

Product datasheet for **SC202509**

Cytokeratin 7 (KRT7) (NM_005556) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	Cytokeratin 7 (KRT7) (NM_005556) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	KRT7
Synonyms:	CK7; K2C7; K7; SCL
ACCN:	NM_005556
Insert Size:	191 bp
Insert Sequence:	>SC202509 3'UTR clone of NM_005556 The sequence shown below is from the reference sequence of NM_005556. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC TCCGCCAGTCGCAGGAGTGCCCGCGACTGAGCCGCCTCCCACCACTCCACTCCTCCAGCCACCACCCAC AATCACAAGAAGATTCCCACCCCTGCCTCCCATGCCTGGTCCCAAGACAGTGAGACAGTCTGGAAAGTG ATGTCAGAATAGCTTCCAATAAAGCAGCCTCATTCTGAGGCCTGAGTGATCCA ACGCGTAAGCGGCCGCGCATCTAGATTGAAAGAAATGACCGACCAAGCGACGCCCAACCTGCCATCA CGAGATTCGATTCCACCGCCCTTCTATGAAAGG
Restriction Sites:	Sgfl-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:	<u>NM_005556.4</u>



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Summary: The protein encoded by this gene is a member of the keratin gene family. The type II cytokeratins consist of basic or neutral proteins which are arranged in pairs of heterotypic keratin chains coexpressed during differentiation of simple and stratified epithelial tissues. This type II cytokeratin is specifically expressed in the simple epithelia lining the cavities of the internal organs and in the gland ducts and blood vessels. The genes encoding the type II cytokeratins are clustered in a region of chromosome 12q12-q13. Alternative splicing may result in several transcript variants; however, not all variants have been fully described. [provided by RefSeq, Jul 2008]

Locus ID: 3855

MW: 6.9