

Product datasheet for **SC334807**

TPM1 (NM_001301289) Human Untagged Clone

Product data:

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| Product Type: | Expression Plasmids |
| Product Name: | TPM1 (NM_001301289) Human Untagged Clone |
| Tag: | Tag Free |
| Symbol: | TPM1 |
| Synonyms: | C15orf13; CMD1Y; CMH3; HEL-S-265; HTM-alpha; LVNC9; TMSA |
| Mammalian Cell Selection: | None |
| Vector: | <u>pCMV6-XL5</u> |
| E. coli Selection: | Ampicillin (100 ug/mL) |
| Fully Sequenced ORF: | >NCBI ORF sequence for NM_001301289, the custom clone sequence may differ by one or more nucleotides |

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ATGGCGGGGAGTAGCTCGCTGGAGGCGGTGCGCAGGAAGATCCGGAGCCTGCAGGAGCAGGCGGACGCCG
CTGAGGAGCGCGGGCACCCCTGCAGCGGAGCTGGACCACGAGAGGAAGCTGAGGGAGACCCGCTGAAGC
CGACGTAGCTTCTCTGAACAGACGCATCCAGCTGGTTGAGGAAGAGTTGGATCGTGCCCAAGGAGCGTCTG
GCAACAGCTTTGCAGAAGCTGGAGGAAGCTGAGAAGGCAGCAGATGAGAGTGAGAGGCCATGAAAGTCA
TTGAGAGTCGAGCCAAAAAGATGAAGAAAAATGGAAATTCAGGAGATCCAAGTAAAGAGGCCAAGCA
CATTGCTGAAGATGCCGACCGAAATATGAAGAGGTGGCCGTAAGCTGGTCATCATTGAGAGCGACCTG
GAACGTGCAGAGGAGCGGCTGAGCTCTCAGAAGGCAAAATGTGCCGAGCTGAAGAAGAATTGAAAAGT
TGACGAACAACCTTGAAGTCACTGGAGGCTCAGGCTGAGAAGTACTCGCAGAAGGAAGACAGATATGAGGA
AGAGATCAAGGTCTTTCCGACAAGCTGAAGGAGGCTGAGACTCGGGCTGAGTTTGGGAGAGGTGAGTA
ACTAAATTGGAGAAAAGCATTGATGACTTAGAAGAGAAAGTGGCTCATGCCAAAGAAGAAAACCTTAGTA
TGCATCAGATGCTGGATCAGACTTTACTGGAGTTAAACAACATGTGA
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| Restriction Sites: | Sgfl-MluI |
| ACCN: | NM_001301289 |
| 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). |



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| 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_001301289.1, NP_001288218.1</u> |
| RefSeq Size: | 1629 bp |
| RefSeq ORF: | 747 bp |
| Locus ID: | 7168 |
| Cytogenetics: | 15q22.2 |
| Protein Families: | Druggable Genome |
| Protein Pathways: | Cardiac muscle contraction, Dilated cardiomyopathy, Hypertrophic cardiomyopathy (HCM) |
| Gene Summary: | <p>This gene is a member of the tropomyosin family of highly conserved, widely distributed actin-binding proteins involved in the contractile system of striated and smooth muscles and the cytoskeleton of non-muscle cells. Tropomyosin is composed of two alpha-helical chains arranged as a coiled-coil. It is polymerized end to end along the two grooves of actin filaments and provides stability to the filaments. The encoded protein is one type of alpha helical chain that forms the predominant tropomyosin of striated muscle, where it also functions in association with the troponin complex to regulate the calcium-dependent interaction of actin and myosin during muscle contraction. In smooth muscle and non-muscle cells, alternatively spliced transcript variants encoding a range of isoforms have been described. Mutations in this gene are associated with type 3 familial hypertrophic cardiomyopathy. [provided by RefSeq, Jul 2008]</p> <p>Transcript Variant: This variant (Tpm1.8, also known as variant 9) contains alternate in-frame exons in the 5' and 3' coding region, compared to variant Tpm1.1. It encodes isoform Tpm1.8cy, which has distinct N- and C-termini and is shorter than isoform Tpm1.1st. Variants Tpm1.8, Tpm1.9 and Tpm1.13 encode isoforms that are the same length, but have distinct protein sequences. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.</p> |