PROTEIN SEQUENCING

Protein sequencing is the use of experimental methods to determine the amino acid sequence in a protein and its post-translation modifications. Precise protein sequence is vital in understanding protein functions, interactions, structural features, localization, and protein-drug interactions.

COMPARATIVE ANALYSIS OF PROTEIN SEQUENCING METHODS

MASS SPECTROMETRY BASED PROTEIN SEQUENCING

Key Features:

- Higher sequence coverage without a limit of protein intact mass.
- Identification of post-translational modifications (PTMs), crucial for understanding protein functions and interactions.

Suitability:

- Ideal for full-length sequencing of purified protein with or without reference sequence

EDMAN BASED PROTEIN SEQUENCING

Key Features:

- Sequential N-terminal amino acid sequencing provides accurate sequence info for N-term unblocked proteins or peptides.
- No requirement for reference amino acid sequence, allowing the sequencing of any protein or peptide directly.

Suitability:

- Best suited for proteins or peptides that reference sequence info is not necessary, especially useful in de novo sequencing or when validating recombinant proteins.

NANOPORE PROTEIN SEQUENCING

Key Features:

- Real-time sequencing capabilities allow for the rapid analysis of proteins.
- Long-read capabilities make it possible to sequence entire proteins in a single run.

Suitability:

- Appropriate for research needing quick turnaround times and for studying large proteins or complexes that are difficult to analyze with other methods.

SINGLE MOLECULE FLUORESCENCE SEQUENCING

Key Features:

- Direct observation of protein synthesis and folding, providing insights into the dynamics of these processes.
- Single-molecule resolution allows for the study of heterogeneity within populations of molecules.

Suitability:

- Particularly useful for detailed studies of protein translation, folding mechanisms, and for investigating molecular dynamics at the single-molecule level.

COMPARATIVE ANALYSIS SUMMARY

Aspect	Mass Spectrometry	Edman Sequencing	Nanopore Sequencing	Single Molecule Fluorescence Sequencing
Sensitivity	High	Moderate	Variable	Variable
Sequence Coverage	High	N-term	Variable	Variable
Post-translational Modification (PTM) Identification	Yes	Limited	Limited	Limited
Real-time Sequencing	No	No	Yes	Yes
Long-read Capabilities	No	No	Yes	No
Data Interpretation Complexity	High	Low	Moderate	Moderate
Equipment Cost	High	Moderate	High	Moderate
Throughput	Moderate to High	Low	Moderate	Low to Moderate

FEATURE SERVICE IN CREATIVE PROTEOMICS

- Protein N-Terminal Sequencing

Analyzing the amino acid sequence of the N-terminus of proteins helps to identify proteins, enrich protein databases and understand protein function.

- Protein De Novo Sequencing

Inferring the primary sequence of proteins without relying on a reference genome helps to study unknown proteomic domains, identify novel proteins and examine specific protein modifications.

- Protein C-Terminal Sequencing

Determine the sequence of the C-terminus of a protein and understand the sequence of the completed protein as well as understand it in terms of recognition, localization and function.

- Protein Full-Length Sequencing

Whole proteins or important fragments are sequenced to help confirm protein structure models, analyze protein interactions, and for clinical diagnostic applications

APPLICATION OF PROTEIN SEQUENCING

Medical Research

Evolutionary Studies

Drug Discovery

Environmental Monitoring

Food Industry

Industrial Biotechnology

contact us

Creative Proteomics