

Rabbit anti-Human, Mouse H3F3A Polyclonal Antibody | anti-H3F3A antibody

H3F3A Antibody

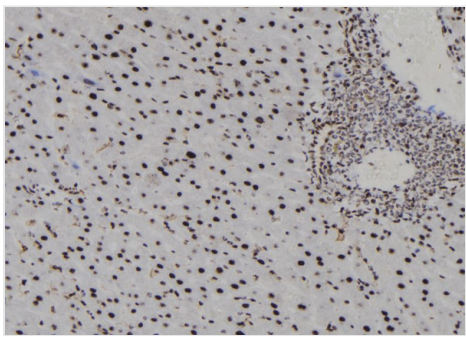
CATALOG #	HOST	REACTIVITY	APPLICATIONS
AAA327352	Rabbit	Human, Mouse	ELISA, Immunohistochemistry, Western Blot

PRODUCT SYNONYMS

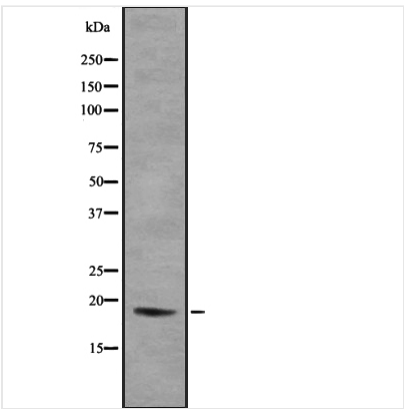
H3F3A; Polyclonal Antibody; H3F3A Antibody; H3 histone family 3A; H3 histone family 3B; H3 histone; family 3B (H3.3B); H3.3; H3.3A; H3.3B; H33_HUMAN; H3F3; H3f3b; Histone H3.3; Histone H3.3Q; Histone H3.A; Histone H3.B; MGC87782; MGC87783; anti-H3F3A antibody

PRODUCT SPECIFICATIONS

Host	Rabbit
Reactivity	Human, Mouse
Clonality	Polyclonal
Isotype	IgG
Specificity	H3F3A antibody detects endogenous levels of total H3F3A
Purity/Purification	The antiserum was purified by peptide affinity chromatography using SulfoLink Coupling Resin.
Form/Format	Liquid Phosphate buffered saline, pH 7.4, 150mM NaCl, 0.02% sodium azide and 50% glycerol.
Concentration	1mg/ml (varies by lot)
Sequence Length	136
Applicable Applications for anti-H3F3A antibody	ELISA, IHC (Immunohistochemistry), WB (Western Blot)
Immunogen	A synthesized peptide derived from human H3F3A
Subcellular Location	Nucleus. Chromosome.
Tissue Specificity	Expressed throughout the cell cycle independently of DNA synthesis.
Predicted Cross Reactivity	Pig, Zebrafish, Bovine, Chicken, Xenopus
Similarity	Pig (100%), Zebrafish (100%), Bovine (100%), Chicken (100%), Xenopus (100%)
Conjugation	Unconjugated
Preparation and Storage	Store at -20 degree C. Stable for 12 months from date of receipt.



IHC (Immunohistochemistry)
AAA327352 at 1/100 staining Mouse liver tissue by IHC-P. The sample was formaldehyde fixed and a heat mediated antigen retrieval step in citrate buffer was performed. The sample was then blocked and incubated with the antibody for 1.5 hours at 22 degree C. An HRP conjugated goat anti-rabbit antibody was used as the secondary.



WB (Western Blot)
Western blot analysis of H3F3A using HuvEc whole lysates.

Related Product Information for anti-H3F3A antibody

Function: Variant histone H3 which replaces conventional H3 in a wide range of nucleosomes in active genes. Constitutes the predominant form of histone H3 in non-dividing cells and is incorporated into chromatin independently of DNA synthesis. Deposited at sites of nucleosomal displacement throughout transcribed genes, suggesting that it represents an epigenetic imprint of transcriptionally active chromatin. 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.

Subunit Structure: The nucleosome is a histone octamer containing two molecules each of H2A, H2B, H3 and H4 assembled in one H3-H4 heterotetramer and two H2A-H2B heterodimers. The octamer wraps approximately 147 bp of DNA. Interacts with HIRA, a chaperone required for its incorporation into nucleosomes. Interacts with ZMYND11; when trimethylated at 'Lys-36' (H3.3K36me3).

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). Acetylation at Lys-123 (H3K122ac) by EP300/p300 plays a central role in chromatin structure: localizes at the surface of the histone octamer and stimulates transcription, possibly by promoting nucleosome instability. 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. Specifically enriched in modifications associated with active chromatin such as methylation at Lys-5 (H3K4me), Lys-37 and Lys-80. 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), which are linked to gene repression, are underrepresented. 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. Monomethylation at Lys-57 (H3K56me1) by EHMT2/G9A in G1 phase promotes interaction with PCNA and is required for DNA replication. Phosphorylated at Thr-4 (H3T3ph) by 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 MAP3K20 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-42 (H3Y41ph) by JAK2 promotes exclusion of CBX5 (HP1 alpha) from chromatin. Phosphorylation on Ser-32 (H3S31ph) is specific to regions bordering centromeres in metaphase chromosomes. Ubiquitinated. Monoubiquitinated by RAG1 in lymphoid cells, monoubiquitination is required for V(D)J recombination (By similarity). Lysine deamination at Lys-5 (H3K4all) to form allysine is mediated by LOXL2. Allysine formation by LOXL2 only takes place on H3K4me3 and results in gene repression. Crotonylation (Kcr) is specifically present in male germ cells and marks testis-specific genes in post-meiotic cells, including X-linked genes that escape sex chromosome inactivation in haploid cells. Crotonylation marks active promoters and enhancers and confers resistance to transcriptional repressors. It is also associated with post-meiotically activated genes on autosomes. Butyrylation of histones marks active promoters and competes with histone acetylation. It is present during late spermatogenesis. Succinylation at Lys-80 (H3K79succ) by KAT2A takes place with a maximum frequency around the transcription start sites of genes (PubMed:29211711). It gives a specific tag for epigenetic transcription activation (PubMed:29211711).

Similarity: Specific interaction of trimethylated form at 'Lys-36' (H3.3K36me3) with ZMYND11 is mediated by the encapsulation of Ser-32 residue with a composite pocket formed by the tandem bromo-PWWP domains. Belongs to the histone H3 family.

NCBI AND UNIPROT INFORMATION

NCBI GI #	4504279
NCBI GeneID	3020
NCBI Accession #	NP_002098.1
NCBI GenBank Nucleotide #	NM_002107.4
UniProt Accession #	P84243; P06351; P33155; Q5VV55; Q5VV56; Q66I33; Q9V3W4
Molecular Weight	Observed: 19 kDa Predicted: 16 kDa
NCBI Official Full Name	histone H3.3
NCBI Official Synonym Full Names	H3 histone family member 3A
NCBI Official Symbol	H3F3A
NCBI Official Synonym Symbols	H3F3; H3.3A
NCBI Protein Information	histone H3.3
UniProt Protein Name	Histone H3.3
UniProt Gene Name	H3F3A
UniProt Synonym Gene Names	H3.3A; H3F3

For Research Use Only. Not for use in diagnostic or therapeutic procedures. Small volumes of product may become entrapped in the seal of the vial during shipment and storage; if necessary, briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the cap.

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