Instructions 11-0026-18 AG

HiTrap™ Capto™ Q, 1 ml and 5 ml
HiTrap Capto ViralQ, 5 ml
HiTrap Capto S, 1 ml and 5 ml
HiTrap Capto DEAE, 1 ml and 5 ml

Capto Q, Capto S and Capto DEAE are ion exchange BioProcess™ media for capture and intermediate purification of proteins. HiTrap Capto Q, HiTrap Capto S and HiTrap Capto DEAE are prepacked 1 ml and 5 ml columns for screening of selectivity, binding and elution conditions, as well as small scale purifications.

Capto ViralQ is in all respects identical to Capto Q, but in addition it provides a license to be used for virus purification as described in the section "Product description", page 3. These instructions will not further discriminate between Capto Q and Capto ViralQ.

HiTrap Capto Q, Capto S and Capto DEAE 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™ systems, but can also be operated with a syringe or a peristaltic pump.

Table of contents

Please 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, please 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	5 bar (0.5 MPa)	5 bar (0.5 MPa)

Note: *The pressure over the packed bed varies depending on a range of parameters such as the characteristics of the chromatography medium, 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 or 2
Stop plug female, 1/16"	For sealing bottom of HiTrap column	2, 5 or 7

Medium properties

Capto Q, Capto S and Capto DEAE are high capacity, strong anion, strong cation and weak anion exchangers, respectively. The ligands, Q, S and DEAE, are coupled to a chemically modified, high flow agarose matrix. The high flow agarose matrix provides particle rigidity without compromising the pore size. In addition, dextran surface extenders coats the agarose matrix. This combination allows for fast mass transfer, resulting in high dynamic binding capacities of Capto Q, Capto S and Capto DEAE at high flow rates. This makes the media suitable for high volume process scale applications. The characteristics of Capto Q, Capto S and Capto DEAE are listed in Table 2, Table 3 and Table 4, respectively.

Table 2. Characteristics of Capto Q.

Matrix	High flow agarose with a dextran surface extender
Ion exchange type	Strong anion, Q
Charged group	$-N^+(CH_3)_3$
Total ionic capacity	0.16–0.22 mmol Cl^-/ml medium
Particle size[1]	90 µm (d_{50v})
Flow velocity	700 cm/h in a 1 m column with 20 cm bed height at 20°C using process buffers with the same viscosity as water at < 3 bar (0.3 MPa)
Dynamic binding capacity[2]	> 100 mg BSA/ml medium > 150 mg ovalbumin/ml medium
pH working range	2 to 12
pH stability[3]	
short term	2 to 14
long term	2 to 12
Working temperature	4°C to 30°C
Chemical stability	All commonly used aqueous buffers, 1 M acetic acid, 1 M NaOH[4], 8 M urea, 6 M guanidine hydrochloride, 30% isopropanol and 70% ethanol
Avoid	Oxidizing agents, anionic detergents
Storage	20% ethanol

[1] d_{50v} is the medium particle size of the cumulative volume distribution.

[2] Dynamic binding capacity at 10% breakthrough as measured at a residence time of 1 min, 600 cm/h in a Tricorn™ 5/100 column with 10 cm bed height in a 50 mM Tris-HCl buffer, pH 8.0.
Note: *1 min residence time corresponds to 1 ml/min (HiTrap 1 ml), 5 ml/min (HiTrap 5 ml).*

[3] **Short term pH:** pH interval where the medium can be subjected to cleaning- or sanitization in-place without significant change in function.
Long term pH: pH interval where the medium can be operated without significant change in function.

[4] No significant change in dynamic binding capacity and carbon content after 1 week storage in 1 M NaOH at 40°C.

Table 3. Characteristics of Capto S.

Matrix	High flow agarose with a dextran surface extender
Ion exchange type	Strong cation, S
Charged group	$-SO^{3-}$
Total ionic capacity	0.11–0.14 mmol Na^+/ml medium
Particle size[1]	90 µm (d_{50v})
Flow velocity	700 cm/h in a 1 m column with 20 cm bed height at 20°C using process buffers with the same viscosity as water at < 3 bar (0.3 MPa)
Dynamic binding capacity[2]	> 120 mg lysozyme/ml medium
pH working range	4 to 12
pH stability[3]	
short term	3 to 14
long term	4 to 12
Working temperature[4]	4°C to 30°C
Chemical stability	All commonly used aqueous buffers, 1 M NaOH[5], 8 M urea, 6 M guanidine hydrochloride, 30% isopropanol and 70% ethanol
Avoid	Oxidizing agents, cationic detergents, long exposure (1 week, 40°C) to pH < 3
Storage	0.2 M sodium acetate in 20% ethanol

[1] d_{50v} is the median particle size of the cumulative volume distribution.

