

Product datasheet for MC225297

Cnot1 (NM_178078) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Cnot1 (NM_178078) Mouse Untagged Clone
Tag: Tag Free
Symbol: Cnot1
Synonyms: 6030411K04Rik; AA815922; D830048B13
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC225297 representing NM_178078
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGATCGCC**

ATGAATCTTGACTCGCTCTCGTGGCCTTGTCTCAAATCAGCTACCTGGTGGACAATTTAACCAAGAAAA
 ACTACCGAGCCAGCCAGCAGGAAATACAGCATATTGTGAATCGGCACGGTCTGAGGCAGACAGGCATTT
 ATTACGCTGCCTATTTTCACATGTGGATTTTCAGTGGCGATGGTAAAAGCAGTGGCAAAGATTTCCATCAG
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 CCATTGATAATCCATTGCACTACCAAGAAGATTTAAAGCCTGCACCCCACTTATTTGCCAGCTGAGTAA
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ATCCTAACTCTGCCATTATTTTGCCTATGCATGGCATGGGCAGGGGCAGTCTCCATCAATTTCGCCAACT
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TCGAAATCATTTGGTTAACATGCAGCAGTATGATCTTCATCTTGCTCAGTCGATGGAGAATGGCTTGAAC
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TACTGAGGCAGATCTGTCCATACCATGAAACCCTCATGAGAAATTAATGCTCATTCCAGAGGCAATGC
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AGGGACTCAGGCTATCGCACACATCCACAACAAGGGCAGCAGCCCTCAATGAGCACCATCACCCACTCA
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CAATTGCGAACCAGCTACGGTACCCAAACAGCCACACTCACTTTCAGCTGCACAATGTTGTACCTTTT
TGCTGAGGCGAACACTGAGGCAATCCAGGAACAGATCACAAAGGTTCTCTTGAACGTTGATTGTAAT
AGGCCACATCCTTGGGTCTTCTTATCACCTTCATTGAGCTGATTA AAAACCCAGCATTTAAGTTCTGGA
ACCATGAATTTGTACTGTGCCCCAGAGATTGAAAAGTTATTTTCAGTCTGTTGCACAGTGTGCATGGG
ACAGAAGCAGGCTCAGCAAGTATGGAGGGGACCGGTGCCAGT TAG

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:

SgfI-MluI

ACCN:

NM_178078

Insert Size:

7116 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).

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_178078.2](#), [NP_835179.1](#)

RefSeq Size: 8375 bp

RefSeq ORF: 7116 bp

Locus ID: 234594

UniProt ID: [Q6ZQ08](#)

Cytogenetics: 8 D1

Gene Summary: Scaffolding component of the CCR4-NOT complex which is one of the major cellular mRNA deadenylases and is linked to various cellular processes including bulk mRNA degradation, miRNA-mediated repression, translational repression during translational initiation and general transcription regulation. Additional complex functions may be a consequence of its influence on mRNA expression. Its scaffolding function implies its interaction with the catalytic complex module and diverse RNA-binding proteins mediating the complex recruitment to selected mRNA 3' UTRs. Involved in degradation of AU-rich element (ARE)-containing mRNAs probably via association with ZFP36. Mediates the recruitment of the CCR4-NOT complex to miRNA targets and to the RISC complex via association with TNRC6A, TNRC6B or TNRC6C. Acts as a transcriptional repressor. Represses the ligand-dependent transcriptional activation by nuclear receptors. Involved in the maintenance of embryonic stem (ES) cell identity; prevents their differentiation towards extraembryonic trophectoderm lineages.[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) has an additional in-frame exon in the 3' coding region, compared to variant 1. It encodes isoform 2, which is longer than isoform 1. 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.