HiTrap™ MabSelect™, 1 mL and 5 mL
HiTrap MabSelect Xtra™, 1 mL and 5 mL

HiTrap MabSelect and HiTrap MabSelect Xtra are 1 mL and 5 mL ready to use columns, prepacked with MabSelect and MabSelect Xtra, respectively.

The protein A-derived ligand is produced in *Escherichia coli* and is free from components from mammalian origin.

MabSelect is designed for fast purification of monoclonal antibodies from large sample volumes due to its compatibility with high flow rates and high pressure when scaling up.

MabSelect Xtra is designed for maximum binding capacity, which allows binding from samples with high expression levels of the monoclonal antibody.

Both resins are ideal for the purification of monoclonal antibodies from lab to process scale.

The design of the HiTrap column, together with the prepacked high flow matrix and high dynamic binding capacity provides fast, simple, and easy separations in a convenient format.

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Read these instructions carefully before using HiTrap columns.

Intended use

HiTrap columns are intended for research use only, and shall not be used in any clinical or *in vitro* procedures for diagnostic purposes.

Safety

For use and handling of the product in a safe way, refer to the Safety Data Sheet.

1 Product description

HiTrap column characteristics

The columns are made of biocompatible polypropylene that does not interact with biomolecules.

The columns are delivered with a stopper at the inlet and a snap-off end at the outlet. Table 1 lists the characteristics of HiTrap columns.

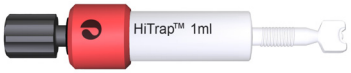

Fig 1. HiTrap, 1 mL column.

Fig 2. HiTrap, 5 mL column.

Note: *HiTrap columns cannot be opened or refilled.*

Note: *Make sure that the connector is tight to prevent leakage.*

Table 1. Characteristics of HiTrap columns

Column volume (CV)	1 mL	5 mL
Column dimensions	0.7 × 2.5 cm	1.6 × 2.5 cm
Column hardware pressure limit	0.5 MPa (5 bar)	0.5 MPa (5 bar)

Note: *The pressure over the packed bed varies depending on a range of parameters such as the characteristics of the chromatography resin, sample/liquid viscosity, and the column tubing used.*

Supplied Connector kit with HiTrap column

Connectors supplied	Usage	No. supplied
Union 1/16" male/ luer female	For connection of syringe to HiTrap column	1
Stop plug female, 1/16"	For sealing bottom of HiTrap column	2, 5 or 7

Resin properties

MabSelect

The recombinant protein A is produced in *Escherichia coli*. Fermentation and subsequent purification of the protein A are done in the absence of mammalian products. The recombinant protein A has been specially engineered to favor an oriented coupling that gives an affinity resin with enhanced binding capacity for IgG.

The specificity of binding to the Fc region of IgG is similar to that of native protein A, and provides excellent purification in one step. The epoxy-based coupling chemistry gives low ligand leakage.

MabSelect is designed to tolerate high flow rates and high pressure with its specially developed base matrix. In combination with low ligand leakage, this makes MabSelect well suited for the purification of monoclonal antibodies from lab to process scale.

The characteristics of HiTrap MabSelect are summarized in Table 2.

MabSelect Xtra

MabSelect Xtra addresses the increasing levels of expression found in monoclonal antibody feedstocks. The resin is engineered to give up to 30% higher dynamic binding capacities than other Protein-A based resins.

The recombinant protein A used in MabSelect Xtra is produced in *Escherichia coli.* Fermentation and subsequent purification are performed in the absence of mammalian products. The recombinant protein has been specially engineered to favor an oriented coupling that gives an affinity resin with enhanced binding capacity for IgG.

The specificity of binding to the Fc region of IgG is similar to that of native protein A and provides excellent purification in one step. High capacity and the specially engineered base matrix, make MabSelect Xtra well suited for purifying monoclonal antibodies from lab to process scale. The characteristics of HiTrap MabSelect Xtra are summarized in Table 3.

