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Product datasheet for MC217132

Ate1 (NM_001029895) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Ate1 (NM_001029895) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Ate1
Synonyms:	AI225793; AW547406
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin

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Fully Sequenced ORF:

>MC217132 representing NM_001029895
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCCGCGATCGCC

ATGGCCTCGGTGGTGGAATACAAGGGCCTGAAGGCCGGCTACTACTGCGGCTACTGCGAGTCCAGGGAGG
GCAAGACGTCGTGTGGCATGTGGGCACATTCCATGACAGTGCAGGATTATCAGGATCTTATAGACCGAGG
ATGGAGAAGAAGTGGGAAATATGTGTACAAACCTGTCATGGATCAAACATGCTGTCCTCAGTATACAATA
AGGTGTCATCCTTTACAGTTTCAGCCATCAAAATCTCACAAGAAAGTTTTGAAAAAAATGCTGAAATTTC
TGGCTAAAGGAGAGATCTCGAAAGGCAATTGTGAGGATGAGCCCATGGATTCTACAGTGGAGGATGCTGT
TGACGGTGACTTTGCATTAATTAACAAGCTGGATATAAAGTGTGATCTCAAAACACTCAGTGACCTCAAA
GGAAGCATAGAGAGTGAAGAGAAGGAGAAAGAAAAGAGTATAAAGAAAGAAGGGTCTAAAGAATTCATTC
ATCCACAATCTATAGAGGAGAAGTTGGGCTCTGGTGAACCATCACATCCAATCAAAGTTCATATTGGTCC
TAAGCCAGGCAAAGGGGCTGACTTGAGTAAGCCTCCATGTCGGAAAGCAAGGGAAATGAGGAAAGAAAGG
CAAAGATTAAAACGGATGCAGCAGGCCTCAGCTGCAGCCTCGGAGGCTCAAGGTCAGCCAGTCTGTTTGT
TACCAAAGGCTAAATCCAACCAGCCCAAGTCACTGGAAGATTTGATTTTTCAATCTTTACCAGAAAATGC
ATCGCACAAGTTAGAGGTGAGGGTGGTAAGATCTTCTCCACCAAGTCCTCAGTTCAGAGCCACATTTCAG
GAGTCTTACCAGGTCTATAAACGCTACCAGATGGTTGTTCACAAGGACCCGCCTGATAAGCCAACCGTGA
GCCAGTTTACAAGATTCCTTTGCAGCTCACCATTGGAGGCAGAGCACCCTGCTGATGGACCAGAATGTGG
TTATGGCTCCTTTCACCAGCAGTACTGGCTCGATGGGAAGATCATTGCTGTGGGGGTGTTAGACATTCTC
CCGTACTGTGTGTCTTCTGTGTATCTCTACTACGATCCTGATTATTCATTTCTGTCTTTGGGTGTCTATT
CAGCATTAAGAGAAATTGCTTTTACTAGACAACTGCATGAGAAAACATCGCAACTCAGCTATTATTATAT
GGGTTTCTACATTCATTCCTGTCCCAAGATGAGATACAAGGGTCAATATAGACCTTCTGATTTGCTGTGT
CCTGAGACGTATGTCTGGGTGCCCATTGAGCAGTGCCTGCCTTCTCTGGACAACTCCAAGTACTGCCGTT
TCAACCAGGACCCCGAAGCAGAGGATGAAGGACGCAGTAAGGAACTTGACCGACTAAGGGTGTTTCACAG
ACGATCTGCCATGCCTTACGGTGTTTATAAGAATCACCAAGAAGACCCAAGTGAGGAGGCTGGTGTGCTG
GAGTATGCAAACCTCGTAGGACAGAAGTGCTCGGAGAGGATGCTGCTGTTCAGACACTGA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI

ACCN: NM_001029895

Insert Size: 1530 bp

OTI Disclaimer: Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).

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:	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_001029895.3, NP_001025066.1
RefSeq Size:	5020 bp
RefSeq ORF:	1530 bp
Locus ID:	11907
Cytogenetics:	7 F3
Gene Summary:	Involved in the post-translational conjugation of arginine to the N-terminal aspartate or glutamate of a protein. This arginylation is required for degradation of the protein via the ubiquitin pathway. Does not arginylate cysteine residues.[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (3) uses an alternate 5' structure, compared to variant 1. This difference causes translation initiation at an upstream AUG and results in an isoform (3) that has a distinct N-terminus and is shorter, compared to isoform 1. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.