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%
quantified (any zero)	0	0%
quantified (any NaN)	0	0%
identified (total)	0	0%
identified (unique modified)	0	0%
identified (unique stripped)	0	0%

Table 1: Total number of quantified and identified peptides. (any zero) corresponds to peptides which are absent in one or more samples. (any NaN) corresponds to peptides which could not be quantified due to overlapping peptide features.

modification	specificity	number
no mods reported		

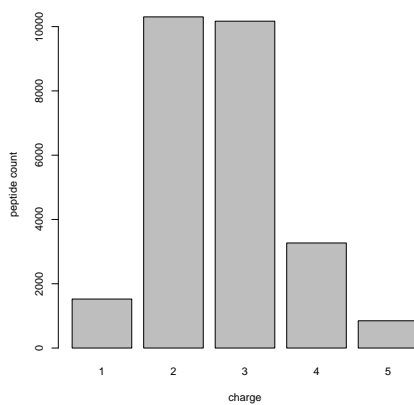Table 2: Statistics of modifications.

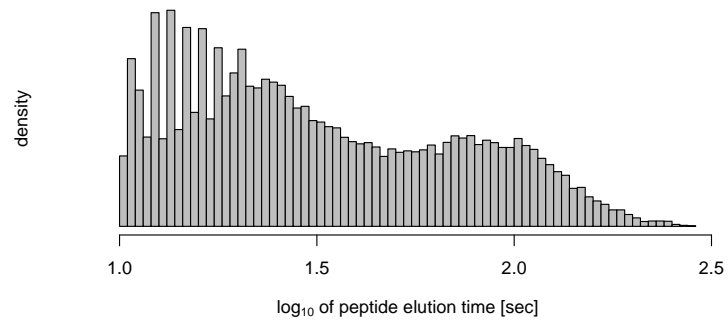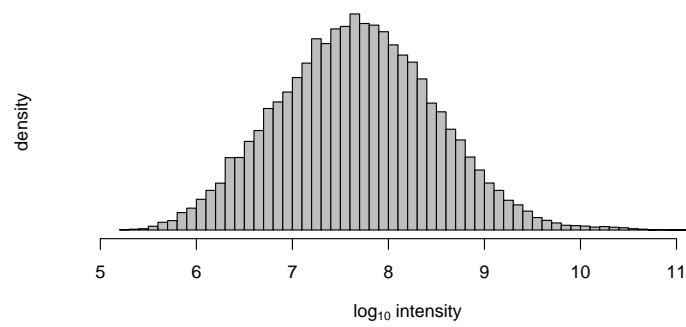Figure 1: Charge distribution of peptide quantifications.

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.

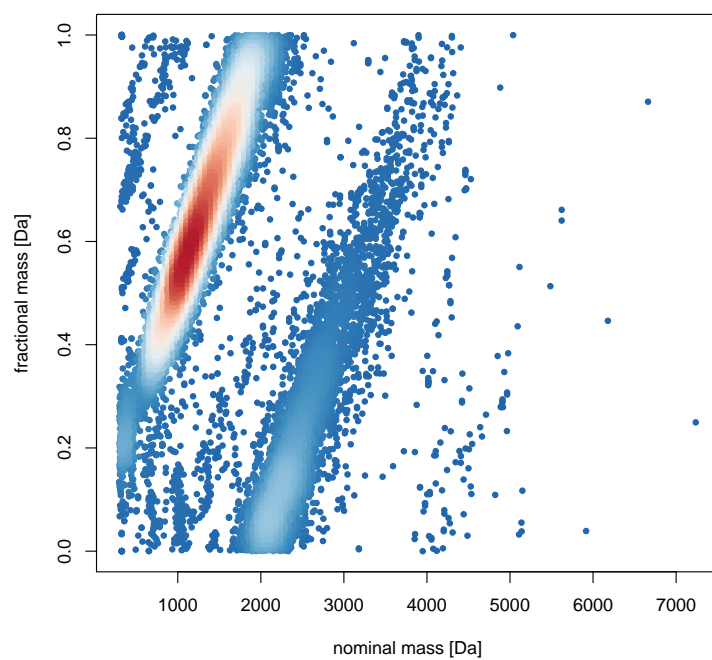Figure 4: Kendrick nominal fractional mass plot

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

Table 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.