

Product datasheet for SC205381

WDR45 (NM_001029896) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Symbol: WDR45

Synonyms: JM5; NBIA4; NBIA5; WDRX1; WIPI-4; WIPI4

Mammalian Cell Neomycin

Selection:

Vector: pMirTarget (PS100062)

ACCN: NM_001029896

Insert Size: 391 bp

Insert Sequence: >SC205381 3'UTR clone of NM_001029896

The sequence shown below is from the reference sequence of NM_001029896. The complete sequence

of this clone may contain minor differences, such as $\ensuremath{\mathsf{SNPs}}\xspace.$

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

GATGATCTCCGATGTGATGAATACGAATAAAAGGCCCTTAATGGCA

CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGG

Restriction Sites: Sgfl-Mlul

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).



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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_001029896.2</u>

Summary: This gene encodes a member of the WD repeat protein family. WD repeats are minimally

conserved regions of approximately 40 amino acids typically bracketed by gly-his and trp-asp (GH-WD), which may facilitate formation of heterotrimeric or multiprotein complexes. Members of this family are involved in a variety of cellular processes, including cell cycle progression, signal transduction, apoptosis, and gene regulation. This gene has a pseudogene at chromosome 4q31.3. Multiple alternatively spliced transcript variants encoding distinct isoforms have been found for this gene, but the biological validity and full-length nature of

some variants have not been determined. [provided by RefSeq, Jul 2008]

Locus ID: 11152

MW: 14.4