and set the unit box accordingly.
- Set MS2 tolerance to 10.

The form should now look like:

Import Peptide Search

### Adjust Search Settings

MS Amanda search settings:

MS1 tolerance: 5 Unit: ppm

MS2 tolerance: 10 Unit: ppm

Fragment ions: b, y

Max variable mods: 3

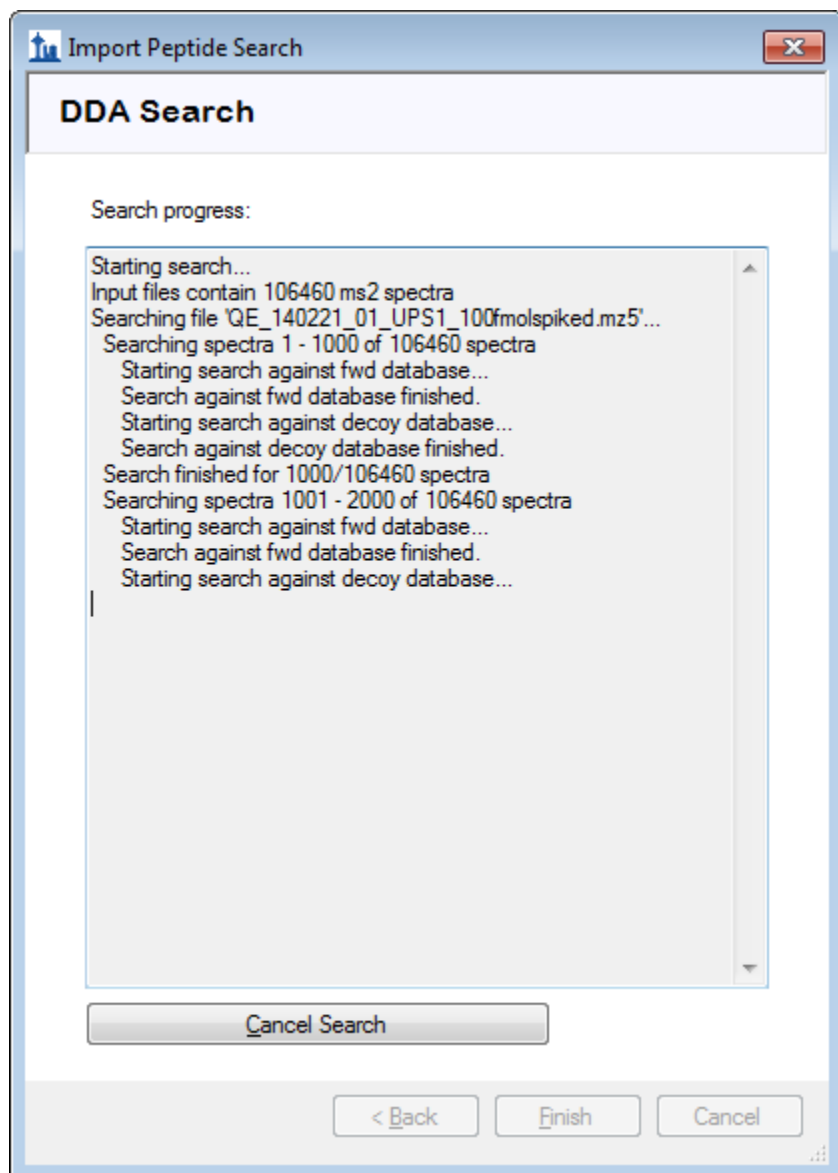
Additional Settings

< Back Next > Cancel

To start the search:

- Click the **Next** button.

