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.

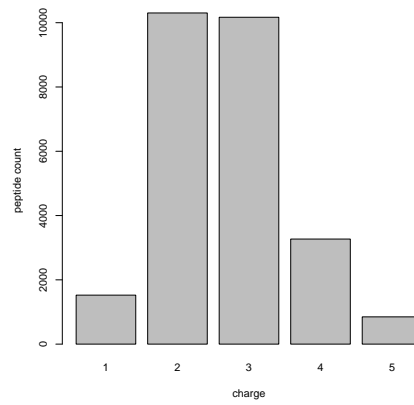| sample	finite	zero	nan
1	26113	0	0

Table 3: Statistics of quantifications.

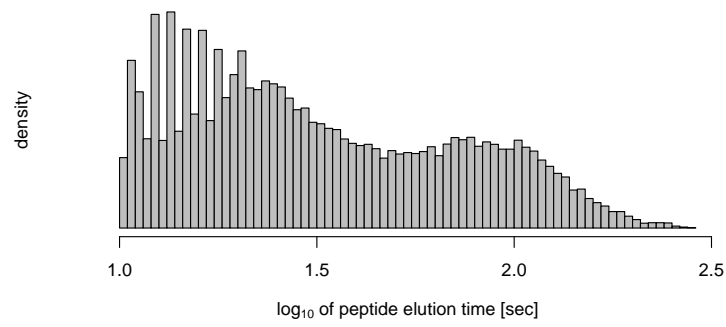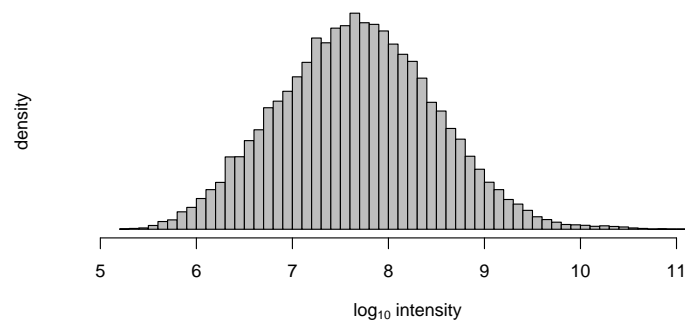Figure 1: Charge distribution of peptide quantifications.

Figure 2: Elution time distribution of peptide quantifications. Note that the elution time is logarithmic. For example, 2.0 corresponds to 100.0 sec.

(a) peptide abundances 1, median(intensity) $= 46,365,100$
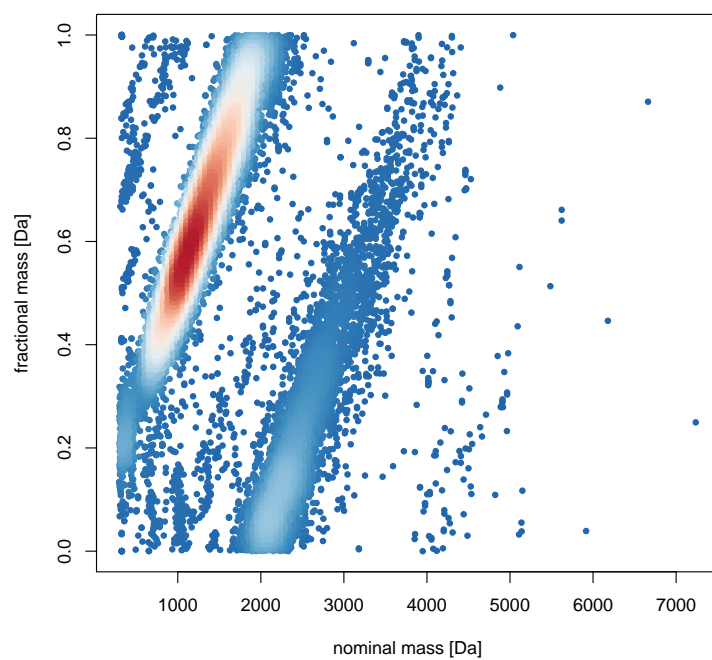
Figure 3: peptide abundance distributions.

Figure 4: Kendrick nominal fractional mass plot

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

Table 4: 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 5: Proteins of interest.