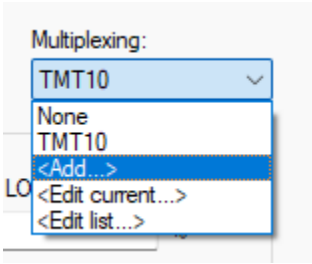
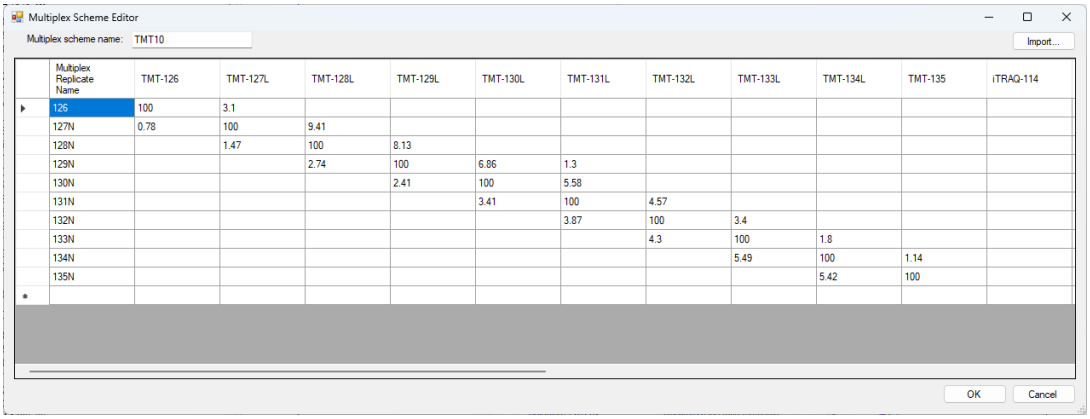
Here is how I think some of the TMT features in the next version of Skyline should work.

1. On the "Quantification" tab of the Peptide Settings dialog, there will be a "Multiplexing" dropdown where you can define a new multiplexing scheme.



This brings up the Multiplex Scheme editor with one column for each reporter ion, and you then get to add rows for each "Multiplex Replicate" and then specify how much signal each of those reporter ions is expected to contribute to a particular multiplex replicate:

