

## Product datasheet

# Histone H3 (pan-methyl K27) Quantification Kit (Colorimetric) ab115074

### Overview

<b>Product name</b>	Histone H3 (pan-methyl K27) Quantification Kit (Colorimetric)
<b>Detection method</b>	Colorimetric
<b>Sample type</b>	Tissue, Adherent cells, Suspension cells
<b>Assay type</b>	Quantitative
<b>Assay time</b>	2h 30m
<b>Species reactivity</b>	<b>Reacts with:</b> Mouse, Human

**Predicted to work with:** Mammals 

### Product overview

Methylation of histone H3 at lysine 27 has an important role in transcription repression and it is catalyzed by G9a and Polycomb Groups enzymes such as EZH2. H3 (mono-methyl K27), a modification enriched at pericentromeric heterochromatin, is broadly distributed throughout all euchromatic sites and participates in silencing gene expression. H3 (di-methyl K27) and H3 (tri-methyl K27) are the facultative heterochromatin mark which promotes the recruitment of PcG proteins for gene silencing.

Histone H3 (pan-methyl K27) Quantification Kit (Colorimetric) (ab115074) allows the user to specifically measure global mono-, di-, and tri-methylation of histone H3K27 colorimetrically using a variety of mammalian cells including fresh and frozen tissues, cultured adherent and suspension cells.

**Platform** Microplate reader

### Properties

**Storage instructions** Please refer to protocols.

Components	Identifier	96 tests
10X Wash Buffer		1 x 20ml
8-Well Sample Strips (with Frame)		1 x 9 units
8-Well Standard Control Strips	Green Ringed	1 x 3 units
Antibody Buffer		1 x 12ml

Components	Identifier	96 tests
Color Developer		1 x 10ml
Detection Antibody, 1 mg/mL		1 x 10µl
Standard Control, 100 µg/mL		1 x 20µl
Stop Solution		1 x 6ml

### Function

Core component of nucleosome. Nucleosomes wrap and compact DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post-translational modifications of histones, also called histone code, and nucleosome remodeling.

### Sequence similarities

Belongs to the histone H3 family.

### Developmental stage

Expressed during S phase, then expression strongly decreases as cell division slows down during the process of differentiation.

### Post-translational modifications

Acetylation is generally linked to gene activation. Acetylation on Lys-10 (H3K9ac) impairs methylation at Arg-9 (H3R8me2s). Acetylation on Lys-19 (H3K18ac) and Lys-24 (H3K24ac) favors methylation at Arg-18 (H3R17me).

Citrullination at Arg-9 (H3R8ci) and/or Arg-18 (H3R17ci) by PAD4 impairs methylation and represses transcription.

Asymmetric dimethylation at Arg-18 (H3R17me2a) by CARM1 is linked to gene activation.

Symmetric dimethylation at Arg-9 (H3R8me2s) by PRMT5 is linked to gene repression.

Asymmetric dimethylation at Arg-3 (H3R2me2a) by PRMT6 is linked to gene repression and is mutually exclusive with H3 Lys-5 methylation (H3K4me2 and H3K4me3). H3R2me2a is present at the 3' of genes regardless of their transcription state and is enriched on inactive promoters, while it is absent on active promoters.

Methylation at Lys-5 (H3K4me), Lys-37 (H3K36me) and Lys-80 (H3K79me) are linked to gene activation. Methylation at Lys-5 (H3K4me) facilitates subsequent acetylation of H3 and H4.

Methylation at Lys-80 (H3K79me) is associated with DNA double-strand break (DSB) responses and is a specific target for TP53BP1. Methylation at Lys-10 (H3K9me) and Lys-28 (H3K27me) are linked to gene repression. Methylation at Lys-10 (H3K9me) is a specific target for HP1 proteins (CBX1, CBX3 and CBX5) and prevents subsequent phosphorylation at Ser-11 (H3S10ph) and acetylation of H3 and H4. Methylation at Lys-5 (H3K4me) and Lys-80 (H3K79me) require preliminary monoubiquitination of H2B at 'Lys-120'. Methylation at Lys-10 (H3K9me) and Lys-28 (H3K27me) are enriched in inactive X chromosome chromatin.

Phosphorylated at Thr-4 (H3T3ph) by GSG2/haspin during prophase and dephosphorylated during anaphase. Phosphorylation at Ser-11 (H3S10ph) by AURKB is crucial for chromosome condensation and cell-cycle progression during mitosis and meiosis. In addition phosphorylation at Ser-11 (H3S10ph) by RPS6KA4 and RPS6KA5 is important during interphase because it enables the transcription of genes following external stimulation, like mitogens, stress, growth factors or UV irradiation and result in the activation of genes, such as c-fos and c-jun.

Phosphorylation at Ser-11 (H3S10ph), which is linked to gene activation, prevents methylation at Lys-10 (H3K9me) but facilitates acetylation of H3 and H4. Phosphorylation at Ser-11 (H3S10ph) by AURKB mediates the dissociation of HP1 proteins (CBX1, CBX3 and CBX5) from heterochromatin. Phosphorylation at Ser-11 (H3S10ph) is also an essential regulatory mechanism for neoplastic cell transformation. Phosphorylated at Ser-29 (H3S28ph) by MLTK isoform 1, RPS6KA5 or AURKB during mitosis or upon ultraviolet B irradiation. Phosphorylation at Thr-7 (H3T6ph) by PRKCBB is a specific tag for epigenetic transcriptional activation that

prevents demethylation of Lys-5 (H3K4me) by LSD1/KDM1A. At centromeres, specifically phosphorylated at Thr-12 (H3T11ph) from prophase to early anaphase, by DAPK3 and PKN1. Phosphorylation at Thr-12 (H3T11ph) by PKN1 is a specific tag for epigenetic transcriptional activation that promotes demethylation of Lys-10 (H3K9me) by KDM4C/JMJD2C. Phosphorylation at Tyr-42 (H3Y41ph) by JAK2 promotes exclusion of CBX5 (HP1 alpha) from chromatin.

Monoubiquitinated by RAG1 in lymphoid cells, monoubiquitination is required for V(D)J recombination (By similarity). Ubiquitinated by the CUL4-DDB-RBX1 complex in response to ultraviolet irradiation. This may weaken the interaction between histones and DNA and facilitate DNA accessibility to repair proteins.

#### Cellular localization

Nucleus. Chromosome.

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