

## **Product datasheet for SC331081**

## MFF (NM\_001277065) Human Untagged Clone

## **Product data:**

**Product Type:** Expression Plasmids

**Product Name:** MFF (NM\_001277065) Human Untagged Clone

Tag: Tag Free
Symbol: MFF

Synonyms: C2orf33; EMPF2; GL004

Vector: pCMV6-Entry (PS100001)

Fully Sequenced ORF: >SC331081 representing NM\_001277065.

Blue=Insert sequence Red=Cloning site Green=Tag(s)

TGGCTGCTTAATAGCTGGCTCTGGTTTCGCCGCTAG

**Restriction Sites:** Sgfl-Mlul

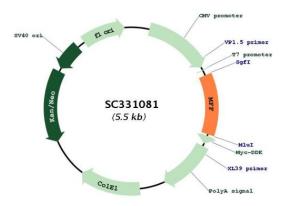
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## Plasmid Map:



**ACCN:** NM\_001277065

**Insert Size:** 657 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: <u>NM 001277065.1</u>

RefSeq Size: 1805 bp
RefSeq ORF: 657 bp
Locus ID: 56947
UniProt ID: Q9GZY8
Cytogenetics: 2q36.3

**Protein Families:** Transmembrane

MW: 25.1 kDa

**Gene Summary:** This is a nuclear gene encoding a protein that functions in mitochondrial and peroxisomal

fission. The encoded protein recruits dynamin-1-like protein (DNM1L) to mitochondria. There are multiple pseudogenes for this gene on chromosomes 1, 5, and X. Alternative splicing

results in multiple transcript variants. [provided by RefSeq, Mar 2013]

Transcript Variant: This variant (6) differs in the 5' UTR, lacks a portion of the 5' coding region

and an lacks three in-frame exons, compared to variant 1. It initiates translation at a downstream in-frame start codon. The encoded isoform (e) is shorter and has a shorter N-

terminus than isoform a. Both variants 6 and 7 encode the same isoform (e).