GE Healthcare
Life Sciences

Instructions 28-9339-49 AE **Prepacked columns**

HiScreen™ MabSelect SuRe™
HiScreen MabSelect SuRe LX
HiScreen MabSelect™
HiScreen MabSelect Xtra™

HiScreen MabSelect SuRe, HiScreen MabSelect SuRe LX, HiScreen MabSelect and HiScreen MabSelect Xtra are ready to use columns, prepacked with MabSelect SuRe, MabSelect SuRe LX, MabSelect and MabSelect Xtra media, respectively. These prepacked 4.7 ml columns are ideal for optimization of methods and parameters, such as selectivity, binding and elution conditions, as well as small scale purifications.

HiScreen MabSelect SuRe, HiScreen MabSelect SuRe LX, HiScreen MabSelect and HiScreen MabSelect Xtra columns provide fast, reproducible and easy separations in a convenient format. The columns are used in an optimal way with liquid chromatography systems such as ÄKTA™.

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Please read these instructions carefully before using the HiScreen columns.

Intended use
HiScreen 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, please refer to the Safety Data Sheet.

1 Product description

HiScreen column characteristics

HiScreen columns are made of biocompatible polypropylene that does not interact with biomolecules. The columns are delivered with stoppers at the inlet and outlet. The arrow on the column label indicates the column orientation and the recommended flow direction, see Figure 1.

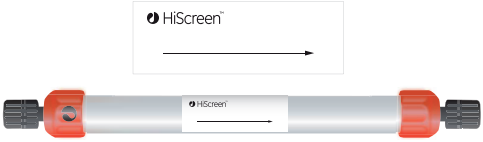

Fig 1. HiScreen column

For easy scaling-up and when a higher bed height is required, two columns can easily be connected in series using a union to give 20 cm bed height (see Section *Scaling up*).

Note: *HiScreen columns cannot be opened or refilled*

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

Table 1. Characteristics of HiScreen column

Column volume (CV)	4.7 ml
Column dimensions	0.77 × 10 cm
Column hardware pressure limit [1]	8 bar (0.8 MPa)

[1] The pressure over the packed bed varies depending on a range of parameters such as the characteristics of the chromatography medium and the column tubing used.

Properties of MabSelect media

MabSelect chromatography media are designed to tolerate high flow rates and high pressure with its specially developed base matrix. This in combination with low ligand leakage makes MabSelect media well suited for purification of monoclonal antibodies from lab to manufacturing. The protein A-derived ligand is produced in *Escherichia coli*. Fermentation and subsequent purification are performed in the absence of animal products.

The characteristics of the MabSelect SuRe, HiScreen MabSelect SuRe LX, MabSelect and MabSelect Xtra media are summarized in Table 2 and 3.

MabSelect SuRe

The protein A-derived ligand has been specially engineered to create an affinity medium with enhanced alkali stability and high binding capacity for IgG. The medium is stable in as high concentration as 0.5 M NaOH. The specificity of binding to the Fc region of IgG is similar to that of conventional protein A and provides excellent purification in one step.

MabSelect SuRe LX

This chromatography medium is optimized for high dynamic binding capacity for high titer cultures of antibodies. The medium is designed with the same alkali-tolerant, protein A-derived ligand as in MabSelect SuRe. This makes also this chromatography medium stable in as high concentration as 0.5 M NaOH.

Table 2. Characteristics of MabSelect SuRe and MabSelect SuRe LX

	MabSelect SuRe	MabSelect SuRe LX
Matrix	Rigid, highly cross-linked agarose	
Average particle size (d_{50v}) [1]	85 µm	85 µm
Ligand	Alkali-stabilized protein A-derived (*E. coli*)	
Ligand coupling method	Epoxy activation	Epoxy activation
Binding capacity	~ 30 mg human IgG/ml medium [2]	~ 60 mg human IgG/ml medium [3]
Recommended flow velocity [4]	120 to 250 cm/h	75 to 150 cm/h
Maximum flow velocity [4]	500 cm/h	500 cm/h
pH stability [5]		
Working range	3 to 12	3 to 12
Cleaning-in-place	2 to 14	3 to 13
Chemical stability	No significant change in chromatographic performance after 1 week storage using 8 M urea, 6 M guanidine hydrochloride, 2% benzyl alcohol or 20% ethanol	
Working temperature	4°C to 40°C	4°C to 40°C
Storage	2°C to 8°C in 20% ethanol	2°C to 8°C in 20% ethanol

1 d_{50v} is the average particle size of the cumulative volume distribution.

