FT-Gebaflex

GeBAflex-tubes Extraction and Dialysis Kits

Here is the next generation technology in **electro-elution/extraction** of biological macromolecules from polyacrylamide or agarose gel as well as for **convenient dialysis** of small-volume samples.

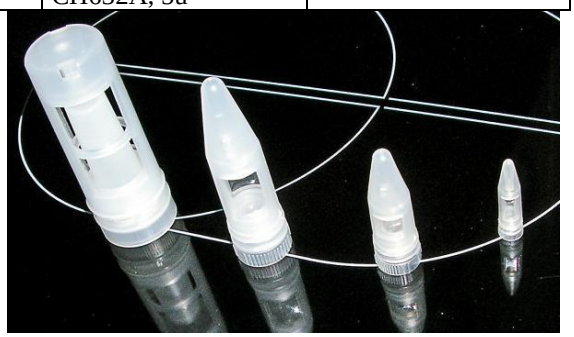
GeBAflex-tube gel dialysis and extraction kits are based on a single eppendorf-like tube, containing a hemi-permeable membrane. The sample (solution, gel slice,...) is simply deposited in the device.
For **dialysis** applications, the device is loaded with sample and then is placed on a floating boy in a beaker filled with buffer to allow for standard dialysis, with high rate. Dialyzed biomolecules (for desalting, buffer exchange, ...) are then recovered.
For **extraction** applications, the device is loaded with gel slices and placed on a support tray, then in an electrophoresis tank, and a current is applied. Electroeluted biomolecules are recovered in solution inside the device.

Many downstream applications are possible: bioassays, MS, purifications, ... as well ligand complexes analysis, sequencing, PCR amplification,... See below.

Following sizes GebaFlex tubes and membranes cut-off are available, provided with accessories (floating boy for the dialysis kits, support tray and extraction buffer for the extraction kits):

Dialysis kits (Include GeBAflex-tube floating boy, handbook)

MWCO	MINI (10-250 µL)	MIDI (50-800 µL)	MAXI (100-3000 µL) §	MEGA (3-20ml) #
1 000 Da		CD195A, 5u S		CH633A#, 5u S
3 500 Da		U2707A, 10 u S,T U2707B, 30 u *	AA740A, 5 u S AA740B, 15 u *	CH634A#, 10u S CH634G#, 30u
6 000 - 8 000 Da	AZ389A, 10 u S AZ389B, 30 u *	U2708A, 10 u S,T U2708B, 30 u	AA742A, 5 u S AA742B, 15 u *	CH635A#, 10u S CH635F#, 30u
12 000 - 14 000 Da	AZ390A, 10 u S AZ390B, 30 u *		AA741A, 5 u S AA741B, 15 u *	CH636A#, 10u S CH636F#, 30u
25 000 Da	CH629A, 5u SS		CH631A, 5u S	
50 000 Da			CH632A, 5u S	



***** Items are available in larger size (50&100u), and (^{T}) as economic packaging (without box and floating rack) : #U2707D (MIDI, 3500MWCO, 30 tubes) and #U2708D (MIDI, 6-800MWCO, 30tubes). Some trial sizes are available as well (^{S}).
§ two caps are provided with MAXI devices to easily adjust the dialysis volume of GeBAflex-tube between 100µl-2ml and 100µl-3ml.

Mega tubes are provided with a cap designed for max 20ml sample sizes as cat.numbers terminated by '1'. Change the last digit of the cat.# by 'B' for 15ml sample size, and 'C' for 10ml sample size.

Storage: Room temperature (>36 months for dialysis kits, >12months for extraction kits)
For long storage, keep in a cool place at relative humidity 35% at least.

Extraction kits (Include GeBAflex-tube dialysis kit + electroelution supporting tray + 3 solutions $^{\&}$)

Extraction kits are no more available. Please order separately the Gebaflex dialysis tubes + the needed extraction buffers + supporting trays.

