CUTANA™ CUT&Tag Kit with Primer Set 2

Catalog No	14-1102-48s2	**Pack Size**	48 Reactions
Lot No	26075004-01	**Kit Version**	v4

DESCRIPTION

The CUTANA™ CUT&Tag Kit offers a comprehensive solution for ultra-sensitive mapping of histone post-translational modifications (PTMs). In CUT&Tag, antibody-bound chromatin is selectively cleaved with fusion protein pAG-Tn5, which simultaneously adds sequencing adapters. Tagmented fragments bypass traditional library prep with CUTANA™ CUT&Tag Kit's exclusive Direct-to-PCR strategy, enabling users to go from cells to PCR-amplified sequencing libraries in one tube with minimal sample loss. The recommended input for CUT&Tag is 100,000 native nuclei per reaction. Comparable data can be generated down to 10,000 nuclei, and the protocol is also validated for whole cells, cryopreserved samples, and lightly cross-linked nuclei or cells. CUT&Tag provides robust profiling for histone PTMs; for chromatin-associated proteins (e.g., transcription factors), CUTANA™ CUT&RUN is recommended (EpiCypher 14-1048, EpiCypher 14-1001).

The CUT&Tag Kit Version 4 (v4) now includes two new Wash Buffer Enhancers, CUTANA™ DNA Purification Beads, and improvements to the CUT&Tag protocol. CUTANA™ DNA Purification Beads are optimized for high yield DNA clean up with precise size selection, while the CUTANA™ Wash Buffer Enhancers reduce clumping and improve bead handling. Protocol improvements amplify sample preservation with changes to nuclei resuspension and refine reaction handling to increase yields for difficult targets. The protocol is also designed for compatibility with multi-channel pipetting for increased throughput and reproducibility. Positive (H3K4me3 and H3K27me3) and negative (IgG) control antibodies are paired with the SNAP-CUTANA™ K-MetStat Panel of nucleosome spike-in controls (see **Figure 2** on product page at epicypher.com/14-1102) to continuously monitor workflows and guide troubleshooting. CUTANA™ CUT&Tag Kits are bench-tested and scientist-approved, providing users with quality reagents for precision mapping.

KIT CONTENTS

Item	Cat No	Item	Cat No
8-strip Tubes	10-0009t	Pre-Wash Buffer	21-1002t
0.5 M EDTA	21-1006t	5% Digitonin	21-1004t
5 M NaCl	21-1013t	1 M Spermidine	21-1005t
1 M MgCl2	21-1015t	CUTANA™ Wash Buffer Enhancer 1	21-1028t
SNAP-CUTANA™ K-MetStat Panel	19-1002t	CUTANA™ Wash Buffer Enhancer 2	15-1030t
SDS Release Buffer	21-1017t	Rabbit IgG Negative Control Antibody	13-0042t
SDS Quench Buffer	21-1018t	H3K27me3 Positive Control Antibody	13-0055t
CUTANA™ DNA Purification Beads	21-1407t	H3K4me3 Positive Control Antibody	13-0060t
0.1X TE Buffer	21-1025t	Anti-Rabbit Secondary Antibody	13-0047t
ConA Beads	21-1401t	pAG-Tn5	15-1017t
Bead Activation Buffer	21-1001t	Non-Hot Start 2X PCR Master Mix	15-1018t
Pre-Nuclei Extraction Buffer	21-1021t		
Multiplexing Primers	This kit includes combinatorial dual indices for multiplexed sequencing of up to 48 reactions. Pair with EpiCypher 14-1102-48s1 or 14-1102-24s3 for multiplexing up to 96 or 72 reactions respectively.		

TECHNICAL INFORMATION

Storage OPEN KIT IMMEDIATELY and store components at room temperature, 4°C, and -20°C as indicated (see **User Manual corresponding to Kit Version 4**).

Instructions for Use See User Manual corresponding to Kit Version 4. This kit is not compatible with previous user manuals.

SAFETY INFORMATION

Item	Cat No	Chemical	Signal Word	Pictogram
0.5 M EDTA	21-1006t	EDTA	Warning	
1 M Spermidine	21-1005t	Spermidine	Warning	
5% Digitonin	21-1004t	Digitonin, DMSO	Danger	
Non-Hot Start 2X PCR Master Mix	15-1018t	DMSO	Warning	
SDS Quench Buffer	21-1018t	X-100	Danger	

CERTIFICATE OF ANALYSIS

Quality Control Metrics

Functional Testing (CUT&Tag)
Each lot of CUTANA™ CUT&Tag Kit is functionally validated by comparison to a previous lot and to established EpiCypher internal controls. CUT&Tag is performed on 100k native K562 cells with 0.5 µg of IgG (EpiCypher 13-0042), H3K4me3 (EpiCypher 13-0060), or H3K27me3 (EpiCypher 13-0055) antibodies using the CUTANA™ CUT&Tag Kit. Libraries are sequenced on an Illumina NextSeq2000 with paired-end sequencing (2x50 bp). Assessment is based on metrics including DNA yields, library fragment size distribution, SNAP-CUTANA™ spike-in control performance, and genome-wide enrichment patterns. Pass

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APPROVED BY

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SENIOR DIRECTOR OF PRODUCT MANAGEMENT

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