

Report for PEP Section in mzTab File

example_1

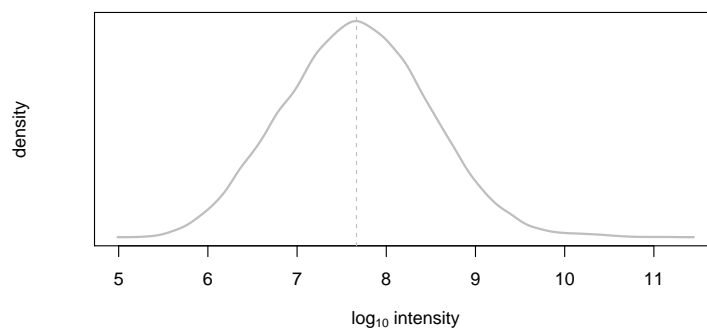
The PEP section of the **mzTab** file contains 26,113 quantified peptide features measured in 1 samples.

| | 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.

| modification | specificity | number |
|------------------|-------------|--------|
| no mods reported | | |

Table 2: Statistics of modifications.



(a) peptide abundances 1, median(intensity) = 46,365,100

Figure 1: peptide abundance distributions.

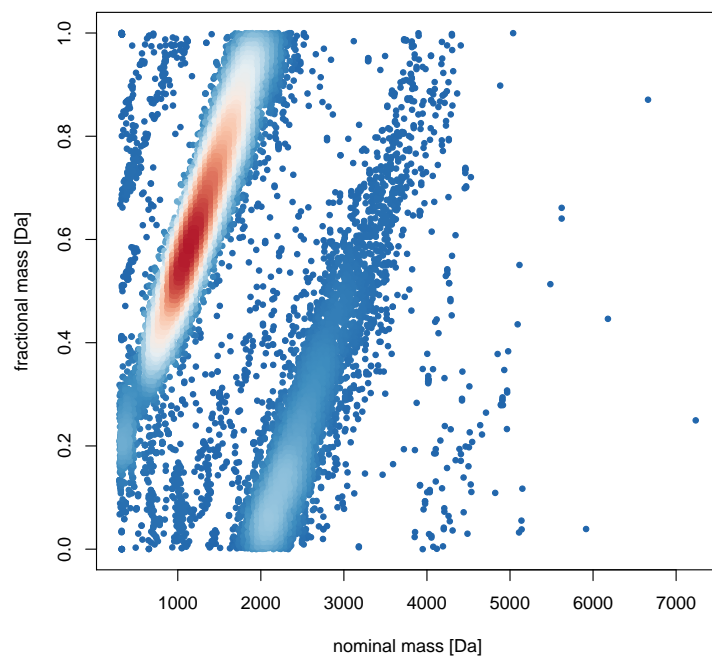


Figure 2: Kendrick nominal fractional mass plot

| 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.