Capturem™ His-Tagged Purification 96 Protocol-At-A-Glance

I. Introduction

This protocol is provided for **Capturem His-Tagged Purification 96** (Cat. No. 635714), a single-use disposable 96-well plate that allows simple, rapid purification of his-tagged proteins from mammalian or bacterial cell samples in up to 1 ml of clarified lysate per well, using either vacuum filtration or centrifugation. This plate is suitable for use under native or denaturing conditions, in the presence of additives such as DTT (up to 10 mM), βME (up to 30 mM), TCEP (up to 5 mM), EDTA (up to 10 mM), or glycerol (see reagent compatibility table for more information).

II. Materials and Reagents

A. Components

- 1 Capturem 96 Nickel Plate

B. Additional Materials Required

- **Lysis Buffer:** We recommend using xTractor™ Buffer (Cat. Nos. 635625, 635626, or 635671), but you may substitute your standard lysis buffer.
- **Wash Buffer:** 20 mM Na_3PO_4, 150 mM NaCl, pH 7.6
- **Elution Buffer**: 20 mM Na_3PO_4, 500 mM NaCl, 500 mM imidazole, pH 7.6
- **96-well collection plates:** Each purification will require four standard 96-well collection plates. These plates should be used throughout the protocol to collect flowthrough and wash samples that will be saved for SDS-PAGE analysis and/or colorimetric protein assays, e.g., Bradford assays.
- **96-well plate filtration device:** The Capturem 96 Nickel Plate is compatible with standard 96-well plate filtration devices, such as the NucleoVac 96 Vacuum Manifold (Cat. No. 740681).
- **96-well plate centrifuge:** The Capturem 96 Nickel Plate is compatible with standard 96-well plate centrifuges.
- **Multi-channel pipette**

III. Sample Preparation

Express your his-tagged protein(s) of interest in 1 ml cultures grown in 96-well plates or 2–5 ml cultures grown in 6-well plates. Before beginning the protein purification protocol in Section IV, it is necessary to prepare crude cell lysates from each culture and clarify the lysates by centrifugation or filtration. We recommend using xTractor Buffer (Section II) for lysis. Lysis protocols using xTractor Buffer are provided in the xTractor Buffer & xTractor Buffer Kit User Manual. Individual protocols are also available for preparing cell lysates from bacterial, mammalian, baculovirus, and yeast cultures.

- **Bacterial Cell Samples**
  We recommend starting with a fresh or frozen cell pellet from 2–5 ml of overnight bacterial culture, which should yield 200–1,000 µl of cleared lysate.

  NOTE: When working with bacterial cells, the volume of lysate (containing the overexpressed his-tagged protein of interest) is determined by the amount of wet cell pellet obtained from a starting culture volume of 2–5 ml. For example, a log-phase *E. coli* culture (O.D. = 0.6–0.8), induced for 2–4 hours, would be expected to provide ~20–80 mg of bacterial pellet from 2–5 ml of culture. We recommend adding ~400 µl of xTractor Buffer to each ~20 mg of wet bacterial cell pellet.

- **Mammalian Cell Samples**
  We recommend starting with a fresh or frozen cell pellet from 2 ml of mammalian cell culture, (e.g., from from a single well of a 6-well culture plate), which should be resuspended in 100–500 µl xTractor Buffer, yielding up to 600 µl of cleared lysate). Adherent cells may be harvested by treating them with trypsin and spinning them down, or scraping them directly from the well in the presence of xTractor Buffer. Suspension cells may be harvested by spinning down the liquid culture.

  NOTE: When lysing mammalian cells, you may substitute your standard lysis buffer for xTractor Buffer.

IV. His-Tagged Protein Purification

Purification of his-tagged proteins from the cleared cell lysates prepared in Section III may be performed using vacuum filtration (Protocol A) or centrifugation in a standard 96-well plate centrifuge (Protocol B).

A. Protocol: Protein Purification Using Vacuum Filtration

1. Assemble the Capturem 96 Nickel Plate in a 96-well plate filtration device together with a 96-well collection plate (supplied by the user—see Section II.B).
2. Add 400 µl Lysis Buffer or PBS to each well of the Capturem 96 Nickel Plate using a multi-channel pipette, to equilibrate the wells. Use vacuum (~0.6–0.7 bar) to run the buffer through the Capturem plate wells into the collection plate. Remove the flowthrough and discard it along with the collection plate. Reassemble the Capturem 96 Nickel Plate in the 96-well plate filtration device together with a new collection plate.

