SNF2L/SMARCA1 CUTANA™ CUT&RUN Antibody

Catalog No	13-2005	**Type**	Polyclonal
Lot No	21013001-39	**Host**	Rabbit
Pack Size	100 µL	**Concentration**	1,000 µg/mL
Applications	CUT&RUN, IP, IHC	**Reactivity**	Human, Mouse (predicted)

DESCRIPTION

This antibody meets EpiCypher's "CUTANA Compatible" criteria for performance in Cleavage Under Targets and Release Using Nuclease (CUT&RUN) and/or Cleavage Under Targets and Tagmentation (CUT&Tag) approaches to genomic mapping. Every lot of a CUTANA Compatible antibody is tested in the indicated approach using EpiCypher optimized protocols (epicypher.com/protocols) and determined to yield peaks that show a genomic distribution pattern consistent with reported function(s) of the target protein. SNF2L/SMARCA1 antibody produces CUT&RUN peaks above background (**Figure 1**) that overlap with H3K4me3 (**Figures 1-2**), consistent with its known role as the ATP-dependent helicase subunit of the NURF ISWI chromatin remodeler complex [1].

TECHNICAL INFORMATION

Immunogen	Between amino acids 1004 and 1054
Storage	Stable for 1 year at 4°C from date of receipt
Formulation	Antigen affinity-purified antibody in Tris-citrate/phosphate buffer pH 7-8, 0.09% sodium azide

RECOMMENDED DILUTION

CUT&RUN	0.5 µg per reaction	**Immunoprecipitation**	2 - 10 µg/mg lysate
Immunohistochemistry	1:1,000 - 1:5,000		

Epitope retrieval with citrate buffer pH 6.0 is recommended for FFPE tissue sections

GENE & PROTEIN INFORMATION

UniProt ID	P28370
Gene Name	SMARCA1
Protein Name	Probable global transcription activator SNF2L1
Target Size	123 kDa
Alternate Names	SNF2L1, ATP-dependent helicase SMARCA1, Nucleosome-remodeling factor subunit SNF2L, SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 1

REFERENCES

[1] Wysocka et al. *Nature* (2006). PMID: 16728976

VALIDATION DATA

CUT&RUN Methods

CUT&RUN was performed on 500k native or fixed (0.1% formaldehyde, 1 min) K562 cells with 0.5 µg of either SNF2L, H3K4me3 positive control (EpiCypher 13-0041), or IgG negative control (EpiCypher 13-0042) antibodies using the CUTANA™ ChIC/CUT&RUN Kit v2.0 (EpiCypher 14-1048). Library preparation was performed with 5 ng of DNA (or the total amount recovered if less than 5 ng) using the CUTANA™ CUT&RUN Library Prep Kit (EpiCypher 14-1001/14-1002). Both kit protocols were adapted for high throughput Tecan liquid handling. Libraries were run on an Illumina NextSeq2000 with paired-end sequencing (2x50 bp). Sample sequencing depth was 12.3 million reads (SNF2L native), 10.4 million reads (SNF2L 0.1% fixation), 4.1 million reads (H3K4me3), and 2.4 million reads (IgG). Data were aligned to the hg19 genome using Bowtie2. Data were filtered to remove duplicates, multi-aligned reads, and ENCODE DAC Exclusion List regions.

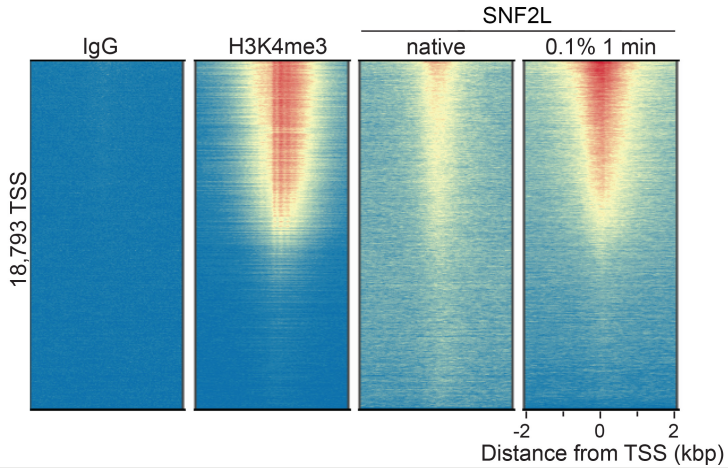

FIGURE 1 SNF2L peaks in CUT&RUN. CUT&RUN was performed as described above. Peaks were called with MACS2. Heatmaps show SNF2L peaks relative to IgG negative control antibody and H3K4me3 positive control antibody in aligned rows ranked by intensity (top to bottom) and colored such that red indicates high localized enrichment and blue denotes background signal. All rows aligned to SNF2L antibody with moderate fixation (0.1% formaldehyde, 1 min), which improved signal vs. native conditions.

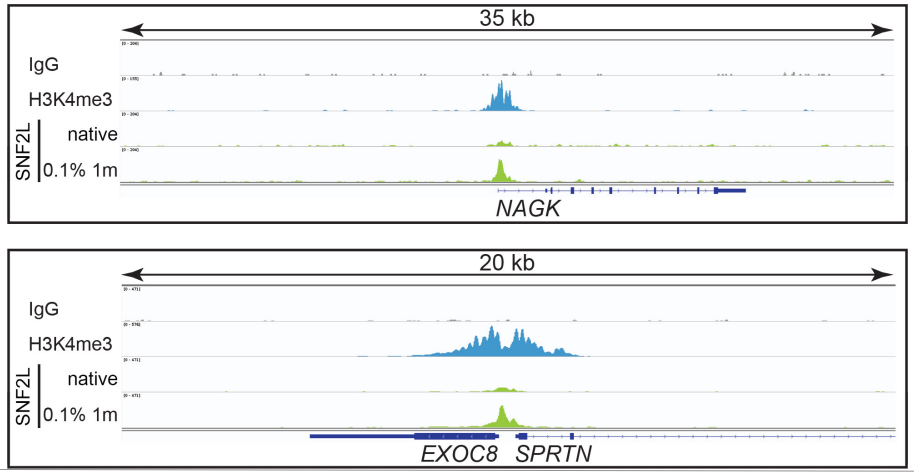

FIGURE 2 SNF2L CUT&RUN representative browser tracks. CUT&RUN was performed as described above. Gene browser shots were generated using the Integrative Genomics Viewer (IGV, Broad Institute). Two gene loci show overlap of SNF2L and H3K4me3 peaks, consistent with its reported function as a member of the NURF ISWI chromatin remodeler complex [1]. Improved signal recovery with moderate fixation (0.1% formaldehyde, 1 min), is notable.

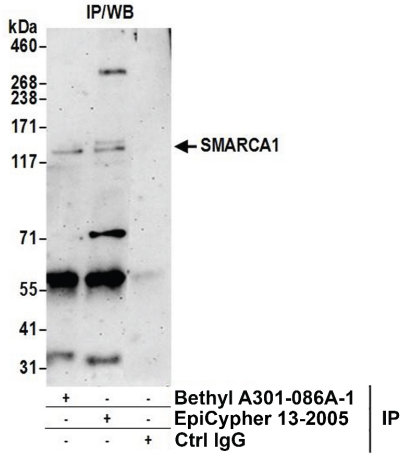

FIGURE 3 Immunoprecipitation data. EpiCypher SNF2L antibody (6 µg) was used to immunoprecipitate whole cell lysates (0.5 mg or 1.0 mg per IP reaction; 20% of IP loaded) isolated from HeLa cells using NETN lysis buffer. A negative control IgG antibody and positive control SNF2L antibody (Bethyl Laboratories A301-086A-1) were also used to demonstrate the specificity of the IP. Immunoprecipitates were loaded onto a 4-8% SDS-PAGE gel (20% of IP loaded) and probed via western blot with EpiCypher SNF2L antibody at a dilution of 1:1,000.

VALIDATION DATA

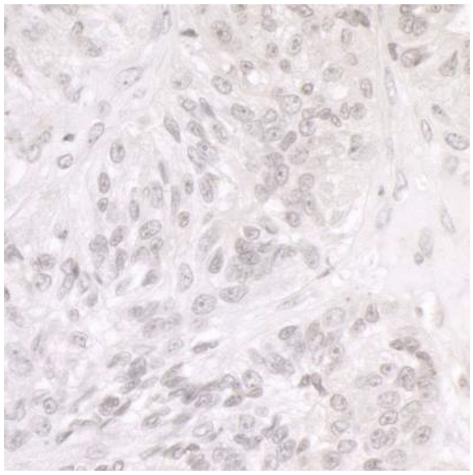

FIGURE 4 **Immunohistochemistry data.** FFPE section of human ovarian carcinoma using SNF2L antibody at a dilution of 1:1,000.