

CL7/Im7 Expression & Purification Protocol: Membrane Proteins

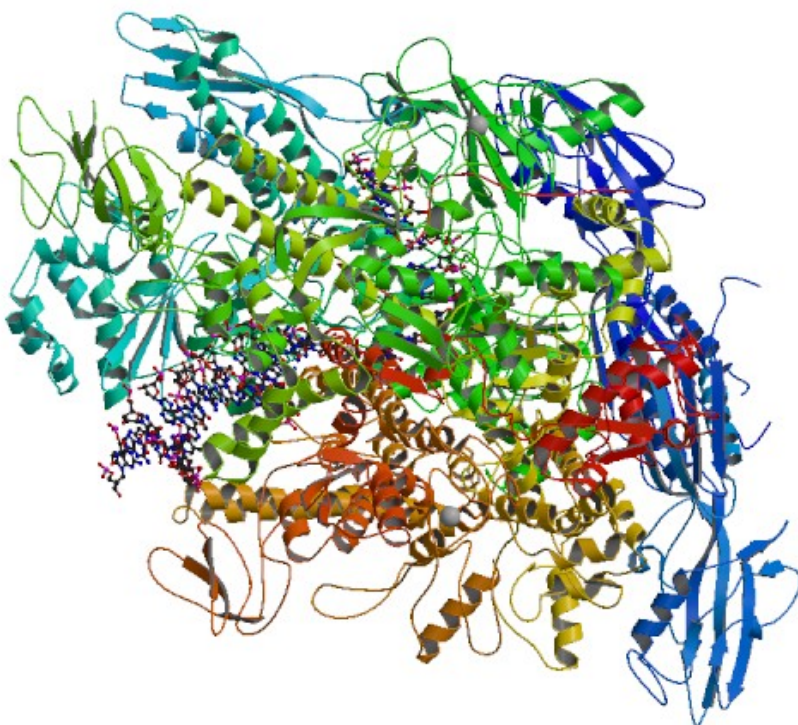


Table of Contents

INTRODUCTION	1
Figure 1	1
1. PLASMID CONSTRUCTION AND PREPARATION	2
2. CELL CULTURE AND LYSIS.....	3
Cell culture	3
Cell lysis.....	3
3. PROTEIN PURIFICATION OF MEMBRANE PROTEINS.....	5
3.1 Non-chromatographic step – Option 1 – Ultracentrifugation	
Protocol.....	5
Example (YidC)	5
3.2. Non-chromatographic Option 2 – PEI precipitation	6
Protocol.....	6
Example (YidC)	7
Figure 3.3	7
3.3 Chromatographic purification of membrane proteins	8
Protocol.....	8
Examples (YidC and Calnexin)	10
Figure 3.4	10
4. ON-COLUMN PROTEOLYTIC ELUTION OF A TARGET PROTEIN.....	11
Chromatography mode	11
Example.....	11
Gravity mode.....	11
5. CLEANING & REGENERATING THE IM7 COLUMN IN GRAVITY MODE	13
Cleaning.....	13
Guanidine Cleaning Protocol	13
Glycine Cleaning Protocol	13
Regeneration.....	13
Example.....	14

For research use only.

Licensing Information

TriAltus Bioscience holds the exclusive, worldwide license to the CL7 protein purification technology platform. It was licensed from the University of Alabama at Birmingham (UAB) in Birmingham, Alabama, USA. An international patent filing has been made with protection being sought in the United States, Europe, and other major markets. The CL7 purification technology is available for research use. For commercial use or resale, contact us at sales@trialtusbioscience.com to discuss commercial licensing.

