# CleanDTR

## BIGDYE® SEQUENCING CLEAN UP SYSTEM - UTILIZING PARAMAGNETIC BEADS



### **Description**

CleanDTR is an efficient paramagnetic bead-based system, designed to remove unincorporated dye terminators from a Sanger sequencing reaction. The CleanDTR process involves three simple steps: bind, wash and elute. By selectively binding the sequencing product to the magnetic particles, unincorporated dyes, nucleotides, salts and primers will be removed during ethanol washes. This principle allows for elution of the pure Sanger Sequencing product in the elution buffer of choice. The protocol can be adapted to your current liquid handling workstation (e.g. Beckman, Hamilton, Tecan, Caliper, Perkin Elmer, Agilent and Eppendorf), utilizing your current protocol, but it can also be used manually.

#### **Features**

- · Long Phred 20 read lengths averaging over 800 bps
- Pass rates over 85% or higher
- Efficient elimination of sequencing reaction contaminants
- Reduce BigDye® usage, due to increased average signal strength

#### **Applications**

• Clean up of sequencing product for both ABI and MegaBACE platforms

#### **Supported Chemistries**

- BigDye® versions 1.0, 1.1, 2.0, 3.0 and 3.1
- DYEnamic ET

#### Comparative Analysis of CleanDTR vs CleanSEQ®

		Signal Strength	CRL	QV
Plasmid DNA*	CleanDTR	2155	636	56
	CleanSEQ	2096	635	55

		Signal Strength	CRL	QV
PCR <sup>1)</sup> : 1.8 kB PCR Fragments*	CleanDTR	1044	844	50
	CleanSEQ	872	776	50

#### \* All samples (plasmid and PCR products) are a median of 16 samples in 5 µl reactions using a 1/32 BigDye® dilution and are processed on a ABI 3730 sequencer. NB: No dye blob(s) and/or ski slope effect were observed.

### **Ordering Information**

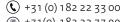
Cat No	Product Description	Preps <sup>2)</sup>	
CDTR-0005	CleanDTR (5 mL)	500/1,000	
CDTR-0050	CleanDTR (50 mL)	5,000 / 10,000	
CDTR-0500	CleanDTR (500 mL)	50.0/100,000	

<sup>1)</sup> The PCR process is covered by patents owned by Roche Molecular Systems, Inc., and F. Hoffman-La Roche, Ltd.

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Coenecoop 75 2741 PH Waddinxveen The Netherlands



**(4)** +31(0) 182 22 33 99



<sup>2) 96-</sup> or 384-well format