

# 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
identified (total)	0
identified (unique modified)	0
identified (unique stripped)	0

Table 1: Total number of quantified and identified peptides.

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

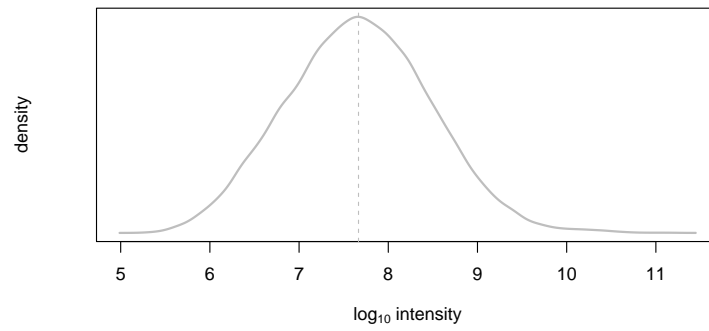
Table 2: Peptides of interest. Note that the script requires a vector of *stripped* peptides sequences, but in the above table we list the *modified* peptide sequences.

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

Table 3: Proteins of interest.

modification	specificity	number
no mods reported		

Table 4: Statistics of modifications.



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

Figure 1: peptide abundance distributions.

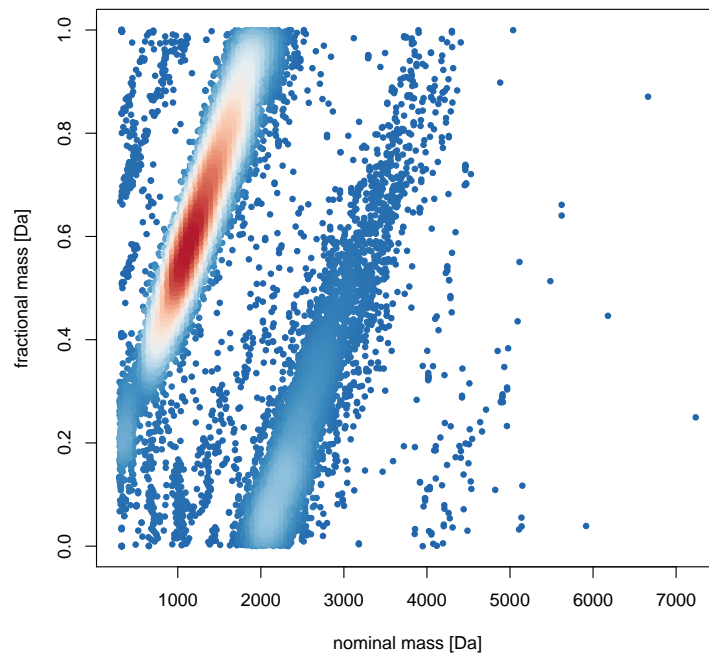


Figure 2: Kendrick nominal fractional mass plot