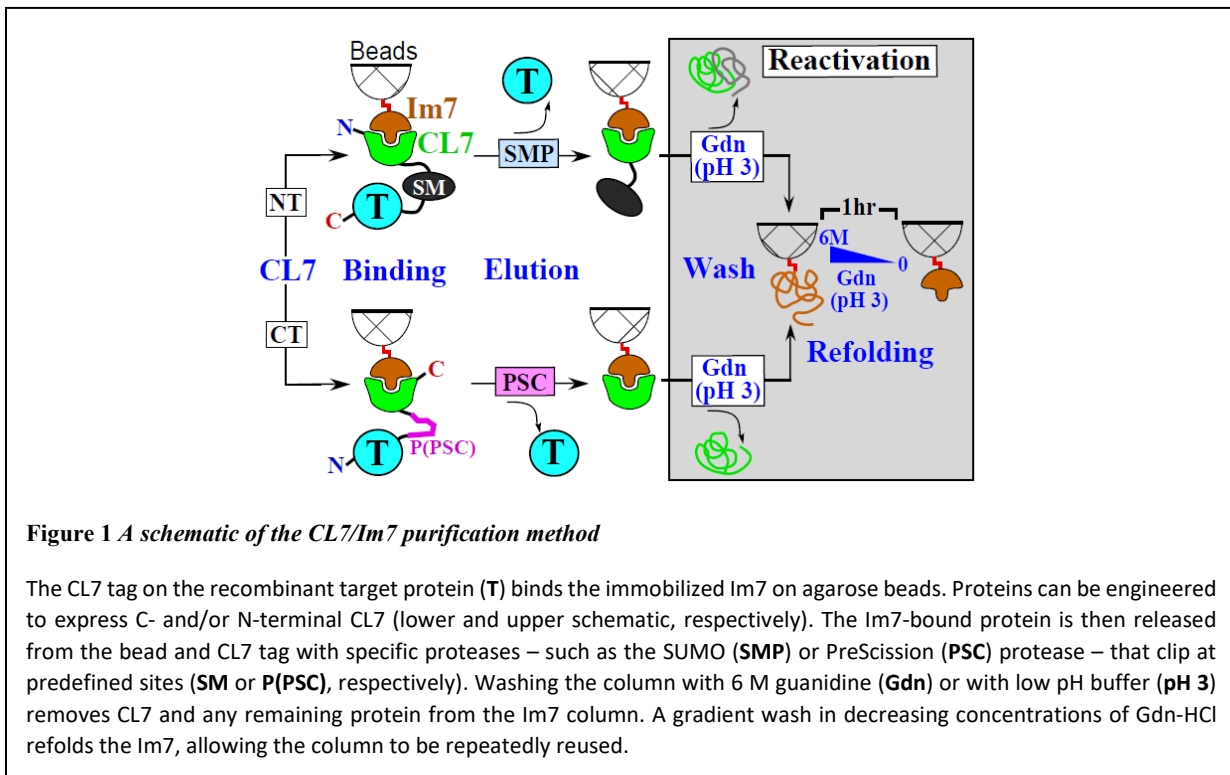
Trademarks

The Company name, the terms “TriAltus” and “TriAltus Bioscience”, the Company logo, and all related names, logos, product and service names, designs, and slogans are trademarks of the Company or its affiliates or licensors. You must not use such marks without the prior written permission of the Company. All other names, logos, product and service names, designs, and slogans on this Website are the trademarks of their respective owners.

Introduction

TriAltus's proprietary high purity, high activity, and high yield (HHH) purification method is based on the ultrahigh affinity interaction between CL7 – a variant of Colicin E7 DNase (CE7) that lacks DNase and DNA-binding activity – and Immunity Protein 7 (Im7), which inhibits CE7. CL7 binds Im7 with a K_d of $\sim 10^{14} - 10^{17}$ M.

With the TriAltus CL7/Im7 purification method, the target protein is expressed with an N- or C-terminal CL7 tag. The CL7-tagged protein is then loaded in high-salt buffer onto an Im7 column. CL7 stably binds the covalently crosslinked Im7 on the column's agarose beads with high affinity. Finally, the target protein ("T" in **Fig. 1**) is released from the CL7 tag via proteolytic cleavage



The TriAltus system outperforms His-trap and other traditional purification methods in efficiency and purity.

1. Efficiency

In a single-step, the CL7/Im7 method purifies many difficult-to-isolate proteins that elude traditional multistep methods.

2. Purity

Compared with other tagging systems, the CL7/Im7 method significantly increases the purity level of the end product and maintains or improves the activity of the protein product. Protein purity improves because the Im7 interacts specifically with CL7; does not interact with untagged cellular components; and CL7/Im7 binding is not affected by widely used protein purification reagents, such as polyethyleneimine (PEI), detergents, reducing agents (β -mercaptoethanol, DTT, TCEP) and metal chelating agents (EDTA).

