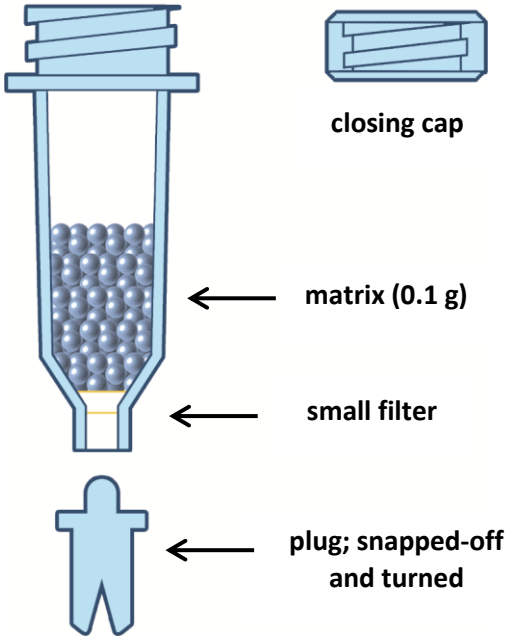
MobiSpin Ni-IDA Columns for His-Tag Purification



binding capacity: 12 mg

Mo Bi Tec
MOLECULAR BIOTECHNOLOGY

Contents

1. Features

- Easy, fast, and cost-effective routine purification of recombinant polyhistidine-tagged proteins:
  - under native and denaturing conditions
  - starting from diverse expression systems, e.g., *E. coli*, yeast, insect, and mammalian cells
- Very high binding capacity: up to 12 mg protein per spin column
- Excellent protein recovery rate of > 90%
- Simultaneous processing of multiple samples
- Easy test of experimental protocols by His_6-GFP (bacterial expression vector available)
- Columns are pre-packed and long-term storable at room temperature

2. Introduction

MobiSpin Ni-IDA columns with silica-based resin provide a fast and convenient routine tool for purification of recombinant polyhistidine-tagged proteins by spinning. In contrast to the large MoBiTec Ni-IDA columns, MobiSpin Ni-IDA is an ideal tool for quick purification of a large number of His_6-tagged proteins extracted from small culture volumes within a short time. The form-stable silica matrix is pre-charged with Ni^{2+} ions and allows purification on the principle of Immobilized Metal Ion Affinity Chromatography (IMAC). Binding of proteins is based on the interaction between the polyhistidine tag of a recombinant protein and immobilized Ni^{2+} ions. The chelating group of the Ni-IDA resin is based on iminodiacetic acid (IDA), which enables strong and efficient binding of target proteins to the IMAC matrix.

In contrast to traditional IDA matrices, MobiSpin Ni-IDA is an optimized matrix with low density of IDA ligands. This non-saturating surface concentration of IDA eliminates almost all non-specific interactions of contaminating host proteins with the adsorbent. As a result, MobiSpin Ni-IDA provides much higher target protein purity.
IDA is a tridentate chelator which occupies three of the six binding sites in the coordination sphere of the Ni^{2+} ion. The remaining three coordination sites are usually occupied by water molecules and can be exchanged with histidine residues of recombinant protein (Fig. 1).

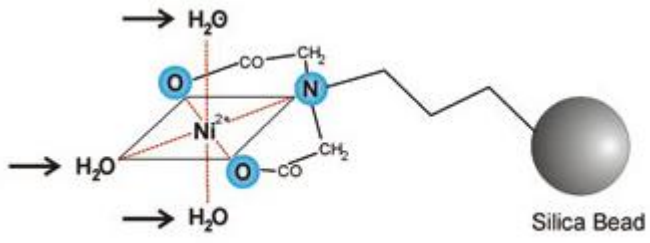


Fig.1: Silica-based Ni-IDA matrix. Schematic drawing of IDA in complex with Ni^{2+}.

3. Product Contents

3.1. Kit components

Order#	Product	Components included
PR-HTK105	MobiSpin Ni-IDA Columns	5 columns with matrix (dry), pre-packed; user manual
PR-HTK110	MobiSpin Ni-IDA Columns	10 columns with matrix (dry), pre-packed; user manual

3.2. Storage and expiration date

MobiSpin Ni-IDA Columns are storable at room temperature for at least 1 year.