2 Determined at 10% breakthrough by frontal analysis at a mobile phase velocity of 500 cm/h in a column with a bed height of 20 cm, i.e. residence time is 2.4 min. Residence time is equal to bed height (cm) divided by nominal flow velocity (cm/h) during sample loading. Nominal flow velocity is equal to volumetric flow rate (ml/h) divided by column cross-sectional area (cm^2).

3 Determined at 10% breakthrough by frontal analysis at a mobile phase velocity of 100 cm/h in a column with a bed height of 10 cm, i.e. residence time is 6.0 min. Residence time is equal to bed height (cm) divided by nominal flow velocity (cm/h) during sample loading. Nominal flow velocity is equal to volumetric flow rate (ml/h) divided by column cross-sectional area (cm^2).

4 Water at room temperature.
For viscous buffers and samples the flow velocity must be optimized. Starting with a low flow rate is recommended.

5 Working range: pH interval where the medium can be handled without significant change in function.
Cleaning-in-place: pH interval where the medium can be subjected to cleaning-in-place without significant change in function.
pH below 3 is sometimes required to elute strongly bound antibody species. However protein ligands may hydrolyze at verey low pH.

MabSelect

The recombinant protein A has been specially engineered to favor an oriented coupling that gives an affinity chromatography medium 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 ensures low ligand leakage.

MabSelect Xtra

MabSelect Xtra addresses the increasing levels of expression found in monoclonal antibody feedstocks. The chromatography medium is engineered to give up to 30% higher dynamic binding capacity than other protein A based media. The recombinant protein A has been specially engineered to favor an oriented coupling that results in an 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.

Table 3. Characteristics of MabSelect and MabSelect Xtra

	MabSelect	MabSelect Xtra
Matrix	Rigid, highly cross-linked agarose	
Average particle size (d_{50v}) [1]	85 µm	75 µm
Ligand	Recombinant protein A (*E. coli*)	
Ligand coupling method	Epoxy activation	Epoxy activation
Binding capacity [2]	~ 30 mg human IgG/ml medium	~ 40 mg human IgG/ml medium
Recommended flow velocity [3]	120 to 250 cm/h	50 to 150 cm/h
Maximum flow velocity [3]	500 cm/h	300 cm/h
pH stability [4]		
Working range	3 to 10	3 to 10
Cleaning-in-place	2 to 12	2 to 12
Chemical stability	No significant change in chromatographic performance after 1 week storage using 8 M urea, 6 M guanidine hydrochloride, 2% benzyl alcohol or 20% ethanol	
Working temperature	4°C to 40°C	4°C to 40°C
Storage	2°C to 8°C in 20% ethanol	2°C to 8°C in 20% ethanol

1 d_{50v} is the average particle size of the cumulative volume distribution.

2 Determined at 10% breakthrough by frontal analysis at a mobile phase velocity of 500 cm/h (MabSelect) or 250 cm/h (MabSelect Xtra) in a column with a bed height of 20 cm (MabSelect) or 10 cm (MabSelect Xtra), i.e. residence time is 2.4 min. Residence time is equal to bed height (cm) divided by nominal flow velocity (cm/h) during sample loading. Nominal flow velocity is equal to volumetric flow rate (ml/h) divided by column cross-sectional area (cm^2).

3 Water at room temperature.
For viscous buffers and samples the flow velocity must be optimized. Starting with a low flow rate is recommended.

4 Working range: pH interval where the medium can be handled without significant change in function.
Cleaning-in-place: pH interval where the medium can be subjected to cleaning-in-place without significant change in function.
pH below 3 is sometimes required to elute strongly bound antibody species. However protein ligands may hydrolyze at verey low pH.

