Associate proteins when populating peptide tree (need background proteome)

Can edit report format and add protein name to output

Skyline will give info on a peptide basis – need to combine this information in excel output and do statistics

One peptide could be upregulated while others are not – could be modified, a fluke, etc. (would see from high stdev)

For output: standard deviation, mean total area, area normalized

Total area = expression value of peptide

Cv total area will give you an idea of if you have an outlier (if it is high)

Use proteome db as background proteome so can annotate

Import proteins -> click on protein -> unfilter -> lists all possible peptides for the protein (this is to populate the peptide tree)

Make a separate document for each treatment – 4 documents of 12 raw files each

View -> ion types -> check b and y ions to check distributions (want good dist of y ions, b are usually less abundant)

Can look at replicate comparisons of retention times – they should be in the same time frame (want to make sure they are the ~same)

Can deselect bad peptides by clicking on proteins in peptide tree

Make sure peptide is present in at least 2 tech reps and in a certain number of biological replicates