

Product datasheet for MC226370

Tnf (NM_001278601) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Tnf (NM_001278601) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Tnf
Synonyms:	DI; DIF; Tn; TNF-; TNF-a; TNF-alpha; Tnfa; TNFalpha; Tnfs; Tnfsf1a; TNFSF2; Tnlg1f
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC226370 representing NM_001278601 Red=Cloning site Blue=ORF Orange=Stop codon

TTTGTAAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGATCGCC**

ATGAGCACAGAAAGCATGATCCGCGACGTGGAAGTGGCAGAAGAGGCACTCCCCAAAAGATGGGGGGCT
 TCCAGAACTCCAGGCGGTGCCTATGTCTCAGCCTCTTCTCATTCTGCTGTGGCAGGGGCCACCACGCT
 CTTCTGTCTACTGAACCTCGGGGTGATCGGTCCCCAAAGGGATGAGAAGTCCCAAATGGCCTCCCTCTC
 ATCAGTTCTATGGCCAGACCCTCACACTCACAACCACCAAGTGGAGGAGCAGCTGGAGTGGCTGAGCC
 AGCGCGCCAACGCCCTCCTGGCCAACGGCATGGATCTCAAAGACAACCAACTAGTGGTGCCAGCCGATGG
 GTTGATACCTTGCTACTCCAGGTTCTCTTCAAGGGACAAGGCTGCCCGACTACGTGCTCCTCACCCAC
 ACCGTCAGCCGATTTGCTATCTCATACCAGGAGAAAGTCAACCTCCTCTGCGCTCAAGAGCCCTGCC
 CCAAGGACACCCCTGAGGGGGCTGAGCTCAAACCTGGTATGAGCCCATATACCTGGGAGGAGTCTTCCA
 GCTGGAGAAGGGGGACCAACTCAGCGCTGAGGTCAATCTGCCCAAGTACTTAGACTTTGCGGAGTCCGGG
 CAGGTCTACTTTGGAGTCATTGCTCT**TGA**

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:	SgfI-MluI
ACCN:	NM_001278601
Insert Size:	660 bp


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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.
Note:	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
RefSeq:	<u>NM_001278601.1, NP_001265530.1</u>
RefSeq Size:	1605 bp
RefSeq ORF:	660 bp
Locus ID:	21926
UniProt ID:	<u>P06804</u>
Cytogenetics:	17 18.59 cM
Gene Summary:	<p>This gene encodes a multifunctional proinflammatory cytokine that belongs to the tumor necrosis factor (TNF) superfamily. Members of this family are classified based on primary sequence, function, and structure. This protein is synthesized as a type-II transmembrane protein and is reported to be cleaved into products that exert distinct biological functions. It plays an important role in the innate immune response as well as regulating homeostasis but is also implicated in diseases of chronic inflammation. In mouse deficiency of this gene is associated with defects in response to bacterial infection, with defects in forming organized follicular dendritic cell networks and germinal centers, and with a lack of primary B cell follicles. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jun 2013]</p> <p>Transcript Variant: This variant (2) lacks an alternate in-frame exon in the 5' coding region compared to variant 1. It encodes isoform 2 which is shorter compared to isoform 1.</p> <p>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>