3.3. Equipment and materials to be supplied by user

- Microliter pipettes
- Appropriate centrifuge (≥ 10,000 x g) and tubes for collection and centrifugation (size depends on culture volume)
- Sonicator
- Lysozyme
- Phenylmethylsulfonyl fluoride (PMSF)
- DNase I
- 0.45 µm membrane filter (optional)
- 500 mM EDTA and 5 mM $MgSO_4$ (only for preparation of periplasmic proteins)
- Buffers according to protocol (composition of all buffers see §3.4.)

3.4. Buffer compositions

Lysis-Equilibration-Wash Buffer (LEW Buffer)

- 50 mM NaH_2PO_4
- 300 mM NaCl

Adjust pH to 8.0 using NaOH

Required for following protocols:
6.3.1. Preparation of cleared lysates under native conditions
6.3.2. Preparation of cleared lysates under denaturing conditions

Elution Buffer

- 50 mM NaH_2PO_4
- 300 mM NaCl
- 250 mM imidazole

Adjust pH to 8.0 using NaOH

Required for the following protocol:
6.3.1. Preparation of cleared lysates under native conditions

Denaturing Solubilization Buffer

Please prepare shortly before use!

- 50 mM NaH_2PO_4
- 300 mM NaCl
- 8 M urea

Adjust pH to 8.0 using NaOH

Required for the following protocol:
6.3.2. Preparation of cleared lysates under denaturing conditions

Denaturing Elution Buffer

Please prepare shortly before use!

- 50 mM NaH_2PO_4
- 300 mM NaCl
- 8 M urea
- 250 mM imidazole

Adjust pH to 8.0 using NaOH

Required for the following protocol:
6.3.2. Preparation of cleared lysates under denaturing conditions

Sucrose Buffer

- 30 mM Tris/HCl
- 20% sucrose

Adjust pH to 8.0

Required for the following protocol:
6.2. Purification of periplasmic polyhistidine-tagged proteins

4. Terms and Conditions

For research use only. NOT recommended or intended for the diagnosis of human or animal diseases. Do NOT USE internally or externally in humans or animals. All chemicals should be considered potentially hazardous. Only persons trained in laboratory techniques and familiar with the principles of good laboratory practice should handle these products. Suitable protective clothing such as laboratory overalls, safety glasses, and gloves should be worn. Care should be taken to avoid contact with skin or eyes; if contact should occur, wash immediately with water (See Material Safety Data Sheet(s)).

Product warranty is limited to our liability to replace this product. All other warranties, expressed or implied, including but not limited to any implied warranties of merchantability or usefulness for a particular purpose, are excluded and do not apply. We shall have no liability for any direct, indirect, consequential, or incidental damages arising out of the use, the results of use, or the inability to use this product.

5. Technical Information

5.1. Protein binding

Proteins with different numbers of polyhistidine tags fused either to the amino or to the carboxy terminus can bind to the Ni-IDA matrix with very high affinity. Even when the tag is not completely accessible (e.g., under native conditions) it will bind as long as more than two histidine residues are available for interaction. In general, the smaller the number of accessible histidine residues the weaker is the binding.

5.2. Binding capacity

Maximum binding capacity of the MobiSpin Ni-IDA Column is 12 mg of recombinant protein as tested for histidine-tagged green fluorescent protein (His_6-GFP, 32 kDa). The actual yield obtained depends on the concentration of the histidine-tagged fusion protein as well as its total amount in the loaded sample.
Maximal recovery: For a maximal recovery (> 90%, tested with purified His_6-GFP) we recommend loading up to 7 mg of polyhistidine-tagged protein in a volume of 300-700 µl.
Maximum yield: To obtain a maximum yield (with lower recovery values) we recommend loading even higher amounts of polyhistidine-tagged protein (up to 20 mg of cleared protein lysate). A high concentration and a high overall amount will result in the highest possible yield.

5.3. Purification of secretory proteins

Producing proteins by secretion can be beneficial for proper folding, disulfide bond formation, and for directing toxic proteins out of the cell. In addition, purification may be easier since the proteins can be purified directly from the corresponding compartment (periplasmic space or culture medium) having a lower amount of total protein.
Secretory proteins contain a signal peptide that addresses them for the export into the periplasmic space (e.g., *E. coli*) or into the culture medium (e.g., *Bacillus* spec.).

