

Product datasheet for SC305093

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OriGene Technologies, Inc.

C1orf135 (AUNIP) (NM_024037) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: C1orf135 (AUNIP) (NM_024037) Human Untagged Clone

Tag: Tag Free Symbol: AUNIP

Synonyms: AIBP; C1orf135

Mammalian Cell

Selection:

Neomycin

Vector: pCMV6-Entry (PS100001)

E. coli Selection: Kanamycin (25 ug/mL)

Fully Sequenced ORF: >SC305093 representing NM_024037.

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

GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC

ATGAGGCGGACAGGCCCCGAGGAGGAGGCCTGCGGCGTGTGGCTGGACGCGGCGCGCTGAAGAGGCGG ACCTTGCAGCCAGGAAAGACAAATGGCAGTGACCAGAAGAGTGTTTCATCTCATACAGAAAGTCAGATC AACAAAGAGTCCAAGAAAAATGCGACCCAGCTAGACCATTTGATCCCAGGCTTAGCACACGATTGCATG GCATCCCCTTTAGCCACTTCAACCACTGCAGACATCCAGGAAGCTGGACTCTCTCCTCAGTCCCTCCAG ACTTCTGGCCACCACAGAATGAAAACCCCATTTTCAACTGAGCTATCTTTGCTCCAGCCTGATACTCCA GACTGTGCTGGAGATAGTCATACCCCACTGGCTTTTTCCTTCACCGAGGACTTGGAAAGTTCTTGTTTG CTAGACCGAAAGGAAGAAAAAGGGGATTCTGCCAGGAAATGGGAATGGCTTCATGAGTCTAAGAAGAAC TATCAGAGTATGGAGAAACACCAAACTACCTGGGGACAAATGCTGTCAGCCCTTAGGCAAGACTAAA TTGGAAAGAAAGGTGTCTGCCAAAGAAAACAGGCAGGCCCCTGTCCTCCAAACATACAGGGAATCC TGGAATGGAGAAACATAGAATCAGTGAAACAAAGCCGTAGTCCAGTTTCTGTGTTTTTCCTGGGACAAT GAAAAGAATGACAAGGACTCCTGGAGTCAACTTTTCACTGAAGATTCTCAAGGCCAGCGGGTCATTGCC CACAACACTAGAGCTCCTTTTCAAGATGTAACCAATAACTGGAATTGGGACTTAGGGCCGTTTCCTAAC AGTCCTTGGGCTCAGTGCCAGGAGGATGGGCCAACTCAAAATCTGAAGCCTGATTTGCTCTTTACCCAG GACTCTGAAGGTAATCAAGTTATCAGACACCAATTCTAA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGGATCTGGCAGCAAATGATATCCTGGAT

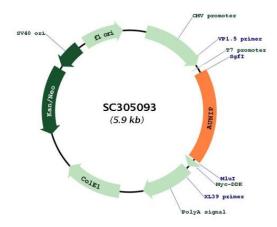
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

Restriction Sites: Sgfl-Mlul





Plasmid Map:



ACCN: NM_024037 **Insert Size:** 1074 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 024037.2

RefSeq Size: 2178 bp RefSeq ORF: 1074 bp Locus ID: 79000



C1orf135 (AUNIP) (NM_024037) Human Untagged Clone - SC305093

 UniProt ID:
 Q9H7T9

 Cytogenetics:
 1p36.11

 MW:
 40.3 kDa

Gene Summary: DNA-binding protein that accumulates at DNA double-strand breaks (DSBs) following DNA

damage and promotes DNA resection and homologous recombination (PubMed:29042561). Serves as a sensor of DNA damage: binds DNA with a strong preference for DNA substrates that mimic structures generated at stalled replication forks, and anchors RBBP8/CtIP to DSB sites to promote DNA end resection and ensuing homologous recombination repair (PubMed:29042561). Inhibits non-homologous end joining (NHEJ) (PubMed:29042561). Required for the dynamic movement of AURKA at the centrosomes and spindle apparatus

during the cell cycle (PubMed:20596670).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) uses an alternate 3' terminal exon, compared to variant 1. It encodes isoform 2 which is shorter and has a distinct C-terminus, 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.