

Product datasheet for SC330782

ZNF706 (NM_001267709) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Tag: Tag Free

Symbol: ZNF706

Synonyms: HSPC038; PNAS-106; PNAS-113

Vector: pCMV6-Entry (PS100001)

Fully Sequenced ORF: >SC330782 representing NM_001267709.

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

GAATTAGCTGATGTTCAGGCATAA

Restriction Sites: Sgfl-Mlul

ACCN: NM_001267709

Insert Size: 231 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.



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Note: Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um

filter is required.

RefSeq: <u>NM_001267709.1</u>

RefSeq Size: 2668 bp

RefSeq ORF: 231 bp

Locus ID: 51123

UniProt ID: Q9Y5V0

Cytogenetics: 8q22.3

MW: 8.5 kDa

Gene Summary: Transcription repressor involved in the exit of embryonic stem cells (ESCs) from self-renewal.

Acts by repressing expression of KLF4.[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (5) differs in the 5' UTR compared to variant 1. Variants 1, 3, 4 and 5 encode the same protein. 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.