



## EPIGENOMIC PROFILING

# Cleavage Under Targets and Release Using Nuclease (CUT&RUN)

## Brief Description of Technology

CUT&RUN is a widely applicable chromatin profiling method that is an attractive alternative to ChIP-based applications.

### BUSINESS OPPORTUNITY

Non-exclusive license  
Exclusive license

### TECHNOLOGY TYPE

Research tool  
Method

### STAGE OF DEVELOPMENT

Method validated, currently developing adaptations and refining method

### PATENT INFORMATION

US Provisional patent

### INVESTIGATOR

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### LEARN MORE

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## Technology Overview

For over 30 years, chromatin immunoprecipitation [ChIP] has been the leading method of mapping protein-DNA interactions. The readout strategies have evolved but the fundamentals of ChIP have remained fairly constant. Researchers in the Henikoff Lab developed CUT&RUN, a novel method superior to ChIP. CUT&RUN is an epigenomic profiling strategy in which antibody-targeted controlled cleavage by micrococcal nuclease releases specific protein-DNA complexes into the supernatant for paired-end DNA sequencing. CUT&RUN is performed *in situ* and avoids crosslinking and solubilization issues. This allows for both quantitative high-resolution chromatin mapping and probing of the local chromatin environment. CUT&RUN is widely applicable and has mapped where transcription factors bind to DNA from yeast and human cells.

## Applications

- *In situ* mapping of protein-DNA interactions at base-pair resolution
- Transcription factor and chromatin profiling
- 3D contact mapping
- Proteomics analysis

## Advantages

- Simple, cost effective procedure completed within a day
- Outperforms ChIP protocols in resolution, signal-to-noise, and depth of sequencing required
- Allows chromatin mapping in small number of cells
- Opportunities for robotic automation

## Market Overview

ChIP is the industry standard for mapping protein-DNA interactions; however, limitations exist. Progress has been made, notably leveraging next generation sequencing to advance ChIP-based technologies. However, there still is a need for better quantitative mapping methods for protein-DNA interactions, like CUT&RUN.