To show that our method is a fully polynomial-time approximation scheme, we derive a bound on the length of a *DMS* set. After trimming, successive elements DMS_i and DMS_i' of *DMS* must have a relationship:

$$\frac{DMS_i'}{DMS_i} > 1 + \varepsilon$$

Therefore, each possible *DMS* set contain up to $\log_{1+\varepsilon} PML_{val}$ values.

$$\log_{1+\varepsilon} PMS_{val} = \frac{\ln PMS_{val}}{\ln 1 + \varepsilon}$$

Since $\frac{x}{1+x} \leq \ln(1+x) \leq x$ and $0 < \varepsilon < 1$:

$$\frac{\ln PMS_{val}}{\ln 1 + \varepsilon} \leq \frac{(1+\varepsilon)\ln PMS_{val}}{\varepsilon} \leq \frac{2\ln PMS_{val}}{\varepsilon}$$

From the equation above, this bound is polynomial in the size of the input PMS_{val}. It is also polynomial in the size of the set *DMS* since ε is directly proportional to the number of cysteine-containing peptides *k* (according to Eq. 2), which are combined to form each set DMS_i.

Since the running time of APROX-DMS routine is polynomial in the length of each set DMS_i and the same proof can be used to demonstrate the polynomial running time characteristic of the APROX-FMS routine, our method is a fully polynomial-time approximation scheme.