[2] Dynamic binding capacity at 10% breakthrough as measured at a residence time of 1 min, 600 cm/h in a Tricorn 5/100 column with 10 cm bed height, in a 30 mM Na-phosphate buffer, pH 6.8.
Note: *1 min residence time corresponds to 1 ml/min (HiTrap 1 ml), 5 ml/min (HiTrap 5 ml).*

[3] **Short term pH**: pH interval where the medium can be subjected to cleaning- or sanitization in-place without significant change in function.
Long term pH: pH interval where the medium can be operated without significant change in function.

[4] Low temperature can decrease capacity of Capto S.

[5] No significant change in dynamic binding capacity and carbon content after 1 week storage in 1 M NaOH at 40°C.

Table 4. Characteristics of Capto DEAE.

Matrix	High flow agarose with a dextran surface extender
Ion exchange type	Weak anion, DEAE
Charged group	$-N^+H(CH_2CH_3)_2$
Total ionic capacity	0.29–0.35 mmol Cl^-/ml medium
Particle size[1]	90 µm (d_{50v})
Flow velocity	700 cm/h in a 1 m column with 20 cm bed height at 20°C using process buffers with the same viscosity as water at < 3 bar (0.3 MPa)
Dynamic binding capacity[2]	> 90 mg ovalbumin/ml medium
pH working range[3]	2 to 9. *See* titration curve, Fig 3
pH stability[4]	
short term	2 to 14
long term	2 to 12
Working temperature[5]	4°C to 30°C
Chemical stability	All commonly used aqueous buffers, 1 M acetic acid, 1 M NaOH[6], 8 M urea, 6 M guanidine hydrochloride, 30% isopropanol and 70% ethanol
Avoid	Oxidizing agents, anionic detergents,
Storage	20% ethanol

[1] d_{50v} is the median particle size of the cumulative volume distribution.

[2] Dynamic binding capacity at 10% breakthrough as measured at a residence time of 1 min, 600 cm/h in a Tricorn 5/100 column with 10 cm bed height, in a 50 mM Tris-HCl buffer, pH 8.0.

Note: *1 min residence time corresponds to 1 ml/min (HiTrap 1 ml), 5 ml/min (HiTrap 5 ml).*

[3] The recommended working pH range for DEAE ion exchangers is for most protein separations the optimal. DEAE media, although predominantly weak anion exchangers, are not possible to fully discharge by raising the pH due to a minor content of quaternarized amine groups. It is therefore possible to use DEAE media at higher pH values for separations of e.g. highly charged species as nucleotides.

[4] **Short term pH:** pH interval where the medium can be subjected to cleaning- or sanitization in- place without significant change in function.
Long term pH: pH interval where the medium can be operated without significant change in function.

[5] Low temperature can decrease capacity of Capto DEAE.

[6] No significant change in dynamic binding capacity and carbon content after 1 week storage in 1 M NaOH at 40°C.

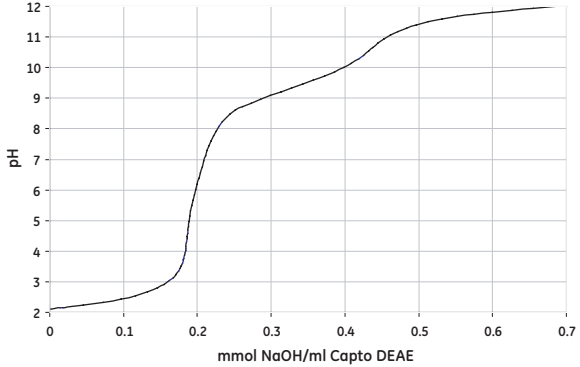

Fig 3. Titration curve for Capto DEAE. Capto DEAE has both weak and strong ion exchange properties. At pH ~ 5 most of the weak ion exchange ligands are protonated and positively charged. With increasing pH the ligands will gradually lose bound protons and thus charge. At a pH between 10 and 11 all weak ion exchange ligands are uncharged and only permanently positively charged quaternary ammonium groups remains.

