

## **Product datasheet for SC325832**

## TCF7 (NM\_001134851) Human Untagged Clone

**Product data:** 

**Product Type:** Expression Plasmids

Product Name: TCF7 (NM\_001134851) Human Untagged Clone

Tag: Tag Free Symbol: TCF7

Synonyms: TCF-1

Mammalian Cell Neomycin

Selection:

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

Fully Sequenced ORF: >SC325832 representing NM\_001134851.

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

GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC

GGTAATGGACAAGAGTCACTGTCCATGTCTTCTTCTTCTAGCCCAGCT<mark>TGA</mark>

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT

TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

**Restriction Sites:** Sgfl-Mlul



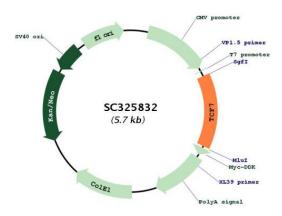
**OriGene Technologies, Inc.** 9620 Medical Center Drive, Ste 200

CN: techsupport@origene.cn

Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com



## Plasmid Map:



**ACCN:** NM\_001134851

**Insert Size:** 810 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).

**OTI Annotation:** This TrueClone is provided through our Custom Cloning Process that includes sub-cloning

into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

**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 001134851.2</u>

RefSeq Size: 3322 bp



## TCF7 (NM\_001134851) Human Untagged Clone - SC325832

 RefSeq ORF:
 810 bp

 Locus ID:
 6932

 UniProt ID:
 P36402

 Cytogenetics:
 5q31.1

**Protein Families:** Druggable Genome, ES Cell Differentiation/IPS, Transcription Factors

**Protein Pathways:** Acute myeloid leukemia, Adherens junction, Arrhythmogenic right ventricular

cardiomyopathy (ARVC), Basal cell carcinoma, Colorectal cancer, Endometrial cancer,

Melanogenesis, Pathways in cancer, Prostate cancer, Thyroid cancer, Wnt signaling pathway

MW: 30.3 kDa

**Gene Summary:** This gene encodes a member of the T-cell factor/lymphoid enhancer-binding factor family of

high mobility group (HMG) box transcriptional activators. This gene is expressed

predominantly in T-cells and plays a critical role in natural killer cell and innate lymphoid cell

development. The encoded protein forms a complex with beta-catenin and activates transcription through a Wnt/beta-catenin signaling pathway. Mice with a knockout of this gene are viable and fertile, but display a block in T-lymphocyte differentiation. Alternative splicing results in multiple transcript variants. Naturally-occurring isoforms lacking the N-terminal beta-catenin interaction domain may act as dominant negative regulators of Wnt

signaling. [provided by RefSeq, Oct 2016]

Transcript Variant: This variant (3, also known as A), differs in the 5' UTR, has multiple coding region differences, uses a downstream start codon, and differs in the 3' UTR, compared to variant 1. The resulting isoform (3) is shorter at the N-terminus and has a distinct C-terminus, compared to 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.