1. Open blank document and check that the document is in “proteomics” mode



1. Settings -> peptide settings
	1. Digestion tab: Add a “No Enzyme” option in the enzyme drop down list, where it ‘cleaves’ at A, unless followed by ARNDCQEGHILKMFPSTWYV
		1. For background proteome, import a FASTA file with human amelogenin protein sequences
	2. Library tab: build a new library by adding DAT files from Mascot searched data (export Mascot identifications as DAT files and load into Skyline)
	3. Modifications tab: unselect carbamidomethyl, and add an oxidation of methionine modification
2. Settings -> transition settings
	1. Full-scan tab: in the MS/MS filtering section, select DDA as acquisition method, and TOF as product mass analyzer
3. Edit->insert->peptides
	1. In the columns, type in
		1. SMIRPPY | AMELY
		2. SIRPPYPSYG | AMELX
		3. SIRPPYPSYGYEPMG | AMELX
	2. These peptides should now appear in the targets window
4. This can then be exported as a transition list which creates an excel spreadsheet with all of the transitions Skyline will scan for
5. File->import->results, click ok. You can then load in spectral data