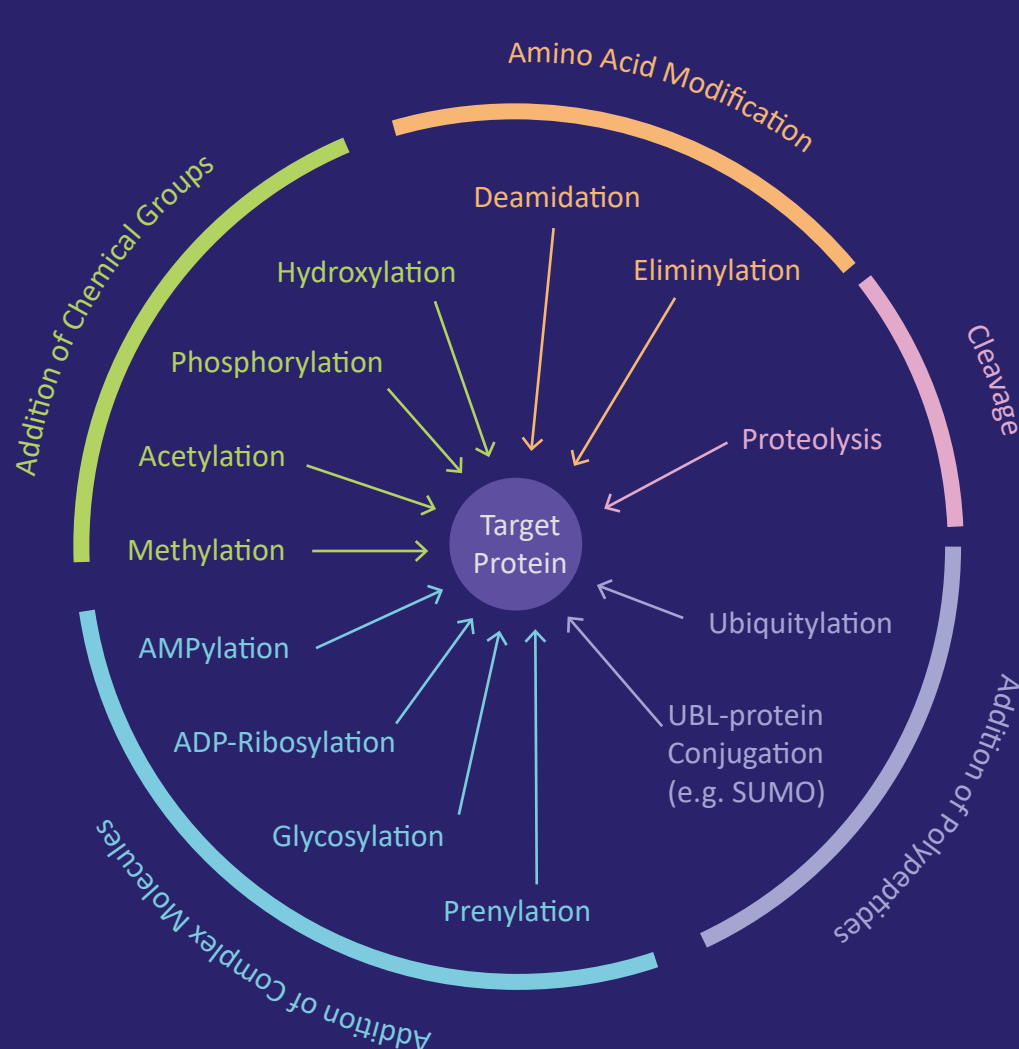


# HOW TO ANALYZE PROTEIN POST-TRANSLATIONAL MODIFICATIONS

Protein post-translational modification (PTM) refers to covalently binding chemical moieties to the amino acid side chains of proteins. More than 400 types of PTMs are known, and almost all proteins can undergo PTMs. Meanwhile, the same protein can achieve multiple PTMs simultaneously.

## TYPE OF POST-TRANSLATIONAL MODIFICATIONS



The physicochemical properties of the protein will significantly change when it undergoes PTM, altering protein conformation and thus directly changing the binding ability and protein functions. Although protein expression levels may remain the same, protein functions are significantly changed if the state of post-translational modification is altered.

The effects of PTM on protein functions are diverse, which are manifested in the following three aspects: (1) Multiple functions may be given when one type of post-translational modification is made to a protein; (2) Different protein functions may be revealed when the same type of post-translational modification is made to one protein but at different amino side chains; (3) Different post-translational modifications may be applied to one protein and lead to changes in protein functions and biological processes of different complexities.