1. Plasmid construction and preparation

TriAltus's CL7-tagged template vectors are derived from the commercial pET28a expression vector (Invitrogen). The CL7 vectors contain either an N- or C-terminal CL7 tag and may include additional tags, such as His.

1. To insert a coding nucleotide sequence into a TriAltus vector, simply use the appropriate restriction sites, according to the plasmid's respective Genebank file on the [product page](#). Transform a cloning strain such as DH5 α to make DNA preps and verify the insert sequence.
2. The resulting expression plasmids may be transformed into BL21 (DE3) (Invitrogen) competent cells or their derivatives.
3. Culture the cells according to the manufacturer's instructions.

Note 1.1 | The target nucleotide sequence may require optimization – such as reducing the codon G/C content to ~43-45% – for expression in *E. coli*. Original, non-optimized codons inserted into vectors – especially those that encode N-terminal CL7 tags – may significantly decrease the expression level of the full-length protein.

Note 1.2 | Compared with BL21 (DE3) cells, BL21 Star™ (DE3) (Invitrogen) competent cells generally increase target protein expression.

2. Cell culture and lysis

Use the BL21 (DE3) expression strain culture from [section 1](#) with the following expression and lysis protocols.

Cell culture

1. Plate agar Petri plates with enough culture to produce 100-200 colonies on the plate.
2. Grow colonies overnight at 37°C (~17 h).
3. The next day, scrape the colonies from the plate into a 1L flask containing 0.5L [TB media](#) (for 2 plates, use 1L media, etc.).
4. Rinse the agar with a small amount of additional media and scrape any remaining culture into the flask.
5. Grow bacteria in a shaking incubator at 37°C and 200 rpm until the OD₅₆₀ of the culture reaches ~0.7-0.8 (~2-2.5 h).
6. Reduce the temperature to 18-20°C and continue to incubate until the OD₅₆₀ reaches ~1.
7. Add 0.1 mM [isopropyl β-D-1-thiogalactopyranoside](#) (IPTG) to induce overexpression.
8. Grow the cells overnight for ~20-24 h.
9. Centrifuge the culture at 4,000 *g* for ~30 min, decant the supernatant, and freeze the cell pellets at -80°C.

Cell lysis

Note | *Different classes of proteins – namely DNA-/RNA-binding proteins and membrane proteins – require unique buffer modifications. Please refer to [section 3](#) for specific lysis buffer recommendations.*

1. Suspend the frozen cell pellet from above in the appropriate lysis buffer (see [table 3.2](#)) at 1 g cells/10 mL buffer.
2. A. Use a high-pressure homogenizer at 4°C and ~15,000 PSI for ~3 min (for ~3 g cells) to disrupt the cells.

OR

B. Use sonication to disrupt the cells. We recommend the following parameters with the Fisher Sonic Dismembrator Model 500 (500 W power):

- a. For 4 g of cells
 - Suspend cells in 40 mL of lysis buffer in a conical Falcon tube on ice
 - Use 58% power amplitude, 5 sec pulse/15 sec pause for 20 min
- b. For 100 g of cells
 - Suspend cells in 1 L of lysis buffer on ice

- Use 58% power amplitude, 5 sec pulse/15 sec pause for ~110 min
 - Use a magnetic mixer to uniformly cool the lysate during sonication
3. Centrifuge the lysates at 40,000 g for 20 min.
 4. Filter the lysate through a 45- μ m filter.
 5. Load the lysate onto an equilibrated Im7 column, according to the protocol in section 3.

Note 2.1 | In ~90% of cases, the above protocol resulted in the best cell growth and protein expression. If poor cell growth or expression is observed, consider modifying the protocol as necessary. For example, increase the IPTG concentration in step 7 to 1 mM and/or the temperature in step 6 to 30-37°C.

3. Protein Purification of Membrane Proteins

Due to their hydrophobicity, membrane proteins (MPs) form strong, nonspecific hydrophobic contacts with each other, soluble cytoplasmic proteins and/or NAs, making purification difficult. Direct MP purification from cell lysates is a challenge with traditional methods.

Two precipitation methods can be used with the CL7/Im7 method to minimize contamination during MP purification: ultracentrifugation or PEI precipitation.