5.4. Purification under native and denaturing conditions

Polyhistidine-tagged proteins can be purified under native or denaturing conditions. Which condition is chosen depends on diverse considerations: protein location and solubility, the accessibility of the polyhistidine-tag, and whether biological activity must be retained.
Depending on the expression system and the host, recombinant proteins will accumulate in the cytoplasm or will be secreted into the periplasmic space or into the culture medium. In most cases, secreted proteins are correctly folded and soluble. Intracellularly accumulated recombinant protein remains either in a soluble form or aggregates as insoluble misfolded protein in inclusion bodies.

Native conditions: In case of a soluble protein (purified from cytoplasm, periplasm, or supernatant) with good accessibility of the polyhistidine-tag, protein can be purified under native conditions (see protocol “6.3.1. Preparation of cleared lysates under native conditions”). Native conditions may also be used if co-purification of associated proteins is desired.

Denaturing conditions: In case of inclusion body formation, the polyhistidine-tagged protein has to be extracted from the cell pellet using urea as denaturant (see protocol “6.3.2. Preparation of cleared lysates under denaturing conditions”). Denaturing conditions can also be an option for improving the accessibility of the polyhistidine-tag.

Table 1: How to find the proper purification conditions: please choose

Native conditions if …	**Denaturing conditions if …**
protein is soluble	protein aggregates (e.g., inclusion bodies)
polyhistidine-tag is well accessible	the polyhistidine-tag is poorly accessible
co-purification of associated proteins is desired.	

5.5. Culture volume

The recommended culture volume complies with the concentration of the polyhistidine-tagged protein in the culture. The latter typically varies from < 10 mg/l up to 100 mg/l depending on cell density and expression level.

Table 2: Culture size guide

Expression level	Recommended culture volume	Recommended pellet wet weight (*E. coli*)	Estimated amount of poly-histidine-tagged protein in sample
High (~100 mg/l)	40-200 ml	160-800 mg	~4-20 mg
Low (~10 mg/l)	0.4-2 l	1.6-8 g	~4-20 mg

6. Protocols

The following protocols and procedures, including the buffers made by the user, can be tested, before applying the user's His-tagged protein, by using MoBiTec´s His_6-GFP bacterial expression vector. His_6-GFP protein extracted from *E. coli*, can be detected by eye when loaded on, washed on, and eluted from the MobiSpin Ni-IDA column. Every step can be quantified easily.

