CUTANA™ DNA Purification Kit

Catalog No	14-0050	**Pack Size**	50 Preps
Lot No	23132005-01	**Kit Version**	v2

DESCRIPTION

Cleavage Under Targets & Release Using Nuclease (CUT&RUN) utilizes an immunotethering approach to specifically release genomic fragments of interest into solution, enabling next-generation sequencing and genomic mapping with unprecedented sensitivity. High yield purification and concentration of partitioned chromatin DNA is an essential step - one that requires a workflow specifically compatible with low starting material. Utilizing tapered cleanup columns designed for low elution volumes (as low as 6 µL), this kit produces purified, concentrated DNA ready for library preparation and next-generation sequencing (**Figure 1**). The user-friendly workflow can be completed in just 30 minutes. The columns recover > 50 bp DNA fragments, making the DNA Purification Kit ideal for a variety of CUT&RUN targets, including histone PTMs and chromatin associated proteins.

KIT CONTENTS

Item	Cat. No.	Item	Cat. No.
DNA Cleanup Columns	10-0010	DNA Wash Buffer	21-1009
DNA Collection Tubes	10-0011	DNA Elution Buffer	21-1010
DNA Binding Buffer	21-1008		

TECHNICAL INFORMATION

Storage	Store at room temperature. Stable for 6 months from date of shipment.
Instructions for Use	**See User Manual corresponding to Kit Version 2**. This kit is not compatible with previous user manuals.

REFERENCES

VALIDATION DATA

CUT&RUN Methods

CUT&RUN was performed on 500k K562 cells with 0.5 µg of either IgG (EpiCypher 13-0042), H3K4me3 (EpiCypher 13-0041), H3K27me3 (ThermoFisher MA5-11198), or CTCF (EpiCypher 13-2014) antibodies using the ChIC/CUT&RUN Kit v3.0 (EpiCypher 14-1048). DNA was purified with the CUTANA™ DNA Purification Kit and prepared for Illumina sequencing with the CUTANA™ CUT&RUN Library Prep Kit (EpiCypher 14-1001/14-1002).

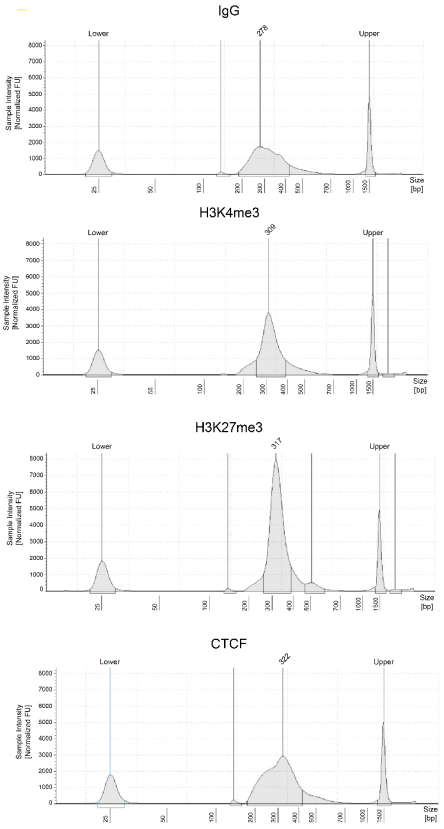

FIGURE 1 CUT&RUN DNA fragment size distribution analysis. CUT&RUN was performed as described above. Library DNA was analyzed by Agilent TapeStation®, which confirmed that mononucleosomes were predominantly enriched in CUT&RUN (~300 bp peaks represents 150 bp nucleosomes + sequencing adapters).