

Product datasheet for **SC336146**

TENT2 (NM_001297745) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	TENT2 (NM_001297745) Human Untagged Clone
Tag:	Tag Free
Symbol:	TENT2
Synonyms:	APD4; GLD2; PAPD4; TUT2
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC336146 representing NM_001297745. Blue=Insert sequence Red=Cloning site Green=Tag(s)

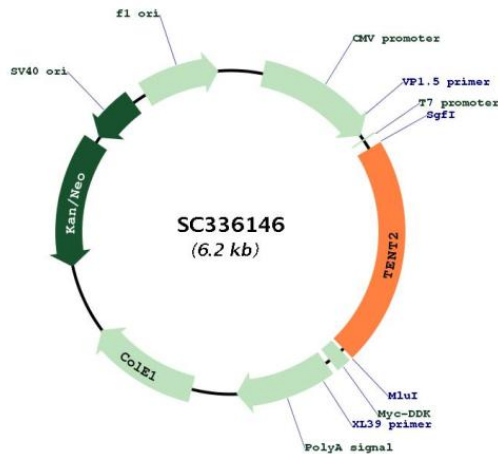
```
GCTCGTTTGTAGTGAACCGTCAGAATTTTGTAAATACGACTACTATAGGGCGCCGGGAATTCGTGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGTTCCCAAACCTCAATTTGGGTGCGCCACCCTTCACTCCAATCATCAACAACATAATAAATTCTTT
ACCCTGTCACCTACTGTTTATTCACACCAGCAGCTTATAGATGCACAATCAACTTTCAGAATGCAGAC
TTGTCTAGAGCTGTGTCATTACAGCAGCTGACATATGAAATGTCAGTCCAATACAGACCTCAGCTTCC
CCATTATTTGAGGAAGGAAGAGATTAAGCGATGAAAAAACCTTCTCTTGACGGTAAACGGCAACGT
TTCCATTACCCCAAGAGCCAAGTGTAGTTAACCAGATAGTGCCTTTATCAGGTGAACGAAGATAC
TCAATGCCACCATTGTTTCATACACATTATGTACCAGATATAGTCAGATGTGTTCCACCTTTTCGAGAA
ATTGCATTTTAGAACCTAGAGAAATCACACTGCCTGAGGCCAAAGATAAGTTGAGTCAGCAGATACTG
GAGTTATTTGAAACATGTGAGCAGCAAATAAGTGATTTAAAGAAGAAAGAACTCTGTGCAACACAGCTG
CAGAGAGAAATTCAGCTGTTATTTCCACAAAGCAGACTTTTTTTGGTTGGGTCTCTTTAAATGGATTT
GGTACCCGGAGCAGTGATGGTGATTTATGCCTAGTTGTTAAGGAAGAACCATGTTTTTTTCAGGTAAT
CAGAAGACTGAAGCAGGCATATACTCACCTTAGTCCATAAACTTCTGTAAGTACTAGACTTTCCGGCTAC
ATTGAGAGACCTCAGCTGATTCGAGCAAAGTGCATTTGTGAAGTTCAGGGATAAAGTCAGTTGTGTG
GAGTTTGACTTGAATGTAACAATATTGTTGGAATAAGAAACACATTCCTTCTCAGAAGTATGCATAC
CCCCTACCTGAACCCATCCTTCCATCCCTCCAAAAATTTACCCAGAGTCTTTTAGTCCTGCTATACAG
CTGCACCTGTACATCAAGCTCCATGTAATGTTCCCTCCTTACCTCTCAAAGAATGAATCAAACCTTGGG
GACCTCTTACTGGGCTTTCTTAAATATTATGCTACAGAATTTGACTGGAATAGTCAAATGATTTTCAGTT
CGTGAAGCCAAAGCCATTCCAAGCCTGATGGTATTGAATGGAGAAATAATACATCTGTGTAGAAGAA
CCTTTTGTGGAACAAATACAGCCAGAGCAGTGCACGAAAAGCAGAAATTTGATATGATCAAGGATCAA
TTTTTAAAGTCATGGCACAGATTGAAAAACAAGAGAGATTTGAACAGTATACTACCTGTAAGAGCTGCT
GTCCTGAAAAGATAA
ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGCGC
```



[View online »](#)

Restriction Sites: SgfI-MluI

Plasmid Map:



ACCN: NM_001297745

Insert Size: 1326 bp

OTI Disclaimer: Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).

Components: The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).

Reconstitution Method:

1. Centrifuge at 5,000xg for 5min.
2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.
3. Close the tube and incubate for 10 minutes at room temperature.
4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.
5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.

RefSeq: [NM_001297745.1](#)

RefSeq Size: 3397 bp

RefSeq ORF: 1326 bp

Locus ID: 167153

Cytogenetics: 5q14.1

MW: 51.1 kDa

Gene Summary:

Cytoplasmic poly(A) RNA polymerase that adds successive AMP monomers to the 3'-end of specific RNAs, forming a poly(A) tail. In contrast to the canonical nuclear poly(A) RNA polymerase, it only adds poly(A) to selected cytoplasmic mRNAs (PubMed:15070731). Does not play a role in replication-dependent histone mRNA degradation (PubMed:18172165). Adds a single nucleotide to the 3' end of specific miRNAs, monoadenylation stabilizes and prolongs the activity of some but not all miRNAs (PubMed:23200856).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (5) lacks an in-frame coding exon, compared to variant 1. The resulting isoform (3) lacks an internal segment, compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.