3.1 Non-chromatographic step - Option 1 – Ultracentrifugation

A pre-chromatography, ultracentrifugation step improves purification by precipitating and purifying the MP fraction from most NAs and soluble cytoplasmic proteins. The resulting pellet is then solubilized with high concentrations of nondenaturing detergent, which also removes/exchanges the natural lipids bound to the MP surface.

Protocol

1. Ultracentrifuge the lysate – Follow the protocol detailed in [section 2](#); then, ultracentrifuge the filtered lysate at 120,000 *g* for 1.5 h.

2. Solubilize the pellet – Dissolve the pellet containing the membrane fraction in solubilization buffer** with a volume equal to ~1/5-1/2 of the lysate volume, to a final protein concentration of ~2-4 mg/mL.

3. Ultracentrifuge the lysate – Centrifuge the lysate at 120,000 *g* for 30 min and then discard the pellet.

****Solubilization buffer 1** | 0.2-0.9 M NaCl, 20 mM Tris (pH 8.0), 5% glycerol, 0.1 mM phenylmethylsulfonyl fluoride (PMSF), 1.5% n-dodecyl β -D-maltoside (DDM)

Example (YidC)

B. halodurans **YidC** membrane integrase (non-induced cells) is an “all”-membrane protein, without bulky extramembrane domains. The gene sequence was optimized for *E. coli* codon usage and cloned in the pET28a vector with the C-terminal CL7 tag. When cells were cultivated without IPTG to modestly overexpress MPs, ultracentrifugation produced a large pellet, corresponding to the membrane fraction (MF). Solubilization of the MF with 1.5% DDM resulted in a pool of cellular MPs with a prominent YidC gel band (**Fig. 3.3A**). When cells were induced with IPTG, the [PEI solubilization method](#) (section 3.2) was required for efficient YidC extraction.

3.2 Non-chromatographic step - Option 2 – PEI precipitation

When the target MP is greatly overexpressed, polyethyleneimine (PEI) precipitation provides better results than the ultracentrifugation method, efficiently purifying MPs from NAs and soluble cellular proteins. The resulting samples exhibit equivalent or better purity than that of ultracentrifuged samples.

Protocol

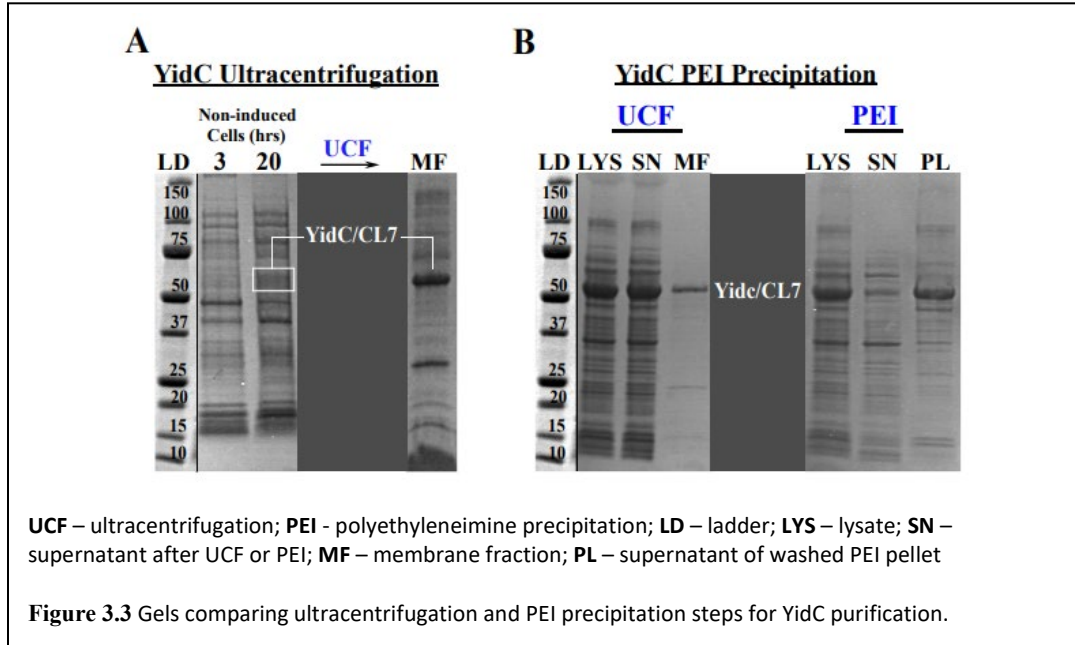
1. *Dilute the lysate* – Follow the protocol detailed in [section 2](#); then, dilute the lysate with an appropriate detergent-free buffer to reach an OD₂₆₀ ~25 and a salt (NaCl) concentration of ~0.3-0.35 M.
2. *Add PEI to the lysate* – Add 10% PEI stock solution to lysate in three aliquots to a final concentration of 0.06%. At each step, gently mix the suspension for ~5-10 min. After the final step, centrifuge the suspension at 3,000-5,000 *g* for 15 min.
3. *Solubilize the pellet* – Wash the final PEI pellets with solubilization buffer 2** for 10-15 min. with a volume of solubilization buffer equal to ~1/5-1/2 of the original lysate volume, to a final protein concentration of ~2-4 mg/mL. Centrifuge the suspension at 3,000-5,000 *g* for 15 min and discard the pellet.

