Report for `PSM` Section in `mzTab` File
## example

|	total		non-redundant	
PSMs	32,927	100%	29,775	100%
unique PSMs	29,471	89.5%	26,823	90.09%
target PSMs	22,235	67.53%	19,340	64.95%
decoy PSMs	8,959	27.21%	8,739	29.35%
target + decoy PSMs	35	0.11%	32	0.11%
unmapped PSMs	0	0%	0	0%

Table 1: Number of PSMs. Two PSMs are considered *non-redundant* if they differ in amino acid sequence. They are considered *redundant*, if they differ merely in modifications. A PSM is considered *unique*, if its amino acid sequence can be mapped uniquely to a single protein. The sequence can appear in either target proteins, decoy proteins, both or neither of them.

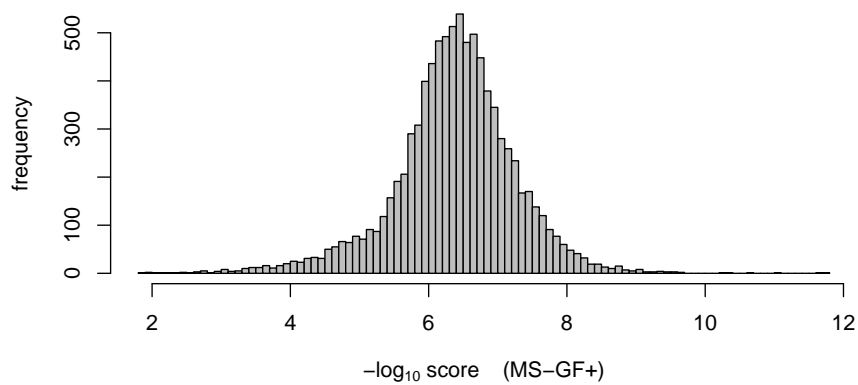| mod	specificity	number
Carbamidomethyl	C	11234
Oxidation	M	7944

Table 2: Statistics of modifications.
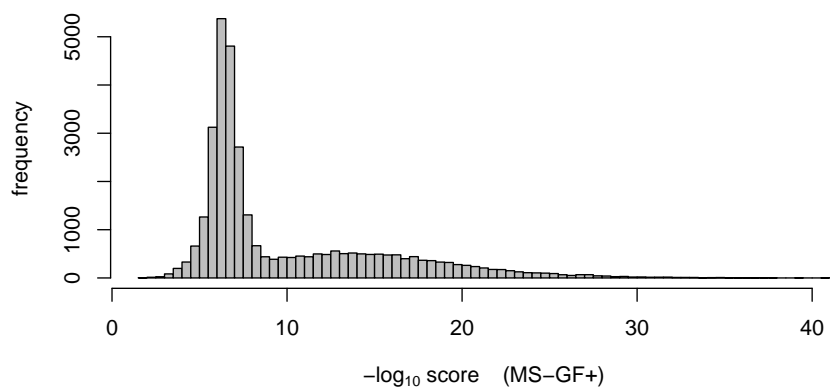
(a) 32,927 PSMs
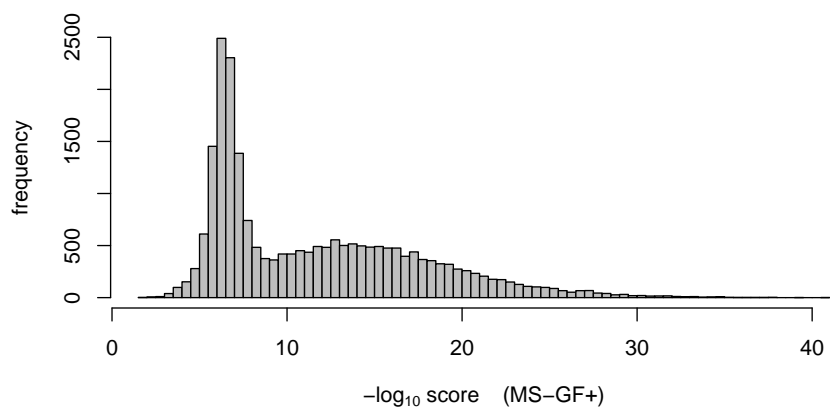
(b) 22,235 target PSMs

(c) 8,959 decoy PSMs

Figure 1: Score distribution of `search_engine_score[1]`.