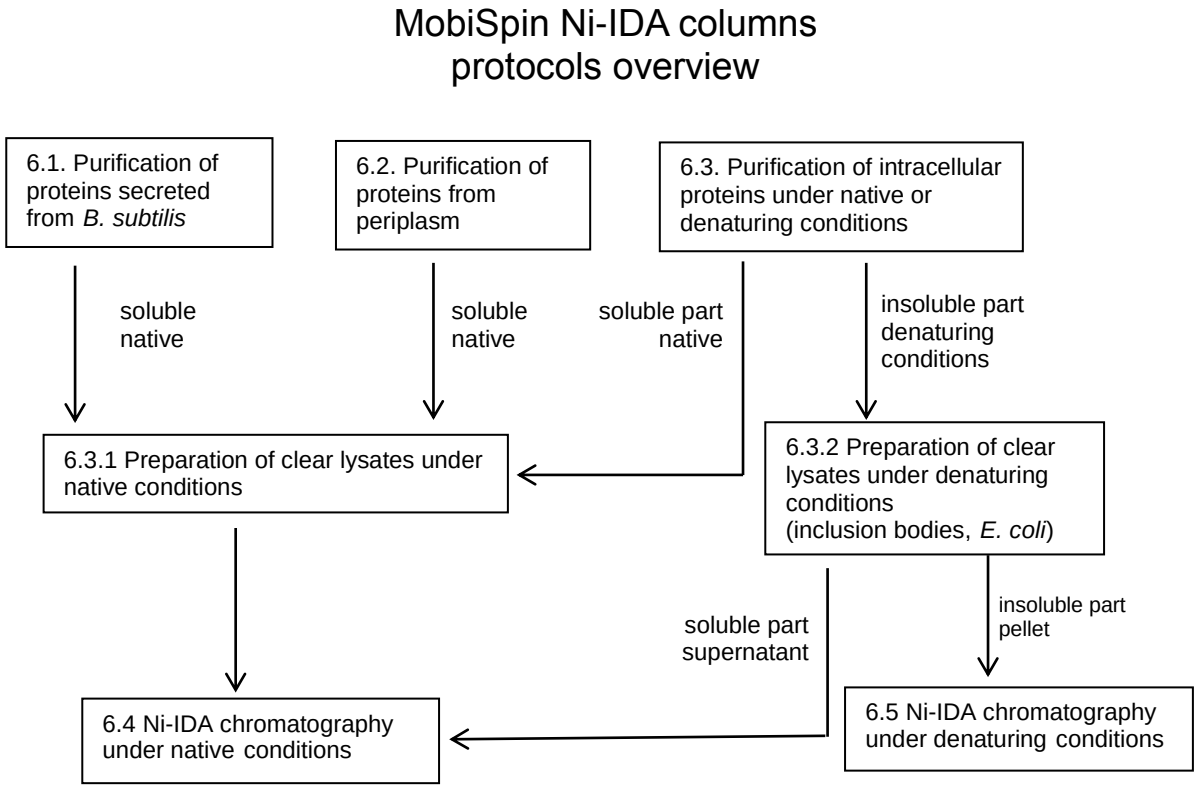


Fig. 2: Protocols overview for purification of secreted, periplasmic, and/ or intracellular recombinant polyhistidine-tagged proteins under native and denaturing conditions.

6.1. Purification of secreted polyhistidine-tagged proteins from the supernatant (e.g., *Bacillus subtilis*)

For preparation of secreted polyhistidine-tagged proteins, cells and supernatant will be separated by centrifugation (15 min, 4,500 x g to 6,000 x g, 4 °C). The clear supernatant can be directly applied to MobiSpin Ni-IDA columns. Please follow the protocol "6.3.1. Preparation of cleared lysates under native conditions"

6.2. Purification of periplasmic polyhistidine-tagged proteins

Periplasmic proteins can be separated from cytoplasmic proteins by osmotic shock preparation. The obtained osmotic shock fluid can then be subjected to MobiSpin Ni-IDA columns.

- Harvest the cells from expression culture by centrifugation (15 min, 4,500 x g to 6,000 x g, 4 °C).
- Resuspend cell pellet in Sucrose Buffer at 80 ml per gram wet weight.
- Keep the cells on ice and add 500 mM EDTA solution dropwise to 1 mM final concentration.
- Incubate the cells on ice for 5-10 min with gentle agitation.
- Centrifuge the cell suspension at 8,000 x g for 20 min at 4 °C.
- Remove supernatant completely and resuspend the pellet in equal volume of ice-cold 5 mM $MgSO_4$ solution.
- Shake or stir for 10 min in an ice bath.
- Centrifuge at 8,000 x g for 20 min at 4 °C.
- Carefully transfer the supernatant (containing the periplasmic proteins) to a clean tube without disturbing the pellet.
- If the supernatant is not clear, centrifuge a second time or filter through a 0.45 µm membrane to avoid clogging of the Ni-IDA column with insoluble material.
- Dialyze the supernatant extensively against LEW buffer.
- Store supernatant on ice.
- Proceed with protocol “6.3.1. Preparation of cleared lysates under native conditions”.

6.3. Purification of intracellular polyhistidine-tagged proteins under native or denaturing conditions

For purification of intracellular polyhistidine-tagged proteins under native conditions, a considerable portion of the protein should be present in soluble form. If so, please follow protocol “6.3.1. Preparation of cleared lysates under native conditions”.

High levels of recombinant protein expression might lead to the formation of insoluble aggregates; in *E. coli*, these are known as inclusion bodies.
During preparation of intracellular recombinant protein, cells are disrupted and cell pellets are separated from the soluble fraction by centrifugation. In contrast to soluble protein that remains in the supernatant, the inclusion bodies will sediment with the cell debris, and the polyhistidine-tagged protein has to be extracted from cell pellet using urea as denaturant. 8 M urea completely solubilizes the inclusion bodies and His_6-tagged proteins. Under these denaturing conditions, the His_6-tag on a protein will be fully exposed so that binding to the Ni-IDA matrix is enabled. If most of the His_6-tagged protein is localized within inclusion bodies, please follow protocol “6.3.2. Preparation of cleared lysates under denaturing conditions”.

