abcam

Product datasheet

Histone H4 (di-methyl R3) Quantification Kit (Colorimetric) ab156914

2 Images

Overview

Product name	Histone H4 (di-methyl R3) Quantification Kit (Colorimetric)
Detection method	Colorimetric
Sample type	Cell culture extracts, Tissue Extracts, Nuclear Extracts
Assay type	Quantitative
Sensitivity	>= 0.5 ng/well
Range	100 ng/well - 2000 ng/well
Assay time	3h 30m
Species reactivity	**Reacts with:** Plants, Mammals, Fungi
Product overview	Histone H4 (di-methyl R3) Quantification Kit (Colorimetric) (ab156914) is suitable for specifically measuring global histone H4 arginine 3 di-methylation from a broad range of species such as mammals, plants, fungi, and bacteria, in a variety of forms including cultured cells and fresh tissues.
Notes	Arginine histone methylation is one of the many important epigenetic marks, and is essential for the regulation of multiple cellular processes. Arginine methylation of histones H3 (Arg2, 8, 17, 26) and H4 (Arg3) promotes transcriptional activation and is mediated by a family of protein arginine methyltransferases (PRMTs). There are 9 types of PRMTs found in humans but only 7 members are reported to methylate histones. They can mediate mono or dimethylation of arginine residues. These enzymes use S-adenosyl-methionine (SAM) as a methyl donor and transfer it to the guanidinium side chain of arginine. Based on the position of methyl group addition, the PRMTs can be classified into type I (CARM1, PRMT1, PRMT2, PRMT3, PRMT6, and PRMT8) and type II (PRMT5 and PRMT7). Symmetric di-methylation of histone H4 arg3 (H4R3) are catalyzed by type II PRMTs, which are found to be strongly implicated in diseases like cancer. For example, PRMT5 plays a role in the repression ofcertain tumor suppressor genes such as RB tumor suppressors while PRMT7 overexpression is observed in breast cancer. The global H4R3 di-methylation can be changed by inhibition or activation of type II PRMTs. Therefore, quantitative detection of global symmetric di-methyl histone H4R3 would provide useful information for better understanding epigenetic regulation of gene activation and silencing, as well as for developing PRMT-targeted drugs.
Platform	Microplate reader

Properties

Storage instructions	Please refer to protocols.

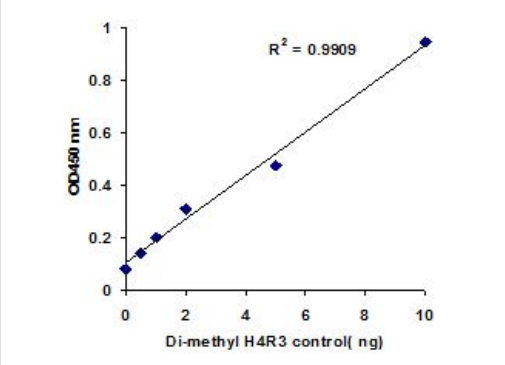
Components	48 tests	96 tests
1000X Capture Antibody	1 x 5µl	1 x 10µl
10X Wash Buffer	1 x 14ml	1 x 28ml
2000X Detection Antibody	1 x 6µl	1 x 12µl
8-Well Assay Strips (with Frame)	1 x 6 units	1 x 12 units
Adhesive Covering Film	1 unit	1 unit
Blocking Buffer	1 x 10ml	1 x 20ml
Developer Solution	1 x 5ml	1 x 10ml
Enhancer Solution	1 x 6µl	1 x 12µl
H4R3me2 Control, 50 µg/mL	1 x 10µl	1 x 20µl
Histone Buffer	1 x 4ml	1 x 8ml
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.

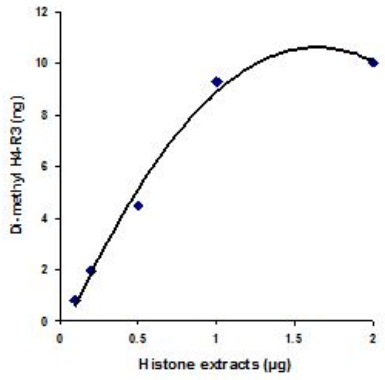
Cellular localization Nucleus. Chromosome.

Images



Standard Curve

Illustrated standard curve generated with H4R3me2 Control.



Typical data

Histone extracts were prepared from MDA-231 cells using Histone Extraction Kit (ab113476) and the amount of H4R3me2 was measured using Abcam's Histone H3 (di-methyl R4) Quantification Kit (Colorimetric) (ab156914).

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