

Product datasheet for **SC205961**

TRIM14 (NM_033220) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones
Product Name: TRIM14 (NM_033220) Human 3' UTR Clone
Vector: pMirTarget (PS100062)
Symbol: TRIM14
Synonyms: KIAA0129
ACCN: NM_033220
Insert Size: 472 bp
Insert Sequence: >SC205961 3'UTR clone of NM_033220

The sequence shown below is from the reference sequence of NM_033220. The complete sequence of this clone may contain minor differences, such as SNPs.

Blue=Stop Codon Red=Cloning site

```
GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC
GGGGCCATCAGCATCCCCCGCTGCCCTAGGGGCCAGGACCGCGTGACAGCCTCCAGAATGTCATGGA
AGCAGAATCGTACAGTATGTTCCCTTCTGCATATGCTGCTTCTCACTCAGCATATTTCTTGAGATG
CATCCAGGCTGCTGCACGCATCAATAGTTCATTCTGGCTGGGCGCGGTGCTCACGCCTGTAATCCCA
GCGCTTTGGGAGGCCGATGTGGGTGGATACAAGGTCAGGAGTTTGAGACTAGCCTGGCCAAGATGGTG
AAACCCCATCTCTGCAAAAAATACAAAAATTAGCCGGGACCATGGCATGTGCCTGTAATCCCTGTAC
TCAGGAGGCTGAGGAAGGAGAATCACTTGAACCCGGGACGCGGAGTTGCAGTGAGCCGAGATCACACC
ACTGCACTCCAGCCTGGCAATAGAGTGAGACTCCGTTTCAAAAAAAAAAAAAAAAAAAAA
ACGCGTAAGCGGCCGCGCATCTAGATTGAAAGAAATGACCGACCAAGCGACGCCCAACCTGCCATCA
CGAGATTTGATTCCACCGCCCTTCTATGAAAGG
```

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: [NM_033220.1](#)



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Summary: The protein encoded by this gene is a member of the tripartite motif (TRIM) family. The TRIM motif includes three zinc-binding domains, a RING, a B-box type 1 and a B-box type 2, and a coiled-coil region. The protein localizes to cytoplasmic bodies and its function has not been determined. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Mar 2010]

Locus ID: 9830

MW: 17.3