# abcam

# Product datasheet

# Histone H4 (mono-methyl K20) Quantification Kit (Fluorometric) abl 15094

#### Overview

Product name Histone H4 (mono-methyl K20) Quantification Kit (Fluorometric)

**Detection method** Fluorescent

Sample type Tissue, Adherent cells, Suspension cells

Sensitivity 1 ng/well

Range 10 ng/well - 2000 ng/well

Assay time 2h 30m

Species reactivity Reacts with: Mouse, Human

Predicted to work with: Mammals

**Product overview** Methylation of histone H4 at lysine 20 is catalyzed by SET9 and SUV4.20h among other methyl

transferases in mammalian cells. H4 (mono-methyl K20) is involved in the maintenance of the

proper higher order structure of DNA and is consequently essential for chromosome

condensation. It is also involved in gene silencing.

Histone H4 (mono-methyl K20) Quantification Kit (Fluorometric) (ab115094) enables the user to measure global mono-methylation of histone H4K20. The global H4K20 mono-methylation can also be changed by inhibition or activation of HMTs, making quantitative detection of global mono-methyl histone H4K20 useful in developing a better understanding of epigenetic regulation of gene activation/repression and for developing HMT-targeted drugs. ab115094 is suitable for use with a variety of mammalian cells including fresh and frozen tissues, and cultured adherent

and suspension cells.

**Platform** Microplate reader

# **Properties**

**Storage instructions** Please refer to protocols.

Components	Identifier	48 tests	96 tests
10X Wash Buffer		1 x 10ml	1 x 20ml
8-Well Sample Strips (with Frame)		4 units	9 units

1

Components	Identifier	48 tests	96 tests
8-Well Standard Control Strips	Green Ringed	2 units	3 units
Antibody Buffer		1 x 6ml	1 x 12ml
Detecting Antibody, 1 mg/mL		1 x 5µl	1 x 10µl
Fluoro Developer		1 x 12µl	1 x 24µl
Fluoro Dilution		1 x 4ml	1 x 8ml
Fluoro Enhancer		1 x 12µl	1 x 24µl
Signal Enhancer		1 x 120µl	1 x 240µl
Signal Report Solution		1 x 5µl	1 x 10µl
Standard Control, 100 μg/mL		1 x 10µl	1 x 20µl

#### **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

Post-translational modifications

Belongs to the histone H4 family.

Acetylation at Lys-6 (H4K5ac), Lys-9 (H4K8ac), Lys-13 (H4K12ac) and Lys-17 (H4K16ac) occurs in coding regions of the genome but not in heterochromatin.

Citrullination at Arg-4 (H4R3ci) by PADI4 impairs methylation.

Monomethylation and asymmetric dimethylation at Arg-4 (H4R3me1 and H4R3me2a, respectively) by PRMT1 favors acetylation at Lys-9 (H4K8ac) and Lys-13 (H4K12ac).

Demethylation is performed by JMJD6. Symmetric dimethylation on Arg-4 (H4R3me2s) by the

PRDM1/PRMT5 complex may play a crucial role in the germ-cell lineage.

Monomethylated, dimethylated or trimethylated at Lys-21 (H4K20me1, H4K20me2, H4K20me3).

Monomethylation is performed by SET8. Trimethylation is performed by SUV420H1 and

SUV420H2 and induces gene silencing.

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. Monoubiquitinated at Lys-92 of histone H4 (H4K91ub1) in response to DNA damage. The exact role of H4K91ub1 in DNA damage response is still unclear but it may function as a licensing signal for additional histone H4 post-translational modifications such as H4 Lys-21

methylation (H4K20me).

Sumoylated, which is associated with transcriptional repression.

### **Cellular localization**

Nucleus. Chromosome.

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