

Product datasheet for SC321115

HNMT (NM_006895) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: HNMT (NM_006895) Human Untagged Clone

Tag: Tag Free
Symbol: HNMT

Synonyms: HMT; HNMT-S1; HNMT-S2; MRT51

Mammalian Cell

Selection:

Neomycin

Vector:pCMV6-AC (PS100020)E. coli Selection:Ampicillin (100 ug/mL)

Fully Sequenced ORF: >OriGene sequence for NM_006895.2

GAGAAAACCAAATATGGCATCTTCCATGAGGAGCTTGTTTTCTGACCACGGGAAATATGT GGACAAGAAGCTGCCAGGCATAATAGGAAGGATTGGAGACACAAAATCAGAAATTAAGAT TCTAAGCATAGGCGGAGGTGCAGGTGAAATTGATCTTCAAATTCTCTCCAAAGTTCAGGC TCAATACCCAGGAGTTTGTATCAACAATGAAGTTGTTGAGCCAAGTGCTGAACAAATTGC CAAATACAAAGAGCTTGTAGCCAAGACATCGAACCTCGAGAACGTAAAGTTTGCTTGGCA TAAGGAGACATCATCTGAATACCAAAGTAGAATGTTGGAGAAAAAGGAGCTTCAAAAGTG GGACTTTATTCATATGATTCAAATGCTGTATTATGTAAAAGACATCCCAGCTACCCTGAA ATTCTTCCATAGTCTCTTAGGTACCAATGCTAAGATGCTCATTATTGTTGTGTCAGGAAG CAGTGGCTGGGACAAGCTGTGGAAAAAGTACGGATCACGCTTTCCCCAGGATGACCTCTG CCAGTATATCACATCAGATGACCTCACTCAGATGCTGGACAACCTAGGGCTTAAGTATGA GTGCTATGACCTTTTGTCCACCATGGATATATCTGACTGCTTTATTGATGGTGATGAAAA TGGAGACCTGCTTTGGGATTTTTTGACTGAAACCTGCAACTTTAATGCCACAGCACCACC GGGGAAGGTTCTTTTTAATAATACTCTGAGTTTCATAGTGATTGAGGCATAACTATCAAT TTAAAATCACAAACTCATCCATTAATGTAGATAAAGCACTGTTTGGATATGAGATGTAGC AAATTCCAATACATTATTGGACTTCCATTTGGAATCATATGGGATACTGCTGGTCTTATC CTGTCCCTCCAGGTAGAGAGACCACAAGCAGGCTCAACATAACATAAGCTAGAAAAA TGAAATTTTCTAGAATACTAATAAAATACATACTATAGATTCTTTATTAGTGAAGTATGC ACTAATCAATACTTTGAACACAAAGCCTGTGTTACTGATTTGGCCGTTTTGTGAAGAAAC ATTTATCTTTGTACGTTCTTCTATTGTGCTTTCTATCTAATTTTTATTAATTTGTAAGAG AA

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Restriction Sites: Please inquire

ACCN: NM_006895

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 006895.2, NP 008826.1

 RefSeq Size:
 3373 bp

 RefSeq ORF:
 879 bp

 Locus ID:
 3176

 UniProt ID:
 P50135

 Cytogenetics:
 2q22.1

Protein Families: Druggable Genome

Protein Pathways: Histidine metabolism



Gene Summary:

In mammals, histamine is metabolized by two major pathways: N(tau)-methylation via histamine N-methyltransferase and oxidative deamination via diamine oxidase. This gene encodes the first enzyme which is found in the cytosol and uses S-adenosyl-L-methionine as the methyl donor. In the mammalian brain, the neurotransmitter activity of histamine is controlled by N(tau)-methylation as diamine oxidase is not found in the central nervous system. A common genetic polymorphism affects the activity levels of this gene product in red blood cells. Multiple alternatively spliced transcript variants that encode different proteins have been found for this gene. [provided by RefSeq, Jul 2008]

Transcript Variant: This variant (1) represents the longest transcript and it encodes the longest protein (isoform 1). Sequence Note: The RefSeq transcript and protein were derived from transcript and genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.