

Product datasheet for SC209386

TAZ (NM_000116) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: TAZ (NM_000116) Human 3' UTR Clone

Symbol: TAZ

Synonyms: BTHS; CMD3A; EFE; EFE2; G4.5; LVNCX; TAZ; Taz1

Mammalian Cell

Selection:

Neomycin

Vector: pMirTarget (PS100062)

ACCN: NM_000116

Insert Size: 752 bp

Insert Sequence: >SC209386 3'UTR clone of NM_000116

The sequence shown below is from the reference sequence of NM_000116. The complete

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

GGCCTGGGTTTTCATGTTTTTGAAACAGAACCATAAAGCATATGTGTTGGCTTGTTAAAA

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).



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TAZ (NM_000116) Human 3' UTR Clone - SC209386

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 000116.5</u>

Summary: This gene encodes a protein that is expressed at high levels in cardiac and skeletal muscle.

Mutations in this gene have been associated with a number of clinical disorders including

Barth syndrome, dilated cardiomyopathy (DCM), hypertrophic DCM, endocardial fibroelastosis, and left ventricular noncompaction (LVNC). Multiple transcript variants encoding different isoforms have been described. A long form and a short form of each of these isoforms is produced; the short form lacks a hydrophobic leader sequence and may exist as a cytoplasmic protein rather than being membrane-bound. Other alternatively spliced transcripts have been described but the full-length nature of all these transcripts is

not known. [provided by RefSeq, Jul 2008]

Locus ID: 6901 **MW:** 26.9