Table 2. Characteristics of HiTrap MabSelect

Matrix	Highly cross-linked agarose, spherical	
Particle size, d_{50v}[1]	~ 85 µm	
Ligand	Recombinant protein A (*E. coli*)	
Coupling chemistry	Epoxy	
Dynamic binding capacity, Q_{B10}[2]	~ 30 mg human IgG/mL resin	
	1 mL column	**5 mL column**
Recommended operating flow rate[3]	0.5 mL/min	2.5 mL/min
Maximum operating flow rate[4]	4 mL/min	20 mL/min
Chemical stability	Stable to commonly used aqueous buffers, 10 mM NaOH (pH 12), 0.1 M sodium citrate/HCl (pH 3), 6 M Gua-HCl, 8 M urea, 20% ethanol, 2% benzyl alcohol	
pH stability, operational[5]	3 to 10[6]	
pH stability, CIP[7]	3 to 12[6, 8]	
Temperature stability	2°C to 40°C	
Delivery conditions	20% ethanol	
Storage	20% ethanol, 2°C to 8°C	

1 Median particle size of the cumulative volume distribution

2 Dynamic binding capacity at 10% breakthrough by frontal analysis at a mobile phase velocity of 500 cm/h in an XK 16/20 column at 20 cm bed height (2.4 min residence time) for human IgG in 0.020 M NaH_2PO_4, pH 7.4. Residence time is equal to bed height (cm) divided by flow velocity (cm/h) during sample loading. Flow velocity (cm/h) is equal to flow rate (mL/h) divided by column cross-sectional area (cm^2).

3 At room temperature in buffers with the same viscosity as water.

4 At room temperature in H_2O

5 pH range where resin can be operated without significant change in function

6 pH below 3 is sometimes required to elute strongly bound IgG species. However, protein ligands can hydrolyze at pH below 2.

7 pH range where resin can be subjected to cleaning- or sanitization-in-place without significant change in function

8 Reducing agent, for example 100 mM 1-thioglycerol followed by 15 mM NaOH, is among the most efficient CIP for MabSelect.

Note: *The dynamic binding capacity can be optimized for process development. Increased residence time gives higher dynamic binding capacity.*

Table 3. Characteristics of HiTrap MabSelect Xtra

Matrix	Highly cross-linked agarose, spherical	
Particle size, d_{50v}[1]	~ 75 µm	
Ligand	Recombinant protein A (*E. coli*)	
Coupling chemistry	Epoxy	
Dynamic binding capacity, Q_{B10}[2]	~ 40 mg human IgG/mL resin	
	1 mL column	**5 mL column**
Recommended operating flow rate[3]	0.5 mL/min	2.5 mL/min
Maximum operating flow rate[4]	4 mL/min	20 mL/min
Chemical stability	Stable to commonly used aqueous buffers, 10 mM NaOH (pH 12), 0.1 M sodium citrate/HCl (pH 3), 6 M Gua-HCl, 8 M urea, 20% ethanol, 2% benzyl alcohol	
pH stability, operational[5]	3 to 10[6]	
pH stability, CIP[7]	3 to 12[6, 8]	
Temperature stability	2°C to 40°C	
Delivery conditions	20% ethanol	
Storage	20% ethanol, 2°C to 8°C	

[1] Median particle size of the cumulative volume distribution

[2] Dynamic binding capacity at 10% breakthrough by frontal analysis at a mobile phase velocity of 250 cm/h in an XK 16/20 column at 10 cm bed height (2.4 min residence time) for human IgG in 0.020 M NaH_2PO_4, pH 7.4. Residence time is equal to bed height (cm) divided by flow velocity (cm/h) during sample loading. Flow velocity (cm/h) is equal to flow rate (mL/h) divided by column cross-sectional area (cm^2).

[3] At room temperature in buffers with the same viscosity as water.

[4] At room temperature in H_2O

[5] pH range where resin can be operated without significant change in function

[6] pH below 3 is sometimes required to elute strongly bound IgG species. However, protein ligands can hydrolyze at pH below 2.

[7] pH range where resin can be subjected to cleaning- or sanitization-in-place without significant change in function

[8] Reducing agent, for example 100 mM 1-thioglycerol followed by 15 mM NaOH, is among the most efficient CIP for MabSelect.

