

Product datasheet for **MC228045**

Nmt2 (NM_001290370) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Nmt2 (NM_001290370) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Nmt2
Synonyms:	A930001K02Rik; AI605445; AU044698; hNMT-2
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin



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Fully Sequenced ORF: >MC228045 representing NM_001290370
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGATCGCC**

ATGGCGGAGGACAGCGAGTCTGCGGCCAGCCAGCAGACCTAGAGCTGGACGACCAGGACACGTGCGGAA
 TAGACGGAGACAATGAGGAGGAGACCGAACACGCCAAAGGAAGCCCTGGAGGGGATTTGGGAGCAAAAA
 GAAAAAGAAAGAAAACAAAAGAGAAAAAAGGAGAAGCCAAATTCTGGGGGTACCAAGTCCGACTCTGCATCT
 GACTCCCAGGAGATTAAGATTTCAGCAGTCTTCTAAAAATCCCACCATCCCTATTCAGAAGCTACAAGACA
 TCCAGAGAGCAATGGAGCTGCTGTCTGCATGCCAAGGCCAGCCAGGAACATTGATGAGGCCACAAAACG
 CAGATACCAGTTTTGGGACACACAGCCAGTGCCCAAATGAATGAAGTCATAACATCTCATGGTGAATT
 GAACCAGACAAAGACAATATCCGCCAGGAACCATATTCTTTGCCGAAGGTTTTATGTGGGACACTTTAG
 ACTTGAGTAATGCCGAAGTGCTGAAGGAGCTGTATACGTTGCTGAATGAGAATTATGTGGAAGACGATGA
 CAATATGTTCCGCTTTGACTATTCACTGAGTTTCTGCTGTGGGCTCTGCSCCCCCAGGATGGCTTCTG
 CAGTGGCACTGTGGAGTCCGAGTGTCTTCAAATAAAAAGTTAGTAGGTTTCATAAGTGCCATTCCAGCAA
 ACATCCGAATTTATGATAGTGTGAAGAGGATGGTAGAAATCAACTTTCTTTGTGTCCATAAGAACTGAG
 ATCAAAACGGGTAGCCCCAGTGTGATTCGAGAAATAACCAGAAGAGTGAACCTGGAAGGCATCTTTCAG
 GCTGTGTATACTGCGGGAGTAGTTCTTCTTAAGCCTGTGGCCACTTGACAGTATTGGCACCAGTCCCTAA
 ACCCCAGGAACTGGTGGAAAGTGAATTTTCTCACCTGAGTAGAAACATGACCTTACAGAGAACGATGAA
 GCTTTACAGACTTCCAGATGTTACAAAGACTTCAGGTTTGAGACCAATGGAACAAAAGACATCAAAGCA
 GTCCGAGAGCTAATCAACATCTACTTGAAGCAGTTTCTACTAGCTCCAGTATGGATGACGCAGAAGTGG
 CCCACTGGTTCCTGCCAGGGAGCACATCATTGACACGTTTGTAGTGGAGAACCCAGTGGGAAGCTGAC
 TGACTTCTGAGCTTCTACACTCTCCCCTCCACGGTTATGCACCACCAGCTCACAAAAGCCTCAAGGCT
 GCCTATTCCTTCTACAACATTCACACAGAGACACCCCTGCTGGACCTCATGAATGATGCGCTCATTATAG
 CCAAAATTGAAAGGATTTGATGTGTTCAATGCACTAGATTTGATGGAAAATAAGACCTTCTTGAAAAA
 AAAGTTTGGTATAGGAGATGGCAACTTACAGTATTATTTGTACAACCTGGAGGTGTCCAGGGACAGACTCT
 GAAAAGGTTGGACTTGTCTACAG**TAG**

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

- Restriction Sites:** Sgfl-Mlul
- ACCN:** NM_001290370
- Insert Size:** 1497 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:** 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.
RefSeq:	<u>NM_001290370.1</u> , <u>NP_001277299.1</u>
RefSeq Size:	4368 bp
RefSeq ORF:	1497 bp
Locus ID:	18108
Cytogenetics:	2 A1
Gene Summary:	<p>Adds a myristoyl group to the N-terminal glycine residue of certain cellular and viral proteins. [UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (4) lacks two alternate exons that result in the loss of an in-frame segment in the 5' coding region, compared to variant 1. The encoded isoform (d) is shorter than isoform a. 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>