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Product datasheet for SC328248

NUDT16 (NM_001171905) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	NUDT16 (NM_001171905) Human Untagged Clone
Tag:	Tag Free
Symbol:	NUDT16
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC328248 representing NM_001171905. Blue=Insert sequence Red=Cloning site Green=Tag(s) GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGCAGATGCGCTTCGATGGACGCCTGGGCTTCCCCGGCGGATTCGTGGACACGCAGGACAGAAGCCTA GAGGACGGGCTGAACCGCGAGCTGCGCGAGGAGCTGGGCGAAGCGGCTGCCGCTTTCCGCGTGGAGCGC ACTGACTACCGCAGCTCCCACGTCGGGTCAGGGCCACGCGTTGTGGCCCACTTCTATGCCAAGCGTCTG ACGCTCGAGGAGCTGTTGGCTGTGGAGGCCGGCGCAACACGCGCCAAGGACCACGGGCTGGAGGTGCTG GGCCTGGTGCGAGTGCCCCTGTATACCCTGCGGGATGGTGTAGGAGGCCTGCCTACCTTCCTGGAGAAT TCCTTTATTGGCTCTGCGCGGGAGCAGTTACTTGAAGCAGCCCTCCATGGACCCATGAAAACTGAGATG AGGACCTTGGTACTAGGGAGGGAGGGAAGGACGTGGGAATGTTTTCTTATTGGATCTGAGAGATGA AGCGGACCGACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGAT ATCCTGGATTACAAGGATGACGACGATAAGGTTTAA
Restriction Sites:	SgfI-RsrII

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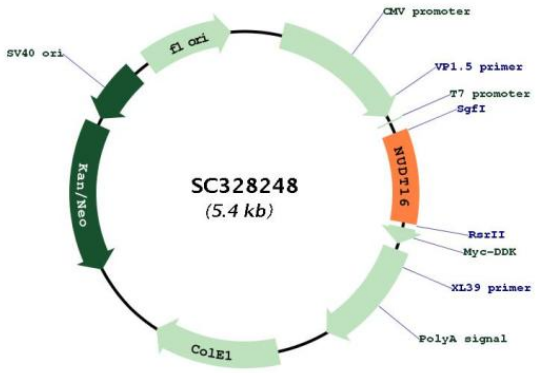
Plasmid Map:



ACCN:	NM_001171905
Insert Size:	480 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_001171905.1
RefSeq Size:	5943 bp
RefSeq ORF:	480 bp
Locus ID:	131870
UniProt ID:	Q96DE0
Cytogenetics:	3q22.1
MW:	17.7 kDa
Gene Summary:	RNA-binding and decapping enzyme that catalyzes the cleavage of the cap structure of snoRNAs and mRNAs in a metal-dependent manner. Part of the U8 snoRNP complex that is required for the accumulation of mature 5.8S and 28S rRNA. Has diphosphatase activity and removes m7G and/or m227G caps from U8 snoRNA and leaves a 5'monophosphate on the RNA. Catalyzes also the cleavage of the cap structure on mRNAs. Does not hydrolyze cap analog structures like 7-methylguanosine nucleoside triphosphate (m7GpppG). Also hydrolysis m7G- and m227G U3-capped RNAs but with less efficiencies. Has broad substrate specificity with manganese or cobalt as cofactor and can act on various RNA species. Binds to the U8 snoRNA; metal is not required for RNA-binding. May play a role in the regulation of snoRNAs and mRNAs degradation. Acts also as a phosphatase; hydrolyzes the non-canonical purine nucleotides inosine diphosphate (IDP) and deoxyinosine diphosphate (dITP) as well as guanosine diphosphate (GDP), deoxyguanosine diphosphate (dGDP), xanthine diphosphate (XDP), inosine triphosphate (ITP) and deoxyinosine triphosphate (ITP) to their respective monophosphate derivatives and does not distinguish between the deoxy- and ribose forms (PubMed:20385596, PubMed:26121039). The order of activity with different substrates is IDP > dIDP >> GDP = dGDP > XDP = ITP = dITP (PubMed:20385596). Binds strongly to GTP, ITP and XTP. Participates in the hydrolysis of dIDP/IDP and probably excludes non-canonical purines from RNA and DNA precursor pools, thus preventing their incorporation into RNA and DNA and avoiding chromosomal lesions (PubMed:20385596).[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (3) has multiple differences, compared to variant 1. The encoded isoform (3) is shorter at the N-terminus and has a distinct C-terminus, 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.