# Filtering of MaxQuant evidence.txt output by PIF for TMT quantitation

## Using the script:

1. Open in an RStudio project folder.
2. Add the evidence.txt file in the same folder as the script.
3. Add the msms.txt file in the same folder as the script.
4. Open the script pif\_filtering\_evidence\_file\_for\_MSstats\_fromMSMS.R in RStudio.
5. Modify the Top\_N criteria you want (line 9 of the script, 2 is default)
6. Modify the PIF cut-off you want to set (0.65 is default)
7. Execute the rest.

## Output:

A .txt will be generated in the same folder with the name evidence\_top\_X\_PIF\_peptides.txt where X would correspond to your desired Top\_N criteria.

**Note**: You might need to change the name of this file to evidence.txt when using it as input of other scripts for preprocessing.

A secondary filtered\_out\_proteins\_non\_quantifiable\_peptides.txt file will also be generated if the whole script is executed. This file would have the same format as the evidence.txt file and would only include the list of proteins that were excluded because were identified with unquantifiable peptides.