2 Performing a separation

Sample preparation

Adjust the sample to the composition of the start buffer by buffer exchange using HiTrap Desalting or HiPrep™ 26/10 Desalting columns, *see* Table 5. Before application to the column, the samples can be centrifuged or filtered through a 0.45 µm filter.

Sample preparation without clarification of sample

The following sample preparation procedure is aimed to give a sample, sufficiently homogenized to be applied directly to the column without prior clarification. The protocol below has been used successfully in our own laboratories, but other established procedures may also work.

1. Dilution of cell paste: Add 5–10 ml of start buffer for each gram of cell paste.
2. **Enzymatic lysis:** 0.2 mg/ml lysozyme, 20 µg/ml DNAse, 1 mM $MgCl_2$, 1 mM Pefabloc™ SC or PMSF (final concentrations). Stir for 30 min at room temperature or 4°C depending on the sensitivity of the target protein.
3. **Mechanical lysis:** Sonication on ice for approx. 10 min, homogenization with a French press or other homogenizer or freeze/thaw, repeated at least five times.

   Mechanical lysis time may have to be extended compared with standard protocols to secure an optimized lysate for sample loading (to prevent clogging of the column and back pressure problems). Different proteins have different sensitivity to cell lysis and care must be taken to avoid frothing and overheating of the sample.
4. Adjust the pH of the lysate. The pH should be at least 0.5 units below (cation exchangers) or 0.5 units above (anion exchangers) the pI of the target molecule. Do not use strong bases or acids for pH-adjustment (precipitation risk). Apply the unclarified lysate on the column directly after preparation.

Note: *If the sonicated or homogenized unclarified cell lysate is frozen before use, precipitation and aggregation may increase. New sonication of the lysate can then prevent increased back pressure problems when loading on the column.*

Table 5. Prepacked columns for desalting and buffer exchange

Column	Code No.	Loading volume	Elution volume	Comments	Application
HiPrep 26/10 Desalting	17-5087-01	2.5–15 ml	7.5–20 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	0.25–1.5 ml	1.0–2.0 ml	Prepacked with Sephadex G-25 Superfine. Requires a syringe or pump to run.	
PD-10 Desalting	17-0851-01	1.0–2.5 ml[1] 1.75–2.5 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– 0.5 ml[1] 0.2–0.5 ml[2]	1.0 ml[1] Up to 0.5 ml[2]		
PD MidiTrap™ G-25	28-9180-08	0.5–1.0 ml[1] 0.75–1.0 ml[2]	1.5 ml[1] Up to 1.0 ml[2]		

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

Choice of start and elution buffer

The elution buffer is usually of the same composition and pH as the start buffer, but it contains additional salt, most often sodium chloride. The pH of the start buffer should be at least 0.5–1 pH unit above the pI of the target molecule when using an anion exchanger and at least 0.5-1 pH unit below the pI when using a cation exchanger.

The buffer species and buffer concentration are important for reproducible and robust methods. Table 6 and Table 7 show suitable buffers for anion and cation exchangers, respectively, and suggested starting concentrations. The buffer concentration should be at least 10 mM, and only rarely above 100 mM.

For samples with unknown charge properties, try the following:

Anion exchange (Q and DEAE)

Start buffer: 20 mM Tris-HCl, pH 8.0

Elution buffer: 20 mM Tris-HCl, 1 M NaCl, pH 8.0

Cation exchange (S)

Start buffer: 50 mM sodium acetate, pH 5.0

Elution buffer: 50 mM sodium acetate, 1 M NaCl, pH 5.0

or

Start buffer: 50 mM MES, pH 6.0

Elution buffer: 50 mM MES, 1 M NaCl, pH 6.0

Table 6. Buffers for anion exchange chromatography.

