**Human H3F3C (Histone H3.3C) knockout HEK293T cell lysate ab258444**

**Overview**

**Product name**

Human H3F3C (Histone H3.3C) knockout HEK293T cell lysate

**Product overview**

Access thousands of knockout cell lysates, generated from commonly used cancer cell lines. 
See here for more information on knockout cell lysates.

**User storage instructions:** After reconstitution, store the lysate at -80°C.

**Parental Cell Line**

HEK293T

**Organism**

Human

**Mutation description**

Knockout achieved by using CRISPR/Cas9, Homozygous: 4 bp deletion in exon 1.

**Passage number**

<20

**Knockout validation**

Sanger Sequencing

**Reconstitution notes**

To use as WB control, resuspend the lyophilizate in 50 µL of LDS* Sample Buffer to have a final concentration of 2 mg/ml. For reducing conditions, we recommend a final concentration of 0.1 M DTT.

*Usage of SDS sample buffer is not recommended with these lyophilized lysates.

**Notes**

Abcam has not and does not intend to apply for the REACH Authorisation of customers’ uses of products that contain European Authorisation list (Annex XIV) substances.

It is the responsibility of our customers to check the necessity of application of REACH Authorisation, and any other relevant authorisations, for their intended uses.

This product is subject to limited use licenses from The Broad Institute and ERS Genomics Limited, and is developed with patented technology. For full details of the limited use licenses and relevant patents please refer to our limited use license and patent pages.

**Properties**

**Storage instructions**

Store at -80°C. Please refer to protocols.
<table>
<thead>
<tr>
<th>Components</th>
<th>1 kit</th>
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<tbody>
<tr>
<td>Human H3F3C knockout HEK293T cell lysate (Lyophilized)</td>
<td>1 x 100µg</td>
</tr>
<tr>
<td>Human Wild Type HEK293T cell lysate (Lyophilized)</td>
<td>1 x 100µg</td>
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</table>

**Cell type**
- epithelial

**STR Analysis**
- Amelogenin X: 8, 9
- D13S317: 12, 14
- D7S820: 11
- D16S539: 9, 13
- vWA: 16, 19
- TH01: 7, 9.3
- TPOX: 11
- CSF1PO: 11, 12

**Target**

**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. Hominid-specific H3.5/H3F3C preferentially colocalizes with euchromatin, and it is associated with actively transcribed genes.

**Tissue specificity**
Specifically expressed in the seminiferous tubules of testis.

**Sequence similarities**
Belongs to the histone H3 family.

**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) is linked to gene activation. Methylation at Lys-5 (H3K4me) facilitates subsequent acetylation of H3 and H4. 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) requires preliminary monoubiquitination at H2B at ‘Lys-120’. Methylation at Lys-10 (H3K9me) and Lys-28 (H3K27me) are enriched in inactive X chromosome chromatin. Monomethylation at Lys-56 (H3K56me1) by EHMT2/G9A in G1 phase promotes interaction with PCNA and is required for DNA replication. 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 PRKCB 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-41 (H3Y41ph) by JAK2 promotes exclusion of CBX5 (HP1 alpha) from chromatin.

Lysine deamination at Lys-5 (H3K4all) to form allysine is mediated by LOXL2. Allylsine formation by LOXL2 only takes place on H3K4me3 and results in gene repression.

Cellular localization

Nucleus. Chromosome.

Images

<table>
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