

Product datasheet for **SC306093**

A1CF (NM_138933) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	A1CF (NM_138933) Human Untagged Clone
Tag:	Tag Free
Symbol:	A1CF
Synonyms:	ACF; ACF64; ACF65; APOBEC1CF; ASP
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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Fully Sequenced ORF: >SC306093 representing NM_138933.
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGGCCGGGAATTCGTGCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCCGCATCGCC
ATGGAAGCAGTGTGTCTGGGCACATGCCAGAGCCAGAAGCGAGCATGAGCACAGCAATTCCTGGCCTC
AAAAAAGGAAATATGCTTTGCAGTCCATCATTGCAAACCTTGTGAAAAGGAAATGGACAAAGA
AAATATGGTGGCCCTCCACCTGGTTGGGATGCTGCACCCCTGAAAGGGGCTGTGAAATTTTATTGGA
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GAAGCCAAGAATGCAATCAAGCAACTTAATAATTAGAAATTAGAAATGGGCGCCTCTTAGGGTTTGT
GCCAGTGTGGACAACCGCATTATTTGTTGGGGCATCCAAAAACAAAAAGAGAGAAGAAATCTTA
TCGGAGATGAAAAAGTTACTGAAGGTGTGTCGATGTCATCGTCTACCAAGCGCTGCAGATAAAACC
AAAAACCGAGGCTTTCCTTTCGTTGGAGTATGAGAGTATCGAGCAGCTGCCATGGCGAGGAGAACTG
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ATGATTGAAAAGGAATCAACAATATCAAAACAGGTGCTGTGGAGAGGGTGAAGAAAATTCGAGACTAT
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GGCACAGGTGGAAGGGGACCATGCTGCAAGGAGAGTATACCTACTCTTTGGGCCAAGTTTATGATCCC
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GCACCCGTGTCTGCAGCCAGCTCAAGCAAGCGGTAACCCCTGGACAAGACTTAGCAGCATATAACAAC
TATGAGGTCTACCAACTTTTGCAGTACTGCCGAGGGGATGGATATGGCACCTCTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
  
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Restriction Sites: SgfI-MluI

Plasmid Map: □

ACCN: NM_138933

Insert Size: 1785 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: This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

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_138933.2](#)

RefSeq Size: 9364 bp

RefSeq ORF: 1785 bp

Locus ID: 29974

UniProt ID: [Q9NQ94](#)

Cytogenetics: 10q11.23

MW: 65 kDa

Gene Summary: Mammalian apolipoprotein B mRNA undergoes site-specific C to U deamination, which is mediated by a multi-component enzyme complex containing a minimal core composed of APOBEC-1 and a complementation factor encoded by this gene. The gene product has three non-identical RNA recognition motifs and belongs to the hnRNP R family of RNA-binding proteins. It has been proposed that this complementation factor functions as an RNA-binding subunit and docks APOBEC-1 to deaminate the upstream cytidine. Studies suggest that the protein may also be involved in other RNA editing or RNA processing events. Several transcript variants encoding a few different isoforms have been found for this gene. [provided by RefSeq, Nov 2010]

Transcript Variant: This variant (3) differs in the 5' UTR and lacks an alternate in-frame segment compared to variant 5. The resulting isoform (3) lacks a short internal segment compared to isoform 4. Variants 3 and 6 both encode the same isoform (3). 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.