pH interval	Substance	Conc. (mM)	Counter-ion	pK_a (25°C)[1]
4.3–5.3	N-Methylpiperazine	20	Cl^-	4.75
4.8–5.8	Piperazine	20	Cl^- or $HCOO^-$	5.33
5.5–6.5	L-Histidine	20	Cl^-	6.04
6.0–7.0	Bis-Tris	20	Cl^-	6.48
6.2–7.2	Bis-Tris propane	20	Cl^-	6.65
8.6–9.6	Bis-Tris propane	20	Cl^-	9.10
7.3–8.3	Triethanolamine	20	Cl^- or CH_3COO^-	7.76
7.6–8.6	Tris	20	Cl^-	8.07
8.0–9.0	N-Methyldiethanolamine	20	SO_4^{2-}	8.52
8.0–9.0	N-Methyldiethanolamine	50	Cl^- or CH_3COO^-	8.52
8.4–9.4	Diethanolamine	20 at pH 8.4 50 at pH 8.8	Cl^-	8.88
8.4–9.4	Propane 1,3-diamino	20	Cl^-	8.88
9.0–10.0	Ethanolamine	20	Cl^-	9.50
9.2–10.2	Piperazine	20	Cl^-	9.73
10.0–11.0	Propane 1,3-diamino	20	Cl^-	10.55
10.6–11.6	Piperidine	20	Cl^-	11.12

[1] Handbook of chemistry and physics, 83rd edition, CRC, 2002–2003.

Table 7. Buffers for cation exchange chromatography

pH interval	Substance	Conc. (mM)	Counter-ion	pK_a (25°C)[1]
1.4–2.4	Maleic acid	20	Na^+	1.92
2.6–3.6	Methyl malonic acid	20	Na^+ or Li^+	3.07
2.6–3.6	Citric acid	20	Na^+	3.13
3.3–4.3	Lactic acid	50	Na^+	3.86
3.3–4.3	Formic acid	50	Na^+ or Li^+	3.75
3.7–4.7	Succinic acid	50	Na^+	4.21
5.1–6.1	Succinic acid	50	Na^+	5.64
4.3–5.3	Acetic acid	50	Na^+ or Li^+	4.75
5.2–6.2	Methyl malonic acid	50	Na^+ or Li^+	5.76
5.6–6.6	MES	50	Na^+ or Li^+	6.27
6.7–7.7	Phosphate	50	Na^+	7.20
7.0–8.0	HEPES	50	Na^+ or Li^+	7.56
7.8–8.8	BICINE	50	Na^+	8.33

[1] Handbook of chemistry and physics, 83rd edition, CRC, 2002.2003.

First time use or after long term storage

Flow: 1 ml/min (HiTrap 1 ml), 5 ml/min (HiTrap 5 ml).

1. Remove the stopper and connect the column to the system (or syringe) with a drop-to-drop connection to avoid introducing air into the column.
2. Remove the snap-off end at the column outlet and wash with 1 column volume of distilled water. This step ensures removal of ethanol and avoids the precipitation of buffer salts upon exposure to ethanol. The step can be omitted if precipitation is not likely to be a problem.
3. Wash with 5 column volumes of start buffer.
4. Wash with 5 column volumes of elution buffer.
5. Wash with 5 column volumes of start buffer.

Separation by gradient elution

Linear ionic strength gradients should always be used for method development or when starting with an unknown sample. Linear ionic strength gradients are easy to prepare and very reproducible when generated by a suitable chromatography system. The results obtained can then serve as a base from which to optimize the separation.

Flow: 1 ml/min (HiTrap 1 ml), 5 ml/min (HiTrap 5 ml). Collect fractions throughout the separation.

1. Equilibrate the column with at least 5 column volumes of start buffer for Capto Q and Capto S and at least 10 column volumes of start buffer for Capto DEAE or until the UV baseline, eluent pH and conductivity are stable.
2. Adjust the sample to the chosen starting pH and conductivity and apply to the column.
3. Wash with 5–10 column volumes of start buffer or until no material appears in the effluent.
4. Begin elution using a gradient volume of 10–20 column volumes and an increasing salt concentration up to 0.5 M NaCl (50% elution buffer).
5. Wash with 5 column volumes of 1 M NaCl (100% elution buffer) to elute any remaining ionically bound material.
6. Re-equilibrate with 5–10 column volumes of start buffer or until the UV baseline, eluent pH, and conductivity reach the required values.

Screening of selectivity

HiTrap columns are a convenient format for screening the selectivity of different ion exchange media.

