P501/P601/P602/P603/P604:
PEPTIDE MAPPING & PROTEIN THERAPEUTICS CHARACTERIZZATION

APPLICATION

- Comprehensive characterization of purified proteins to be developed for therapeutics
- Protein sequence confirmation and PTM mapping
- Comparative analysis of biosimilars with reference standards
- Evaluation of purified or partially purified protein samples including therapeutics products at the early stage of development
- Confirmation of full amino acid sequence and PTM mapping;
- N-linked glycosylation sites mapping and profiling of N-linked glycans of pure mAbs

SUITABLE SAMPLE TYPE

- Purified protein, in solution or dried

MINIMUM SAMPLE REQUIREMENT

- Purity >95%
- ≥10 µg/sample is recommended for optimal results
- Detection limit: ≥0.1 µg
- *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