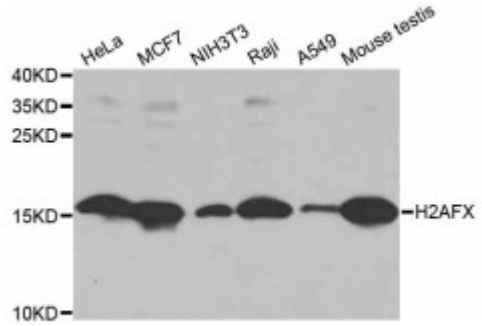
Anti-H2AFX Antibody



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 encodes a replication-independent histone that is a member of the histone H2A family, and generates two transcripts through the use of the conserved stem-loop termination motif, and the polyA addition motif.

Model	STJ113704
Host	Rabbit
Reactivity	Human, Mouse
Applications	WB
Immunogen	A synthetic peptide corresponding to a sequence within amino acids 50 to the C-terminus of human H2AFX (NP_002096.1).
Gene ID	3014
Gene Symbol	H2AFX
Dilution range	WB 1:500 - 1:2000
Purification	Affinity purification
Note	For Research Use Only (RUO).
Protein Name	Histone H2AX H2a/x Histone H2A.X

Molecular Weight	15.145 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:4739OMIM:601772Reactome:R-HSA-1221632
Alternative Names	Histone H2AX H2a/x Histone H2A.X
Function	Variant histone H2A which replaces conventional H2A in a subset of nucleosomes, 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, Required for checkpoint-mediated arrest of cell cycle progression in response to low doses of ionizing radiation and for efficient repair of DNA double strand breaks (DSBs) specifically when modified by C-terminal phosphorylation,
Cellular Localization	Nucleus
Post-translational Modifications	Phosphorylated on Ser-140 (to form gamma-H2AX or H2AX139ph) in response to DNA double strand breaks (DSBs) generated by exogenous genotoxic agents and by stalled replication forks, and may also occur during meiotic recombination events and immunoglobulin class switching in lymphocytes, Phosphorylation can extend up to several thousand nucleosomes from the actual site of the DSB and may mark the surrounding chromatin for recruitment of proteins required for DNA damage signaling and repair, Widespread phosphorylation may also serve to amplify the damage signal or aid repair of persistent lesions, Phosphorylation of Ser-140 (H2AX139ph) in response to ionizing radiation is mediated by both ATM and PRKDC while defects in DNA replication induce Ser-140 phosphorylation (H2AX139ph) subsequent to activation of ATR and PRKDC, Dephosphorylation of Ser-140 by PP2A is required for DNA DSB repair, In meiosis, Ser-140 phosphorylation (H2AX139ph) may occur at synaptonemal complexes during leptotene as an ATM-dependent response to the formation of programmed DSBs by SPO11, Ser-140 phosphorylation (H2AX139ph) may subsequently occurs at unsynapsed regions of both autosomes and the XY bivalent during zygotene, downstream of ATR and BRCA1 activation, Ser-140 phosphorylation (H2AX139ph) may also be required for transcriptional repression of unsynapsed chromatin and meiotic sex chromosome inactivation (MSCI), whereby the X and Y chromosomes condense in pachytene to form the heterochromatic XY-body, During immunoglobulin class switch recombination in lymphocytes, Ser-140 phosphorylation (H2AX139ph) may occur at sites of DNA-recombination subsequent to activation of the activation-induced cytidine deaminase AICDA, Phosphorylation at Tyr-143 (H2AXY142ph) by BAZ1B/WSTF determines the relative recruitment of either DNA repair or pro-apoptotic factors, Phosphorylation at Tyr-143 (H2AXY142ph) favors the recruitment of APBB1/FE65 and pro-apoptosis

factors such as MAPK8/JNK1, triggering apoptosis, In contrast, dephosphorylation of Tyr-143 by EYA proteins (EYA1, EYA2, EYA3 or EYA4) favors the recruitment of MDC1-containing DNA repair complexes to the tail of phosphorylated Ser-140 (H2AX139ph),