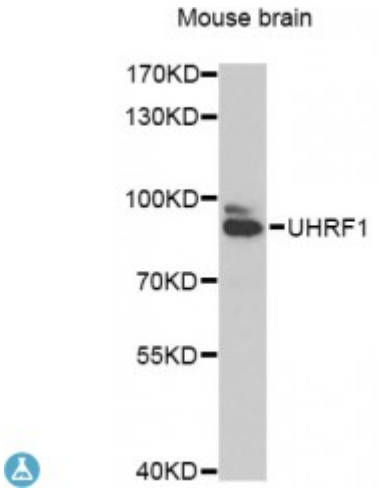
Anti-UHRF1 Antibody



Description	This gene encodes a member of a subfamily of RING-finger type E3 ubiquitin ligases. The protein binds to specific DNA sequences, and recruits a histone deacetylase to regulate gene expression. Its expression peaks at late G1 phase and continues during G2 and M phases of the cell cycle. It plays a major role in the G1/S transition by regulating topoisomerase IIalpha and retinoblastoma gene expression, and functions in the p53-dependent DNA damage checkpoint. It is regarded as a hub protein for the integration of epigenetic information. This gene is up-regulated in various cancers, and it is therefore considered to be a therapeutic target. Multiple transcript variants encoding different isoforms have been found for this gene. A related pseudogene exists on chromosome 12.

Model	STJ114463
Host	Rabbit
Reactivity	Mouse
Applications	WB
Immunogen	Recombinant fusion protein containing a sequence corresponding to amino acids 139-298 of human UHRF1 (NP_037414.3).
Gene ID	29128
Gene Symbol	UHRF1
Dilution range	WB 1:500 - 1:2000
Tissue Specificity	Expressed in thymus, bone marrow, testis, lung and heart, Overexpressed in breast cancer

Purification	Affinity purification
Note	For Research Use Only (RUO).
Protein Name	E3 ubiquitin-protein ligase UHRF1
Molecular Weight	89.814 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:12556OMIM:607990Reactome:R-HSA-5334118
Alternative Names	E3 ubiquitin-protein ligase UHRF1
Function	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,
Cellular Localization	Nucleus,
Post-translational Modifications	Phosphorylation at Ser-298 of the linker region decreases the binding to H3K9me3, Phosphorylation at Ser-639 by CDK1 during M phase impairs interaction with USP7, preventing deubiquitination and leading to degradation by the proteasome,