

Product datasheet for **MC229247**

Trim24 (NM_001272076) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Trim24 (NM_001272076) Mouse Untagged Clone
Tag: Tag Free
Symbol: Trim24
Synonyms: A130082H20Rik; AI447469; D430004I05Rik; Tif; TIF1; TIF1-alpha; Tif1a; TIF1alpha
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC229247 representing NM_001272076
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGGATCGCC**

ATGGCAGATATTTTTGATTACACTTTTATCGGTGGGTGTGGAGATGCTTGTCCACATGCGCATGTGGAA
GTCAGAGGATAACTTGGAAAAGTCAGTTCTTTCCATCCTGTGTTTCGTCCCATGGATAAACTGCTGTCAC
TGGTGATGAGCAAGTTGGAGTCATTCGATGCCAGTTTGCAGTCAAGAGTGTGCTGAGAGACACATCATA
GACAACTTTTTGTGAAGGACACCACTGAAGTTCCCTAGTAGTACAGTAGAAAAGTCTAATCAGGTATGTA
CAAGCTGTGAAGACAATGCAGAAGCTAATGGGTTTTGTGTAGAGTGTGTTGAATGGCTCTGCAAGACATG
TATTAGAGCTCACCAGAGGGTGAAGTTCACAAAAGACCACACAGTCAGGCAGAAAAGAAGAAGTATCTCCA
GAGGCAGTTGGGGTGACCACTCAGCGACCAAGTGTGTTTGTCCCTCCATAAAAAGGAGCAGTTGAACTTT
ACTGTGAAACATGTGATAAACTGACCTGTCGAGACTGCCAGCTGCTAGAACAACAAAGAACACAGGTATCA
ATTTATAGAAGAAGCTTTTCAGAATCAAAAAGTGATCATAGATACTCTAATCACCAAACTGATGGAAAA
ACAAAATATAAAGTATACAGGAAATCAGATCCAAAATAGGATAATTGAAATAAATCAAAACAAAAGC
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GCTGCACCAGCTTGAGAGTCTTGCAAAGGACCATCGAATGAAACTCATGCAACAACAGCAGGAAGTGGCT
GGGCTTTCTAAGCAGTTAGAGCACGTCATGCATTTTTCTAAATGGGCTGTTTCCAGTGGCAGCAGCACAG
CCTTGCTGTACAGCAAGCGGCTGATTACATACAGGTTACGGCACCTTCTTCGTGCAAGGTGTGATGCTTC
TCCTGTGACCAACACCACCATCCAGTTTCACTGTGATCCTAGTTTCTGGGCTCAAATAATTATCAACTTG
GGTTCTTTAGTAATCGAGGATAAAGAGAGCCAGCCACAAATGCCTAAGCAGAATCCTGTCGTGGAGCAGA
GTTACAGCCACCAGGTGGTTTACCTTCCAACAGTTATCCAAGTCCCAACACAGATCAGCCTAGCTCA
GTTACGACTCCAGCATATTCAGCAACAGGTAATGGCTCAGAGGCAACAGGTGCAACGGAGGCCAGCACCT
GTGGGTTTACAAACCTAGAATGCAGGGGCCATCCAGCAGCCTCCATCTCTCATCAGCATCCGCCAC
CAGCTTAATAAACTTTTCAAGTACAGCCCTAAGCCCAATGGACCAGTTCTTCCTCTTATCCTCAGCA
GCTGAGATATTCACCAAGCCAGAATGTACCTCGGCAGACAACAATAAAGCCCAACCCCTTGCAAATGGCT
TTTTTGGCTCAACAGGCCATAAAACAGTGGCAGATCAGCAGTGTACAGGCTCCGCCACAACCTGCCAGCA



