

CUTANA™  
CUT&RUN Services  
For scaled epigenomic  
analyses



MJS  
BioLynx 

 CHROMATOGRAPHIC  
SPECIALTIES INC.

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# CUTANA™ CUT&RUN Services

Chromatin mapping made simple

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## The challenge

Biomedical and pharmaceutical researchers are increasingly turning to epigenomic analyses for identification of new cell types, biomarkers, and drug targets. Mapping the genomic enrichment of transcription factors, chromatin modifying enzymes, and histone post-translational modifications (PTMs) is essential to drive these efforts.

To fully achieve these goals, scientists need access to genomics expertise and supporting infrastructure, including customized high-throughput workflows and bioinformatics pipelines.

## Our solution

EpiCypher is pioneering the development of CUT&RUN chromatin mapping assays, which provide massive improvements in throughput, data quality, and sensitivity compared to ChIP-based methods.

To meet the needs of our research partners, we developed automated CUTANA CUT&RUN Services. Our services offer exclusive access to EpiCypher's genomics experts, guaranteeing strong support from experimental design to data analysis. This turnkey solution delivers rapid, high-resolution chromatin mapping at scale – unlocking the epigenome to advance biological discovery.



The perfect partnership:  
your project & our experts

# CUTANA™ CUT&RUN Services

At a glance

## The workflow

## Our expertise

Detailed, end-to-end experimental design

>10,000 reactions to date  
Automated 96-well assay  
Standardized controls  
High reproducibility

Expert optimization for your sample and target

>100 sample types  
Primary and FACS-isolated  
Drug-treated and stimulated  
Tissues, including biopsies

Reliable profiling using automated assays and standardized controls

>1,000 antibodies tested  
Transcription factors  
Chromatin modifiers  
Histone PTMs

Comprehensive data report and presentation by our scientists

Tailored bioinformatics  
CUT&RUN-optimized pipeline  
Raw and processed files  
Preliminary visualization

Scalable protocols from pilot tests to high-throughput studies

Limitless applications  
Cell identity fingerprinting  
Biomarker discovery  
Drug mechanism of action

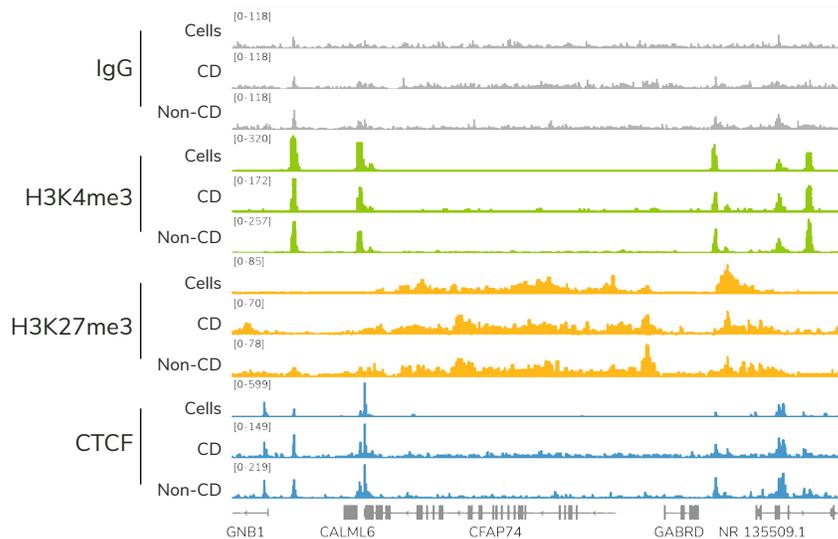
# CUTANA™ CUT&RUN Services

## Validated applications

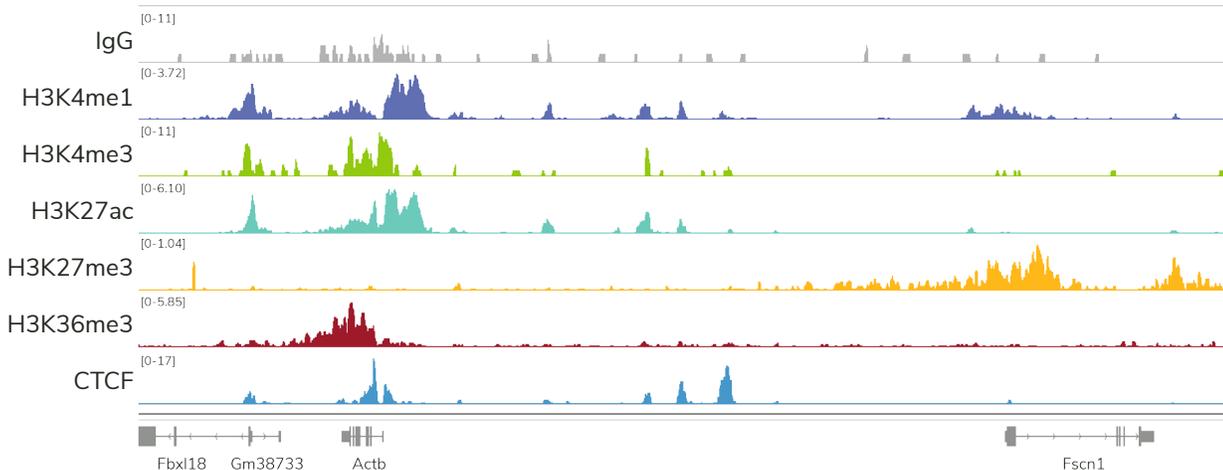
Our team provides detailed, end-to-end experimental design and expert optimization for targets and cell types, including high-value clinical samples.

## High-resolution chromatin profiling from biopsies

Flash-frozen patient samples yield high-quality genomic data. Colon biopsies from Crohn's Disease (CD) and healthy (Non-CD) patients were compared to cultured colon cells (Cells) using CUT&RUN. Sequencing tracks demonstrate robust profiles for histone PTMs and chromatin-associated proteins from each sample.



## Map diverse targets to illuminate the chromatin landscape



High-resolution chromatin profiling using 10,000 FACS-isolated innate lymphoid cells identifies unique genomic compartments, including active regulatory elements (H3K4me1, H3K27ac), promoters (H3K4me3), gene bodies (H3K36me3), repressed genes (H3K27me3), and transcription factor binding sites (CTCF).

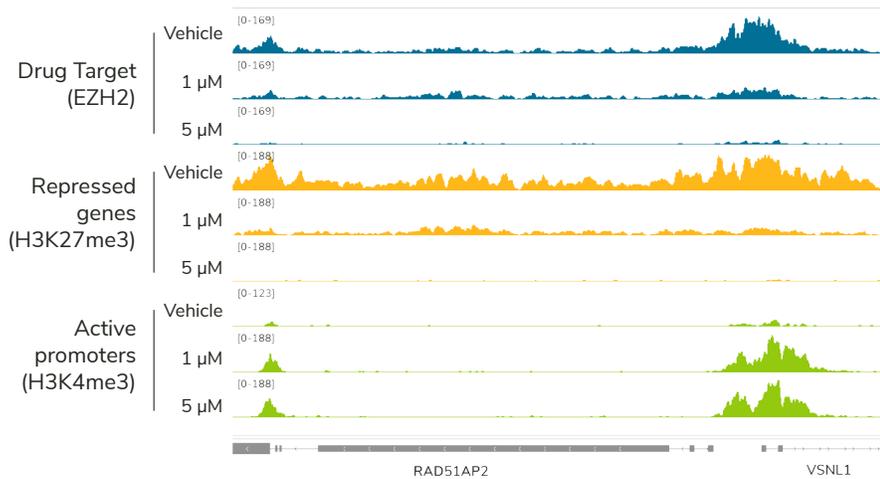
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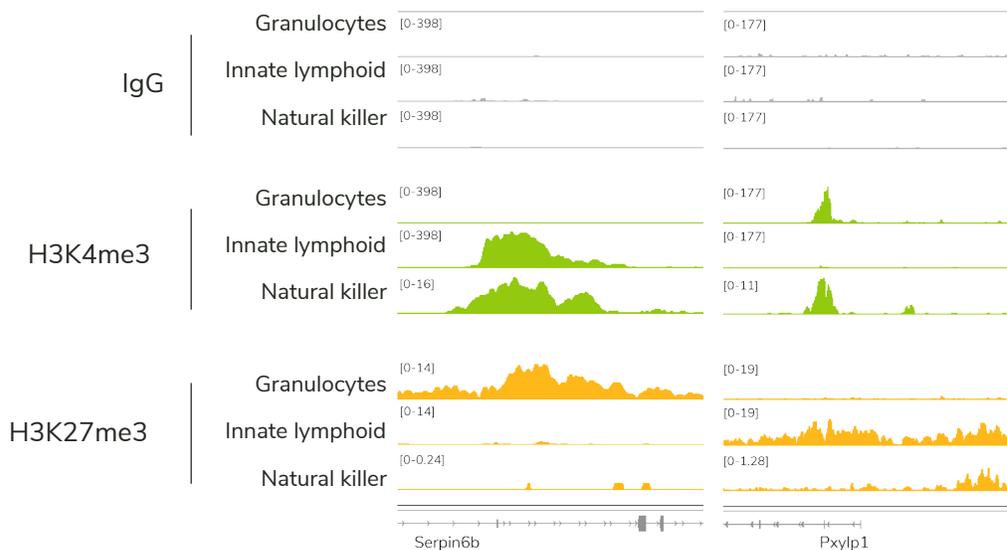
Our scaled workflows have limitless applications, ranging from pilot studies aimed at defining gene regulatory mechanisms to large-scale drug screening.

## Uncover drug mechanism of action

Epigenetic inhibitor treatment alters chromatin structure. Cultured glioma cells were treated with the clinically-approved epigenetic inhibitor Tazverik, which targets the histone H3K27 methyltransferase EZH2. Cells exhibit dose-dependent loss of EZH2 and H3K27me3 with concomitant increases in the activating mark H3K4me3, consistent with Tazverik activity.



## Reveal cell-specific epigenomic profiles



Investigate unique cell types and uncover novel regulatory pathways using CUTANA CUT&RUN Services. Here, FACS-isolated immune cells from a multi-site consortium reveal distinct H3K4me3 (promoters) and H3K27me3 (repressed genes) profiles across granulocytes, innate lymphoid cells, and natural killer cells.

# CUTANA™ CUT&RUN Services

## Our approach

Our automated workflows include multiple quality control steps. Together we review tailored bioinformatic analyses and quality control metrics to ensure you receive data you can trust.

## Standardized controls and stringent quality metrics

Designated controls create checkpoints for ongoing project risk evaluation.

**Sample preparation:** Viability staining to assess cell and nuclei integrity

**Spike-in controls:** Proprietary approach to confirm experimental success

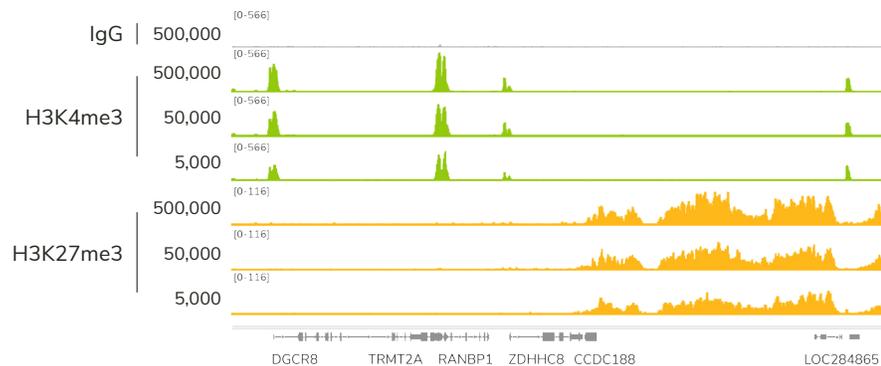
**Pre-sequencing:** DNA yield, sequencing library size and concentration

**Post-sequencing:** Sequencing and control metrics, genomic enrichment



## Robust, proven protocols

CUTANA CUT&RUN Service protocols were developed for the most challenging studies, enabling low-input applications. Across a 100-fold dilution of cells and two different histone PTMs, our protocol shows high signal-to-noise and reproducible genomic profiles.



## Expert bioinformatic processing

Our bioinformaticians developed a CUT&RUN-optimized pipeline that we use to analyze sequencing data. You receive raw and processed files that can immediately be used to perform downstream analyses and derive biological insights in your lab.

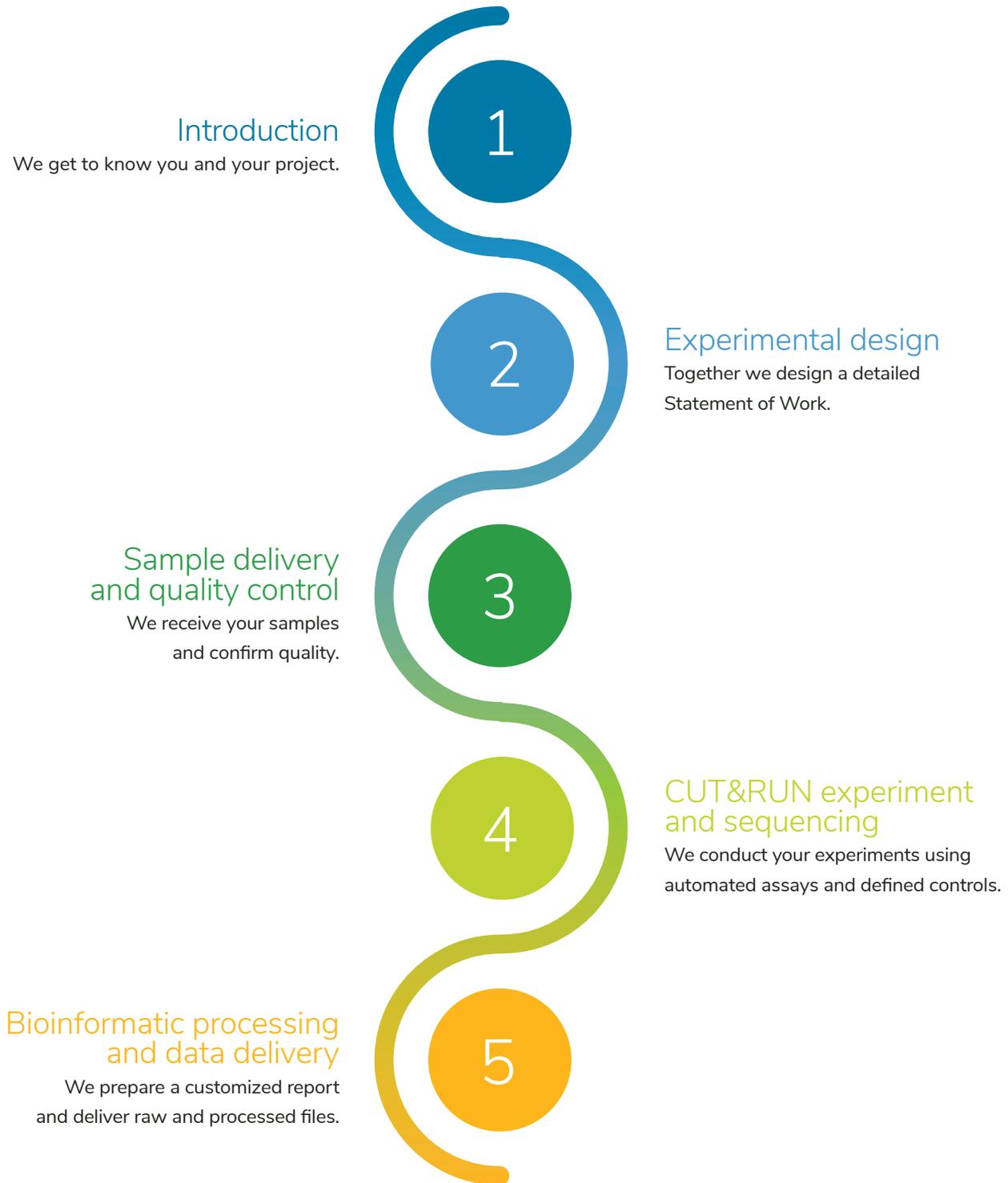
To see a sample data report, email [services@epicypher.com](mailto:services@epicypher.com)



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## Project roadmap

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