2 General process development

HiScreen column format is ideal to use for parameter and method optimization and for robustness testing when developing a new purification process. The small column volume, 4.7 ml, and the 10 cm bed height makes it possible to perform scalable experiments at relevant process flow rates. If necessary, two columns can easily be connected in series with a union to give 20 cm bed height (see Section *Scaling up*).

The figure below outlines typical steps during general process development.

Already from start in process development it is necessary to consider process cost, cleaning of the medium and environmental constraints.

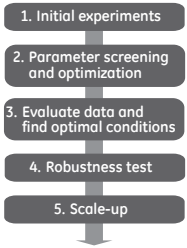

Fig 2. Typical steps during process development.

Design of Experiments (DoE) is an effective tool for investigating the effect of several parameters on protein recovery in order to establish the optimal purification protocol.

A common approach in DoE is to define a reference experiment (center point) and perform representative experiments around that point. Some initial experiments are required in order to define the center point and the variable ranges. DoE may be used for parameter screening and optimization as well as robustness testing.

The robustness of a process is a measure of its capacity to remain unaffected by small, but deliberate variations in method parameters, and provides an indication of its reliability during normal usage. An objective of a robustness test is the evaluation of factors potentially causing variability in the responses of the method, for example, purity and yield. For this purpose, small variations in method parameters are introduced.

For scale-up, see Section *Scaling up*.

3 Optimization

Preferred ligands

In general, most IgGs can be purified using protein A, but for some IgG, protein G is the preferred ligand. See Table 4 for relative binding strengths for protein A and protein G.

Optimizing elution

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. The pH of the eluted fractions is normally neutralized using a basic solution.

Step-wise 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.

Removal of leached protein A from final product

The ligand leakage from the MabSelect media is generally low. For example, MabSelect SuRe gives 5 to 20 ppm (ng ligand/mg antibody) of leached ligand in eluate. However, in some monoclonal antibody applications it is necessary to eliminate leached ligand from the final product.

A number of chromatographic solutions can be used for removal of leached ligand, such as ion exchange chromatography or gel filtration chromatography, but the proposed solution is to use Capto™ adhere, which is a medium designed for removal of contaminants after using MabSelect media.

The optimal conditions for removal of leached ligand must be evaluated for each individual antibody. For more details, please refer to www.gelifesciences.com/bioprocess or HiScreen Capto adhere instructions (28-9337-90).

Automated buffer preparation

Users of ÄKTA chromatography systems with BufferPrep or BufferPro functionality can select from a range of buffer recipes to conveniently screen media over a range of pH values and elution conditions.

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		+/-	++

* ++++ = strong binding; ++ = medium binding; - = weak or no binding

† Purify using HiTrap™ IgM and HiTrap IgY Purification HP columns, respectively.

4 Operation

Optimal conditions must be evaluated for each sample. Flow rate, buffer composition, pH, gradient elution, CIP conditions and length of each step are examples of factors that may effect purification.

Prepare buffers

The following buffers are recommended:

Start 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 media, an increased binding capacity will be achieved by including 2.5 M NaCl in the binding buffer.*

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

Prepare the sample

Step	Action
1	Adjust the sample to the composition of the start buffer, using one of these methods: • Dilute the sample with start buffer. • Exchange buffer using a HiPrep™ 26/10 Desalting, HiTrap™ Desalting or PD-10 Desalting column (see Table below).
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 longevity of the column when loading large sample volumes.