6.3.1. Preparation of cleared lysates under native conditions (*E. coli*)

- Prepare LEW buffer (Lysis-Equilibration-Wash Buffer) and Elution Buffer as described in “3.4. Buffer compositions”.
- Harvest the cells from expression culture by centrifugation (15 min, 4,500 x g to 6,000 x g, 4 °C).
- Remove supernatant and store pellet at -20 °C or proceed immediately. Please perform all steps on ice!
- Thoroughly resuspend the pellet in LEW buffer (~1.25 – 5.0 mg polyhistidine-tagged protein/ 1 ml LEW, see also table 3 below), by pipetting up and down or vortexing until complete resuspension is achieved (no cell aggregates visible anymore). Add lysozyme

to a final concentration of 1 mg/ml and protease inhibitor (e.g., 0.1 mM PMSF final concentration). Stir the solution on ice for 30 min.

- Sonicate the suspension on ice according to the instructions provided by the manufacturer (e.g. 10 x 15 sec burst with 20 sec rest (amplitude of 20%).
- Carefully check samples appearance after sonication. If the lysate is still viscous from incomplete fragmentation of DNA, add 5 µg/ml DNase I and stir on ice for additional 15 min.
- Centrifuge the crude lysate at 10,000 x g for 30 min at 4 °C to remove cellular debris.
- Carefully transfer the supernatant to a clean tube without disturbing the pellet.
- If the supernatant is not clear, centrifuge a second time or filter through a 0.45 µm membrane to avoid clogging of the Ni-IDA column with insoluble material.
- Store supernatant on ice.

Proceed with chapter “6.4. Ni-IDA chromatography under native conditions”.

Table 3: LEW buffer volume guide

Expression level	Recommended culture volume	Recommended pellet wet weight	Ratio pellet weight/LEW volume	Volume of LEW for re-suspension
High (~100 mg/l)	40 ml (min.)	0.16 g (min.)	1:5	0.8 ml
	200 ml (max.)	0.8 g (max.)	1:5	4.0 ml
Low (~10 mg/l)	400 ml (min.)	1.6 g (min.)	1:2	3.2 ml
	2 l (max.)	8 g (max.)	1:2	16.0 ml

6.3.2. Preparation of cleared lysates under denaturing conditions (*E. coli*)

High levels of expression of recombinant proteins in a variety of expression systems can lead to the formation of insoluble aggregates; in *E. coli*, these are known as inclusion bodies. Strong denaturants such as 8 M urea completely solubilize inclusion bodies and 6xHis-tagged proteins. Under these conditions, the His_6-tagged protein will be fully exposed so that binding to the Ni-IDA matrix may be improved.

For preparation of intracellular recombinant proteins, cells are disrupted and cell pellets are separated from the soluble fraction by centrifugation, whereas inclusion bodies will sediment with the cell debris and the soluble recombinant protein remains in the supernatant. The clear supernatant can be directly applied to MobiSpin Ni-IDA Columns (follow protocol “6.4. Ni-IDA chromatography under native conditions”). In case of inclusion body formation, the His_6-tagged protein has to be extracted from the cell pellet using urea as denaturant (follow the protocol below).

Isolation of inclusion bodies

- Harvest the cells from expression culture by centrifugation (15 min, 4,500 x g to 6,000 x g, 4 °C).
- Remove supernatant and store pellet at -20 °C or proceed immediately. Please perform all steps on ice!
- Thoroughly resuspend the pellet in LEW buffer (~1.25-5.0 mg polyhistidine-tagged protein/1 ml LEW, see Table 3), by pipetting up and down or vortexing until complete

resuspension is achieved (no cell aggregates visible anymore). Add lysozyme to a final concentration of 1 mg/ml and protease inhibitor (e.g., 0.1 mM PMSF final concentration). Stir the solution on ice for 30 min.

- Sonicate the suspension on ice according to the instructions provided by the manufacturer (e.g., 10 x 15 sec burst with 20 sec rest (amplitude of 20%).
- Carefully check protein sample appearance after sonication. If the lysate is still viscous from incomplete fragmentation of DNA, add 5 µg/ml DNase I and stir on ice for additional 15 min.
- Centrifuge the crude lysate at 10,000 x g for 30 min at 4 °C to collect inclusion bodies. Discard the supernatant and keep the pellet on ice.

