

Methylation Sequencing



Methylation Matters: Explore the Epigenome

DNA methylation is one of the most common epigenetic modifications that fundamentally influence gene expression, cellular differentiation, and genomic imprinting. Without any change in the DNA sequence itself, gene activity and function can be regulated by DNA methylation. DNA methyltransferases mediate the regulation of gene activity and function by transferring a methyl group to the fifth carbon of the cytosine ring. In mammals, the resulting 5-methylcytosines (5-mC) and 5-hydroxymethylcytosines (5-hmC) occur mainly in cytosine-phosphate-guanine (CpG) dinucleotides. However, methylation can also be found in non-CpG contexts in other organisms.

Changes in the epigenetic signature, especially in DNA methylation, have been reported to happen in normal cell development and aging. However, alterations in DNA methylation are also closely associated with diseases like cancer, metabolic disorders, and neurological diseases. Global hypomethylation and locus-specific hypermethylation of CpG islands have been shown to increase genomic instability and promote tumor progression.

High-quality methylation data analysis can be used for:

- ✗ Biomarker discovery
- ✗ Clinical studies with methylation-associated treatments or other clinical and scientific applications
- ✗ Exploration of cell differentiation mechanisms, characteristic methylation profiles, and specific tissue development

Explore Our Product Portfolio for Methylation Sequencing

	WGM Classic	WGM Flex
Species	Human	Diverse
DNA quality	High molecular weight DNA	Various quality (e.g., fragmented DNA)
Cytosine conversion method	Enzymatic	
Sequencing platform	Illumina	
Output	90 Gb	Flexible
Included deliverables	Project report & FASTQ files	

We offer Whole Genome Methylation Sequencing (WGM) products using an enzyme-based method (enzymatic Methyl-Seq, EM-seq™) to realize your research studies.

Want to Discover More?
We invite you to take a look at our website.
www.cephg.com/methylation-sequencing





About Us

CeGaT was founded in 2009 in Tübingen, Germany. Our scientists are specialized in next-generation sequencing (NGS) for genetic diagnostics, and we also provide a variety of sequencing services for research purposes and pharma solutions. Our sequencing service portfolio is complemented by analyses suited for microbiome, immunology, and translational oncology studies.

Our dedicated project management team of scientists and bio-informaticians works closely with you to develop the best strategy to realize your project. Depending on its scope, we select the most suitable library preparation and conditions on our sequencing platforms.

**We would be pleased to provide you with our excellent service.
Contact us today to start planning your next project.**



Accredited by DAKKS according to
DIN EN ISO/IEC 17025:2018



CLIA CERTIFIED ID: 99D2130225

CeGaT GmbH
Research & Pharma Solutions
Paul-Ehrlich-Str. 23
72076 Tübingen
Germany

Phone: +49707156544-333

Fax: +49 707156544-56

Email: rps@cegat.com

Web: www.cegat.com/rps