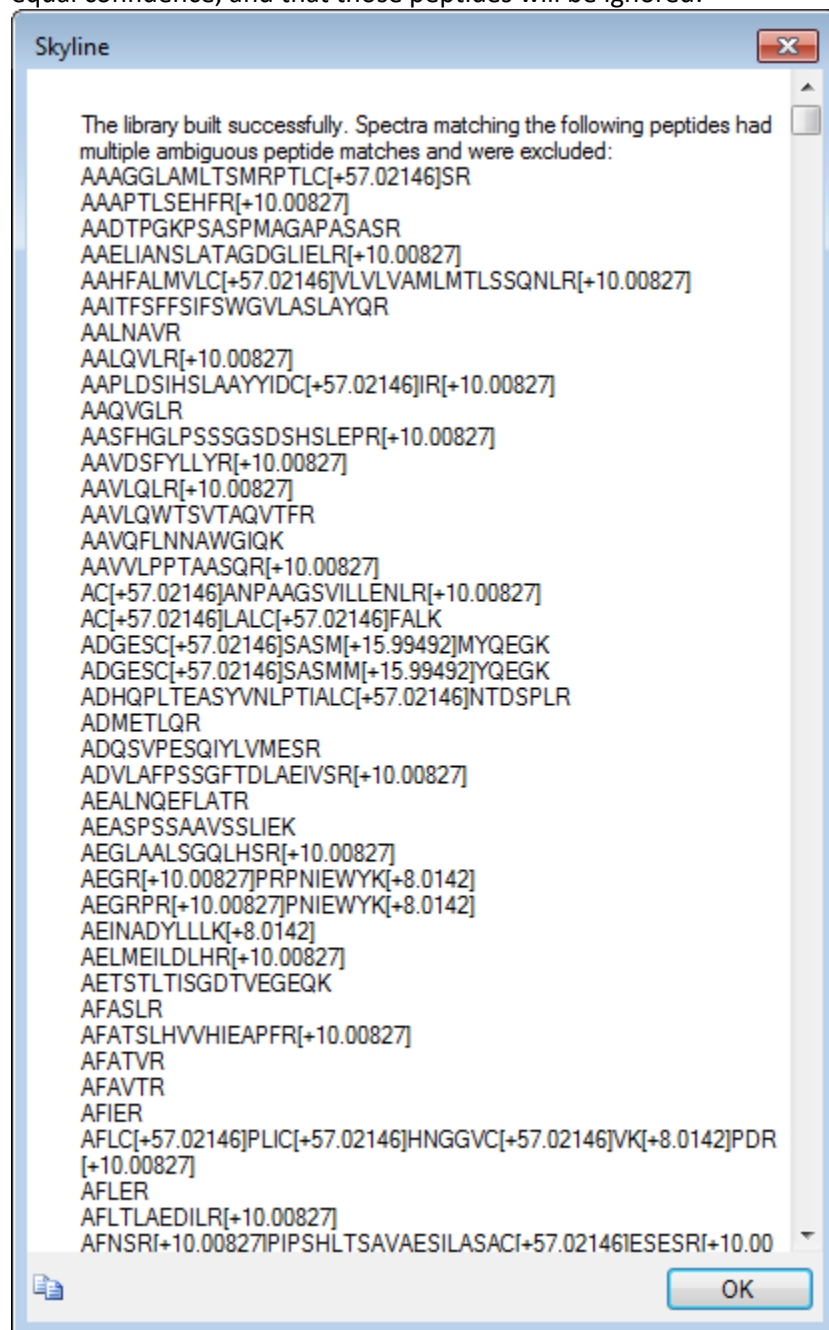
The **DDA Search** page will show you the progress of the search. You may also cancel the search here.



After the search is finished:

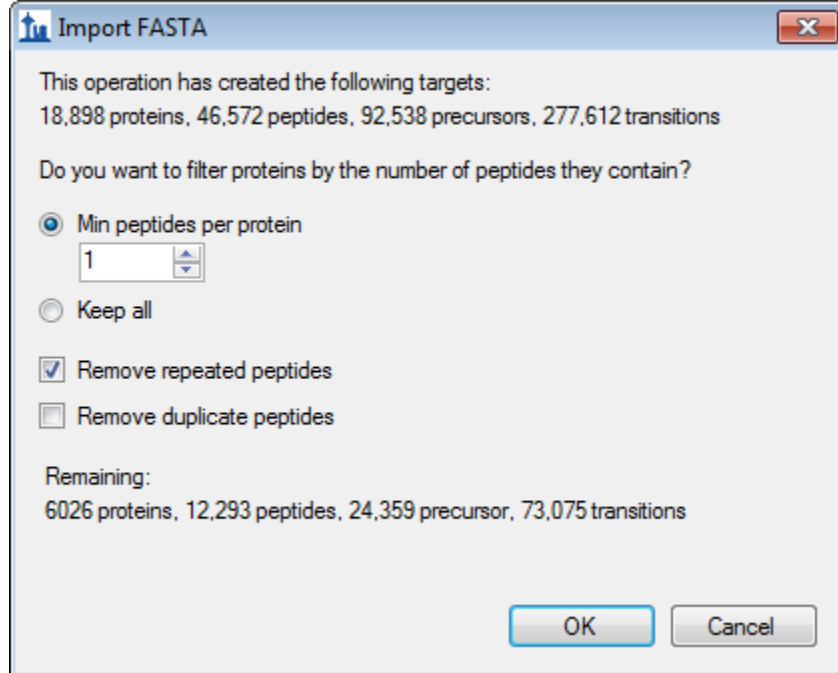
- Click the **Finish** button.

Skyline will then start to build a spectral library from the search results. A message box will pop up to warn you that there were some spectra that could be interpreted as multiple different peptides with equal confidence, and that those peptides will be ignored:



- Click the **OK** button to dismiss the message.

Skyline will then start to import the library into your document. When that is finished it will ask you to set criteria for including proteins in the document:



The image shows a Windows-style dialog box titled "Import FASTA". It contains the following text and controls:

- Header: "Import FASTA" with a close button (X).
- Text: "This operation has created the following targets:"
- Text: "18,898 proteins, 46,572 peptides, 92,538 precursors, 277,612 transitions"
- Text: "Do you want to filter proteins by the number of peptides they contain?"
- Radio button: "Min peptides per protein" (selected). Below it is a spin box with the value "1".
- Radio button: "Keep all".
- Checkbox: "Remove repeated peptides" (checked).
- Checkbox: "Remove duplicate peptides" (unchecked).
- Text: "Remaining:"
- Text: "6026 proteins, 12,293 peptides, 24,359 precursor, 73,075 transitions"
- Buttons: "OK" and "Cancel".