Note: *The dynamic binding capacity can be optimized for process development. Increased residence time gives higher dynamic binding capacity.*

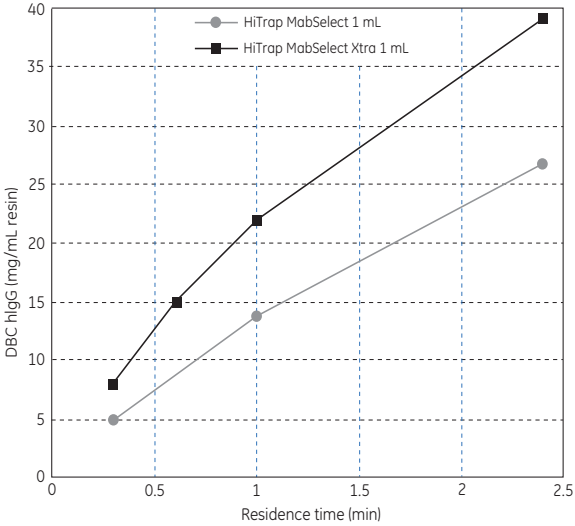

Fig 3. Dynamic binding capacity (DBC) versus residence time for HiTrap MabSelect 1 mL and HiTrap MabSelect Xtra 1 mL. Sample: 1 mg/mL human IgG (hIgG) Gammanorm™ (Octapharma); Binding buffer: 20 mM phosphate, 150 mM NaCl, pH 7.4; Elution buffer: 100 mM sodium citrate, pH 3.0. Also see Fig 4 on page 13.

Preferred ligands

Most IgG can be purified using protein A, but for some IgG protein G is the preferred ligand. Refer to Table 4 for relative binding strengths for protein A and protein G.

Table 4. Relative binding strengths for protein A and protein G

Species	Subclass	Protein A binding	Protein G binding
Human	IgA	variable	–
	IgD	–	–
	IgE	–	–
	IgG_1	++++	++++
	IgG_2	++++	++++
	IgG_3	–	++++
	IgG_4	++++	++++
	IgM*	variable	–
Avian egg yolk	IgY†	–	–
Cow		++	++++
Dog		++	+
Goat		–	++
Guinea pig	IgG_1	++++	++
	IgG_2	++++	++
Hamster		+	++
Horse		++	++++
Koala		–	+
Llama		–	+
Monkey (rhesus)		++++	++++
Mouse	IgG_1	+	++++
	IgG_{2a}	++++	++++
	IgG_{2b}	+++	+++
	IgG_3	++	+++
	IgM*	variable	–
Pig		+++	+++
Rabbit	no distinction	++++	+++
Rat	IgG_1	–	+
	IgG_{2a}	–	++++
	IgG_{2b}	–	++
	IgG_3	+	++
Sheep		+/–	++

* Purify using HiTrap IgM Purification HP columns.
† Purify using HiTrap IgY Purification HP columns.
++++ = strong binding
++ = medium binding
– = weak or no binding

2 Operation

Preparation of buffers

Water and chemicals used for buffer preparation must be of high purity. Filter buffers through a 0.22 µm or a 0.45 µm filter before use.

Recommended buffers

Binding buffer: 20 mM sodium phosphate, 0.15 M NaCl, pH 7.2

Elution buffer: 0.1 M sodium citrate, pH 3.0 to 3.6

Note: *When purifying mouse IgG_1 on protein A resin, an increased binding capacity will be achieved by including 2.5 M NaCl in the binding buffer.*

Preparation of the sample

1. If needed, adjust the sample to the composition of the start buffer using one of these two methods:
   - Dilute the sample with start buffer.
   - Exchange buffer using a Prepacked columns for desalting, refer to Table 5**.**
2. Filter the sample through a 0.45 µm filter or centrifuge immediately before loading it to the column. This prevents clogging and increases the life time of the column when loading large sample volumes.

Prepacked columns for desalting

The prepacked columns described in Table 5 are used for desalting, buffer exchange, and cleanup of proteins and other large biomolecules (Mr > 5000).

