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RNF8 antibody - C-terminal region
Rabbit Polyclonal Antibody
Catalog # AI11669

Specification

RNF8 antibody - C-terminal region - Product Information

Application	**IHC, WB**
Primary Accession	O76064
Other Accession	NM_003958, NP_003949
Reactivity	**Human, Mouse, Rat, Rabbit, Pig, Horse, Bovine, Dog**
Predicted	**Human, Mouse, Rat, Horse, Bovine**
Host	**Rabbit**
Clonality	**Polyclonal**
Calculated MW	**55kDa KDa**

RNF8 antibody - C-terminal region - Additional Information

Gene ID 9025

Alias Symbol	**FLJ12013, KIAA0646**

Other Names
E3 ubiquitin-protein ligase RNF8, hRNF8, 6.3.2.-, RING finger protein 8, RNF8, KIAA0646

Format
Liquid. Purified antibody supplied in 1x PBS buffer with 0.09% (w/v) sodium azide and 2% sucrose.

Reconstitution & Storage
Add 100 ul of distilled water. Final anti-RNF8 antibody concentration is 1 mg/ml in PBS buffer with 2% sucrose. For longer periods of storage, store at 20°C. Avoid repeat freeze-thaw cycles.

Precautions
RNF8 antibody - C-terminal region is for research use only and not for use in diagnostic or therapeutic procedures.

RNF8 antibody - C-terminal region - Protein Information

Name RNF8 {ECO:0000255|HAMAP-Rule:MF_03067}

Synonyms KIAA0646

Function
E3 ubiquitin-protein ligase that plays a key role in DNA damage signaling via 2 distinct roles: by mediating the 'Lys-63'-linked ubiquitination of histones H2A and H2AX and promoting the recruitment of DNA repair proteins at double-strand breaks (DSBs) sites, and by catalyzing 'Lys-48'-linked ubiquitination to remove target proteins from DNA damage sites. Following DNA DSBs, it is recruited to the sites of damage by ATM-phosphorylated MDC1 and catalyzes the 'Lys-63'-linked ubiquitination of histones H2A and H2AX, thereby promoting the formation of

TP53BP1 and BRCA1 ionizing radiation-induced foci (IRIF). Also controls the recruitment of UIMC1-BRCC3 (RAP80-BRCC36) and PAXIP1/PTIP to DNA damage sites. Also recruited at DNA interstrand cross-links (ICLs) sites and catalyzes 'Lys-63'-linked ubiquitination of histones H2A and H2AX, leading to recruitment of FAAP20/C1orf86 and Fanconi anemia (FA) complex, followed by interstrand cross-link repair. H2A ubiquitination also mediates the ATM-dependent transcriptional silencing at regions flanking DSBs in cis, a mechanism to avoid collision between transcription and repair intermediates. Promotes the formation of 'Lys-63'-linked polyubiquitin chains via interactions with the specific ubiquitin-conjugating UBE2N/UBC13 and ubiquitinates non- histone substrates such as PCNA. Substrates that are polyubiquitinated at 'Lys-63' are usually not targeted for degradation. Also catalyzes the formation of 'Lys-48'-linked polyubiquitin chains via interaction with the ubiquitin-conjugating UBE2L6/UBCH8, leading to degradation of substrate proteins such as CHEK2, JMJD2A/KDM4A and KU80/XRCC5: it is still unclear how the preference toward 'Lys-48'- versus 'Lys-63'- linked ubiquitination is regulated but it could be due to RNF8 ability to interact with specific E2 specific ligases. For instance, interaction with phosphorylated HERC2 promotes the association between RNF8 and UBE2N/UBC13 and favors the specific formation of 'Lys-63'- linked ubiquitin chains. Promotes non-homologous end joining (NHEJ) by promoting the 'Lys-48'-linked ubiquitination and degradation the of KU80/XRCC5. Following DNA damage, mediates the ubiquitination and degradation of JMJD2A/KDM4A in collaboration with RNF168, leading to unmask H4K20me2 mark and promote the recruitment of TP53BP1 at DNA damage sites (PubMed:11322894, PubMed:14981089, PubMed:17724460, PubMed:18001824, PubMed:18001825, PubMed:18006705, PubMed:18077395, PubMed:18337245, PubMed:18948756, PubMed:19015238, PubMed:19124460, PubMed:19202061, PubMed:19203578, PubMed:19203579, PubMed:20550933, PubMed:21558560, PubMed:21857671, PubMed:21911360, PubMed:22266820, PubMed:22373579, PubMed:22531782, PubMed:22705371, PubMed:22865450, PubMed:22980979). Following DNA damage, mediates the ubiquitination and degradation of POLD4/p12, a subunit of DNA polymerase delta. In the absence of POLD4, DNA polymerase delta complex exhibits higher proofreading activity (PubMed:23233665). In addition to its function in damage signaling, also plays a role in higher-order chromatin structure by mediating extensive chromatin decondensation. Involved in the activation of ATM by promoting histone H2B ubiquitination, which indirectly triggers histone H4 'Lys-16' acetylation (H4K16ac), establishing a chromatin environment that promotes efficient activation of ATM kinase. Required in the testis, where it plays a role in the replacement of histones during spermatogenesis. At uncapped telomeres, promotes the joining of deprotected chromosome ends by inducing H2A ubiquitination and TP53BP1 recruitment, suggesting that it may enhance cancer development by aggravating telomere-induced genome instability in case of telomeric crisis. Promotes the assembly of RAD51 at DNA DSBs in the absence of BRCA1 and TP53BP1 Also involved in class switch recombination in immune system, via its role in regulation of DSBs repair. May be required for proper exit from mitosis after spindle checkpoint activation and