Accessories

Supporting tray (for 1-4 MINI GeBAflex-tubes) RC7750, 1 unit
Supporting tray (for 1-4 MIDI GeBAflex-tubes) BI2920, 1 unit
Supporting tray (for 1-3 MAXI GeBAflex-tube) RC7770, 1 unit
Caps for Mega: RC7700(20ml), RC7690(15ml) and RC7680(10ml)

Floating tray (for 1-9 MINI GeBAflex-tubes) RC7760, 1 unit
Floating rack (for 1-4 MIDI GeBAflex-tubes) BI2930, 1 unit
Floating rack (for 1-7 MAXI GeBAflex-tubes) RC7780, 1 unit
Floating rack (for 1 MEGA GeBAflex-tube) RC7710, 1 unit

Precipitation TCA reagent (for protein) AXJTH0/1/2/3 (2ml for 8 Mini or 2 Midi / 10ml for 40 Mini or 14 Midi or 3 Maxi / 30ml for 120 Mini or 42 Midi or 10Maxi / 60ml for 240 Mini or 85 Mini or 6 Maxi)
MS Solution (for SDS removal) AXJTL0/1/2
(2ml for 80 Mini, 28 Midi, 6 Maxi / 10ml for 400 Mini, 142 Midi, 33 Maxi / 30ml for 1200 Mini, 428 Midi, 100 Maxi)
Precipitation Kac reagent (for DNA and RNA) AXJTP0/1/2
(2ml sufficient for 80 Mini, 28 Midi, 6 Maxi / 10ml for 400 Mini, 142 Midi, 33 Maxi / 30ml for 1200 Mini, 428 Midi, 100 Maxi)

Applications & key features

GebaFlex tubes are particularly suited for desalting, and for rapid and high yield extraction of Protein, RNA, DNA and complexes of RNA-protein, DNA-protein and Protein-Protein from any gel matrix.

Characteristics

-**Volume**: 10-250µl, 50-800µl, 100-3000µl, or 3-20ml
-**MWCO**: 3500, 6000-8000, 12000-14000, 25 000 or 50 000Da
-membrane is made of **ultra-clean regenerated cellulose** (sulfur and heavy metal free and EDTA treated)
-GeBAflex-tubes are autoclaved and are bacterial free
-All kit buffers are filtered, autoclaved and are bacterial free

Dialysis uses examples

GeBAflex-tubes provide efficient dialysis / desalting of any biomolecule:
. Removing excess reagents in labeling and conjugations
. Removing salts, surfactants, detergents, solvents, buffers
. Buffer exchange (for storage, assays,...), pH adjustement
. Purified fractions, tissue/cell extracts, virus, particules..
. Recombinant proteins, peptides,... (desalting/purification, refolding,...)
. Nucleic acid samples (desalting/purification, ethidium bromide removal,...)

Features

- **Recovery**: > 97%
- **Cut off**: 1 000 to 50 000 MWCO
- **Volume for Dialysis**: 50 µl to 20ml
- **Purity**: no contamination with Protease, RNase, DNase and PCR products.
- **Ready to use**: single use, no need for cleaning or autoclaving.

See directions for use below.

Extraction (Electro-elution) uses examples

GeBAflex-tubes provide high yields of pure proteins and nucleic acids, for direct use in down-stream applications such as:

- Proteins recovered or purified from gels for:

. Immunization of laboratory animals.
. Mass spectrometry analysis (MW determination, structural characterization and identification)
. HPLC analysis for peptide sequencing; Peptide mapping
. Recover proteins and simultaneously remove ampholytes from proteins run on isoelectric focusing gels.
. Purification of very small Protein quantities.
. Protein - nucleic acids complexes analysis.
. Dialyze purified proteins found to have amino termini blocked to sequencing (unblock /buffer suitable for enz. or chem. cleavage)

- DNA or RNA recovered or purified from gels for:

. RNA structure mapping.
. Purification of RNA transcripts.
. Removal of RNA contamination from in vitro transcription RNA.
. Complex formation between nucleic acids and Proteins.
. Radioactive and fluorescent sequencing.

See directions for use below.

Features

- **Recovery**: Protein > 75%, RNA or DNA > 90%.
- **Starting Amount**: 0.5-5 µg of proteins and nucleic acids (Mini & Midi), or 20µg (Maxi)
- **Extraction limits**: DNA > 20 bp, RNA or oligonucleotides > 20 nucleotides, Protein > 1000 MW
- **Purity**: No contamination with Protease, RNase, DNase and PCR products. Heavy metal presence tested.
- **Ready to use**: Single use, no need for cleaning or autoclaving.

Directions for use - Dialysis

A: Dialysis protocol

Choose the suitable GebaFlex device (and cap) (Mini, Midi, Maxi, Mega), depending your sample size:

Sample volume	Device / config.
(10-250 µL)	MINI
(50-800 µL)	MIDI
(100µL-2ml) (2ml-3ml)	MAXI – with 2ml cap MAXI – with 3ml cap
(7-20ml) (5-15ml) (3-10ml)	MEGA – with 20ml cap MEGA – with 15ml cap MEGA – with 10ml cap

1. Fill the GeBAflex-tube with dH_2O or desired buffer*, to rinse it. Empty the tube.
Rem: use max volume: 250µl for Mini, 0.8 ml for Midi, 2/3ml for $Maxi_{-2/3}$, and 20ml for $Mega_{-10/15/20}$. No leak should be observed.

2. Load sample into the GeBAflex-tube.
Close the tube with appropriate cap
Rem: sample volume should be in following range:

3. Position the loaded GeBAflex-tube on floating rack[a]
Place for a sufficient time [c,c3] in a stirred[c1] beaker containing large volume[c2] of the desired buffer[b]

Notes:

[a] **Floating racks** can hold 1-7 Midi GeBAflex-tube(s), or 1 Mega* tube.
*For Mega tubes, adjust floating balance rack heigh for upright floating; i.e; up middle height of the Mega tube if dialysing 5ml).

[b] The **choice of buffer** depends on downstream application. A standard buffers include PBS, TBS,...

[c] One usually expect to reach more or less **complete dialysis** with 2 to 4 changes, that can be achieved with a proper balance of bath volume, agitation and time. As a guideline, perform typically **3 changes**
(i.e. 1-2H with 100 sample vol. of buffer, 2-6H with 1000 vol. and overnight with 1000 vol.).

[c1]-Adjust the **stir bar speed** for proper agitation of the buffer around the dialysis device. Avoid forming foam.

[c2]-Use **sufficient bath volume** of the desired buffer to dialyze efficiently.
Bath volume can be lowered for a rapid first dialysis, but should be sufficient at the end, depending on dialysis duration, agitation and the number of buffer changes. Think dialysis would theorically (at equilibrium,...) "dilute" small molecules of your sample for each change by a factor = dialysis bath / sample volume.
As guideline, *use at least >100-fold the volume of sample, and up to 1000 or more for long and final dialysis*.

[c3]-Allow dialysis to perform for a **sufficient time**.
Low-molecular weight salts and buffers (e.g., Tris·Cl and KPO_4) equilibrate usually within 3 hours, but time increase with sample volume, and considerably with viscous samples. Sufficient dialysis can be achieved i.e. within 1H for 0.1ml sample in 1000 vol of bath. A quick pre-dialysis step shoud be at least 30min for 0.1ml sample in 100 vol of bath. But again time should be sufficient at the end of the dialysis process, and the exact dialysis equilibration time should ideally be determined – monitoring undesired low species in sample.
Now, *2-3 changes with 1-4H duration are sufficient in most cases*.

4. Change the dialysis buffer as necessary, typically 2-3 times (see notes above).
Check if necessary dialysis completion anylysis the sample.
Note: the sample volume may increase depending onsome configurations of sample / buffer compositions (osmosis). In case of large volume increase, let your sample evaporate on the bench top, or even using a fan. See protocol C0 below.

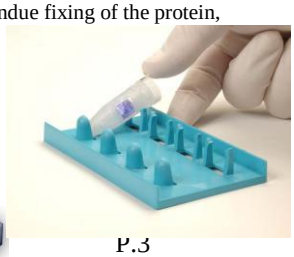
5. Transfer the sample carefully with pipette from the GeBAflex-tube to a clean tube.

B: Extraction from PolyAcrylamide Gels

This protocol is outlined for proteins from polyacrylaminde gels (min 0.5µg/MIDI, 20µg/MAXI), but applies also for nucleic acids from polyacrylaminde or agarose gels.

1. Fill the GeBAflex-tube with dH_2O; incubate for at least 5 min. empty the tube.
Note: use 0.8 ml for Midi, 2/3ml for $Maxi_{-2/3}$. No leak should be observed.

2. After staining the gel (see note), excise the gel slice containing the protein with a clean, sharp scalpel.
IMPORTANT:
-Fixation of proteins before electro elution (e.g. fixation with methanol, acetic acid, etc) is not recommended; fixation greatly reduces extraction yield.
-It is recomended to use the CooBlue staining solution #UP47255A, that will yield a sensitive protein staining without undue fixing of the protein, and result in highest recovery yield of proteins from the gel.
-Minimize the size of the gel slice by removing extra gel. Maximum gel slice size 2 cm x 1 cm.



3. Transfer the gel slice to a GeBAflex-tube.
Maximum size of the gel slice that can be inserted into the tube: 1cmx0.5cm (Midi) or 2 cm x 1 cm (Maxi)
For larger gel slices, use several GebaFlex units as needed.
Fill the tube with protein-running buffer.
Note: use 0.7-0.8 ml for Midi, 2-3ml for Maxi.

Close the tube gently.
Avoid air bubbles in the tube. Use 3 ml cap for Maxi GeBAflex-tubes.

4. Place the GeBAflex-tube in the provided supporting tray (see image).
The supporting tray can hold 1-4 Midi GeBAflex-tube(s) or 1-3 Maxi GeBAflex-tube(s).
Position the arrow on the cap face-up.

5. Place the supporting tray containing the GeBAflex-tube(s) in a horizontal electrophoresis tank containing protein running buffer (see image 2).
protein-running buffer: 250 mM Tricine pH 8.5, 0.025% SDS and 25 mM Tris-Base
IMPORTANT: Immerse fully the GeBAflex-tube(s) with the tray in the buffer.
The two membranes of the GeBAflex-tube must be in **perpendicular to the electric field** to permit the electric current to pass through the tube. Cover the supportingtray: height is 1.5cm (Mini) and 2.4cm (Midi)

3 Maxi GebaFlex ready for electroelution

6. Pass electric current (usually at 100 volt) until protein exits from the gel slice.
IMPORTANT: **Electro-elution time** is to be adjusted for each individual sample. It takes at least 150-165 min for BSA protein to be electro-eluted from a 10% SDS-PAGE slice, size 1 X 2 cm. For other proteins, increase or decrease electro elution time presented in Table 1 below, by 30%.
DNA/RNA application:
The elution time need to be adjusted of each individual sample – see tables 2 3 below. Follow nucleic acid eluted out of the gel with hand-held lamp or table.

7. Reverse the polarity of the electric current for 120 seconds.
This step will release the protein from the membrane.

8. Open the GeBAflex-tube gently, pipetting the protein-containing solution up and down carefully (at least 5 times) and transfer the solution to a clean tube.
Do the pipetting on the inner side of the membrane. Important Notes:
i. Use the extracted protein directly.
ii. Concentrate the extracted protein by ProteoConN or ProteoConD kits.
iii. Precipitate the extracted protein by standard precipitation protocols (see below protocols C1 & C2/MS).
iv. Dialyze directly the extracted protein with a clean GeBAflex-tube (see below).
DNA/RNA application:
Concentrate the extracted nucleic acid by standad concentrations methods (see protocol C3 below)

B2.Elution Time Table1 – for Proteins

The elution time depends on the size of the protein molecule to be eluted, the applied voltage, the size of gel slice, the ratio of the polyacrylamide:bisacrylamide and the percentage of the polyacrylamide gel. Electro-elution time at the elution step was to be adjusted for each individual sample.

Table 1: Minimum time needed to extract different-sized proteins from 10% SDS-polyacrylamide gel (29:1 polyacrylamide:bisacrylamide) at 100 V, in 1X PRB: 0.192M Glycine, 0.025M Tris-base and 0.1% SDS
.

Protein (kDa)	Time (min) Midi GebaFlex	Time (min) Maxi GebaFlex
128	140-150	
116	120-130	180-190
81	105-115	
66.2	85-95	150-160
50	75-85	
45	65-75	30-140
40	60-70	
35		110-120
29	55-65	70-80
25		55-65
19-26	45-55	
14.4	35-45	50-60

B2'.Elution Time Table2 – for Nucleic acids

The elution time depends on the size of the nucleic acid fragment, the concentration of the gel, the size of the gel slice, the ratio of the polyacrylamide:bisacrylamide and the applied voltage.
IMPORTANT: The electro-elution time at the elution step needs to be adjusted for each individual sample.

Table 2: Minimum time needed to extract various DNA fragments from 4% polyacrylamide gel (29:1 polyacrylamide:bisacrylamide) at 100 volt in 1X TBE buffer using MAXI GebaFlex.

Fragment size (bp)	Time (min)
100	10-15
200	15-20
500	30-35
1 000	50-60
1 400	75-80

Table 3: Minimum time needed to extract DNA fragments from 1% agarose gel at 100 volt in 1XTAE buffer using MAXI GebaFlex.

