

Outline

- What roles do amino acid sequences play in protein structure?
- What are the elements of secondary structure in proteins, and how are they formed?
- How do polypeptides fold into three-dimensional protein structures?

How can you determine the primary structure of proteins?

TABLE 3–7

The Specificity of Some Common Methods for Fragmenting Polypeptide Chains

Reagent (biological source)*	Cleavage points [†]
Trypsin (bovine pancreas)	Lys, Arg (C)
<i>Submaxillarius</i> protease (mouse submaxillary gland)	Arg (C)
Chymotrypsin (bovine pancreas)	Phe, Trp, Tyr (C)
<i>Staphylococcus aureus</i> V8 protease (bacterium <i>S. aureus</i>)	Asp, Glu (C)
Asp-N-protease (bacterium <i>Pseudomonas fragi</i>)	Asp, Glu (N)
Pepsin (porcine stomach)	Leu, Phe, Trp, Tyr (N)
Endoproteinase Lys C (bacterium <i>Lysobacter enzymogenes</i>)	Lys (C)
Cyanogen bromide	Met (C)

*All reagents except cyanogen bromide are proteases. All are available from commercial sources.

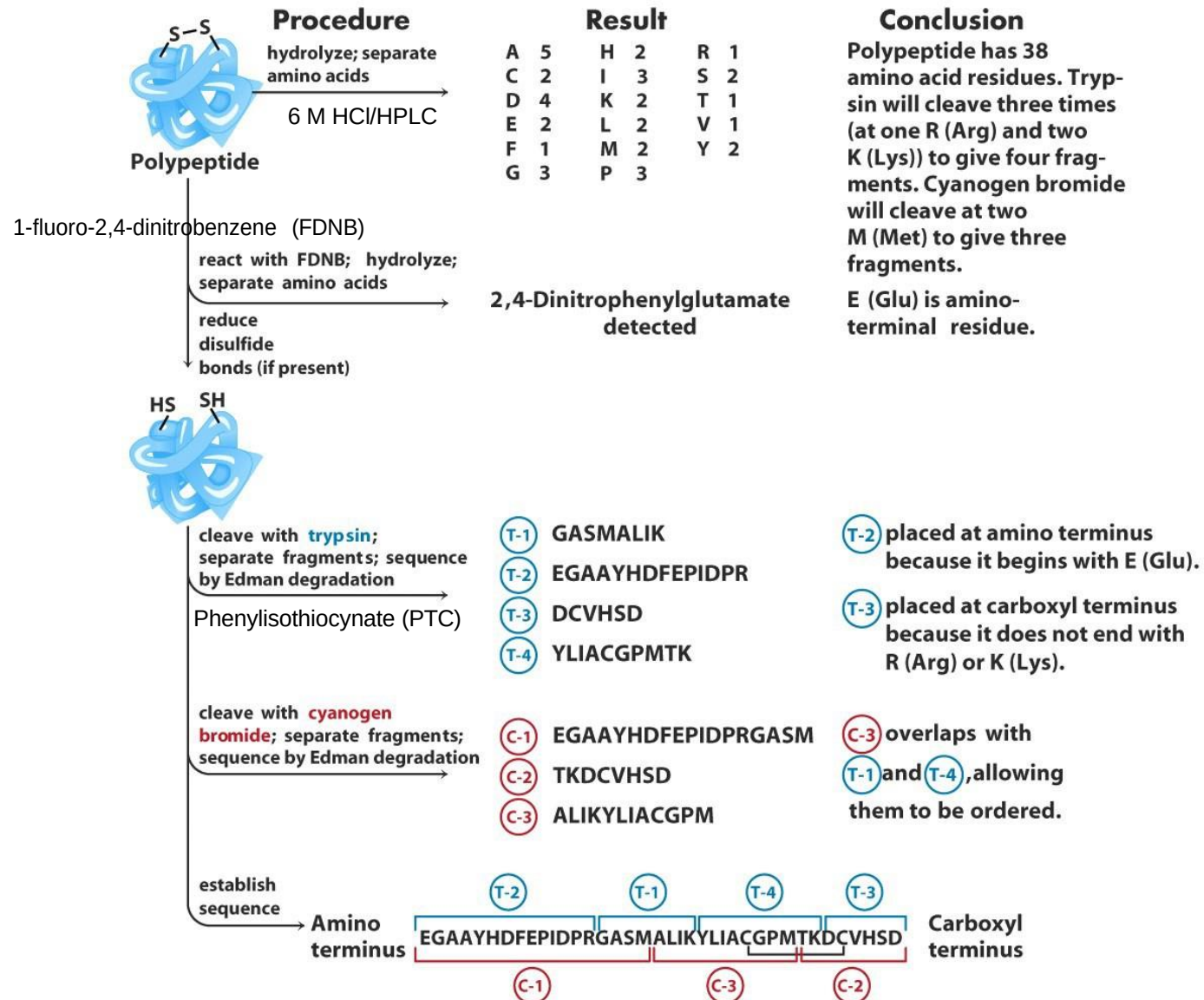
[†]Residues furnishing the primary recognition point for the protease or reagent; peptide bond cleavage occurs on either the carbonyl (C) or the amino (N) side of the indicated amino acid residues.

