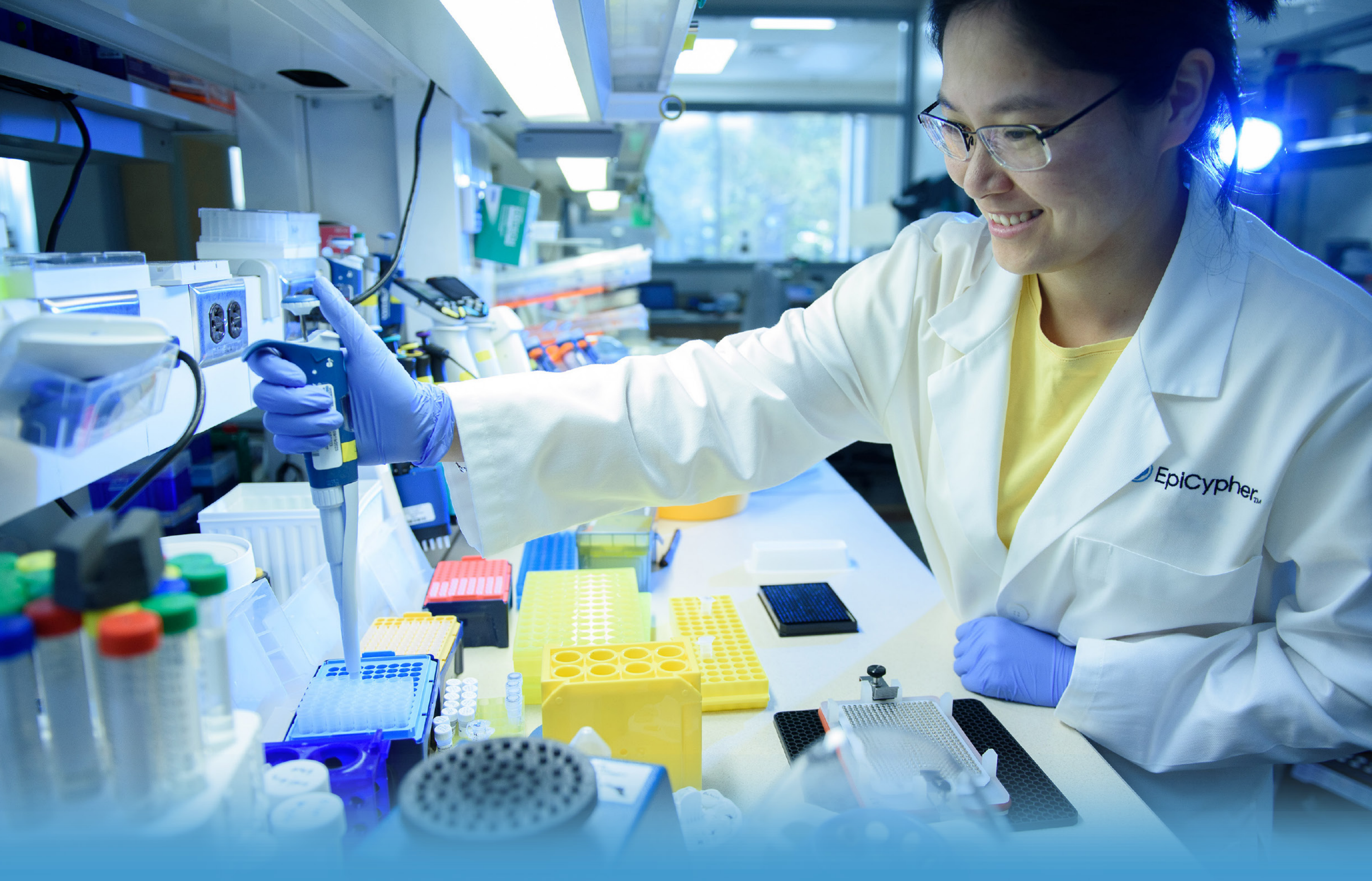

CUTANA™ GENOMIC SERVICES

- ✓ Uncover regulatory drivers of gene expression
- ✓ Unlock drug mechanism of action (MoA)
- ✓ Identify biomarkers for patient stratification
- ✓ Reveal mechanisms of drug resistance

EpiCypher®

Bringing Epigenetics to Life

CUTANA™ Genomic Services

EpiCypher®

If you are looking for a dependable CRO to help with drug discovery and development, you may find that many are limited to using traditional gene and protein expression assays such as RNA-seq and proteomics. Those approaches capture downstream effects of drug treatment but fail to reveal direct mechanisms of action. In other words, they may show **what** changed, but not **why**.

