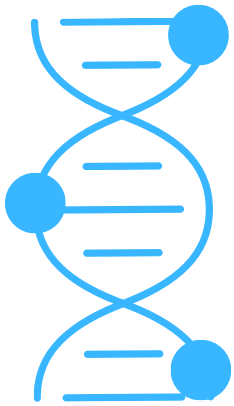
Enzymatic Methyl-seq

admera health
Welcome To The Advanced Molecular Era



Admera Health offers methyl-seq services leveraging advanced enzymatic technology for exceptional data quality, high-throughput capacity, and comprehensive analysis, Our team ensures rapid turnaround and provide white-glove service with personalized 1:1 support and transparent communication at every stage.

Enzymatic Methyl-seq (EM-seq), an enzyme-based approach, offers superior sequencing performance with higher library yields, even base coverage, larger insert sizes, more CpG site detections, and less GC bias.

EM-seq Service Tiers

Global EM-seq: Our partners from New England Biolabs (NEB) offers a complete end-to-end, methylome analysis solution using the NEBNext Enzymatic Methyl-seq library prep kit. EM-seq uses a two-step enzymatic process that is less destructive to the DNA and generates Illumina-compatible libraries. Global EM-seq is similar to whole genome bisulfite sequencing (WGBS).

Targeted EM-seq: Combine EM-seq with Twist Bioscience's Human Methylome Panel to target 3.98M biologically relevant CpG sites across the genome for an accurate, sensitive, & high-performance hybrid-capture system perfect for cancer, functional genomics, & developmental biology investigations.

How Does EM-seq Compare to Bisulfite Sequencing?

Superior Library Preparation	Enzyme conversion is less harsh to DNA vs. chemical treatment Similar conversion efficiency vs. bisulfite conversion Greater DNA insert sizes
Greater Sequencing Performance	Higher quality sequencing data from EM-seq libraries Lower library duplication rates Less severe GC bias with greater CpG coverage

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Workflow

Mechanical Fragmentation
Diluted genomic DNA (gDNA) is sheared using a focused-ultrasonicator

EM-seq Library Preparation
Sheared gDNA is end repaired & A-tailed for subsequent ligation of Universal Adapters for the NEBNext EM-seq workflow

Methylation Conversion
A two-step enzymatic conversion process distinguishes between unmethylated and methylated cytosines (5mC & 5hmC)

Methylome Enrichment **Targeted EM-seq workflow*
The Twist Human Methylome Panel targets 3.98M CpG sites with 123 Mb of genomic content to investigate biological relevant methylation markers

Next-Generation Sequencing
EM-seq libraries are sequenced at 2x150 bp using an Illumina NovaSeq® 6000 or NovaSeq® X Plus

Bioinformatics
High-quality reads are aligned using the DRAGEN Methylation pipeline and other computational tools for differential methylation analysis

Superior Support for Your Methylome Research

Exceptional Data Quality
Stringent quality control steps ensure consistency for high-quality data delivery

Rapid Delivery
Industry-leading turnaround time to get the data in your hands within 7-10 business days

High-Throughput Capacity
Our state-of-the-art technology and custom coverage capabilities provide the necessary throughput to support data-driven projects

White-Glove Service
Responsive, 1:1 support for all projects and communicate outcomes for each step of the EM-seq workflow

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