

# ProteoTrap™

Protein Purification Resins

## Protocol

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### 1.0. Storage of ProteoTrap™ resin

The resin is supplied as 50% (v/v) slurry in 10mM Tris/300 mM NaCl/1mM EDTA, pH 8.0. The product is shipped at ambient temperature but should be stored at 4C.

### 1.1. Materials required (but not supplied)

For small sample volumes you may need only a microfuge and 1.5 ml tubes. For larger volumes (up to 20 ml) the purification of binding proteins is conveniently carried out using disposable polypropylene columns. A simple mixing device (e.g. rotary shaker or end-over-end mixer) may also be useful.

### 1.2. Overview of procedure

ProteoTrap™ resin is added to a crude protein extract and the suspension is gently mixed. After a period of incubation the resin is transferred to a disposable column and washed to remove non-bound or loosely adsorbed material. Finally, the column is eluted with buffer containing a competing ligand.

Since ProteoTrap™ resin may be used to capture many purine-binding proteins the instructions below provide only general guidance on the use of resin. You may need to modify the conditions to facilitate the binding of your particular biomolecule of interest.

### 1.3 Buffers

For simplicity we would recommend that you start with the same buffer for the equilibration, binding and wash steps. The elution buffer is prepared by adding a competing ligand.

#### 1.4.1 Types of buffers

The buffer and pH must be compatible with the biomolecule of interest. Tris (pH 7.5-8.5) and Hepes (pH 7.0-8.0) are commonly used but other buffers may also be suitable.

### **1.4.2 Metal ions**

ATP-binding proteins usually recognise ATP-magnesium ion complexes rather than free ATP. It is usual to include MgCl<sub>2</sub> (at least 10 mM) in all column buffers to facilitate metal-dependent interactions with the resin.

### **1.4.3 Salts**

To prevent non-specific electrostatic interactions with the matrix include 100mM–500mM NaCl, KCl or other salt in the buffer.

### **1.4.4 Thiols**

Thiols are often included in buffers to prevent oxidation of cysteine residues. A final concentration of 1 mM DTT is commonly used. DTT is not stable and should be added to the buffer immediately before use.

### **1.4.5 Protease inhibitors**

Protease inhibitors (e.g. PMSF, benzamidine) may or may not be required, depending on the sensitivity of the protein of interest to proteolysis. It is also advisable to carry out the binding and wash steps in a cold room or fridge using ice-cold buffers.

### **1.4.6 Detergents**

Detergents (e.g. Triton X-100) are sometimes used to prevent non-specific hydrophobic interactions. Since the resin and spacer are hydrophilic a detergent may not be necessary. However, if a detergent is required try relatively low concentrations (0.02-0.1%) in the first instance.

## **1.5 Chromatography steps**

Make sure the resin has been fully equilibrated with the column equilibration buffer before commencing the purification procedure. Dialyse or desalt the sample into the same buffer before application to the resin.

### **1.5.1 Binding step**

If you do not have access to an automated chromatography system a batch-binding method may be used. Protein samples with volumes of 0.5-1.0 ml should be incubated in 1.5ml tubes with 50-100 ml of ProteoTrap™ resin. For larger sample volumes the incubation should

be carried out in 10 ml, 30 ml or 50 ml tubes (or in a capped disposable column with an integral upper reservoir). Allow at least 1 hour at 4°C for binding to take place, and agitate the sample at regular intervals to prevent settling of the resin.

If you have a pump system the recommended flow rate in the first instance is 0.1-0.25 ml/min for columns that are 1-5ml in size, though you may wish to explore higher flow rates especially if the volume of material to be processed is large.

### **1.5.2 Wash step**

If incubations have been carried out in small tubes, the resin should be subjected to five or more cycles of washing and centrifugation (e.g. in a microfuge for 3-4 seconds) using ice-cold buffers. On a larger scale it is easier to transfer the suspension to a disposable polypropylene column and to allow the non-bound material to drip through under the force of gravity. Add the wash buffer carefully down the inner surface of the column and try not to disturb the resin otherwise the wash buffer will mix with the non-bound material, leading to less efficient washing of the resin. It is important to remove all of the non-bound material prior to elution. The absence of protein in the washes is easily verified with a dye-based protein detection reagent (e.g. Bradford reagent) or with a UV monitor.

### **1.5.3 Elution step**

It is important to appreciate in affinity chromatography that the eluting ligand (competing ligand or 'displacer') does not usually drive the bound protein from the resin; rather, it associates with proteins that dissociate from the resin and prevents their rebinding. The concentration of the displacer has to be sufficiently high to compete with any unoccupied ligand sites on the resin and sufficient time has to be allowed for dissociation to take place. Resins with a high ligand density (8-12 mmol/ml; 8-12 mM) may need a higher concentration of competing ligand for efficient elution than resins with a low density (1-2 mmol/ml; ~1-2 mM). If ATP is used as the competing ligand the concentration should be 5-10 mM.

## **FAQ Q1. What is the best buffer to use?**

There is no 'right' answer here. In the absence of any information on the binding requirements of the protein(s) of interest a good starting point is a buffer containing 20 mM Hepes, 100-500 mM NaCl (or KCl), 20 mM MgCl<sub>2</sub> and 1 mM DTT, pH 7.5. Alternatively, try experimenting with several buffer conditions using small amounts of resin in 1.5 ml tubes. After the wash step, elute with ATP or other competing ligand and analyse the eluted proteins by SDS-PAGE. The purification method can then be scaled up using the preferred buffer conditions.

## **Q2. Are there any other ways of eluting binding proteins from ProteoTrap™ resin?**

Yes. While ATP is the obvious choice, ligands that are structurally related to ATP may be used (e.g. NADH, AMP, adenosine) to elute a specific subset of the ATP-binding proteins. Drugs that are known to bind to ATP-binding proteins might also be used. If preservation of biological activity is not required, aliquots of resin may be boiled with SDS sample buffer prior to gel electrophoresis.



Havnaasveien 21, 3135 Toroed, Norway  
tel: +47 33 61 07 18, fax: +47 33 40 14 44  
[www.amebioscience.com](http://www.amebioscience.com)