CUTANA™ Anti-GST Tag Antibody

Catalog No	13-0073	**Type**	Polyclonal
Lot No	24318001-88	**Host**	Rabbit
Pack Size	100 µg	**Concentration**	0.5 mg/mL
Applications	CUT&RUN, WB	**Reactivity**	GST Tag

DESCRIPTION

Unlock the full potential of Reader CUT&RUN with our high-affinity CUTANA™ Anti-GST Tag Antibody, specifically developed to support chromatin profiling applications wherein a GST-tagged reader protein replaces the traditional primary antibody in directing the selective cleavage and release of target chromatin fragments by pAG-MNase [1]. For example, this antibody is used in CUTANA™ meCUT&RUN (EpiCypher Kit 14-1060-24), a modified CUT&RUN workflow in which a GST-tagged MeCP2 methyl binding domain is used to enrich regions of chromatin with symmetrically methylated CpGs, enabling streamlined, high-resolution mapping of DNA methylation.

Engineered for superior performance in low-background, high-resolution CUT&RUN assays, this antibody offers exceptional sensitivity and specificity for detecting GST-fusion proteins bound to chromatin. Whether studying histone modifications, DNA methylation, or other epigenetic readers, this antibody is the ideal tool for enabling precise, reproducible mapping using GST-tagged fusion constructs.

TECHNICAL INFORMATION

Immunogen	Glutathione-S-Transferase (GST)
Storage	Stable for 1 year at 4°C from date of receipt
Formulation	Antigen affinity-purified antibody in phosphate buffered saline (PBS), 0.09% sodium azide

RECOMMENDED DILUTION

CUT&RUN:	0.5 µg per reaction	**Western Blot:**	1:500 - 1:15,000

REFERENCES

[1] Marunde et al. *eLife* (2024). PMID: 38319148

VALIDATION DATA

CUT&RUN Methods

meCUT&RUN was performed starting with 500k K562 cells with either 2.5 µL of 20X GST-MeCP2 (EpiCypher 15-2002) added as the primary binding reagent or 0.5 µg of a secondary antibody-only control (anti-GST antibody) to determine background cleavage. Library preparation was performed using 5 ng of meCUT&RUN-enriched DNA (or the total amount recovered if less than 5 ng) using the CUTANA™ CUT&RUN Library Prep Kit (EpiCypher 14-1001/14-1002). Libraries were run on an Illumina NextSeq2000 with paired-end sequencing (2x50 bp). Sample sequencing depth was 7.7 million reads (anti-GST) and 8.4 million reads (GST-MeCP2). Data were aligned to the hg38 genome using Bowtie2. Data were filtered to remove duplicates, multi-aligned reads, and ENCODE DAC Exclusion List regions.

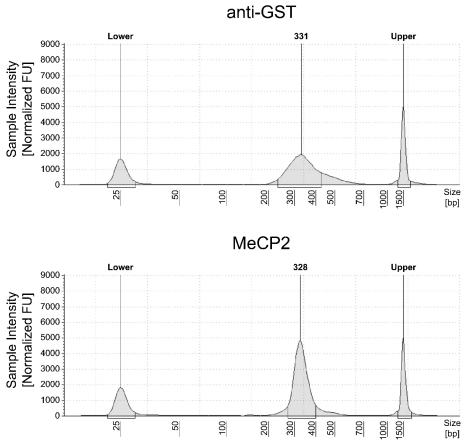

FIGURE 1 meCUT&RUN DNA fragment size distribution analysis. meCUT&RUN was performed as described above. Library DNA was analyzed by Agilent TapeStation®. This analysis confirmed that mononucleosomes were predominantly enriched in meCUT&RUN (~300 bp peaks represent 150 bp nucleosomes + sequencing adapters).

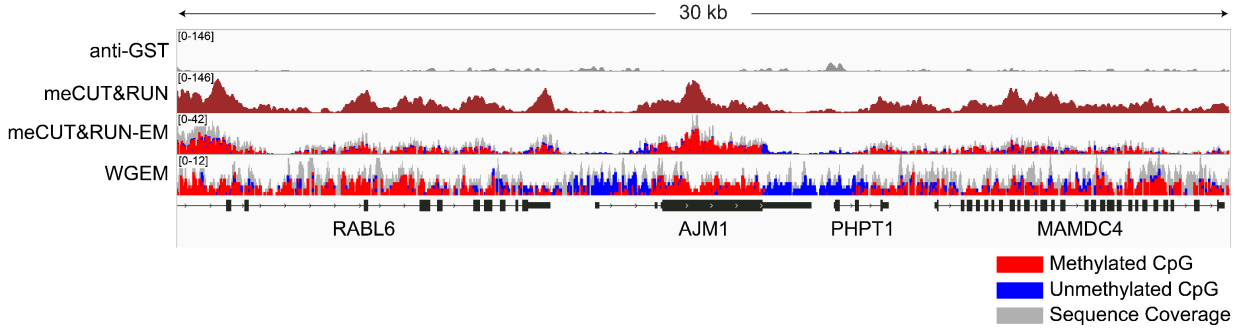

FIGURE 2 Gene browser tracks. meCUT&RUN was performed as described above. A 30 kb window at the AJM1 gene is shown for anti-GST antibody and meCUT&RUN. Tracks are also shown with representative data for meCUT&RUN followed by EM-seq (meCUT&RUN-EM) and whole genome EM-seq (WGEM), using the New England Biolabs NEBNext® Enzymatic Methyl-seq v2 Kit (NEB E8015). The meCUT&RUN kit produced the expected genomic distribution, showing enrichment of methylated DNA that approximates the methylated CpG pattern observed in WGEM. Images were generated using the Integrative Genomics Viewer (IGV, Broad Institute).

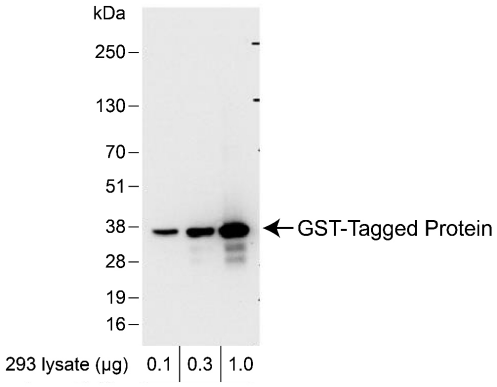

FIGURE 3 Western blot data. Western analysis of GST Tag in 0.1, 0.3, or 1.0 µg of HEK293 cell lysate expressing a GST-tag fusion protein. Lysate was resolved via SDS-PAGE and detected with a 1:7,500 dilution of EpiCypher anti-GST Tag antibody.