

P301/P302/P303: PTM PROFILING AND QUANTITATIVE PROTEOMICS

APPLICATION

- Identification of novel PTM sites
- Signaling cascade studies
- Phosphoproteome change studies upon activation treatment
- Phosphoproteome signaling transduction studies
- Physiological state studies of a subcellular compartment's phosphoproteome
- Evolutionary conservation of phosphorylation studies

SUITABLE SAMPLE TYPE

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

MINIMUM SAMPLE REQUIREMENT

- ≥ 2 million cells
- ≥ 20 mg tissue
- ≥ 500 μg of total protein in cell or tissue lysate
- ≥ 100 μg subcellular organelles
- ≥ 60 μl serum/plasma, body fluids, or cell culture medium
- *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