Solubilization of inclusion bodies

- Resuspend the pellet in 10 ml LEW buffer to wash the inclusion bodies. Centrifuge the suspension at 10,000 x g for 30 min at 4° C and discard the supernatant.
- Resuspend the pellet in 2 ml “Denaturing Solubilization Buffer” to solubilize the inclusion bodies. For complete solubilization it may be necessary to vortex or sonicate the solution. Stir the suspension for further 60 min on ice.
- Centrifuge at 10,000 x g for 30 min at 20 °C to remove any remaining insoluble material. Carefully transfer the supernatant to a clean tube without disturbing the pellet.
- If the supernatant is not clear, centrifuge a second time or filter through a 0.45 µm membrane to avoid clogging of the MobiSpin Ni-IDA column with insoluble material.
- Store supernatant at 4 °C.

Proceed with chapter “6.5. Ni-IDA chromatography under denaturing conditions”.

6.4. Ni-IDA chromatography under native conditions

Column equilibration

Equilibrate the spin column with 0.7 ml LEW buffer. Centrifuge at 600 x g for 1 min and discard the fluid subsequently.

Binding

Add the cleared lysate (2 x 0.4 ml, total volume of 0.8 ml) to the pre-equilibrated spin column and thoroughly mix protein sample with matrix by inverting the column. Leave the column for 30 sec on ice and spin it down by centrifugation at 600 x g for 1 min at 4 ºC. You may store the first centrifugation flow for protein assay and SDS-PAGE analysis.

Washing

Wash the column three times with 0.7 ml LEW buffer (3 x 0.7 ml) by centrifugation at 600 x g for 1 min at 4 ºC. Discard the fluid after each centrifugation. It is recommended mixing the column by gentle inverting each time before centrifugation.

Elution

Elute the bound polyhistidine-tagged protein in 4 fractions by adding 1.6 ml Elution Buffer containing 250 mM Imidazol (4 x 0.4 ml) and collect separately. Centrifuge at 600 x g for 1 min at 4 ºC and place the spin column in a new 2 ml tube each time.

Note: Commonly, 90% of the eluted protein can be found within the first 0.8 ml of elution. Use protein assay and/or SDS-PAGE analysis to determine which fraction(s) contain(s) the majority of the polyhistidine-tagged protein.

6.5. Ni-IDA chromatography under denaturing conditions

Column Equilibration
Equilibrate the spin column with 0.7 ml of “Denaturing Solubilization Buffer”. Centrifuge at 600 x g for 1 min and discard the fluid subsequently.

Binding
Add the cleared lysate (2x 0.4 ml, total volume of 0.8 ml) to the pre-equilibrated equilibrated spin column and mix protein sample with matrix thoroughly by inverting the column. Leave the column for 30 sec on ice and spin it down by centrifugation at 600 x g for 1 min at 4 ºC. You may store the first centrifugation flow for protein assay and SDS-PAGE analysis.

Washing
Wash the column three times with 0.7 ml of “Denaturing Solubilization Buffer” (3 x 0.7 ml) by centrifugation at 600 x g for 1 min at 4 ºC. Discard the fluid after each centrifugation. It is recommended mixing the column by gentle inverting each time before centrifugation.

Elution
Elute the polyhistidine-tagged protein in 4 fractions by adding 1.6 ml of “Denaturing Elution Buffer” divided in a suitable number of fractions (4 x 0.4 ml) and collect separately. Centrifuge at 600 x g for 1 min at 4 ºC and place the spin column in a new 2 ml tube each time.

Note: Commonly, 90% of the eluted protein can be found within the first 0.8 ml of elution. Use protein assay and/or SDS-PAGE analysis to determine which fraction(s) contain(s) the majority of the polyhistidine-tagged protein.

6.6. Compatibility of reagents

Buffer components that chelate metal ions, such as EDTA and EGTA, should not be used since they strip Ni^{2+} ions from the matrix. Do not use buffers with pH > 8.4 since silica dissolves in solutions of high pH.

