

## **Product datasheet for SC210133**

## PRDM8 (NM\_001099403) Human 3' UTR Clone

**Product data:** 

Product Type: 3' UTR Clones

Symbol: PRDM8

**Synonyms:** EPM10; KMT8D; PFM5

Mammalian Cell Neomycin

Selection:

Vector: pMirTarget (PS100062)

**ACCN:** NM\_001099403

Insert Size: 827 bp

Insert Sequence: >SC210133 3'UTR clone of NM\_001099403

The sequence shown below is from the reference sequence of NM\_001099403. The complete sequence

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCCGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

Restriction Sites: Sgfl-Mlul



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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.

Note: Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um

filter is required.

**RefSeq:** <u>NM\_001099403.2</u>

Summary: This gene encodes a protein that belongs to a conserved family of histone methyltransferases

that predominantly act as negative regulators of transcription. The encoded protein contains an N-terminal Su(var)3-9, Enhancer-of-zeste, and Trithorax (SET) domain and a double zinc-finger domain. Knockout of this gene in mouse results in mistargeting by neurons of the dorsal telencephalon, abnormal itch-like behavior, and impaired differentiation of rod bipolar cells. In

humans, the protein has been shown to interact with the phosphatase laforin and the ubiquitin ligase malin, which regulate glycogen construction in the cytoplasm. Alternative

splicing results in multiple transcript variants. [provided by RefSeq, Feb 2016]

**Locus ID:** 56978

MW: 32