

# P101: PROTEIN IDENTIFICATION OF GEL BAND SAMPLES

## APPLICATION

- Determine protein identity
- Detect specific post-translational modifications (e.g., Phosphorylation, Acetylation, Methylation, Ubiquitination, etc.)

## SUITABLE SAMPLE TYPE

- SDS-PAGE Gel Band or 2D-PAGE Gel Spot
- Protein(s) in a visible silver stain or blue stain band can be identified

## MINIMUM SAMPLE REQUIREMENT

- 10 ng/protein for protein identification; 100 ng/protein for post-translational modifications analysis
- *Please contact us for any specific samples or requirements*

## SAMPLE PREPARATION

- Take an image of the SDS-PAGE Gel or 2D-PAGE Gel prior to slicing the target gel band(s)
- Slice the target gel band (size  $\leq 3$  mm x 3.5 mm x 1.5mm) and place it into a new 1.5 mL tube
- Label it with a proper name and store at 4°C prior to shipping
- Gel-band samples can be shipped at room temperature

## GENERAL SAMPLE GUIDELINES FOR MASS SPECTROMETRY ANALYSIS

- ✓ **Protein Identification:** Any biological sample; detection limit  $\geq 1$  ng/purified protein,  $\geq 0.1$   $\mu\text{g}$ /mixture of proteins
- ✓ **Protein Profiling (Quantitative Proteomics):** Any biological sample; (e.g., tissue, cells, protein lysates, serum/plasma, etc.) with minimum requirements of  $>100$   $\mu\text{g}$ /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  $\geq 0.1$   $\mu\text{g}$ /sample
- ✓ **Intact Protein MW Analysis:**  $\geq 5$   $\mu\text{g}$ /sample of any purified protein  $\leq 180$  kDa
- ✓ **Peptide mapping:**  $\geq 20$   $\mu\text{g}$ /sample of any purified protein with a purity  $>90\%$  for 100% sequence coverage

# P102: PROTEIN IDENTIFICATION OF MIXTURE SAMPLES

## 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

- Purified protein, in solution or dried
- Purified protein complex, in solution or dried
- Fresh frozen cell/tissue lysate, body fluids, or cell culture medium
- Subcellular organelles such as Mitochondria, Lysosomes, Exosomes, etc.
- Protein mixture from pull-down, immunoprecipitation (IP), co-immunoprecipitation (co-IP), or other approaches
- Purified protein complex/mixture on Protein A/G agarose beads, Dynabeads, or on the surface of other solid materials

## MINIMUM SAMPLE REQUIREMENT

- 10 ng/protein for protein identification; 100 ng/protein for post-translational modifications analysis
- 5-25 µg of total protein/sample is recommended for optimal results
- Detection limit:  $\geq 1$  ng/protein,  $\geq 0.1$  µg/mixture of proteins
- *Please contact us for any specific samples or requirements*

## SAMPLE PREPARATION

- Store the samples at  $-20^{\circ}\text{C}$  or  $-80^{\circ}\text{C}$  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  $\geq 1$  ng/purified protein,  $\geq 0.1$  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  $\geq 0.1$  µg/sample
- ✓ **Intact Protein MW Analysis:**  $\geq 5$  µg/sample of any purified protein  $\leq 180$  kDa
- ✓ **Peptide mapping:**  $\geq 20$  µg/sample of any purified protein with a purity  $>90\%$  for 100% sequence coverage