

# Report for PEP Section in mzTab File

## example\_1

The PEP section of the **mzTab** file contains 26,113 quantified peptide features measured in 1 samples.

	number of peptides	
quantified	26,113	100%
identified (total)	0	0%
identified (unique modified)	0	0%
identified (unique stripped)	0	0%

Table 1: Total number of quantified and identified peptides.

modification	specificity	number
no mods reported		

Table 2: Statistics of modifications.

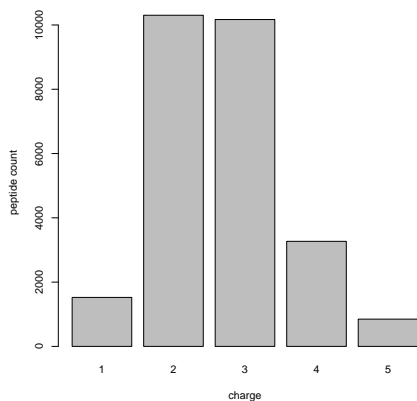
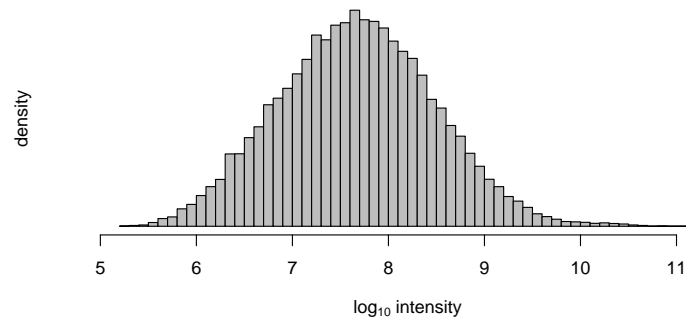


Figure 1: Charge distribution of peptide quantifications.



(a) peptide abundances 1,  $\text{median}(\text{intensity}) = 46,365,100$

Figure 2: peptide abundance distributions.

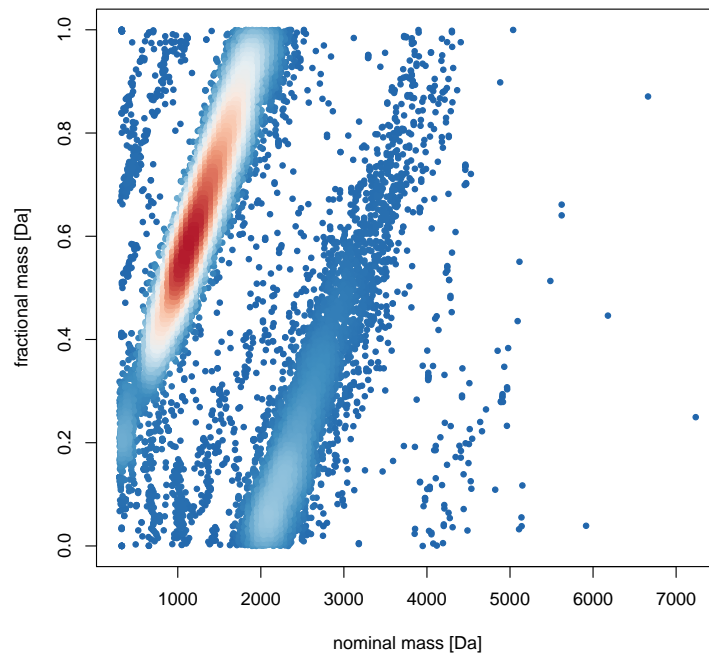


Figure 3: Kendrick nominal fractional mass plot

modified sequence	accession	charge	retention time	m/z
no sequences reported				

Table 3: Peptides of interest. Please note that the script requires a vector of *stripped* peptides sequences, but in the above table we list the *modified* peptide sequences.

modified sequence	accession	charge	retention time	m/z
no accessions reported				

Table 4: Proteins of interest.