METHODS FOR MEASURING PROTEIN-DNA INTERACTIONS WITH LONG-READ DNA SEQUENCING

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PATENT STATUS

Country	Type	Number	Dated	Case
Patent Cooperation Treaty	Reference for National Filings	WO 2022/256469	12/08/2022	2021-127

Patent Pending

BRIEF DESCRIPTION

The inventors present a method to modify DNA at the site of protein-DNA interactions in intact nuclei that takes advantage of the ability for long-read DNA sequencing platforms to detect base pair modifications, such as methylation, to map the location of interactions.

Current techniques for profiling protein-DNA interactions with sequencing are limited by short-read DNA sequencing technology, which precludes the mapping of protein-DNA interactions in highly repetitive regions of the genome.

SUGGESTED USES

Suggested uses for this technology include:

- as a research tool in academic and commercial labs to map protein-DNA interactions human cells and other organisms.
- identifying regulatory mechanisms associated with protein binding in the genome that may lead to therapeutic insight. For example, investigators could elucidate the mechanisms of genetic diseases by coupling this invention with functional genomic screens of genetic variants associated with chromatin organization.

ADVANTAGES

The new method presented by the inventors maps protein-DNA interactions genome-wide, including highly repetitive areas of the genome.

In contrast, other high-throughput DNA sequencing platforms can only sequence short snippets of DNA molecules, typically around 200 base pairs in length.

RELATED MATERIALS

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OTHER INFORMATION

KEYWORDS

chromatin organization, protein-DNA interactions, epigenomics, genomics, DNA sequencing

CATEGORIZED AS

- **Biotechnology**
  - Genomics
  - Health
- **Medical**
  - Research Tools
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