Fragment size (bp)	Time (min)
500	10-15
1 000	15-20
2 000	25-30
5 000	40-45
8 000	50-55
10 000	55-60

B3.Protein Extraction from Polyacrylamide Gel compatible with MALDI-MS by Maxi GeBAflex-tube

(Matrix-assisted Laser Desorption/Ionization Mass Spectrometry)

Introduction

Sodium dodecylsulfate-polyacrylamide gel electrophoresis (SDS-PAGE) is a widely used technique for the separation and molecular weight estimation of individual proteins. However, the accuracy of this molecular weight determination is often inadequate for protein characterization. More recently Matrix-assisted Laser Desorption/Ionization Mass Spectrometry (MALDI-TOFMS) has found widespread use for the determination of molecular mass of intact proteins isolated from gels.

The isolation of proteins from gels with the newly developed GeBAflex-tube electro-elution system provides 80% recovery yields. This combination of SDS-PAGE, GeBAflex-tube electro-elution system and MALDI-TOFMS is attractive. It provides a much more accurate determination of protein molecular weight. Moreover, even difficult proteins to analyze such as integral membrane proteins (hydrophobic) or high molecular mass proteins can be analyzed. This unique method provides a powerful means for characterizing endogenous proteins of wide molecular weight range separated by SDS-PAGE.

The combination of the three methods provides significantly improved protein yield and SDS free samples. The end result is a MALDI-MS analysis with greater sensitivity. The GeBAflex-tube tool provides high protein yield recovery, and the MS buffer contained in the GeBAflex-tube kit thoroughly removes the SDS.

Electro-elution of proteins from gel
Follow protocol B above.

Protein concentration and SDS removal
Follow protocol C2 below.

B4.DNA/RNA Extraction from Electrophoresis Gels using GebaFlex tubes

Electro-elution of nucleic acids (DNA/RNA) from agarose or polyacrylamide gels
Follow protocol B for proteins above – with minor modifications outlined in brown.

Protein concentration and SDS removal
Follow protocol C2 below.

C: Directions for use – Concentration

C0a: Sample concentration by evaporation using water absorbant.

GeBAflex-tubes are suit for sample concentration using absorbants like PEG solution, of for superior result, using the spectragel absorbant #292600 (does not contaminated the sample by small PEGs ; superior concentration rate).

C0b: Sample concentration by evaporation using GebaFlex tubes

GeBAflex-tubes are ideally suited for sample concentration via evaporation. Dialysis and concentration in the same device reduce protein loss. Unlike closed-system centrifuge-type devices, sample concentration can be easily monitored in the GeBAflex-tubes.

1. Place a sample in the GeBAflex-tube or use already dialyzed sample and place it on microtube rack stand (horizontal).
2. Let your sample evaporate

Use a fan or better a neutral gas (nitrogen) to aerate the inferior membrane, increasin evaporation across the membrane.
Make sure to check from time to time to prevent evaporation to dryness.

Note: When concentrating by evaporation the water from your sample, the small molecule (buffer salts, reducing agents, etc.) will also be concentrated ! Hence, it is wise to dialyze first before concentrating.

C1: Trichloroacetic acid precipitation procedure / Precipitation TCA Reagent #BI2941

1. Add equal volume of TCA #BI2941 to the microcentrifuge tube containing the extracted protein solution.
   For example, add 700µl of 20% TCA to a 700 µl sample/Midi size [scale up for 3ml sample/Maxi size, or 20ml sample/Mega size]
2. Incubate 40-60 min on ice or 4°C.
3. Spin in a microcentrifuge at 4°C for 30 min at 14 000 RPM.
4. Discard supernatant carefully.
5. Add 500µl cold acetone for 60min and spin at -20°C for 15 min at 14 000 RPM. [2ml for Maxi size; 14ml for Mega]
   To increase protein precipitation yield incubate the samples at –20°C for 1H or up overnight.
6. Discard supernatant and air-dry the pellet.
6. Resuspend the pellet using 0.1M NaOH or dH_2O.
   Use at least 20 µl for Midi size [100µl for Maxi size, 700µl for Mega size] to perform resuspension
   If dH_2O is used for resuspension, incubate the sample for 5 min in 60°C, resuspend the sample and incubate 5 min more at 60°C.

C2: MS precipitation procedure / recommended when protein-bound SDS needs to be removed / #BI2947

1. Add MS buffer #BI2947 at 1:10 by volume to the protein containing solution and mix properly.
   For example, add 80µl of MS buffer to a 0.8 ml sample/Midi size [scale up for 3ml sample/Maxi size, or 20ml sample/Mega size]
2. Incubate for 15 min at room temperature.

