

Product datasheet for SC212220

SUMF2 (NM_001042470) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: SUMF2 (NM_001042470) Human 3' UTR Clone

Symbol: SUMF2
Synonyms: pFGE

Mammalian Cell Neomycin

Selection:

Vector: pMirTarget (PS100062)

ACCN: NM_001042470

Insert Size: 1088 bp

Insert Sequence: >SC212220 3'UTR clone of NM_001042470

The sequence shown below is from the reference sequence of NM_001042470. The complete

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

 ${\sf TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC}$

 ${\tt ACTGTCACTGGATGTCATGGGGCCAATAAAATCTCCTGCAATTGTGTATCTCA}$

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

Restriction Sites: Sgfl-Mlul



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SUMF2 (NM_001042470) Human 3' UTR Clone - SC212220

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 001042470.3

Summary: The catalytic sites of sulfatases are only active if they contain a unique amino acid, C-alpha-

formylglycine (FGly). The FGly residue is posttranslationally generated from a cysteine by enzymes with FGly-generating activity. The gene described in this record is a member of the sulfatase-modifying factor family and encodes a protein with a DUF323 domain that localizes to the lumen of the endoplasmic reticulum. This protein has low levels of FGly-generating activity but can heterodimerize with another family member - a protein with high levels of FGly-generating activity. Alternate transcriptional splice variants, encoding different isoforms,

have been characterized. [provided by RefSeq, Jul 2008]

Locus ID: 25870 **MW:** 40.8