Table 5. Prepacked columns for desalting

Column	Loading volume	Elution volume
HiPrep™ 26/10 Desalting[1]	2.5 to 15 mL	7.5 to 20 mL
HiTrap Desalting[2]	0.25 to 1.5 mL	1.0 to 2.0 mL
PD-10 Desalting[3]	1.0 to 2.5 mL[4] 1.75 to 2.5 mL[5]	3.5 mL Up to 2.5 mL
PD MiniTrap G-25	0.1 to 2.5 mL[4] 0.2 to 0.5 mL[5]	1.0 mL Up to 0.5 mL
PD MidiTrap G-25	0.5 to 1 mL[4] 0.75 to 1 mL[5]	1.5 mL Up to 1.0 mL

[1] Prepacked with Sephadex™ G-25™ Fine, requires a pump or a chromatography system to run.

[2] Prepacked with Sephadex G-25 Superfine, requires a syringe or pump to run.

[3] Prepacked with Sephadex G-25, can be run by the gravity flow or centrifugation.

[4] Volumes with gravity elution.

[5] Volumes with centrifugation.

Purification

Note: *A blank run, including CIP, is recommended before the first run with antibody feed. This decreases the ligand leakage during the chromatography step.*

Note: *The recommended operating flow rate for HiTrap MabSelect and HiTrap MabSelect Xtra is 0.5 or 2.5 mL/min for 1 and 5 mL column, respectively.*

1 If the eluted sample needs to be neutralized, add an alkaline buffer as 1 M Tris-HCl, pH 9.0, to the collection tubes.

2 Remove the stopper from the inlet and the snap-off end at the column outlet.

3 Connect the column to the system with 1/16" male connectors (28401081).

Note: *Make a drop-to-drop connection to prevent air from entering the column.*

Note: *Make sure that the connectors are tight to prevent leakage.*

4 Wash with 5 column volumes (CV) of distilled water to remove the ethanol. This prevents precipitation of buffer salts at exposure to ethanol.

Note: *The viscosity for 20% ethanol is higher than for water. For this step, do not use a higher flow rate than the recommended 0.5 or 2.5 mL/min for 1 and 5 mL column, respectively.*

5 Equilibrate the column with start buffer for at least 5 CV, or until the UV baseline, eluent pH, and conductivity are stable.

6 Load sample onto the column.

7 Wash with 5 to 10 CV binding buffer or until the UV trace of the effluent returns to near base line.

8 Elute by linear gradient elution or a step elution:

- *Step elution*
  Elute with 2 to 5 CV elution buffer
- *Linear gradient elution*
  Elute with 0-100% elution buffer in 10 to 20 CV

9 Wash the column with 5 CV elution buffer.

10 Re-equilibrate the column with 5-10 CV binding buffer.

11 If required, clean the column, refer to Section *Cleaning-in-place (CIP).*

12 If required, perform a buffer exchange or a desalting of the collected eluted fractions. Refer to Table 5 for recommended columns.

3 Optimization

When optimizing binding conditions, one important parameter to check is the flow rate, as the residence time is important for binding capacity, see Figure 3 on page 8 and Figure 4 below.

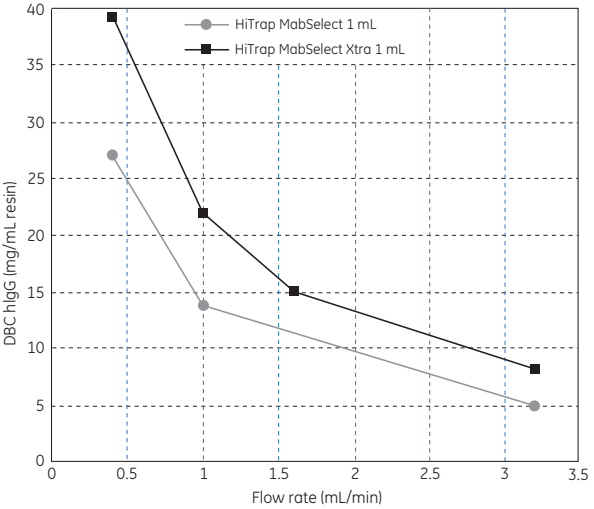

Fig 4. Dynamic binding capacity (DBC) versus flow rate for HiTrap MabSelect 1 mL and HiTrap MabSelect Xtra 1 mL. Sample: 1 mg/mL human IgG (hIgG) Gammanorm (Octapharma); Binding buffer: 20 mM phosphate, 150 mM NaCl, pH 7.4; Elution buffer: 100 mM sodium citrate, pH 3.0. Also see Figure 3 on page 8.

