

Product datasheet for SC207413

GTF2H2 (NM_001515) Human 3' UTR Clone

Product data:

OriGene Technologies, Inc.

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Product Type:	3' UTR Clones
Product Name:	GTF2H2 (NM_001515) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	GTF2H2
Synonyms:	BTF2; BTF2 p44; BTF2P44; p44; T-BTF2P44; TFIIH
ACCN:	NM_001515
Insert Size:	360 bp
Insert Sequence:	>SC207413 3'UTR clone of NM_001515 The sequence shown below is from the reference sequence of NM_001515. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site
	GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAA <mark>GCGATCGCC</mark> CATAAGATTCCAGCTCCTTCAGGTGTTTGATTCCAGCATGTAGTATACATTGTATGTGTTAAAAAGAAA TTTGCAACTGTGAATAAAAGGACTTCTTTAGAAGAAGCTTCATTTAAAACATGAAAGGATAATCTGACT TAAGAAACTTTTTGCTAAGAAAAGGTAATATTTTATTAAAATTTTAAATTTGTGTTGT
Restriction Sites:	Sgfl-Mlul
OTI Disclaimer:	Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).
Components:	The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.
RefSeq:	<u>NM 001515.4</u>



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	GTF2H2 (NM_001515) Human 3' UTR Clone – SC207413
Summary:	This gene is part of a 500 kb inverted duplication on chromosome 5q13. This duplicated region contains at least four genes and repetitive elements which make it prone to rearrangements and deletions. The repetitiveness and complexity of the sequence have also caused difficulty in determining the organization of this genomic region. This gene is within the telomeric copy of the duplication. Deletion of this gene sometimes accompanies deletion of the neighboring SMN1 gene in spinal muscular atrophy (SMA) patients but it is unclear if deletion of this gene contributes to the SMA phenotype. This gene encodes the 44 kDa subunit of RNA polymerase II transcription initiation factor IIH which is involved in basal transcription and nucleotide excision repair. Transcript variants for this gene have been described, but their full length nature has not been determined. A second copy of this gene within the centromeric copy of the duplication has been described in the literature. It is reported to be different by either two or four base pairs; however, no sequence data is currently available for the centromeric copy of the gene. [provided by RefSeq, Jul 2008]
Locus ID:	2966
MW:	14

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