

Product datasheet for MC208057

Snx12 (NM_018875) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: Snx12 (NM_018875) Mouse Untagged Clone

Tag: Tag Free Symbol: Snx12

Synonyms: 2610001F05Rik; AW045757; SDP8

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

Cell Selection: Neomycin

Fully Sequenced ORF: >MC208057 representing NM_018875

Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC

GCCGCGATCGCC

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT

ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: Sgfl-Mlul ACCN: NM_018875

Insert Size: 501 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).



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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 018875.2, NP 061363.2

RefSeq Size: 1000 bp
RefSeq ORF: 501 bp
Locus ID: 55988
UniProt ID: 070493
Cytogenetics: X D

Gene Summary: May be involved in several stages of intracellular trafficking.[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (3) differs in the 3' coding region and UTR, compared to variant 1. It encodes isoform 3 which has a longer, distinct C-terminus, compared to isoform 1. An inframe AUG is located 45 codons upstream of the annotated translation start site but is not being annotated as a start site since it is not conserved and is in a weak Kozak sequence

context.