EpiCypher's **CUTANA™ Genomic Services** go beyond traditionally used assays to provide a direct view into **gene regulation**, the "software" that controls disease- and cell-type-specific expression programs. By mapping chromatin-level changes, we can transform indirect readouts into mechanistic evidence and reveal how your treatment perturbs regulatory pathways in cells.

With expert-led, industry-validated **CUT&RUN, Fiber-seq,** and **DNA Methylation Services**, we connect molecular intervention to its regulatory impact. This provides a clearer MoA definition, earlier resistance detection, and more confident decision-making throughout your drug discovery and development.

Partner With the Experts:

- ✓ Over **30,000** genomic assays performed using rigorously standardized workflows
- ✓ More than **1,000** antibodies screened for accurate profiling of transcription regulators
- ✓ Over **100** sample types tested, including drug-treated cells and precious patient tissues
- ✓ **30+** co-authored publications across cancer, immunology, and other disease areas

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Featured Customers

FOGHORN® THERAPEUTICS

biomea FUSION™

ImmGen

Dave Lahr, PhD
Sr. Director of Bioinformatics
Foghorn Therapeutics

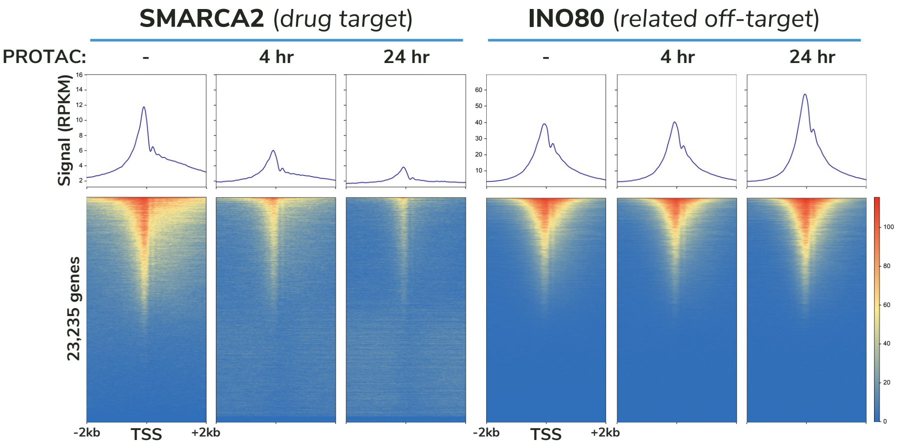
> *"Access to EpiCypher's high-throughput workflows and expertise has been amazing. Through their platform, we were able to systematically test a variety of compound concentrations and time points that enabled us to understand both short- and long-term drug effects in cellular models. The throughput, cost, and reliability of their system also allowed us to scale up our experiments without compromising data integrity, thus enhancing the efficiency of our preclinical studies."*

Selected Publications Using Our Services

- Agustinus *et al.* Epigenetic dysregulation from chromosomal transit in micronuclei. Nature **619**, 176-183 (2023). PMID: 37286593.
- Baysoy *et al.* The interweaved signatures of common-gamma-chain cytokines across immunologic lineages. Journal of Experimental Medicine **220** (2023). PMID: 36976164.
- Asberry *et al.* Reprogramming landscape highlighted by dynamic transcriptomes in therapy-induced neuroendocrine differentiation. Computational and Structural Biotechnology Journal **20**, 5873-5885 (2022). PMID: 36382181.

Applications

EpiCypher supports every phase of drug development, from target ID to scaled clinical research. Our technologies enable direct insights into treatment effects, as illustrated in a case study of a Proteolysis Targeting Chimera (PROTAC) compound in development. This drug exploits a synthetic lethality vulnerability in cancers characterized by mutations in SMARCA2/4, functionally redundant subunits of the SWI/SNF chromatin remodeling complex.

