Datasheet for ABIN6950951

CUTANA™ pAG-MNase for ChIC/CUT&RUN Assays

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Overview

Quantity:	50 reactions
Target:	Nuclease
Host:	Escherichia coli (E. coli)
Application:	Chromatin Immunocleavage (ChIC), Cleavage Under Targets and Release Using Nuclease (CUT&RUN)

Product Details

Purpose:	This construct of Protein A and G fused to Micrococcal Nuclease is useful in performing CUT&RUN. The pAG-MNase fusion enzyme may be used in conjunction with any of our **CUT&RUN Product Sets**.
Brand:	CUTANA™
Characteristics:	Recombinantly produced in E. coli, CUTANA™ pAGMNase for ChIC/CUT&RUN Workflows is a fusion of Proteins A and G to Micrococcal Nuclease. This construct is useful in performing Chromatin Immunocleavage (ChIC) and Cleavage Under Targets and Release Using Nuclease (CUT&RUN). CUTANA pAG-MNase contains a C-terminal 6xHis epitope tag.

Target Details

Target:	Nuclease
Abstract:	Nuclease Products
Molecular Weight:	44 kDa

Application Details

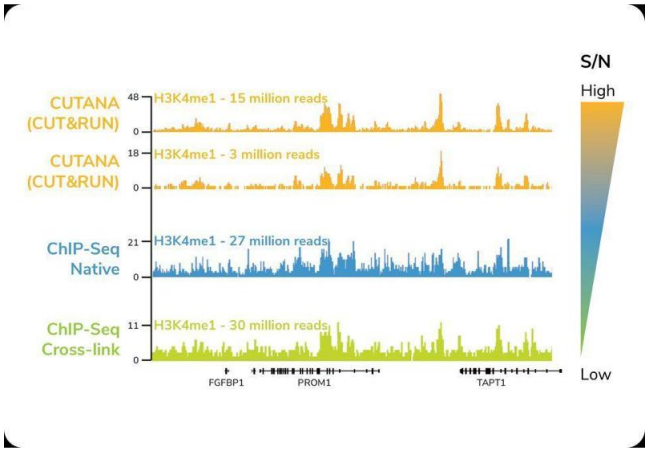
Application Notes:	This product is sufficient to perform 50/250 CUT&RUN reactions. Recommended use: 2.5 µL of the supplied enzyme into a 50 µL CUT&RUN reaction (20X dilution).
Comment:	CUTANA pAG-MNase, the essential reagent for ChIC/CUT&RUN workflows: • First-in-class commercial product for ChIC/CUT&RUN assays • Optimized fusion of Proteins A and G with Micrococcal Nuclease (pAG-MNase) enables direct compatibility with a broad range of antibody isotypes • 50 and 250 reaction pack sizes, enabling greater experimental throughput
Restrictions:	For Research Use only

Handling

Concentration:	20 X
Buffer:	Provided as a 20X stock in 10 mM Tris HCl pH 7.5, 150 mM NaCl, 1 mM EDTA, and 50 % glycerol.
Handling Advice:	Avoid freeze-thaw cycles
Storage:	-20 °C
Storage Comment:	Stable for one year at -20°C from date of receipt. The protein is not subject to freeze/thaw under these conditions.
Expiry Date:	12 months

Publications

Product cited in:	Meers, Bryson, Henikoff, Henikoff: "Improved CUT&RUN chromatin profiling tools." in: **eLife**, Vol. 8, (2019) (PubMed). Skene, Henikoff, Henikoff: "Targeted in situ genome-wide profiling with high efficiency for low cell numbers." in: **Nature protocols**, Vol. 13, Issue 5, pp. 1006-1019, (2019) (PubMed). Skene, Henikoff: "An efficient targeted nuclease strategy for high-resolution mapping of DNA binding sites." in: **eLife**, Vol. 6, (2018) (PubMed). Schmid, Durussel, Laemmli: "ChIC and ChEC; genomic mapping of chromatin proteins." in: **Molecular cell**, Vol. 16, Issue 1, pp. 147-57, (2004) (PubMed).



Cleavage Under Targets and Release Using Nuclease

Image 1. A representative 350 kb region of an H3K4me1 profile in K-562 cells, generated using CUTANA (yellow panels), native ChIP-seq (blue panels), or cross-linked ChIP-seq (green panels). All data were generated by EpiCypher and are expressed as reads per million (RPM). Color- coded gradient (to left) represents signal/noise (S/N) ratios determined by genome-wide analysis (bamFingerprint data, not shown).

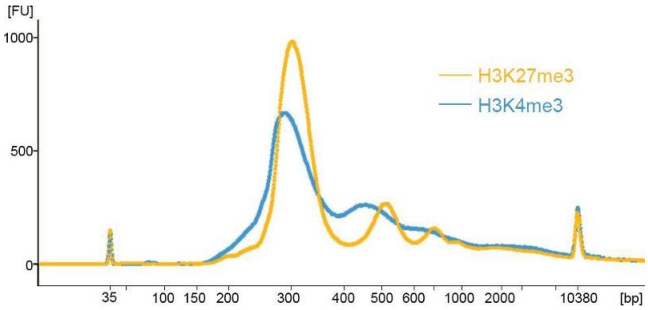
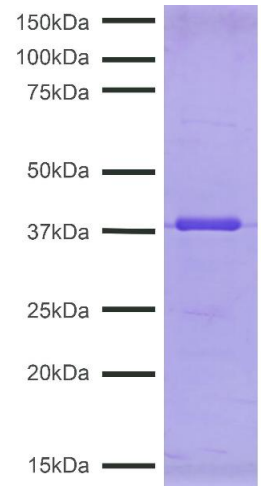


Image 2. Size Distribution of Released Chromatin:CUT&RUN was performed using CUTANA™ pAG-MNase (1:20 dilution) with 0.5 million K-562 cells. Purified DNA was subjected to sequencing library preparation using an NEBNext® Ultra™ II DNA Library Prep Kit for Illumina®. Agilent Bioanalyzer traces for libraries derived from H3K4me3 CUT&RUN (blue track) and H3K27me3 CUT&RUN (orange track) are shown. Excised DNA is highly enriched for mononucleosomes (peak at 300 bp reflects 150 bp insert size).



SDS-PAGE

Image 3. Protein Gel Data: CUTANA™ pAG-MNase (1 µg) was resolved via SDS-PAGE and stained with Coomassie blue. The migration and molecular weight of the protein standards are indicated.

Please check the product details page for more images. Overall 5 images are available for ABIN6950951.