Table 3-7

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Short peptides can be sequenced



Mass Spectrometry of biological macromolecules



Mass spectrometry (MS) provides the most accurate mass measurements of biomolecules.

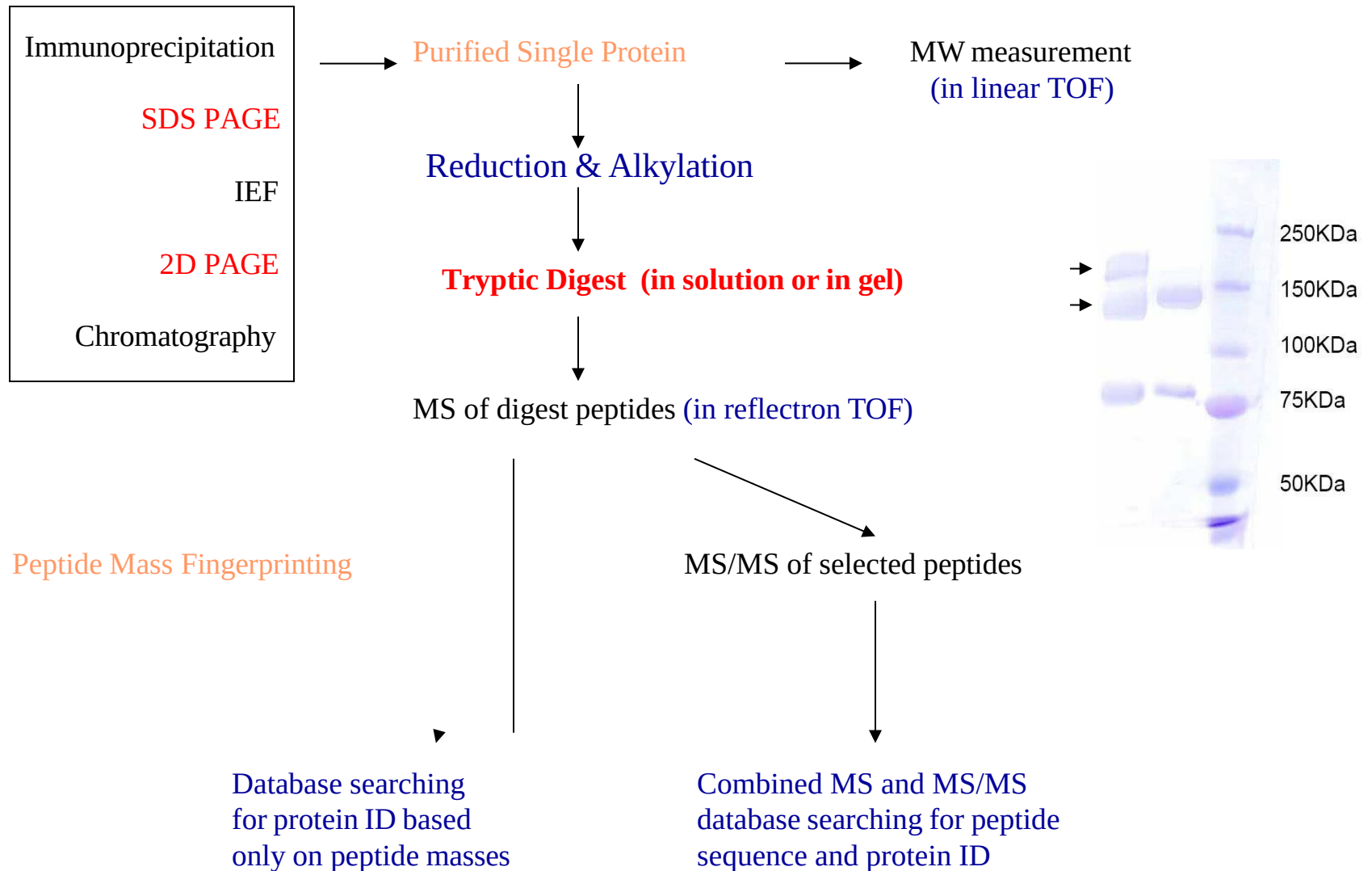
Why MS?

-Proteomics

**Characterize Proteins in Tissues or Whole Cells
(10,000 to 20,000 proteins at a given time)**

- **Protein Identification (Sequence verification)**
- **Posttranslational modifications**
- **Mutation analysis**
- **Splice variants**
- **Expression level quantification**
- **Cellular localization**
- **Binding partners**

MALDI based Protein ID



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