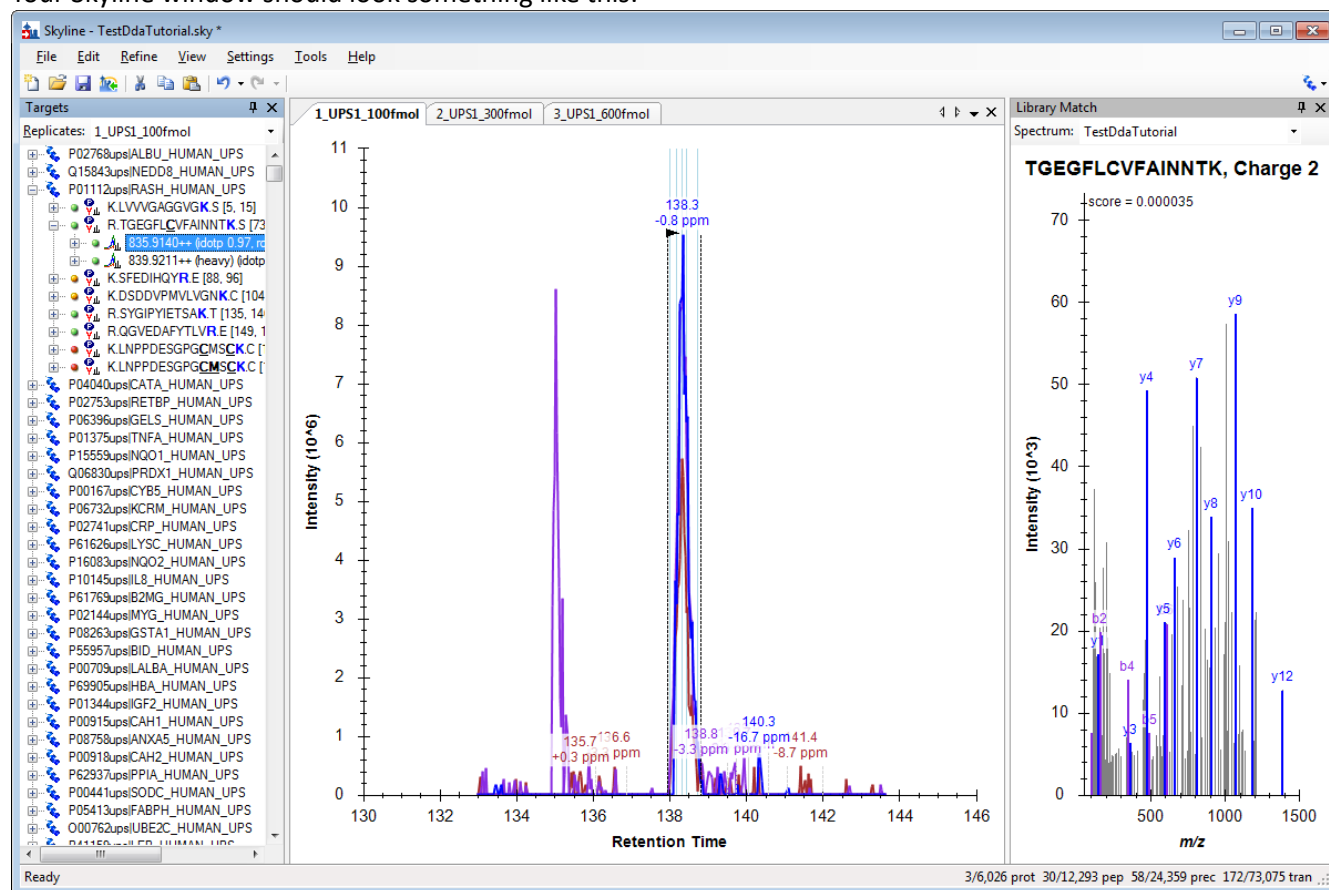
- Check the box to **Remove repeated peptides** (i.e. keep first protein for non-unique peptides).
- Click the **OK** button.



After the proteins are imported into the document, you will see the main Skyline window with the UPS proteins at the top of the Targets view. You should see **6,026** proteins there (counted in the status bar).

- Click on the [+] icon next to the third protein P01112ups|RASH\_HUMAN\_UPS.
- Click on the [+] icon next to that protein's third peptide R.TGEGFLCVFAINNTK.S.
- Click on that peptide's first precursor 835.9140++ and the chromatogram for that precursor and the MS/MS spectrum for that peptide will appear. (Note that the bold, underlined residue "**C**" in the peptide sequence indicates a carbamidomethyl cysteine).
- If you do not see the MS/MS spectrum, on the **View** menu, click **Library Match**.
- If you do not see as many annotated peaks as in the image below, on the **View** menu, choose **Ion Types** and check **B** and **Y**.
- If you do not see the entire chromatogram for the peptide, on the **View** menu, choose **Auto-Zoom** and click **None** (Shift-F11).

Your Skyline window should look something like this:



