

## **Product datasheet for SC322975**

## ABIN3 (TNIP3) (NM 001128843) Human Untagged Clone

**Product data:** 

**Product Type:** Expression Plasmids

Product Name: ABIN3 (TNIP3) (NM\_001128843) Human Untagged Clone

Tag: Tag Free Symbol: ABIN3

Synonyms: ABIN-3; LIND

Mammalian Cell Neomycin

Selection:

Vector:pCMV6-Entry (PS100001)E. coli Selection:Kanamycin (25 ug/mL)

Fully Sequenced ORF: >SC322975 representing NM\_001128843.

Blue=Insert sequence Red=Cloning site Green=Tag(s)

GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC

TGTGAAAGCATGGAGCTGGACAAAAAAATCCAGGATCTGATTGAGAGAAATGCGTCTCCTCATCCAAAA CGGTTCACCCCAGAGGCCATGCCAACTCACAGAAATCTATGTTCTCTGAAGACTCCAGGAAAAACAGCT TCCATGGCACATTTTGTACAGGGCACATCTAGAATGATTGCCGCAGAAAGTTCTACGGAGCATAAAGAG TGTGCTGAACCATCAACAAGAAAGAACTTGATGAATTCTCTTGAACAAAAGATAAGGTGTTTGGAAAAA CAAAGAAAAGAGCTCCTGGAAGTTAACCAGCAATGGGATCAGCAATTTAGAAGTATGAAAGAGTTATAT GAAAGAAAGGTAGCAGAGCTGAAGACGAAACTGGACGCCGCGGAAAGATTCCTCAGCACGCGGGAGAAG GACCGGCTGCAGCGGGAGAGAAGGAAAAGGAACGCCTAAATGAAGAATTACATGAATTGAAAGAAGAG AATAAACTTTTAAAGGGAAAAAATACTCTTGCGAACAAGGAAAAGGAACATTACGAATGTGAAATAAAA CGCCTCAATAAGGCTCTTCAGGATGCCTTGAATATCAAGTGTTCATTTTCCGAGGACTGTTTGAGGAAG TCTCGAGTGGAATTCTGCCATGAGGAGATGAGAACAGAAATGGAAGTTCTGAAGCAGCAGGTGCAAATA CAAATTAATGAAACTTCCCAATCCCAGTTGAACAGGCTGAATTCCCAGATAAAAGCTTGTCAGATGGAG AAAGAAAACTAGAAAAGCAATTAAAACAGATGTATTGCCCACCCTGTAACTGCGGCTTGGTTTTCCAC CTGCAAGATCCATGGGTACCAACAGGCCCTGGAGCTGTGCAGAAGCAACGGGAGCACCCAGTTTATCCT

**ACGCGTACGCGGCCGCTC**GAGCAGAAACTCATCTCAGAAGAGGGATCTGGCAGCAAATGATATCCTGGAT

TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

**Restriction Sites:** Sgfl-Mlul



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## ABIN3 (TNIP3) (NM\_001128843) Human Untagged Clone - SC322975

**ACCN:** NM 001128843

**Insert Size:** 1110 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:** <u>NM 001128843.2</u>

 RefSeq Size:
 2410 bp

 RefSeq ORF:
 1110 bp

 Locus ID:
 79931

 UniProt ID:
 Q96KP6

 Cytogenetics:
 4q27

**MW:** 44.1 kDa

**Gene Summary:** Binds to zinc finger protein TNFAIP3 and inhibits NF-kappa-B activation induced by tumor

necrosis factor, Toll-like receptor 4 (TLR4), interleukin-1 and 12-O-tetradecanoylphorbol-13-acetate. Overexpression inhibits NF-kappa-B-dependent gene expression in response to lipopolysaccharide at a level downstream of TRAF6 and upstream of IKBKB. NF-kappa-B

inhibition is independent of TNFAIP3 binding.[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) differs in the 5' UTR and initiates translation at an alternate start codon, and lacks an exon in the 3' coding region which results in a frameshift compared to variant 1. The encoded protein (isoform 2) has distinct N- and C-termini and is longer than 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.