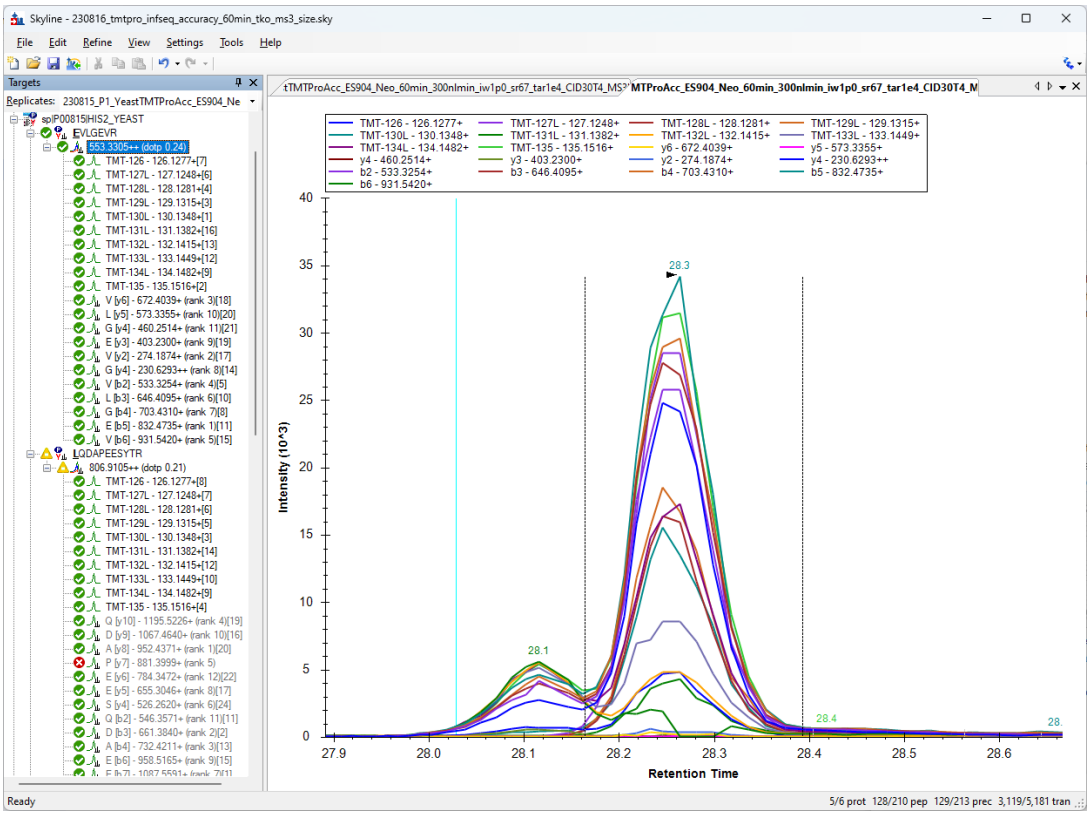


Multiplex Replicate Name	TMT-126	TMT-127L	TMT-128L	TMT-129L	TMT-130L	TMT-131L	TMT-132L	TMT-133L	TMT-134L	TMT-135	iTRAQ-114
126	100	3.1									
127N	0.78	100	9.41								
128N		1.47	100	8.13							
129N			2.74	100	6.86	1.3					
130N				2.41	100	5.58					
131N					3.41	100	4.57				
132N						3.87	100	3.4			
133N							4.3	100	1.8		
134N								5.49	100	1.14	
135N									5.42	100	

Users can either type all those numbers in manually, or they can use the "Import..." button to read that from the "AnalysisDefinition" table inside of a Proteome Discoverer .msf file.

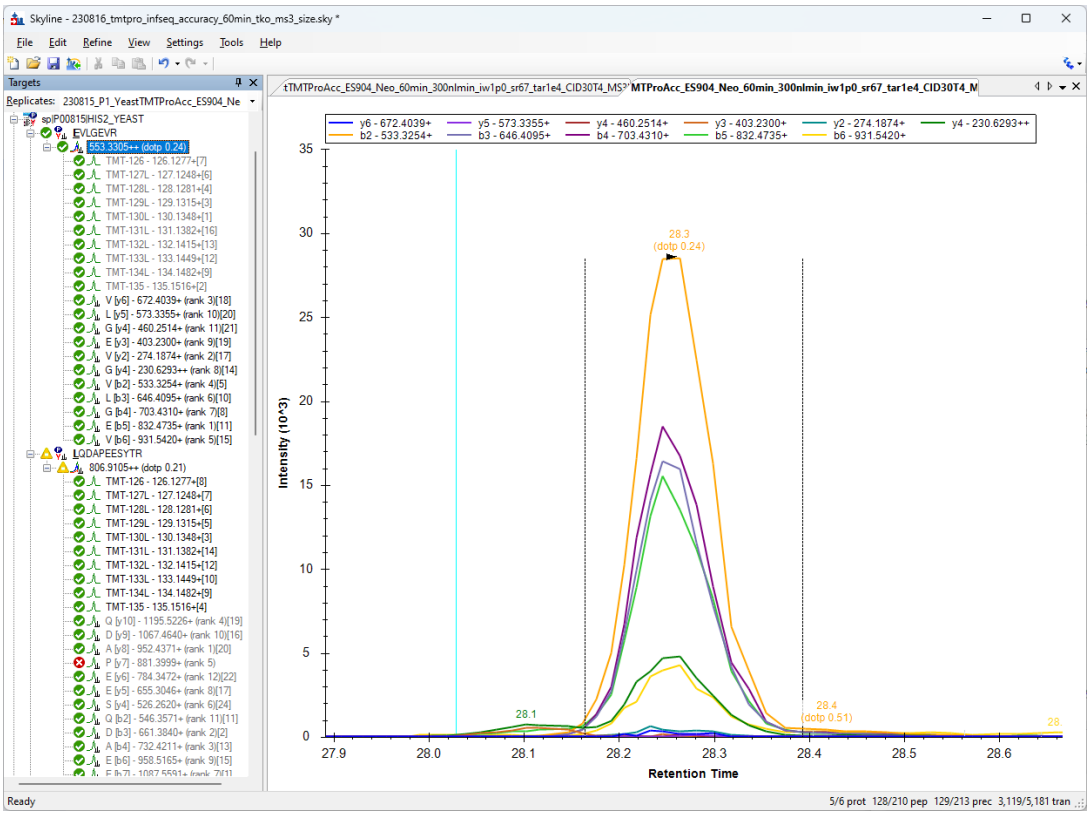
The numbers in this table were typed in manually by me because this dataset seemed to be from a low resolution instrument so it seemed like the correct thing to sum the values for the C and N labeled TMT tags. I imagine that Skyline should also have the smarts to do that.

Here is some PRM data which shows some ordinary transitions and some reporter ions.



One feature that would probably be useful might be to see the reporter ions separately from the ordinary transitions.

Here's what the ordinary transitions look like:



Here's what the reporter ions look like: