**Potein sequences**

* The amino acid sequences of proteins are direct reflections of mRNA sequences and therefore closely related to the structures of the genes coding for their synthesis. For this reason, comparisons of proteins from different microorganisms are very useful taxonomically.
* The most direct approach is to determine the amino acid sequence of proteins with the same function.
* If the sequences of proteins with the same function are similar, the organisms possessing them are probably closely related.
* The sequences of cytochromes and other electron transport proteins, histones, heat-shock proteins, transcription and translation proteins, and a variety of metabolic enzymes have been used in taxonomic studies.
* Because protein sequencing is slow and expensive, more indirect methods of comparing proteins frequently have been employed.
* The electrophoretic mobility of proteins is useful in studying relationships at the species and subspecies levels.
* Antibodies can discriminate between very similar proteins, and immunologic techniques are used to compare proteins from different microorganisms.

**Signature sequences**

* Signature sequences are contiguous patterns of amino acids 10-50 residues long that are associated with a particular structure or function in proteins.
* Signature sequences in proteins could be defined as regions in the alignments where a specific change is observed in the primary structure of a protein in all members of one or more taxa but not in the other taxa.
* The changes in the sequence could be either the presence of particular amino acid substitutions or specific deletions or insertions (i.e., indels)
* In all cases, the signatures must be flanked by regions that are conserved in all the sequences under consideration. These conserved regions serve as anchors to ensure that the observed signature is not an artifact resulting from improper alignment or from sequencing errors.