## **Refolding on Column Standard Operating Procedure**

Date: 1/11/05 Author: N. Oganesyan Edited by: R. Kim

**Reference:** Oganesyan, N., Kim, S. –H., Kim, R. (2004) On-column Chemical Refolding of Proteins. PharmaGenomics **4**: 22-26.

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Materials/Reagents/Equipment	Vendor
Resin: Ni-NTA Agarose (store at 2-8 <sup>0</sup> C)	QIAGEN
	Catalog # 30230
Urea Solution is made fresh each time.	Mol. Biol.Grade, Research Organics
	Catalog # 9692U
	MW: 60.6g
β-cyclodextrin	Sigma C4767 MW:1135 g
Triton X-100	Sigma T8787
1 CMC: 0.23 mM=0.015%	MW: 647 g

**Purpose:** Refolding of proteins that are expressed as inclusion bodies. This is a procedure for His tagged Proteins.

Note: Urea should be made fresh each time.

Preparation of 8 M urea: Weigh urea and place in a beaker, bring to 20 mM Tris, pH 8. Place beaker in a larger container containing water and heat over low heat until dissolved using a magnetic stir bar. DO NOT heat urea to high temperatures. Bring solution to desired final volume, pH of the solution is ~ pH 8.2. Allow solution to cool, do not place in the refrigerator (it will crystallize).

If protein has 1 or more cysteines: add 20 mM beta-mercaptoethanol (βME) in step 1. <u>Before binding the protein to Ni-NTA, dilute the sample 1:1 to bring it to 10 mM</u> βME.

- 1. Dissolve inclusion body (IB) protein at a ratio of 1 gm IB/3 ml of 8 M urea/20 mM Tris, pH 8 (Buffer A). Put over a magnetic stirrer for 1 hr at room temperature, stirring slowly. If sample is not going into solution and large particles remain, sonicate 3 x 10 seconds. Spin 15,000 rpm, 20 min in Sorvall centrifuge. Keep supernatant, there should be not much of a pellet.
- 2. Equilibrate Ni-NTA resin with Buffer A (calculate amount of resin needed by using a ratio of 5 mg target protein/ml resin).
- 3. Bind protein to Ni-NTA overnight at room temp in a batch mode, rocking, in a 50 ml plastic conical tube. It is important to incubate overnight for good binding. After binding, pour resin into a BioRad Econo column.

- 4. Wash column with buffer A (5 CV) +/- 10 mM βME, followed by 5 CV buffer A/20 mM imidazole. Keep 10 mM βME in all buffers if cysteines are present.
- 5. Wash column with 10 CV of 0.1% Triton X100/20 mM Tris, pH 7.5/0.5 M NaCl or a detergent of your choice. Let it drip slowly.
- Slowly wash column with 10 CV of 5 mM β-cyclodextrin/20 mM Tris, pH 7.5/0.1 M NaCl. The cyclodextrin removes all the detergent from the protein.
- 7. Wash column with 10 CV of 0.1 M NaCl/20 mM Tris, pH 7.5.
- 8. Elute target with 300/600 mM imidazole /20 mM Tris, pH 7.5/0.1 M NaCl or buffer of your choice.
- 9. Concentrate protein and run size exclusion chromatography column, do dynamic light scattering assay, and run sample on native gel, SDS/PAGE. Perform circular dichroism measurement. If protein is not pure enough, perform ion exchange chromatography on the sample.