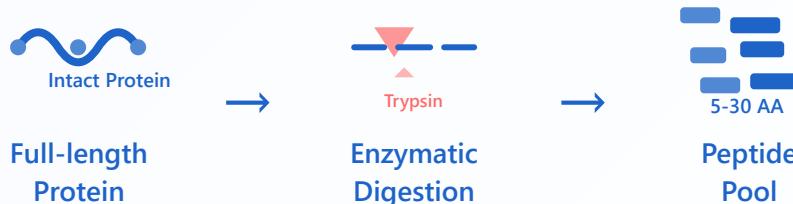


Bottom-up Proteomics



Protein Digestion

- Enzymatic cleavage into peptides
- 5-30 amino acid peptides
- Most common workflow

Trypsin Specificity

- Cleaves after K and R residues
- Predictable peptide generation
- Optimal MS-friendly peptides

Peptide Separation

- Reverse-phase liquid chromatography
- Gradient elution
- Online LC-MS coupling

Data Complexity

- Thousands of peptides
- Multiple charge states
- Requires computational analysis