## Affinity chromatography

- It is a method of separating biochemical mixtures based on a highly specific interaction that occurs between stationary phase and molecule of interest present in the mobile phase.
- Examples of such interactions include antigen- antibody/enzyme-substrate/receptor-ligand interaction etc.
- One of the members from the above example will be included in the stationary phase and the other will be in the mobile phase.
- Because these members are highly selective and have high affinity for each other, thus, method is called as affinity chromatography.
- The molecules bind with the stationary phase and those that do not bind are eluted first.
- The bound molecules are eluted with an eluting solvent of high salt concentration by *competitive interaction*.

Receptor Biomolecule	Ligand
Antigen	Antibody
Antibody	Antigen
Poly T or Poly U	Poly A tail of mRNA
Poly lysine (+ charge)	rRNA (- charge)
Ni <sup>2+</sup>	6X His-tagged fusion protein
Glutathione	GST-tagged fusion protein
Maltose	MBP-tagged fusion protein
Concanavalin - A	Glycoproteins
Protein – A / G	Antibody



## Significance:

- It is highly specific method for purification.
- It is efficient and quick as it is a single step purification method.
- It is used to separate glycoprotein from proteins.
- It is used to separate metalloenzyme from non-metal enzyme.

## Significance in case of genetic engineering:

For easy purification of recombinant proteins from other host proteins this method is applied as is outlined below:

1. Vectors are designed in such a way that recombinant proteins will have affinity tags at one of their ends i.e. N-terminal or C-terminal. This is shown in the figure below for His-tag.



DNA sequence coding for histidine cluster is engineered in the vector in such a manner that after restriction digestion & ligation the gene of interest will have His-tag at N-terminal or C-terminal.

We call it histidine cluster because it has continuous presence of 6-9 or sometimes 10 Histidine amino acids. More commonly, it is referred to as 6X His-tag if sequence has 6 His amino acids or polyHis-tag for tags having more amino acids.

2. When recombinant protein is expressed, it will have the His-tag fused in its structure. This is the reason all such tags are also called as fusion tags. In the figure below you will find the tags at N-terminal on top and at C-terminal at the bottom.



- 3. These recombinant proteins having tags are present in the bacterial cell along with the usual bacterial proteins (usual bacterial proteins are called as endogenous protein).
- 4. When bacterial cells are lysed, the lysate contains endogenous proteins as well as recombinant proteins.
- 5. The presence of tags in the recombinant proteins helps in its separation from endogenous proteins. Principle for the same is shown in the figure below:



6. The method which is used for separation of His tagged proteins is affinity chromatography. The specific variant used here is called as Ni-NTA affinity chromatography. In this, NTA is the chelating agent and stands for Nitrilotriacetic acid. It is attached to the sepharose beads and chelates the Ni<sup>2+</sup> ions. These Ni<sup>2+</sup> ions bind to the imidazole ring present in the side chain of His-tag present in the recombinant fusion proteins. This is shown below.



- 7. After recombinant proteins are bound to the Ni-NTA beads present in the column, they are washed using a buffer that contains 10-25 mM of imidazole. This helps remove non-specific binding of endogenous proteins. After washing, elution is done using a higher concentration of imidazole usually in the range of 100-500 mM concentration.
- 8. The imidazole competes with the His side chain for binding to the Ni<sup>2+</sup> and in this process the recombinant protein is released from the column and is collected. This process is called as elution.
- 9. We can also use cobalt (Co<sup>2+</sup>) or copper (Cu<sup>2+</sup>) ions in place of Ni<sup>2+</sup> ions for isolation of His-tagged recombinant proteins using affinity chromatography.

The workflow outline for the whole process is shown in the figure below:

