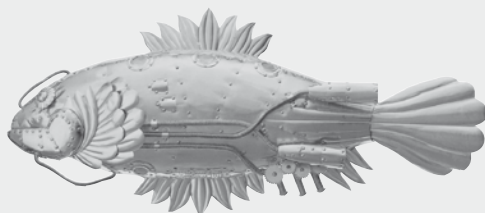
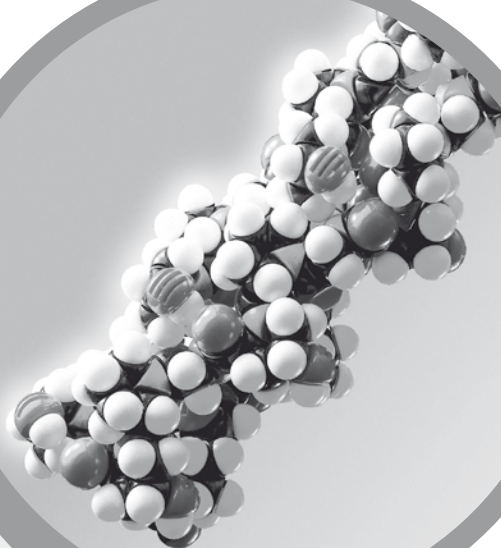




Protein & Peptide with Shodex Columns



Shodex[®]

TECHNICAL NOTEBOOK

No. 7

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1. Introduction

The analysis of proteins and peptides is essential to food science, biomolecular, and pharmaceutical studies. One of the most useful tools for this purpose is HPLC, which relies on wide variety of separation techniques. The main separation modes used for the analysis of proteins by HPLC are: Size exclusion chromatography, Reversed phase chromatography, Ion exchange chromatography, Hydrophobic interaction chromatography and Affinity chromatography. In addition, Multi mode chromatography, which combines Size exclusion and Reversed phase chromatography (or Ion exchange chromatography) can also be used. In this technical notebook, we will first review each separation mechanism, and then introduce the corresponding Shodex columns along with relevant application data.

2. Separation of Protein and Peptide by HPLC

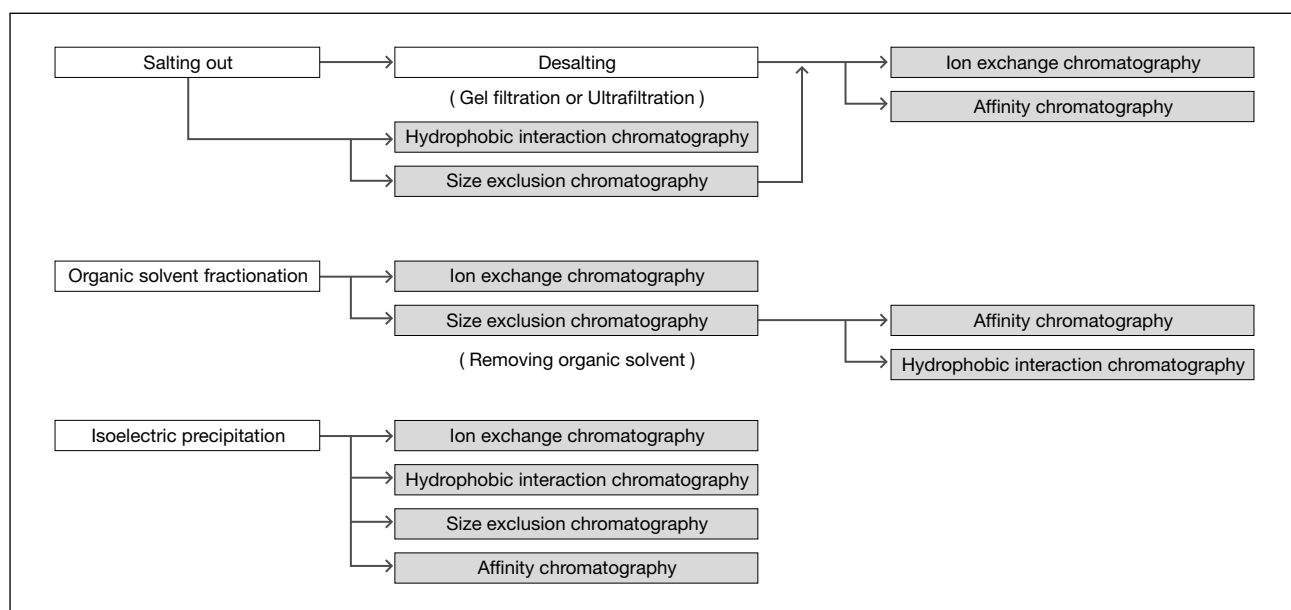
In order to plan the separation and purification of proteins or peptides, it is necessary to study the character of the target substances and select a suitable separation mode. Accordingly to choose a suitable separation mode, one must first consider which of the following case best describes the analytes:

- (1) The case where there is large difference of molecular weight between the target substance and the matrix
→ Size exclusion chromatography
- (2) The case where the difference in isoelectric points between the target substance and the matrix is greater than 1
→ Ion exchange chromatography
- (3) The case where there is the difference in hydrophobicity between the target substance and the matrix
→ Reversed phase chromatography, Hydrophobic interaction chromatography
- (4) The case where a resin with affinity to the target substance is available
→ Affinity chromatography
- (5) The pH, salt concentration, and thermostability of the target substance

When analysis is the main purpose, studying points (1) – (4) is enough for the selection of a suitable separation mode. If purification is the main purpose, studying aspect (5) is also necessary in order to prevent protein denaturation.

Usually, a combination of several separation modes is used for separation and purification. A model purification scheme is shown in Figure 1. For an unknown sample, Size exclusion chromatography is usually suitable because all substances are eluted within a limited time in order of molecular size.

Fig. 1 Model separation & purification scheme



Shodex provides columns corresponding to each of the above mentioned-separation modes for the analysis of proteins and peptides. Figures 2-1 & 2-2 can be used for the selection of a suitable column, and each separation mode is explained in chapter 3.

Fig. 2-1 Shodex column selection guide (Size exclusion, Reversed phase)

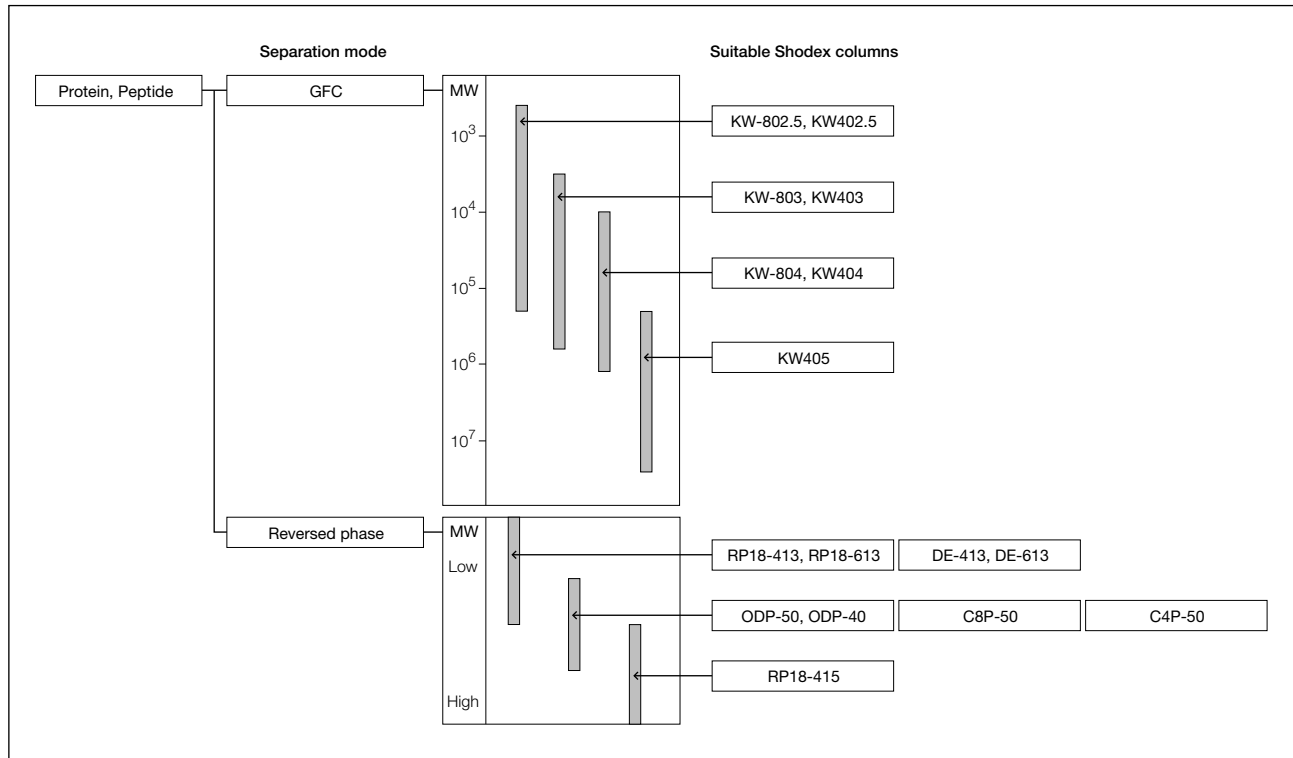
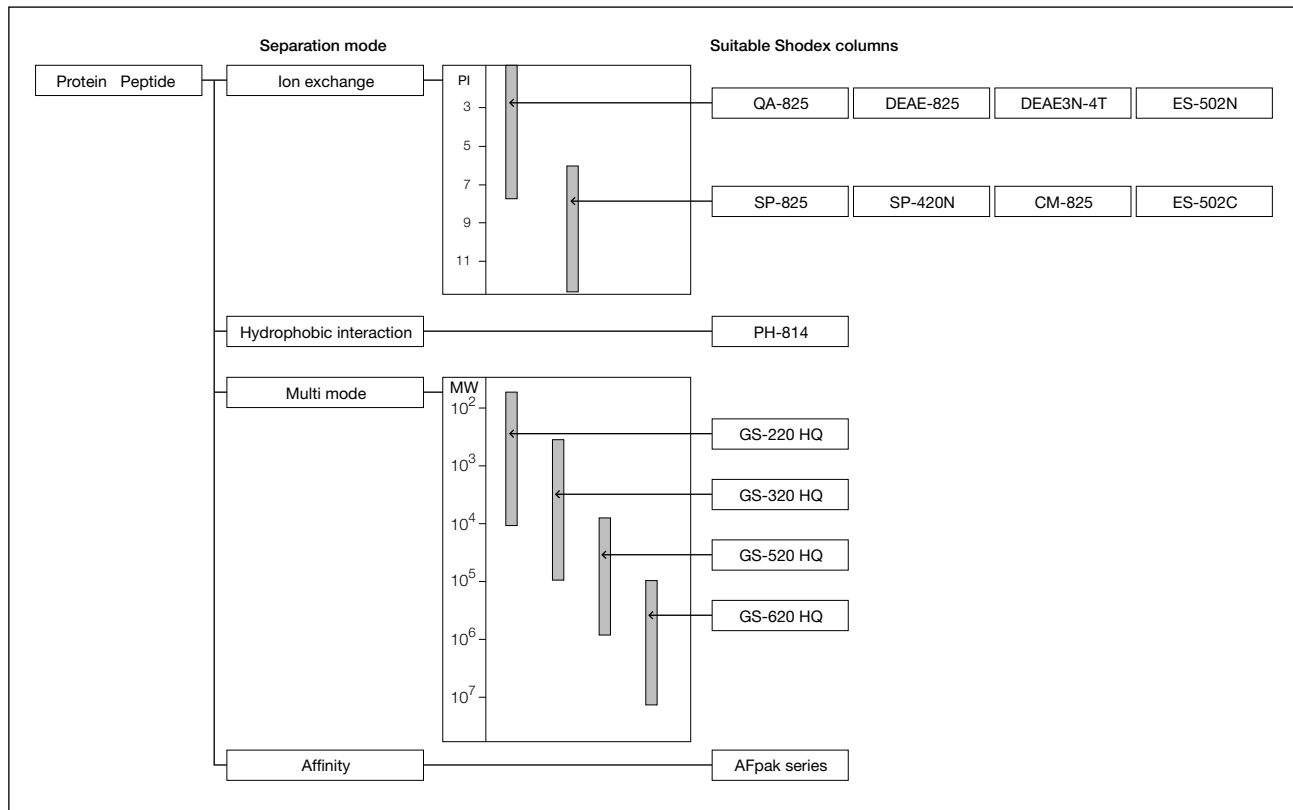


Fig. 2-2 Shodex column selection guide (Ion exchange, Hydrophobic interaction, Multi mode, Affinity)



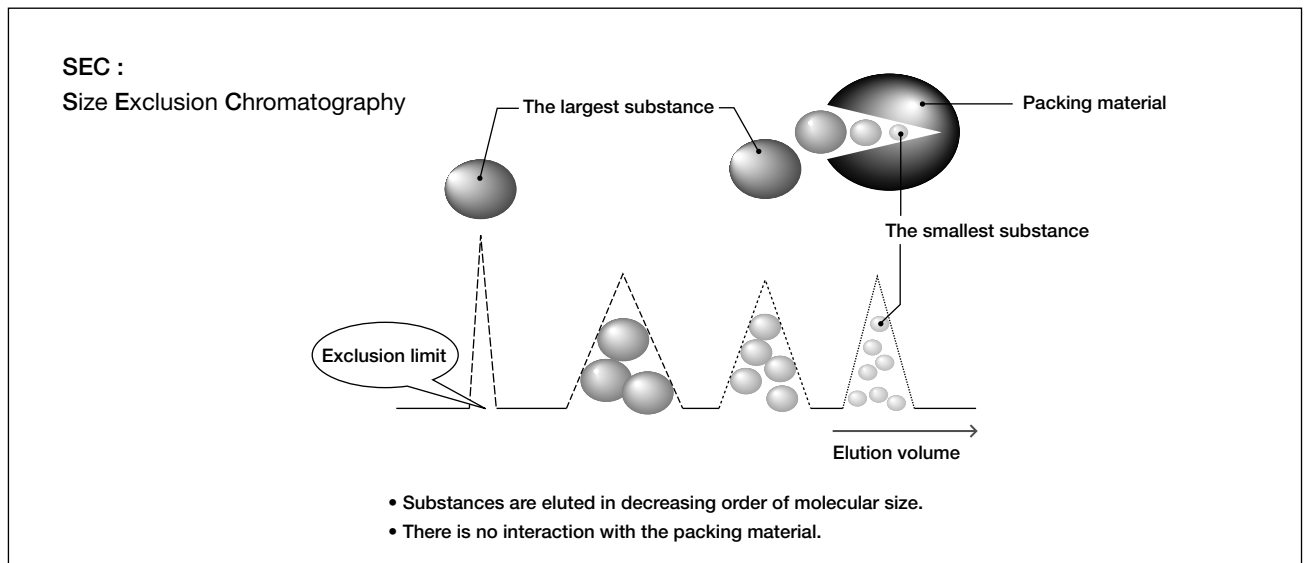
3. Separation modes

3-1. Size exclusion chromatography

3-1-1. Separation mechanism

Size exclusion chromatography (SEC) relies on the separation of molecules based on their size whereby larger molecules, which have a larger 3-dimensional volume in the eluent, elute faster. The principle of size exclusion chromatography is shown in Figure 3.

Fig. 3 The principle of SEC



The packing material has a network of small wedged holes called pores. When proteins are introduced into a column, they diffuse into pores by capillary action. Proteins which are larger than the pore size cannot penetrate into the pore and move forward with eluent, therefore eluting from the column earlier. On the other hand, proteins smaller than the pore size can get into the pore and elute from the column later. With SEC, proteins are eluted from the largest one on.

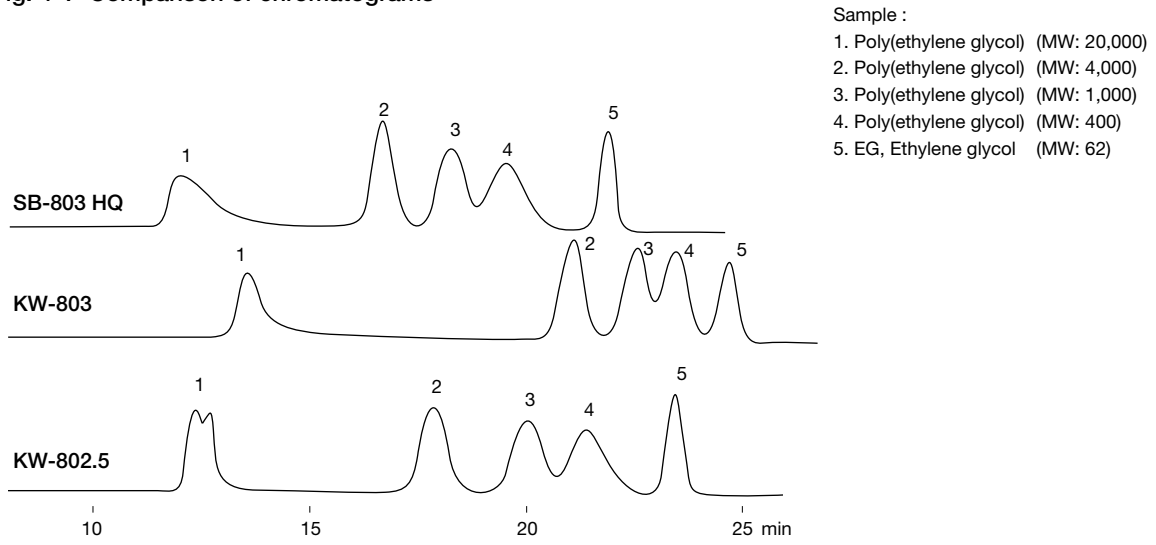
SEC has a disadvantage, which is a low loading capacity and the impossibility to increase the capacity factor (k') above 1.0. SEC is therefore not suitable for the separation of complex samples. In spite of that, SEC is frequently used as the first screening method for the separation of unknown proteins, because of the following three reasons: (1) The eluent can be easily selected. (2) It is possible to separate by molecular size. (3) The purification ratio is effective.

3-1-2. Introduction of Shodex columns

Two types of base materials can be packed into a column, i.e. silica-based, and polymer-based materials. Generally speaking for proteins and peptides analysis, silica-based stationary phases show the best separation performance because the base material has a smaller pore size distribution. On the other hand, polymer-based stationary phases are at an advantage in alkaline eluents of pH higher than 7.5, because silica gel dissolves in alkaline eluents. Figure 4 shows the comparison chromatograms of a Polyethylene glycol (PEG) mixture between the polymer-based column OHPak SB-803 HQ and the silica-based PROTEIN KW-803 & KW-802.5. OHPak SB-803 HQ is suitable for the analysis of synthetic polymers with a wider molecular range thanks to its wider pore size distribution. On the other hand, the PROTEIN KW-803 & KW-802.5 columns are suitable for the analysis of proteins thanks to their narrower pore size distribution.

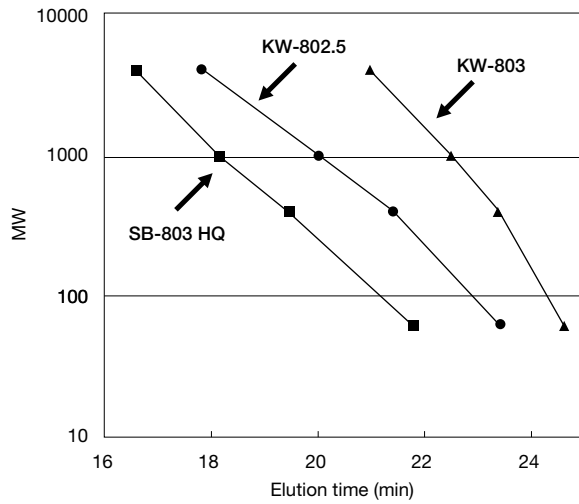
Fig. 4 Comparison between silica-based columns KW-803 & KW-802.5 and polymer-based column SB-803 HQ

Fig. 4-1 Comparison of chromatograms



Columns : Shodex OHpak SB-803 HQ or PROTEIN KW-802.5 or KW-803 (8.0mmID x 300mm each)
 Eluent : H₂O
 Flow rate : 0.5mL/min
 Detector : Shodex RI
 Column temp. : 30°C

Fig. 4-2 Comparison of calibration curves

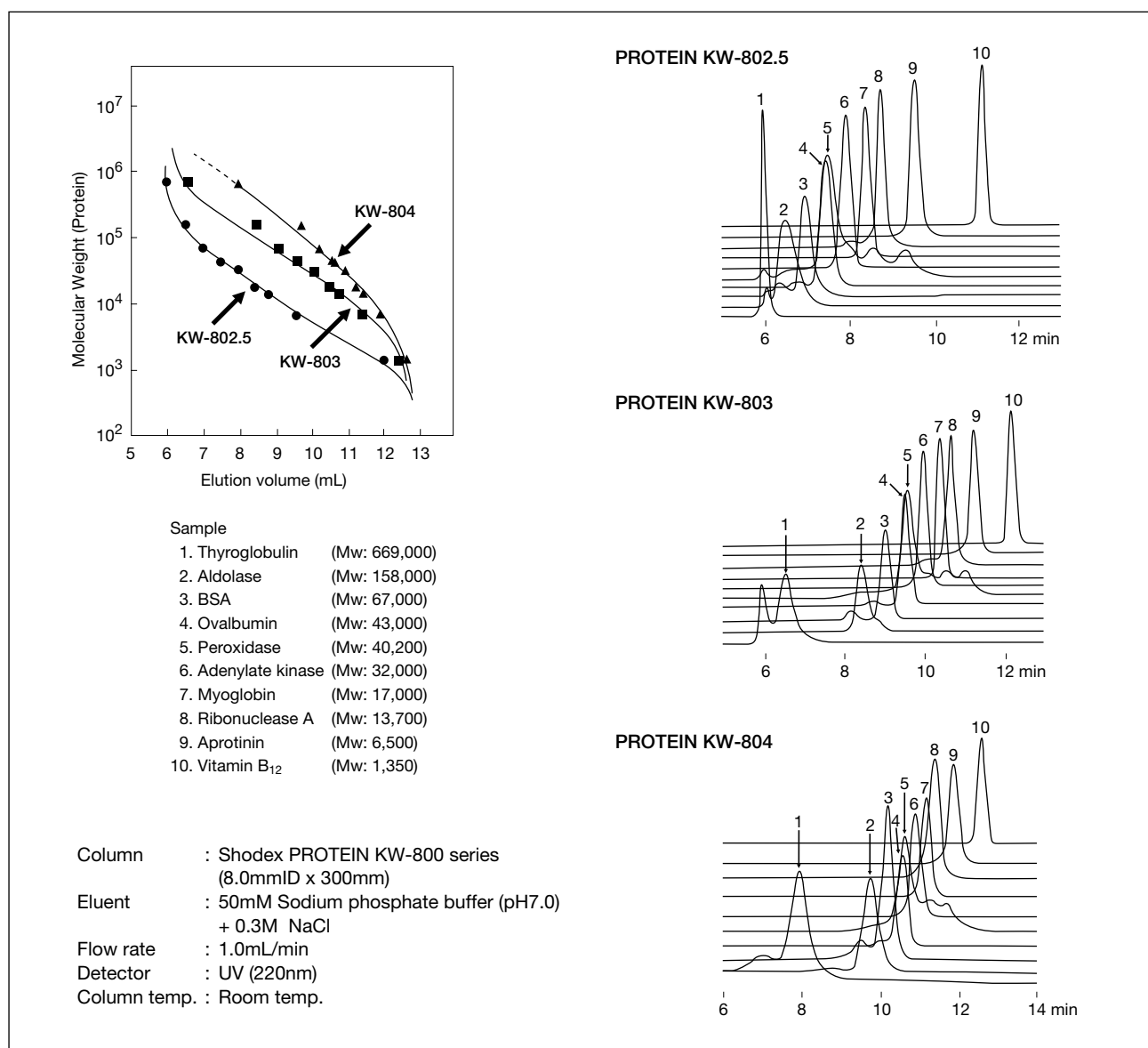


● **PROTEIN KW-800 series (Silica-based)**

The packing material of the Shodex PROTEIN KW-800 series is based on silica particles whose surface is coated with a hydrophilic polymer. This column is for aqueous SEC, and indexed in the Shodex catalogue under Gel filtration chromatography (GFC). It enjoys a positive reputation thanks to its high recovery ratio of proteins and peptide. The PROTEIN KW-800 series comprises three kinds of columns, differing in pore and particle size.

Figure 5 shows the analysis of a mixture of 10 standard proteins with the PROTEIN KW-800 series.

Fig. 5 Calibration curve of the PROTEIN KW-800 series



The PROTEIN KW-800 series line-up

PROTEIN KW-800 series	Size (mm) I.D. x L	Plate Number (TP/column)	Exclusion Limit		Particle Size (μm)	Pore Size (Å)	
			Pullulan	Protein		Max.	Avg.
KW-802.5	8.0 x 300	> 21,000	60,000	150,000	5	400	150
KW-803	8.0 x 300	> 21,000	170,000	700,000	5	1,000	300
KW-804	8.0 x 300	> 16,000	500,000	1,000,000	7	1,500	500
KW-G	6.0 x 50	(Guard column)	—	—	7	—	—

● KW400 series (Silica-based)

The Shodex KW400-4F series is the high-performance semi-micro column version of the KW-800 series. The theoretical plate number and the sensitivity are improved by reducing the diameter of the packed particle to 3 micrometers.

KW405-4F, the newest addition to the KW400 line-up, has a larger pore size than any columns in the existing KW-800 series, and can analyze proteins whose molecular weight is larger than 1,000,000. It enables the scientist to carry out the analysis of protein complexes. Figure 6 shows the calibration curves of the KW400 series with proteins.

Fig. 6 Calibration curves of the KW400-4F series

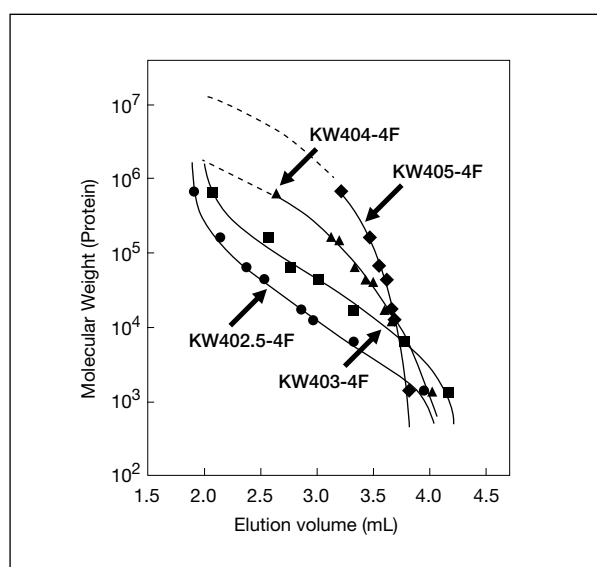
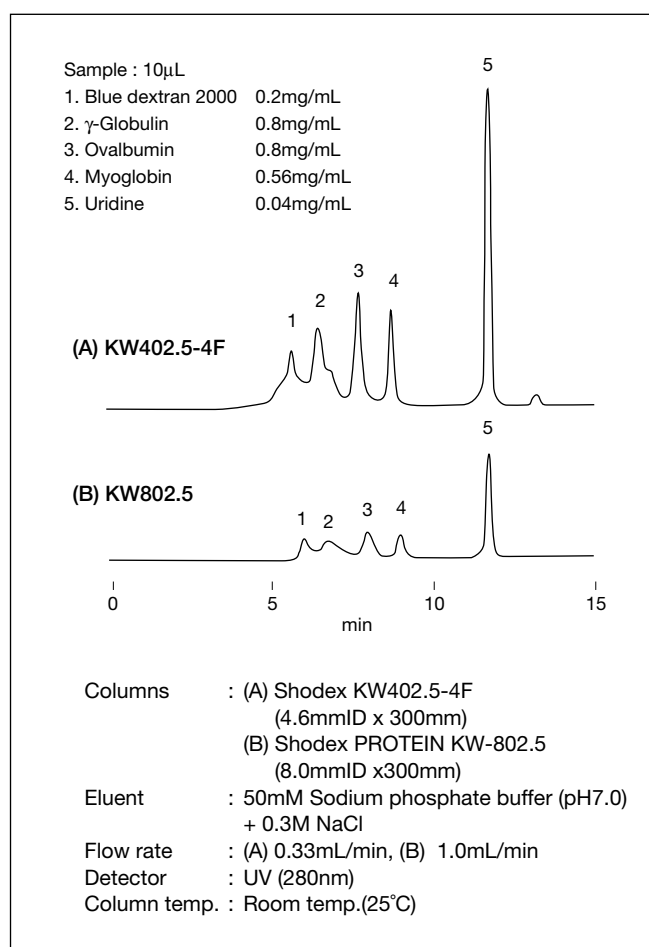


Figure 7 shows the comparison between the high-performance semi-micro column KW402.5-4F and the original PROTEIN KW-802.5 column for protein analysis. The KW400-4F series exhibits approximately a 1.5 times higher theoretical plate number and 4 times better sensitivity compared to the KW-800 series.

Fig. 7 Comparison between KW402.5-4F and KW-802.5 columns



The KW400 series line-up

KW400 series	Size (mm) I.D. x L	Plate Number (TP/column)	Exclusion Limit		Particle Size (μ m)	Pore Size (\AA)	
			Pullulan	Protein		Max.	Avg.
KW402.5-4F	4.6 x 300	> 35,000	60,000	150,000	3	400	150
KW403-4F	4.6 x 300	> 35,000	150,000	600,000	3	800	250
KW404-4F	4.6 x 300	> 25,000	500,000	1,000,000	5	1,500	500
KW405-4F	4.6 x 300	> 25,000	1,300,000	20,000,000	5	2,000	1,000
KW400G-4A	4.6 x 10	(Guard column)	—	—	5	—	—

The following semi-micro and micro columns can be prepared.

• Inner diameter : 2.0mm, 1.0mm • Length : 250mm, 150mm, 50mm

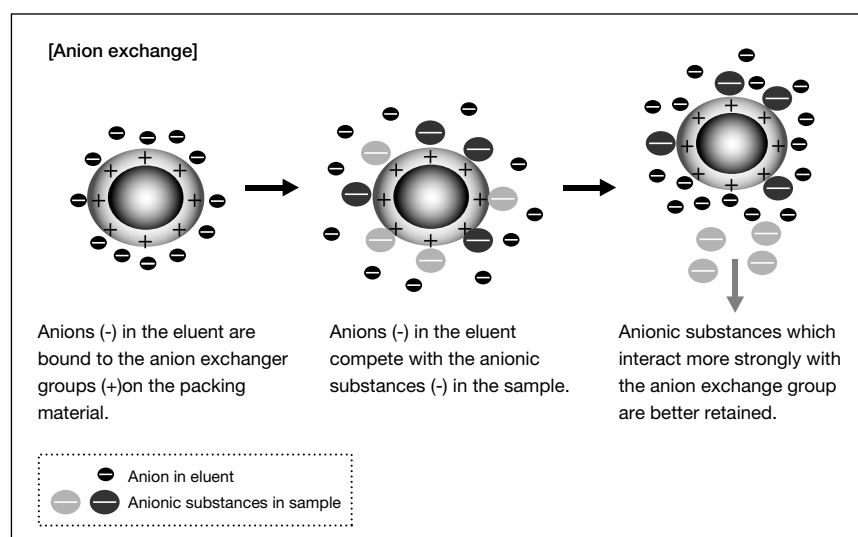
3-2. Ion exchange chromatography

3-2-1. Separation mechanism

Ion exchange chromatography is an analytical method relying on the interaction of ion-charges between the surface of proteins and the surface of the packing material. Packing materials with a positive surface charge are called “anion exchangers” and those with a negative surface charge are called “cation exchangers”.

Obtaining some information about the isoelectric point (pI) of proteins is useful for selecting suitable analytical conditions. Proteins consist of amino acids, and are amphoteric compounds, so there is pH at which the total sum of electrical charges becomes zero in the solution. That pH is called isoelectric point (pI). Around the pI, the electrical charge on the surface of proteins is neutralized and such proteins cannot easily adsorb on the surface of the packing material. In some cases, proteins precipitate around the pI, a phenomenon known as “isoelectric precipitation”. In order to adsorb the target protein, the pH of the eluent must be adjusted at more than 1.0 pH unit from pI. When the pH is more acidic than the pI, a cation exchanger should be used, and when the pH is more alkaline than the pI, an anion exchanger should be selected. Figure 8 shows the mechanism of an anion exchanger.

Fig. 8 The mechanism of anion exchange separations



Hereinafter, we describe the mechanism of an ion exchange separation through the example of a Diethylaminoethyl (DEAE)-based anion exchange resin. In the case of the separation of a protein whose pI is 7, the pH of the eluent should be adjusted to 8, to make the protein anionic. The DEAE ion exchanger should be equilibrated with a buffer solution with chloride (Cl^-) as the counter ion. When the protein, which has negative charge as an anion, is introduced into the column, it binds to the DEAE ion exchanger while removing Cl^- . If a

protein with a pI of 9 is mixed in the sample, that protein exists as cation and goes through the DEAE ion exchanger without adsorption.

In order to elute the adsorbed proteins, there are two methods. One elution method is the gradual concentration increase of salts such as sodium chloride (NaCl) in the eluent, and another method is the gradual change of pH in the eluent. The first method is used more prevalently. Hereinafter we will discuss the salt concentration gradient method. When the concentration of NaCl increases in the eluent, the concentration of Cl^- increases and competes for adsorption against previously adsorbed negatively charged proteins, thus removing proteins from the anion exchanger.

The situation of the separation also depends on the type of ion exchanger. An ion exchanger is classified not only by anion or cation exchanger type, but also by the strength of the exchanger resulting from differences in functional groups. The difference between a strong and a weak exchanger is not a difference in the binding strength for proteins but the difference in the effect of pH change in the eluent, i.e. the difference in buffering capacity. Strong ion exchangers can keep the same electrical charge and adsorb proteins in a wider pH range, while weak ion exchangers are affected by pH changes in the eluent, readily changing the ion exchange capacity.

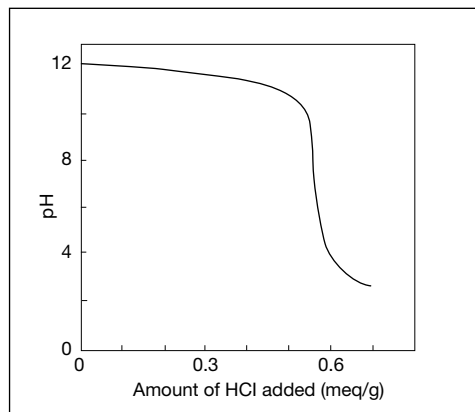
In the next chapter, we show how to optimize analytical conditions using Shodex ion exchange chromatography columns.

3-2-2. Introduction of Shodex columns

3-2-2-1. Anion exchange

- Strong anion exchange IEC QA-825
- Weak anion exchange IEC DEAE-825, Asahipak ES-502N 7C

Fig. 9 IEC QA-825 (Quaternary ammonium)



A strong anion exchange resin with a quaternary ammonium functional group is packed into the IEC QA-825 column. This column can be used at a wider pH range because the pKa of the ion exchange base is 11.7 (Figure 9).

Figure 10 shows the separation of five kinds of proteins with IEC QA-825. Conalbumin is eluted earlier at a pH higher than 6.0 because the pI of Conalbumin is between 6.0 and 6.8. On the other hand, the isoelectric points of other proteins, namely Transferrin, Ovalbumin and Trypsin inhibitor are lower than 6.0 so these elute consecutively throughout the gradual the salt concentration increase.

Fig. 10 QA-825

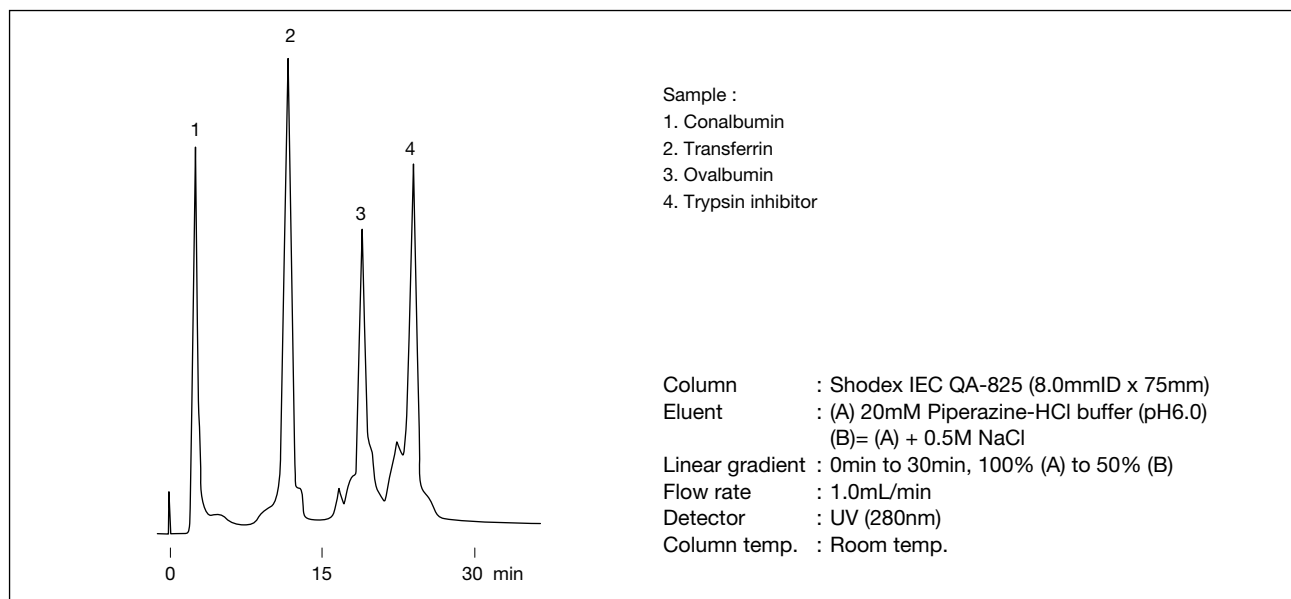
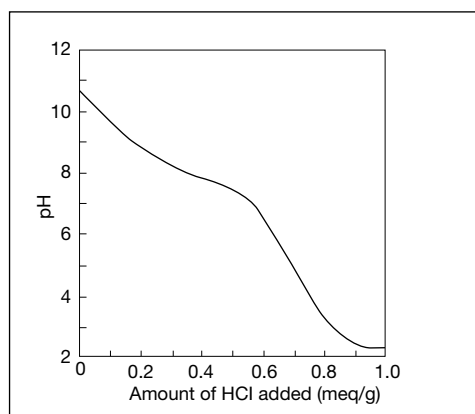


Fig. 11 IEC DEAE-825/Asahipak ES-502N 7C (DEAE base)



A weak anion exchange resin with a diethylaminoethyl (DEAE) functional group is packed into IEC DEAE-825 and Asahipak ES-502N columns. These columns are suitable for the separation of acidic proteins because the pKa of the ion exchanger is about 7.8 (Figure 11).

Figure 12 shows the effect of pH on the separation of proteins on weak anion exchange chromatography column IEC DEAE-825. Under acidic eluents, the four kinds of protein can be separated well but under alkaline eluents, the separation worsens with increasing pH. It is due to the ion exchanger not being properly ionized at alkali pH.

Weak anion exchangers (DEAE) are preferably used for protein analysis, even though the pH range for protein retention is narrower than the range for a strong anion exchanger, because milder analytical conditions can be used.

Fig. 12

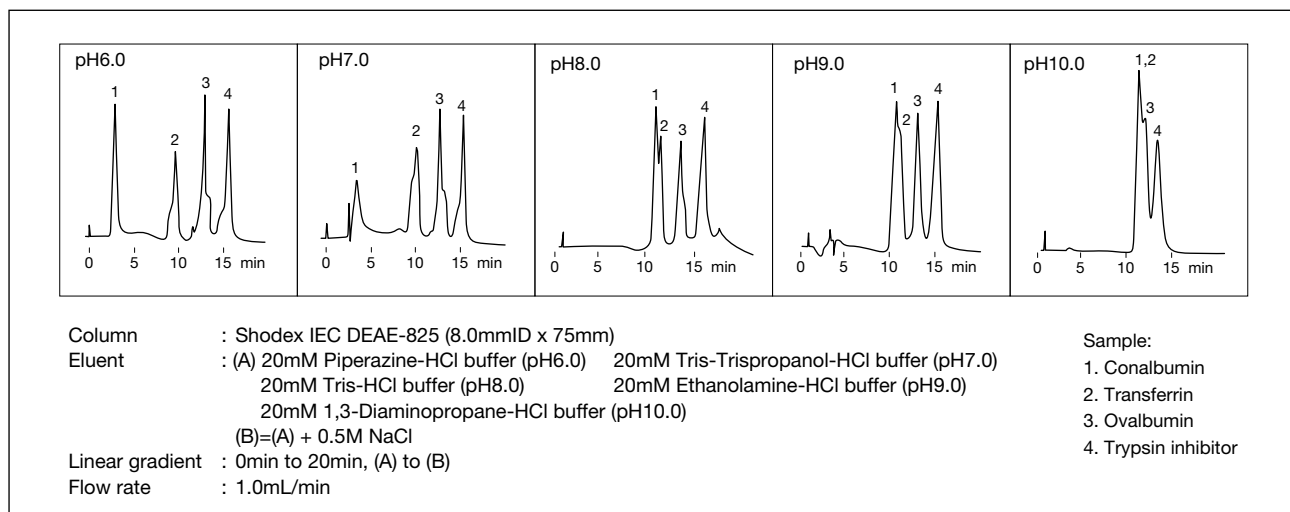
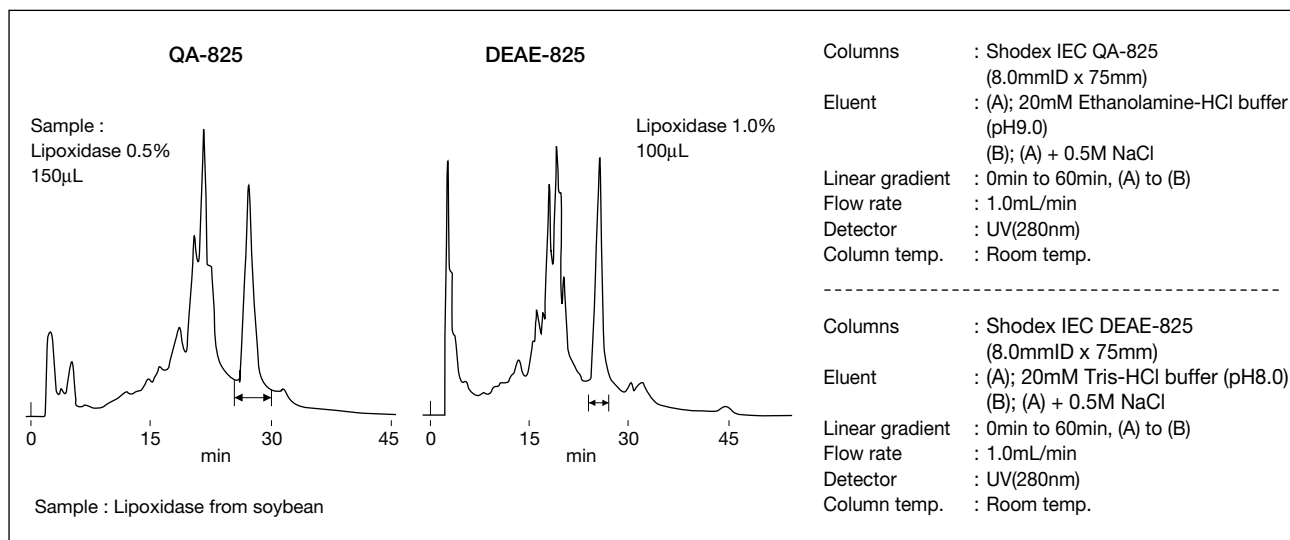


Figure 13 shows the analysis of Lipoxidase (reagent grade) with the IEC QA-825 (strong anion exchange resin) and IEC DEAE-825 (weak anion exchange resin). Enzymatic activity was detected in the range delimited by double arrows.

Fig. 13 Comparison between QA-825 and DEAE-825



Anion exchange

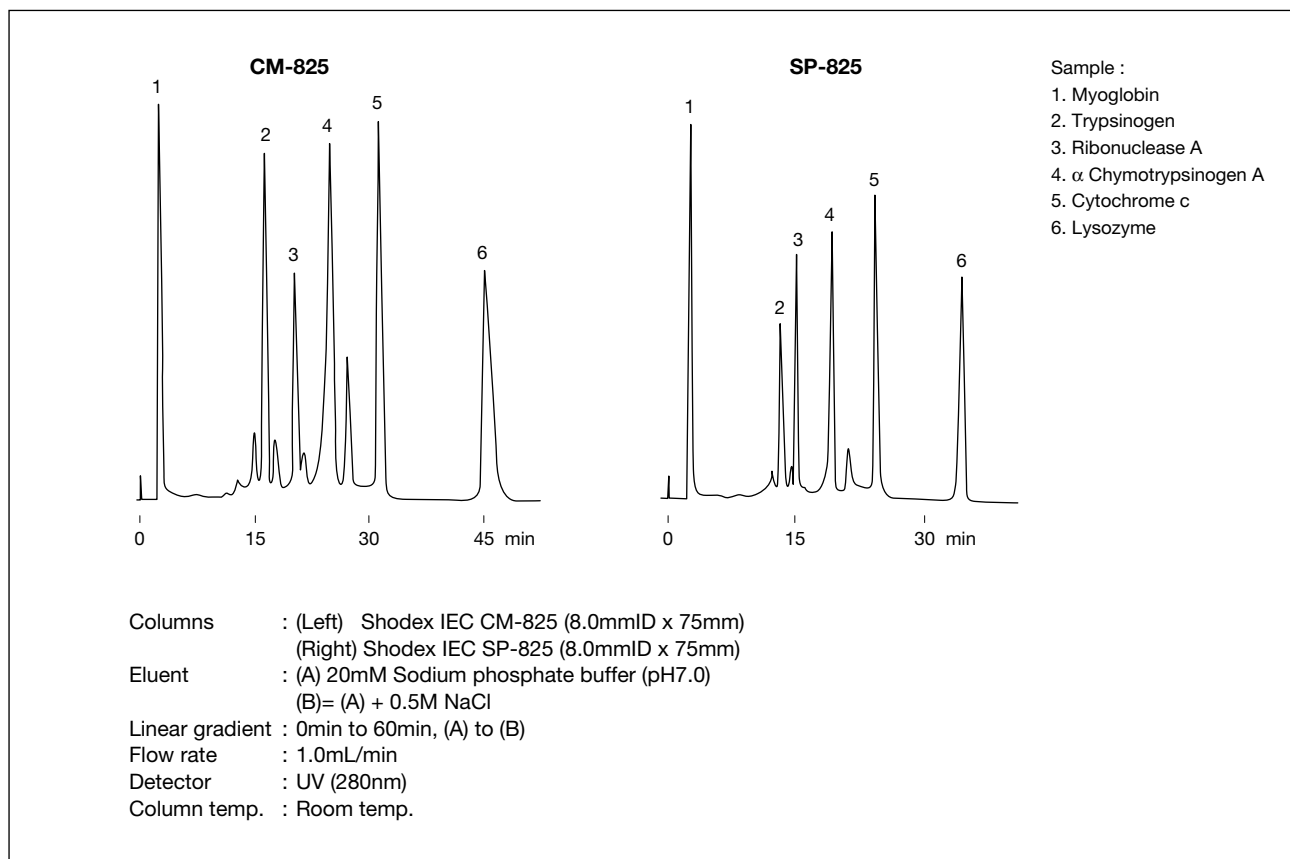
Product	Type	Size (mm) ID x L	Base material	Ion Exchange Capacity (meq/g)	Pore size (Å)	Particle size (μm)
IEC QA-825	Strong	8.0 x 75	Polyhydroxymethacrylate	0.45	5,000	12
IEC DEAE-825	Weak	8.0 x 75	Polyhydroxymethacrylate	0.6	5,000	8
Asahipak ES-502N 7C	Weak	7.5 x 100	Polyvinyl alcohol	0.55	2,000	9

The following semi-micro and micro columns can be prepared.

- Inner diameter : 2.0mm, 1.0mm, 0.8mm, 0.5mm, 0.3mm • Length : 150mm, 50mm, 35mm

Figure 17 shows the separation of six kinds of proteins including Trypsinogen with the IEC CM-825 (weak cation exchange resin) and IEC SP-825 (strong cation exchange) columns. The elution patterns are similar but the elution is faster with SP-825 than with CM-825.

Fig. 17 Comparison between CM-825 and SP-825



Cation exchange

Product	Type	Size (mm) ID x L	Base material	Ion Exchange Capacity (meq/g)	Pore size (Å)	Particle size (μ m)
IEC SP-825	Strong	8.0 x 75	Polyhydroxymethacrylate	0.4	5,000	8
IEC CM-825	Weak	8.0 x 75	Polyhydroxymethacrylate	0.4	5,000	8
Asahipak ES-502C 7C	Weak	7.5 x 100	Polyvinyl alcohol	0.55	2,000	9

The following semi-micro and micro columns can be prepared.

- Inner diameter : 2.0mm, 1.0mm, 0.8mm, 0.5mm, 0.3mm
- Length : 150mm, 50mm, 35mm

3-2-2-3. Non-porous gel (Fast analysis)

- Anion exchange DEAE3N-4T
- Cation exchange SP-420N

For fast analysis, columns packed with a non-porous gel are effective. A non-porous gel is made of packing material that does not have pores. The particle diameter of a non-porous gel can be shortened and the compressive strength of the gel is high, so it can be used for fast analysis with increased eluent flow rates.

<Maximum flow rate>

DEAE-825, SP-825 (porous resin) : 1.5ml/min
 DEAE3N-4T, SP-420N (non-porous resin) : 2.0ml/min

A disadvantage though, is that the maximum protein loading volume of non-porous gel is reduced.

<Maximum protein loading volume>

DEAE-825, SP-825 (porous resin) : 1,000µg/column
 DEAE3N-4T, SP-420N (non-porous resin) : 20µg/column

[Packing material schematic]

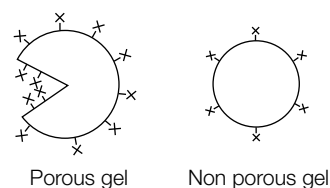
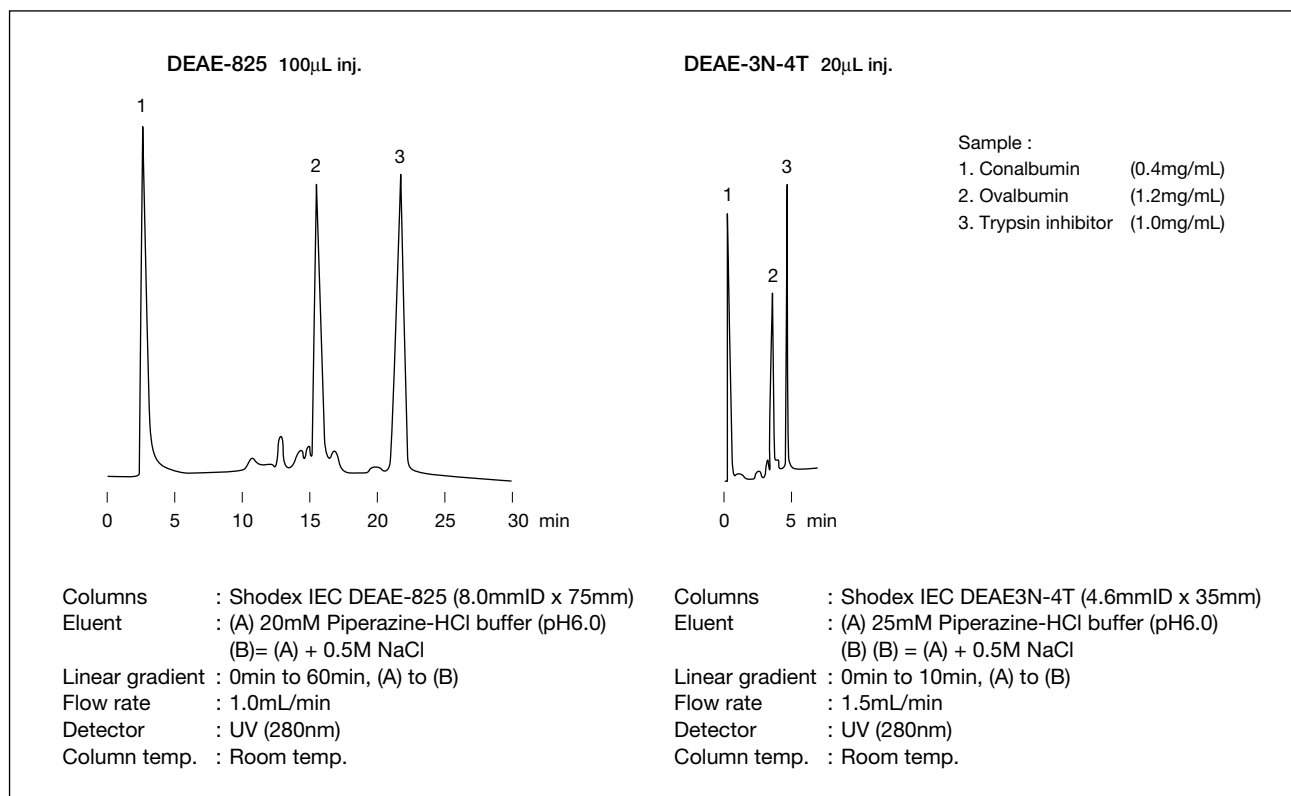


Figure 18 shows the separation of proteins with IEC DEAE3N-4T (non-porous weak anion exchange resin). The analytical time with DEAE3N-4T is shorter than the time with IEC DEAE-825, which is packed with a porous weak anion exchange resin.

Fig. 18 Comparison between DEAE-825 and DEAE3N-4T (Non-porous)



Non-porous

Product	Type	Size (mm) ID x L	Base material	Ion Exchange Capacity (meq/g)	Pore size (Å)	Particle size (µm)
IEC DEAE3N-4T	Strong anion	4.6 x 35	Polyhydroxymethacrylate	0.4	—	2.5
IEC SP-420N	Strong cation	4.6 x 35	Polyhydroxymethacrylate	0.3	—	2.5

The following semi-micro and micro columns can be prepared.

- Inner diameter : 2.0mm, 1.0mm, 0.8mm, 0.5mm, 0.3mm
- Length : 50mm, 35mm

(Appendix) Selection of a suitable buffer for the eluent

A buffer with a sufficient buffering power at the pH of the eluent and with an ion of identical electrical charge to that of the ion exchanger should be selected for the eluent. The table below shows some examples. We recommend the use of a salt solution of NaCl, KCl, Na₂SO₄ or K₂SO₄, possibly in combination with a buffer solution. The total salt concentration should remain within the 20mM to 600mM range.

PH	Cation Exchange Resin
3.8 ~ 4.3	Sodium formate
4.3	Sodium succinate
4.8 ~ 5.2	Sodium acetate
5.0 ~ 6.0	Sodium malonate
5.5 ~ 6.7	MES
6.7 ~ 7.6	Sodium phosphate
7.6 ~ 8.2	HEPES
8.2 ~ 8.7	BICINE

PH	Anion Exchange Resin
4.8 ~ 5.0	N-Methylpiperazine HCl
5.0 ~ 6.0	Piperazine HCl
5.8 ~ 6.4	Bis Tris HCl
6.4 ~ 7.3	Bis Tris Propane HCl
7.3 ~ 7.7	Triethanolamine HCl
7.5 ~ 8.0	Tris HCl
8.0 ~ 8.5	N-Methyldiethanolamine HCl
8.4 ~ 8.8	Diethanolamine HCl
8.5 ~ 9.0	1,3-Diaminopropane HCl
9.0 ~ 9.5	Ethanolamine HCl

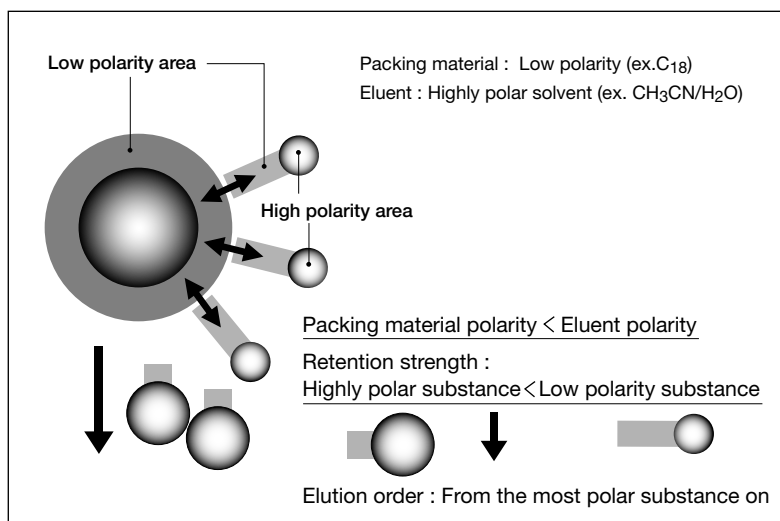
- MES : 2-(N-morpholino)ethanesulfonic acid
 HEPES : 4-(2-hydroxymethyl)-1-piperazine ethanesulfonic acid
 BICINE : N,N-bis(2-hydroxyethyl)glycine
 Tris : tris(hydroxymethyl)aminomethane
 Bis Tris : Bis(2-hydroxyethyl)iminotris(hydroxymethyl)methane
 Bis Tris propane : 1,3-Bis[tris(hydroxymethyl)methylamino]propane

3-3. Reversed phase chromatography

3-3-1. Separation mechanism

The separation mode of reversed phase chromatography is based on the hydrophobic interactions governing the distribution/adsorption equilibrium between nonpolar amino acids in proteins and the surface of the packing material (See Figure 19). The surface of the packing material's polymer- or silica-based gel is bound with a hydrophobic functional group such as octadecyl (C₁₈). Some types of polymer gels can be used for reversed phase chromatography without the need for a functional group because the base material in itself is hydrophobic. Proteins with a higher hydrophobicity are retained more strongly, so proteins are eluted from the most hydrophilic one on.

Fig. 19 Separation mechanism of reversed phase chromatography



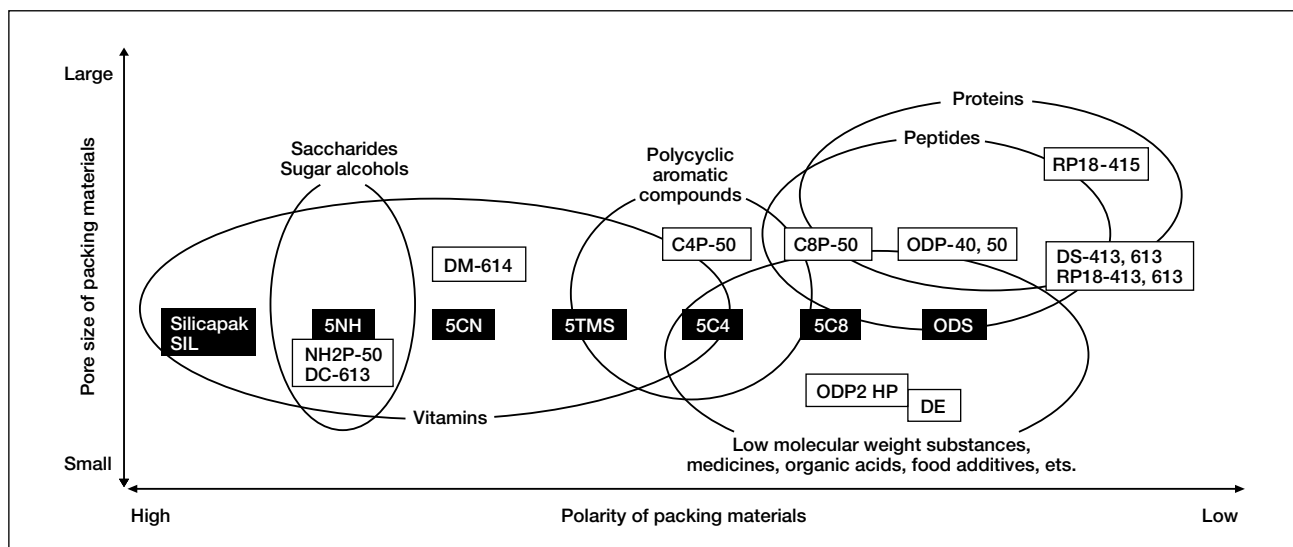
3-3-2. Introduction of Shodex columns

- Asahipak ODP, C8P, C4P series
- ODP2 HP series
- RSpak RP18, DS, DE series

In order to separate the target substance well, several kinds of columns are available with varying polarity and gel pore sizes (Figure 20). A smaller pore size is suitable for peptides, and larger pore size is suitable for proteins.

The RSpak RP18-415 column has the largest pore size (about 450 Å) in the Shodex lineup and is suitable for protein analysis. The pore size of Asahipak ODP, C8P and C4P columns is about 250 Å and these can be used for analyzing both proteins and peptides. The RSpak DE column has a smaller pore size (about 25 Å) and is suitable for analyzing smaller molecules like oligopeptides. The above-mentioned columns are polymer-based but can be used with similar analytical condition as silica-based ODS columns. In case the adsorption of the target substance is not sufficient with DE-613, DE-413 or ODS columns, RSpak RP18-413 and RP18-613 are recommended.

Fig. 20 Characteristics and applications of packing materials for normal & reversed phase columns



The chromatogram and recovery rate of proteins with the polymer-based reversed phase chromatography column RSpak RP18-415 are shown in Figure 21. The figure shows that the proteins and peptides are analyzed in 25 minutes with a high recovery rate. The maximum durable pressure is 22 MPa, so the flow rate can be increased for faster analysis.

Fig. 21

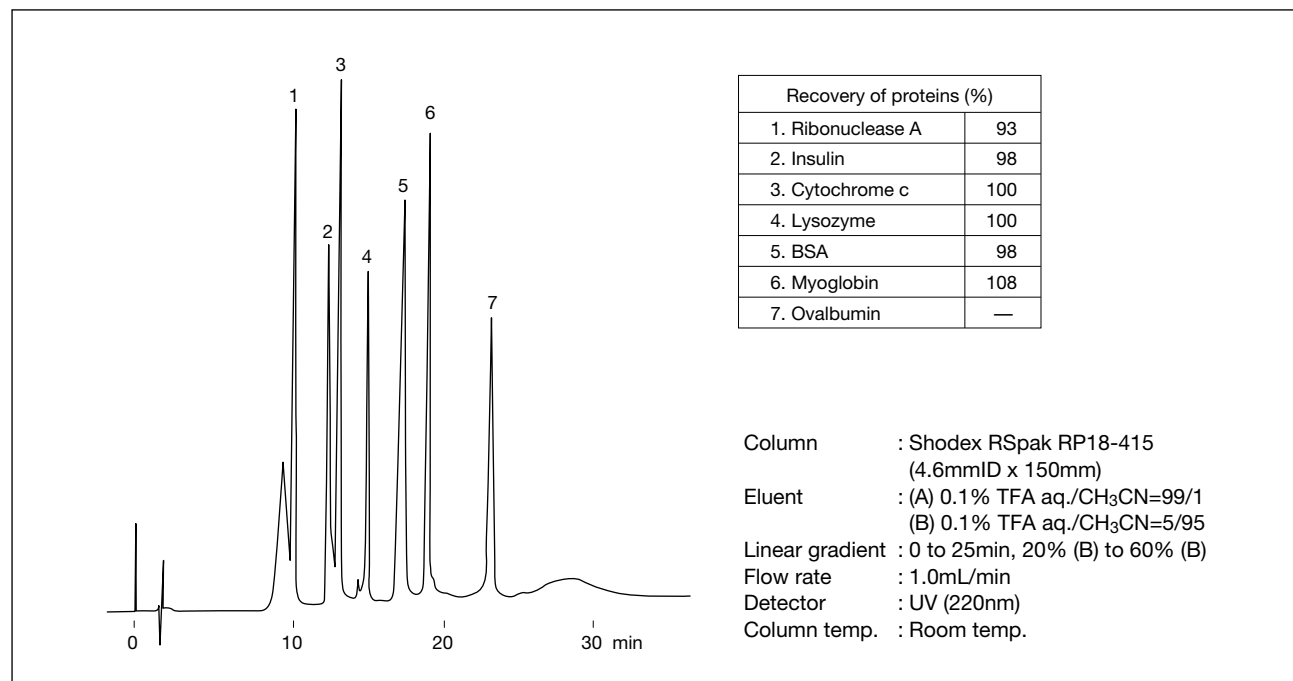


Figure 22 shows the chromatogram of a mixed sample including proteins and peptides with gradient elution. The polymer-based Asahipak ODP-50 6D column is used for its excellent elution volume reproducibility for proteins and peptides. In addition, the results show a high recovery rate.

Fig. 22

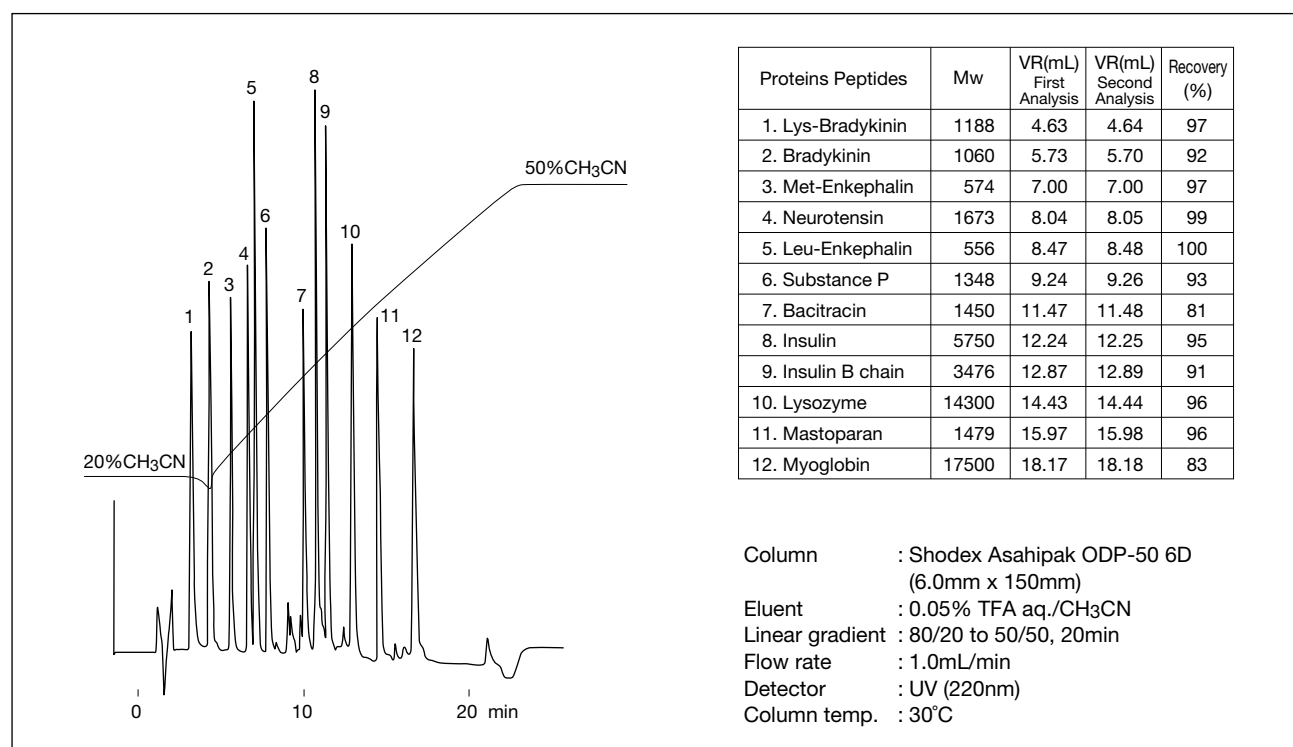


Figure 23 shows the separation of dipeptides with the polymer-based RSpak DE-613.

Fig. 23

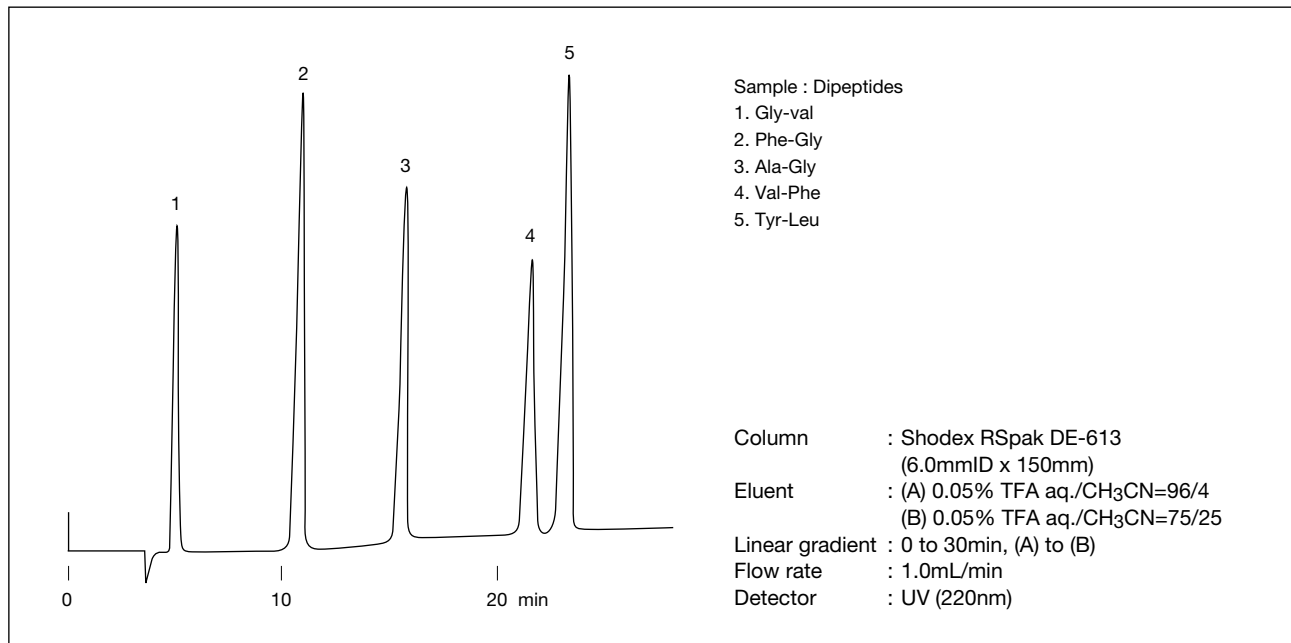
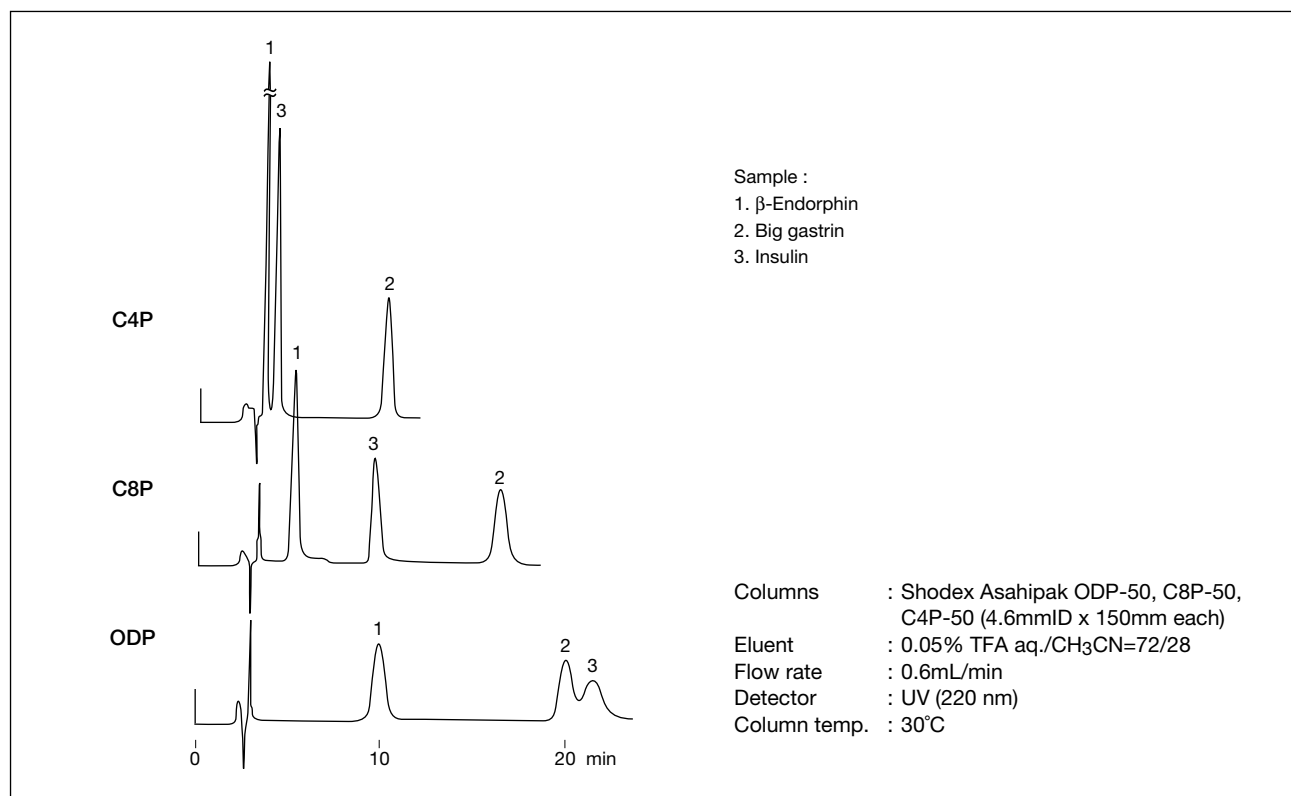


Figure 24 shows the comparison of the retention of 3 kinds proteins with the polymer-based reversed phase chromatography columns Asahipak ODP-50, C8P-50 and C4P-50. The Octadecyl functional group (C₁₈) is bonded onto the base material of ODP-50, the Octyl group (C₈) is on C8P-50, and the Butyl group (C₄) is on C4P-50. The shorter alkyl chain has the weakest hydrophobic interaction. If the retention of the ODP-50 column is too strong, it is recommended to use C8P-50 or C4P-50 because the ratio of organic solvent in the eluent can be reduced and the analytical conditions for proteins and peptides can be milder.

Fig. 24



The Shodex Asahipak series line-up

Product	Size (mm) ID x L	Functional group	Base material	Pore size (Å)	Plate number (TPN/column)	Particle size (µm)
ODP-40 4D	4.6 x 150	Octadecyl	Polyvinyl alcohol	250	> 11,000	4
ODP-40 4E	4.6 x 250	Octadecyl	Polyvinyl alcohol	250	> 17,000	4
ODP-50 6D	6.0 x 150	Octadecyl	Polyvinyl alcohol	250	> 9,000	5
ODP-50 6E	6.0 x 250	Octadecyl	Polyvinyl alcohol	250	> 14,000	5
ODP-50G 6A	6.0 x 10	Octadecyl	Polyvinyl alcohol	—	(Guard column)	5
ODP-50 4B	4.6 x 50	Octadecyl	Polyvinyl alcohol	250	> 2,500	5
ODP-50 4D	4.6 x 150	Octadecyl	Polyvinyl alcohol	250	> 9,000	5
ODP-50 4E	4.6 x 250	Octadecyl	Polyvinyl alcohol	250	> 14,000	5
ODP-50G 4A	4.6 x 10	Octadecyl	Polyvinyl alcohol	—	(Guard column)	5
ODP-50 2D	2.0 x 150	Octadecyl	Polyvinyl alcohol	250	> 5,000	5
ODP-50G 2A	2.0 x 10	Octadecyl	Polyvinyl alcohol	—	(Guard column)	5
C8P-50 4D	4.6 x 150	Octyl	Polyvinyl alcohol	250	> 7,000	5
C8P-50 4E	4.6 x 250	Octyl	Polyvinyl alcohol	250	> 11,000	5
C8P-50G 4A	4.6 x 10	Octyl	Polyvinyl alcohol	—	(Guard column)	5
C4P-50 4D	4.6 x 150	Butyl	Polyvinyl alcohol	250	> 6,000	5
C4P-50 4E	4.6 x 250	Butyl	Polyvinyl alcohol	250	> 9,000	5
C4P-50G 4A	4.6 x 10	Butyl	Polyvinyl alcohol	—	(Guard column)	5

The following semi-micro and micro columns can be prepared for ODP-40.

- Inner diameter : 2.0mm, 1.0mm, 0.8mm, 0.5mm, 0.3mm
- Length : 250mm, 150mm, 50mm

The Shodex RSpak series line-up

Product	Size (mm) ID x L	Functional group	Base material	Pore size (Å)	Plate number (TPN/column)	Particle size (µm)
RP18-415	4.6 x 150	—	Styrene divinylbenzene copolymer	450	> 5,000	6
RP18-613	6.0 x 150	—	Styrene divinylbenzene copolymer	200	> 13,000	3.5
RP18-413	4.6 x 150	—	Styrene divinylbenzene copolymer	200	> 11,000	3.5
RP18-G	4.6 x 10	—	Styrene divinylbenzene copolymer	—	(Guard column)	6
DS-613	6.0 x 150	—	Styrene divinylbenzene copolymer	200	> 6,500	6
DS-413	4.6 x 150	—	Styrene divinylbenzene copolymer	200	> 11,000	4
DS-G	4.6 x 10	—	Styrene divinylbenzene copolymer	—	(Guard column)	10
DE-613	6.0 x 150	—	Polymethacrylate	25	> 7,000	6
DE-413	4.6 x 150	—	Polymethacrylate	25	> 11,000	4
DE-413L	4.6 x 250	—	Polymethacrylate	25	> 17,000	4
DE-413S	4.6 x 50	—	Polymethacrylate	25	> 3,000	4
DE-G	4.6 x 150	—	Polymethacrylate	—	(Guard column)	10
DE-213	2.0 x 150	—	Polymethacrylate	25	> 3,000	4
DE-SG	2.0 x 10	—	Polymethacrylate	—	(Guard column)	6

The following semi-micro and micro columns can be prepared for DE-413.

- Inner diameter : 2.0mm, 1.0mm, 0.8mm, 0.5mm, 0.3mm
- Length : 250mm, 150mm, 50mm

3-4. Hydrophobic interaction chromatography

3-4-1. Separation mechanism

The mechanism of hydrophobic interaction chromatography is based on the hydrophobic interaction between proteins and the surface of the packing material. It is like reversed phase chromatography, however eluent conditions differ. As the salt concentration increases, the hydrophobicity of the protein surface also increases and the protein adsorbs onto the packed material. This effect is similar to the "salting out" of proteins, a procedure usually carried out with ammonium sulfate. After adsorption, the adsorbed protein is eluted by decreasing the salt concentration thus weakening the hydrophobic interaction with the packing material.

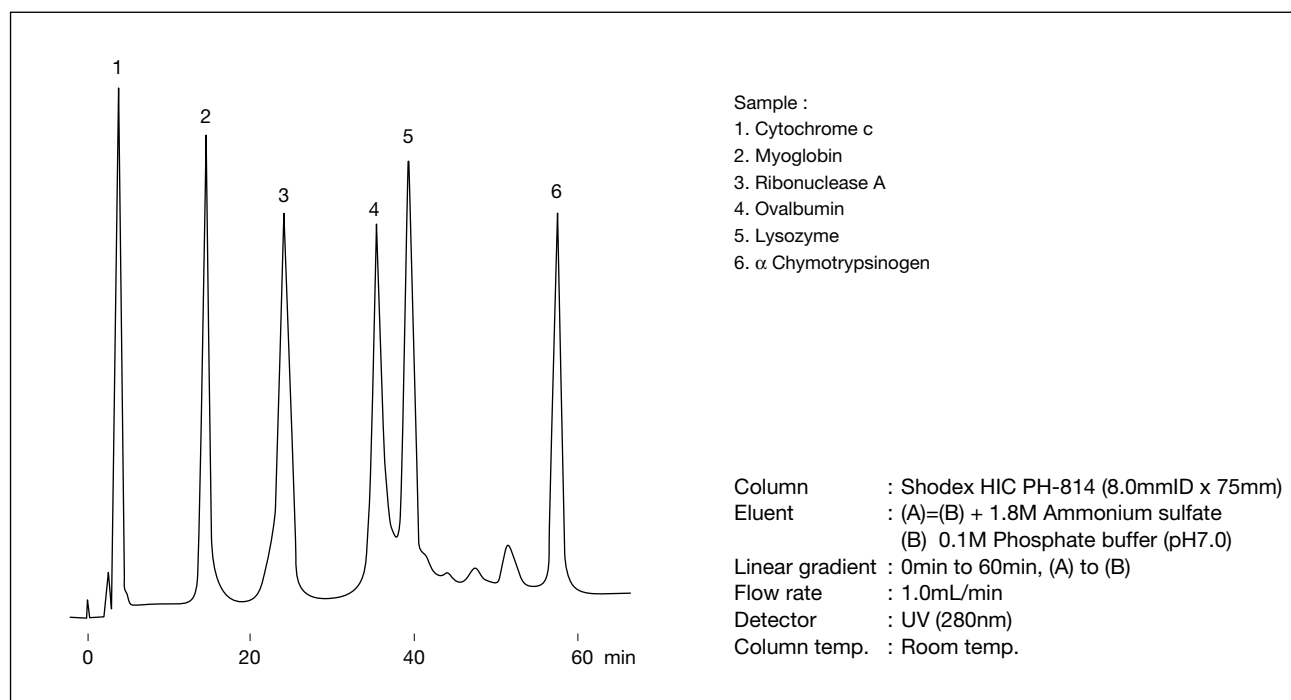
The protein is adsorbed under high salt concentration, so this separation mode is usable after ammonium sulfate precipitation or ion exchange chromatography. Moreover a less hydrophobic base like phenyl is used as the functional group, hence the analytical conditions for proteins are milder than the conditions of reversed phase chromatography, preserving the bio-activity of protein.

3-4-2. Introduction of Shodex columns

● HIC PH-814

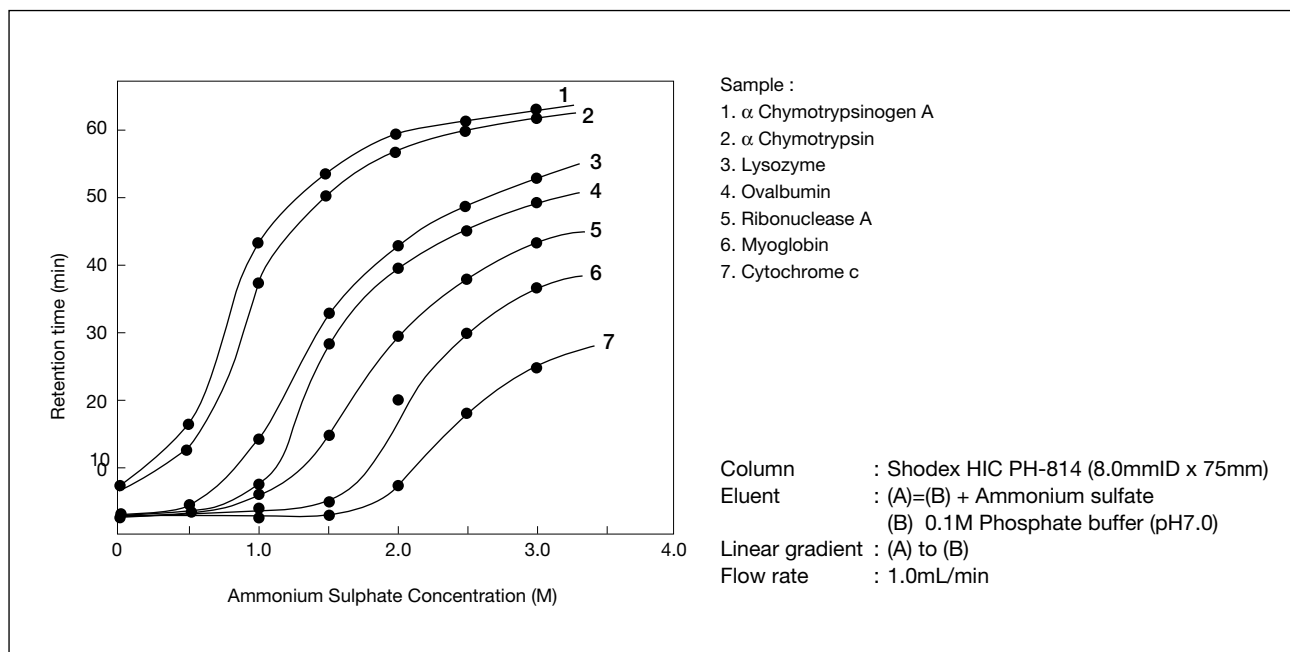
Shodex HIC PH-814 is a column for hydrophobic interaction chromatography, with a phenyl group bound to the packing material as a hydrophobic ligand. Figure 25 shows the separation of 6 kinds of proteins with HIC PH-814.

Fig. 25



The effect of the ammonium sulfate concentration in the eluent on protein separation with HIC PH-814 is illustrated in Figure 26. The retention of proteins is controlled not only by the salt concentration but also by pH and temperature. The retention is stronger at higher pH or temperatures and weaker under lower pH and temperatures.

Fig. 26



The Shodex HIC PH-814 column

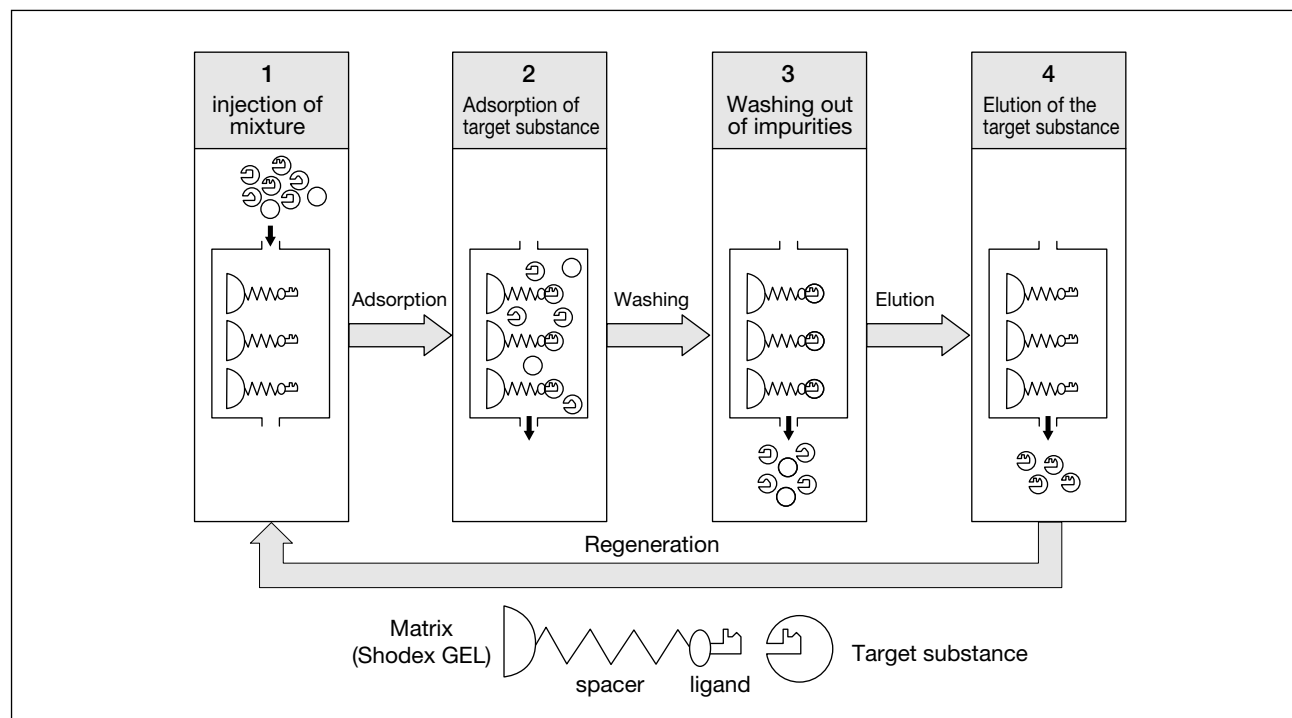
Product	Size (mm) ID x L	Functional group	Base material	Pore size (Å)	Particle size (μ m)
HIC PH-814	8.0 x 75	Phenyl	Polyhydroxymethacrylate	2,000	10

3-5. Affinity chromatography

3-5-1. Separation mechanism

Affinity chromatography is a highly selective separation method relying on biochemical interaction. The mechanism is explained in Figure 27.

Fig. 27



- 1) Inject sample into an initially equilibrated affinity chromatography column (AFpak).
- 2) Only the substances with affinity for the ligand are retained in the column.
- 3) Substances with no affinity for the ligand are eluted from the column without interacting with the stationary phase.
- 4) The substances retained in the column can be eluted by changing the pH or salt or organic solvent concentrations of the eluent.

3-5-2. Introduction of Shodex columns

● AFpak series

The rigid polymer-based packing material used with the various ligands for Shodex AFpak columns, has the following advantages.

- 1) High-speed and high-pressure (5~10 MPa) analysis
- 2) Minimizes the detachment of ligands, ensuring highly reproducible analyses

Application data with each AFpak column is shown below.

Fig. 28 Ovalbumin

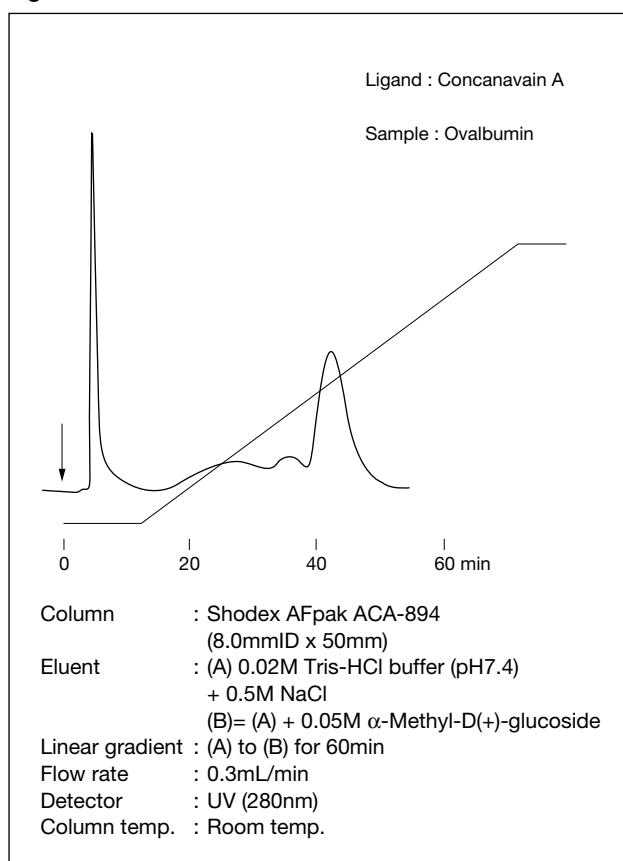


Fig. 29 α 1 Antitrypsin

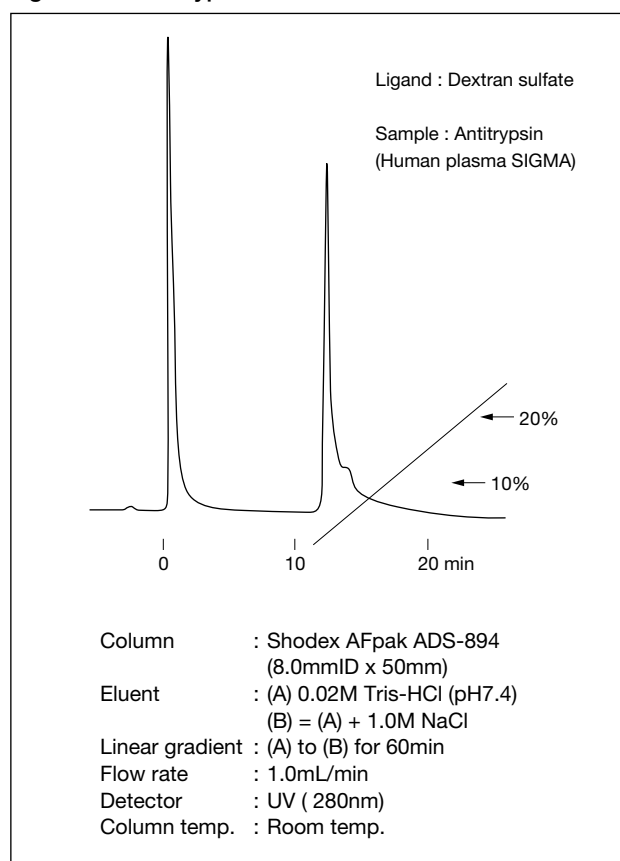


Fig. 30 Bovine serum albumin

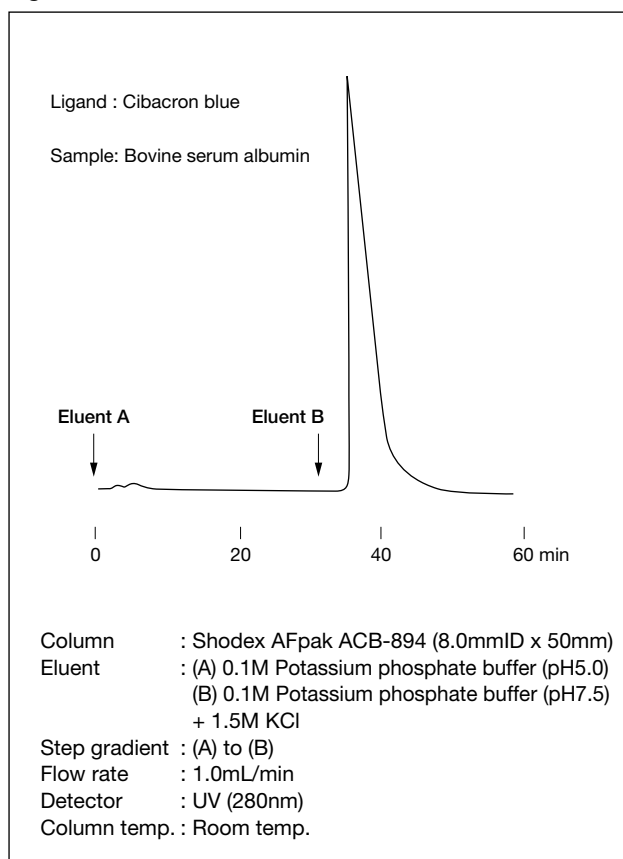


Fig. 31 Ovalbumin / Conalbumin / Lysozyme

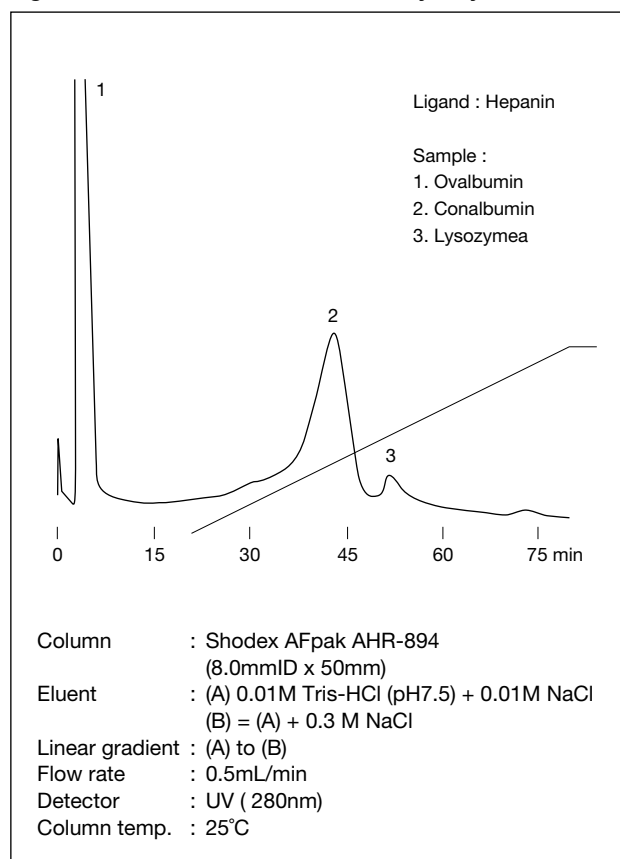


Fig. 32 Glutathione S-transferase

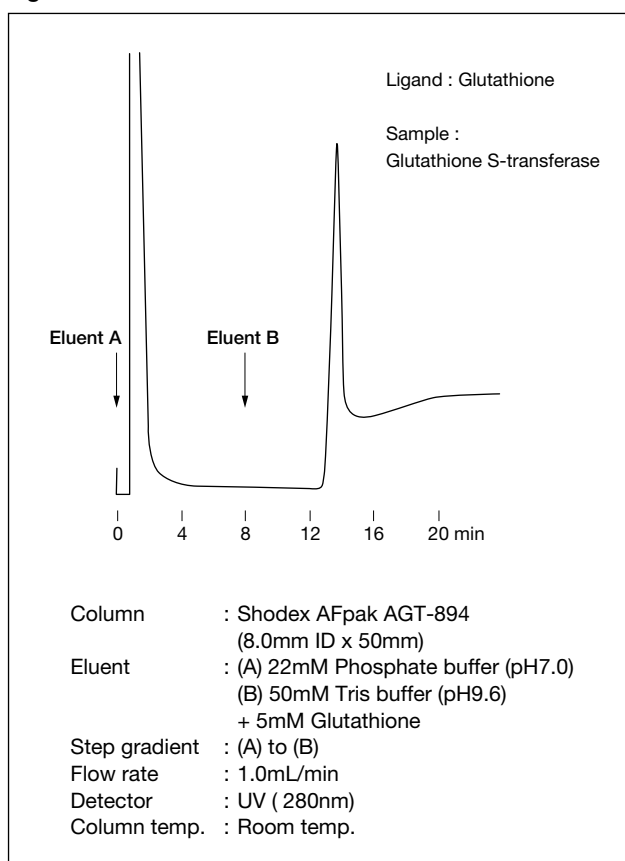


Fig. 33 L-lactate dehydrogenasepsin

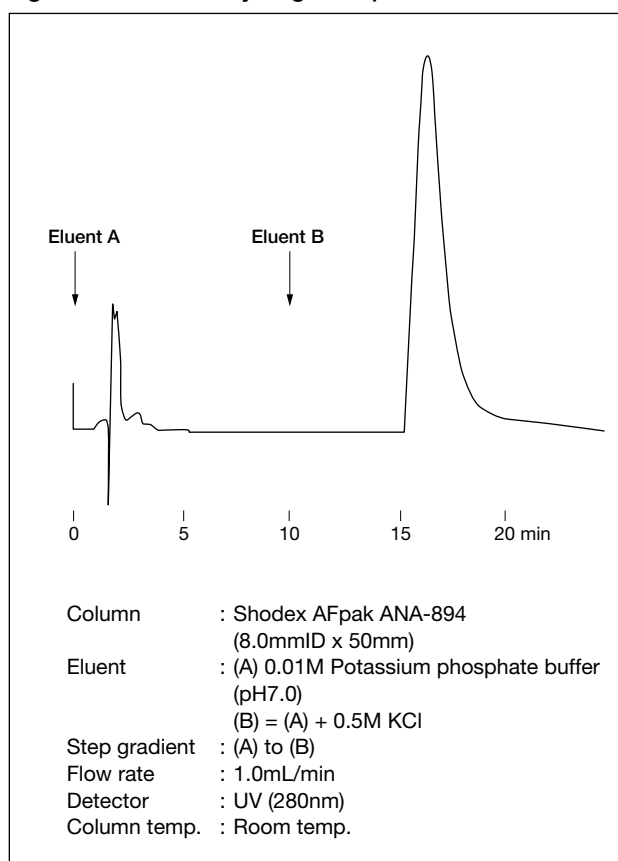


Fig. 34 Super oxide dismutase

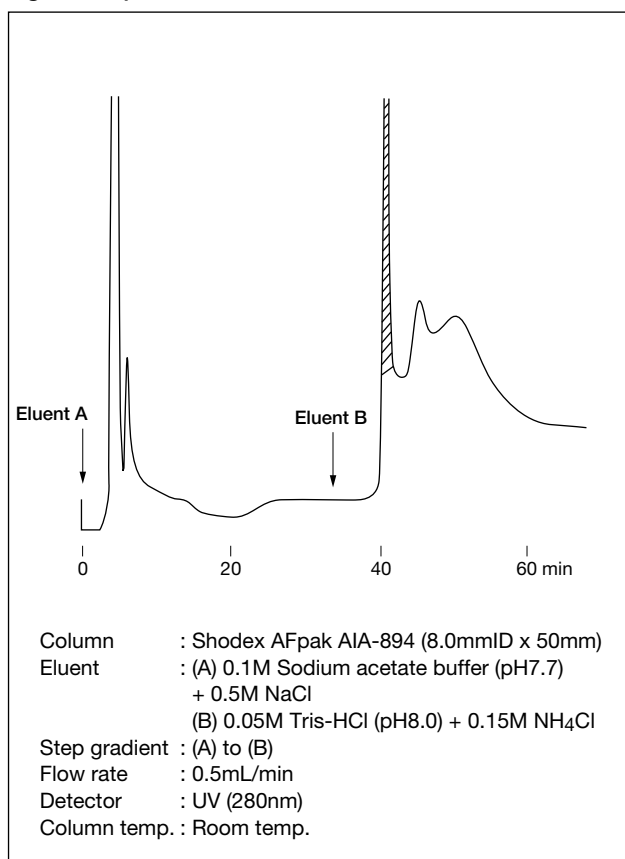


Fig. 35 Fibrinogen (Sigma)

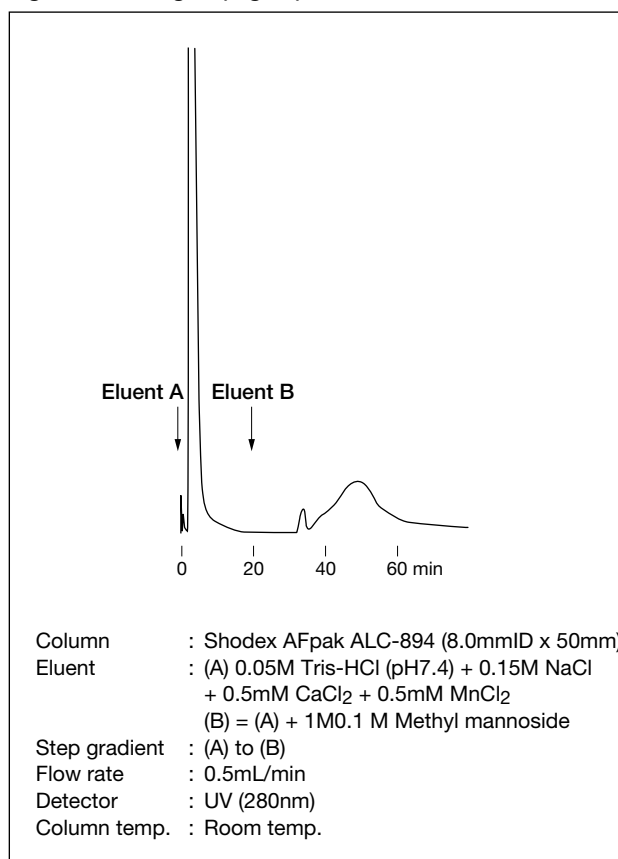


Fig. 36 Plasminogen (from bovine plasma, Sigma)

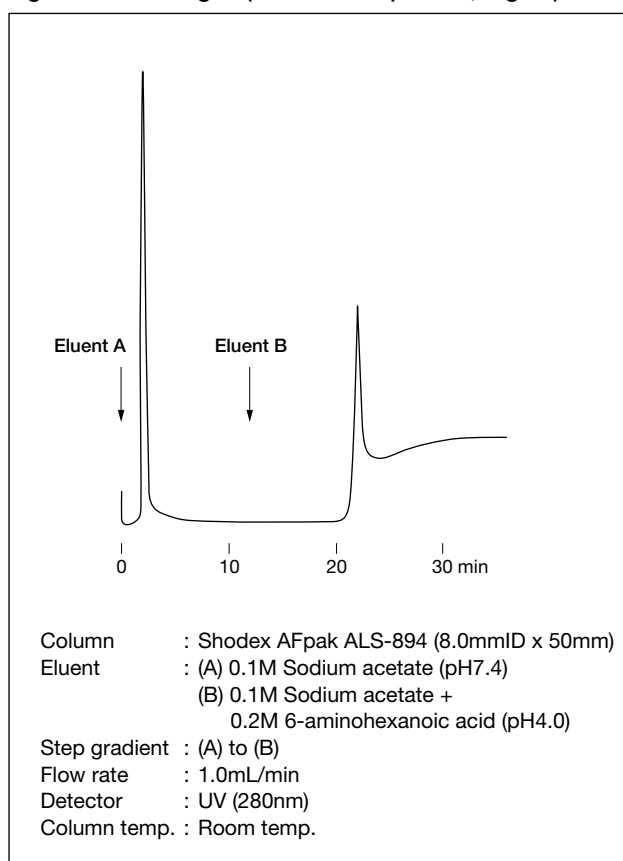


Fig. 37 Human serum

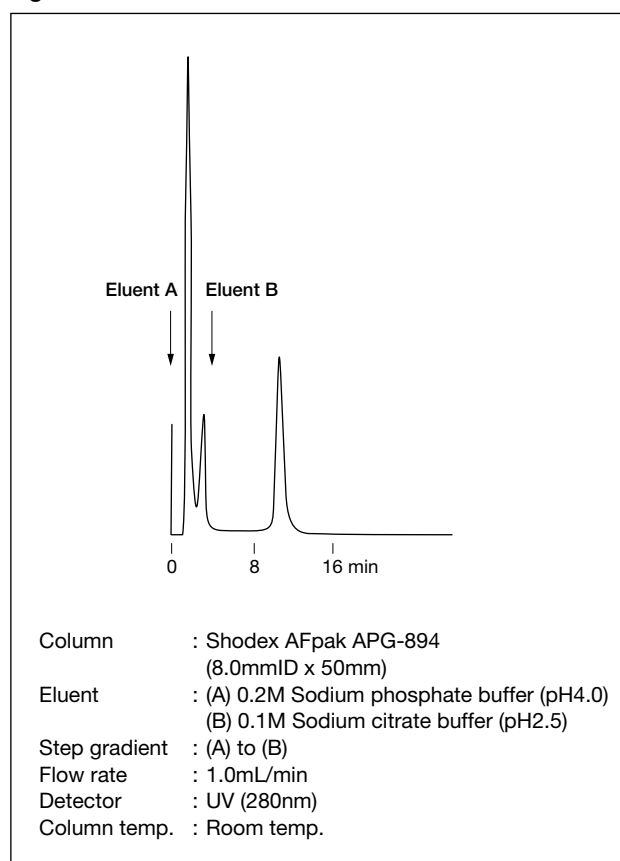


Fig. 38 Globulin Bovine γ -globulin (Sigma)

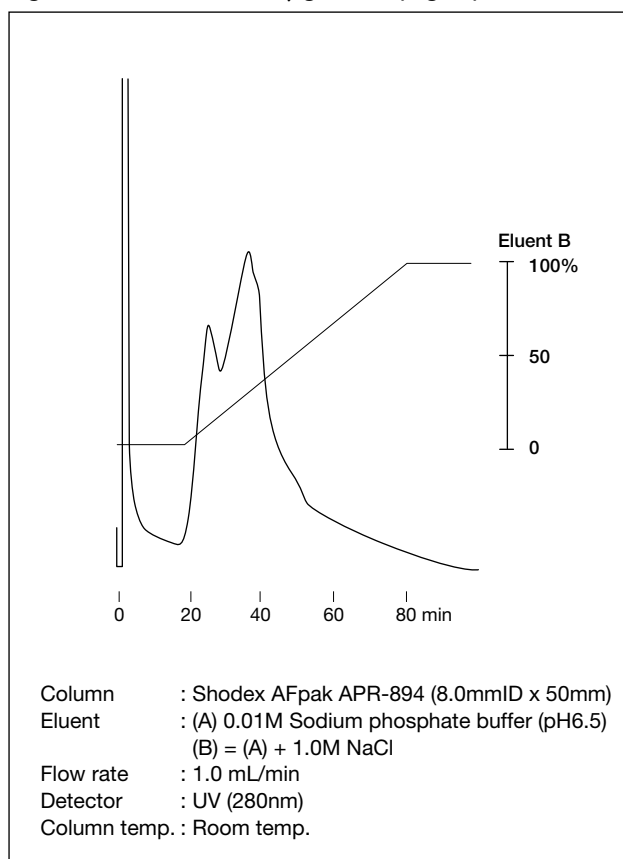


Fig. 39 Bovine γ -globulin Globulin

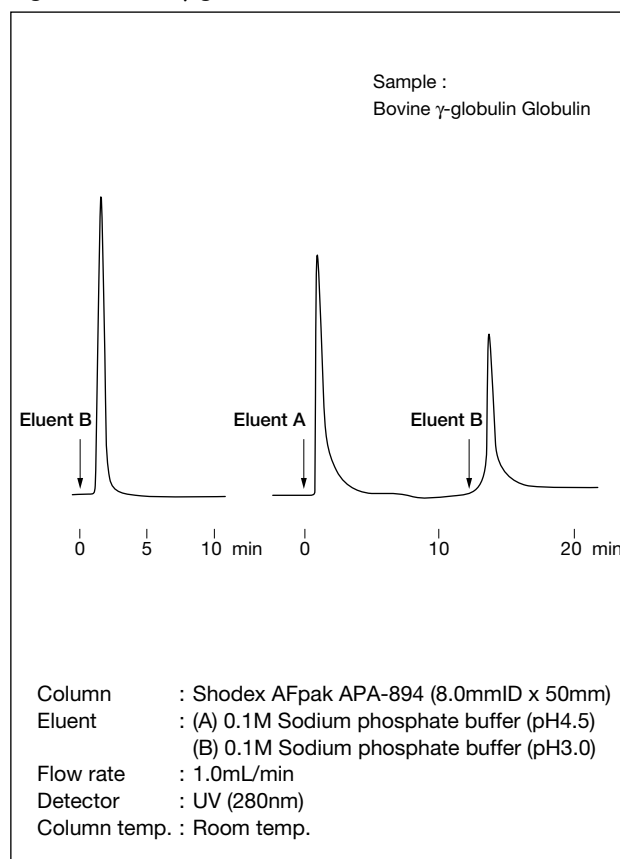


Fig. 40 Globulin Human γ -globulin (Sigma)

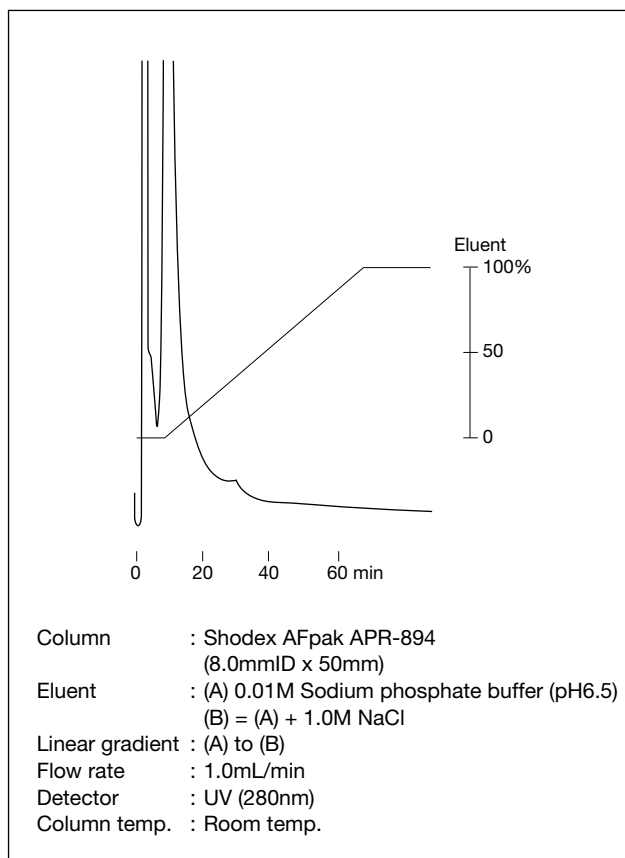


Fig. 41 Human IgM (Sigma)

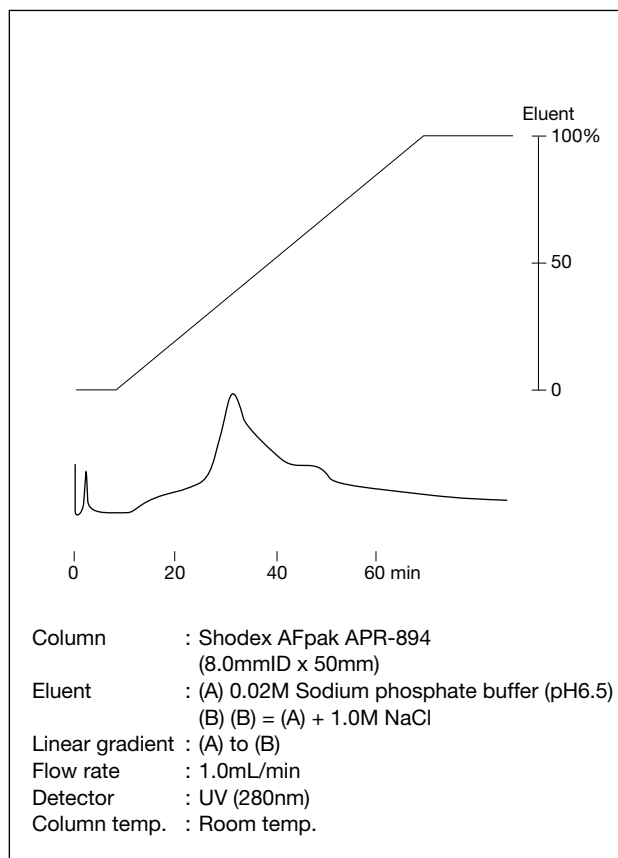


Fig. 42 Human serum albumin (Sigma)

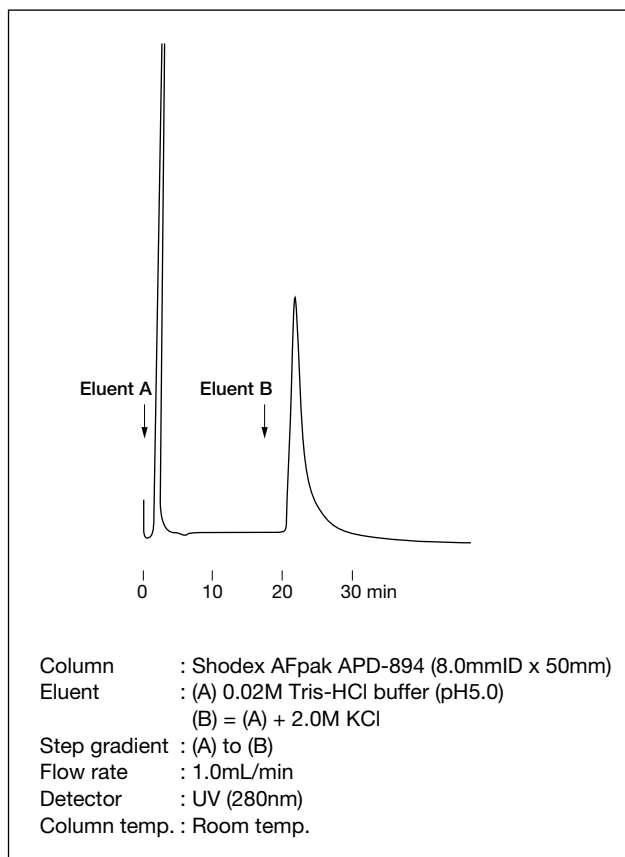


Fig. 43 C-Reactive protein (Sigma)

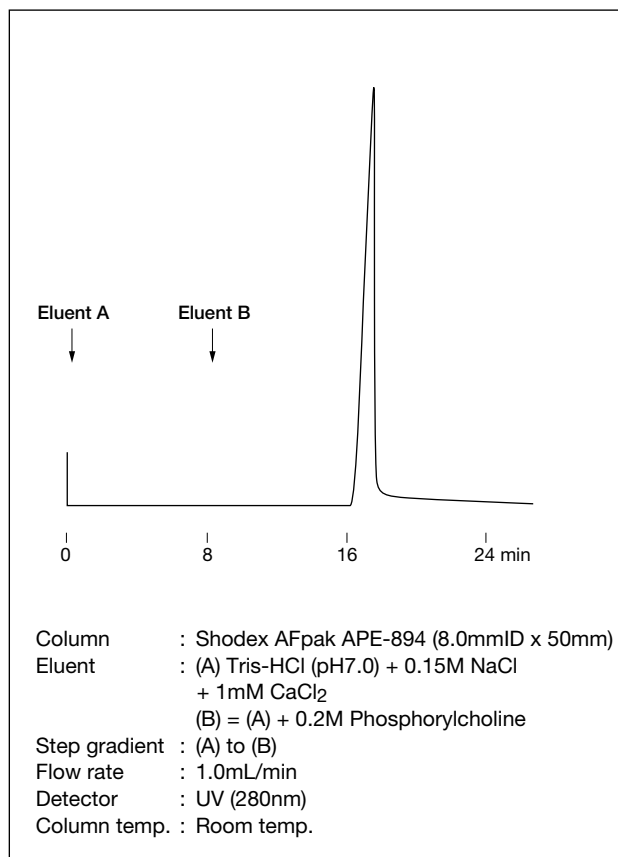


Fig. 44 Trypsin

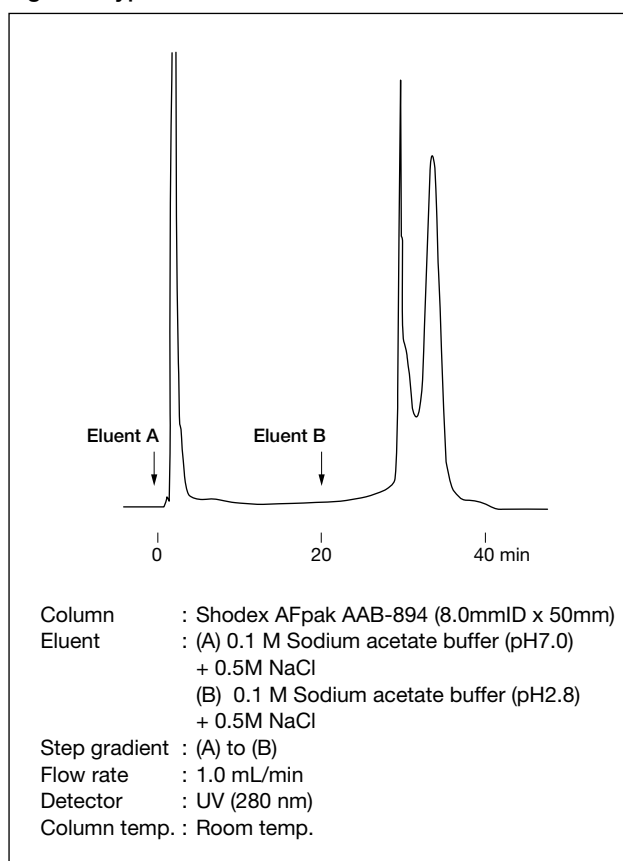


Fig. 45 Adenosine phosphate

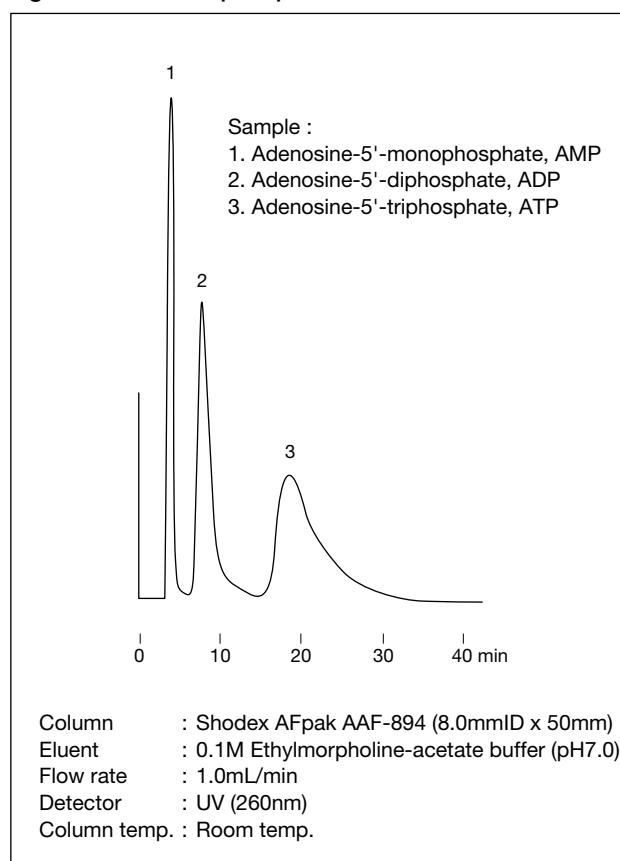


Fig. 46 0.1% Avidin, 10 μ L

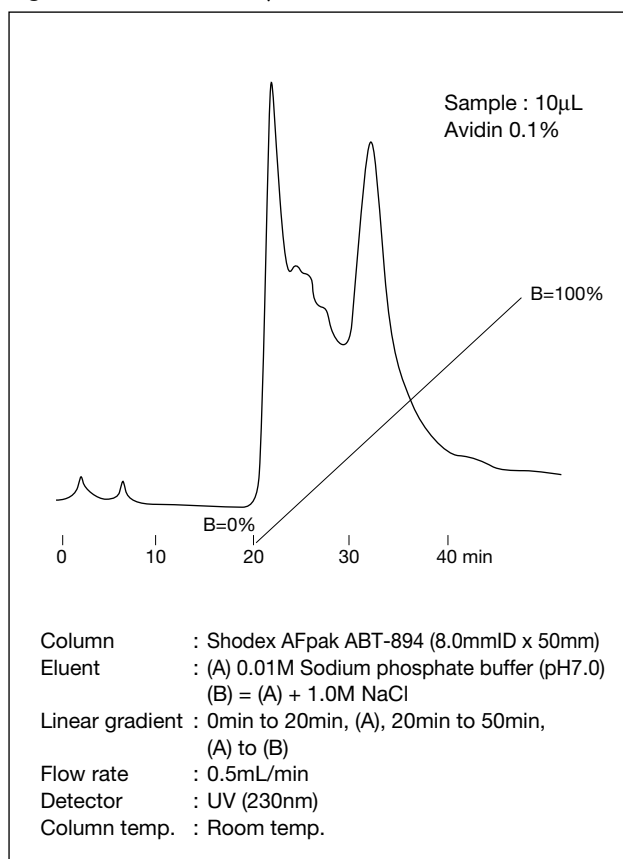


Fig. 47 Chymotrypsin

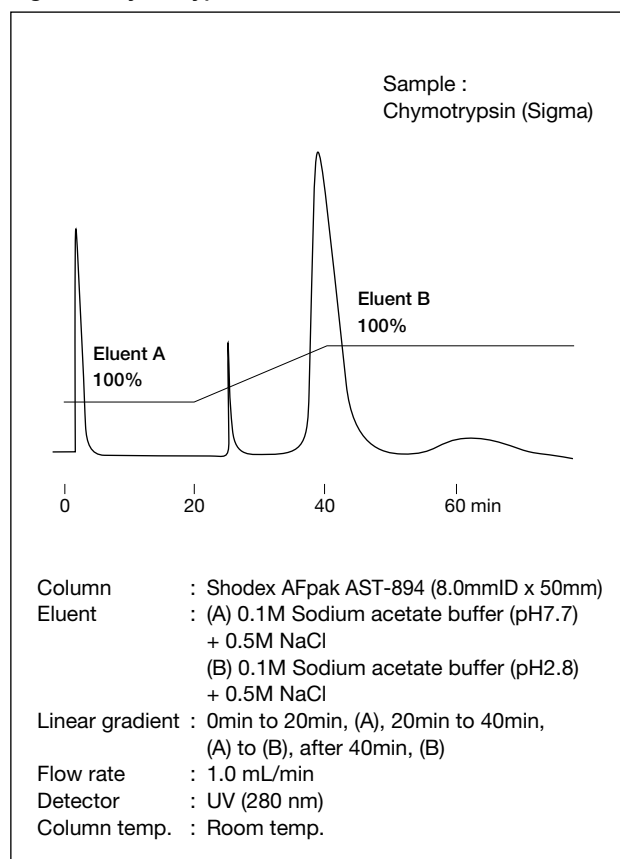


Fig. 48 Lysozyme

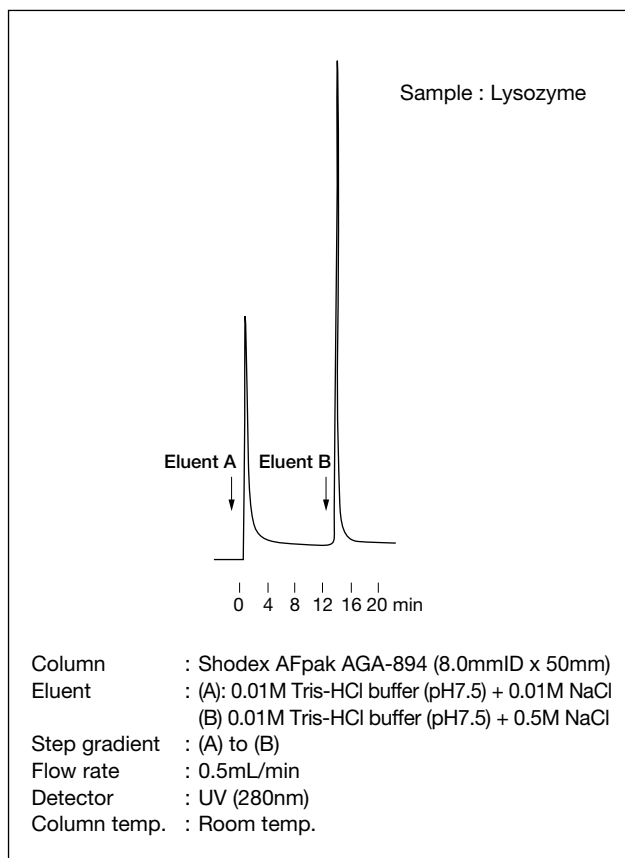


Fig. 49 Lysozyme

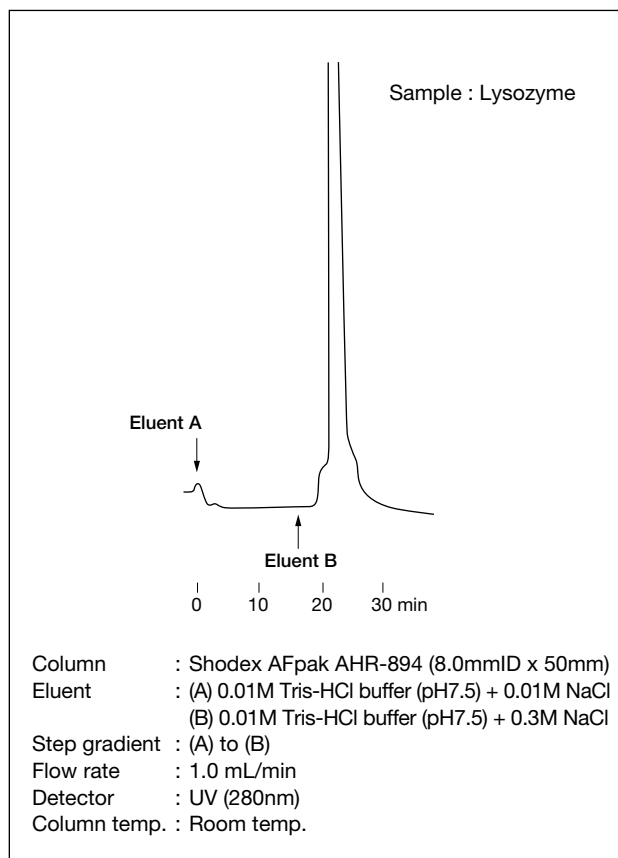


Fig. 50 Fibronectin

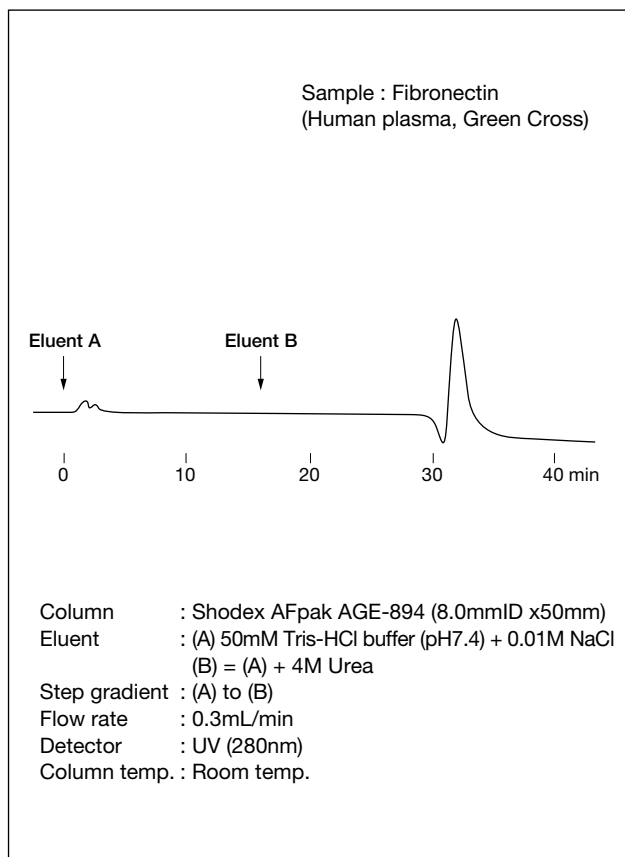
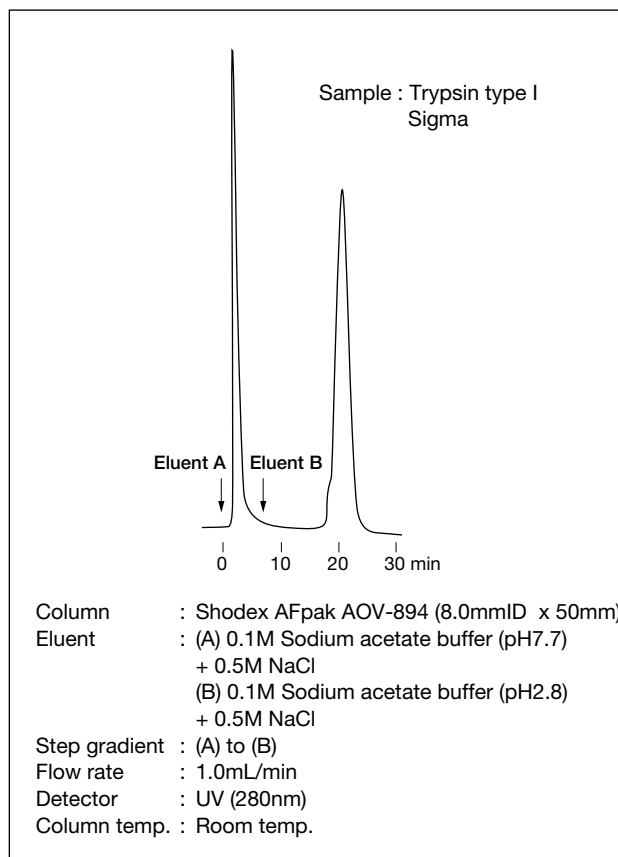


Fig. 51 Trypsin (type I)



The Shodex AFpak (Column size : I.D. 8.0mm x L 50mm)

Product AFpak	Ligand	Application	Ligand load /gel(g)	Capacity	Particle size (µm)
AAB-894	Aminobenzamidine	Serine protease	100µmol	—	18
AAM-894	5'AMP	NAD, ATP dependent enzymes	10µmol	Lactic dehydronase 1.5mg/g	18
AAP-894	Aprotinin	Serine proteases	5mg	Trypsin 3mg/g	18
ABT-894	Biotin	Avidin	—	Avidin 9mg/g	18
ACA-894	Concanavalin A (ConA)	Glycoprotein, polysaccharides	15mg	—	18
ACB-894	Cibacron Blue	Albumin, NDA dependent enzymes	40µmol	BSA 20mg/column	18
ADS-894	Dextran sulfate	Lipoproteins, blood coagulation factors	30mg	LDL 5mg/g	18
AED-894	Ethylenediamine diacetic acid	Nucleic acids, serum proteins	30µmol	—	18
AGA-894	N-acetyl-glucosamine	Lectins, carbohydrate metabolizing enzymes	—	Lysozyme 0.6mg	18
AGE-894	Gelatin	Fibronectin	30mg	Fibronectin 150mg/g	18
AGT-894	Glutathione	Enzymes related to glutathione	50µmol	—	18
AHR-894	Heparin	Lipoproteins, blood coagulation factors	5mg	Lysozyme 4mg/column	18
AIA-894	Iminodiacetic acid	Interferon, serum proteins	70µmol	BSA 70mg/column	18
ALC-894	Lentil lectin	Glycoproteins, polysaccharides	6-7mg	—	18
ALS-894	Lysine (LCA)	Plasminogen, plasminogen activator, RNA, DNA	—	Plasminogen 54µg/g	18
ANA-894	NAD	NAD-Dependent dehydrogenase	10µmol	Lactic dehydronase 1.4mg/g	18
AOV-894	Ovomucoid	Trypsin-like protease	10mg	Trypin 100mg/g	18
APA-894	Protein A	Human IgG, immune complexes	4mg	IgG Human 20mg/g	18
APB-894	Aminophenyl boronic acid	Nucleic acids and catecholamines	800µmol	Sorbitol 0.2mg/column	10
APD-894	Procion red	NAD, NADP, interferon enzymes	40-60µmol	BSA 72mg/g	18
APE-894	Phosphorylethanolamine	C-reactive protein, enzymes	—	C-reactive protein 0.91mg/g	18
APG-894	Protein G	IgG immune complex	4-5mg	IgG Humnan 10mg/g	18
APH-894	Phenyl alanine	Subtilisin Carlsberg	50µmol	Subtilisin Carlsberg 9mg/g	18
APR-894	Proteamine	IgM	4-5mg	IgM Human 1.9mg/column	18
ARC-894	RCA-I	Glycoproteins, polysaccharides	20mg	—	18
AST-894	Soybean trypsin inhibitor	Trypsin-like proteases	20mg	Trypsin 100mg/g	18
AWG-894	Wheat germ agglutinin (WGA)	Glycoproteins, polysaccharides	14mg	—	18
ACH-494	Choline oxydase, acetylcholine esterase	Choline, acetylcholine	—	—	18

The following semi-micro and micro columns can be prepared.

- Inner diameter : 2.0mm, 1.0mm, 0.8mm, 0.5mm, 0.3mm
- Length : 50mm, 35mm

3-6. Multi mode chromatography

3-6-1. Separation mechanism

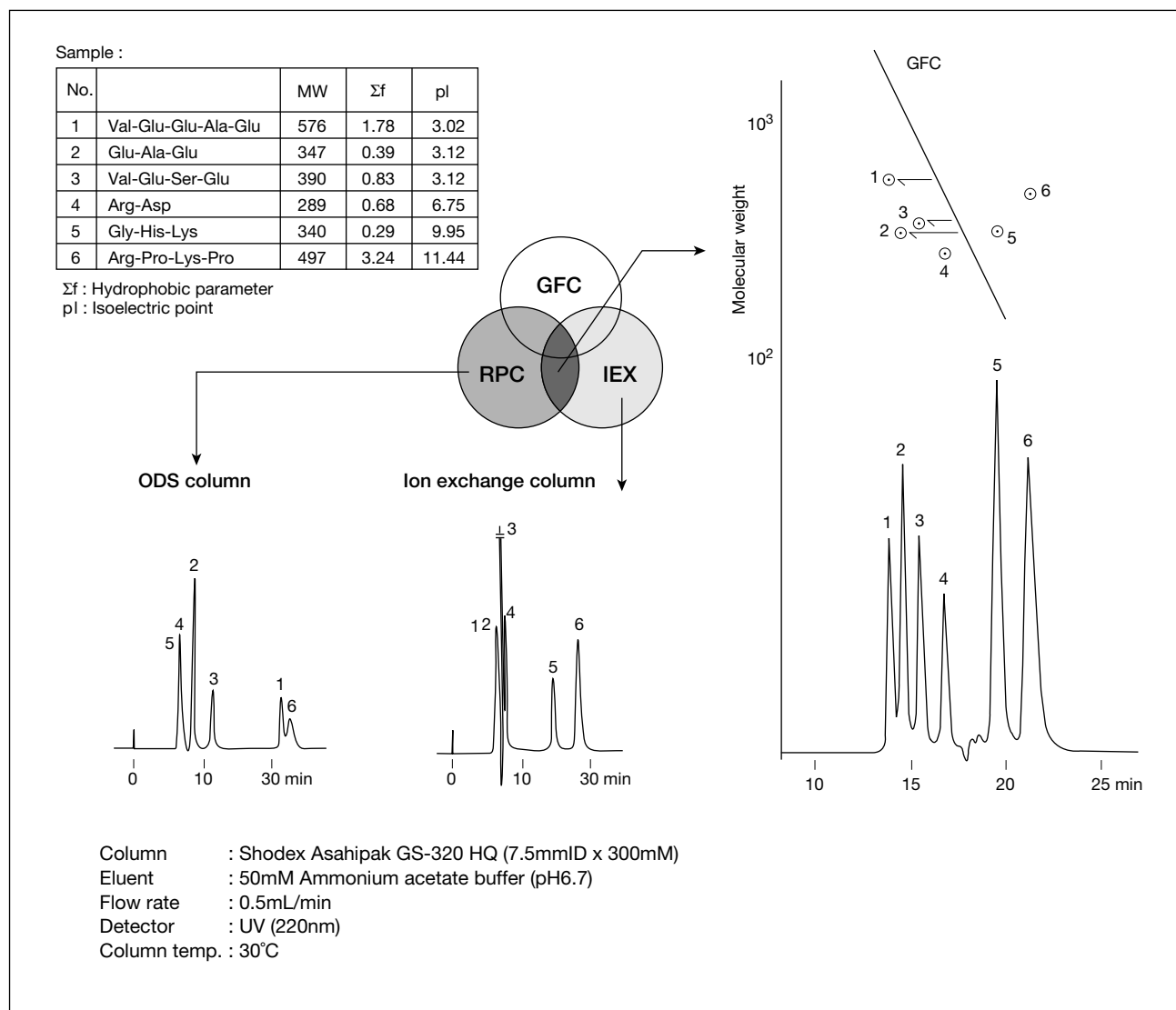
Multi mode chromatography is an analytical method combining several separation modes. When a single separation mode is not enough for separating the target substance, an improvement can be expected by using multi mode chromatography. The balance between the separation modes involved can be controlled by changing the eluent composition.

3-6-2. Introduction of Shodex columns

● Asahipak GS series

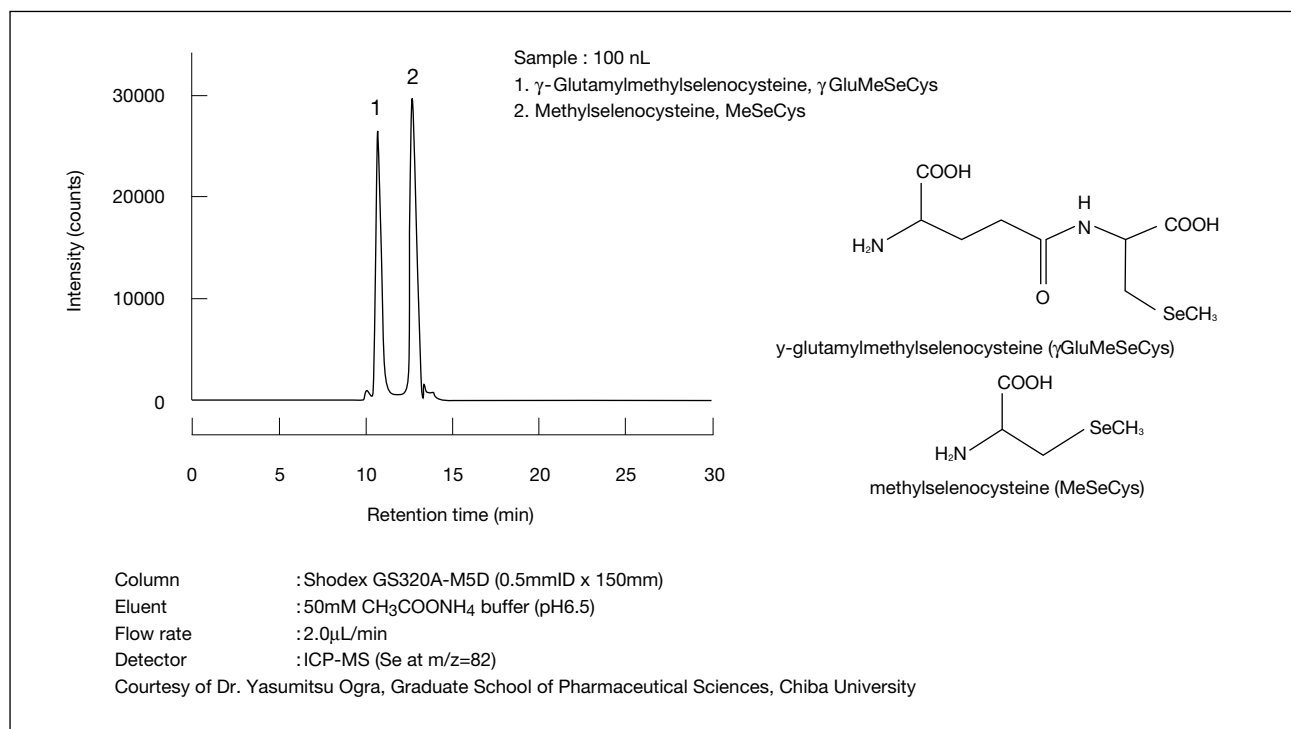
The Shodex Asahipak GS-HQ series mainly relies on size exclusion chromatography but also works in multi mode with the combination of reversed phase and ion exchange modes. One can therefore expect different separation patterns from those obtained by standard size exclusion chromatography. The GS-HQ series is particularly suited for the separation of hydrophilic peptides, especially acidic peptides and basic peptides (See Figure 52). The base material is a polymer, resulting in the following advantages; 1) usable at a wide pH range, 2) washable with alkaline solutions, 3) column durability.

Fig. 52



Metal-bonded amino acids can be analyzed by multi mode chromatography. Figure 53 shows the investigation of metal-bonded amino acids which is important for the study of how metals are metabolized in the human body. Selenized amino acids are analyzed using the micro column GS320A-M5D (0.5 mm ID x 150 mm) and ICP/MS. The sensitivity of the analysis using this micro column is higher than with a conventional type column.

Fig. 53



The Shodex Asahipak GS series

Product	Size (mm) ID x L	Plate Number (TP/column)	Exclusion Limit (Pullulan)	Particle size (μ m)	Pore size (\AA)		Usable pH range
					Max.	Avg	
GS-220 HQ	7.5 x 300	> 19,000	3,000	6	150		2 to 9
GS-320 HQ	7.5 x 300	> 19,000	40,000	6	400		2 to 12
GS-520 HQ	7.5 x 300	> 18,000	300,000	7	2,000		2 to 12
GS-620 HQ	7.5 x 300	>18,000	2,000,000	7	7,000		2 to 12
GS-2G 7B	7.5 x 50	(Guard column)	—	9	—		2 to 12

Max. usable organic solvent concentrations:

GS-320 HQ, GS-520 HQ, GS-620 HQ : 100% Methanol, 50% Acetonitrile

GS-220 HQ : 30% Methanol, 50% Acetonitrile

The following semi-micro and micro columns can be prepared.

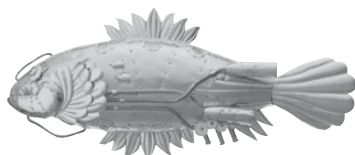
• Inner diameter : 4.6mm, 2.0mm, 1.0mm, 0.8mm, 0.5mm, 0.3mm • Length : 250mm, 150mm, 50mm

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