

Product datasheet for SC204831

SARS2 (NM 001145901) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: SARS2 (NM_001145901) Human 3' UTR Clone

Symbol: SARS2

Synonyms: mtSerRS; SARSM; SerRS; SerRSmt; SERS; SYS

Mammalian Cell

Selection:

Neomycin

Vector: pMirTarget (PS100062)

ACCN: NM_001145901

Insert Size: 370 bp

Insert Sequence: >SC204831 3'UTR clone of NM_001145901

The sequence shown below is from the reference sequence of NM_001145901. The complete

sequence of this clone may contain minor differences, such as SNPs.

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

GTCCCCAATAAATGGTCAGGACAAA

ACGCGTAAGCGGCCGCGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

Restriction Sites: Sgfl-Mlul

OTI Disclaimer: Our molecular clone sequence data has been matched to the sequence identifier above as a

point of reference. Note that the complete sequence of this clone is largely the same as the

reference sequence but may contain minor differences, e.g., single nucleotide

polymorphisms (SNPs).

Components: The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The

package also includes 100 pmols of both the corresponding 5' and 3' vector primers in

separate vials.



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SARS2 (NM_001145901) Human 3' UTR Clone - SC204831

RefSeq: <u>NM 001145901.2</u>

Summary: This gene encodes the mitochondrial seryl-tRNA synthethase precursor, a member of the

class II tRNA synthetase family. The mature enzyme catalyzes the ligation of Serine to tRNA(Ser) and participates in the biosynthesis of selenocysteinyl-tRNA(sec) in mitochondria. The enzyme contains an N-terminal tRNA binding domain and a core catalytic domain. It functions in a homodimeric form, which is stabilized by tRNA binding. This gene is regulated by a bidirectional promoter that also controls the expression of mitochondrial ribosomal protein S12. Both genes are within the critical interval for the autosomal dominant deafness locus DFNA4 and might be linked to this disease. Multiple transcript variants encoding different isoforms have been identified for this gene. [provided by RefSeq, Mar 2009]

Locus ID: 54938 MW: 13.3