

Product datasheet for **SC324751**

TAF12 (NM_001135218) Human Untagged Clone

Product data:

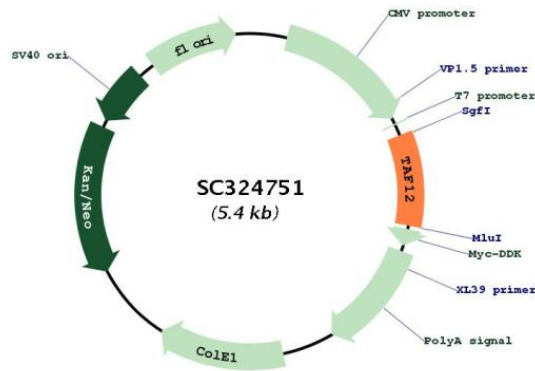
Product Type:	Expression Plasmids
Product Name:	TAF12 (NM_001135218) Human Untagged Clone
Tag:	Tag Free
Symbol:	TAF12
Synonyms:	TAF2J; TAFII20
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC324751 representing NM_001135218. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGAACCAGTTTGGCCCTCAGCCCTAATCAACCTCTCCAATTTCTCATCCATAAAACGGAAACCAGCC
AGCACCCCTCCACAAGGCTCCATGGCCAATAGTACTGCAGTGGTAAAGATACCAGGCACTCCTGGGGCA
GGAGGTCGCTTAGCCCTGAAAACAATCAGGTATTGACCAAGAAGAAATTACAGGACTTAGTAAGAGAA
GTGGATCCTAATGAGCAGTTGGATGAAGATGTGGAGGAGATGCTGCTGCAGATTGCTGATGATTTTATC
GAGAGTGTGGTGACAGCAGCCTGTCAGCTTGC CGGCATCGCAAGTCTAGCACCTGGAGGTGAAAGAT
GTCCAGCTGCATTTAGAGCGCCAGTGGACATGTGGATCCAGGATTTGGCTCTGAAGAAATCCGACCC
TACAAAAAAGCTTGCACCACAGAAGCTCACAACAGAGAATGGCATTGATCCGAAAAACAACCAAGAAA
TAA
ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGCC
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Restriction Sites: Sgfl-MluI



[View online »](#)

Plasmid Map:


ACCN:	NM_001135218
Insert Size:	486 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: [NM_001135218.1](#)

RefSeq Size: 1466 bp

RefSeq ORF: 486 bp

Locus ID: 6883

UniProt ID: [Q16514](#)

Cytogenetics: 1p35.3

Protein Families: Transcription Factors

Protein Pathways: Basal transcription factors

MW: 17.9 kDa

Gene Summary: Control of transcription by RNA polymerase II involves the basal transcription machinery which is a collection of proteins. These proteins with RNA polymerase II, assemble into complexes which are modulated by transactivator proteins that bind to cis-regulatory elements located adjacent to the transcription start site. Some modulators interact directly with the basal complex, whereas others may act as bridging proteins linking transactivators to the basal transcription factors. Some of these associated factors are weakly attached while others are tightly associated with TBP in the TFIID complex. Among the latter are the TAF proteins. Different TAFs are predicted to mediate the function of distinct transcriptional activators for a variety of gene promoters and RNA polymerases. TAF12 interacts directly with TBP as well as with TAF2I. Two transcript variants encoding the same protein have been found for this gene. [provided by RefSeq, Sep 2008]

Transcript Variant: This variant (1) represents the longer transcript. Variants 1 and 2 both 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.