

Product datasheet for **SC202972**

NR2C1 (NM_001032287) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	NR2C1 (NM_001032287) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	NR2C1
Synonyms:	TR2
ACCN:	NM_001032287
Insert Size:	240 bp
Insert Sequence:	>SC202972 3'UTR clone of NM_001032287 The sequence shown below is from the reference sequence of NM_001032287. The complete sequence of this clone may contain minor differences, such as SNPs. Blue =Stop Codon Red =Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC CACAATAGTCTTCAACAAGCAGAGGGGTAAATCACCTTAAAATGTCATCAAAAATAGATCTACTAGAAGG CAGCATCACATTCCCATTACTTATGGACTCTACCCCTGGTTCATGTCTTATATGCCTGTAATGGTT ATAAAGCCTACCTTCAGGAAAGCTATGGTTGACTAATTACTAATGGATGGGTTTTAAACATGTCCCTCT ACAATAAATTAATCCTTTATTGTAATACTTTA ACGCGT AAGCGGCCGCGCATCTAGATTGAAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA CGAGATTCGATTCCACCGCCCTTCTATGAAAGG
Restriction Sites:	SgfI-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_001032287.3</u>



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Summary: This gene encodes a nuclear hormone receptor characterized by a highly conserved DNA binding domain (DBD), a variable hinge region, and a carboxy-terminal ligand binding domain (LBD) that is typical for all members of the steroid/thyroid hormone receptor superfamily. This protein also belongs to a large family of ligand-inducible transcription factors that regulate gene expression by binding to specific DNA sequences within promoters of target genes. Multiple alternatively spliced transcript variants have been described, but the full-length nature of some of these variants has not been determined. [provided by RefSeq, Jul 2008]

Locus ID: 7181

MW: 9.3