abcam

Product datasheet

Histone H3 (di-methyl K4) Quantification Kit (Colorimetric, Circulating) ab233496

2 Images

Overview

Product name	Histone H3 (di-methyl K4) Quantification Kit (Colorimetric, Circulating)
Detection method	Colorimetric
Sample type	Serum, Plasma, Other biological fluids
Assay type	Quantitative
Sensitivity	0.5 ng/well
Assay time	2h 30m
Species reactivity	**Reacts with:** Mouse, Rat, Human
Product overview	Histone H3 (di-methyl K4) Quantification Kit (Colorimetric, Circulating) (ab233496) is a convenient package of tools designed to specifically measure circulating dimethyl histone H3K4 (H3K4me2) from biological fluid samples such as plasma and serum from human, mouse or rat. This kit only recognizes H3K4me2 with no cross-reactivity with unmodified H3 or other modifications at the same lysine site. The amount of plasma or serum for each assay can be 10-40 µl with an optimal amount of 30 µl.
Notes	Epigenetic activation or inactivation of genes plays a critical role in many important human diseases, especially in cancer. A major mechanism for epigenetic gene inactivation is methylation of CpG islands in genomic DNA caused by DNA methyltransferases. Histone methyltransferases (HMTs) control or regulate DNA methylation through chromatin-dependent transcriptional repression or activation. HMTs transfer 1-3 methyl groups from S-adenosyl-L-methionine to the lysine and arginine residues of histone proteins. NSD3 is the major histone methyltransferase that catalyzes dimethylation of histone H3 at lysine 4 (H3-K4) in mammalian cells. LSD2 and JARIDs are the major histone demethylase that demethylates H3K4. H3K4me2 has been viewed as a signature mark of highly transcribed genes, which is placed exclusively in the 5'- region downstream of the promoter. The H3K4me2 can also be changed by inhibition or activation of HMTs. Circulating histone H3K4me2 in plasma or serum has been observed and demonstrated as the marker for many different diseases or pathological changes such as cancer progression. Therefore, detection of circulating H3K4me2 would provide useful information for a better understanding of epigenetic regulation of gene activation and silencing, histone modification-associated pathological processes, screening of disease-related biomarkers, as well as for developing histone modification-targeted drugs.
Platform	Microplate reader

Properties

Storage instructions Please refer to protocols.

Components	1 x 48 tests	1 x 96 tests
10X Wash Buffer	1 x 14ml	1 x 28ml
8-Well Assay Strip	4 units	10 units
Adhesive Covering Film	1 unit	1 unit
Control Assay Strips	2 units	2 units
Detection Antibody	1 x 6µl	1 x 12µl
Developer Solution	1 x 5ml	1 x 10ml
Histone Assay Buffer	1 x 4ml	1 x 8ml
Standard Control	1 x 10µl	1 x 20µl
Stop Solution	1 x 5ml	1 x 10ml

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.

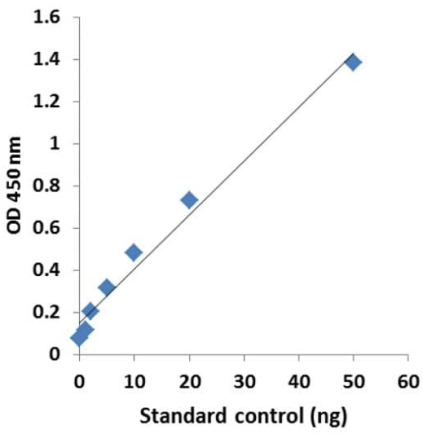
Developmental stage Expressed during S phase, then expression strongly decreases as cell division slows down during the process of differentiation.

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 PADI4 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.

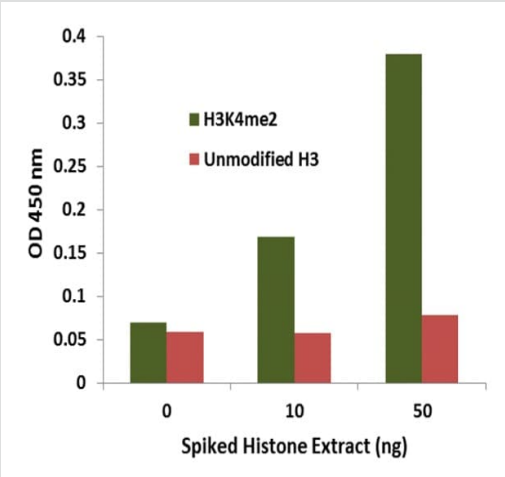
Cellular localization Nucleus. Chromosome.

Images



Example Standard Curve

Standard Curve



Example Data

Histone extracts were prepared from HL-60 (Human promyelocytic leukemia cell line) cells and spiked into bovine plasma at different concentrations. The amount of H3K4me2 was measured using Histone H3 (di-methyl K4) Quantification Kit (Colorimetric, Circulating) (ab233496).

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