Table 5. Prepacked columns for desalting

Column	Code No.	Loading volume	Elution volume	Comments	Application
HiPrep 26/10 Desalting	17-5087-01	2.5 to 15 ml	7.5 to 20 ml	Prepacked with Sephadex™ G-25 Fine. Requires a laboratory pump or a chromatography system to run.	For desalting and buffer exchange of protein extracts (M_r > 5000).
HiTrap Desalting	17-1408-01	0.25 to 1.5 ml	1.0 to 2.0 ml	Prepacked with Sephadex G-25 Superfine. Requires a syringe or pump to run.	
PD-10 Desalting	17-0851-01	1.0 to 2.5 ml[1] 1.75 to 2.5 ml[2]	3.5 ml[1] up to 2.5 ml[2]	Prepacked with Sephadex G-25 Medium. Runs by gravity flow or centrifugation	For desalting, buffer exchange, and cleanup of proteins and other large biomolecules (M_r > 5000).
PD MiniTrap™ G-25	28-9180-07	0.1 to 0.5 ml[1] 0.2 to 0.5 ml[2]	1.0 ml[1] up to 0.5 ml[2]		
PD MidiTrap™ G-25	28-9180-08	0.5 to 1.0 ml[1] 0.75 to 1.0 ml[2]	1.5 ml[1] up to 1.0 ml[2]		

[1] Volumes with gravity elution
[2] Volumes with centrifugation

Recommended flow rates

Table 6. Recommended flow rates for HiScreen MabSelect columns. A lower flow rate is recommended for CIP.

Column type	Flow velocity (cm/h)	Flow rate (ml/min)
MabSelect	120 to 250	0.9 to 2
MabSelect Xtra	50 to 150	0.4 to 1.2
MabSelect SuRe	120 to 250	0.9 to 2
MabSelect SuRe LX	75 to 150	0.6 to 1.2

Purification

Flow rate: See Table 6 for recommended flow rates for the different MabSelect columns.

Column tubing: Choose the optimal tubing kit for the column and the application you intend to run. (i.d.: 0.25, 0.50 or 0.75 [mm]). A tubing with wider inner diameter gives broader peaks whereas a tubing with a smaller inner diameter gives higher back pressure.

Step	Action
1	Prepare collection tubes by adding 60 to 200 µl of 1 M Tris-HCl, pH 9.0 per ml of fraction to be collected.
2	Remove the stoppers and connect the column to the system. Avoid introducing air into the column. ***Note:*** *To prevent leakage, ensure that the connectors are tight. Use fingertight 1/16" connector (28-4010-81).*
3	Wash out the ethanol with at least 5 column volumes (CV) of distilled water or start buffer.
4	Equilibrate the column with 10 CV of start buffer at 2.3 or 3.9 ml/min (300 or 500 cm/h), see Table 6 above.
5	Load the sample onto the column.
6	Wash with 5 to 10 CV of start buffer or until the UV trace of the effluent returns to near baseline.

Step	Action
7	Elute, either by linear gradient elution or a step elution, see below. If required, the collected eluted fractions can be buffer exchanged or desalted using columns listed in Table 5. Collect fractions into tubes containing 60 to 200 µl of 1 M Tris-HCl, pH 9.0 per ml of fraction to be collected. • *Linear gradient elution* Elute with 0-100% elution buffer in 10 to 20 CV • *Step elution* Elute with 2 to 5 CV of elution buffer
8	Wash the column with 5 CV of elution buffer.
9	Wash the column with 3 CV of start buffer.
10	If required, perform a cleaning-in-place to clean the column, see Section *Cleaning-in-place (CIP)*.
11	Re-equilibrate the column with 5 to 10 CV of start buffer or until the UV baseline, eluent pH, and conductivity reach the required values. ***Note:*** *Do not exceed the maximum recommended flow and back pressure for the column.*

5 Cleaning-in-place (CIP)

General description

Correct preparation of samples and buffers should maintain columns in good condition. However, reduced performance, increased back pressure or blockage indicates that the column medium needs cleaning.

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

CIP should be performed regularly to prevent the build-up of contaminants and to maintain the capacity, flow properties and general performance of prepacked columns. CIP is usually performed after the elution.

It is recommended to perform a CIP:

- When an increase in back pressure is seen.
- If reduced column performance is observed.
- Before first time use or after long term storage.
- Between runs when the same column is used for purification of different proteins to prevent possible cross-contamination.
- After every run with real feed.

CIP protocols

The nature of the sample will ultimately determine the final CIP protocol so the CIP procedure below may require optimization. Concentration, contact time and frequency are typically the main parameters to vary during the optimization of the CIP. The CIP procedures below removes common contaminants.

