



CUTANA™
CUT&RUN Services
For scaled epigenomic
analyses

CUTANA™ CUT&RUN Services

Chromatin mapping made simple

The challenge

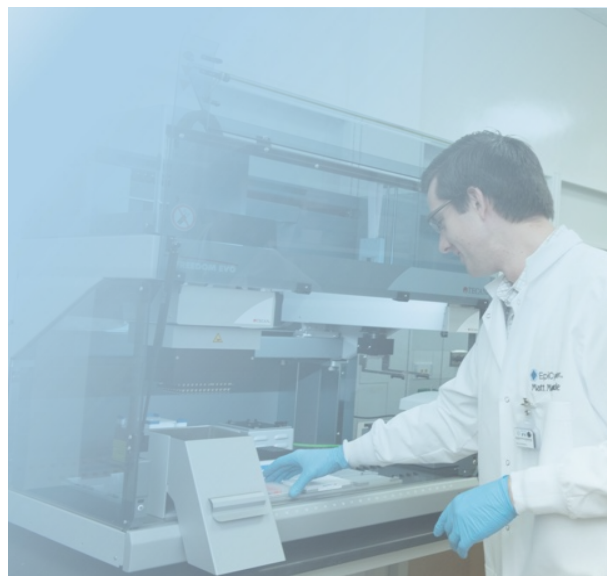
Biomedical and pharmaceutical researchers are increasingly turning to epigenomic analyses for identification of new cell types, biomarkers, and drug targets. Mapping the genomic enrichment of transcription factors, chromatin modifying enzymes, and histone post-translational modifications (PTMs) is essential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

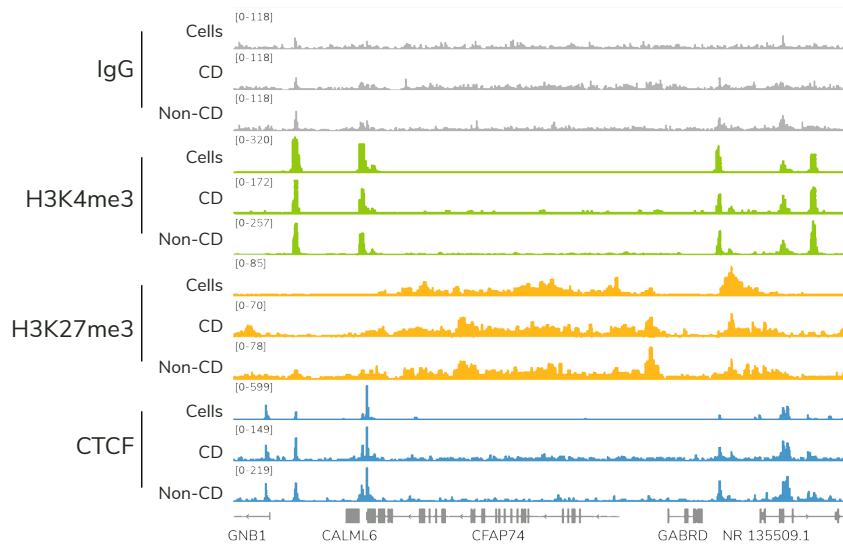
CUTANA™ CUT&RUN Services

Validated applications

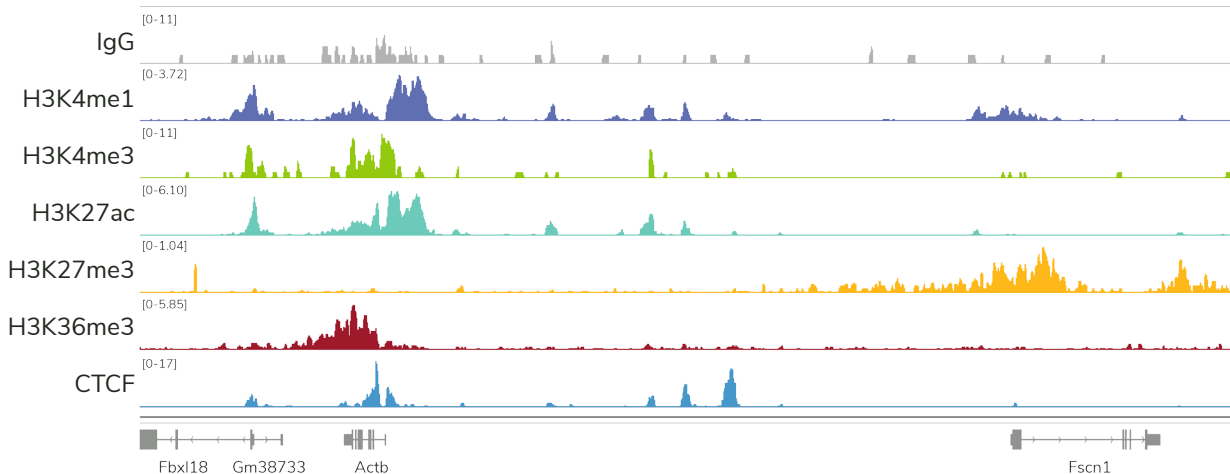
Our team provides detailed, end-to-end experimental design and expert optimization for targets and cell types, including high-value clinical samples.

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).

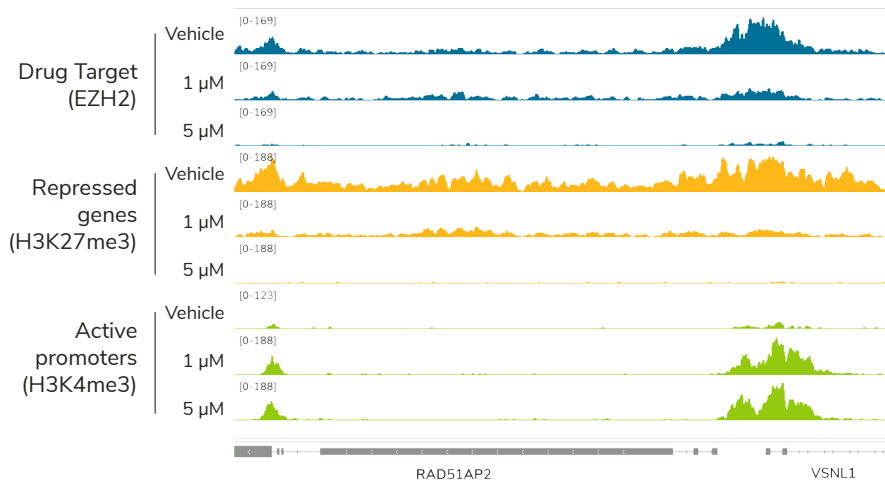
CUTANA™ CUT&RUN Services

Validated applications

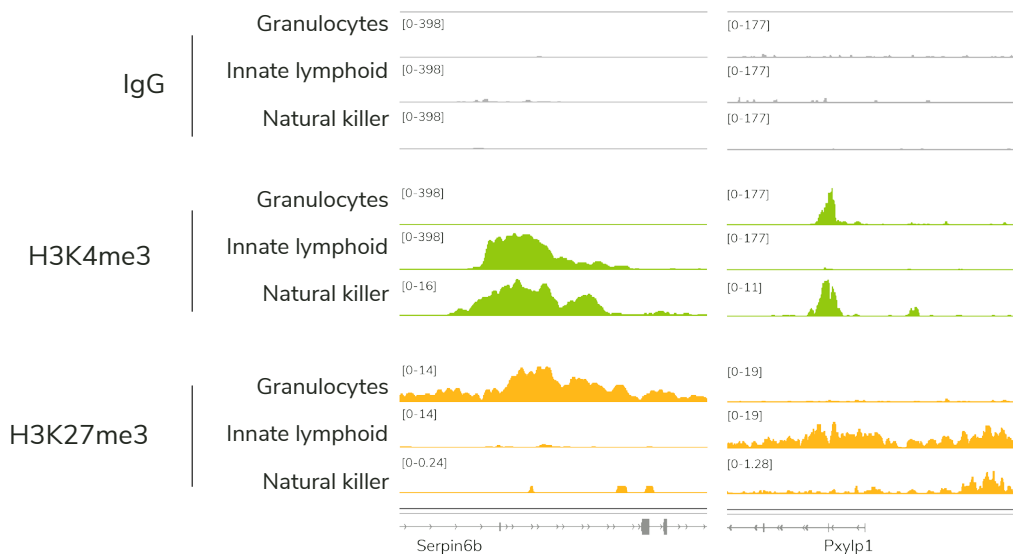
Our scaled workflows have limitless applications, ranging from pilot studies aimed at defining gene regulatory mechanisms to large-scale drug screening.

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

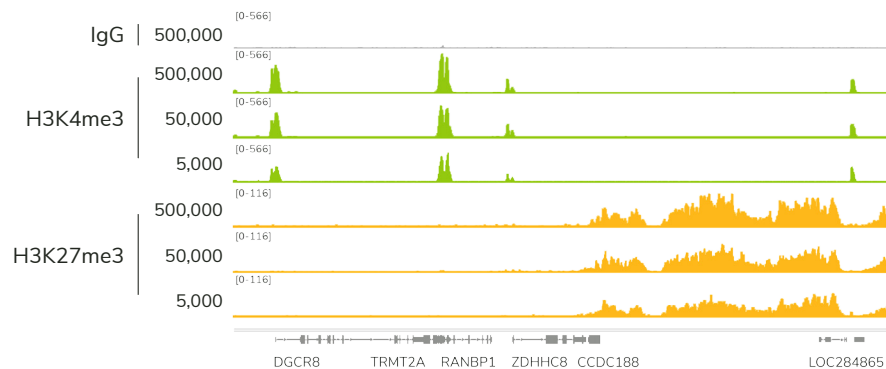
Pre-sequencing: DNA yield, sequencing library size and concentration

