

Product datasheet for **SC334837**

TGIF (TGIF1) (NM_001278686) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	TGIF (TGIF1) (NM_001278686) Human Untagged Clone
Tag:	Tag Free
Symbol:	TGIF1
Synonyms:	HPE4; TGIF
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>NCBI ORF sequence for NM_001278686, the custom clone sequence may differ by one or more nucleotides

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ATGGACATTCCTTGGACCTTCTTCATCCGCTGGCTCAGGCAAGAGAAGGAGAAGGGGCAACCTACCCA  
AGGAGTCTGTGCAGATTCTCGGGATTGGCTGTATGAGCACCGTTACAATGCCTATCCTTCAGAGCAAGA  
AAAAGCGTTGCTGTCCCAGCAAACACACCTGTCTACGCTACAGGTCTGTAAGTGGTTCATCAACGCCCGC  
CGCAGGCTCCTCCTGACATGCTGAGAAAGGATGGCAAAGATCCAATCAGTTCACAATTTCCCGCCGTG  
GGGCAAGATTTCTGAAACGAGCTCTGTGGAGTCCGTGATGGGCATCAAAAATTTCATGCCAGCTCTAGA  
GGAGACCCATTTCAATCCTGTACAGCTGGGCCAAACCAACCTAGGGAGGCCACTGTCTCCTAAGCCG  
TCATCCCCGGGATCAGTTTTGGCTCGTCCATCAGTGATCTGCCATACCACTGTGACTGCATTGAAAGATG  
TCCCTTTCTCTCTGCCAGTCGGTCCGGTGTGGGACAAAACACAGATATACAGCAGATAGCGGCCAAAAA  
CTTCACAGACACCTCTCTCATGTACCCAGAGGACACTTGTAAATCTGGACCAAGTACGAATACACAGAGT  
GGTCTTTTCAACACTCCTCCCCCTACTCCACCGGACCTCAACCAGGACTTCAGTGGATTTTCAGCTTCTAG  
TGGATGTTGCACTCAAACGGGCTGCAGAGATGGAGCTTCAGGCAAACTTACAGCTTAA
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Restriction Sites:	Sgfl-MluI
ACCN:	NM_001278686
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:	<ol style="list-style-type: none">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_001278686.1</u> , <u>NP_001265615.1</u>
RefSeq Size:	1553 bp
RefSeq ORF:	759 bp
Locus ID:	7050
UniProt ID:	<u>Q15583</u>
Cytogenetics:	18p11.31
Protein Families:	Druggable Genome, Stem cell - Pluripotency, Stem cell relevant signaling - TGFb/BMP signaling pathway, Transcription Factors
Gene Summary:	<p>The protein encoded by this gene is a member of the three-amino acid loop extension (TALE) superclass of atypical homeodomains. TALE homeobox proteins are highly conserved transcription regulators. This particular homeodomain binds to a previously characterized retinoid X receptor responsive element from the cellular retinol-binding protein II promoter. In addition to its role in inhibiting 9-cis-retinoic acid-dependent RXR alpha transcription activation of the retinoic acid responsive element, the protein is an active transcriptional co-repressor of SMAD2 and may participate in the transmission of nuclear signals during development and in the adult. Mutations in this gene are associated with holoprosencephaly type 4, which is a structural anomaly of the brain. Alternative splicing has been observed at this locus and multiple splice variants encoding distinct isoforms are described. [provided by RefSeq, Jul 2013]</p> <p>Transcript Variant: This variant (11) includes two alternate 5' exons, which result in a different 5' UTR and a downstream translation start codon, compared to variant 1. The resulting isoform (d) has a shorter N-terminus, compared to isoform a. Variants 5, 6, 7, 8, and 11 encode the same isoform d. 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.</p>