Product datasheet for SC332866

C1orf2 (FAM189B) (NM_001267608) Human Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: C1orf2 (FAM189B) (NM_001267608) Human Untagged Clone
Tag: Tag Free
Symbol: FAM189B
Synonyms: C1orf2; COTE1
Vector: pCMV6 series
Fully Sequenced ORF: 

>NCBI ORF sequence for NM_001267608, the custom clone sequence may differ by one or more nucleotides

ATGATGCCCTGCCTAGTGACTCCAGCCGCTCGCTGACCAGCCGGCCCAGCACCAGGGGCCTTACCCACC
TCCGCCTCCACAGGACCCCTGGCTGACGGCCCTGGCTGACCAGCCGGCCCAGCACCAGGGGCCTTACCCACC
TCCGCCTCCACCGACCCTGGCTGCAGGCCCTGCTTACGCTGGGGCTGGTCCAAGTGCTCCTGGGCATCCT
GGTGGTCACCTTCAGCATGGTGGCCTCTTCCGTCACCACCACCGAGAGCATCAAGAGGTCCTGCCCGTCT
TGGGCTGGGTTCTGCTGCTATTGTCTGCTGATCAAATCTTCCCCCTGAGCATCTGCA

Restriction Sites:  

SgfI-MluI

ACCN:  

NM_001267608

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).

RefSeq:  

NM_001267608.1, NP_001254537.1

RefSeq Size:  

3154 bp

RefSeq ORF:  

1953 bp

Locus ID:  

10712

Cytogenetics:  

1q22

Protein Families:  

Transmembrane
Gene Summary: This gene is located near the gene for the lysosomal enzyme glucosylceramidase; a deficiency in this enzyme is associated with Gaucher disease. The encoded protein has been identified as a potential binding partner of a WW domain-containing protein which is involved in apoptosis and tumor suppression. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Dec 2010]

Transcript Variant: This variant (3) lacks an in-frame exon in the 5’ coding region, compared to variant 1. It encodes isoform c which is shorter than 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.