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Product datasheet

Histone H3 (di-methyl K36) Quantification Kit (Fluorometric) ab115078

概述

产品名称	Histone H3 (di-methyl K36) Quantification试剂盒(Fluorometric)
检测方法	Fluorescent
样品类型	Tissue, Adherent cells, Suspension cells
检测类型	Quantitative
检测时间	2h 30m
种属反应性	**与反应:** Mouse, Human **预测可用于:** Mammals
产品概述	Methylation of histone H3 at lysine 36 seems to be coupled to the proces of active transcriptional elongation and it is enriched towards the 3' end of target genes. However, when present within protein-coding regions it prevents inappropriate transcriptional initiation of intragenic sequences. In particular, H3 (di-methyl K36) is associated with transcriptionally active genes. Abcam's Histone H3 (di-methyl K36) Quantification Kit (Fluorometric) (ab115078) allows the user to specifically measure global di-methylation of histone H3K36 fluorometrically using a variety of mammalian cells including fresh and frozen tissues, cultured adherent and suspension cells.
平台	Microplate reader

性能

存放说明	Please refer to protocols.

组件	标识符	48 tests	96 tests
10X Wash Buffer		1 x 10ml	1 x 20ml
8-Well Sample Strips (with Frame)		4 units	1 x 9 units
8-Well Standard Control Strips	Green Ringed	2 units	3 units
Antibody Buffer		1 x 6ml	1 x 12ml
Detection Antibody, 1 mg/mL		1 x 5µl	1 x 10µl

组件	标识符	48 tests	96 tests
Fluoro Developer		1 x 12µl	1 x 24µl
Fluoro Dilution		1 x 4ml	1 x 8ml
Fluoro Enhancer		1 x 12µl	1 x 24µl
Standard Control, 100 µg/mL		1 x 10µl	1 x 20µl

功能

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.

序列相似性

Belongs to the histone H3 family.

发展阶段

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

翻译后修饰

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.
细胞定位	Nucleus. Chromosome.