

Product datasheet for **MC216505**

Samd8 (NM_026283) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Samd8 (NM_026283) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Samd8
Synonyms:	1110053F04Rik; 1700010P07Rik; SMSr
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin



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Fully Sequenced ORF: >MC216505 representing NM_026283
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**GCGATCGCC**

ATGCCCGTGGTAGCCGAGCCGGCTCCCGCTGCGCTCCGGCTCCCTCCCCGGCCTTCGGTCTGACTC
 TCAAGGCGCTGCGCCCCGCTACGCGCCGAGGACCCCGACTCCAACGGCGACTTAGACACCGGCTCCGA
 GCTGGGTCCCGGAGCCCGGCTCCACCCGCGGAGGAAGTAGAGAAAGAAATGGCAGGTCCTAGTCAACTC
 TGCATTGCGCGTGGACTACCAAGCATGTGGCTGTGTGGCTGAAGGACGAAGTTTCTTTGAGTATGTGG
 ACATTTTATGCAACAAGCACCGCCTTGATGGAATCACATTGCTCACGCTGACTGAATATGATCTCCGCTC
 TCCTCCTCTGGAAATCAAAGTCTAGGAGACATTAACCGTTAATGCTCTCAGTCCGAAAATTGCAGAAA
 ATACATACTGATTTTTGGAAGAGATGGGCTACAACAGTGACAGTCTATGAGTCCCAGTACTCCATTCC
 TTAGTGCTCTTCAGAGTGCAGACTGGCTCTGTAAACGGAGAGCCACACACAGCTGTGATGGGCCATCCC
 TGACTTGAGTTCTGATCAGTACCAGTACATGAATGGCAAAAACAACATTCTGCTCGAAGACTGGACCCA
 GAGTACTGGAAGACCATCCTGAGTTGTGTATATGTTTTATAGTATTTGGGTTTACGTCTTTCATTATGG
 TTATTGTTTCATGAGCGTGTGCCTGACATGCAGACCTACCCACCACTCCCAGATATATTCCTAGACAGTGT
 TCCTAGGATCCCGTGGGCTTCTCCATGACCGAAGTGTGTGGCGTGATTCTGTGCTACATTTGGATCCTG
 GTTCTTCTTCCACAAGCACAGGTCAATCCTTCTGCGAAGGCTCTGTAGTCTGATGGGCACTGTATTCT
 TGCTTCGCTGTTTACCATGTTTGTGACCTCCCTCTCCGTGCCAGGACAGCACCTGCAGTGTACTGGAAA
 GATATA TGAAGTGTGTGGGAGAACTACGACGGGCATTTGCCATCTGGAGCGGCTTTGGAATGACTCTG
 ACTGGCGTCCACACTTGTGGAGACTACATGTTCCAGTGGCCACACAGTTGTTCTAACCATGCTGAATTTCT
 TTGTCACAGAGTATACCAAGAAGCTGGAATTTCTTGCACACTCTATCCTGGTTCTCAACCTCTTGG
 AATCTTCTTCATCTTGGCTGCCCATGAACATTATCCATTGATGTGTTTATTGCCTTTTATACACAACA
 AGACTCTTTTTGTACTACCATACTCTGGCTAACCCAGAGCGTATCATCAGAGTAGGAGAGCGAGGATTT
 GGTTCCTATGTTTTCTTCTTGAATGCAATGTTAATGGCACAGTACCTAATGAATATTGTTGGCCATT
 TTCTAAACCAGCAATAATGAAAAGACTAATTGGATGA

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: Sgfl-MluI

ACCN: NM_026283

Insert Size: 1437 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).

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_026283.2](#), [NP_080559.1](#)

RefSeq Size: 6997 bp

RefSeq ORF: 1437 bp

Locus ID: 67630

UniProt ID: [Q9DA37](#)

Cytogenetics: 14 A3

Gene Summary: sphingomyelin synthases synthesize sphingolipids through transfer of a phosphatidyl head group on to the primary hydroxyl of ceramide. SAMD8 is an endoplasmic reticulum (ER) transferase that has no sphingomyelin synthase activity but can convert phosphatidylethanolamine (PE) and ceramide to ceramide phosphatidylethanolamine (CPE) albeit with low product yield. Appears to operate as a ceramide sensor to control ceramide homeostasis in the endoplasmic reticulum rather than a converter of ceramides. Seems to be critical for the integrity of the early secretory pathway (By similarity).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (1) encodes the longest 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.