

Product datasheet for SC210804

SMARCA2 (NM_003070) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Symbol: SMARCA2

Synonyms: BAF190; BIS; BRM; hBRM; hSNF2a; NCBRS; SNF2; SNF2L2; SNF2LA; Sth1p; SWI2

Mammalian Cell Neomycin

Selection:

Vector: pMirTarget (PS100062)

ACCN: NM_003070

Insert Size: 911 bp

Insert Sequence: >SC210804 3'UTR clone of NM_003070

The sequence shown below is from the reference sequence of NM_003070. The complete sequence of

this clone may contain minor differences, such as $\ensuremath{\mathsf{SNPs}}\xspace.$

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

Restriction Sites: Sgfl-Mlul



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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.

Note: Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um

filter is required.

RefSeq: <u>NM_003070.5</u>

Summary: The protein encoded by this gene is a member of the SWI/SNF family of proteins and is highly

similar to the brahma protein of Drosophila. Members of this family have helicase and ATPase activities and are thought to regulate transcription of certain genes by altering the chromatin

structure around those genes. The encoded protein is part of the large ATP-dependent chromatin remodeling complex SNF/SWI, which is required for transcriptional activation of genes normally repressed by chromatin. Alternatively spliced transcript variants encoding different isoforms have been found for this gene, which contains a trinucleotide repeat (CAG)

length polymorphism. [provided by RefSeq, Jan 2014]

Locus ID: 6595

MW: 36.2