

Product datasheet for **SC308079**

TCF7 (NM_201632) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	TCF7 (NM_201632) Human Untagged Clone
Tag:	Tag Free
Symbol:	TCF7
Synonyms:	TCF-1
Vector:	<u>pCMV6 series</u>
Fully Sequenced ORF:	>NCBI ORF sequence for NM_201632, the custom clone sequence may differ by one or more nucleotides ATGTACAAAGAGACCGTCTACTCCGCCCTCAATCTGCTCATGCATTACCCACCCCTCG GGAGCAGGGCAGCACCCCGCCGCTGCACAAGGCAATCAGCCCCCAC GGTGTCCCCAACTCTCTCTCTACGAACATTTCAACAGCCACATCCCACCCCTGCACCT GCGGACATCAGCCAGAAGCAAGTTCACAGGCCTCTGCAGACCCCTGACCTCTCTGGCTTC TACTCCCTGACCTCAGGCAGCATGGGGCAGCTCCCCCACTGTGAGCTGGTTACCCAC CCATCCTTGATGCTAGGTTCTGGTGTACCTGGTCACCCAGCAGCCATCCCCACCCGGCC ATTGTGCCCCCTCAGGGAAGCAGGAGCTGCAGCCCTTCGACCGCAACCTGAAGACACAA GCAGAGTCCAAGGCAGAGAAGGAGGCCAAGAAGCCAACCATCAAGAAGCCCTCAATGCC TTCATGCTGTACATGAAGGAGATGAGAGCCAAGGTCATTGCAGAGTGCACACTTAAGGAG AGCGCTGCCATCAACCAGATCCTGGGCCGAGGTGGCACGCGCTGTCGCGAGAAGAGCAG GCCAAGTACTATGAGCTGGCCCGCAAGGAGAGGCGCTGCACATGCAGCTATACCCAGGC TGGTCAGCGCGGGACAACACGGGAAGAAGAAGAGGCGGTTCGAGGGAAAAGCACCACAGAA TCCACCACAGGAGGAAAAAGAAATGCATTTCGGTACTTACCCGGAGAAGGCCGCTGCCCA GCCCGTTCCTCCGATGACAGTGCTCTAG
Restriction Sites:	Please inquire
ACCN:	NM_201632
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).



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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: [NM_201632.1](#), [NP_963963.1](#)

RefSeq Size: 2821 bp

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

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 (2, also known as B), differs in the 5' UTR, has multiple coding region differences, and uses a downstream start codon, compared to variant 1. The resulting isoform (2) is shorter at the N-terminus, compared to isoform 1. Both variants 2 and 5 encode the same isoform. 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.