may regulate cytokinesis. May play a role in the regulation of RXRA-mediated transcriptional activity. Not involved in RXRA ubiquitination by UBE2E2 (PubMed:11322894, PubMed:14981089, PubMed:17724460, PubMed:18001824, PubMed:18001825, PubMed:18006705, PubMed:18077395, PubMed:18337245, PubMed:18948756, PubMed:19015238, PubMed:19124460, PubMed:19202061, PubMed:19203578, PubMed:19203579, PubMed:20550933, PubMed:21558560, PubMed:21857671, PubMed:21911360, PubMed:22266820, PubMed:22373579, PubMed:22531782, PubMed:22705371, PubMed:22865450, PubMed:22980979).

Cellular Location
Nucleus {ECO:0000255|HAMAP-Rule:MF_03067, ECO:0000269|PubMed:11322894, ECO:0000269|PubMed:14981089, ECO:0000269|PubMed:16215985, ECO:0000269|PubMed:23233665}. Cytoplasm {ECO:0000255|HAMAP-Rule:MF_03067}. Midbody {ECO:0000255|HAMAP- Rule:MF_03067}. Chromosome, telomere {ECO:0000255|HAMAP-Rule:MF_03067} Note=Recruited at uncapped telomeres (By similarity). Following DNA damage, such as double-strand breaks, recruited to the sites of damage (PubMed:18001824, PubMed:18077395, PubMed:22266820, PubMed:23233665) During prophase, concomitant with nuclear envelope breakdown, localizes throughout the cell, with a dotted pattern. In telophase, again in the nucleus and also with a discrete dotted pattern in the cytoplasm. In late telophase and during cytokinesis, localizes in the midbody of the tubulin bridge joining the daughter cells. Does not seem to be associated with condensed chromosomes at any time during the cell cycle. During spermatogenesis, sequestered in the cytoplasm by PIWIL1: RNF8 is released following ubiquitination and degradation of PIWIL1 {ECO:0000255|HAMAP-Rule:MF_03067, ECO:0000269|PubMed:18001824, ECO:0000269|PubMed:18077395, ECO:0000269|PubMed:22266820, ECO:0000269|PubMed:23233665}

Tissue Location
Ubiquitous. In fetal tissues, highest expression in brain, thymus and liver. In adult tissues, highest levels in brain and testis, lowest levels in peripheral blood cells

RNF8 antibody - C-terminal region - Protocols

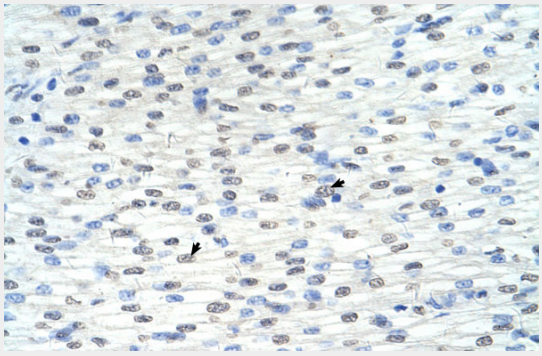
Provided below are standard protocols that you may find useful for product applications.

- Western Blot
- Blocking Peptides

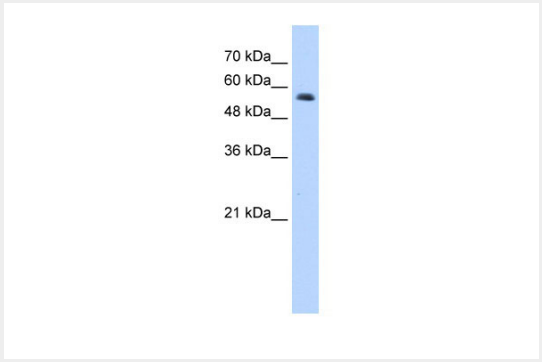
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- Dot Blot
- Immunohistochemistry
- Immunofluorescence
- Immunoprecipitation
- Flow Cytomety
- Cell Culture

RNF8 antibody - C-terminal region - Images



Human Heart



RNF8 antibody - C-terminal region - References

Lehner,B. (2004) Genome Res. 14 (7), 1315-1323 Reconstitution and Storage:For short term use, store at 2-8C up to 1 week. For long term storage, store at -20C in small aliquots to prevent freeze-thaw cycles.