

Product datasheet

Anti-gamma H2A.X (phospho S139) antibody - C-terminal ab228655

3 Images

Overview

Product name	Anti-gamma H2A.X (phospho S139) antibody - C-terminal
Description	Rabbit polyclonal to gamma H2A.X (phospho S139) - C-terminal
Host species	Rabbit
Tested applications	Suitable for: WB, IHC-P, IHC - Wholemount
Species reactivity	Reacts with: Zebrafish
Immunogen	Synthetic peptide within Zebrafish Histone H2A.X (C terminal) (phospho S139). The exact sequence is proprietary. Database link: Q7ZUY3
Positive control	IHC-Wm: 24 hours post-fertilization (UV-irradiated) and 2 days-post-fertilization zebrafish embryos. WB: UVC treated 3dpf zebrafish embryos extracts.

Properties

Form	Liquid
Storage instructions	Shipped at 4°C. Store at +4°C short term (1-2 weeks). Upon delivery aliquot. Store at -20°C long term. Avoid freeze / thaw cycle.
Storage buffer	pH: 7.00 Preservative: 0.025% Proclin Constituents: PBS, 1% BSA, 20% Glycerol
Purity	Immunogen affinity purified
Clonality	Polyclonal
Isotype	IgG

Applications

Our [Abpromise guarantee](#) covers the use of **ab228655** in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Application	Abreviews	Notes
WB		1/500 - 1/3000. Predicted molecular weight: 15 kDa.
IHC-P		1/100 - 1/2000.
IHC - Wholemount		1/100 - 1/500.

Target

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.

Sequence similarities

Belongs to the histone H2A family.

Developmental stage

Synthesized in G1 as well as in S-phase.

Domain

The [ST]-Q motif constitutes a recognition sequence for kinases from the PI3/PI4-kinase family.

Post-translational modifications

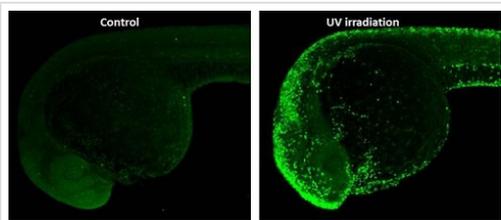
Phosphorylated on Ser-140 (to form gamma-H2AFX or H2AX139ph) in response to DNA double strand breaks (DSBs) generated by exogenous genotoxic agents and by stalled replication forks, and may also occur during meiotic recombination events and immunoglobulin class switching in lymphocytes. Phosphorylation 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). Monoubiquitination of Lys-120 (H2AXK119ub) by RING1 and RNF2/RING2 complex gives a specific tag for epigenetic transcriptional repression. Following DNA double-strand breaks

(DSBs), it is ubiquitinated through 'Lys-63' linkage of ubiquitin moieties by the E2 ligase UBE2N and the E3 ligases RNF8 and RNF168, leading to the recruitment of repair proteins to sites of DNA damage. Monoubiquitination and ionizing radiation-induced 'Lys-63'-linked ubiquitination are distinct events.

Cellular localization

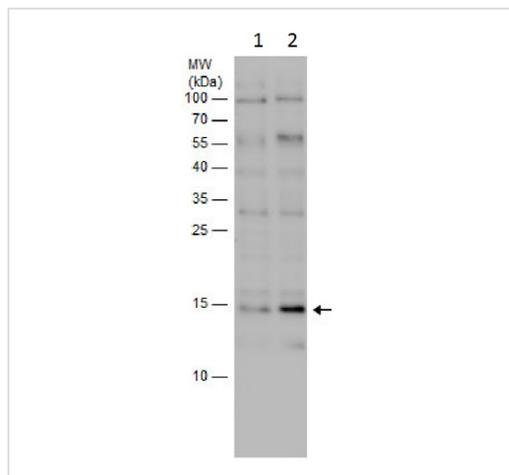
Nucleus. Chromosome.

Images



IHC - Wholemount - Anti-gamma H2A.X (phospho S139) antibody - C-terminal (ab228655)

24 hours-post-fertilization, UV-irradiated zebrafish embryo stained for Histone H2A.X (phospho S139) with ab228655 (green) at 1/100 dilution in immunohistochemical wholemount analysis.



Western blot - Anti-gamma H2A.X (phospho S139) antibody - C-terminal (ab228655)

All lanes : Anti-gamma H2A.X (phospho S139) antibody - C-terminal (ab228655) at 1/1000 dilution

Lane 1 : 3dpf zebrafish embryo whole cell extract

Lane 2 : 3dpf zebrafish embryos treated with 8000 J/m² UVC, whole cell extract

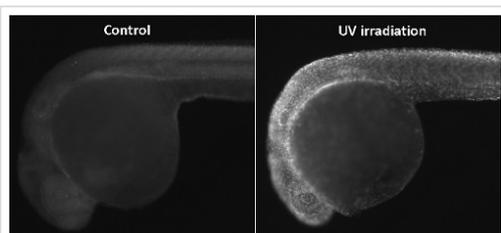
Secondary

All lanes : HRP-conjugated anti-rabbit IgG

Developed using the ECL technique.

Predicted band size: 15 kDa

15% SDS-PAGE



IHC - Wholemount - Anti-gamma H2A.X (phospho S139) antibody - C-terminal (ab228655)

2 days-post-fertilization zebrafish embryo stained for Histone H2A.X (phospho S139) with ab228655 at a 1:100 dilution in immunohistochemical wholemount analysis.

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