Crosslinked peptide support in Skyline Nicholas Shulman, Alex Zelter, Michael MacCoss, Brendan MacLean

University of Washington Genome Sciences, Seattle, WA, United States

Overview

- Skyline is a freely-available, open-source Windows client application for analyzing and viewing many types of mass spectrometry data including SRM, DIA/SWATH, DDA and PRM
- Skyline has traditionally been used to predict m/z values of peptide fragment ions in order to extract chromatograms from LC-MS/MS data.
- The next release of Skyline, version 20.2, will have support for crosslinked peptides.
- Crosslinked peptides are two or more ordinary peptides linked together by a chemical crosslinker

Defining crosslinkers in Skyline

Crosslinked peptides in Skyline are modeled as a main peptide with a special "crosslinker" modification on it.

OK

has a chemical formula which describes the set of atoms that are added to (or subtracted from) the chemical formulas of the two unlinked peptides. OK

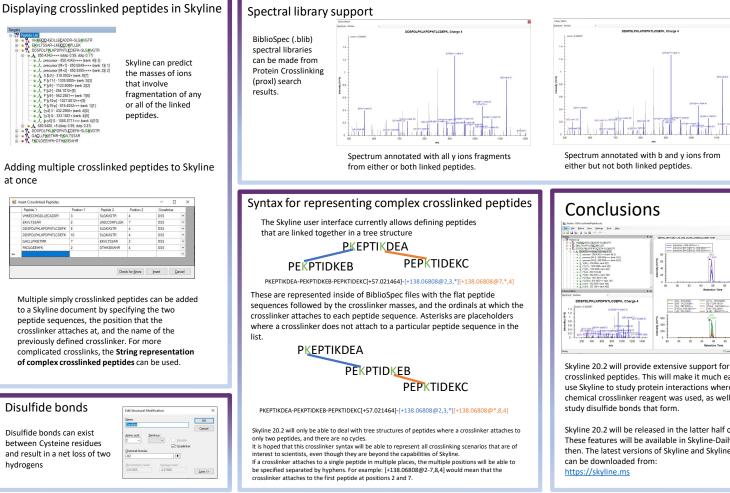
A crosslinker modification



dit Linked Peptide	-		
Linked peptide sequence:			
DOSPOLPKLKPDPNTLCD	FK		
Crosslink attaches at residue	number:		
8			
Edt Modifications			
Eak Modifications			
	OK	Can	cel

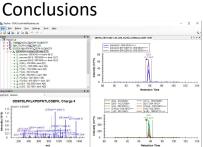
When a crosslinker modification is chosen. the Edit Linked Peptide dialog appears and allows the user to specify the amino acid sequence of the linked peptide and the location that the crosslinker attaches

Carol





https://skyline.ms



crosslinked peptides. This will make it much easier to use Skyline to study protein interactions where a chemical crosslinker reagent was used, as well as to

Skyline 20.2 will be released in the latter half of 2002. These features will be available in Skyline-Daily before then. The latest versions of Skyline and Skyline-Daily