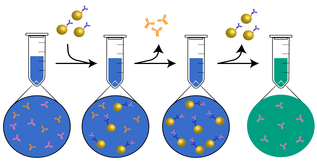
CO-IMMUNOPRECIPITATION MASS SPECTROMETRY

Co-immunoprecipitation (Co-IP) is a widely used method for investigating protein-protein interactions in a complex mixture. However, combining Co-IP with mass spectrometry (MS) analysis has revolutionized the way researchers identify and characterize protein interactions. This advanced technique offers an unprecedented level of resolution, sensitivity, and accuracy in detecting even weak protein interactions.

Principles and Workflow of Co-IP-MS

The central principle of Co-immunoprecipitation Mass Spectrometry (Co-IP-MS) involves the selective capture of protein complexes by specific antibodies, followed by the identification and quantification of individual proteins within these complexes using mass spectrometry.

Co-IP selectively captures protein complexes using antibodies that target a particular protein within the complex. The antibody-protein complexes are captured on solid supports like beads. After washing to remove non-specifically bound proteins, the proteins are eluted from the solid support.

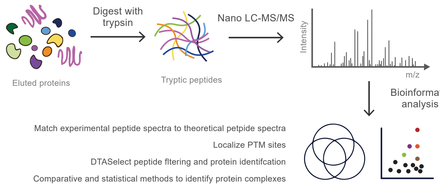


Co-immunoprecipitation

The eluted protein complex is then subjected to enzymatic digestion, typically using trypsin, to break down the proteins into smaller peptide fragments. These peptides are analyzed by mass spectrometry, where they are ionized, separated based on their mass-to-charge ratios, and detected and quantified.

The mass spectrometry data is analyzed using bioinformatics tools and databases to identify the proteins present in the complex. Comparative analysis can be performed to assess changes in protein composition between different samples or conditions.

By combining the selectivity of Co-IP with the high sensitivity and resolution of mass spectrometry, Co-IP-MS enables the identification and quantification of proteins within complexes, mapping of intricate protein interaction networks, and detection of even weak or transient protein interactions.



Why choose CoIP-MS?

1 Identification of protein complex components

Co-IP-MS enables the identification of all proteins within a protein complex, including novel and previously unknown interacting partners, without prior knowledge of their identities. This is a major advantage over techniques like Western blotting which require prior knowledge of potential interactors.

2 Quantification of protein interactions

Co-IP-MS allows for the quantification of protein interactions by comparing the abundance of proteins within different Co-IP samples. This provides insights into changes in interaction strengths, stoichiometry, and dynamics under different conditions.

3 Mapping protein interaction networks

By analyzing multiple Co-IP experiments systematically, we can construct comprehensive protein interaction networks, depicting the connections between proteins and their functional relationships within biological systems.

4 No prior knowledge required

A major advantage of Co-IP-MS over traditional Co-IP is that it does not require prior knowledge of the potential interacting partners. Mass spectrometry can identify all co-precipitated proteins, enabling the discovery of novel interactions.

5 High throughput analysis

Co-IP-MS enables high-throughput analysis of protein complexes and interactions, facilitating the study of complex biological processes and systems.

6 Physiologically relevant interactions

Co-IP preserves the native conformations of proteins, allowing the identification of physiologically relevant protein-protein interactions.

CoIP-MS in Creative Proteomics

Customer Sample Requirements

Sample Types: Fresh or properly preserved tissues, cells, or protein samples.

Tissue Samples:

- Animal Tissue: >400 mg/sample
- Plant Tissue: >2 g/sample

Cell Samples:

- Cell Count: >2 x 10^7 cells/sample

Protein Samples:

- Lysate Total Protein: >2 mg total protein/sample

Please ensure that all samples meet the specified criteria for optimal analysis.

Authenticity of Immunoprecipitation Results

- Ensure that the co-precipitated proteins are precipitated by the added antibodies, not exogenous non-specific proteins. Monoclonal antibodies have the advantages of high specificity, mass production and easy standardization, etc. The use of monoclonal antibodies helps to avoid contamination.
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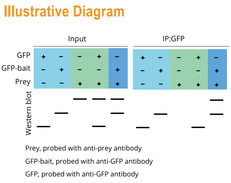
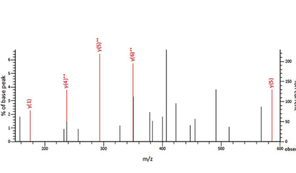
- Ensure that the antibody is specific, and that if the antibody does not bind to the antigen in the cytosol, it will not cause a coimmunoprecipitation reaction.
- Make sure that protein-protein interactions occur in the cell and not as a result of cell lysis.

Illustrative Diagram





LC-MS/MS

Contact Us

Creative Proteomics