

Single Cell Xenopus TMT Analysis

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Data Organization

```
pepRaw = pepRaw %>% mutate(run = c('ctrl','a','b','c','d','e')[match(pepRaw$file, files)]) %>%  
  group_by(file, `Annotated Sequence`) %>% mutate(pepID = letters[1:n()]) %>% ungroup() %>%  
  select(file, run, pepID, everything())  
  
pepTidy = pepRaw %>% gather(key = label, value = intensity, '126':'131') %>%  
  select(run, label, intensity, everything(), -file) %>%  
  mutate(condition = ifelse(run == 'ctrl', 'ctrl', c('ctrl', 0, 20, 40, 60, 80)[match(label, c(126:131))]),  
         intensity = as.numeric(intensity)) %>%  
  select(run, label, condition, everything())
```

Variance and Covariance Between Cells Before Normalization