3. Add 20% TCA at 1:2 by volume and mix properly.
   For example, add 440µl of 20% TCA to a 880 µl sample. [1.65ml for 3.3ml/Maxi size; 11ml for 22ml/Mega]
4. Incubate for 1 hour at 4°C.
5. Centrifuge the sample at 4°C for 30 min at 14 000 RPM.
6. Carefully descent the supernatant without disturbing the pellet.
7. Add 2 ml of ice-cold acetone.
8. Incubate at –20°C for 30 min and centrifuge the sample at 4°C for 30 min at 14 000 RPM.
   To increase protein precipitation yield incubate the samples over night at –20°C.
9. Carefully descent the supernatant without disturbing the pellet. Air-dry the pellet.
10. Resuspend the pellet in a suitable buffer solution or 0.1M NaOH.
    Use at least 20 µl for Midi size [100µl for Maxi size, 700µl/Mega size] to perform resuspension
    If dH_2O is used for resuspension, incubate the sample for 5 min in 60°C, resuspend the sample and incubate 5 min more at 60°C.

C3: DNA or RNA precipitation procedure (GeBAflex-tube) / Precipitation Buffer (Kac) #BI2943

1. Add 0.1 volume of KAc #BI2943 and 0.7-1 volume of isopropanol to the solution.
   Mix gently by inverting the tube several times.

For example,
add 70µl of 3M KAc and 500-700µl isopropanol to a 700µl sample/MIDI size [scale up for 3ml sample/Maxi size, or 20ml sample/Mega size]
Note: addition of carrier (e.g. 20 µg tRNA or 20 µg glycogen) to the solution will increase the efficiency of precipitation. [80µg/Maxi size]

2. Incubate at –20°C for 10 min.
3. Centrifuge the sample at 4°C for 30 min at 14 000 RPM.
4. Carefully discard the supernatant without disturbing the pellet.
5. Wash the pellet with 0.5 ml of cooled 70% ethanol. [2ml/Maxi size]
6. Centrifuge at 4°C for 5 min at 14 000 RPM.

Note: Centrifuge the tube in the same orientation as previously to recover the DNA or RNA in a compact pellet.

7. Air-dry the pellet for 5-20 min.

Note: Do not overdry the pellet (e.g., by using a vacuum evaporator), as this will make the DNA, especially if it is of high molecular weight, difficult to redissolve.

8. Redissolve the DNA or RNA in a suitable buffer.

Note: Use a buffer with pH >8.0 for redissolving, as DNA does not dissolve readily in acidic buffers.

For mass spectrometric analysis, appropriate solution compatible with MALDI-MS should be determined according protein characteristic. Samples should also be diluted appropppriately with MALDI-MS protocols.

Use at least 100 µl to perform resuspension.

Troubleshooting Guide

Problem	Cause	Comments and suggestions
Low yield	Insufficient elution time	Increase elution time.Increase applied voltage.
	Current polarity was not reversed	Reverse the polarity of the current for 120 second.
	Incomplete emptying of the tube from the macromolecules-containing solution	Make sure to empty all the macromolecules containing solution at the end of elution.
	Ineffective precipitation	Use suitable precipitation procedures.
	Tube not fully immersed in the buffer of the electrophoresis tank	Fully immerse the tube in the buffer of the electrophoresis tank.
	Gel slice not fully immersed in the buffer inside the tube	Fully immerse the gel slice in buffer inside the tube
	More than one gel slice into the tube	Don't fill the tube with several gel slices, for large gel slices use more than one tube
	The electric current don't pass through the tube	The two membranes of the GeBAflex-tube must be parallel to the electric field
Long elution time	Low applied voltage	Increase applied voltage.
	Gel slice is not fully immersed in the buffer inside the tube	Fully immerse the gel slice in buffer inside the tube
	Tube not fully immersed in the buffer of the electrophoresis tank	Fully immerse the tube in the buffer of the electrophoresis tank.
Macromolecules containing solution reduced after elution	Membrane not wetted before elution	Wet the membrane for 5 min with dH2O before elution
	Pinhole in the membrane, due to careless handling of the tube	Change tube
Presence of air bubbles in the tube	Insufficient dH2O or running buffer inside the tube	After inserting the gel slice in the tube, fill the tube to the top .

Other information

Related products:
See BioSciences Innovations catalogue and e-search tool:
Buffers: i.e.PBS #UP68723A
Other dialysis tools: i.e. CelluSep tubings, Desalting columns #UP848742
CooBlue Protein Gel Stains #UPG4562A

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