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Product datasheet for SC200784

NDUFB9 (NM_005005) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	NDUFB9 (NM_005005) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	NDUFB9
Synonyms:	B22; CI-B22; LYRM3; MC1DN24; UQOR22
ACCN:	NM_005005
Insert Size:	117 bp
Insert Sequence:	>SC200784 3'UTR clone of NM_005005 The sequence shown below is from the reference sequence of NM_005005. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC GTGACCAGACCCCGGGAGCGGCCCATGTAGAAAGAGAGAGACCTCATCTTTCATGCTTGCAAGTGAAAT ATGTTACAGAACATGCACTTGCCCTAATAAAAAATCAGTGAAATGGTC ACGCGTAAGCGGCCGCGGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG
Restriction Sites:	SgfI-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:	NM_005005.3

View online »

Summary: The protein encoded by this gene is a subunit of the mitochondrial oxidative phosphorylation complex I (nicotinamide adenine dinucleotide: ubiquinone oxidoreductase). Complex I is localized to the inner mitochondrial membrane and functions to dehydrogenate nicotinamide adenine dinucleotide and to shuttle electrons to coenzyme Q. Complex I deficiency is the most common defect found in oxidative phosphorylation disorders and results in a range of conditions, including lethal neonatal disease, hypertrophic cardiomyopathy, liver disease, and adult-onset neurodegenerative disorders. Pseudogenes of this gene are found on chromosomes five, seven and eight. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jul 2015]

Locus ID: 4715

MW: 4.7