

Top-down Proteomics



Intact Protein

Complete sequence + PTMs

VS



Digested Peptides

Fragmented before analysis

Intact Protein Analysis

- No digestion required
- Analyze whole proteins
- 10-80 kDa typical range

PTM Preservation

- Complete modification pattern
- Combinatorial PTM analysis
- Proteoform characterization

Technical Challenges

- Requires high resolution
- Complex spectra interpretation
- Lower sensitivity than bottom-up

Native MS

- Preserve non-covalent interactions
- Protein complexes
- Quaternary structure information