

Product datasheet for SC202408

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CDK5 (NM_001164410) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: CDK5 (NM_001164410) Human 3' UTR Clone

Vector: pMirTarget (PS100062)

Symbol: CDK5

Synonyms: LIS7; PSSALRE ACCN: NM 001164410

Insert Size: 224 bp

Insert Sequence: >SC202408 3'UTR clone of NM_001164410

The sequence shown below is from the reference sequence of NM_001164410. The complete

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

TTGGCTCCTTTCCCACA

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 001164410.3</u>







Summary:

This gene encodes a proline-directed serine/threonine kinase that is a member of the cyclin-dependent kinase family of proteins. Unlike other members of the family, the protein encoded by this gene does not directly control cell cycle regulation. Instead the protein, which is predominantly expressed at high levels in mammalian postmitotic central nervous system neurons, functions in diverse processes such as synaptic plasticity and neuronal migration through phosphorylation of proteins required for cytoskeletal organization, endocytosis and exocytosis, and apoptosis. In humans, an allelic variant of the gene that results in undetectable levels of the protein has been associated with lethal autosomal recessive lissencephaly-7. Alternative splicing results in multiple transcript variants. [provided by RefSeq, May 2015]

Locus ID: 1020

MW: 7.7