

Product datasheet for MC226638

Nudt7 (NM_001290181) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Nudt7 (NM_001290181) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Nudt7
Synonyms:	1300007B24Rik; 2210404C19Rik
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC226638 representing NM_001290181 Red=Cloning site Blue=ORF Orange=Stop codon

TTTGTAAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**CGATCGC**C

ATGGTACAGTCCCTTGAGCTGCCACAGAGGCAACCTTGTCACCTTTGGAAGTTGGATCAAGCGCTCACCT
CGGGCCTCACCTCAAAGTCACCGAGTCAGGTTTGGGAAACAATCTGATAGATGATGCCAAGGCTCGCT
GAGAAAGTCTGATGTCGGGACCAGATATTCTCACCTGCTCTAATAAATTCTGTCTTGTACCACTG
CTGGCCAGAGGAGGAAAGTTGTATTTGATGTTACGGTCCGCTCAGACAAGCTGAAAAGGGAACCTGGAG
AAGTCTGCTTCCCTGGAGGAAAGAGGGACCCGGTGGACACAGATGACACAGCCACTGCTCTCCGTGAAGC
CCAGGAGGAGGTGGGGCTGCATCCCCACCAAGTGAGGTGGTCTCTCACCTGGTGCCATACGTATTTGAT
AATGATGCACTGGTAACCCCGTAGTGGGTTTTCTAGACCACAACCTCCAGGCCAACCTAATGCTGATG
AAGTGAAGGAAGTCTTCTTTGTGCCTTTGGACTATTTCTCCATCCCCAAGTCTACTACCAGAAGCAAAT
CACACAGTCTGGCCGTGATTTTCATGTCATTGCTTCGAGTACAAAGACCCTGAGACTGGTGTGAACCTAC
CTAATCCAGGGAATGACCTCAAAGTGGCTGTGTTGGTGGCCTTAATTATTTTGGAAACAAAGTCTGCCT
TCAAGATTGATTTTGATCTCCATGACCTGATACCGTCTTGTAAGGACCTTCTTTGGAGATATTCTTT
AAGCAAGTT**GA**

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:	SgfI-MluI
ACCN:	NM_001290181
Insert Size:	783 bp



[View online »](#)

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_001290181.1, NP_001277110.1</u>
RefSeq Size:	2839 bp
RefSeq ORF:	783 bp
Locus ID:	67528
UniProt ID:	<u>Q99P30</u>
Cytogenetics:	8 E1
Gene Summary:	<p>Coenzyme A diphosphatase which mediates the cleavage of CoA, CoA esters and oxidized CoA with similar efficiencies, yielding 3',5'-ADP and the corresponding 4'-phosphopantetheine derivative as products. CoA into 3',5'-ADP and 4'-phosphopantetheine. Has no activity toward NDP-sugars, CDP-alcohols, (deoxy)nucleoside 5'-triphosphates, nucleoside 5'-di or monophosphates, diadenosine polyphosphates, NAD, NADH, NADP, NADPH or thymidine-5'-monophospho-p-nitrophenyl ester. May be required to eliminate oxidized CoA from peroxisomes, or regulate CoA and acyl-CoA levels in this organelle in response to metabolic demand. Does not play a role in U8 snoRNA decapping activity. Binds U8 snoRNA.</p> <p>[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (4) contains an alternate 5' terminal exon, and it thus differs in the 5' UTR and initiates translation at an alternate start codon, compared to variant 1. The encoded isoform (4) has a distinct N-terminus and is longer than 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>