

Product datasheet for TA347186

OriGene Technologies, Inc.

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H3FA (HIST1H3A) Rabbit Polyclonal Antibody

Product data:

Product Type: Primary Antibodies

Applications: Dot, ELISA, IF, WB

Recommended Dilution: ELISA (1:100); Dot blotting (1:50,000); Western blotting (1:1,000); ChIP (5ug/ChIP)

Reactivity: Human
Host: Rabbit
Isotype: IgG

Clonality: Polyclonal

Immunogen: The immunogen for anti-H3K79me2 antibody: the region of histone H3 containing the

dimethylated lysine 79 (H3K79me2), using a KLH-conjugated synthetic peptide.

Concentration: lot specific

Purification: Affinity purified polyclonal antibody in PBS containing 0.05% azide and 0.05% ProClin 300.

Conjugation: Unconjugated

Storage: Store at -20°C as received.

Stability: Stable for 12 months from date of receipt.

Gene Name: histone cluster 1, H3a

Database Link: NP 003520

Entrez Gene 8350 Human

P68431

Background: Histones are the main constituents of the protein part of chromosomes of eukaryotic cells.

They are rich in the amino acids arginine and lysine and have been greatly conserved during evolution. Histones pack the DNA into tight masses of chromatin. Two core histones of each class H2A, H2B, H3 and H4 assemble and are wrapped by 146 base pairs of DNA to form one octameric nucleosome. Histone tails undergo numerous post-translational modifications, which either directly or indirectly alter chromatin structure to facilitate transcriptional activation or repression or other nuclear processes. In addition to the genetic code, combinations of the different histone modifications reveal the so-called "histone code". Histone methylation and demethylation is dynamically regulated by respectively histone

methyl transferases and histone demethylases.

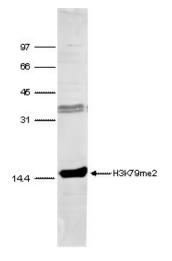




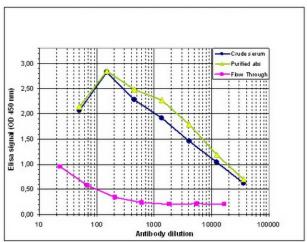
Synonyms: A; H3; H3FA

Protein Pathways: Systemic lupus erythematosus

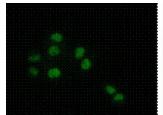
Product images:

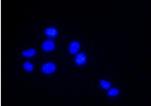


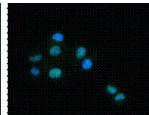
WB using the antibody against H3K79me2 diluted 1:1,000 in TBS-Tween containing 5% skimmed milk. The position of the protein of interest is indicated on the right; the marker (in kDa) is shown on the left.



Determination of the antibody titer To determine the titer of the antibody, an ELISA was performed using a serial dilution of the antibody against human H3K79me2, crude serum and flow through. The antigen used was a peptide containing the histone modification of interest. By plotting the absorbance against the antibody dilution (Figure 3), the titer of the antibody was estimated to be 1:8,000.

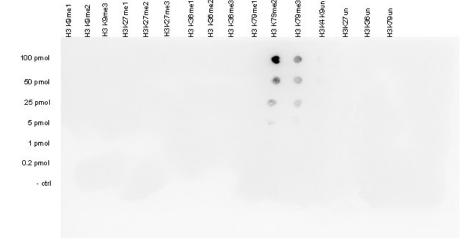




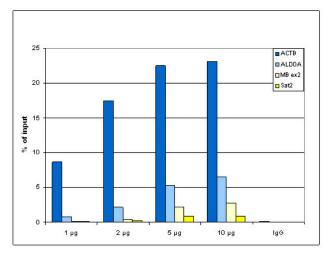


HeLa cells were stained with the antibody against H3K79me2 and with DAPI. Cells were fixed with 4% formaldehyde for 10' and blocked with PBS/TX-100 containing 5% normal goat serum and 1% BSA. The cells were immunofluorescently labelled with the H3K79me2 antibody (left) diluted 1:500 in blocking solution followed by an anti-rabbit antibody conjugated to Alexa488. The middle panel shows staining of the nuclei with DAPI. A merge of the two stainings is shown on the right.

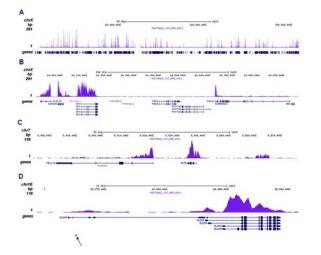




A Dot Blot analysis was performed to test the cross reactivity of the antibody against H3K79me2 with peptides containing other modifications and unmodified sequences of histone H3. One hundred to 0.2 pmol of peptide containing the respective histone modification were spotted on a membrane. The antibody was used at a dilution of 1:50,000. Figure 4 shows a high specificity of the antibody for the modification of interest.



ChIP assays using HeLa cells: ChIP-seq" kit, using sheared chromatin from 1 million cells. A titration of 1, 2, 5 and 10 ug ab was used. IgG (2 ug/IP) was negative control. qPCR primers were specific for the coding regions of the active genes ACTB and ALDOAas positive controls, and for exon 2 of the inactive myoglobin (MB) gene and the Sat2 satellite repeatas negative controls. Image shows the recovery, expressed as a % of input (the relative amount of IP'd DNA compared to input DNA after qPCR).



ChIP was performed with 1 ug of the ab. The 36 bp tags were aligned to the human genome using the ELAND algorithm. Image shows the peak distribution along the complete sequence and a 1 Mb region of the X-chromosome and in a 20 kb region surrounding the ALDOA gene (figure 2D). The position of the amplicon used for validating the ALDOA enrichment is indicated with an arrow.