GE Healthcare
Life Sciences

Fisher Scientific

HiTrap–convenient protein purification

Column Guide

HiTrap

Ion Exchange Chromatography (IEX)

IEX separates proteins with differences in charge. The separation is based on the reversible interaction between a charged protein and an oppositely charged chromatographic medium. Proteins bind as they are loaded onto a column. Conditions are then altered so that bound substances are eluted differentially. This elution is usually performed by increases in salt concentration or changes in pH. Most commonly, samples are eluted with salt (NaCl), using a gradient elution, as shown in Figure 1. Target proteins are concentrated during binding and collected in a purified, concentrated form.

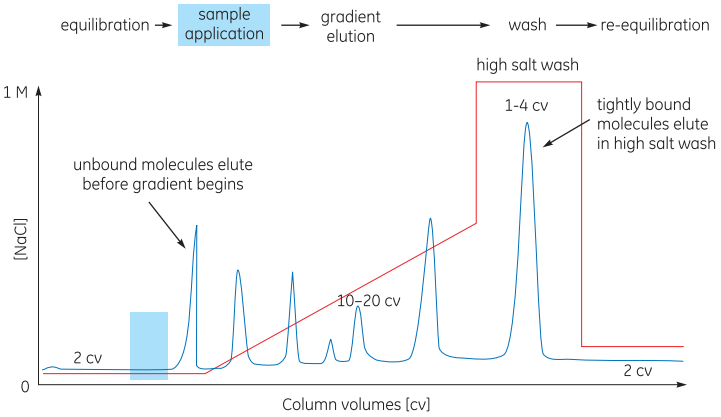


Fig 1. Typical IEX gradient elution.

Choice of ion exchanger

For most purifications it is recommended to begin with a strong exchanger to allow work over a broad pH range during method development.

Strong ion exchangers

Q (anion exchange), S or SP (cation exchange) are fully charged over a broad pH range (pH 2–12).

Weak ion exchangers

DEAE or ANX (anion exchange) and CM (cation exchange) are fully charged over a narrower pH range (pH 2–9, pH 3–10 and pH 6–10, respectively), but give alternative selectivities.

Media selection

HiTrap™ IEX Selection Kit, including seven different IEX media, is used for fast screening of IEX ligands and for method optimization.

See also *Ion Exchange Columns and Media Guide*, 18-1127-31.

Optimization parameters

1. Select ion exchanger.
2. Scout for optimum pH.
3. Select steepest gradient to give acceptable resolution at selected pH.
4. Select highest flow rate that maintains resolution and minimizes separation time.
5. For small scale sample clean up or large scale purifications, transfer to step elution to reduce separation times and buffer consumption, as shown in Figure 2. The different HiTrap IEX columns are ideal for small scale sample clean up.

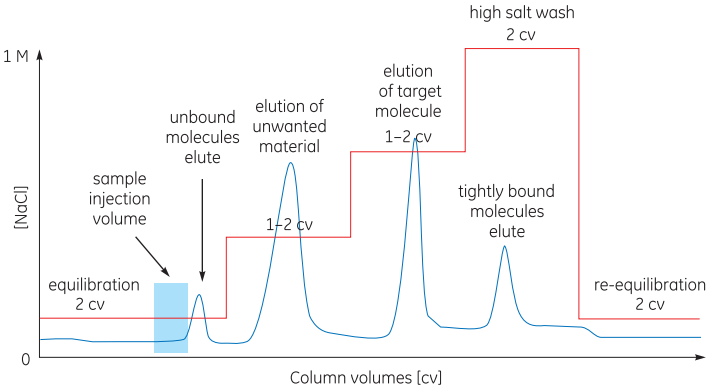


Fig 2. Typical IEX step elution.

Hydrophobic Interaction Chromatography (HIC)

HIC separates proteins with differences in hydrophobicity. The separation is based on the reversible interaction between a protein and the hydrophobic surface of a chromatographic medium. This interaction is enhanced by high ionic strength buffer, which makes HIC an ideal "next step" for purification of proteins that have been precipitated with ammonium sulphate or eluted in high salt during IEX. Samples in high ionic strength solution (e.g., 1.5 M $(NH_4)_2SO_4$) bind as they are loaded onto a column. Conditions are then altered so that the bound substances are eluted differentially. Elution is usually performed by decreases in salt concentration. Changes are made stepwise or with a continuously decreasing salt gradient. Most commonly, samples are eluted with a decreasing gradient of ammonium sulphate concentration. The key stages in a separation are shown in Figure 3. Target proteins are concentrated during binding and collected in a purified, concentrated form.

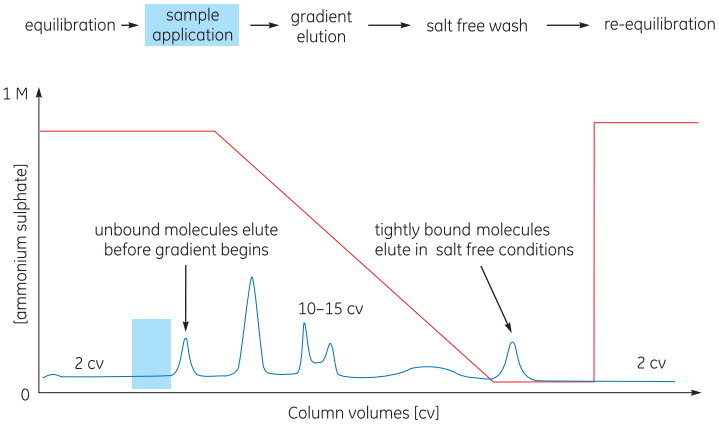


Fig 3. Typical HIC gradient elution.

Choice of hydrophobic ligand and media selection

The hydrophobicity of a protein is difficult to determine. It is recommended to screen for the most suitable media for each application using HiTrap HIC Selection Kit.

Available hydrophobic ligands vary according to their degree of hydrophobicity:

Increasing hydrophobicity →

ether → isopropyl → butyl → octyl → phenyl

Highly hydrophobic proteins bind tightly to highly hydrophobic ligands. Note that with HIC the chromatographic matrix as well as the hydrophobic ligand can affect selectivity.

Begin with a medium of low hydrophobicity if the sample is known to have hydrophobic components.

Select the medium that gives the best resolution and loading capacity at a low salt concentration.

See also *RPC & HIC Columns and Media Guide*, 18-1149-96.

Optimization parameters

1. Select medium.
2. Select optimum gradient to give acceptable resolution. For unknown samples begin with 0%B–100%B (0%B = 1 M ammonium sulphate).
3. Select highest flow rate that maintains resolution and minimizes separation time.
4. For large scale purifications, transfer to step elution to reduce separation times and buffer consumption, as shown in Figure 4.

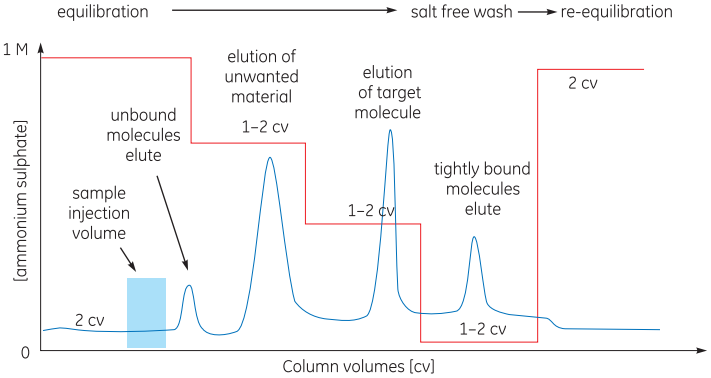


Fig 4. Typical HIC step elution.

Affinity Chromatography (AC)

AC separates proteins on the basis of a reversible interaction between a protein (or group of proteins) and a specific ligand attached to a chromatographic matrix. AC can be used whenever a suitable ligand is available.

The target protein(s) is specifically and reversibly bound by a complementary binding substance (ligand). The sample is applied under conditions that favor specific binding to the ligand. Unbound material is washed away, and the bound target protein is recovered by changing conditions to those favouring desorption. Elution is performed specifically, using a competitive ligand, or non specifically, by changing the pH, ionic strength or polarity. Proteins are concentrated during binding and collected in a purified, concentrated form. The key stages in a separation are shown in Figure 5.

One important application using AC is purification of tagged recombinant proteins, for example histidine-, GST-, MBP-, and/or Strep(II)-tagged..

AC may also be used to remove specific contaminants. For example, HiTrap Benzamidine FF (high sub) removes trypsin-like serine proteases.

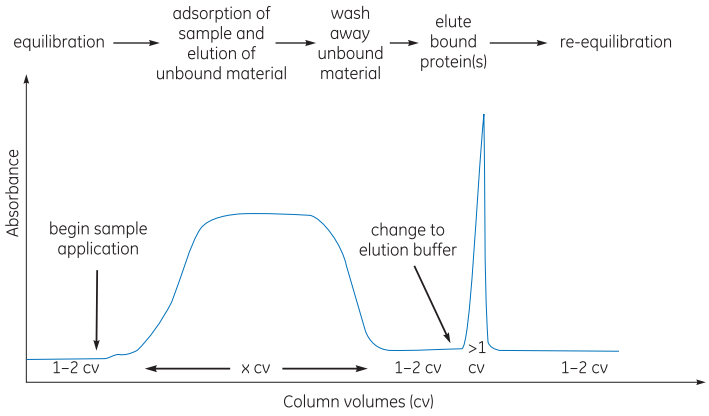


Fig 5. Typical affinity separation.

Media selection

Parameters such as scale of purification and commercial availability of affinity matrices should be considered when selecting affinity media.

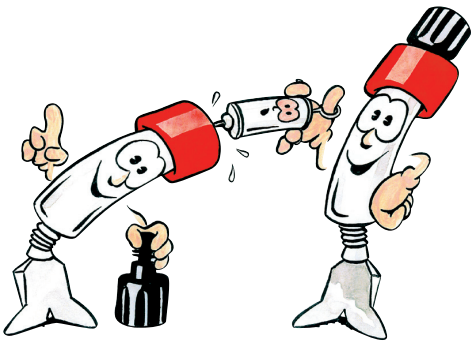
HiTrap affinity columns are ideal for method optimization or small scale purification of target proteins using well-established protocols.

Affinity media can be prepared by coupling a ligand to a selected gel matrix. HiTrap NHS-activated HP is designed specifically to facilitate this process and is supplied with a recommended coupling procedure for coupling primary amines.

See also *Affinity Chromatography Columns and Media Guide*, 18-1121-86.

Optimization parameters

1. Select correct specificity for target protein.
2. Follow manufacturer's recommendations for binding or elution conditions.
3. Select optimum flow rate for sample application to achieve efficient binding.
4. Select optimum flow rate for elution to maximize recovery.
5. Select maximum flow rate for column re-equilibration to minimize run times.



Gel Filtration Chromatography (GF)

Gel filtration (size exclusion) chromatography separates proteins with differences in molecular size. Samples are eluted isocratically (single buffer, no gradient). Since buffer composition does not directly affect resolution, the buffer conditions can be varied to suit the sample type or the requirements for the next purification, analysis or storage step. Proteins are collected in purified form in the chosen buffer.

Sample clean up

Sephadex™ G-25, is ideal for rapid clean up of protein samples.

HiTrap Desalting columns (prepacked with Sephadex G-25) enable fast sample clean up in less than 5 minutes for sample volumes from 0.25 to 1.5 ml, as shown in Figure 6. To increase the maximum sample volume capacity to 3 ml simply connect two columns in series.

HiTrap Desalting columns are ideal for desalting, buffer exchange, and removal of salts, co-factors, labels or other small molecules.

Sample volumes up to 30% of total column volume are loaded when using gel filtration for desalting. The high sample volume gives a separation with minimal sample dilution. Larger sample volumes can be applied but resolution will be reduced.

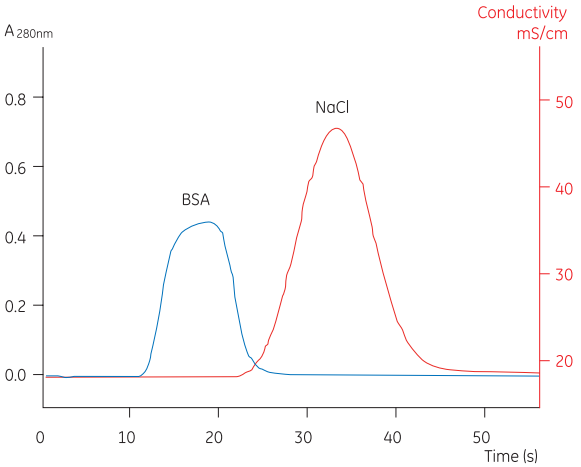


Fig 6. Typical desalting separation.

High resolution separations

For high resolution separations the technique should be used when sample volumes have been minimized. Figure 7 shows a typical high resolution gel filtration separation.

Media selection

Refer to *Gel Filtration Columns and Media Guide,* 18-1124-19.

Optimization parameters for high resolution separations

1. Select medium that gives the best separation of target proteins from contaminants.
2. Select the highest flow rate that maintains resolution and minimizes separation time. Lower flow rates improve resolution of high molecular weight components, whereas faster flow rates may improve resolution of low molecular weight components.
3. Determine the maximum sample volume that can be loaded without significant reduction in resolution (sample volume should be 0.5 to 5% of total column volume).
4. To improve resolution further, increase column length by connecting two columns in series.

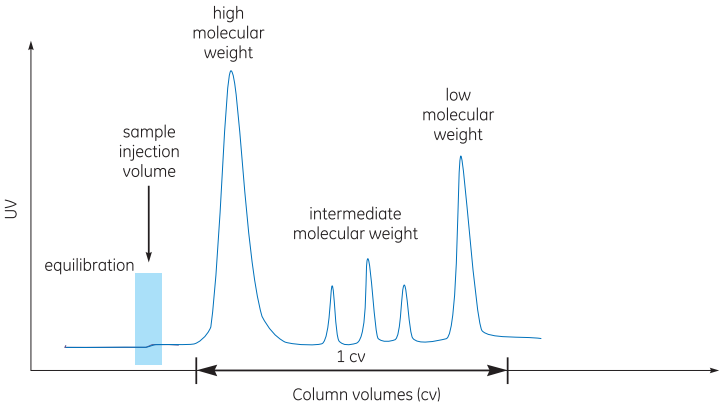
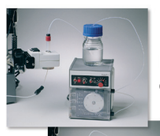


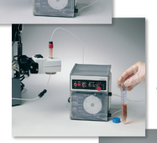
Fig 7. Typical high resolution GF separation.

Convenient Protein Purification HiTrap Columns

Simple protein purification



Equilibrate column



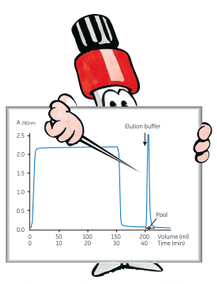
Load sample
Wash

Elute
Collect fractions

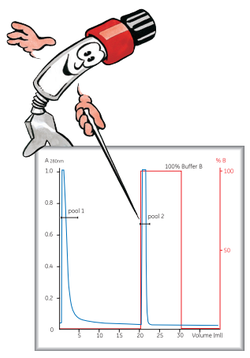
High throughput and scale-up

ÄKTAxpress™

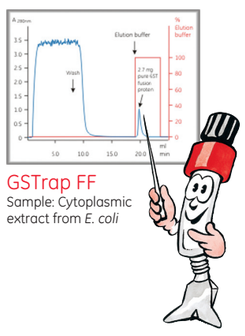
ÄKTAexplorer™



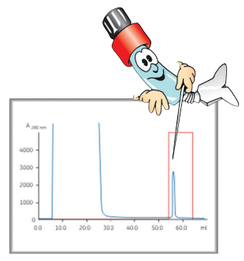
HiTrap rProtein A FF
Sample: Cell culture supernatant containing IgG_1



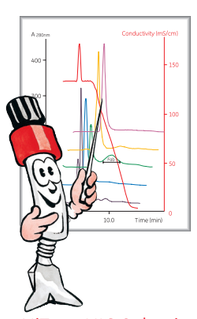
HiTrap Q HP
Sample: Human serum, conditions selected to remove IgG fraction in pool 1



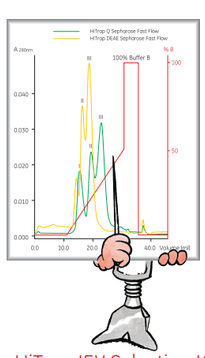
GSTrap FF
Sample: Cytoplasmic extract from *E. coli*



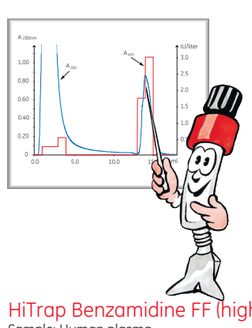
HisTrap HP
Sample: Approx. 12 mg histidine-tagged protein in *E. coli* extract



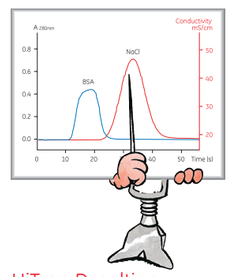
HiTrap HIC Selection Kit
Sample: Recombinant Fab fragment, media screening



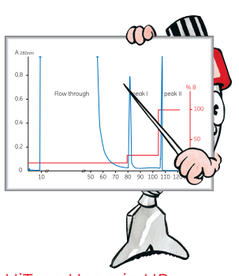
HiTrap IEX Selection Kit
Sample: Ribonuclease A, human apo-transferrin, α-lactalbumin, media selection



HiTrap Benzamidine FF (high sub)
Sample: Human plasma



HiTrap Desalting
Sample: Bovine serum albumin



HiTrap Heparin HP
Sample: Antithrombin III from bovine plasma

ÄKTApurifier™

Sample clean-up in less than 5 minutes

Load sample
Wash

Elute
Collect product

Automated purification

ÄKTAprime™ plus

ÄKTAFPLC™

Affinity

HiTrap columns/kits	Fisher Scientific Cat. No.	Quantity/components	Maximum operating flow rate	Approximate binding capacity per ml media	Applications
Affinity / Isolation of immunoglobulins					
HiTrap MabSelect™	45001462 45001463 45001464	5 × 1 ml 1 × 5 ml 5 × 5 ml	4 ml/min 20 ml/min	Human IgG ~30 mg/ml	Purification of monoclonal IgG for fast purifications from large sample volumes. Prepacked with MabSelect.
HiTrap MabSelect SuRe™	45000008 45000009 45000010	5 × 1 ml 1 × 5 ml 5 × 5 ml	4 ml/min 20 ml/min	Human IgG ~30 mg/ml	Purification of monoclonal IgG with the possibility to perform Cleaning-in-Place (CIP) between runs with 0.1 to 0.5 M NaOH. Prepacked with MabSelect SuRe medium that has a alkali-stabilized protein A ligand.
HiTrap MabSelect Xtra™	45001465 45001466 45001467	5 × 1 ml 1 × 5 ml 5 × 5 ml	4 ml/min 20 ml/min	Human IgG ~40 mg/ml	Purification of monoclonal IgG for fast purifications from large sample volumes. Prepacked with MabSelect Xtra giving increased dynamic binding capacity.
HiTrap rProtein A FF	45000262 45000263 45000264 45000265	5 × 1 ml 2 × 1 ml 1 × 5 ml 5 × 5 ml	4 ml/min 20 ml/min	Human IgG ~50 mg/ml	Monoclonal and polyclonal IgG from ascites fluid, serum and cell culture supernatant IgG classes, fragments and subclasses.
HiTrap Protein A HP	45000049 45000050 45000051 45000052	5 × 1 ml 2 × 1 ml 1 × 5 ml 5 × 5 ml	4 ml/min 20 ml/min	Human IgG ~20 mg/ml	Monoclonal and polyclonal IgG from ascites fluid, serum and cell culture supernatant IgG classes, fragments and subclasses.
HiTrap Protein G HP	45000053 45000054 45000055 45000056	5 × 1 ml 2 × 1 ml 1 × 5 ml 5 × 5 ml	4 ml/min 20 ml/min	Human IgG 25 mg/ml	Monoclonal and polyclonal IgG from ascites fluid, serum and cell culture supernatant IgG classes, fragments and subclasses including human IgG_3 strong affinity to monoclonal mouse IgG_1 and rat IgG.
MAbTrap™ Kit	45000185	HiTrap Protein G HP column (1 × 1 ml), accessories, pre-made buffers	4 ml/min	Human IgG 25 mg/ml	Monoclonal and polyclonal IgG from ascites fluid, serum and cell culture supernatant IgG classes, fragments and subclasses.
HiTrap IgY Purification HP	45000277	1 × 5 ml	20 ml/min	IgY 20 mg/ml	IgY from egg yolk.
HiTrap IgM Purification HP	45000276	5 × 1 ml	4 ml/min	Human IgM 5 mg/ml	Monoclonal and human IgM.
Affinity / Isolation of tagged proteins					
HisTrap™ HP	45000323 45000324 45000325	5 × 1 ml 1 × 5 ml 5 × 5 ml	4 ml/min 20 ml/min	$(Histidine)_6$-tagged protein (M, 43 000) at least 40 mg/ml	Histidine-tagged proteins. HisTrap HP columns are prepacked with Ni Sepharose™ High Performance, a Ni^{2+} precharged medium. Optimized for high performance purifications of histidine-tagged proteins.
HisTrap FF	45000336 45000326	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	$(Histidine)_6$-tagged protein (M, 43 000) ~40 mg/ml	Histidine-tagged proteins. HisTrap FF columns are prepacked with Ni Sepharose 6 Fast Flow, a Ni^{2+} precharged medium. Optimized for large sample volumes and scale-up.
HisTrap FF crude	45000000 45000335	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	$(Histidine)_6$-tagged protein (M, 43 000) ~40 mg/ml	Histidine-tagged protein. HisTrap FF crude columns are prepacked with Ni Sepharose 6 Fast Flow and optimized for direct loading of sonicated unclarified cell lysate without any sample pretreatment such as centrifugation and filtration.
HisTrap FF crude Kit	45001428	HisTrap FF crude columns (3 × 1 ml), accessories, pre-made buffers	4 ml/min	(Histidine)6-tagged protein (Mr 43 000) at least 40 mg/ml	Histidine-tagged proteins. HisTrap FF crude columns are prepacked with Ni Sepharose 6 Fast Flow.
HiTrap Chelating HP (see below) HiTrap IMAC HP (see below) HiTrap IMAC FF (see below)					
GSTrap™ HP	45000332 45000333 45000334	5 × 1 ml 1 × 5 ml 5 × 5 ml	4 ml/min 15 ml/min	GST-tagged protein (M, 63 000) ~10 mg/ml	Glutathione S-transferase (GST) tagged proteins produced using the pGEX series of expression vectors, other glutathione S-transferases and glutathione-dependent proteins. Prepacked with Glutathione Sepharose High Performance.
GSTrap FF	45000281 45000282 45000283 45000284	5 × 1 ml 2 × 1 ml 1 × 5 ml 5 × 5 ml	4 ml/min 15 ml/min	~10 mg GST/ml GST-tagged protein (M, 43 000) ~10 mg/ml	Glutathione S-transferase (GST) tagged proteins produced using the pGEX series of expression vectors, other glutathione S-transferases and glutathione-dependent proteins. Prepacked with Glutathione Sepharose 6 Fast Flow.
GSTrap 4B	45001429 45001430 45001431	5 × 1 ml 1 × 5 ml 5 × 5 ml	1 ml/min 5 ml/min	~10 mg GST/ml	Glutathione S-transferase (GST) tagged proteins produced using the pGEX series of expression vectors, other glutathione S-transferases and glutathione-dependent proteins. Prepacked with Glutathione Sepharose 4B.
MBPTrap™ HP	45001540 45001541 45001542	5 × 1 ml 1 × 5 ml 5 × 5 m	4 ml/min 20 ml/min	MBP-tagged protein (M_r ~70 000, multimer in solution) ~7 mg/ml medium MBP-tagged protein (M_r ~158 000, multimer in solution) ~16 mg/ml medium	Purification of MBP (Maltose Binding Protein)-tagged proteins. Prepacked HiTrap columns with Dextrin Sepharose High Performance. Optimized for high performance purificationss of MBP-tagged proteins
StrepTrap™ HP	45001519 45001520 45001521	5 × 1 ml 1 × 5 ml 5 × 5 ml	4 ml/min 20 ml/min	Strep(II)-tagged protein (M, 37 400) ~6 mg/ml medium	Purification of Strep(II)-tagged proteins. Prepacked HiTrap columns with StrepTactin™ Sepharose High Performance. Optimized for high performance purifications of Strep(II)-tagged proteins.
HiTrap Streptavidin HP	45000278	5 × 1 ml	4 ml/min	Biotinylated BSA 6 mg/ml	Biotin and biotinylated molecules, such as biotin-tagged fusion proteins. Strep-tagged proteins.
Affinity / Group specific media					
HiTrap IMAC HP	45000163 45000164	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	$(Histidine)_6$-tagged protein (M, 43 000) ~40 mg/ml	Optimization of purification of histidine-tagged proteins with usage of other metal ions than Ni^{2+}. HiTrap IMAC HP is prepacked with IMAC Sepharose High Performance.
HiTrap IMAC FF	45000167 45000168	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	$(Histidine)_6$-tagged protein (M, 43 000) ~40 mg/ml	Optimization of purification of histidine-tagged proteins with usage of other metal ions than Ni^{2+}. HiTrap IMAC FF is prepacked with IMAC Sepharose 6 Fast Flow.
HiTrap Chelating HP	45000060 45000061 45000062	5 × 1 ml 1 × 5 ml 5 × 5 ml	4 ml/min 20 ml/min	$(Histidine)_6$-tagged protein (M, 27 600) ~12 mg/ml	Proteins and peptides with exposed amino acids: His (Cys, Trp), e.g., α_2-macroglobulin and interferon, histidine-tagged proteins. Optimizing purification of histidine-tagged proteins by charging with different metal ions.
GSTrap HP (see above) GSTrap FF (see above) GSTrap 4B (see above)					
HiTrap Blue HP	45000063 45000064	5 × 1 ml 1 × 5 ml	4 ml/min 20 ml/min	HSA (M_r 68 000) 20 mg/ml	Albumin, nucleotide requiring enzymes, coagulation factors.
HiTrap Streptavidin HP	45000278	5 × 1 ml	4 ml/min	Biotinylated BSA 6 mg/ml	Biotin and biotinylated molecules, such as biotin-tagged proteins.
HiTrap Heparin HP	45000057 45000058	5 × 1 ml 1 × 5 ml	4 ml/min 20 ml/min	Antithrombin III (bovine) ~3 mg/ml	Antithrombin III and other coagulation factors, lipoprotein lipases, DNA binding proteins, protein synthesis factors.
HiTrap Benzamidine FF (high sub)	45000288 45000289 45000290	5 × 1 ml 2 × 1 ml 1 × 5 ml	4 ml/min 20 ml/min	≥ 35 mg trypsin/ml	Trypsin and trypsin-like serine proteases (e.g., thrombin and factor Xa).
Affinity / Matrix for preparation of affinity media					
HiTrap NHS-activated HP	45000137 45000138	5 × 1 ml 1 × 5 ml	4 ml/min 20 ml/min	Ligand specific	For coupling of primary amines.
IEX					
HiTrap IEX Selection Kit	45000368	7 × 1 ml columns HiTrap Q FF, HiTrap SP FF, HiTrap DEAE FF, HiTrap CM FF, HiTrap ANX FF (high sub), HiTrap Q XL, HiTrap SP XL	4 ml/min	As listed below	Media selection, method scouting.
HiTrap Q FF	45000258 45000293	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	HSA (M, 68 000) 120 mg/ml	Small scale, fast separation of sample, ideal for scale-up.
HiTrap SP FF	45000259 45000294	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	Ribonuclease A (M_r 13 700) 70 mg/ml	Small scale, fast separation of sample, ideal for scale-up.
HiTrap DEAE FF	45000260 45000291	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	HSA (M_r 68 000) 110 mg/ml	Small scale, fast separation of sample, ideal for scale-up.
HiTrap CM FF	45000261 45000292	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	Ribonuclease A (M_r 13 700) 50 mg/ml	Small scale, fast separation of sample, ideal for scale-up.
HiTrap ANX FF (high sub)	45000299 45000300	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	BSA (M_r 67 000) 43 mg/ml	Small scale, fast separation of sample, ideal for scale-up, particulary useful for separation of high molecular mass proteins.
HiTrap Q XL	45000295 45000296	5 × 1ml 5 × 5 ml	4 ml/min 20 ml/min	BSA (M_r 67 000) >130 mg/ml	Small scale, fast separation of sample, ideal for scale-up, in certain applications very high loading capacity.
HiTrap SP XL	45000297 45000298	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	Lysozyme (M_r 14 300) >160 mg /ml	Small scale, fast separation of sample, ideal for scale-up, in certain applications very high loading capacity.
HiTrap Q HP	45000193 45000194	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	HSA (M_r 68 000) 50 mg/ml	Small scale, high resolution separation of sample.
HiTrap SP HP	45000191 45000192	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	Ribonuclease A (M_r 13 700) 55 mg/ml	Small scale, high resolution separation of sample.
HiTrap Capto™ Q	45000002 45000003	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	Minimum 100 mg BSA/ml (10% breakthrough, 1 min residence time)	Fast separation of sample, ideal for scale-up, high binding capacity at high flow rate.
HiTrap Capto DEAE	45001525 45001526	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	Ovalbumin (M_r 67 000) > 90 mg	Fast separation of sample, ideal for scaling-up, high binding capacity at high flow rate.
HiTrap Capto S	45000337 45000338	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	Minimum 120 mg lysozyme/ml medium (10% breakthrough, 1 min residence time)	Fast separation of sample, ideal for scale-up, high binding capacity at high flow rate.
HiTrap Capto MMC	45000004 45000005	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	BSA (M_r 67 000) >45 mg at 30 mS/cm	Fast separation of sample, ideal for scale-up, high binding capacity at high flow rate. Capto MMC is a multimodel cation exchanger that gives different selectivity compared with traditional ion exchangers.
HiTrap Capto adhere	45001438 45001439	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	Not available	Fast separation of sample, ideal for scaling-up, high binding capacity at high flow rate. HiTrap Capto adhere is a multimodal anion exchanger that gives different selectivity compared with traditional ion exchangers.
HIC					
HiTrap HIC Selection Kit	45001471	7 x 1mL Phenyl Sepharose™ High Performance, Butyl Sepharose™ High Performance, Phenyl Sepharose™ 6 Fast Flow (low sub) and Phenyl Sepharose™ 6 Fast Flow (high sub), Butyl-S Sepharose 6 Fast Flow, Butyl Sepharose™ 4 Fast Flow, Octyl Sepharose™ 4 Fast Flow	4 ml/min		Media selection, method scouting.
HiTrap Phenyl FF (high sub)	45000249 45000317	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	40 µmol/ml	Small scale, fast separation of sample, ideal for scale-up.
HiTrap Phenyl FF (low sub)	45000248 45000318	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	25 µmol/ml	Small scale, fast separation of sample, ideal for scale-up.
HiTrap Phenyl HP	45000247 45000319	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	25 µmol/ml	Small scale, high resolution separation of sample.
HiTrap Butyl FF	45000250 45000321	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	40 µmol/ml	Small scale, fast separation of sample, ideal for scale-up.
HiTrap Butyl-S FF	45000174 45000175	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	10 µmol/ml	Small scale, fast separation of sample, ideal for scale-up.
HiTrap Butyl HP	45001469 45001470	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	25 µmol/ml	Small scale, fast separation of sample, ideal for scale-up.
HiTrap Octyl FF	45000251 45000320	5 × 1 ml 5 × 5 ml	4 ml/min 20 ml/min	5 µmol/ml	Small scale, high resolution separation of sample.
Desalting					
HiTrap Desalting	45000252	5 × 5 ml	15 ml/min	Sample loading capacity: 1.5 ml (non-binding technique)	Separation by size (biomolecules M_r > 5 000).

Media:
FF – Sepharose Fast Flow
HP – Sepharose High Performance

BioProcess™ media includes regulatory support.

*Available by special order. Please contact your local GE Healthcare representative.

Recommended separation conditions:
All HiTrap columns are supplied with a detailed protocol to ensure an optimal result.

Fast and easy scale-up:
For fast scaling-up, two or more HiTrap columns can be connected in series by screwing the end of one into the top of the next (backpressure will increase).

GE Healthcare Bio-Sciences AB, a General Electric Company.

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

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