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GCTCCTCCTCCACGCCGTCCAGCCCCACAATCACAAGTGCAGCTGGGTACGATGGAAAAGCTTTTAGTTC
ACCCATGATTGATCTGAGTGCACCGGTGGGAGGGTCTTACAATCTTCTTCTTCCAGATATTGATTGT
TCAAGTACTATAATGTTGGACAACATTGCAAGGAAAGACACAGGTGTAGATCACGCCCCAGCCGAGGCCTC
CGTCAAACAGAACGGTGCAGTACCAAATTCATCAGTGCCATCTCCAGGCCTTGCAGGGCCTGTTACTAT
GACTAGCGTCCATCCCCAATACGTTACCTAGTGCCTCCAGTGTGGAAGTCGAGGAAGCTCTGGCTCT
TCCAGCAAACCAGCAGGAGCTGATTCTACTCACAAGTCCCAGTAGTCATGCTGGAGCCAATTCGAATAA
AACAGGAAAACAGTGGACCACCTGAAAAATTATGATTTTCTGTTTATAGTAAAAACAAGAATCAGATGA
AGAATCTAGACCTCAAAATACTAACTATCCAAGAAGCATACTTACCTCCCTCCTCTTAAACAGCAGTCAG
AGCTCTGCTTCTGAGGAAACCGTGTACGATCTGATGCCCTGATAGTACAGGAGATCAGCCTGGACTCC
ATCAAGAAAATTCCTCAAATGGAAAGTCTGAGTGGTCGGATGCCTCCCAGAAAGTCCCCTGTGCATGTCGG
AGAGACGAGGAAGGAGGATGACCCCAATGAAGACTGGTGTGCTGTTTGTCAAAATGGTGGGGAACCTCTA
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GAGAATGGATCTGTACTTTCTGCCGAGACTTATCTAAGCCAGAGGTTGACTATGATTGTGATGTTCCCG
TCACCACTCAGAGAAAACGAAAAGTGAAGGCCTTACTAAGTTAACCCAATAGACAAAAGGAAATGTGAA
CGCCTACTTCTGTTTCTTACTGCCATGAAATGAGCCTGGCTTCCAAGACCCTGTCTCTCTAACTGTGC
CTGATTATTATAAAATAATTAACCCCAATGGACTTGTCAACCATCAAGAAAAGACTTCCAGGAGGATTA
TTGCATGTATACAAAGCCTGAAGACTTTGTAGCTGATTTTAGATTGATCTTTCAAAACTGTGCTGAATTC
AATGAGCCTGATTCTGAAGTAGCCAATGCTGGTATAAACTTGAAAGCTATTTTGAAGAACTTCTAAAGA
ATCTTTATCCAGAAAAAGGTTTCTAAGGTAGAATTCAGGCAATGAAGCAGAAGACTGTAAGTTCAGTGA
CGACTCAGACGATGACTTTGTACAGCCCCGGAAGAAGCGTCTCAAGAGCACCGAGGATCGCCAGCTGCTT
AAGTAA
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ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA
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- Restriction Sites:** Sgfl-Mlul
- ACCN:** NM_001272076
- Insert Size:** 2946 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:**
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_001272076.1](#), [NP_001259005.1](#)
- RefSeq Size:** 5771 bp

RefSeq ORF: 2946 bp

Locus ID: 21848

UniProt ID: [Q64127](#)

Cytogenetics: 6 B1

Gene Summary: The protein encoded by this gene is part of the tripartite-motif containing family (TRIM), which are typified by the RING, B-box type 1, B-box type 2, and coiled-coil region domains. This protein, which also contains a PHD/TTC finger and bromodomain important for regulating nuclear receptors and binding chromatin, has important roles in differentiation, development, and tissue homeostasis. This protein has been reported to regulate the activity of the tumor suppressor p53 and of the retinoic acid receptor. A translocation event between this gene and Braf transforming gene, which results in the fusion protein T18, has been reported in hepatocellular carcinomas. Alternative splicing results in multiple transcript variants that encode different protein isoforms. [provided by RefSeq, Jan 2013]
Transcript Variant: This variant (3) differs in the 5' UTR and 5' coding region, and uses an alternate start codon, compared to variant 1. The encoded isoform (3) has a distinct and shorter N-terminus that lacks the N-terminal RING domain, 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.