

Rabbit anti-Human, Mouse ATRX Polyclonal Antibody | anti-ATRX antibody

ATRX Antibody

CATALOG #	HOST	REACTIVITY	APPLICATIONS
AAA321015	Rabbit	Human, Mouse	ELISA, Immunocytochemistry, Immunofluorescence, Western Blot

PRODUCT SYNONYMS

ATRX; Polyclonal Antibody; ATRX Antibody; Alpha thalassemia/mental retardation syndrome X linked homolog; ATP dependent helicase ATRX; ATP-dependent helicase ATRX; ATR2; Atrx; ATRX_HUMAN; DNA dependent ATPase and helicase; Helicase 2; X linked; MGC2094; MRXHF1; RAD54; RAD54L; SFM1; SHS; Transcriptional regulator ATRX; X linked helicase II; X linked nuclear protein; X-linked helicase II; X-linked nuclear protein; XH2; XNP; Znf HX; Znf-HX; anti-ATRX antibody

PRODUCT SPECIFICATIONS

Host	Rabbit
Reactivity	Human, Mouse
Clonality	Polyclonal
Isotype	IgG
Specificity	ATRX antibody detects endogenous levels of ATRX
Purity/Purification	The antiserum was purified by peptide affinity chromatography using SulfoLink Coupling Resin.
Form/Format	Liquid Phosphate buffered saline, pH 7.4, 150mM NaCl, 0.02% sodium azide and 50% glycerol.
Concentration	1mg/ml (varies by lot)
Sequence Length	2492
Applicable Applications for anti-ATRX antibody	ELISA, ICC (Immunocytochemistry), IF (Immunofluorescence), WB (Western Blot)
Immunogen	A synthesized peptide derived from human ATRX
Subcellular Location	Nucleus. Chromosome, Telomere. Nucleus, PML Body. Associated with pericentromeric heterochromatin during interphase and mitosis, probably by interacting with CBX5/HP1 alpha. Colocalizes with histone H3.3, DAXX, HIRA and ASF1A at PML-nuclear bodies. Colocalizes with cohesin (SMC1 and SMC3) and MECP2 at the maternal H19 ICR (By similarity).
Tissue Specificity	Ubiquitous.
Predicted Cross Reactivity	Bovine, Rabbit, Dog
Similarity	Bovine (100%), Rabbit (100%), Dog (100%)
Conjugation	Unconjugated
Preparation and Storage	Store at -20 degree C. Stable for 12 months from date of receipt.



WB (Western Blot)
Western blot analysis of extracts from 293, using ATRX Antibody.



IF (Immunofluorescence)
AAA321015 staining HeLa cells by IF/ICC. The sample were fixed with PFA and permeabilized in 0.1% Triton X-100, then blocked in 10% serum for 45 minutes at 25 degree C. The primary antibody was diluted at 1/200 and incubated with the sample for 1 hour at 37 degree C. An Alexa Fluor 594 conjugated goat anti-rabbit IgG (H+L) antibody, diluted at 1/600, was used as secondary antibody.

ADDITIONAL INFORMATION

Related Product Information for anti-ATRX antibody

Description: The protein encoded by this gene contains an ATPase/helicase domain, and thus it belongs to the SWI/SNF family of chromatin remodeling proteins. The mutations of this gene are associated with an X-linked mental retardation (XLMR) syndrome most often accompanied by alpha-thalassemia (ATRX) syndrome. Theses mutations have been shown to cause diverse changes in the pattern of DNA methylation, which may provide a link between chromatin remodeling, DNA methylation, and gene expression in developmental processes. This protein is found to undergo cell cycle-dependent phosphorylation, which regulates its nuclear matrix and chromatin association, and suggests its involvement in the gene regulation at interphase and chromosomal segregation in mitosis. Three alternatively spliced transcript variants encoding distinct isoforms have been reported.

