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Product datasheet for SC308729

TRIM14 (NM_033219) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	TRIM14 (NM_033219) Human Untagged Clone
Tag:	Tag Free
Symbol:	TRIM14
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC308729 representing NM_033219. Blue=Insert sequence Red=Cloning site Green=Tag(s) GTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTA CCGAGGAGATCTGCCGCCGCGATCGCCGGCGCGCCC ATGGCGGGCGCGGCGACCGGGAGCCGGACCCCTGGGAGGTCGGAGCTTGTCGAGGGATGCGGCTGGCGC TGCCCGGAGCATGGCGACCGCGTGGCTGAGCTCTTCTGTCGCCGCTGCCGCCGCTGCGTGTGCGCGCTT TGCCCGGTGCTGGGCGCGCACCGTGGCCACCCTGTGGGCCTGGCGCTGGAGGCAGCGGTGCACGTGCAG AAACTCAGCCAAGAATGTTTAAAGCAGCTGGCAATCAAGAAGCAGCAGCACATTGACAACATAACCCAG ATAGAAGATGCCACCGAGAAGCTCAAGGCTAATGCAGAGTCAAGTAAAACCTGGCTGAAGGGGAAATTC ACTGAACTCAGATTACTACTTGACGAAGAGGAAGCGCTGGCCAAGAAATTCATTGATAAAAACACGCAG CTTACCCTCCAGGTGTACAGGGAACAAGCTGACTCTTGCAGAGAGCAACTTGACATCATGAATGATCTC TCCAACAGGGTCTGGAGTATCAGCCAGGAGCCCGATCCTGTCCAGAGGCTTCAGGCATACACGGCCACC GAGCAGGAGATGCAGCAGCAGATGAGCCTCGGGGAGCTGTGCCATCCCGTGCCCCTCTCCTTTGAGCCC GTCAAGAGCTTCTTTAAGGGCCTCGTGGAAGCCGTGGAGAGTACATTACAGACGCCATTGGACATTCGC CTTAAGGAAAGCATAAACTGCCAGCTCTCAGACCCTTCCAGCACCAAGCCAGGTACCTTGTTGAAAACC AGCCCCTCACCAGAGCGATCGCTATTGCTGAAATACGCGCGCACGCCCACGCTGGATCCTGACACGATG CACGCGCGCCTGCGCCTGTCCGCCGATCGCCTGACGGTGCGCTGCGGCCTGCTGGGCAGCCTGGGGCCC GTGCCCGTGCTGCGGTTCGACGCGCTCTGGCAAGTGCTGGCTCGTGACTGCTTCGCCACCGGCCGCCAC TACTGGGAGGTTGACGTGCAGGAGGCGGGCGCCGGCTGGTGGGTGGGCGCGGCCTACGCCTCCCTTCGG CGCCGCGGGGCCTCGGCCGCCGCCCGCCTGGGCTGCAACCGCCAGTCCTGGTGCCTCAAGCGCTACGAC CTTGAGTACTGGGCCTTCCACGACGGCCAGCGCAGCCGCCTGCGGCCCCGCGACGACCTCGACCGGCTC GGCGTCTTCCTGGACTACGAGGCCGGCGTCCTCGCCTTCTACGACGTGACGGGCGGCATGAGCCACCTG CATACCTTCCGCGCCACGTTCCAGGAGCCGCTCTACCCGGCCCTGCGGCTCTGGGAGGGGGCCATCAGC ATCCCCCGGCTGCCCTAG ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
Restriction Sites:	AscI-MluI

View online »

Plasmid Map:	
ACCN:	NM_033219
Insert Size:	1329 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:	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_033219.2
RefSeq Size:	1654 bp
RefSeq ORF:	1329 bp
Locus ID:	9830
UniProt ID:	Q14142
Cytogenetics:	9q22.33
Protein Families:	Druggable Genome
MW:	49.8 kDa
Gene 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] Transcript Variant: This variant (2, also referred to as alpha) is alternatively spliced in the 3' UTR, compared to variant 1. Both variants encode the same protein. 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.