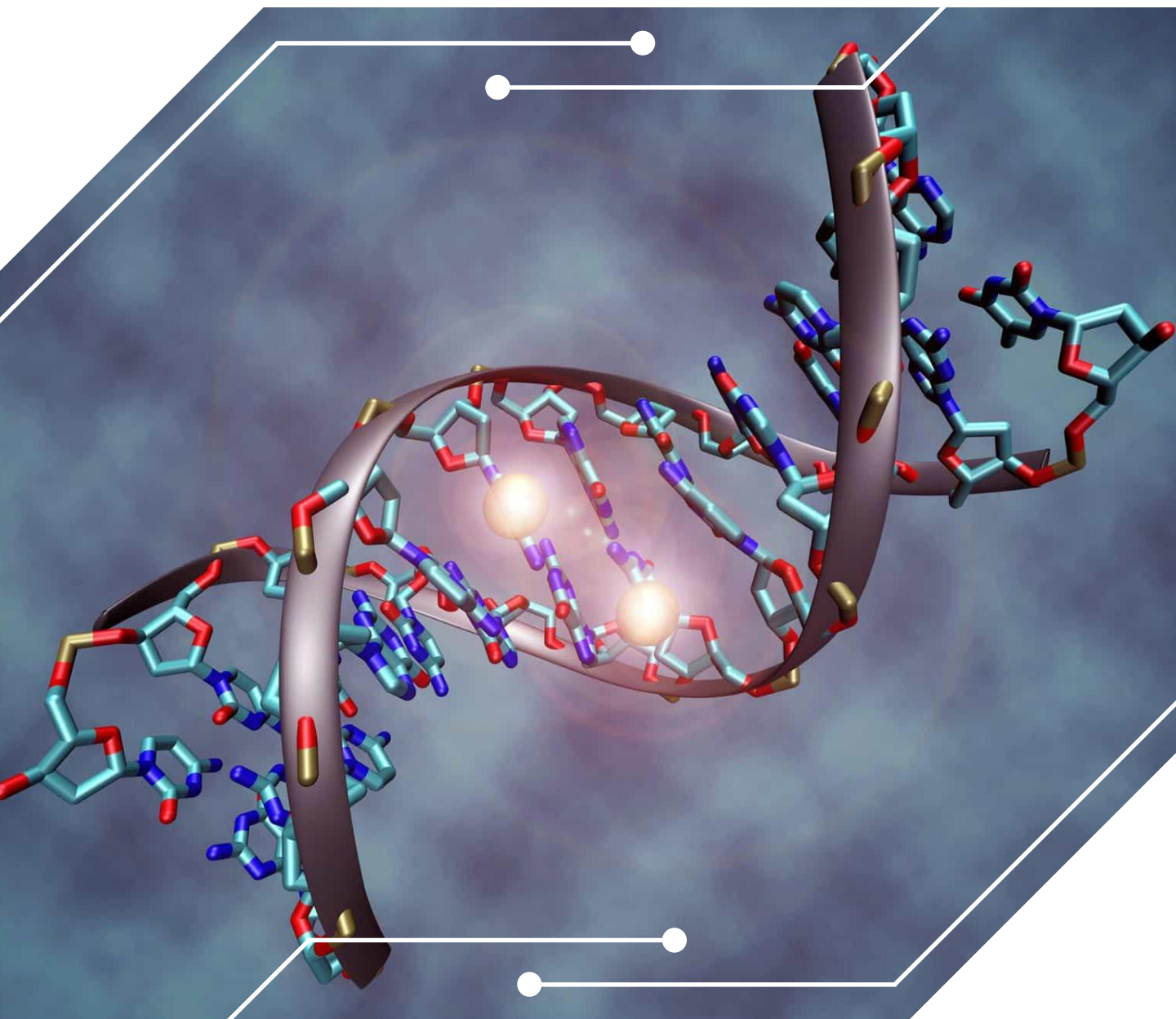




CD Genomics

The Genomics Services Company



**Powerful Solutions for
Exploring Epigenomic
Changes**

Epigenomics at CD Genomics

We provide a wide range of epigenomics sequencing services to meet the needs and budget of our clients. They can be used for many purposes, including detection of various methylations, elucidation of mechanisms of complex disease, disease diagnosis, and translational discovery.

Service	Description	Specification
 Whole Genome Bisulfite Sequencing	The gold-standard approach to identifying individually methylated cytosines on a genome-wide scale at base-pair resolution.	<ul style="list-style-type: none"> ◆ HiSeq platforms, PE 150 ◆ Sequencing depth > 20X ◆ More than 80% of bases with a \geqQ30 quality score
 Targeted Bisulfite Sequencing	An accurate, economic technology for DNA methylation analysis of target regions based on hybridization or PCR amplification.	<ul style="list-style-type: none"> ◆ HiSeq platforms, PE 150 ◆ Sequencing depth > 100X ◆ More than 80% of bases with a \geqQ30 quality score
 Reduced Representation Bisulfite Sequencing	A genome-wide DNA methylation analysis combining restriction enzyme digestion with bisulfite sequencing to enrich a CpG-dense fraction of the genome.	<ul style="list-style-type: none"> ◆ Illumina HiSeq X Ten, paired-end 150 bp ◆ > 50M clean reads ◆ More than 80% of bases with a \geqQ30 quality score
 MeDIP Sequencing	MeDIP-seq combines methylated DNA immunoprecipitation with the NGS for epigenetic studies at genome-wide level or any given regions of interest.	<ul style="list-style-type: none"> ◆ Illumina HiSeq4000, PE 150 ◆ 50M reads or 10 G data per sample ◆ More than 80% of bases with a \geqQ30 quality score
 MethylRAD-Seq	MethylRAD uses methylated modified dependent endonuclease for <i>de novo</i> methylation analysis.	<ul style="list-style-type: none"> ◆ Illumina HiSeq X-ten, PE 150 ◆ 30 M reads per Gb genome size
 ChIP-Seq	The technique combines chromatin immunoprecipitation (ChIP) with NGS to measure genome-wide DNA-associated proteins.	<ul style="list-style-type: none"> ◆ Illumina HiSeq, SE 50 ◆ \geq10M clean reads (transcription factor), \geq20 M clean reads (histone proteins)
 EpiTYPER DNA Methylation Analysis	A MALDI-TOF mass spectrometry-based bisulfate sequencing method that enables genome-wide DNA methylation analysis.	<ul style="list-style-type: none"> ◆ EpiTYPER MassARRAY platform ◆ Down to 5% differences in methylation detection ◆ High precision (5% CV)