



CM Beads 6FF DEAE Beads 6FF

SP Beads 6FF Q Beads 6FF

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1. Product Description

CM, SP, DEAE, Q Beads 6FF are part of Ion exchange Resin which is widely used in biomedical and bioengineering for separation and purification of proteins, nucleic acids and polypeptides. The base matrix of **CM, SP, DEAE, Q Beads 6FF** is 6% highly cross-linked agarose which gives the ion exchange resin chemical and physical stability. The characteristics such as capacity, elution behavior and pressure/flow rate are unaffected by the solutions commonly used in process chromatography and cleaning procedures, for details see table under each respective ion exchange resin. Fig.1 is the pressure/flow rate curves of the matrix.

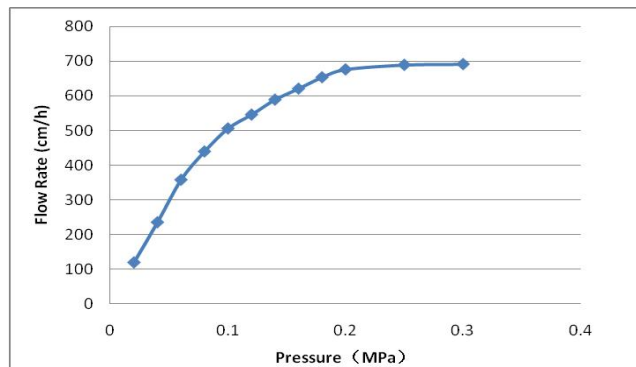


Fig.1. A typical pressure/flow rate curve for **CM, SP, DEAE, Q Beads 6FF**

CM Beads 6FF

CM Beads 6FF is a weak cation exchange resin. The ion exchange group is a carboxy methyl group, see below.

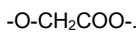


Table 1. Characteristics of **CM Beads 6FF**

Item	Description
Matrix	Highly cross-linked 6% agarose
Ion exchange type	Weak cation
Total ionic capacity	0.09-0.13mmol H ⁺ /ml medium
Particle Size	45-165 μm
Flow rate	300-600 cm/h
pH stability	4-13
Storage buffer	1×PBS containing 20% ethanol
Storage	4°C - 30°C

SP Beads 6FF

SP Beads 6FF is a strong cation exchange resin. The ion exchange group is a sulphopropyl group, see below.

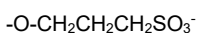


Table 2. Characteristics of **SP Beads 6FF**

Item	Description
Matrix	Highly cross-linked 6% agarose
Ion exchange type	Strong cation
Ion exchange capacity	0.18-0.25mmol H ⁺ /ml medium





Particle Size	45-165 μ m
Flow rate	400-700 cm/h
pH stability	4-13
Storage buffer	20% ethanol, 0.2M sodium acetate
Storage	4°C - 30°C

DEAE Beads 6FF

DEAE Beads 6FF is a weak anion exchange resin. The ion exchange group is a diethylaminoethyl group, see below.

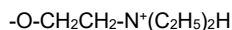


Table 3. Characteristics of **DEAE Beads 6FF**

Item	Description
Matrix	Highly cross-linked 6% agarose
Ion exchange type	Weak anion
Ion exchange capacity	0.11-0.16mmol Cl ⁻ /ml medium
Particle Size	45-165 μ m
Flow rate	300-600 cm/h
pH stability	2-12
Storage buffer	1× PBS containing 20% ethanol
Storage	4°C - 30°C

Q Beads 6FF

Q Beads 6FF is a strong anion exchange resin. The ion exchange group is a quaternary amine group, see below.



Table 4. Characteristics of **Q Beads 6FF**

Item	Description
Matrix	Highly cross-linked 6% agarose
Ion exchange type	Strong anion
Ion exchange capacity	0.18-0.25mmol Cl ⁻ /ml medium
Particle Size	45-165 μ m
Flow rate	400-700 cm/h
pH stability	2-12
Storage buffer	1×PBS containing 20% ethanol
Storage	4°C - 30°C

2. Purification Procedure

2.1 Buffer Preparation

Water and chemicals used for buffer preparation should be high purity. It is recommended to filter the buffers by passing them through a 0.22 μ m or 0.45 μ m filter before use.

2.2 Sample Preparation

It is recommended to filter the sample solution by passing them through a 0.22 μ m or 0.45 μ m filter before use.

2.3 Packing Columns

- 1) Remove air from the column dead spaces by flushing the end-piece and adapter with packing buffer. Make sure no air has been trapped under the column net.
- 2) Close the column outlet leaving the net covered with packing buffer.
- 3) Resuspend the beads stored in its container by shaking (avoid magnetic stirring the sedimented medium). Pouring the slurry down a glass rod held against the column wall will minimize the introduction of air bubbles.

If using a packing reservoir, immediately fill the remainder of the column and reservoir with packing buffer. Mount the adapter or lid of the





packing reservoir and connect the column to a pump. Avoid trapping air bubbles under the adapter or in the inlet tubing.

4) Open the bottom outlet of the column and set the pump to run at the desired flow velocity. Ideally, the medium is packed at a constant pressure of approximately 3 bar (0.3 MPa). If the packing equipment does not include a pressure gauge, use a packing flow velocity of approximately 400 cm/h (10 cm bed height, 25°C, low viscosity buffer). If the recommended pressure or flow velocity can not be obtained, use the maximum flow velocity the of the pump. This should also give a well-packed bed. Do not exceed 75% of the packing flow velocity in subsequent chromatographic procedures.

5) When the bed has stabilized, mark the position of the bed surface. Close the bottom outlet and stop the pump.

If using a packing reservoir, disconnect the reservoir and fit the adapter to the column. If using the column, carefully place the top filter on top of the bed before fitting the adapter.

6) With the adapter inlet disconnected, adjust the adapter to the bed surface.

7) Connect the pump, open the bottom outlet and continue packing. The bed will be further compressed at this point and a space will be formed between the bed surface and the adapter.

8) Close the bottom outlet. Disconnect the column inlet and push the adapter a further 2-3mm. Connect the pump. The column is now ready to use.

2.4 Sample Purification

1) Fill the pump tubing with binding buffer. Connect the column to purification system, “drop to drop” to avoid introducing air into the column.

2) Wash the column with 10 column volumes of binding buffer.

3) Apply the sample, using a syringe fitted to the connector or by pumping it onto the column.

4) Wash with 5 to 10 column volumes of binding buffer or until no material appears in the effluent.

5) Elute with Elution Buffer using a stepwise or linear gradient. For one-step elution, 5 column volumes are usually enough. Other volumes may be required if the interaction is difficult to break. Linear gradient elution can be used to separate proteins of different binding strengths with a small gradient, such as 20 column volumes or more.

2.5 Analysis

Identify the fractions containing the target protein. using UV absorbance, SDS-PAGE, or western blot.

3. Clean-in-Place

After each separation, elute any reversibly bound material either with a high ionic strength solution (e.g. 1M NaCl in buffer) or by increasing pH. Regenerate the beads by washing with at least 5 bed volumes of buffer, or until the column effluent shows stable conductivity and pH values.

Cleaning-in-place (CIP) is a cleaning procedure that removes contaminants such as lipids, precipitates, or denatured proteins that may remain in the packed column after regeneration. Regular CIP also prevents the build-up of these contaminants in the media bed and helps to maintain the capacity, flow properties and general performance of the media.

A specific CIP protocol should be designed for each process according to the type of contaminants present. CIP cycle is generally recommended every 1-5 separation cycles.

Remove the ionically bound proteins

Wash with 3-4 column volumes of 2M NaCl. Contact time 10-15min.

Remove the precipitation or hydrophobically bound proteins or lipoproteins

Wash with at least 2 column volumes of 1M NaOH . Contact time 1-2h.

Remove lipids and very hydrophobic proteins

Wash with 2-4 column volumes of 0.5% non-ionic detergent, 70% ethanol or 30% isopropanol. Contact time 1-2h.

4. Troubleshooting

Problem	Probable Cause	Solution
Back pressure is too high	Column is clogged	Cleaning in place(part 3).
	Sample solution contains precipitate	Filtering the sample solution by passing them through a 0.22µm or 0.45µm filter.
Eluate is not pure	The medium repeat too much times.	Cleaning in place(part 3).
	Wash is not enough.	Increase the volume of Wash Buffer.





5. Related Products

Product	Cat. No.	Size
Q Beads 6FF	SI001025	25 ml
	SI001100	100 ml
	SI001500	500 ml
	SI00101L	1 L
	SI00110L	10 L
SP Beads 6FF	SI003025	25 ml
	SI003100	100 ml
	SI003500	500 ml
	SI00301L	1 L
	SI00310L	10 L
DEAE Beads 6FF	SI005025	25 ml
	SI005100	100 ml
	SI005500	500 ml
	SI00501L	1 L
	SI00510L	10 L
CM Beads 6FF	SI007025	25 ml
	SI007100	100 ml
	SI007500	500 ml
	SI00701L	1 L
	SI00710L	10 L

