P201/P202/P203: PROTEIN PROFILING AND QUANTITATIVE PROTEOMICS

APPLICATION

- Determine protein identity, interactomics, protein profiling, and quantitate proteins (relative) in any given sample
- Detect specific post-translational modifications (e.g., Phosphorylation, Acetylation, Methylation, Ubiquitination, etc.)

SUITABLE SAMPLE TYPE

- Frozen cell pellet or tissue
- Cell or tissue protein lysate
- Serum/plasma, body fluids, or cell culture medium
- Subcellular organelles such as Mitochondria, Lysosomes, and Exosomes

MINIMUM SAMPLE REQUIREMENT

- ≥1 million cells
- ≥5mg tissue
- ≥100 µg of total protein in cell or tissue lysate
- ≥30 µl serum/plasma, body fluids, or cell culture medium
- ≥25 µg subcellular organelles
- *Please contact us for any specific samples or requirements*

SAMPLE PREPARATION

- Store the samples at -20°C or -80°C prior to shipping
- Package the samples with dry-ice or chemical blue-ice bag when shipping

GENERAL SAMPLE GUIDELINES FOR MASS SPECTROMETRY ANALYSIS

✓ **Protein Identification:** Any biological sample; detection limit ≥1 ng/purified protein, ≥0.1 µg/mixture of proteins

✓ **Protein Profiling (Quantitative Proteomics):** Any biological sample; (e.g., tissue, cells, protein lysates, serum/plasma, etc.) with minimum requirements of >100 µg/sample of total protein; >5 mg/sample for tissue; or >1 million cells/sample for cell pellets

✓ **PTM Analysis:** Phosphorylation, Acetylation, Methylation, Ubiquitination, etc. with minimum sample requirement of target protein ≥0.1 µg/sample

✓ **Intact Protein MW Analysis:** ≥5 µg/sample of any purified protein ≤180 kDa

✓ **Peptide mapping:** ≥ 20 µg/sample of any purified protein with a purity >90% for 100% sequence coverage