****Solubilization buffer 2** | 0.6-0.8 M NaCl, 20 mM Tris (pH 8.0), 5% glycerol, 1.5% DDM

Note 3.2.2 | To optimize precipitation conditions, apply the PEI treatment to small (1-2 ml) aliquots of the lysate in varying salt concentrations and/or washing volumes. For example, use 0.2, 0.3, and 0.35 M NaCl in the precipitation step and 0.6 and 0.8 M NaCl for the wash (solubilization) step. Load the supernatants from each experiment on a gel and analyze the results to select the best working conditions.

Example (YidC)

The **YidC** gene sequence was optimized for *E. coli* codon usage and expressed with the CL7 tag, greatly increasing protein expression levels following IPTG induction. However, ultracentrifugation did not pellet YidC or other MPs (**Fig. 3.3A**). In contrast, polyethyleneimine (PEI) treatment successfully precipitated YidC (**Fig. 3.3B**).



3.3 Chromatographic purification of membrane proteins

Protocol

1. Dilute the lysate – Dilute the lysate from section [3.1](#) or [3.2](#) above ~8-10 fold with buffer A to yield a final detergent concentration of ~0.25%. (Note that dilution with DDM-free buffer is not recommended; dilution should be done slowly to maintain the DDM micelles, which are essential for the MP structure). Although this dilution step increases the purification time, it may substantially improve the column's binding capacity for the target MP.

2. Load the lysate onto the equilibrated Im7 column (buffer A) – Load lysate onto the Im7 column that has been equilibrated with 5-10 column volumes (CV) of Loading buffer A using a flow rate of 1/10 – 1/4 (CV).

For example, use

- 0.2-0.3 mL/min for a 1-mL column
- 0.5-1.2 mL/min for a 5-mL column
- 2-4 mL/min for a 20-mL column

To improve binding capacity in gravity mode, where it might be difficult to control the actual flow rate, load the lysate repeatedly 2-3 times. For large lysate volumes that require long loading times, alternate between loading and a high-salt wash (buffer A1) (e.g., after each 30-min of loading, wash with high-salt buffer) to remove impurities from the column.

3. Wash the Im7 column with high-salt wash buffer (buffer A1) – Wash the Im7 column with 6-8 CVs of high-salt buffer A1.

4. Wash the Im7 column with no-salt wash buffer (buffer A2) – Wash the Im7 column with 6-8 CVs of no-salt buffer A2.

5. Repeat the wash cycles – Repeat Steps 3 and 4 above two to three times. On a chromatography system, the flow rate may be as high as the column pressure limits allow.

6. Apply protease to elute the target protein (buffer A3) – Equilibrate the column with 2-3 CVs of the buffer A3. Add the elution protease to buffer A3 and perform proteolytic elution for ~1.5-2.5 h according to the Elution Protocol described in [section 4](#).

7. Clean the Im7 column (buffer A4) – Wash the Im7 column with 8-10 CVs of denaturing buffer A4 to remove the bound CL7-tag.

