

Product datasheet for MC210622

N6amt1 (NM_026366) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: N6amt1 (NM_026366) Mouse Untagged Clone

Tag: Tag Free Symbol: N6amt1

Synonyms: 5830445C04Rik; Hemk2; Pred28

Vector:pCMV6-Entry (PS100001)E. coli Selection:Kanamycin (25 ug/mL)

Cell Selection: Neomycin

Fully Sequenced ORF: >MC210622 representing NM_026366

Red=Cloning site Blue=ORF Orange=Stop codon

 ${\tt TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCCC}$

GCCGCGATCGCC

ATGGCGGCGCCGAGTGTCCCCACGCCGTTGTACGGGCACGTGGGTCGCGGAGCCTTCCGCGACGTGTACG
AGCCAGCGGAGGACACGTTCCTGTTACTGGACGCGCTCGAGGCGGCGGCGGCGCGACGCTAGCAGGAGTGGA
AATATGCCTTGAAGTAGGAGCAGGATCTGGTGTGTGTGTCTCCCATTCCTGGCCTCCATGATAGGTCCTCGG
GCCTTATACATGTGCACTGATATCAACCCTGAGGCAGCCGCATGTACCTTGGAAACAGCACGCTGTAACA
GAGTCCATGTTCAGCCAGTGATCACAGATTTGGTGCACGGCTTGCTGCCCAGACTGAAGGGGAAAGTAGA
CCTGCTGGTGTTTAACCCCCCCTATGTAGTGACTCCGCCTGAAGAGGTAGGAAGTCGTGGAATAGAAGCA
GCCTGGGCTGGCGGCAGAAACGGCCGGGAAGTCATGGACAGGTTCTTCCCACTGGCTCCAGAACTCCTCT
CCCCAAGAGGGCTGTTCTACTTAGTTACCGTAAAAGAAAACAATCCCGAGGAAATCTTTAAAACAATGAA
GACAAGAGGTCTGCAAGGGACCACAGCACTTTGCAGGCAAGCAGGCCAAGAAGCCCTGTCAGTCCTCAGG
TTCAGCAAGTCCTAG

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT

ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: Sgfl-Mlul ACCN: NM_026366

Insert Size: 645 bp



OriGene Technologies, Inc. 9620 Medical Center Drive, Ste 200

CN: techsupport@origene.cn

Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com



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: <u>NM 026366.2</u>, <u>NP 080642.1</u>

RefSeq Size: 1791 bp
RefSeq ORF: 645 bp
Locus ID: 67768
UniProt ID: Q6SKR2
Cytogenetics: 16 C3.3

Gene Summary:

Methyltransferase that can methylate both proteins and DNA, and to a lower extent, arsenic (PubMed:20606008, PubMed:26797129). Catalytic subunit of a heterodimer with TRMT112, which catalyzes N5-methylation of Glu residue of proteins with a Gly-Gln-Xaa-Xaa-Arg motif (PubMed:26797129). Methylates ETF1 on 'Gln-185'; ETF1 needs to be complexed to ERF3 in its GTP-bound form to be efficiently methylated (PubMed:20606008, PubMed:26797129). Also acts as a N(6)-adenine-specific DNA methyltransferase by mediating methylation of DNA on the 6th position of adenine (N(6)-methyladenosine) (By similarity). N(6)-methyladenosine (m6A) DNA is significantly enriched in exonic regions and is associated with gene transcriptional activation (By similarity). May also play a role in the modulation of arsenicinduced toxicity by mediating the conversion of monomethylarsonous acid (3+) into the less toxic dimethylarsonic acid (By similarity). It however only plays a limited role in arsenic metabolism compared with AS3MT (By similarity),[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (1) represents the longer transcript and encodes the longer 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.