

Product datasheet for MR226423

Atrx (NM_009530) Mouse Tagged ORF Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Atrx (NM_009530) Mouse Tagged ORF Clone
Tag:	Myc-DDK
Symbol:	Atrx
Synonyms:	4833408C14Rik; AI447451; ATR2; DXHXS6677E; HP1-BP38; Hp1bp2; Hp1bp38; MRXS3; Rad54; RAD54L; XH2; Xnp
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin
ORF Nucleotide Sequence:	>MR226423 representing NM_009530 Red=Cloning site Blue=ORF Green=Tags(s)

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Protein Sequence: >MR226423 representing NM_009530
 Red=Cloning site Green=Tags(s)

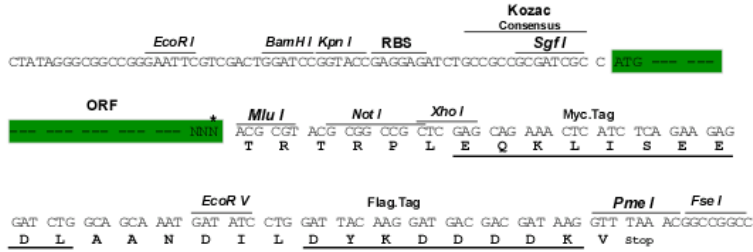
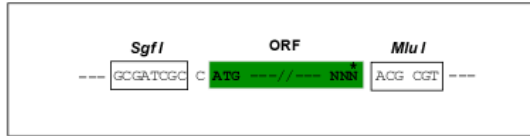
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Restriction Sites: SgfI-MluI

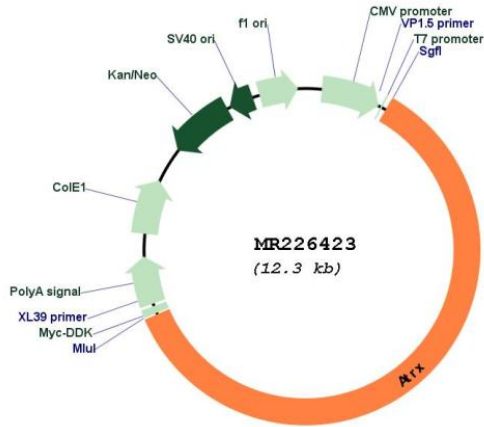
Cloning Scheme:

Cloning sites used for ORF Shutting:



* The last codon before the Stop codon of the ORF

Plasmid Map:



ACCN: NM_009530

ORF Size: 7428 bp

OTI Disclaimer:	The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing variants is recommended prior to use. More info
OTI Annotation:	This clone was engineered to express the complete ORF with an expression tag. Expression varies depending on the nature of the gene.
Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
Reconstitution Method:	<ol style="list-style-type: none"> 1. Centrifuge at 5,000xg for 5min. 2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. 3. Close the tube and incubate for 10 minutes at room temperature. 4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
RefSeq:	NM_009530.2 , NP_033556.2
RefSeq Size:	10244 bp
RefSeq ORF:	7431 bp
Locus ID:	22589
UniProt ID:	Q61687
Cytogenetics:	X 47.26 cM
MW:	279 kDa

Gene Summary:

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 probably implying recruitment of CBX5 to telomeres. Reports on the involvement in transcriptional regulation of telomeric repeat-containing RNA (TERRA) are conflicting; according (PubMed:20211137) is required for its transcriptional repression in embryonic stem cells. Acts as negative regulator of chromatin incorporation of transcriptionally repressive histone H2AFY, particularly at telomeres. 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. 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 (By similarity).[UniProtKB/Swiss-Prot Function]