- When using guanidine (Gdn) on a chromatography system, the flow rate may be as high as the column pressure limits allow.
- The low-pH, Gly buffer elutes the bound CL7-tag slowly and nonuniformly. We recommend a flow rate of 0.5-1 mL/min; the elution may take 1-1.5 h. In gravity mode, follow the protocol described in [section 5](#).

8. Regenerate the Im7 column (buffer A4 & buffer B) – On a chromatography system, exchange denaturing buffer A4 with refolding buffer B using a 1-h gradient (e.g., flow rate – 1 mL/min; gradient volume – 60 ml). In gravity mode, follow the protocol described in [section 5](#).

9). Final Wash (buffer B) – Wash the regenerated Im7 column with 3-4 CVs of buffer B.

Lysis Buffer	Loading Buffer A	Washing Buffer A1	Washing Buffer A2	Elution Buffer A3	Cleaning Buffer A4	Refolding Buffer B
0.2-0.5 M NaCl	0.2-1 M NaCl	1 M NaCl	20 mM Tris (pH 8)	0.2-0.5 M NaCl	6 M Gdn (pH 8) ****	0.5 M NaCl
20 mM Tris (pH 8)	20 mM Tris (pH 8)	20 mM Tris (pH 8)	5% Glycerol	20 mM Tris (pH 8)	OR	20 mM Tris (pH 8)
5% Glycerol	5% Glycerol	5% Glycerol	0.1% DDM	5% Glycerol	0.1 M Gly (pH 3)	5% Glycerol
0.1 mM PMSF	0.1% DDM**	0.1% DDM		0.1% DDM	****	
Inhibitory tablet(s)*				0.2 mM EDTA		
				Elution Protease**		

Table 3.2 Buffers for the lysis and chromatographic purification of MPs

* - add 1 tablet of inhibitory cocktail (Roche) per 30-40 ml of lysate

** - DDM - n-dodecyl- β -D-maltopyranoside; other popular detergents can also be used

*** - details of the proteolytic elution are provided in Section 4

**** - Gdn - Guanidine Hydrochloride; Gly - Glycine

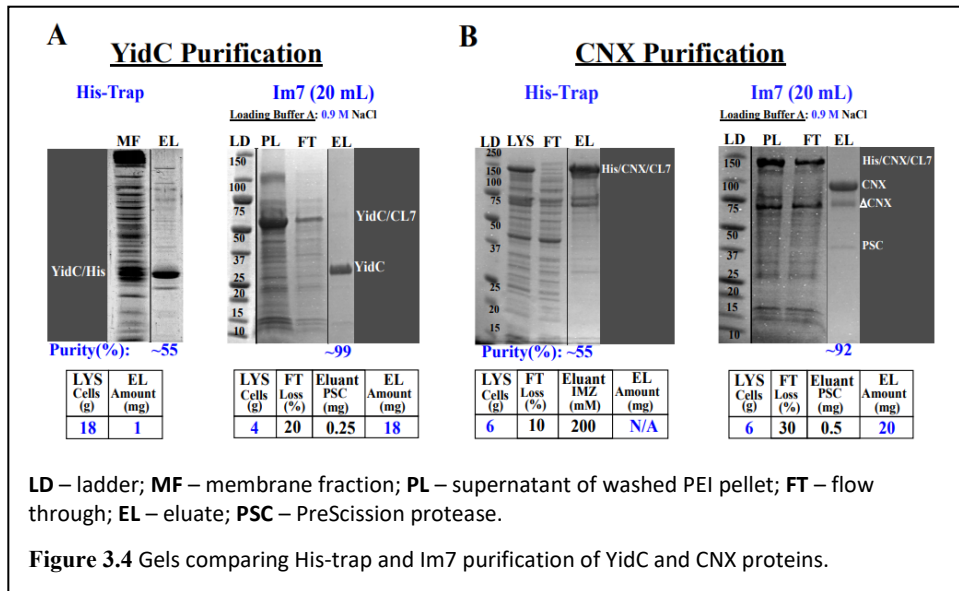
Examples (YidC and Calnexin)

The CL7/Im7 method with PEI precipitation successfully isolates even difficult-to-purify proteins, such as Calnexin.