Optimizing elution conditions

When optimizing elution conditions, determine the highest pH that allows efficient elution of antibody from the column. This will prevent denaturing sensitive antibodies due to exposure to low pH.

Stepwise elution allows the target antibody to be eluted in a more concentrated form, thus decreasing buffer consumption and shortening cycle times. It might be necessary to decrease the flow rate due to the high concentrations of protein in the eluted pool.

Whatever conditions are chosen, HiTrap MabSelect and HiTrap MabSelect Xtra columns can be operated with a syringe, peristaltic pump, or chromatography system.

4 Removal of leached ligand from final product

The ligand leakage from MabSelect and MabSelect Xtra is generally very low. However, in some monoclonal antibody applications it is a requirement to eliminate leached ligand from the final product. There are a number of chromatographic solutions, such as cation exchange chromatography, anion exchange chromatography, or size exclusion chromatography.

The optimal conditions for removal of leached ligand must be evaluated for each individual antibody.

More details can be found in instructions for MabSelect (71502191) and MabSelect Xtra resins (11002602), available for download at www.gelifesciences.com/protein-purification.

5 Cleaning-in-place (CIP)

CIP is the removal of very tightly bound, precipitated or denatured substances from the resin. If such contaminants are allowed to accumulate, they can affect the chromatographic properties of the column, reduce the capacity of the resin and, potentially, come off in subsequent runs. If the fouling is severe, it can block the column, increase back pressure, and reduce flow rate.

Regular CIP prevents the buildup of contaminants and helps to maintain the capacity, flow properties, and general performance of HiTrap MabSelect and HiTrap MabSelect Xtra. When an increase in back pressure is seen, the column must be cleaned. We recommend performing a blank run, including CIP, before the first purification is started to wash out leached protein A.

The CIP protocols below must be used as guidelines for formulating a cleaning protocol specific for the sample applied to the column. The frequency of use will depend on the nature of the sample but it is recommended to use a CIP procedure at least every 5 cycles during normal use.

Depending on the nature of the contaminants, different protocols maybe have to be used in combination. If fouling is severe, the protocols maybe have to be further optimized.

To prevent cross-contamination between different antibodies, CIP must be done in between runs when the same column is used for purification of different antibodies.

Note: *The safest and fastest way to prevent cross-contamination is always to use a new column when starting to purify a new antibody.*

CIP protocol for precipitated or denatured substances using HiTrap MabSelect

1. Wash with 2 column volumes of 10 mM NaOH, contact time approx. 30 min.
2. Wash immediately with at least 5 column volumes of filtered binding buffer at pH 7 to 8.

or

1. Wash with 2 column volumes of 6 M guanidine hydrochloride, contact time approx. 10 min.
2. Wash immediately with at least 5 column volumes of filtered binding buffer at pH 7 to 8.

CIP protocol for hydrophobically bound substances using HiTrap MabSelect

1. Wash the column with 2 column volumes of a nonionic detergent (e.g., conc. 0.1%), contact time approx. 10 min.
2. Wash immediately with at least 5 column volumes of filtered binding buffer at pH 7 to 8.

or

1. Wash the column with 3 to 4 columns volumes of 70% ethanol, contact time approx. 10 min.
2. Wash immediately with at least 5 column volumes of filtered binding buffer at pH 7 to 8. Apply increasing gradients to avoid air bubble formation when using high concentrations of organic solvents.

or

1. Wash the column with 3 to 4 column volumes of 30% isopropanol, contact time approx. 10 min.
2. Wash immediately with at least 5 column volumes of filtered binding buffer at pH 7 to 8. Apply increasing gradients to avoid air bubble formation when using high concentrations of organic solvents.

