

May 07, 2019

## Protein Purification ( Column Cromotography)

DOI

[dx.doi.org/10.17504/protocols.io.2ntgden](https://dx.doi.org/10.17504/protocols.io.2ntgden)



Sevval Uysalcan<sup>1</sup>, Rengin Yamur Akbiyik<sup>2</sup>

<sup>1</sup>Istanbul Bilgi University; <sup>2</sup>Istanbul Bilgi University



**Sevval Uysalcan**

Istanbul Bilgi University

### Create & collaborate more with a free account

Edit and publish protocols, collaborate in communities, share insights through comments, and track progress with run records.

Create free account

OPEN  ACCESS



DOI: <https://dx.doi.org/10.17504/protocols.io.2ntgden>

**Protocol Citation:** Sevval Uysalcan, Rengin Yamur Akbiyik 2019. Protein Purification ( Column Cromotography). **protocols.io** <https://dx.doi.org/10.17504/protocols.io.2ntgden>

**License:** This is an open access protocol distributed under the terms of the **Creative Commons Attribution License**, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

**Protocol status:** In development

**We are still developing and optimizing this protocol**

**Created:** May 07, 2019

**Last Modified:** May 07, 2019

**Protocol Integer ID:** 22963

**Keywords:** purification of protein, purification techniques appropriate for this protein, purification method, purification technique, more of the purification method, purification, proteins in pure form, protein mixture, resulting protein mixture, different protein, protein, concentration of this protein, desired protein, thousands of different protein, enzyme, many enzyme, amino acid composition, cell membrane, nucleus membrane, cell particle

## Abstract

It is very difficult to purify a desired protein from a cell and tissue in a pure state. If the concentration of this protein is low, it is necessary to select the purification techniques appropriate for this protein to separate it from thousands of different proteins and to obtain it in pure form. The methods used in the purification of proteins are quite advanced.


Today, many enzymes and non-enzyme proteins have been isolated in pure and crystalline form. To study the amino acid composition and sequence, molecular weight, and other physical properties of a protein, it is first necessary to purify the protein. In order to isolate proteins from a group of tissues and cells, there are certain procedures that should be done first. In the first stage, the tissue or cell group where the protein we want to work at most is selected. The tissue and cells are homogenized by using buffer solutions to keep the protein we are interested in. The cell membrane and the nucleus membrane must be broken down. This homogenate is then subjected to centrifugation at certain rates to remove cell particles. The resulting protein mixture is then removed in the supernatant state to purify the proteins in pure form using one or more of the purification methods.

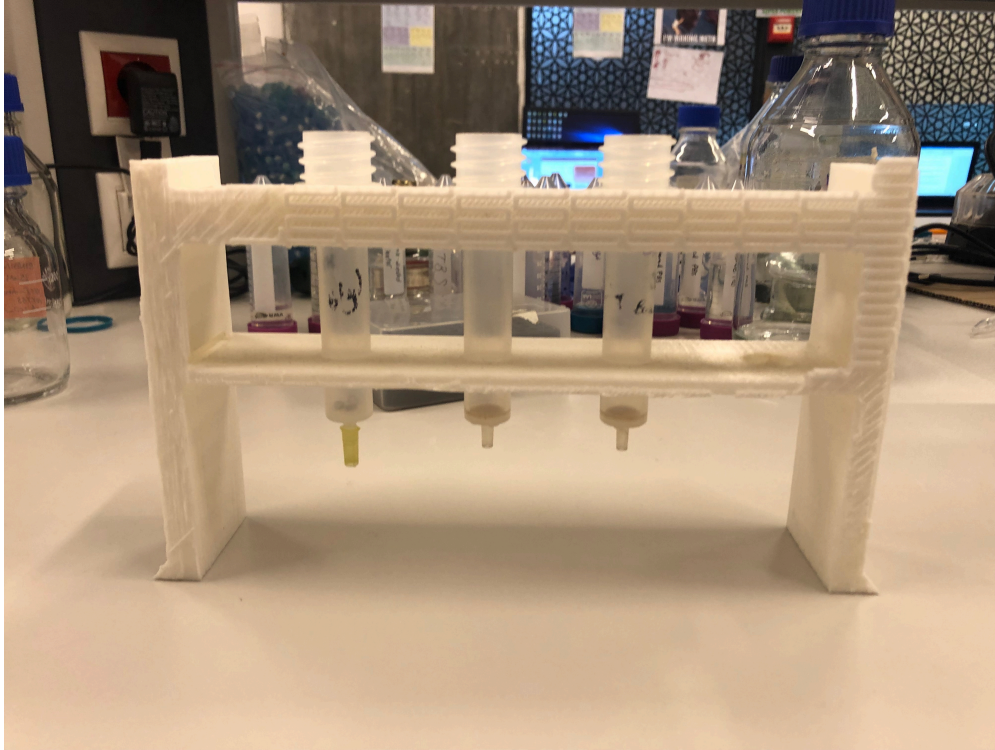
## Guidelines



Binding buffer : 5 ml Immidazole, 20 ml TBS, ddw up to 200 ml.

Wash Buffer : 8 ml Immidazole, 20 ml TBS, ddw up to 200 ml.

## Troubleshooting


- 1 2 ml of resin (Ni-beads) should be put onto columns. Wash column with double distilled water before using resin.  2000  $\mu\text{L}$  Resin



- 2 1X Binding Buffer should be added until fill the whole column.
- 3 When all Binding Buffer is leaked, samples should be put into columns.
- 4 Wash columns and sample until all residues are gone. In the washing step take from sample and from bradford and put into 96 well plate.  
 10  $\mu\text{L}$  sample  
 200  $\mu\text{L}$  Bradford



- 5 As a last step, to keep the protein that is purified from samples, Elution Buffer is added and transferred to new centrifuge tubes.

 1000  $\mu$ L Elution Buffer