A. **YidC** (MW ~ 32 kDa) lysate (processed according to [section 2](#); induced cells) was precipitated in lysis buffer containing 0.3 M NaCl with 0.06% PEI. The PEI pellet was washed with Solubilizing buffer containing 0.6 M NaCl and 1.5% DDM. The resulting supernatant was diluted 10 fold in high-salt, detergent-free buffer (the final NaCl and DDM concentrations in the supernatant were 0.9 M and 0.15%, respectively) and then loaded onto a 20-mL Im7 column at a flow rate of 2 mL/min. A single Im7 purification run provided an extra-pure (~99%) sample of YidC. In contrast, His-Trap purification resulted in only ~55% purity (**Fig. 3.4A**).

B. **Calnexin** (CNX; MW ~65 kDa) is a human, transmembrane chaperone protein. CNX contains a ~35 residue transmembrane segment and two soluble domains on either side of the membrane. Without the CL7/Im7 method, full-length CNX had never been expressed in *E. coli*, and no purification had been reported.

The CNX protein was purified with the TriAltus CL7/Im7 method in essentially the same manner as YidC (induced cells). After PEI precipitation, a single Im7 purification run provided a high-purity (~92%) sample, whereas only ~55% purity was achieved with the His-Trap approach under similar purification conditions (**Fig. 3.4B**).



4. On-column proteolytic elution of a target protein

After loading and washing the Im7 column, the target protein is eluted with the appropriate protease according to the steps below.

Chromatography mode

1. Add elution protease (SUMO (SMP) or PreScission (PSC)) at ~1.5-3% of the expected amount of bound target protein (assuming a saturated column, or using an estimate from gel analysis) (e.g., 0.5 mg protease per 30-40 mg of target protein saturated on a 1 ml Im7 column).
2. Dilute the required amount of protease in 3-4 CVs of Elution buffer A3 plus the volume of the tubing through which the protease is loaded on a column.
3. Fill the loading tubing with the diluted protease at a fast flow rate (4-5 mL/min).
4. Reduce the flow rate to 0.05-0.1 CV/min.
5. Run the protease through the column slowly until the OD₂₆₀ peak – which corresponds to the eluted target protein – returns to baseline.

Note | Allowing the protease to incubate on the column for 20-30 min when the OD₂₆₀ peaks may increase the concentration of the eluted protein. This may be repeated more than once per purification run.

Example

1. Use ~7 mL of tubing to load a 5-mL Im7 cartridge with the protease sample.
2. If the expected amount of bound protein is ~30-40 mg, use ~0.5 mg protease diluted in ~20 mL of elution buffer A3.
3. Load 7 mL protease at 5 mL/min to fill the tubing.
4. Reduce the speed to 0.2 mL/min.
5. Run the protease sample through the column (~1.5 – 2.5 hours) to elute the target protein.

To improve the cleavage efficiency or to increase the concentration of the eluted target, consider interrupting protease loading for 20-30 min to give the protease more time to complete the on-column protein cleavage.

Gravity mode

1. Add elution protease (SUMO (SMP) or PreScission (PSC)) at ~1.5-3% of the expected amount of bound target protein as estimated above in the chromatography mode section (e.g., 0.5 mg protease per 30-40 mg of target protein).
2. After equilibrating the column with Elution buffer A3, drain the column but don't dry the beads entirely.

3. Dilute the required amount of protease in 0.5-1 CV of elution buffer.
4. Add the protease to the beads and incubate for ~1.5 – 2.5 h at 4°C, mixing the beads gently every 5-7 min.
5. To monitor protein elution, collect a 0.3-0.4 mL aliquot from the column every 20-30 min and check the sample concentration with a NanoDrop spectrophotometer. Return the aliquot to the column. When the protein concentration no longer significantly increases, the elution is complete.

Columns typically have a “dead” volume (with no beads) – beneath the bottom frit – where cleavage will not occur. To avoid measuring the “dead” volume, return the first eluted aliquot to the column and collect and measure the next aliquot.

Note 4.1 | Several factors may reduce proteolytic efficiency, resulting in poor protein elution. Use the protocol below to determine the cause of low protein recovery and then modify the protocol according to the respective suggestions.