CIP protocol for precipitated or denatured substances using HiTrap MabSelect Xtra

1. Wash with 2 column volumes of 50 mM NaOH in 1.0 M NaCl, contact time approx. 10 min.
2. Wash immediately with at least 5 column volumes of filtered binding buffer at pH 7 to 8.

or

1. Wash with 2 column volumes of 50 mM NaOH in 0.5 M Na_2SO_4, contact time approx. 10 min.
2. Wash immediately with at least 5 column volumes of filtered binding buffer at pH 7 to 8.

or

1. Wash with 2 column volumes of 6 M guanidine hydrochloride in 10 mM NaOH, contact time approx. 10 min.

2 Wash immediately with at least 5 column volumes of filtered binding buffer at pH 7 to 8.

CIP protocol for hydrophobically bound substances using HiTrap MabSelect Xtra

1 Wash the column with 2 column volumes of a nonionic detergent (e.g., conc. 0.1%), contact time approx. 10 min.

2 Wash immediately with at least 5 column volumes of filtered binding buffer at pH 7 to 8.

or

1 Wash the column with 3 to 4 column volumes of 70% ethanol, contact time approx. 10 min.

2 Wash immediately with at least 5 column volumes of filtered binding buffer at pH 7 to 8. Apply increasing gradients to avoid air bubble formation when using high concentrations of organic solvents.

or

1 Wash the column with 3 to 4 column volumes of 30% isopropanol, contact time approx. 10 min.

2 Wash immediately with at least 5 column volumes of filtered binding buffer at pH 7 to 8. Apply increasing gradients to avoid air bubble formation when using high concentrations of organic solvents.

6 Sanitization

Sanitization reduces microbial contamination of the chromatographic bed to a minimum.

Sanitization protocols for HiTrap MabSelect and HiTrap MabSelect Xtra

1. Equilibrate the column with 0.1 M acetic acid in 20% ethanol.
2. Allow to stand for 1 hour, and wash with at least 5 column volumes of sterile binding buffer.

or

1. Equilibrate the column with 70% ethanol.
2. Allow to stand for 12 hours, and wash with at least 5 column volumes of sterile binding buffer.

7 Scaling up

After optimizing the method at laboratory scale, the process is ready for scaling up. For quick small scale-up of purification, two or three HiTrap columns can be connected in series with a union (18112093) to give increased bed height.

Note: *The back pressure will increase when the columns are connected in series. This can easily be addressed by lowering the flow rate.*

Scaling up is typically performed by keeping bed height and linear flow velocity (cm/h) constant, while increasing bed diameter and volumetric flow rate (mL/min or L/h).

Factors such as clearance of critical impurities may change when column bed height is modified and should be validated using the final bed height.

Bulk resin is available for further scaling up, see *Ordering information*.

MabSelect and MabSelect Xtra belong to the BioProcess range of resins. BioProcess chromatography resins are developed and supported for production scale chromatography. BioProcess

resins are produced with validated methods and are tested to meet manufacturing requirements. Secure ordering and delivery routines give a reliable supply of resins for production scale. Regulatory Support Files (RSF) are available to assist process validation and submissions to regulatory authorities. BioProcess resins cover all purification steps from capture to polishing

A general description of the scaling up procedure is described below.

1. Select bed volume according to required sample load. Keep sample concentration constant.
2. Select column diameter to obtain the desired bed height. The excellent rigidity of the high flow base matrix allows for flexibility in choice of bed heights.
3. The larger equipment used when scaling up may cause some deviations from the method optimized at small scale. In such cases, check the buffer delivery and monitoring systems for time delays or volume changes.

8 Adjusting pressure limits

Pressure generated by the flow through a column affects the packed bed and the column hardware, see Fig 5. Increased pressure is generated when running/using one or a combination of the following conditions:

- High flow rates
- Buffers or sample with high viscosity
- Low temperature
- A flow restrictor

Note: *Exceeding the flow limit (see Table 2 and Table 3) can damage the column*

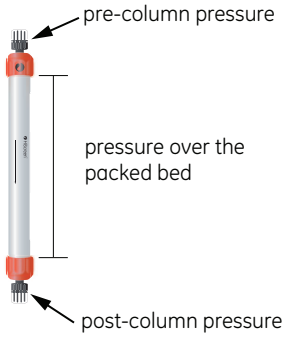

Fig 5. Pre-column and post-column measurements.

ÄKTA™ avant and ÄKTA pure

The system will automatically monitor the pressures (pre-column pressure and pressure over the packed bed, Δp). The pre-column pressure limit is the column hardware pressure limit (see Table 1).