## POST-TRANSLATIONAL MODIFICATION ANALYSIS STRATEGIES

### Bottom-up Strategy

With the bottom-up strategy, a protein is typically digested with enzyme (i.e., trypsin) into peptides in gel or in solution. These peptides can be detected using the mass spectrometer, and modification can be mapped in recovered peptides.

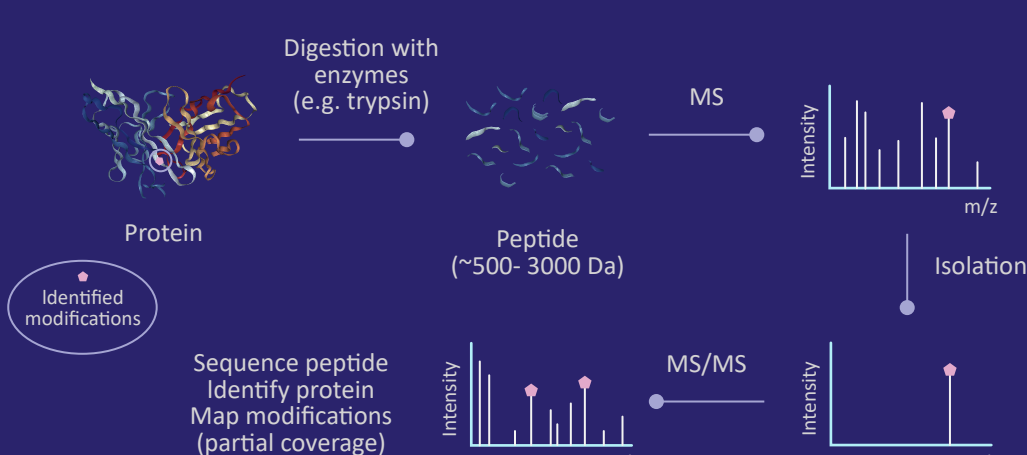
#### Advantage

Higher sensitivity than the top-down method

#### Limitations

Enhanced overall complexity of the sample

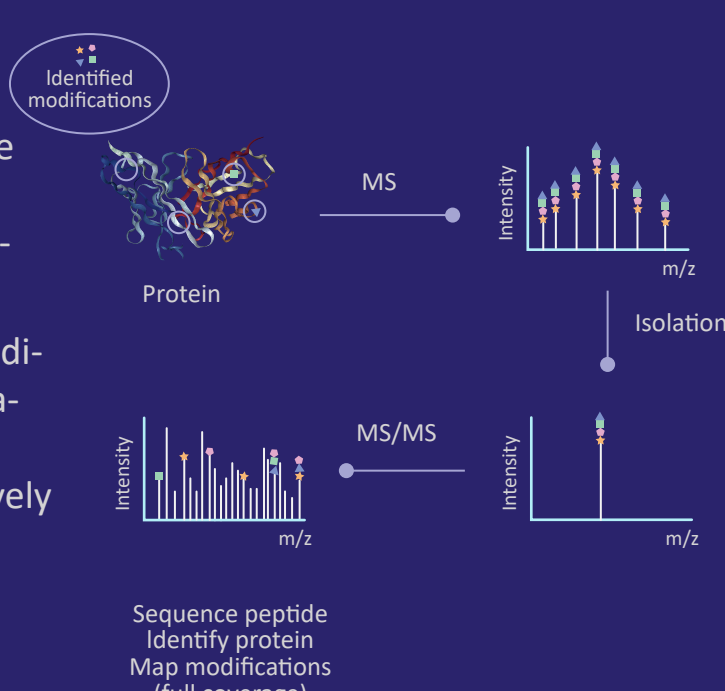
The connection between modifications on disparate portions of a protein can be lost



### Top-down Strategy

The entire protein is analyzed directly in the mass spectrum without the need for digestion, thus revealing the complete identification of all modifications.

It can simultaneously detect all existing modifications, including PTMs (e.g., phosphorylation, proteolysis and acetylation) and sequence variants (e.g., mutants, alternatively spliced isoforms and amino acid polymorphisms) in a single spectrum without prior knowledge.



## PTM ANALYSIS IN CREATIVE PROTEOMICS

### 01 What We Can Do

- Phosphorylation Analysis
- Glycosylation Analysis
- Methylation Analysis
- Acetylation Analysis
- Ubiquitination Analysis
- Nitrosylation Analysis
- Di-Sulfide Bond Localization
- SUMOylation Analysis

### 02 Advantages

- Q Exactive<sup>TM</sup> MS/MS, with the highest resolution.
- Wide and full coverage range: at least 3 enzymes will be used to ensure wide and full coverage.
- Professional data analysis: constantly upgraded bioinformatics analysis systems.