

Product datasheet for **SC216506**

SLC25A25 (NM_001006642) Human 3' UTR Clone

Product data:

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| Product Type: | 3' UTR Clones |
| Product Name: | SLC25A25 (NM_001006642) Human 3' UTR Clone |
| Vector: | pMirTarget (PS100062) |
| Symbol: | SLC25A25 |
| Synonyms: | MCSC; PCSCL; SCAMC-2 |
| ACCN: | NM_001006642 |
| Insert Size: | 1831 bp |



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Insert Sequence: >SC216506 3'UTR clone of NM_001006642
 The sequence shown below is from the reference sequence of NM_001006642. The complete sequence of this clone may contain minor differences, such as SNPs.
 Blue=Stop Codon Red=Cloning site

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GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC
AAGATCACCCCTGGGCGTGCAGTCGCGGTGACGGGGGGAGGGCCGCCCGGCAGTGGACTCGTGATCCTG
GGCCGACGCTGGGGTGTGCAGCCATCTATTCTGTGAATGTGCCAACACTAAGCTGTCTCGAGCCAAG
CTGTGAAAACCCCTAGACGCACCCGACGGGAGGGTGGGAGAGCTGGCAGGCCAGGGCTTGTCTGCTG
ACCCAGCAGACCCTCCTGTTGGTTCAGCGAAGACCACAGGCATTCTTAGGGTCCAGGGTCCAGCAGG
CTCCGGGCTCACATGTGTAAGGACAGGACATTTCTGCAGTGCCTGCCAATAGCGAGCTTGGAGCCTGG
AGGCCGGCTTAGTCTTCCATTTACCCTTGCAGCCAGCTGTTGGCCACGGCCCTGCCCTCTGGTCTG
CCGTGCATCTCCCTGTGCCCTCTTGTGCTGCCTGTCTGCTGAGTAAGGTGGGAGGAGGGCTACAGC
CCACATCCACCCCTCGTCCAATCCATAATCCATGATGAAAGGTGAGGTACGTGGCCTCCAGGCC
TGACTTCCAACCTACAGCATTGACGCCAACTGGCTGTGAAGGAAGAGGAAAGGATCTGGCCTTGTGG
TCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGCATGCTTGGGAGTGACGGGGCTCGGGC
TGCCCTGGCCTGGCTGCACAGAAGGCAAGTCTGGGGCTCATGGTCTCTGAGCTGGCCTGGACCCTGTC
AGGATGGGCCCCACCTCAGAACCAAACTCACTGTCCCACTGTGGCATGAGGGCAGTGGAGCACCATGT
TTGAGGGCGAAGGGCAGAGCGTTTGTGTGTTCTGGGGAGGGAAGGAAAAGGTGTTGGAGGCCCTAATTA
TGGACTGTTGGGAAAAGGGTTTTGTCCAGAAGGACAAGCCGGACAATGAGCGACTTCTGTGCTCCAG
AGGAAGACGAGGGAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGTTCCTGTC
CAACCCAGCAGGGGCGCAGCGGACGCCCCACATTCACCTTGTGCTACTGCTTGGAACCTATTTAT
TTTGTATTTATTTGAACAGAGTTATGTCCTAACTATTTTATAGATTTGTTTAATTAATAGCTTGTGAT
TTTCAAGTTCATTTTTTATTCATATTTATGTTTATGTTGATTGTACCTCCCAAGCCCGCCAGTGGG
ATGGGAGGAGGAGGAGAAGGGGGCCTTGGGCCGCTGCAGTCACATCTGTCCAGAGAAAATCCTTTTGG
GACTGGAGGCAGAAAAGCGGCCAGAAGGCAGCAGCCCTGGCTCCTTTCTTTGGCAGGTTGGGGAAGGG
CTTGCCCCAGCCTTAGGATTTTCAAGGTTTACTGGGGCGTGGAGAGAGAGGGAGGAACCTCAATAAC
CTTGAAGTGGAATCCAGTTATTTCTGCGCTGCGAGGGTTTCTTTATTTCACTTTTTCTGAATGTCA
AGGCAGTGAGGTGCTCTCACTGTGAATTTGTGGTGGGCGGGGCTGGAGGAGAGGGTGGGGACTGGC
TCCGTCCCTCCAGCCTTCTGCTGCCCTTGCTTAAACAATGCCGGCCAACGGCGACCTCACGGTTGCAC
TTCCATTCACACAGAATGACCTGATGAGGAAATCTTCAATAGGATGCAAAGATCAATGCAAAAATTGTT
ATATATGAACATATAACTGGAGTCGTCAAAAAGCAAATTAAGAAAAGAAATTGGACGTTAGAAGTTGTCAT
TTAAAGCAGCCTTCTAATAAAGTTGTTTCAAAGCTGA
ACGCGTAAGCGGCCGCGGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA
CGAGATTCGATTCCACCGCCGCTTCTATGAAAGG
  
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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.

RefSeq: [NM_001006642.4](https://www.ncbi.nlm.nih.gov/nuccore/NM_001006642.4)

Summary:

The protein encoded by this gene belongs to the family of calcium-binding mitochondrial carriers, with a characteristic mitochondrial carrier domain at the C-terminus. These proteins are found in the inner membranes of mitochondria, and function as transport proteins. They shuttle metabolites, nucleotides and cofactors through the mitochondrial membrane and thereby connect and/or regulate cytoplasm and matrix functions. This protein may function as an ATP-Mg/Pi carrier that mediates the transport of Mg-ATP in exchange for phosphate, and likely responsible for the net uptake or efflux of adenine nucleotides into or from the mitochondria. Alternatively spliced transcript variants encoding different isoforms with a common C-terminus but variable N-termini have been described for this gene. [provided by RefSeq, Jul 2012]

Locus ID:

114789

MW:

66.9