## Report for PEP Section in mzTab File example\_1

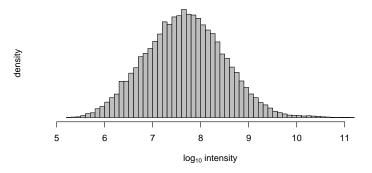
The PEP section of the mzTab file contains 26,113 quantified peptide features measured in 1 samples.

	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.



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

Figure 1: peptide abundance distributions.

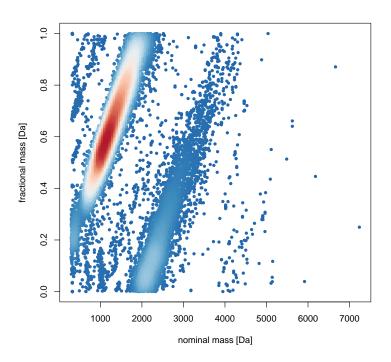


Figure 2: Kendrick nominal fractional mass plot

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.