

Product datasheet for **SC336537**

ATE1 (NM_001288736) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	ATE1 (NM_001288736) Human Untagged Clone
Tag:	Tag Free
Symbol:	ATE1
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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Fully Sequenced ORF: >SC336537 representing NM_001288736.
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

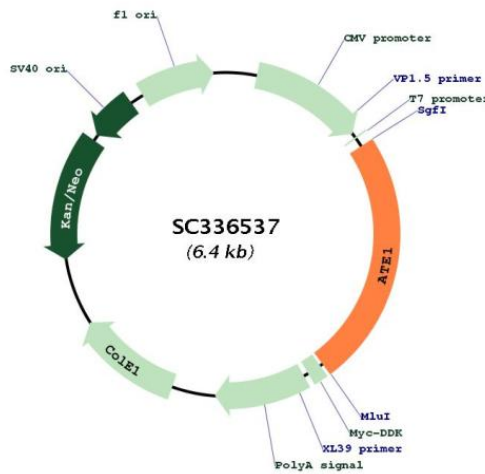
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Restriction Sites:

SgfI-MluI

Plasmid Map:



ACCN:

NM_001288736

Insert Size:	1536 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:	<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_001288736.1
RefSeq Size:	5165 bp
RefSeq ORF:	1536 bp
Locus ID:	11101
UniProt ID:	O95260
Cytogenetics:	10q26.13
MW:	58.1 kDa
Gene Summary:	<p>This gene encodes an arginyltransferase, an enzyme that is involved in posttranslational conjugation of arginine to N-terminal aspartate or glutamate residues. Conjugation of arginine to the N-terminal aspartate or glutamate targets proteins for ubiquitin-dependent degradation. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Dec 2013]</p> <p>Transcript Variant: This variant (5) differs in the 5' UTR and coding region, and uses an alternate in-frame exon in the central coding region, compared to variant 1. The encoded isoform (5) has a shorter and distinct N-terminus and a unique internal segment, compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.</p>