



## Protein Purification and Analysis in Polymerase Chain Reaction

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### DESCRIPTION

Biomolecular techniques are a diverse array of scientific methods used to investigate the structure, function and interactions of biological molecules. These techniques have revolutionized the field of biology by providing researchers with powerful tools to explore the intricate mechanisms underlying life processes. From studying the structure of DNA to unraveling protein-protein interactions, biomolecular techniques have discovered the advancements in various disciplines, including genetics, biochemistry, biotechnology and medicine. DNA sequencing is a fundamental biomolecular technique that allows scientists to determine the precise order of nucleotides in a DNA molecule. The advent of automated sequencing techniques, such as Sanger sequencing and Next-Generation Sequencing (NGS), has revolutionized genomics and enabled researchers to decipher the complete genetic makeup of organisms. DNA sequencing has applications in diverse fields, including gene discovery, genetic disease diagnosis, evolutionary studies, and personalized medicine. It has provided insights into the human genome, identified disease-causing mutations, and facilitated the development of targeted therapies.

Polymerase Chain Reaction (PCR) is a widely used biomolecular technique that allows for the amplification of specific DNA sequences. It enables researchers to produce millions of copies of a target DNA fragment even from a tiny starting amount. PCR has diverse applications including gene cloning, genetic fingerprinting, diagnostics and forensics. It has played a crucial role in the identification and diagnosis of infectious diseases, genetic disorders and cancer. PCR-based techniques such as real-time PCR and reverse transcription PCR (RT-PCR) have further expanded the utility of PCR in quantification and gene expression analysis.

### Protein purification and analysis

Proteins are the workhorses of the cell and understanding their structure and function is essential for unraveling the

complexities of life. Biomolecular techniques for protein purification and analysis, such as chromatography, electrophoresis and mass spectrometry have greatly facilitated protein characterization. Chromatography techniques including affinity chromatography and size-exclusion chromatography enable the isolation and purification of proteins from complex mixtures. Electrophoresis techniques such as SDS-PAGE and two-dimensional gel electrophoresis allow for the separation and identification of proteins based on their size and charge. Mass spectrometry enables the identification and quantification of proteins and their post-translational modifications. Protein-protein interactions play a crucial role in cellular processes and are essential for understanding biological pathways and networks. Biomolecular techniques for studying protein-protein interactions such as yeast two-hybrid assays co-immunoprecipitation and Fluorescence Resonance Energy Transfer (FRET) provide insights into the complex interactions between proteins.

These techniques enable the identification of protein interaction partners the mapping of protein interaction networks and the investigation of protein dynamics. They have contributed to our understanding of various cellular processes including signal transduction, gene regulation and disease mechanisms. Provides information about distances between atoms their chemical environments and interactions with other molecules. NMR spectroscopy has been particularly useful in studying the structures of smaller proteins and elucidating their interactions with ligands or other biomolecules. Cryo-Electron Microscopy (cryo-EM) is a rapidly advancing technique that allows for the visualization of biological macromolecules at near-atomic resolution. It involves freezing samples in vitreous ice and imaging them using an electron microscope. Cryo-EM has revolutionized structural biology by enabling the determination of complex molecular structures, such as large protein assemblies, membrane proteins and viruses which were previously challenging to study using traditional techniques. It has provided unprecedented insights into the architecture and mechanisms of biomolecular complexes.

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