Function: Involved in transcriptional regulation and chromatin remodeling. Facilitates DNA replication in multiple cellular environments and is required for efficient replication of a subset of genomic loci. Binds to DNA tandem repeat sequences in both telomeres and euchromatin and in vitro binds DNA quadruplex structures. May help stabilizing G-rich regions into regular chromatin structures by remodeling G4 DNA and incorporating H3.3-containing nucleosomes. Catalytic component of the chromatin remodeling complex ATRX:DAXX which has ATP-dependent DNA translocase activity and catalyzes the replication-independent deposition of histone H3.3 in pericentric DNA repeats outside S-phase and telomeres, and the in vitro remodeling of H3.3-containing nucleosomes. Its heterochromatin targeting is proposed to involve a combinatorial readout of histone H3 modifications (specifically methylation states of H3K9 and H3K4) and association with CBX5. Involved in maintaining telomere structural integrity in embryonic stem cells which probably implies recruitment of CBX5 to telomers. Reports on the involvement in transcriptional regulation of telomeric repeat-containing RNA (TERRA) are conflicting; according to a report, it is not sufficient to decrease chromatin condensation at telomers nor to increase expression of telomeric RNA in fibroblasts (PubMed:24500201). May be involved in telomere maintenance via recombination in ALT (alternative lengthening of telomeres) cell lines. Acts as negative regulator of chromatin incorporation of transcriptionally repressive histone H2AFY, particularly at telomeres and the alpha-globin cluster in erythroleukemic cells. Participates in the allele-specific gene expression at the imprinted IGF2/H19 gene locus. On the maternal allele, required for the chromatin occupancy of SMC1 and CTCF within the H19 imprinting control region (ICR) and involved in establishment of histone tails modifications in the ICR. May be involved in brain development and facial morphogenesis. Binds to zinc-finger coding genes with atypical chromatin signatures and regulates its H3K9me3 levels. Forms a complex with ZNF274, TRIM28 and SETDB1 to facilitate the deposition and maintenance of H3K9me3 at the 3' exons of zinc-finger genes (PubMed:27029610).

Subunit Structure: Interacts with DAXX to form the chromatin remodeling complex ATRX:DAXX. Probably binds EZH2. Binds annexin V in a calcium and phosphatidylcholine/phosphatidylserine-dependent manner. Interacts directly with CBX5 via the PxVxL motif. Interacts with RAD50, MRE11 and NBN; indicative for an association with the MRN complex. Interacts with histone H2AFY. Interacts with histone H3 peptides methylated at 'Lys-10' with preferences H3K9me3 > H3K9me2 > H3K9me1. Interacts with histone H3 peptides unmethylated at 'Lys-5' (H3K4me0). Interacts with MECP2, SMC1 and SMC3. Interacts with SETDB1, TRIM28 and ZNF274 (PubMed:27029610).

Post-translational Modifications: Phosphorylated at serine residues during mitose. Phosphorylation may promote the release from the nuclear matrix and progression to mitosis.

Similarity: The ADD domain predominantly interacts with histone H3 trimethylated at 'Lys-10'(H3K9me3) (and to a lesser extent H3 mono-or dimethylated at 'Lys-10') and simultaneously to histone H3 unmethylated at 'Lys-5' (H3K4me0). The interaction with H3K9me3 is disrupted by the presence of H3K4me3 suggesting a readout of the combined histone H3 methylation state. Contains one Pro-Xaa-Val-Xaa-Leu (PxVxL) motif, which is required for interaction with chromoshadow domains. This motif requires additional residues -7, -6, +4 and +5 of the central Val which contact the chromoshadow domain. Belongs to the SNF2/RAD54 helicase family.

NCBI AND UNIPROT INFORMATION

NCBI GI #	530788276
NCBI GeneID	546
NCBI Accession #	NP_000480.3
NCBI GenBank Nucleotide #	NM_000489.5
UniProt Accession #	P46100; P51068; Q15886; Q59FB5; Q59H31; Q5H9A2; Q5JWI4; Q7Z2J1; Q9H0Z1; Q9NTS3; D3DTE2
Molecular Weight	Observed: 282 kDa Predicted: 283 kDa
NCBI Official Full Name	transcriptional regulator ATRX isoform 1
NCBI Official Synonym Full Names	ATRX, chromatin remodeler
NCBI Official Symbol	ATRX
NCBI Official Synonym Symbols	JMS; XH2; XNP; MRX52; RAD54; RAD54L; ZNF-HX
NCBI Protein Information	transcriptional regulator ATRX
UniProt Protein Name	Transcriptional regulator ATRX
UniProt Gene Name	ATRX
UniProt Synonym Gene Names	RAD54L; XH2; XNP

For Research Use Only. Not for use in diagnostic or therapeutic procedures. Small volumes of product may become entrapped in the seal of the vial during shipment and storage; if necessary, briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the cap.

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