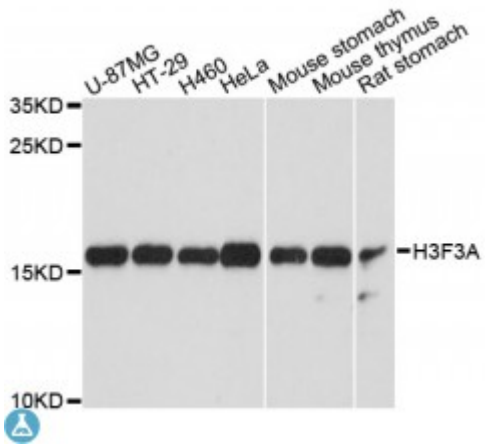
Anti-H3F3A Antibody



Description	Histones are basic nuclear proteins that are responsible for the nucleosome structure of the chromosomal fiber in eukaryotes. Two molecules of each of the four core histones (H2A, H2B, H3, and H4) form an octamer, around which approximately 146 bp of DNA is wrapped in repeating units, called nucleosomes. The linker histone, H1, interacts with linker DNA between nucleosomes and functions in the compaction of chromatin into higher order structures. This gene contains introns and its mRNA is polyadenylated, unlike most histone genes. The protein encoded is a replication-independent member of the histone H3 family.

Model	STJ115766
Host	Rabbit
Reactivity	Human, Mouse, Rat
Applications	WB
Immunogen	Recombinant fusion protein containing a sequence corresponding to amino acids 1-136 of human H3F3A (NP_002098.1).
Gene ID	3020
Gene Symbol	H3F3A
Dilution range	WB 1:500 - 1:2000
Purification	Affinity purification
Note	For Research Use Only (RUO).
Protein Name	Histone H3.3
Molecular Weight	15.328 kDa

Clonality	Polyclonal
Conjugation	Unconjugated
Isotype	IgG
Formulation	PBS with 0.02% sodium azide, 50% glycerol, pH7.3.
Storage Instruction	Store at -20C. Avoid freeze / thaw cycles.
Database Links	HGNC:4764OMIM:137800Reactome:R-HSA-201722
Alternative Names	Histone H3.3
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,
Cellular Localization	Nucleus, Chromosome
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,