Your tool for advancing Epigenetics

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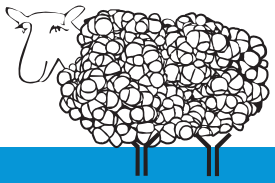
Studying epigenetic modifications and want to use the best kits?

Save time and choose the right tools to detect methylation, histone modifications and DNA-protein interactions.



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Histone modification

Posttranslational histone modifications are important epigenetic modifiers: acetylation, methylation, phosphorylation or sumoylation are reversible covalent processes that can occur at the same time on a given histone. They activate or repress gene transcription by modulating the accessibility of proteins to chromatin.

Histone Acetylation

Acetylation on specific residues on histone H3 and/or histone H4 is generally linked to gene transcriptional activation. Acetylation is regulated by specific histone acetyltransferase (HAT) and histone deacetylase (HDAC) enzymes.

HAT activity kits	Acetylation quantification kits	
HAT activity ab65352	**Histone H3 acetylation** ab115104 – ab115115	**Histone H4 acetylation** ab115116 - ab115123

Histone Methylation

Methylation on histone H3 and/or histone H4 by the addition of one, two or three methyl groups on specific lysine residues can lead to transcriptional repression or activation, depending on the modified residue and the amount of methyl groups added. Methylation is regulated by specific histone methyltransferase (HMT) and histone demethyltransferase (HDMT) enzymes.

HMT activity kits	HDMT activity kits		Methylation quantification kits	
Site specific ab113452 – ab113454	**Site specific** ab113455 ab113457 ab113458	**Inhibitor Screening** ab113456	**Histone H3 methylation** ab115048 – ab115092	**Histone H4 methylation** ab115093 – ab115100

Histone Phosphorylation

Histone phosphorylation on serine and/or threonine residues may have a role on disrupting chromatin structure and possibly provide a signal for the recruitment of non-histone chromosomal proteins to chromatin. Phosphorylation of S10 and S28 on histone H3 has been shown to correlate with chromosome condensation during cell replication and both sites have been used as mitotic markers.

Phosphorylation quantification kits
Histone H3 phosphorylation kits ab115126 – ab115130

DNA methylation

DNA methylation in mammals occurs primarily on the fifth carbon of the cytosine base (5-methylcytosine, 5-mC) of CpG dinucleotides. This reversible covalent addition of the methyl group is involved in chromatin structure, imprinting and gene regulation.

Gene-specific methylation

Gene-specific methylation can be analyzed either by immunoprecipitating the methylated DNA with specific antibodies or by treating the denatured DNA with sodium bisulfite: sodium bisulfite will deaminate all unmethylated cytosine residues to uracil while leaving 5-mC intact.

Bisulfite modification	Methylation capture kits	
DNA bisulfite conversion kits ab117124 – ab117127	**Methylated DNA (5-mC) capture kits** ab117133 ab117135	**Hydroxmethylated DNA (5-hmC) capture kits** ab117134 ab117136

DNA methyltransferase/ demethylase

DNA methyltransferases and demethyltransferases are the enzymes responsible for regulating DNA methylation at the CpG dinucleotides.

DNMT activity	Demethylase activity	Enzyme quantification	Inhibitor screening
Total DNMT activity kits ab113467 ab113468	**Total demethylase activity kits** ab113472	**DNMT level quantification kits** ab113469 (DNMT1) ab113470 (DNMT3A) ab113471 (DNMT3B)	**DNMT inhibitor screening kits** ab113465 (DNMT1) ab113466 (DNMT3B)

Global DNA methylation

A decrease in global DNA methylation levels (DNA hypomethylation) is likely caused by methyl-deficiency due to environmental influences and generally considered a molecular marker for processes such as cancer.

MBD2	DNA methylation	DNA hydroxymethylation
Methyl CpG binding protein activity quantification kits ab113473	**DNA methylation quantification kits** ab117128 ab117129	**DNA hydroxymethylation quantification kits** ab117130 ab117131

DNA/ Protein Interaction

DNA and transcription factors among other proteins are critical for cellular functions such as gene transcription and DNA replication, as well as epigenetic silencing. Identifying the genetic targets of DNA-binding proteins and how they interact with their binding DNA sequences is essential for understanding said cellular functions. In mammalian cells, interactions between transcription factors and promoter sequences of specific genes are primary determinants for establishing spatial and temporal expression patterns of those genes.

In vivo DNA/ protein interaction detection

ChIP (Chromatin Immunoprecipitation) is an established and versatile tool for characterizing *in vivo* how a particular protein binds to specific sequences of genomic loci.

ChIP methyl DNA kits		ChIP general kits		ChIP protein-specific kits	
Methylated DNA ab117133 ab117135	**Hydroxymethylated DNA** ab117134 ab117136	**Cells/tissues** ab117136	**Plants** ab117137	**Methylated histone H3/H4** ab117141 – ab117147	**Methyl CpG binding protein** ab113450 ab113451
				Acetylated histone H3/H4 ab117148 – ab117151	

In vitro DNA/ protein interaction detection

The study *in vitro* of direct interactions between proteins and DNA enables the controlled analysis of transcription factor binding to specific DNA consensus sequences located in gene promoter regions.

ab117139 – **DNA/protein Binding Assay Kit (Colorimetric)**	ab11740 – **DNA/protein Binding Assay Kit (Fluorometric)**

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