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ProductInformation

Benzoylated Naphthoylated DEAE Cellulose

Product Number **B 6385** Storage Temperature 2-8 °C

Product Description

This affinity resin is useful for the isolation of DNA and RNA from crude lysates. This resin can also be used to separate single-stranded from double-stranded DNA.

Regeneration of this resin for re-use may be possible with careful washing using a high ionic-strength buffer (1 M NaCl) to remove non-specifically bound material. However, most cellulose resins are very sensitive to any pressure during use and readily form resin fines, causing up to a 50% loss of binding capacity during regeneration procedures.

Precautions and Disclaimer

For Laboratory Use Only. Not for drug, household or other uses.

Preparation Instructions

This product is preswollen and will yield approximately 1 ml packed resin per gram of solid.

Procedure

For isolation of DNA from lysates, the following procedure is recommended:

- Equilibrate the resin in 300 mM NaCl, 10 mM Tris, 1 mM EDTA.
- 2. Dilute the lysate in the same equilibration buffer until the sample viscosity is similar to water.
- Load samples by either gravity flow or by low pressure chromatography. Batch methods are not recommended since the repeated mixing needed will generate resin fines.
- 4. Wash the column with the equilibration buffer until no more protein or other contaminants come off the column.
- 5. A second wash should be applied using a linear gradient starting with the equilibration buffer and increasing the NaCl concentration to 1.0 M.
- The DNA can be eluted using a gradient of 1.0 M NaCl-Tris-EDTA to 2% caffeine in 1.0 M NaCl-Tris-EDTA. The DNA should elute in the first 2-3 fractions.

References

- Haber, M., et al., Limitations on the stability of benzoylated DEAE-cellulose. Analytical Biochemistry, 139(2), 363-366 (1984).
- Gillam, I., et al., The separation of soluble ribonucleic acids on benzoylated diethylaminoethylcellulose. Biochemistry, 6(10), 3043-3056 (1967).
- 3. Nelson, S.F., et al., Genomic mismatch scanning: a new approach to genetic linkage mapping. Nature Genetics, **4(1)**, 11-18 (1993).

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