

Product datasheet for SC309140

CD95 (FAS) (NM_152871) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: CD95 (FAS) (NM_152871) Human Untagged Clone

Tag: Tag Free

Symbol: FAS

Synonyms: ALPS1A; APO-1; APT1; CD95; FAS1; FASTM; TNFRSF6

Mammalian Cell

Selection:

Neomycin

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

Fully Sequenced ORF: >SC309140 representing NM_152871.

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

GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC

GACTCAGAAAATTCAAACTTCAGAAATGAAATCCAAAGCTTGGTCTAG

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT

TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

Restriction Sites: Sgfl-Mlul

Plasmid Map:

ACCN: NM_152871



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CD95 (FAS) (NM_152871) Human Untagged Clone - SC309140

Insert Size: 945 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 152871.3</u>

 RefSeq Size:
 3888 bp

 RefSeq ORF:
 945 bp

 Locus ID:
 355

 UniProt ID:
 P25445

Cytogenetics: 10q23.31

Protein Families: Druggable Genome, ES Cell Differentiation/IPS, Secreted Protein

Protein Pathways: Allograft rejection, Alzheimer's disease, Apoptosis, Autoimmune thyroid disease, Cytokine-

cytokine receptor interaction, Graft-versus-host disease, MAPK signaling pathway, Natural killer cell mediated cytotoxicity, p53 signaling pathway, Pathways in cancer, Type I diabetes

mellitus

MW: 35.4 kDa



Gene Summary:

The protein encoded by this gene is a member of the TNF-receptor superfamily. This receptor contains a death domain. It has been shown to play a central role in the physiological regulation of programmed cell death, and has been implicated in the pathogenesis of various malignancies and diseases of the immune system. The interaction of this receptor with its ligand allows the formation of a death-inducing signaling complex that includes Fasassociated death domain protein (FADD), caspase 8, and caspase 10. The autoproteolytic processing of the caspases in the complex triggers a downstream caspase cascade, and leads to apoptosis. This receptor has been also shown to activate NF-kappaB, MAPK3/ERK1, and MAPK8/JNK, and is found to be involved in transducing the proliferating signals in normal diploid fibroblast and T cells. Several alternatively spliced transcript variants have been described, some of which are candidates for nonsense-mediated mRNA decay (NMD). The isoforms lacking the transmembrane domain may negatively regulate the apoptosis mediated by the full length isoform. [provided by RefSeq, Mar 2011]

Transcript Variant: This variant (2), also known as FasdeltaTM or soluble FAS, lacks an alternate in-frame exon in the 3' coding region, compared to variant 1. The resulting isoform (2) lacks an internal region, 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.