

## **Product datasheet for SC203945**

## FBXO7 (NM 012179) Human 3' UTR Clone

**Product data:** 

**Product Type:** 3' UTR Clones

**Product Name:** FBXO7 (NM\_012179) Human 3' UTR Clone

Symbol: FBXO7

**Synonyms:** FBX; FBX07; FBX7; PARK15; PKPS

Mammalian Cell

Selection:

Neomycin

**Vector:** pMirTarget (PS100062)

**ACCN:** NM\_012179

**Insert Size:** 329 bp

Insert Sequence: >SC203945 3'UTR clone of NM\_012179

The sequence shown below is from the reference sequence of NM\_012179. The complete

sequence of this clone may contain minor differences, such as SNPs.

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

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 012179.4</u>



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**Summary:** 

This gene encodes a member of the F-box protein family which is characterized by an approximately 40 amino acid motif, the F-box. The F-box proteins constitute one of the four subunits of the ubiquitin protein ligase complex called SCFs (SKP1-cullin-F-box), which function in phosphorylation-dependent ubiquitination. The F-box proteins are divided into 3 classes: Fbws containing WD-40 domains, Fbls containing leucine-rich repeats, and Fbxs containing either different protein-protein interaction modules or no recognizable motifs. The protein encoded by this gene belongs to the Fbxs class and it may play a role in regulation of hematopoiesis. Alternatively spliced transcript variants of this gene have been identified with the full-length natures of only some variants being determined. [provided by RefSeq, Jul 2008]

**Locus ID:** 25793 **MW:** 12.2