

Name:

Roll Number:

(if name or roll number is not filled, ZERO marks will be awarded)

1. Which among the following combinations of Ion Source and Mass Analyzer are compatible with each other: a) Ion trap X ESI b) TOF X MALDI c) TOF X ESI d) Quadrupole X ESI

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2. Calculate the Time of Flight for a protein of mass 15 kDa travelling a distance 0.2 m in TOF mass spectrometer under an accelerating potential difference of 125 V.  
[ $z = 1$ ;  $e = 1.6 \times 10^{-19} \text{ C}$ ]

$$t = 0.2 \times \sqrt{\frac{15000 / 6.022 \times 10^{23}}{2 \times 1.6 \times 10^{-19} \times 125}}$$

$$= 157.8 \mu\text{s}$$

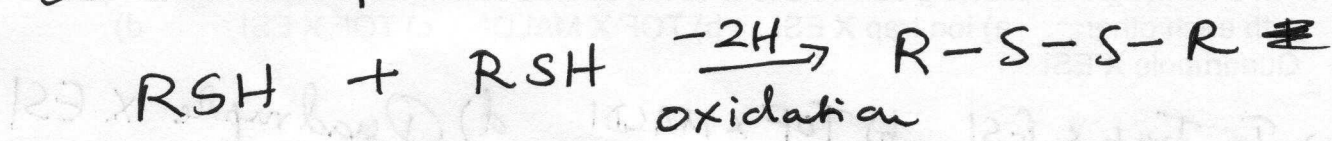
3. Shanti isolated a novel protein with folded structure. She wants to determine which regions in the sequence of protein are least exposed to solvent. How can she proceed?

Shanti can use the HDX technique with Mass Spectrometry.

- exchange protein with  $\text{D}_2\text{O}$  buffer
- Stop exchange by using acidic cond.
- Analyse separated proteolytic fragments by MS
- Exchange sites determined by peptides that show Deuterium mass shifts.
- Sites in seq that show least exchange are least exp.

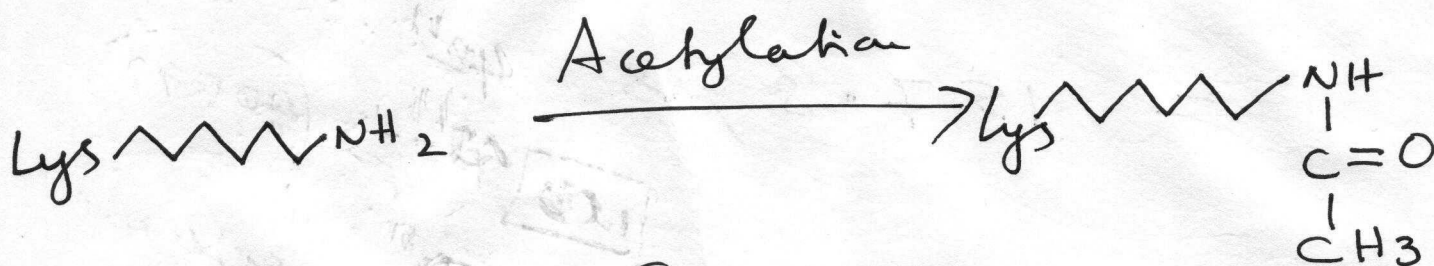
4. A certain protein yields TWO mass values  $X$  and  $2X-2$  from mass spectrometry for a constant  $z$ . Explain the likely origin of the larger mass detected.

The  $2X-2$  mass value can arise from a disulphide bonded dimer



formed under oxidising conditions.

5. Histone proteins are enzymatically acetylated at the Lysine amino group and frequently deacetylated at same position. How can you confirm if the a given histone protein has been acetylated? How can you verify the number of acetylated sites in a given protein?



Addition of  $(43-1) = 42 \text{ Da}$   
indicates likely acetylation

Number of acetylated sites can be calculated by dividing the extra mass due to acetylation by 42.