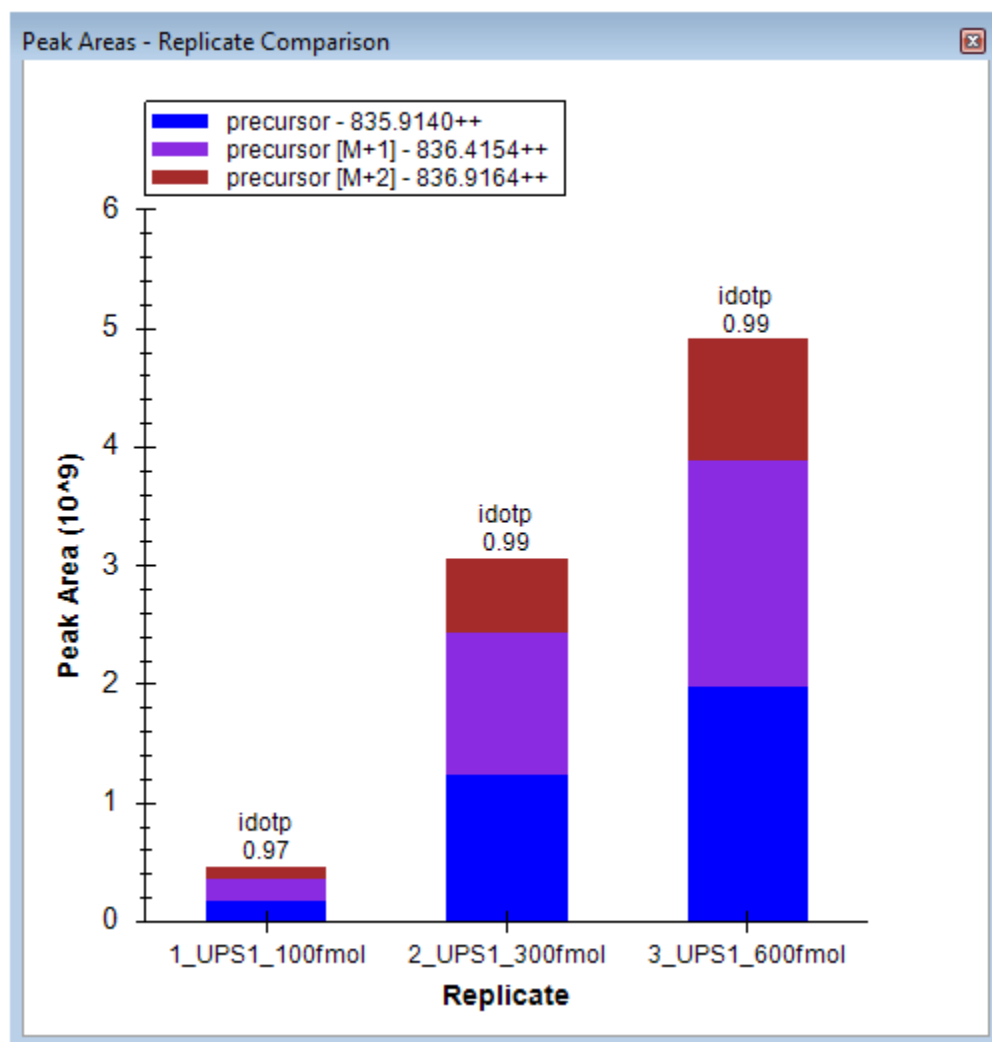
The document is now fully configured for MS1 Filtering with three DDA runs imported. You will see that the chromatogram in this view is approximately 10 minutes in length (133 to 143 minutes), due to the **Use only scans within [5] minutes of MS/MS IDs** setting chosen in the import wizard. Note that when the Skyline document is set up for MS1 Filtering, in the place where you would see product ion transitions (e.g. y-ions) for triple quadrupole SRM experiments, you will now see the different precursor isotope peaks, such as for peptide TGEGFLCVFAINNTK: precursor – 835.9140++, precursor [M+1] – 836.4154++, and precursor [M+2] – 836.9164++.

To configure a few other features that will be helpful in general, especially to visualize certain MS1 Filtering data, perform the following steps:

- On the **Settings** menu, make sure **Integrate All** is checked.

This tells Skyline to treat all chromatograms in a peak group (here precursor ions M, M+1 and M+2) as integrating together, regardless of whether peaks appear to be co-eluting with the largest peak. It no longer impacts the integrated peak areas as it once did.

