

Product datasheet for SC334840

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C12orf43 (NM_001286195) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: C12orf43 (NM_001286195) Human Untagged Clone

Tag: Tag Free Symbol: C12orf43

Synonyms: Custos

Mammalian Cell

Neomycin

Selection:

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

Fully Sequenced ORF: >NCBI ORF sequence for NM_001286195, the custom clone sequence may differ by one or

more nucleotides

Restriction Sites: Sgfl-Mlul

ACCN: NM 001286195

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: <u>NM 001286195.1</u>, <u>NP 001273124.1</u>

 RefSeq Size:
 2518 bp

 RefSeq ORF:
 759 bp

 Locus ID:
 64897

 UniProt ID:
 Q96C57

 Cytogenetics:
 12q24.31

Gene Summary: Plays a role in the regulation of Wnt signaling pathway during early development.

[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (4) uses alternate splice sites at three coding exons, but maintains the reading frame, 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.