

Product datasheet for **MC227458**

Terf1 (NM_001286628) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Terf1 (NM_001286628) Mouse Untagged Clone
Tag: Tag Free
Symbol: Terf1
Synonyms: P; Pin2; Trbf; Trbf1; Trf; Trf1
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC227458 representing NM_001286628
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**GCGATCGCC**

ATGGCGGAGACGGTCTCCTCAGCGGCCCGGACGCGCCGAGCCGTGAGGGCTGGACAGATTCGGATTCTC
 CAGAGCAGGAGGAGGTGGAGACGACGCGGAGCTGCTCCAGTGCCAGCTTCAGCTGGGACCCCGAGAGA
 GATGGAGAACCGCGAGCTTGTGGCTGAGGTGGAGGCCGTGGCTGCGGGCTGGATGCTCGACTTCCTCTGC
 CTGTCTCTGTGCCGAGCCTCCGTGACGCGCCGCTCCGAGGACTTTCGTGCTACTCGTGACAGCGCCGAGG
 CTATTATTCATGGACTACACAGACTTACAGCTTACCAATTGAAAAGTGTGTATATATGTCAGTTTTTGC
 AAGAGTTGCATCTGAAAAGGCCCTTGATGCACAGTTTGAAGTTGATGAGCGTATTACACCCTTGGAAATCA
 GCCCTGATGATTTGGAATCAATTGAAAAGGAACATGACAACTGCATGACGAAATAAAGAATTTAATTA
 AAATTCAGCCTTTAGAAAAGGAAGTTACTTAAGATAATCTCTCAGAAGGATGTGTTCCACTCCCTTTTCCA
 ACACTTCAGCTATAGCTGCATGATGGAGAAAATTCAGAGTTATGTGGGTGATGTGTTAAGTGAAAAATCA
 TCAACTTTTCTAATGAAGGCAGCAACAAAAGTAGTGGAAAATGAGAAAAGCGAGGACACAAGCGCTAAGG
 ATAGGCCAGATGCCCAACACTGGAATGGACTGAAGTTGGTTTGAATAAAGAGAAAAGTGTAAATGG
 CCAGCAGTCTACAGAACTGAACCTTAGTGGATACAGTATCCTCAATAAGGTCTCACAAAGAACGCCTTA
 TCGCAGTTAAAACACAGACGTGCTCCATCAGATTTTCAGTAGGAACGAAGCAAGAACAGGAACTCTTCAGT
 GTGAAACAACGATGAAAAGGAACCGAAGAACCAGTGGAAAGGAATAGATTGTGTCTCAGAGAATCAGCC
 AGACACTGATGACAAAAGTGGACGAGGAAAAGACAGACATGGCTTTGGGAAGAAGACAGAAATTTGAAG
 TGTGGTGTAAAGAAATATGGAGAGGGAAATTTGGCTAAAATACTATCCCATTATAAGTTCAACAACCGAA
 CAAGTGCATGTTAAAAGATAGATGGAGAACAATGAAGAGACTGAACTGATTAG**CTGA**

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI



ACCN:	NM_001286628
Insert Size:	1179 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).
OTI Annotation:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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:	<ol style="list-style-type: none">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:	<u>NM_001286628.1, NP_001273557.1</u>
RefSeq Size:	2181 bp
RefSeq ORF:	1179 bp
Locus ID:	21749
Cytogenetics:	1 4.88 cM
Gene Summary:	<p>This gene encodes a protein that binds to repeats in telomeres to form a nucleoprotein complex that protects against the degradation of chromosomal ends. The encoded protein regulates the length of telomeres and is an integral structural component of the functional telomere. This protein is thought to play a role in spindle formation in mitosis. Mutations in this gene are associated with bone marrow failure. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Nov 2013]</p> <p>Transcript Variant: This variant (2) lacks an in-frame exon in the 5' coding region compared to variant 1. The encoded protein (isoform 2) is shorter than 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.</p>