

Product datasheet for RC203594L4V

OriGene Technologies, Inc.

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FBXO7 (NM_012179) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type: Lentiviral Particles

Product Name: FBXO7 (NM_012179) Human Tagged ORF Clone Lentiviral Particle

Symbol: FBXO7

Synonyms: FBX; FBX07; FBX7; PARK15; PKPS

Mammalian Cell

Selection:

Puromycin

Vector: pLenti-C-mGFP-P2A-Puro (PS100093)

Tag: mGFP

ACCN: NM_012179 **ORF Size:** 1566 bp

ORF Nucleotide

The ORF insert of this clone is exactly the same as(RC203594).

Sequence:

Domains:

OTI Disclaimer:

The molecular sequence of this clone aligns with the gene accession number as a point of reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing

variants is recommended prior to use. More info

OTI Annotation: This clone was engineered to express the complete ORF with an expression tag. Expression

varies depending on the nature of the gene.

RefSeg: NM 012179.3

 RefSeq Size:
 2153 bp

 RefSeq ORF:
 1569 bp

 Locus ID:
 25793

 UniProt ID:
 Q9Y3I1

 Cytogenetics:
 22q12.3

Protein Families: Druggable Genome

F-box





ORIGENE

MW: 58.5 kDa

Gene 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]