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UHRF1 Polyclonal Antibody

Catalog # AP73249

Product Information

Application	WB, E
Primary Accession	Q96T88
Reactivity	Human, Rat, Mouse
Host	Rabbit
Clonality	Polyclonal
Calculated MW	89814

Additional Information

Gene ID	29128
Other Names	UHRF1; ICBP90; NP95; RNF106; E3 ubiquitin-protein ligase UHRF1; Inverted CCAAT box-binding protein of 90 kDa; Nuclear protein 95; Nuclear zinc finger protein Np95; HuNp95; hNp95; RING finger protein 106;Transcription factor ICBP90; Ubiquitin-like PHD and RING finger domain-containing protein 1; hUHRF1; Ubiquitin-like-containing PHD and RING finger domains protein 1
Dilution	WB~~Western Blot: 1/500 - 1/2000. ELISA: 1/40000. Not yet tested in other applications. E~~N/A
Format	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.09% (W/V) sodium azide.
Storage Conditions	-20℃

Protein Information

Name	UHRF1 {ECO:0000303|PubMed:17673620, ECO:0000312|HGNC:HGNC:12556}
Function	E3 ubiquitin-protein ligase that acts as a key epigenetic regulator by bridging DNA methylation and chromatin modification (PubMed:10646863, PubMed:15009091, PubMed:19056828, PubMed:23022729, PubMed:24013172, PubMed:27595565, PubMed:30104358, PubMed:30392929, PubMed:30392931, PubMed:39607687). Plays a key role in DNA methylation inheritance by promoting recruitment of DNMT1 to hemimethylated DNA and ensure faithful propagation of the DNA methylation patterns through DNA replication (PubMed:23022729, PubMed:24013172, PubMed:27595565, PubMed:30104358, PubMed:30392929, PubMed:30392931, PubMed:39607687). Acts both as a histone reader and writer: specifically recognizes and binds (1) hemimethylated DNA at replication forks and (2) histone H3 trimethylated at 'Lys-9' and unmethylated at 'Arg-2' (H3K9me3 and H3R2me0, respectively), thereby activating its E3

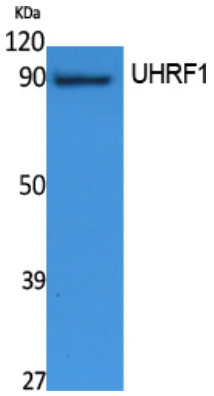
	ubiquitin-protein ligase activity (PubMed:15361834, PubMed:17673620, PubMed:17967883, PubMed:18772889, PubMed:21745816, PubMed:21777816, PubMed:22100450, PubMed:22837395, PubMed:23022729, PubMed:27595565, PubMed:30104358). UHRF1 then mediates histone H3 'Lys-18' monoubiquitination (H3K18ub), a docking site for DNMT1, leading to DNMT1 recruitment and replication- coupled DNA methylation maintenance (PubMed:27595565). Also mediates histone H3 'Lys-14' and 'Lys-23' ubiquitination (H3K14ub and H3K23ub) at lower level (PubMed:24013172, PubMed:27595565). Histone ubiquitin ligase activity also stimulates the methyltransferase activity of SUV39H1 and/or SUV39H2, promoting accumulation of H3K9me3 histone mark to reinformce heterochromatin state (PubMed:39631394). Enriched in pericentric heterochromatin where it recruits different chromatin modifiers required for this chromatin replication. Also localizes to euchromatic regions where it negatively regulates transcription possibly by impacting DNA methylation and histone modifications (PubMed:21777816). Plays a role in DNA repair by cooperating with UHRF2 to ensure recruitment of FANCD2 to interstrand cross-links (ICLs) leading to FANCD2 activation (PubMed:30335751). Also ubiquitinates non- histone proteins, such as histone H3, KIF11 and PML (PubMed:22945642, PubMed:37728657). Acts as a critical player of proper spindle architecture by catalyzing the 'Lys-63'-linked ubiquitination of KIF11, thereby controlling KIF11 localization on the spindle (PubMed:37728657).
Cellular Location	Nucleus {ECO:0000255|PROSITE-ProRule:PRU00358, ECO:0000269|PubMed:10646863, ECO:0000269|PubMed:17673620, ECO:0000269|PubMed:17967883, ECO:0000269|PubMed:19056828, ECO:0000269|PubMed:21777816, ECO:0000269|PubMed:30335751}. Chromosome Note=Associated with replicating DNA from early to late S phase, including at replicating pericentric heterochromatin (PubMed:17673620) Also localizes to euchromatic regions (PubMed:21777816). In non-S-phase cells, homogeneously distributed through the nucleus (By similarity) {ECO:0000250|UniProtKB:Q8VDF2, ECO:0000269|PubMed:17673620, ECO:0000269|PubMed:21777816}
Tissue Location	Expressed in thymus, bone marrow, testis, lung and heart. Overexpressed in breast cancer.

Background

Multidomain protein that acts as a key epigenetic regulator by bridging DNA methylation and chromatin modification. Specifically recognizes and binds hemimethylated DNA at replication forks via its YDG domain and recruits DNMT1 methyltransferase to ensure faithful propagation of the DNA methylation patterns through DNA replication. In addition to its role in maintenance of DNA methylation, also plays a key role in chromatin modification: through its tudor-like regions and PHD- type zinc fingers, specifically recognizes and binds histone H3 trimethylated at 'Lys-9' (H3K9me3) and unmethylated at 'Arg-2' (H3R2me0), respectively, and recruits chromatin proteins. Enriched in pericentric heterochromatin where it recruits different chromatin modifiers required for this chromatin replication. Also localizes to euchromatic regions where it negatively regulates transcription possibly by impacting DNA methylation and histone modifications. Has E3 ubiquitin-protein ligase activity by mediating the ubiquitination of target proteins such as histone H3 and PML. It is still unclear how E3 ubiquitin-protein ligase activity is related to its role in chromatin in vivo. May be involved in DNA repair.

Images

Western Blot analysis of extracts from Jurkat cells, using UHRF1 Polyclonal Antibody.. Secondary antibody was diluted at 1:20000 cells nucleus extracted by Minute TM



Cytoplasmic and Nuclear Fractionation kit (SC-003,Inventbiotech,MN,USA).

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