Note: *Avoid the direct contact between low-pH elution buffer and high-pH NaOH solution on the column by equilibrating with, for example, binding buffer. (Mixing acid and alkaline solutions might cause a rise in temperature in the column).*

Note: *An acid regeneration (pH 3) before CIP is recommended if antibodies were not eluted completely.*

Flow rate: For increased contact time and due to the viscosity of the CIP solutions it is recommended to use a lower flow rate than during the purification.

HiScreen MabSelect SuRe and HiScreen MabSelect SuRe LX

These are alkali-tolerant chromatography media allowing the use of up to 0.5 M NaOH as CIP agent.

Step	Action
1	Wash the column with 3 column volumes (CV) of start buffer.
2	Wash with at least 2 CV of 0.1 to 0.5 M NaOH. Contact time 10 to 15 minutes.
3	Wash immediately with at least 5 CV of start buffer.

HiScreen MabSelect and HiScreen MabSelect Xtra

These media can withstand up to 50 mM NaOH and it is therefore recommended to use other cleaning agents as well.

To remove...	Then...
Precipitated or denaturated substances	1 Wash with 2 column volumes (CV) of 6 M guanidine hydrochloride, contact time at least 10 min. 2 Wash immediately with at least 5 CV of filtered start buffer at pH 7 to 8 or 1 2 CV of 50 mM NaOH in 1.0 M NaCl or 50 mM NaOH in 0.5 M Na_2SO_4, contact time approx. 10 min. 2 Wash immediately with at least 5 CV of filtered start buffer at pH 7 to 8.
Hydrophobically bound substances	1 Wash with 2 column volumes (CV) of a non-ionic detergent (e.g. conc. 0.1%), contact time approximately 10 min. 2 Wash immediately with at least 5 CV of start buffer at pH 7 to 8. or 1 3 to 4 CV of 70% ethanol or 30% isopropanol, contact time approximately 10 min. Increasing gradients may be applied to avoid air bubble formation when using high concentrations of organic solvents. 2 Wash immediately with at least 5 CV of start buffer at pH 7 to 8.

Sanitization

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

HiScreen MabSelect SuRe and HiScreen MabSelect SuRe LX

HiScreen MabSelect SuRe and HiScreen MabSelect SuRe LX are alkali-tolerant, allowing the use of up to 0.5 M NaOH as sanitizing agent. NaOH is very effective for inactivating viruses, bacteria, yeasts, and endotoxins.

Step	Action
1	Wash the column with 3 column volumes (CV) of start buffer.
2	Wash the column with 0.1 to 0.5 M NaOH. Use a contact time of at least 15 minutes (see the note below).
3	Wash immediately with at least 5 CV of sterile start buffer. ***Note:*** *Higher concentrations of NaOH and/or longer contact time inactivates micro-organisms more effectively. However, these conditions might also lead to a decrease in the dynamic binding capacity. The conditions for sanitization must be designed for efficient sanitization and minimized loss of capacity.*

HiScreen MabSelect and HiScreen MabSelect Xtra

Step	Action
1	Wash 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 (CV) of sterile start buffer.

or

Step	Action
1	Wash the column with 70% ethanol.
2	Allow to stand for 12 hours, and wash with at least 5 CV of sterile start buffer.

6 Scaling up

After optimizing the method at laboratory scale, the process is ready for scaling up.

For quick scale-up of purification, two HiScreen columns can easily be connected in series with a union (18-1120-93) to give 20 cm bed height. Note that the back pressure will increase. This can easily be addressed by lowering the flow rate.

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

Scale-up is typically performed by keeping bed height and flow velocity (cm/h) constant while increasing bed diameter and flow rate (ml/min or l/h).

Bulk media is available for further scale-up, see Section *Ordering information*.

7 Adjusting pressure limits in chromatography system software

Pressure generated by the flow through a column affects the packed bed and the column hardware, see Figure below. 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 3) may damage the column.*

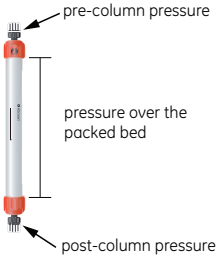

Fig 3. Pre-column and post-column measurements.

