

Product datasheet for **SC200024**

RPL18A (NM_000980) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	RPL18A (NM_000980) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	RPL18A
Synonyms:	L18A
ACCN:	NM_000980
Insert Size:	86 bp
Insert Sequence:	>SC200024 3'UTR clone of NM_000980 The sequence shown below is from the reference sequence of NM_000980. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC ACCACCAAGAGGCCCAACACCTTCTTCTAGGTGCAGGGCCCTCGTCCGGGTGTGCCCAAATAAACTCA GGAACGCCCGGTGCTC ACGCGTAAGCGGCCGCGCATCTAGATTGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA CGAGATTCGATTCCACCGCCGCTTCTATGAAAGG
Restriction Sites:	Sgfl-MluI
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:	<u>NM_000980.4</u>



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Summary: Ribosomes, the organelles that catalyze protein synthesis, consist of a small 40S subunit and a large 60S subunit. Together these subunits are composed of 4 RNA species and approximately 80 structurally distinct proteins. This gene encodes a member of the L18AE family of ribosomal proteins that is a component of the 60S subunit. The encoded protein may play a role in viral replication by interacting with the hepatitis C virus internal ribosome entry site (IRES). This gene is co-transcribed with the U68 snoRNA, located within the third intron. As is typical for genes encoding ribosomal proteins, there are multiple processed pseudogenes of this gene dispersed throughout the genome. [provided by RefSeq, Jul 2012]

Locus ID: 6142

MW: 3.1