

Product datasheet for MC227749

Atf2 (NM_001284369) Mouse Untagged Clone

Tag Free

Neomycin

Atf2

Expression Plasmids

pCMV6-Entry (PS100001)

Kanamycin (25 ug/mL)

Atf2 (NM_001284369) Mouse Untagged Clone

Atf-2; CRE-BP; Creb2; D18875; D130078H02Rik; mXBP; Tg(Gzma-Klra1)7Wum

Product data:

Product Type:

Product Name:

Tag:

Symbol:

Synonyms: Vector:

E. coli Selection:

Cell Selection:

OriGene Technologies, Inc.

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Fully Sequenced ORF:	>MC227749 representing NM_001284369 Red=Cloning site Blue=ORF Orange=Stop codon
	TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC GCC <mark>GCGATCGC</mark> C
	ATGCACTGCCCCTGGGTGTGGGCCAGATCAGACTCCAACGCCAACAAGATTCCTAAAAAACTGTGAAGAAG TGGGTTTGTTCAATGAGTTGGCAAGTCCATTTGAAAATGAATTCAAGAAGGCTTCCGAAGATGACATTAA AAAATGCCTCTAGATTTGTCCCCTCTTGCAACACCCATCATAAGAAGGAAATTGAGGAGCCTTCTGTT GTAGAAACAACTCACCAGGACAGCCCTTTACCTCACCCCGAGTCGACTACCAGTGATGAAAAGGAAGTAC CATTGGCACAAACTGCACAGCCACATCAGCTATCGTTCGT
Restriction Sites:	Sgfl-Mlul
ACCN:	NM_001284369
Insert Size:	1344 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).
OTI Annotation:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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).

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CRIGENE Atf2 (NM_001284369) Mouse Untagged Clone – MC227749

Reconstitution Method:	 Centrifuge at 5,000xg for 5min. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. Close the tube and incubate for 10 minutes at room temperature. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 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:	<u>NM 001284369.1, NP 001271298.1</u>
RefSeq Size:	4140 bp
RefSeq ORF:	1344 bp
Locus ID:	11909
Cytogenetics:	2 C3
Gene Summary:	Transcriptional activator which regulates the transcription of various genes, including those involved in anti-apoptosis, cell growth, and DNA damage response. Dependent on its binding partner, binds to CRE (cAMP response element) consensus sequences (5'-TGACGTCA-3') or to AP-1 (activator protein 1) consensus sequences (5'-TGACTCA-3'). In the nucleus, contributes to global transcription and the DNA damage response, in addition to specific transcriptional activities that are related to cell development, proliferation and death. In the cytoplasm, interacts with and perturbs HK1- and VDAC1-containing complexes at the mitochondrial outer membrane, thereby impairing mitochondrial membrane potential, inducing mitochondrial leakage and promoting cell death. The phosphorylated form (mediated by ATM) plays a role in the DNA damage response and is involved in the ionizing radiation (IR)-induced S phase

checkpoint control and in the recruitment of the MRN complex into the IR-induced foci (IRIF). Exhibits histone acetyltransferase (HAT) activity which specifically acetylates histones H2B and

attenuating its ability to acetylate and activate ATM. Can elicit oncogenic or tumor suppressor activities depending on the tissue or cell type (By similarity).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (3) differs in the 5' UTR, lacks an alternate in-frame exon in the 5' coding region and uses a downstream start codon compared to variant 1. The resulting protein (isoform 2) is shorter compared to isoform 1. Variants 2 and 3 encode the same protein. 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.

H4 in vitro. In concert with CUL3 and RBX1, promotes the degradation of KAT5 thereby

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