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.

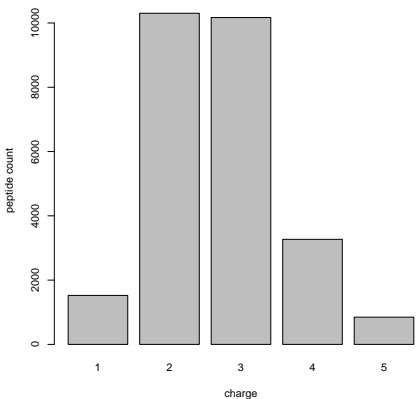| modification	specificity	number
no mods reported		

Table 2: Statistics of modifications.

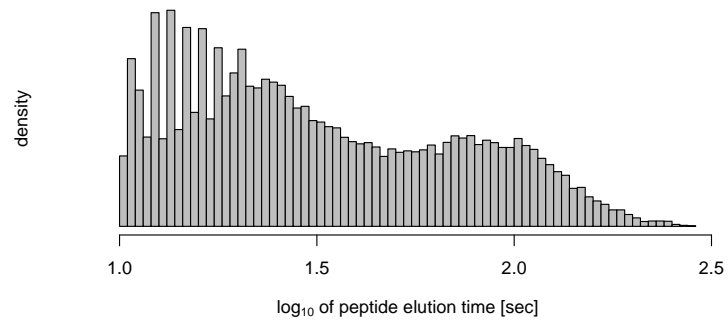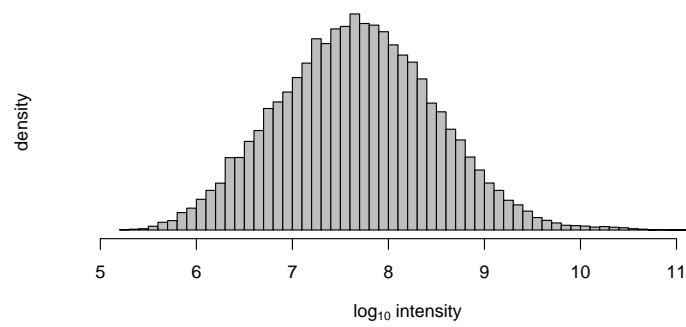Figure 1: Charge distribution of peptide quantifications.

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.

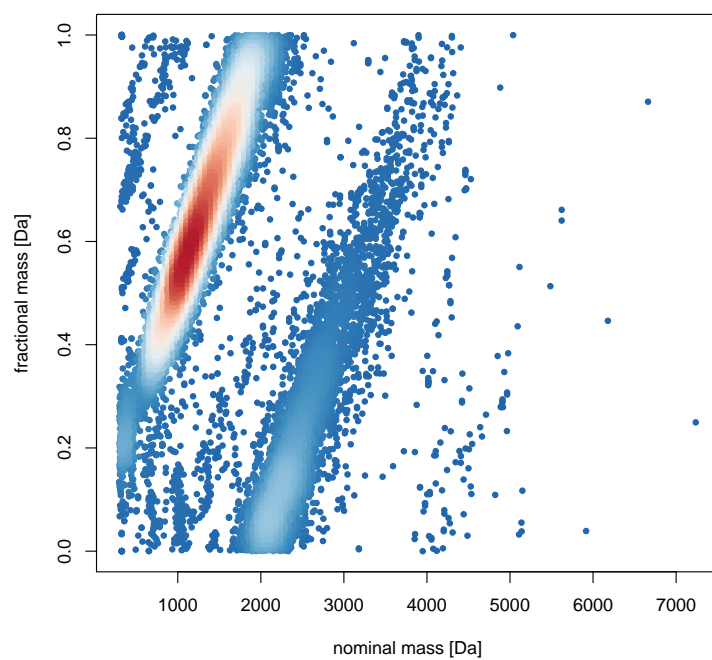Figure 4: Kendrick nominal fractional mass plot

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.