The maximum pressure the packed bed can withstand depends on resin characteristics and sample/liquid viscosity. The measured value also depends on the tubing used to connect the column to the instrument.

ÄKTAexplorer, ÄKTApurifier, ÄKTAFPLC and other systems with pressure sensor in the pump

To obtain optimal functionality, adjust the pressure limit in the software according to the following procedure:

1. Replace the column with a piece of tubing. Run the pump at the maximum intended flow rate. Note the pressure as *total system pressure*, P1.
2. Disconnect the tubing and run the pump at the same flow rate used in step 1. Note that there will be a drip from the column valve. Note this pressure as P2.

3 Calculate the new pressure limit as a sum of P2 and the column hardware pressure limit (see Table 1). Replace the pressure limit in the software with the calculated value.

The actual pressure over the packed bed (Δp) will during run be equal to actual measured pressure - *total system pressure* (P1).

Note: *Repeat the procedure each time the parameters are changed.*

9 Storage

Store HiTrap MabSelect and HiTrap MabSelect Xtra in 20% ethanol at 2°C to 8°C.

10 Troubleshooting

Fault	Possible cause/corrective action
High back pressure during the run.	The column is clogged. Take a new column or perform a cleaning-in-place (CIP).
Unstable pressure curve during sample application.	Remove air bubbles that might have been trapped in the sample pump. De-gas the sample using a vacuum de-gasser.
Gradual broadening of the eluate peak.	Might be due to insufficient elution and CIP caused by contaminants accumulating in the column. Optimize the elution conditions, the CIP protocol and/or perform CIP more frequently.
Gradual decrease in yield.	Too high sample load. Decrease the sample load.
Precipitation during elution.	Optimize the elution conditions, the CIP protocol and/or perform CIP more frequently.
Gradual increase in CIP peaks.	Might be due to insufficient elution or CIP. Optimize the elution conditions, the CIP protocol and/or perform CIP more frequently.

Fault	Possible cause/corrective action
High ligand leakage during the first purifications.	Perform a blank run, including CIP, before the first purification cycle on a new column.

11 Ordering information

Product	Pack size	Product code
HiTrap MabSelect	5 × 1 mL	28408253
	1 × 5 mL	28408255
	5 × 5 mL	28408256
HiTrap MabSelect Xtra	5 × 1 mL	28408258
	1 × 5 mL	28408260
	5 × 5 mL	28408261

Related products	Pack size	Product code
MabSelect	25 mL	17519901
	200 mL[1]	17519902
MabSelect Xtra	25 mL	17526907
	200 mL[1]	17526902
MabSelect SuRe™	25 mL	17543801
	200 mL[1]	17543802
HiTrap MabSelect SuRe	1 × 1 mL	29049104
	5 × 1 mL	11003493
	1 × 5 mL	11003494
	5 × 5 mL	11003495
HiTrap Desalting	1 × 5 mL	29048684
	5 × 5 mL	17140801
	100 × 5 mL[2]	11000329
PD-10 Desalting Column	30	17085101
HiPrep 26/10 Desalting	1 × 53 mL	17508701
	4 × 53 mL	17508702

[1] Larger pack sizes are available.
[2] Pack size available by special order.

Accessories	Quantity	Product code
1/16" male/luer female *(For connection of syringe to top of HiTrap column)*	2	18111251
Tubing connector flangeless/M6 female (*For connection of tubing to bottom of HiTrap* column)	2	18100368
Tubing connector flangeless/M6 male *(For connection of tubing to top of HiTrap column)*	2	18101798
Union 1/16" female/M6 male *(For connection to original FPLC System through bottom of HiTrap column)*	6	18111257
Union M6 female /1/16" male *(For connection to original FPLC System through top of HiTrap column)*	5	18385801
Union luerlock female/M6 female	2	18102712
HiTrap/HiPrep, 1/16" male connector for ÄKTA design	8	28401081
Stop plug female, 1/16" *(For sealing bottom of HiTrap column)*	5	11000464
Fingertight stop plug, 1/16"	5	11000355

Literature	Product code
Antibody Purification Handbook	18103746
Solutions for antibody purification, Selection Guide	28935197
Affinity Chromatography Handbook, Principles and Methods	18102229
Affinity Chromatography Column and Media, Selection Guide	18112186

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