

Product datasheet for SC205660

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FE65 (APBB1) (NM_001164) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: FE65 (APBB1) (NM_001164) Human 3' UTR Clone

Symbol: FE65

Synonyms: FE65; MGC:9072; RIR

Mammalian Cell

Selection:

Neomycin

Vector: pMirTarget (PS100062)

ACCN: NM_001164

Insert Size: 439 bp

The sequence shown below is from the reference sequence of NM_001164. The complete

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

CACTAATAAAGTCTGTCTGCACTGC

ACGCGTAAGCGGCCGCGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA

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 001164.5</u>

Summary: The protein encoded by this gene is a member of the Fe65 protein family. It is an adaptor

protein localized in the nucleus. It interacts with the Alzheimer's disease amyloid precursor protein (APP), transcription factor CP2/LSF/LBP1 and the low-density lipoprotein receptor-related protein. APP functions as a cytosolic anchoring site that can prevent the gene product's nuclear translocation. This encoded protein could play an important role in the pathogenesis of Alzheimer's disease. It is thought to regulate transcription. Also it is observed to block cell cycle progression by downregulating thymidylate synthase expression. Multiple alternatively spliced transcript variants encoding different isoforms have been described for

this gene. [provided by RefSeq, Mar 2012]

Locus ID: 322 MW: 16.5