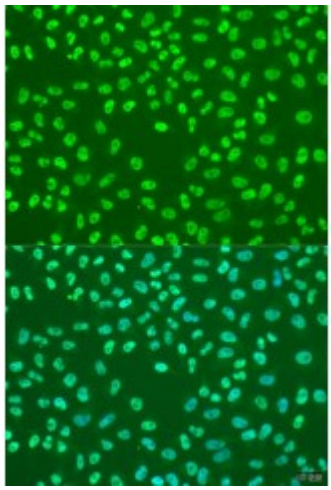
Anti-HIST1H3A Antibody



Description	Histones are basic nuclear proteins that are responsible for the nucleosome structure of the chromosomal fiber in eukaryotes. This structure consists of approximately 146 bp of DNA wrapped around a nucleosome, an octamer composed of pairs of each of the four core histones (H2A, H2B, H3, and H4). The chromatin fiber is further compacted through the interaction of a linker histone, H1, with the DNA between the nucleosomes to form higher order chromatin structures. This gene is intronless and encodes a replication-dependent histone that is a member of the histone H3 family. Transcripts from this gene lack polyA tails; instead, they contain a palindromic termination element. This gene is found in the large histone gene cluster on chromosome 6p22-p21.3.

Model	STJ117852
Host	Rabbit
Reactivity	Human
Applications	IF
Immunogen	Recombinant fusion protein containing a sequence corresponding to amino acids 1-136 of human HIST1H3A (NP_003520.1).
Gene ID	8350
Gene Symbol	HIST1H3A
Dilution range	IF 1:50 - 1:200
Purification	Affinity purification
Note	For Research Use Only (RUO).
Protein Name	Histone H3.1 Histone H3/a Histone H3/b Histone H3/c Histone H3/d Histone

	H3/f Histone H3/h Histone H3/i Histone H3/j Histone H3/k Histone H3/l
Molecular Weight	15.404 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:4766OMIM:137800Reactome:R-HSA-1266695
Alternative Names	Histone H3.1 Histone H3/a Histone H3/b Histone H3/c Histone H3/d Histone H3/f Histone H3/h Histone H3/i Histone H3/j Histone H3/k Histone H3/l
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
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,