ÄKTA avant

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 media 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, the pressure limit in the software may be adjusted according to the following procedure:

Step	Action
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.*

8 Storage

Store HiScreen MabSelect SuRe, HiScreen MabSelect SuRe LX, HiScreen MabSelect and HiScreen MabSelect Xtra in 20% ethanol at 2°C to 8°C.

Do not freeze.

Ensure that the column is tightly sealed to avoid drying out.

9 Troubleshooting

Problem	Possible cause/*corrective action*
High back pressure during the run	The column is clogged. *Clean the column, see Section Cleaning-in-place (CIP).* High viscosity of solutions. *Use lower flow rate.*
Unstable pressure curve during sample loading	Air bubbles trapped in the sample pump. *If possible, degas the sample using a vacuum degasser.*
Gradual broadening of the eluate peak	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	Insufficient elution and CIP. *Optimize the elution conditions, the CIP protocol and/or perform CIP more frequently.*
Precipitation during elution	Sub-optimal elution conditions and CIP. *Optimize the elution conditions, the CIP protocol and/or perform CIP more frequently.*
Gradual increase in CIP peaks	Sub-optimal elution conditions and CIP. *Optimize the elution conditions, the CIP protocol and/or perform CIP more frequently.*
High back pressure during CIP	Proteins precipitated in column. *Optimize elution conditions and/or run acid regeneration (pH 3 or less) before CIP.* *Use lower flow rate.*
High ligand leakage during the first purifications	*Perform a blank run, including CIP, before the first purification cycle on a new column.*
Reduced column performance despite optimized elution and CIP	*Change to a new column. The longevity of the column depends mainly on the sample and sample preparation.*

10 Ordering information

Product	Quantity	Code No.
HiScreen MabSelect	1 × 4.7 ml	28-9269-73
HiScreen MabSelect Xtra	1 × 4.7 ml	28-9269-76
HiScreen MabSelect SuRe	1 × 4.7 ml	28-9269-77
HiScreen MabSelect SuRe LX	1 × 4.7 ml	17-5474-15

Related products	Quantity	Code No
HiTrap MabSelect	5 × 1 ml	28-4082-53
	1 × 5 ml	28-4082-55
	5 × 5 ml	28-4082-56
HiTrap MabSelect Xtra	5 × 1 ml	28-4082-58
	1 × 5 ml	28-4082-60
	5 × 5 ml	28-4082-61
HiTrap MabSelect SuRe	5 × 1 ml	11-0034-93
	1 × 5 ml	11-0034-94
	5 × 5 ml	11-0034-95
MabSelect	25 ml	17-5199-01
	200 ml [1]	17-5199-02
MabSelect Xtra	25 ml	17-5269-07
	200 ml [1]	17-5269-02
MabSelect SuRe	25 ml	17-5438-01
	200 ml [1]	17-5438-02
MabSelect SuRe LX	25 ml	17-5474-01
	200 ml [1]	17-5474-02

[1] Process-scale quantities are available. Please contact your local representative.

Related products	Quantity	Code No
HiTrap Desalting	5 × 5 ml	17-1408-01
HiPrep 26/10 Desalting	1 × 53 ml	17-5087-01
	4 × 53 ml	17-5087-02

Accessories HiScreen	Quantity	Code No
HiTrap/HiPrep, 1/16" male connector for ÄKTA systems *(For connection of columns with 1/16" fittings to ÄKTA systems)*	8	28-4010-81
Union 1/16" male/1/16" male with 0.5 mm i.d. *(For connecting two columns with 1/16" fittings in series)*	2	18-1120-93
Fingertight stop plug, 1/16" [1] *(For sealing a HiScreen column)*	5	11-0003-55

[1] One fingertight stop plug is connected to the inlet and the outlet of each HiScreen column at delivery.

Related literature	Code No.
Antibody Purification Handbook	18-1037-46
Affinity Chromatography Handbook, Principles and Methods	18-1022-29
Affinity Chromatography, Column and Media Selection Guide	18-1121-86
Prepacked chromatography columns for ÄKTA systems, Selection Guide	28-9317-78

For local office contact information, visit
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