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RNF8 Rabbit pAb

Catalog # AP98500

Product Information

Application	IHC-P, IHC-F, IF
Primary Accession	O76064
Other Accession	O76064
Reactivity	Mouse
Predicted	Rat, Pig, Human, Dog, Horse
Host	Rabbit
Clonality	Polyclonal
Calculated MW	55518
Physical State	Liquid
Immunogen	KLH conjugated synthetic peptide derived from human RNF8
Epitope Specificity	331-430/485
Isotype	IgG
Purity	affinity purified by Protein A
Buffer	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.
SIMILARITY	Belongs to the RNF8 family. Contains 1 FHA domain. Contains 1 RING-type zinc finger.
SUBUNIT	Homodimer. Forms a E2-E3 ubiquitin ligase complex composed of the RNF8 homodimer and a E2 heterodimer of UBE2N and UBE2V2. Interacts with class III E2s, including UBE2E1, UBE2E2, and UBE2E3 and with UBE2N. Interacts with RXRA. Interacts (via FHA domain) with ATM-phosphorylated MDC1. Interacts (via FHA domain) with 'Thr-4827' phosphorylated HERC2 (via C-terminus). Interacts (via FHA domain) with phosphorylated human herpesvirus 1 ICP0 protein; leading to RNF8 degradation by the proteasome.
Post-translational modifications	Autoubiquitinated through 'Lys-48' and 'Lys-63' of ubiquitin. 'Lys-63' polyubiquitination is mediated by UBE2N. 'Lys-29'-type polyubiquitination is also observed, but it doesn't require its own functional RING-type zinc finger.
Important Note	This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.
Background Descriptions	The RING finger motif is a specialized DNA-binding zinc finger domain found in many transcriptional regulatory proteins. The ring finger protein (RNF) family includes any protein containing the signature RING finger motif. RNF8 is a ubiquitously expressed nuclear RING finger protein that acts as an E3 ubiquitin-protein ligase. It is required for the ubiquitination of some nuclear proteins and promotes their subsequent degradation. The heterodimeric ubiquitin-conjugating enzyme UBC13 interacts with RNF8, and they co-localize in the nucleus. RNF8 may regulate mediation of UBC13 polyubiquitylation by elongating the ubiquitin chains. RNF8 also binds to Retinoid X receptor alpha (RXR?, a member of the steroid hormone receptor superfamily. It increases RXR?mediated transactivation of the RXR?responsive element (RXRE) promoter in a dose-dependent manner, suggesting that RNF8 is a regulator of RXR?mediated transcriptional activity.

Additional Information

Gene ID	9025
Other Names	hRNF8; RNF8_HUMAN; RNF8; RING finger protein 8; RING-type E3 ubiquitin transferase RNF8; 2.3.2.27; KIAA0646
Dilution	IHC-P=1:100-500,IHC-F=1:100-500,IF=1:100-500
Storage	Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.

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) (PubMed:18001824, PubMed:18006705). Also controls the recruitment of UIMC1-BRCC3 (RAP80-BRCC36) and PAXIP1/PTIP to DNA damage sites (PubMed:18077395, PubMed:19202061). Promotes the recruitment of NBN to DNA damage sites by catalyzing 'Lys-6'-linked ubiquitination of NBN (PubMed:23115235). 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:18001825, PubMed:18337245, PubMed:18948756, PubMed:19015238, PubMed:19124460, PubMed:19203578, PubMed:19203579,

PubMed:20550933, PubMed:21558560, PubMed:21857671, PubMed:21911360, PubMed:22266820, PubMed:22373579, PubMed:22531782, PubMed:22705371, 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 (PubMed:22865450). 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:18001825, PubMed:18337245, PubMed:18948756, PubMed:19015238, PubMed:19124460, PubMed:19203578, PubMed:19203579, PubMed:20550933, PubMed:21558560, PubMed:21857671, PubMed:21911360, PubMed:22266820, PubMed:22373579, PubMed:22531782, PubMed:22705371, 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

Please note: All products are 'FOR RESEARCH USE ONLY. NOT FOR USE IN DIAGNOSTIC OR THERAPEUTIC PROCEDURES'.