3 Optimization

Screening for optimal loading conditions

Scout for optimal loading conditions by testing a range of pH values within which the target protein is known to be stable. If the isoelectric point of the target protein is known, then begin with a narrower pH range, for example, 0.5–1 pH unit away from the isoelectric point. In some cases the sample conductivity is equally important as the pH when scouting for optimal loading conditions. We therefore also recommend to scout for optimal ionic strength by varying the conductivity of the sample between 2–15 mS/cm.

Users of ÄKTA design systems with BufferPrep functionality can select from a range of buffer recipes to test media over a range of pH values and elution conditions.

Flow: 1 ml/min (HiTrap 1 ml), 5 ml/min (HiTrap 5 ml). Collect fractions throughout the separation.

1 Decide what pH values and conductivities are to be investigated. Prepare samples according to this.

2 Start buffers: set up a series of buffers with pH values in the range 5–9 (Capto Q and Capto DEAE) or 4–8 (Capto S) and with 0.5–1 pH unit intervals between each buffer. *See* Table 6 and Table 7 for recommended buffers. Where the conductivity of the buffers should be considered, it can either be adjusted by increasing the buffer concentration or adding sodium chloride.

3 Elution buffers: set up a second series of buffers with the same pH values, but including 1 M NaCl.

4 Equilibrate with at least 5 column volumes of start buffer for Capto Q and Capto S and at least 10 column volumes of start buffer for Capto DEAE or until the UV baseline, eluent pH and conductivity are stable.

5 Apply a known amount of the sample.

6 Wash with at least 5 column volumes of start buffer or until no material appears in the effluent.

7 Elute bound material with elution buffer (3–5 column volumes is usually sufficient, but other volumes may be required dependent on the exact experimental conditions).

8 Analyze all fractions (for example by an activity assay) and determine purity and the amount bound to the column.

9 Perform steps 4–8 for the next buffer pH.

10 Select pH and conductivity: the most suitable buffer should a) allow the target protein to bind and b) recover the protein with as high purity as possible.

Note: *For Capto S and Capto DEAE the dynamic binding capacities for certain proteins decrease at lower temperatures. Screening for buffer concentration will give the optimal dynamic binding capacity at a given temperature.*

Separation by step elution

Reduce separation time and buffer consumption by transferring to a step elution.

Flow: 1 ml/min (HiTrap 1 ml), 5 ml/min (HiTrap 5 ml). Collect fractions throughout the separation.

1 Equilibrate the column with at least 5 column volumes of start buffer for Capto Q and Capto S and at least 10 column volumes of start buffer for Capto DEAE or until the UV baseline, eluent pH, and conductivity are stable.

2 Adjust the sample to the chosen starting pH and conductivity and apply to the column.

3 Wash with 5–10 column volumes of start buffer or until no material appears in the effluent.

4 Elute with 5 column volumes of start buffer including NaCl at chosen concentration.

5 Repeat step 4 at higher NaCl concentrations until the target protein has been eluted.

6 Wash with 5 column volumes of a high salt solution (1 M NaCl in start buffer) to elute any remaining ionically bound material.

7 Re-equilibrate with 5–10 column volumes of start buffer or until the UV baseline, eluent pH, and conductivity reach the required values.

Save time by using higher flow rates during the high salt wash and re-equilibration steps. Do not exceed the maximum recommended flow and back pressure for the column.

Further optimization

HiTrap columns are best suited for initial screening of binding and elution conditions, further optimization is preferably done on a larger column such as Tricorn and XK columns.

4 Cleaning

Correct preparation of samples and buffers, including a high salt wash (1–2 M NaCl) after each separation, should maintain columns in good condition. However, reduced performance, increased back pressure or blockage indicates that the medium needs cleaning.

The following procedure removes common contaminants:

Flow: 1 ml/min (HiTrap 1 ml), 5 ml/min (HiTrap 5 ml),

1 Wash with at least 2 column volumes of 2 M NaCl.

2 Wash with at least 4 column volumes of 1 M NaOH.

3 Wash with at least 2 column volumes of 2 M NaCl.

4 Rinse with at least 2 column volumes of distilled water.

5 Wash with 5 column volumes of start buffer for Capto Q and Capto S and at least 10 column volumes of start buffer for Capto DEAE or until eluent pH and conductivity have reached the required values.

