

# Keyword enrichment test

You have assigned keywords for each protein in your dataset in one column. The multiple keywords are separated by an identifier (e.g. “;”). After testing your dataset for differential abundance, you plan to identify enriched keywords. Use the `kwd_enrichment()` function to test if a specific term of your interest is over-represented in the enriched sub-proteome over the background proteins (complete proteome). see example

```
# you can have the keywords in the same dataframe with your ids.
# e.g. from a central annotation file you can use the append_cols_df function to add
#       annotation in your working dataframe
# create two vectors with the keywords for the significant ids and the background
kwd_col_test <- NS_secreted$Keyword
kwd_col_bg <- bg_secreted$Keyword

# create a vector with the keywords that you aim to test
my_keywords <- c("proteolysis", "transport", "immune system")

# define the separator if multiple keywords are used for each entry
kwd_sep <- ";"

kwd_enrichment(kwd_col_test = significant_ids$keywords,
               kwd_col_bg = background_set$keywords,
               kwd_vector = my_keywords,
               padj_method = "bonferroni")
```