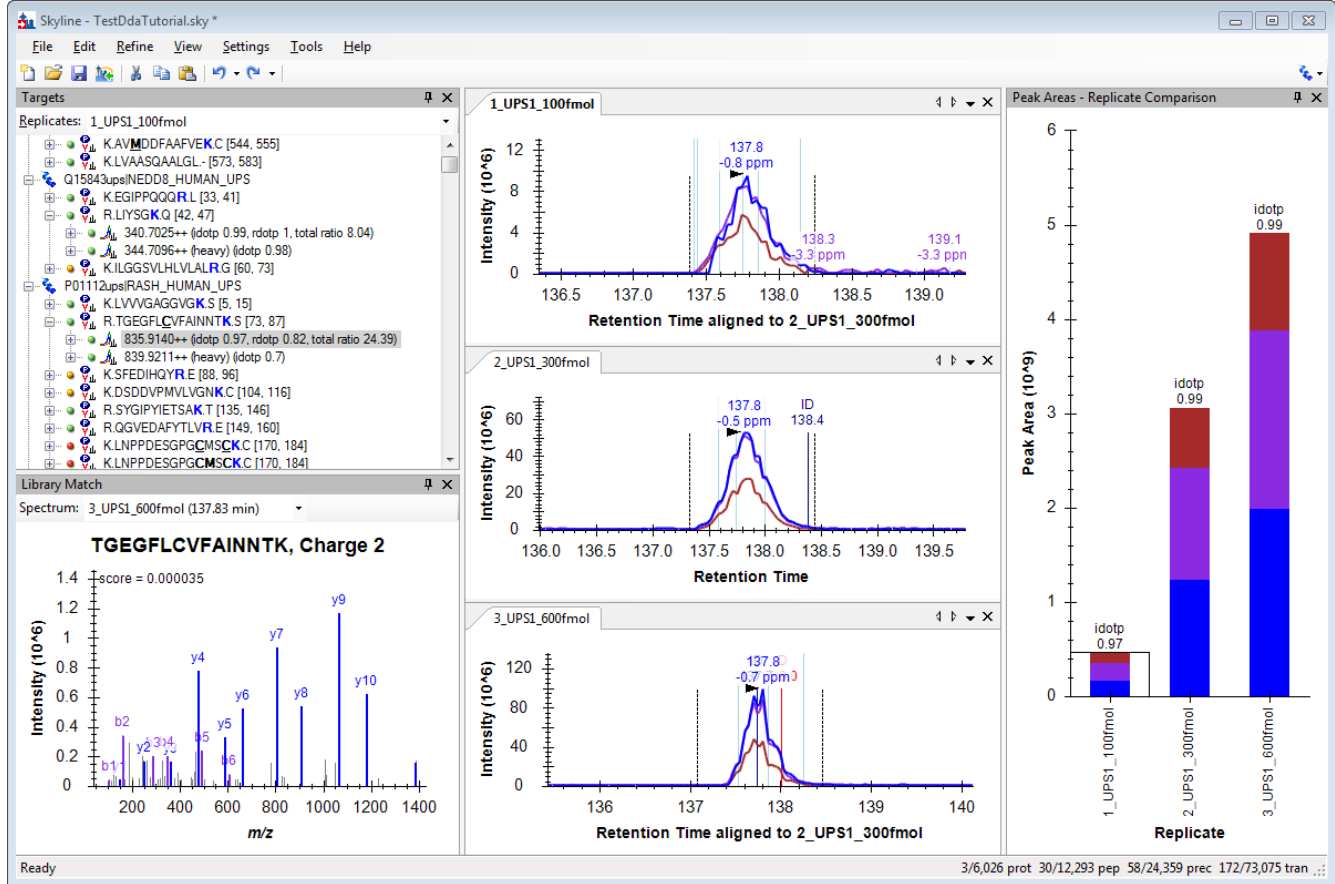
- On the **View** menu, choose **Peak Areas** and click **Replicate Comparison**.



You can dock the **Peak Areas** window to your desired location by doing the following:

- Click and hold down the left mouse button, and then drag it until the mouse cursor is above the **Library Match** view.
- When set of 5 icons arranged in the shape of a cross appears, move the mouse into the lower icon and release the left mouse button to divide the space on the right edge of the Skyline window between the **Peak Areas** and **Library Match** views.
- Move the **Library Match** view to the Targets view by the same process.
- On the **View** menu, choose **Auto-Zoom** and click **Best Peak** (F11).
- On the **View** menu, choose **Arrange Graphs** and click **Column**.

Now your Skyline window should look something like this:



From this point you can follow the normal MS1 full scan filtering workflow covered by another tutorial: [MS1 Full-Scan Filtering](#)