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

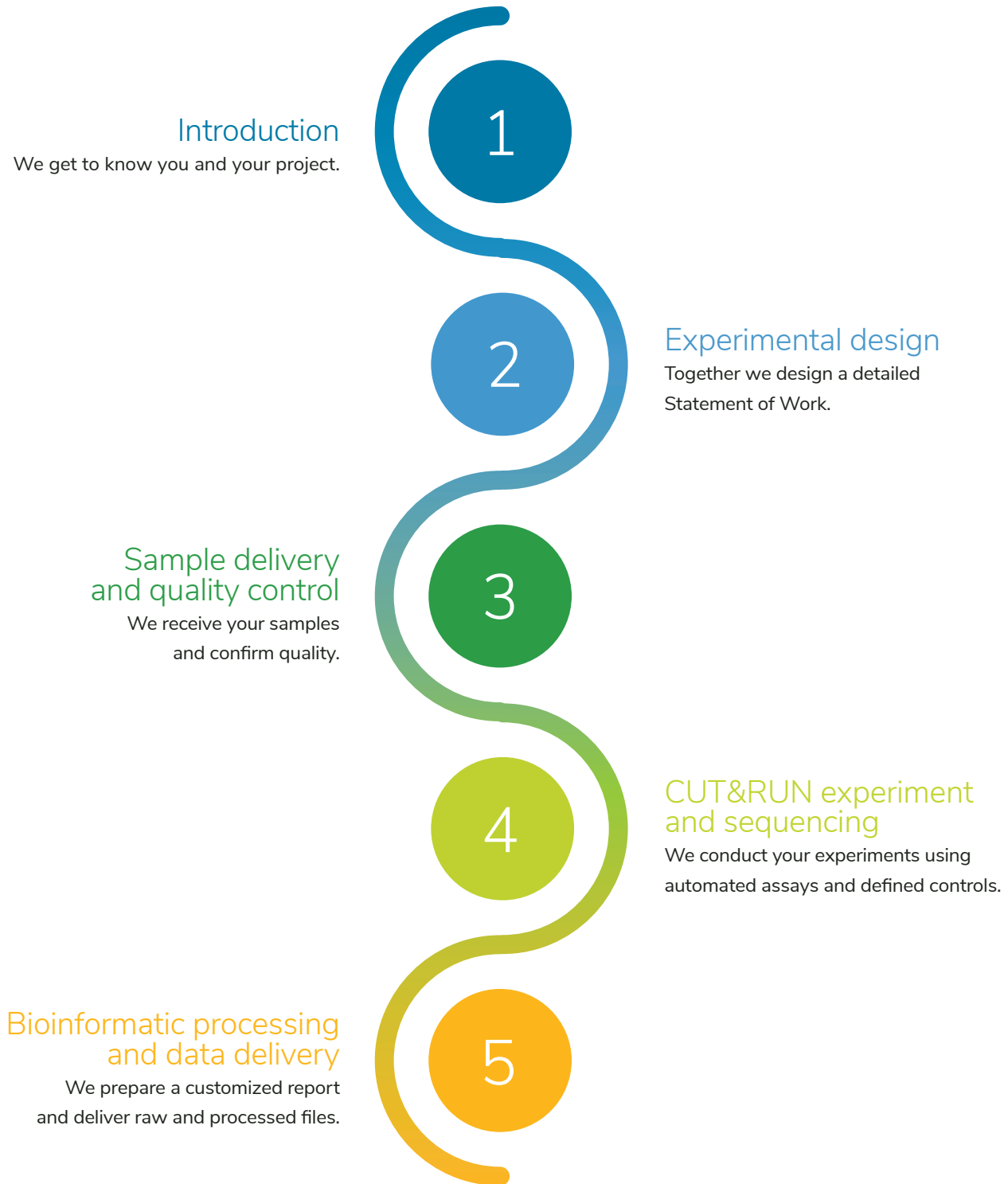
Our bioinformaticians developed a CUT&RUN-optimized pipeline that we use to analyze sequencing data. You receive raw and processed files that can immediately be used to perform downstream analyses and derive biological insights in your lab.

To see a sample data report, email services@epicypher.com



CUTANA™ CUT&RUN Services

Project roadmap



Ready to get started?
Email services@epicypher.com