Data analysis methods (starting from swath processed data):

Load ion areas data

Load FDR data, remove decoys and discard proteins below identification probability threshold

* What is FDR threshold?
* euc\_swath\_reanalysed\_FDR$FDR <- apply(euc\_swath\_reanalysed\_FDR[8:ncol(euc\_swath\_reanalysed\_FDR)],1, function(x) as.numeric(sum(as.numeric(x < 0.01)) > 2) )
* at least three samples where FDR is less than 0.01
* protein areas calculated by Top2top2 analysis of ion areas
* protein molar amounts derived from protein areas relative to ovalbumin GGLEP/DEDT top2/top2avg
  + should double check these calculations really.. then make some good comments on what exactly each line is doing with all the t()’s… maybe could use mutate or something