1. Strip the column with denaturing buffer A4 (~2CV).
2. Measure the eluate’s OD_(260/280) with a NanoDrop spectrophotometer
3. Evaluate a sample of the eluate on a gel using optimized conditions. (**Note** / Before loading the sample on a gel, Gdn should be exchanged for urea by dialysis, as Gdn precipitates when mixed with SDS).
 - a. If the OD_(260/280) ratio is 0.75 (or higher), or several protein bands are observed on the gel, then contamination **(1)** is the likely cause of poor elution efficiency.
 - b. An OD_(260/280) ratio of 0.7 (or less) AND a single dominant band on a gel corresponding to either uncleaved or cleaved target protein indicates that steric hindrance **(2)** or aggregation **(3)**, respectively.

(1) Contaminants (in particular, NAs) may inhibit proteases during the on-column cleavage step. Increasing the salt concentration of Loading buffer A may reduce the number of contaminants and subsequently improve cleavage efficiency.

(2) The binding of target protein – especially large oligomeric proteins – to the column may create steric hindrance that impairs protease cleavage efficiency. Increasing the amount of protease (3-4 fold) in the reaction may improve protein elution. If additional protease is added, an additional purification step (for example, size exclusion, GST or His-Trap chromatography steps) may be required to remove excess protease from the purified, eluted target protein.

(3) An untagged (cleaved from a tag) target protein aggregates/precipitates. In this case, optimizing the Elution buffer conditions to improve solubility of the target protein may help. If it doesn’t, the problem likely exists at, and should be resolved at, the upstream (expression) stage.

5. Cleaning & regenerating the Im7 column in gravity mode

Cleaning

The Im7 column can be cleaned with a guanidine- or glycine-based cleaning buffer (buffer A4) according to the following protocols.

Guanidine Cleaning Protocol

1. Remove Elution buffer A3 from the beads, but do not dry the beads entirely.
2. Add 4 CVs of denaturing buffer A4 (6 M Gdn) to the beads.
3. Equilibrate the column in buffer A4 for 4-5 min.
4. Remove the buffer.
5. Repeat steps 2 and 4 twice (skip the equilibration in step 3).

Glycine Cleaning Protocol

1. Remove Elution buffer A3 from the beads, but do not dry the beads entirely.
2. Add 4 CVs of denaturing buffer A4 (0.1 M Gly) to the beads.
3. Equilibrate the column in buffer A4 for 10-12 min.
4. Remove the buffer.
5. Repeat steps 2 and 4 five to six times (skip the equilibration in step 3).

Regeneration

The Gdn in the cleaning step denatures Im7. Before the column can be reused for another purification, the Im7 must be refolded. Regenerate the Im7 protein according to the following protocol.

1. Add 1-4 CVs of buffer A4 (in total – including the bead volume – the column will contain 2-3 CVs).
2. Dilute buffer A4 by 10% (0.6M) in 10 sequential steps (details below):
 - a. In the first step, elute or exchange with a pipette 10% of the total volume of buffer A4. (use formula in d to calculate the volumes for the next steps).
 - b. Add an equivalent volume of buffer B.
 - c. Equilibrate the column for 5-6 min.
 - d. Repeat steps a-c ten times, referencing the formula below.

$$V_{ra}(N) = V_{tot} \left(1 - \frac{1 - 0.1 * N}{1 - 0.1 * (N - 1)} \right)$$

N - Step # **V_{tot}** – Total buffer Volume; **V_{ra}(N)** – Volume to Remove/Add at Step# **N**

Note | The volume to remove/add will increase with each dilution.
 Buffer A4 will be completely replaced with buffer B after ~50-60 min.

Example

If the bead volume is **2 mL** and the initial volume of buffer A4 in the column (V_{tot}) before regeneration is **4 mL** (bead volume + 1 CV buffer A4 on top of the bead bed), the volume of buffer to elute and add [$V_{ra}(N)$] for each step is provided in **Table 5**.

Dilution Step (N)	0	1	2	3	4	5	6	7	8	9	10
Volume to Add/Remove (mL)	0.000	0.400	0.444	0.500	0.571	0.667	0.800	1.000	1.333	2.000	4.000
$V_{ra}(N)$											
Gdn (%)	100	90	80	70	60	50	40	30	20	10	0

Table 5 Example case of buffer volumes to remove/add if total volume in step 1 of the regeneration protocol is 4 mL