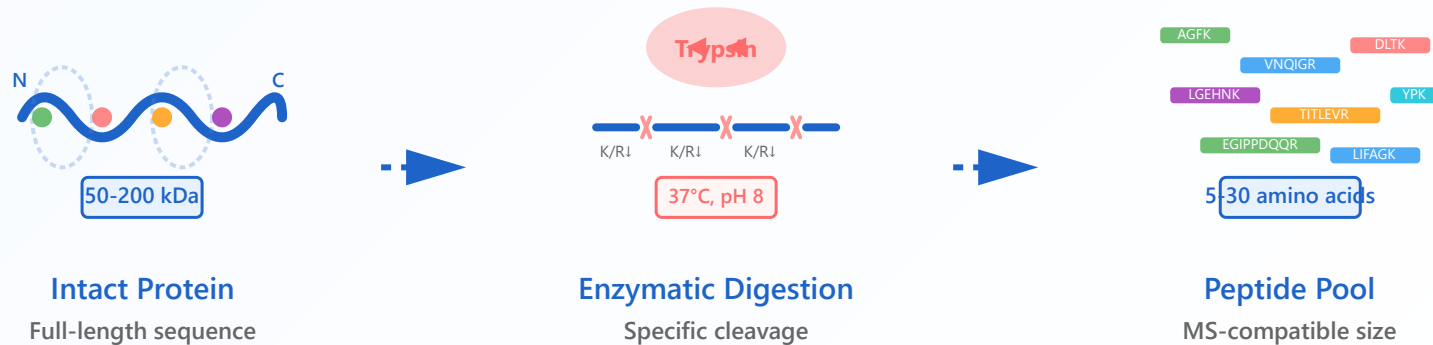


Bottom-up Proteomics



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

