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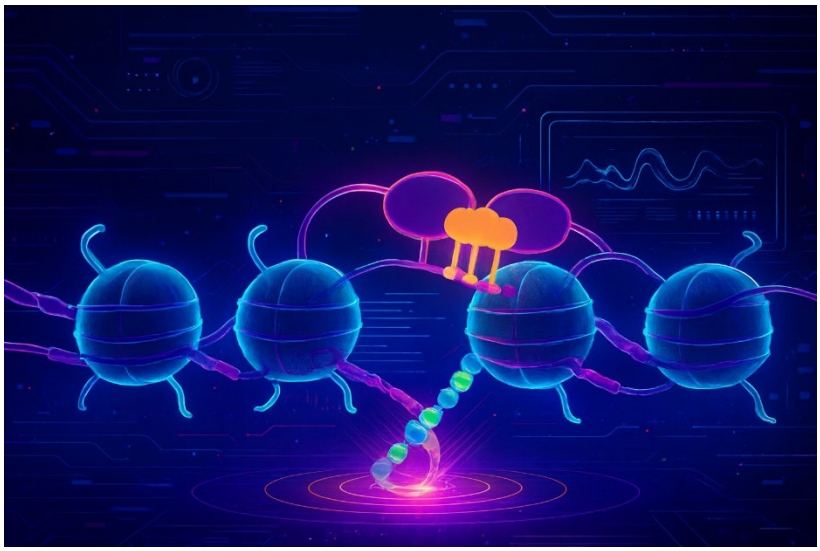
Licensing Opportunity

TTO – Technology Transfer Office

A Novel Fusion-Transposase System for Fast and Specific Methylation Profiling



Examples of MBD binding to CpG rich genomic regions

Ref. Nr

6.2582

Keywords

DNA methylation, epigenetics, diagnostics

Intellectual Property

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Publications

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Description

The analysis of DNA methylation patterns plays a central role in epigenetics research, cancer diagnostics, and the study of gene regulation. Current state-of-the-art methods such as bisulfite sequencing, MeDIP-seq, and enzymatic methyl-seq enable methylation mapping but suffer from several limitations: they often require complex multi-step workflows, large DNA input quantities, and can degrade samples through harsh chemical treatments.
The new technology proposed here overcomes these limitations by fusing methylation-recognition domains directly to a transposase, creating a methylation-directed tagmentation system. This innovation allows simultaneous DNA fragmentation and tagging while discriminating between methylated and unmethylated CpG regions, significantly simplifying workflow, improving precision and lowering sequencing cost.

Advantages

- Direct Methylation-Sensitive Tagmentation for reducing workflow complexity and minimizing sample loss
- High Sensitivity and Low Input Requirement: suitable for challenging samples, such as clinical biopsies or ancient DNA.
- Compatibility with Sequencing Platforms, including NGS

Applications

- Epigenetics and Research Tools
- Clinical and Diagnostics
- Biotechnology and Sequencing Kit Manufacturers
- Agricultural and Environmental Genomics