Skyline User Interface Modes
Skyline was built from the ground up as a proteomics targeted mass spec research tool. By popular demand, Skyline’s support for non-proteomic research has steadily increased over the past several years.

Unfortunately until the Skyline 19.2 release the user interface remained proteomics-centric. Non-proteomics users had to think “molecule” while seeing “peptide”, and it wasn’t always easy knowing which parts of the UI didn’t apply to your work. This was especially true for new users.

But now, Skyline asks what kind of molecules you work with and adjusts its user interface accordingly. The first time you run Skyline you’ll see this:
You can always change your preference later with the new UI Mode control on the Start Page:

and in the Skyline main window.
Three UI Modes Available

• 🌊 **Proteomics**: Traditional Skyline UI. Non-proteomic controls and menus are hidden.

• 🌟 **Molecule**: Proteomics-specific controls and menus are hidden. The words “Peptide” and “Protein” are changed to “Molecule” and “Molecule list” in menus and controls.

• 🌸 **Mixed**: All controls and menus are enabled. “Peptide” and “Protein” are changed to “Molecule” and “Molecule list” except in proteomics-specific controls and menus.
Setting the UI Mode

• For an empty Skyline document, just use the provided control in the Skyline main window or Start Page.

• When you open an existing Skyline document, the UI mode changes automatically if needed, depending on the document contents.

• If you try to change to a UI mode that doesn’t make sense for a loaded document, e.g. “Molecules” for a document with one or more peptides in it, Skyline offers to start a new document.

• Mixed mode works for any kind of document.

• The first time you run Skyline, you will be asked to select an initial UI mode. After that, Skyline defaults to whatever UI mode was last used.
Example: Peptide Settings...

- Min length: 8
- Max length: 25
- Exclude N terminal AAs: 25
- Exclude potential tagged ends
- Exclude peptides containing:
  - Cys
  - Met
  - His
  - NXT/NXS
  - RP/KP
- Auto-select all matching peptides
...becomes Molecule Settings when you select Molecules UI Mode

Note the “Modifications” tab, which makes no sense for non-peptide molecules, is replaced by a “Labels” tab. “Digestion” tab is gone.

Also note the summary line at the bottom of the Skyline window changes from showing “prot” and “pep” counts to “list” and “mol” counts.
Mixed UI Mode

- Allows for Skyline documents with mixed peptide and non-peptide targets
- Basically the previous generation UI, though we do rename “peptide” to “molecule” for controls and menu items that apply to both kinds of targets.