

Product datasheet for SC204939

KRT13 (NM 002274) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: KRT13 (NM_002274) Human 3' UTR Clone

Vector: pMirTarget (PS100062)

Symbol: KRT13

Synonyms: CK13; K13; WSN2

ACCN: NM_002274

Insert Size: 393 bp

Insert Sequence: >SC204939 3'UTR clone of NM_002274

The sequence shown below is from the reference sequence of NM_002274. The complete

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

CCAAAGAAAAGATTATTCAATAAAGTTTCCTGCCTTTCTGCAAACATA

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).

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.

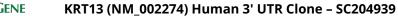
RefSeg: NM 002274.4



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ORIGENE

Summary:

The protein encoded by this gene is a member of the keratin gene family. The keratins are intermediate filament proteins responsible for the structural integrity of epithelial cells and are subdivided into cytokeratins and hair keratins. Most of the type I cytokeratins consist of acidic proteins which are arranged in pairs of heterotypic keratin chains. This type I cytokeratin is paired with keratin 4 and expressed in the suprabasal layers of non-cornified stratified epithelia. Mutations in this gene and keratin 4 have been associated with the autosomal dominant disorder White Sponge Nevus. The type I cytokeratins are clustered in a region of chromosome 17q21.2. Alternative splicing of this gene results in multiple transcript variants; however, not all variants have been described. [provided by RefSeq, Jul 2008]

Locus ID: 3860 MW: 14.4