Reagent	Effect	Comment
β-mercaptoethanol	Prevents formation of disulfide bonds; can reduce Ni^{2+} ions at higher concentrations.	Up to 50 mM in samples has been successfully used in some cases.
DTT, DTE	Can reduce Ni^{2+} ions at higher concentrations.	Up to 10 mM in samples has been successfully used in some cases.
EDTA	Coordinates with Ni^{2+} ions, causing a decrease in capacity at higher concentrations.	Not recommended, but up to 1 mM in samples has been used successfully in some cases.
Ethanol	Prevents hydrophobic interactions between proteins.	Up to 20% can be used; ethanol may precipitate proteins, causing low flow rates and column clogging.
Glutathione reduced	Can reduce Ni^{2+} ions at higher concentrations.	Up to 30 mM in samples has been successfully used in some cases.
Glycerol	Prevents hydrophobic interactions between proteins.	Up to 50% can be used.
GuHCl	Solubilizes proteins.	Up to 6 M can be used.
Imidazole	Binds to immobilized Ni^{2+} ions and competes with the polyhistidine-tagged proteins	Imidazole should not be included in LEW buffer.
SDS	Interacts with Ni^{2+} ions, causing a decrease in capacity.	Not recommended, but up to 0.5% in samples has been used successfully in some cases.
Sodium chloride	Prevents ionic interactions and thus unspecific binding.	up to 2 M can be used, at least 0.3 M should be used
Sodium phosphate	Used in LEW and Elution Buffer in order to buffer the solutions at pH 8.	50 mM is recommended. The pH of any buffer should be adjusted to 8, although in some cases a pH between 7 and 8 can be used.
Tris	Coordinates with Ni^{2+} ions, causing a decrease in capacity.	10 mM may be used, sodium phosphate buffer is recommended
Triton, Tween	Removes background proteins.	Up to 2% can be used.
Urea	Solubilizes proteins.	Use 8 M urea for purification under denaturing conditions.

6.7. Troubleshooting

Problem	Caused by	Suggestions
Sample does not enter the column bed.	Sample/lysate contains insoluble material.	If sample is not clear, use centrifugation or filtration (0.45 µm membrane) to avoid clogging of the column.
	Sample/lysate contains genomic DNA.	Lysate may remain viscous from incomplete shearing of genomic DNA after sonication. Add 5 µg/ml DNase I and incubate on ice for 10 min.
Protein does not bind to the resin.	Vector construct is not correct.	Check if gene of interest and tag have been cloned in-frame.
	Binding conditions are incorrect.	Check composition of buffers and verify pH 7-8. Ensure that there is no chelating or strong reducing reagent or imidazole present.
Protein elutes with wash buffer.	Buffer compositions are incorrect.	Check composition of buffers and verify pH 7-8. Ensure that there is no chelating or strong reducing reagent or imidazole present.
Protein does not elute from column.	Elution conditions are too mild.	Increase concentration of imidazole.
Contamination of other proteins within the eluate.	Insufficient washing.	Use larger volumes for washing.
	Binding and washing conditions are too mild.	Add small amounts of imidazole (1-10 mM). Take care that the imidazole concentration remains low enough to enable binding of the polyhistidine-tagged proteins.
	Contaminating proteins and the polyhistidine-tagged protein are connected *via* disulfide bonds.	Add up to 30 mM β-mercapto-ethanol to reduce disulfide bonds.
	Contaminating proteins are degradation products of polyhistidine-tagged protein.	- Perform cell lysis at 4 °C. - Include protease inhibitor.
	Expression is too low; this leads to increased binding of contaminating proteins.	- Increase expression level. - Increase amount of culture volume or cell pellet weight.

7. Order Information, Shipping, and Storage

Order#	Product	Amount
PR-HTK105	MobiSpin Ni-IDA Columns	5 columns
PR-HTK110	MobiSpin Ni-IDA Columns	10 columns
shipped at room temperature; store columns at room temperature		

Related products:

Order#	Product	Amount
PR-HTK004	MoBiTec Ni-IDA Columns	4 columns
PR-HTK010	MoBiTec Ni-IDA Columns	10 columns
TOPO-HIS01	His_6-GFP bacterial expression vector	10 µg
M105010S	MobiSpinColumn “F” with fixed outlet plug, inserted small 10 µm filter and screw cap	50 columns
M105210S	MobiSpinColumn “F” with fixed outlet plug, inserted large 10 µm filter and screw cap	50 columns
PEG01	pEG-His1 vector	5 µg
PR-SB01-01	SpeedBlot (His)	30 ml

8. Contact and Support

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MoBiTec in your area: Find your local distributor at www.mobitec.com