Note: *For some contaminants a more rigorous CIP procedure can be required for Capto DEAE than for Capto Q and Capto S. For more details, see instructions "Capto S, Capto Q, Capto ViralQ, Capto DEAE", code number 28-4074-52.*

5 Storage

Wash with 2 column volumes of distilled water followed by 2 column volumes of 20% ethanol (Capto Q and Capto DEAE) or 20% ethanol containing 0.2 M sodium acetate (Capto S). Store at 4°C to 30°C. Do not freeze. Ensure that the column is sealed well to avoid drying out.

6 Adjusting pressure limits in chromatography system software

Pressure generated by the flow through a column affects the packed bed and the column hardware, see Fig 4. 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 Tables 2 to 4) may damage the column.*

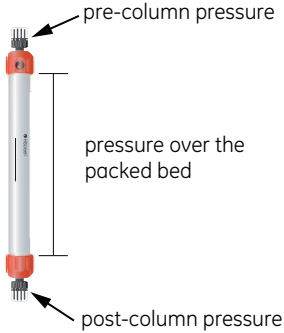

Fig 4. Pre-column and post-column measurements.

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:

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.*

7 Ordering information

Product	Quantity	Code No.
HiTrap Capto Q	5 × 1 ml	11-0013-02
	5 × 5 ml	11-0013-03
HiTrap Capto ViralQ	5 × 5 ml	28-9078-09
HiTrap Capto S	5 × 1 ml	17-5441-22
	5 × 5 ml	17-5441-23
HiTrap Capto DEAE	5 × 1 ml	28-9165-37
	5 × 5 ml	28-9165-40

Related Products	Quantity	Code No.
Capto Q[1]	25 ml	17-5316-10
	100 ml	17-5316-02
	1 L	17-5316-03
Capto ViralQ[1]	25 ml	28-9032-30
Capto S[1]	25 ml	17-5441-10
	100 ml	17-5441-01
Capto DEAE[1]	25 ml	17-5443-10
	100 ml	17-5443-01
	1 L	17-5443-03
HiTrap Desalting	1 × 5 ml	29-0486-84
	5 × 5 ml	17-1408-01
HiPrep 26/10 Desalting	1 × 53 ml	17-5087-01
	4 × 53 ml	17-5087-02

[1] Capto Q, Capto ViralQ, Capto S and Capto DEAE are available in process scale quantities. Please contact your local representative.

Accessories	Quantity	Code No.
1/16" male/luer female *(For connection of syringe to top of HiTrap column)*	2	18-1112-51
Tubing connector flangeless/M6 female *(For connection of tubing to bottom of HiTrap column)*	2	18-1003-68
Tubing connector flangeless/M6 male *(For connection of tubing to top of HiTrap column)*	2	18-1017-98
Union 1/16" female/M6 male *(For connection to original FPLC System through bottom of HiTrap column)*	6	18-1112-57
Union M6 female /1/16" male *(For connection to original FPLC System through top of HiTrap column)*	5	18-3858-01
Union luerlock female/M6 female	2	18-1027-12
HiTrap/HiPrep, 1/16" male connector for ÄKTA design	8	28-4010-81
Stop plug female, 1/16" *(For sealing bottom of HiTrap column)*	5	11-0004-64
Fingertight stop plug, 1/16"	5	11-0003-55

Literature	Code No.
Data File: Capto Q Capto ViralQ, Capto S and Capto DEAE	11-0025-76
Handbook: Ion Exchange Chromatography & Chromatofocusing, Principles and Methods	11-0004-21
Ion Exchange Chromatography Columns and Media, Selection Guide	18-1127-31

For your local office contact information, visit
www.gelifesciences.com/contact

GE Healthcare Bio-Sciences AB
Björkgatan 30
751 84 Uppsala
Sweden

www.gelifesciences.com/hitrap
www.gelifesciences.com/protein-purification

GE Healthcare Europe GmbH
Munzinger Strasse 5,
D-79111 Freiburg,
Germany

GE Healthcare UK Ltd
Amersham Place
Little Chalfont
Buckinghamshire, HP7 9NA
UK

GE Healthcare Bio-Sciences Corp
800 Centennial Avenue
P.O. Box 1327
Piscataway, NJ 08855-1327
USA

GE Healthcare Bio-Sciences KK
Sanken Bldg.
3-25-1, Hyakunincho
Shinjuku-ku, Tokyo 169-0073
Japan

11-0026-18 AG 03/2014