

Affinity Chromatography

What is affinity chromatography?

Purification via affinity chromatography is a powerful technique to separate your protein of interest from your sample. The proteins are marked with "tags" which give them specific binding properties. A suitable immobilized ligand binds to the tagged protein.

Why do we need purified proteins?

Characterisation of proteins e.g. functional assays, structure determination and protein interactions.

Chromatography methods in comparison

Size exclusion

Molecular size

Ion exchange

Net charge

Hydrophobic Interaction

Hydrophobicity

Affinity

Specific binding with tagged proteins

Affinity bead (Core)

- Agarose beads
 - Cross-linked and porous
 - Proteins can flow through pores
 - Hydrophilic
 - Specific bonds
- Agarose bead with magnetic core
 - Magnetic separator
 - Magnetic beads are attracted by separator

Agarose concentration of affinity bead

- Low concentrated agarose: Low degree of crosslinking
- High concentrated agarose: Low degree of crosslinking
- High concentrated agarose: High degree of crosslinking

Affinity bead size in the column

The bead sizes range from 30 µm to 800 µm

- Small affinity beads**
 - Higher ratio of surface to volume
 - Higher binding capacity of the beads
 - Higher pressure resistance
- Large affinity beads**
 - Allows faster flow rate in batch and FPLC experiments
 - Useful for viscous media
 - Useful for scaling-up a purification process

Design the target protein with an Affinity tag

- Choose expression system
 - In vivo
 - In vitro
- Choose the organism for protein expression

Cell-free expression

Components: Amino acids, DNA, Energy components, Plasmid, NTPs, Water

Application: Toxic proteins, DNA binding proteins, Unnatural label or amino acids e.g. isotope label (MNR)

Properties: Easy to manipulate, Costly if large amounts of protein are required

Prokaryotic cell

Processes of transcription and translation occur simultaneously

Advantages: Scalable, Simple culture conditions, High expression level, Less expensive

Eukaryotic cell

Processes: 1. Transcription, 2. mRNA is processed, 3. modified mRNA is exported to the cytoplasm, 4. Translation

Advantages: High-level protein processing, Low - moderate expression level

Affinity tags

Poly Histidin-tag

Sequence: HHHHHH

Specificity of interaction (KD): 10 µM

Protein Yield: Up to 80 [mg] / resin [ml]

Size: 8408-1,937.9 Dalton

Eluent: Imidazol, histidine, or at low pH

Glutathione S-transferase tag (GST)

Removal of Tag after purification possible

Specificity of interaction (KD): 1 µM

Protein Yield: 10-12 [mg] / resin [ml]

Size: 26 kDa

Eluent: Reduced glutathione

Maltose-binding protein (MBP)

Specificity of interaction (KD): 1.2 µM

Protein Yield: 7-16 mg / resin ml

Size: 45 kDa

Eluent: Maltose

Strep-tag

Sequence: WSHHPQFEK

Specificity of interaction (KD): 300 nM

Protein Yield: 9 mg / resin ml

Size: 1,058.1 Dalton

Eluent: Desthiobiotin

Rho1D4-tag

Sequence: TETSQVAPA

Specificity of interaction (KD): 20 nM

Protein Yield: 3-4 mg / resin ml

Size: 902.9 Dalton

Eluent: Rho1D4 peptide, low pH, or protease digest

FLAG-tag

Sequence: DYKDDDDK

Specificity of interaction (KD): 100 nM

Protein Yield: 0.6-1 mg / resin ml

Size: 1,012.9 Dalton

Eluent: DYKDDDDK (FLAG) peptide

Metal ion affinity

Target: His-tagged protein

Ligand: NTA as Chelator and Ni²⁺ ion

6 x Histidin

Enzym substrate specificity

Ligand: Reduced Glutathione (GSH)

Target: Glutathione S-transferase

Ligand: Maltose

Target: Maltose-binding protein

Ligand: Strep-Tactin (Engineered Streptavidin)

Target: Strep-tag II fusion proteins

Antibody-Antigen-Interaction: Each antibody is capable of binding only to a specific antigen

Antibody + Antigen: Rho1D4

Antibody + Antigen: FLAG

Ligand

Ligand	Coordination sites	Nickel binding
Nitrilotriacetic acid (NTA)	4	Light
Iminodiacetic acid (IDA)	3	Weak
INDIGO	5	Strong

Coupled metal ion

Affinity: Cu²⁺ Copper, Ni²⁺ Nickel, Zn²⁺ Zinc, Co²⁺ Cobalt

Specificity: Cu²⁺ > Ni²⁺ > Zn²⁺ > Co²⁺

How to chose tag?

His-tag, GST Tag, MBP Tag, Strep-Tactin tag, Rho1D4-tag, FLAG-tag

← higher protein yield | more expensive, more specific and pure →

Workflow of an Affinity Chromatography

- Cell opening of expression organism by sonification, mechanical disruption etc. followed by centrifugation and cell separation
- The mobile (liquid) phase: Cell lysate with the target protein
- The stationary (solid) phase: Column/ Cartridge filled with affinity beads
- Add lysate to the column
- Protein of interest connects to the beads (matching affinity)
- Unspecific proteins passes the beads
- Add wash buffer to remove remaining unspecific proteins
- Apply elution conditions: e.g. by competition with eluent (or pH change)
- Concentrated purified target protein

Limitations of Affinity Chromatography

- Inaccessible tag sequence

Solution approach: Move the tag to the other terminus of the protein or to an accessible loop within the protein
- Tag degradation by cellulase proteases

Protease
- Affinity tag influences protein expression
 - Tagged proteins may show a lower expression level
 - Affinity tag may cause misfolded proteins
 - Affinity tag may hamper protein activity

Separation methods in the lab

Batch Spin

- Simple and fast method
- No pressure or flow rate control

Gravity Flow Columns

Fast Protein Liquid Chromatography (FPLC)

- Automated system
- Reproducible
- Direct control on pressure, flow rate and the yield

Magnetic Beads

- Simple method
- Automatable and scalable system
- Applicable for small volumes

Subsequent studies

- Combination with an additional chromatography steps
 - Different chromatography e.g. affinity chromatography and size exclusion chromatography
- Control of the purification
 - SDS Page: Purity and quantity of different proteins
 - Western Blot: Analytical technique to detect specific proteins with antibody directed against affinity tag
 - Protein activity detection: ELISA: Immunological assay used to detect and quantify soluble proteins in biological samples
 - SPR (Surface plasmon resonance): Biosensor technique for studying interactions between all classes of biomolecules