

Product datasheet for **SC309634**

TRIM35 (NM_171982) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	TRIM35 (NM_171982) Human Untagged Clone
Tag:	Tag Free
Symbol:	TRIM35
Synonyms:	HLS5; MAIR
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)



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Fully Sequenced ORF: >SC309634 representing NM_171982.
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGGCCGGGAATTCGTGACTG
GATCCGGTACCGAGGAGATCTGCCGCCCGGATCGCC
ATGGAGCGGAGTCCCGACGTGTCCCCGGGCTTCCCGCTCTTCAAGGAGGAGTTGCTCTGCGCCGTC
TGCTACGACCCCTCCCGCAGCAGTCACTCTGCGTGCAGCCACAACCTCTGCGCGGGTGCCTGAGC
CGCTGCTGGGAGGTGCAGGTGTGCGCCACCTGCCAGTGTGCAAAGACCGCGCTACCCGCCGACTG
CGCACCAACCACCCCTCAACAACCTGGTGGAGAAGCTGCTGCGCGAGGAGGCCGAGGGCGCGCTGG
ACCAGCTACCGCTTCTCGCGTGTCTGCCGCTGCACCGCGGACAGCTCAGCCTCTTCTGCCTCGAGGAC
AAGGAGCTGCTGTGCTGCTCCTGCCAGGCCGACCCCGACACCAGGGGACCCGCTGCAGCCGGTGAAG
GACTGCGCCACGACTTTCGGGCAAGTGCAGGAACATGGAGCATGACTGCGGGAGAAGGCCAAGGCC
TTCTGGGCCATGCGGCGCTCTATGAGGCCATCGCCAAGCACAATCAGGTGGAGGCTGCATGGCTGGAA
GGCCGGATCCGGCAGGAGTTTGATAAGCTTCGCGAGTTCTTGAGAGTGGAGGAGCAGGCCATTCTGGAT
GCCATGGCCGAGGAGACAAGGCAGAAGCAACTTCTGGCCGACGAGAAGATGAAGCAGCTCACAGAGGAG
ACGGAGGTGCTGGCACATGAGATCGAGCGGCTGCAGATGGAGATGAAGGAGGACGAGTTTCTTTTCTC
ATGAAACACAAGAGCCGAAAACGCCGACTTCTGCACCATGGAGCCAGAGCCAGTCCAGCCCGGATG
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GAATCTGTACCCTTACGCTTTGACCCCAACACCGCAGCTGGCTGGCTCTCCGTGTCTGACGACCTACC
AGCGTCACCAACCATGGTACCGCGTGCAGGTGGAGAACCCGGAACGCTTCTCCTCGGCGCCCTGCCTG
CTGGGCTCCCGTGTCTTCTCACAGGGCTCGCACGCTGGAGGTGGCCCTTGGGGGGTGCAGAGCTGG
AGGGTGGGCGTGGTACGTGTGCCCAGGACTCGGGCGCTGAGGGCCACTCACACAGTGTACCACGAC
ACAGCTCGGGCTTCTGGTATGCTGCGCACGAGGGCGTGGAGGGGACCAGTGCCTGACCTCGGAC
CCAGCCACGTGCGCCCTGGTCTGGCCATCCACGCGCCCTGCGTGTGGAGCTGGAGTGTGAGGAGGC
GAGCTGTCTTTCTATGACGCGGAGCGCCACTGCCACCTGTACACCTTCCACGCCGCTTTGGGGAGTT
CGCCCTACTTCTACCTGGGGGTGCACGGGGCGCCGGGCTCCAGAGCCTTTCGCGATCTGCCCTTG
CACATCAGTGTCAAGGAAGAAGTGGATGGCTGA
ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
  
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Restriction Sites: SgfI-MluI

ACCN: NM_171982

Insert Size: 1482 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: This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

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:	NM_171982.4
RefSeq Size:	4247 bp
RefSeq ORF:	1482 bp
Locus ID:	23087
UniProt ID:	Q9UPQ4
Cytogenetics:	8p21.2
Protein Families:	Druggable Genome
MW:	56.5 kDa
Gene Summary:	<p>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 function of this protein has not been identified. [provided by RefSeq, Jul 2008]</p> <p>Transcript Variant: This variant (1) represents the longest transcript and encodes the longest 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>