

Product datasheet for **SC337063**

TARS2 (NM_001271895) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	TARS2 (NM_001271895) Human Untagged Clone
Tag:	Tag Free
Symbol:	TARS2
Synonyms:	COXPD21; TARSL1; thrRS
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



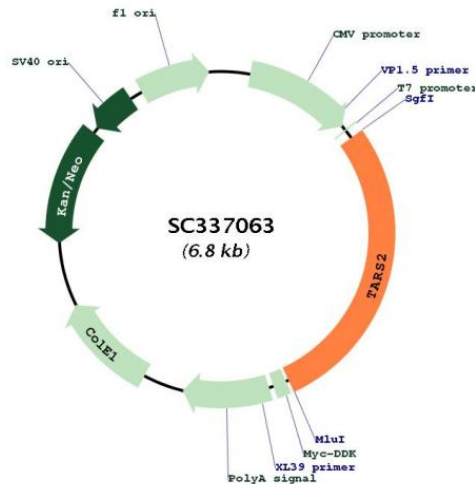
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Fully Sequenced ORF: >SC337063 representing NM_001271895.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGGCCGGGAATTCGTGACTG
GATCCGGTACCGAGGAGATCTGCCGCCCGCATCGCC
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TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
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Restriction Sites: Sgfl-Mlul

Plasmid Map:



ACCN: NM_001271895

Insert Size: 1911 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).

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_001271895.1](#)

RefSeq Size: 2561 bp

RefSeq ORF: 1911 bp

Locus ID: 80222

Cytogenetics: 1q21.2

Protein Pathways: Aminoacyl-tRNA biosynthesis

MW: 71.5 kDa

Gene Summary:

This gene encodes a member of the class-II aminoacyl-tRNA synthetase family. The encoded protein is a mitochondrial aminoacyl-tRNA synthetase. Alternative splicing results in multiple transcript variants. A related pseudogene has been identified on chromosome 4. [provided by RefSeq, Dec 2012]

Transcript Variant: This variant (2) lacks two exons in the coding region, compared to variant 1. The encoded isoform (b) is shorter compared to isoform a.