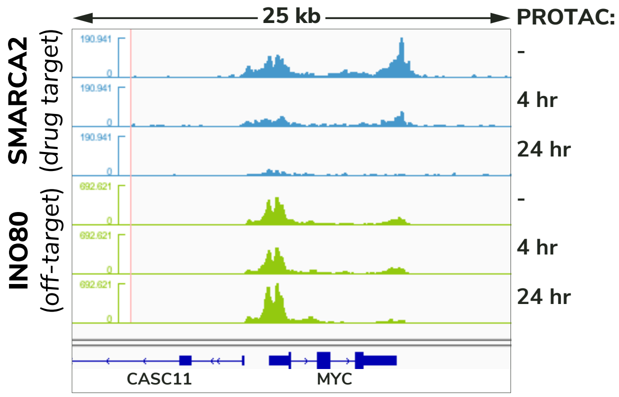


GENOME-WIDE CHROMATIN CHANGES

*CUT&RUN directly profiled chromatin engagement of a SMARCA2-targeted PROTAC in SMARCA4 mutant cancer cells, where SMARCA2 dependency creates a synthetic lethality. Genome-wide heatmaps of protein binding (**red**) over background (**blue**) at annotated transcription start sites (TSS) shows rapid loss of SMARCA2 binding following treatment, confirming on-target degradation. Binding of the related chromatin remodeler INO80 is unchanged, supporting target specificity and minimal off-target activity.*

DRUG RESPONSE AT DISEASE-ASSOCIATED GENES

At the cMYC proto-oncogene, CUT&RUN confirms rapid and selective loss of SMARCA2 binding following PROTAC treatment, with no effect on INO80. These locus-specific results validate target engagement at cancer-relevant genes, link SMARCA2 degradation to transcriptional regulation, and help de-risk drug development by ruling out a likely off-target mechanism.



Typical Project Workflow

Our chromatin biology experts guide study design and execute assays using end-to-end or modular service options.

Define study goals

We align on project objectives, from pilot experiments to high-throughput studies.

Design the experimental plan

A customized study design is developed to address your scientific question.

Prepare and QC samples

We support diverse inputs, including drug-treated cells and clinical specimens.

Run standardized genomic assays

Experiments are performed with validated reagents, defined controls, and rigorous QC.

Deliver and interpret results

You receive a comprehensive data report, secure file transfer, and scientist-led presentation.

CUTANA™ Genomic Services

CUT&RUN

CUT&RUN enables genome-wide mapping of chromatin targets, including transcription factors and epigenetic marks, providing direct, mechanistic insight that expression-based assays miss. Our services combine automation with quantitative spike-in controls to ensure scalability, reproducibility, and cross-sample comparability for translational and preclinical studies.

Fiber-seq

Fiber-seq provides single-molecule, multiomic profiling of chromatin accessibility, protein occupancy, DNA methylation, and sequence on the same DNA fiber. Unlike ATAC-seq or bisulfite sequencing, which isolate individual features, Fiber-seq captures their coordinated state, enabling detailed mechanistic insight into regulatory heterogeneity, drug response, and resistance.

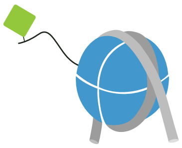
DNA Methylation

Our DNA methylation sequencing technologies overcome the limitations of destructive bisulfite-based methods. By preserving native DNA and enabling multiomic profiling alongside transcription factor binding and chromatin features, EpiCypher's approaches link methylation to function, delivering clearer mechanistic insight into disease biology, drug response, and biomarker strategy.

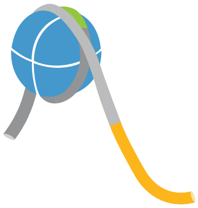
> *"EpiCypher Services team helped us design a strong study, understood our tight deadline, and delivered high-quality results on time. Everything was clear, concise, and on point. Very scientific. That made a huge difference. It's rare to find CROs like this. A lot of CROs are focused on just getting the business done and collecting a paycheck. EpiCypher actually focuses on quality and scientific competence."*

Research Scientist, Team Leader
Clinical Stage Oncology
Pharma Company

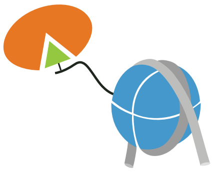
Other Services We Offer



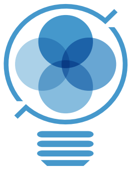
Custom Nucleosome Development Services



EpiDyne® Chromatin Remodeling HTS Assay Services



Captify™ Assay Services for Novel Chromatin Interactions



Custom Services for Assay Development, Automation Tech Transfer & More

Start Your CUTANA™ Genomic Services Project Today
services@epicypher.com | 855.374.2461 | Durham, NC

Tell Us About Your Research Project! ▶