Sample Requirements of MS-Services

1-1 /2. SDS-PAGE analysis

(a) Sample type: Cell pellet、Protein extracts
(b) Sample volume: ≤50 μL
(c) Sample concentration: ≥0.2 μg/μL (Silver stain), ≥1 μg/μL (Coomassie blue stain)
(d) Platform: Hoefer SE260, SE600

1-3 /4. Two-dimension Electrophoresis (IEF/SDS-PAGE)

(a) Sample type: Cell pellet、Protein extracts
(b) Sample volume: ≤150 μL
(c) Sample concentration: ≥1 μg/μL (Silver stain), ≥2 μg/μL (Coomassie blue stain)
(d) Platform: Ettan IPGphor 3 IEF system/Hoefer SE600

1-5. Protein solution concentration, salt removal

(a) Sample type: Protein extracts、Purified protein solution、Body fluid
(b) Sample amount: ≤2 mL
(c) Sample concentration: ≥0.01 μg/μL

1-6. Protein solution concentration, salt removal

(a) Sample type: Protein extracts、Purified protein、Body fluid
(b) Sample amount: ≤50 mL
(c) Sample concentration: ≥0.01 μg/μL

1-7. Plasma abundant proteins (Top-12) removal

(d) Sample type: Human body fluids (serum, plasma, urine, interstitial fluid)
(e) Sample amount: ≥50 μL
(f) Sample concentration: ≥40 μg/μL

2-1. Purified protein: Peptide mapping

(a) Sample type: Purified protein with amino acid sequence
(b) Sample amount: ≥20 pmol (~1 μg for 50 kDa protein)
(c) Sample concentration: ≥2 pmol/μL (~0.1 μg/μL for 50 kDa protein)
(d) Sample purity: ≥50%
(e) Platform: 1DLC, LTQ-Orbitrap MS

2-2. Purified protein: molecular weight determination

(a) Sample type: Purified protein (≤70 kDa)
(b) Sample amount: ≥100 pmol (~5 μg for 50 kDa protein)
(c) Sample concentration: ≥10 pmol/μL (~0.5 μg/μL for 50 kDa protein)
(d) Sample purity: ≥50%
(e) Platform: 1DLC, LTQ-Orbitrap MS

3-1. In-gel protein identification: Basic analysis

(a) Sample type: Gel slice (please provide gel image with staining)
(b) Gel size: ≤3 mm × 8 mm × 1.5 mm (Height × Width × Thickness)
(c) Platform: 1DLC, LTQ-Orbitrap MS

3-2 /3. In-gel protein identification: Standard/Advanced analysis

(a) Sample type: Cell pellet, Protein extracts
(b) Sample volume: ≤50 μL
(c) Sample concentration: ≥0.2 μg/μL (silver stain), ≥1 μg/μL (Coomassie blue stain)
(d) Platform: Hoefer SE260, 1DLC, LTQ-Orbitrap MS

3-4 /5/6. In-solution protein identification: Basic/Standard/Advanced analysis

(a) Sample type: Cell pellet, protein extracts (please provide buffer constituents)
(b) Sample volume: ≤100 μL
(c) Sample concentration: ≥0.1 μg/μL (Basic/Standard analysis), ≥0.5 μg/μL (Advanced analysis)
(d) Platform: 1DLC, 2DLC, LTQ-Orbitrap MS

4-1 /2. Protein interaction: Basic/Standard analysis

(a) Sample type: Immunoprecipitation product (beads or eluents, please provide buffer constituents for solution sample)
(b) Sample amount: Not specified (recommended IP starting materials ≥500 μg)
(c) Sample concentration: Not specified.
(d) Platform: Hoefer SE260, 1DLC, LTQ-Orbitrap MS

4-3. Protein interaction: interacting region analysis

(a) Sample type: Purified protein with amino acid sequence and condition of molecules interaction
(b) Sample amount: ≥200 pmol (~10 μg for 50 kDa protein)
(c) Sample concentration: ≥4.5 pmol/μL (~0.23 μg/μL for 50 kDa protein)
(d) Sample purity: ≥90%
(e) Platform: online-Pepsin-LC, Orbitrap HDX-MS

5a. Quantitative proteome: Basic/Standard/Advanced analysis

(a) Sample type: Cell pellet, Protein extracts (please provide buffer constituents)
(b) Sample amount: ≥5 μg (Basic), ≥10 μg (Standard), ≥20 μg (Advanced) for each group
(c) Sample concentration: ≥0.5 μg/μL (Basic), ≥1 μg/μL (Standard), ≥2 μg/μL (Advanced)
(d) Limitations: Detergents (≤0.2%), Urea (≤1 M); Buffer without Tris-Base, Ammonium Salt, Gly-gly, DTT, Mercaptoethanol
(e) Platform: online-2DLC LTQ-Orbitrap MS

5b. Quantitative phosphoproteome: Basic/Standard/Advanced analysis

(a) Sample type: Cell pellet, Protein extracts (please provide buffer constituents)
(f) Sample amount: ≥10 μg (Basic), 40 μg (Standard), 100 μg (Advanced) for each group
(b) Sample concentration: ≥0.5 μg/μL (Basic), ≥1 μg/μL (Standard), ≥2 μg/μL (Advanced)
(c) Limitations: Detergents (≤0.2%), Urea (≤1 M); Buffer without Tris-Base, Ammonium Salt, Gly-gly, DTT, Mercaptoethanol
(d) Platform: online-2DLC LTQ-Orbitrap MS

6. Protein post-translational modification site analysis

(a) Sample type: Gel slice (please provide gel image with staining), Immunoprecipitation product (beads or eluent), Protein extracts or Purified protein solution (please provide buffer constituents for solution sample)
(b) Gel size: ≤3 mm × 8 mm × 1.5 mm (Height × Width × Thickness)
(c) Sample amount: ≥100 μg (Protein extracts), ≥10 μg (Purified protein solution, purity ≥50%), ≥500 μg (recommended IP starting materials)
(d) Sample concentration: ≥0.25 μg/μL
(e) Platform: PTM-peptide enrichment, 1DLC, LTQ-Orbitrap MS

7. Protein quantification analysis

(a) Sample requirement: Please contact us for further details.

(b) Platform: Bio-Plex System

8-1. Bioinformatics analysis: Metabolic & Signaling pathway analysis

(a) Sample type: Quantitative data of genomic or proteomic analysis

(b) Platform: Please contact us for further details.

8-2. Bioinformatics analysis: Customized database searching

(a) Sample type: MS raw data, Processed MS data (mzML, mzXML, mgf)

(b) Platform: Please contact us for further details.

9. Rush service

(a) Service type: Available for our services with turnaround time ≥2 weeks.

10. Customized service

(a) Sample requirement: Please contact us for further details.

(b) Platform: Please contact us for further details.