   NOTE: The required pressure may vary between 0.2–0.8 bar, depending on the sample. When performing vacuum filtration, use the following formula to convert between different vacuum pressure units:

   Pressure Conversion Formula:
   1 mbar = 100 Pa = 0.750 mm Hg = 14.504 x 10^{-3} psi = 0.987 x 10^{-3} atm
3. Load 200–1,000 µl cleared lysate (from Section III) onto each well of the equilibrated Capturem 96 Nickel Plate. Use a vacuum (~0.6–0.7 bar) to run the buffer through the Capturem plate wells into the collection plate. Save the collection plate containing the lysate flowthrough for protein analysis. Reassemble the Capturem 96 Nickel Plate in the 96-well plate filtration device together with a new collection plate.
4. Add 300 µl Wash Buffer to each well of the Capturem 96 Nickel Plate. Use a vacuum (~0.6–0.7 bar) to run the buffer through the Capturem plate wells into the collection plate. Save the collection plate containing the lysate flowthrough for protein analysis. Reassemble the the Capturem 96 Nickel Plate in the 96-well plate filtration device together with a new collection plate.
5. Add 300 µl Elution Buffer to each well of the Capturem 96 Nickel Plate. Use a vacuum (~0.6–0.7 bar) to run the buffer through the Capturem plate wells into the collection plate. The wells of the collection plate should contain your eluted tagged protein, which is now ready for analysis.

   NOTE: ≥90% of your tagged protein can be eluted with 100 µl of Elution Buffer.
6. Measure the amount of protein in your flowthrough samples from Steps 3 and 4, and your eluate from Step 5, using a Bradford assay or other colorimetric protein analysis method.
7. Analyze the samples that were quantified in Step 6 using SDS-PAGE.

B. Protocol: Protein Purification Using Centrifugation

1. Place the Capturem 96 Nickel Plate securely on top of a 96-well collection plate (supplied by the user—see Section II.B).
2. Add 400 µl Lysis Buffer or PBS to each well of the Capturem 96 Nickel Plate using a multi-channel pipette, to equilibrate the wells. Centrifuge at 2,000 x g for 3 minutes at room temperature. Remove the flowthrough and discard it along with the collection plate. Place the Capturem 96 Nickel Plate securely on top of a new 96-well collection plate.

   NOTE: When performing centrifugation, use the following formula to convert rpm to centrifugal force units (RCF or g) if the centrifuge does not automatically provide this information:

   Centrifugal Force Conversion Formula:
   RCF or $g = (1.12) \times (R) \times (rpm/1000)^2$

   where R is the distance (in millimeters) from the center of the rotor to the end of the spin bucket when held horizontally and away from the center.
3. Load 200–1,000 µl cleared lysate (from Section III) onto each well of the equilibrated Capturem 96 Nickel Plate. Centrifuge at 2,000 x g for 3 minutes at room temperature. Save the collection plate containing the lysate flowthrough for protein analysis. Place the Capturem 96 Nickel Plate securely on top of a new 96-well collection plate.
4. Add 300 µl Wash Buffer to each well of the Capturem 96 Nickel Plate. Centrifuge at 2,000 x g for 3 minutes at room temperature. Save the collection plate containing the lysate flowthrough for protein analysis. Place the Capturem 96 Nickel Plate securely on top of a new 96-well collection plate.
5. Add 300 µl Elution Buffer to each well of the Capturem 96 Nickel Plate. Centrifuge at 2,000 x g for 3 minutes at room temperature. The wells of the collection plate should contain your eluted tagged protein, which is now ready for analysis.

   NOTE: ≥90% of your tagged protein can be eluted with 100 µl of Elution Buffer.
6. Measure the amount of protein in your flowthrough samples from Steps 3 and 4, and your eluate from Step 5, using a Bradford assay or other colorimetric protein analysis method.
7. Analyze the samples that were quantified in Step 6 using SDS-PAGE.

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