

## **Product datasheet for SC211161**

CSRP2BP (KAT14) (NM 020536) Human 3' UTR Clone

## Product data:

**Product Type:** 3' UTR Clones

Product Name: CSRP2BP (KAT14) (NM 020536) Human 3' UTR Clone

Symbol: CSRP2BP

Synonyms: ATAC2; CRP2BP; CSRP2BP; dJ717M23.1; PRO1194

Mammalian Cell

Selection:

Neomycin

**Vector:** pMirTarget (PS100062)

**ACCN:** NM\_020536

**Insert Size:** 606 bp

Insert Sequence: >SC211161 3'UTR clone of NM\_020536

The sequence shown below is from the reference sequence of NM\_020536. The complete

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

TCTTTTGCTGACTTTGGTTACAGTCAGAAAAAAAAAAACTAGATGTTTGTGTCTA

**ACGCGT**AAGCGGCCGCGCATCTAGATTCGAAGAAAATGACCGACCAAGCGACGCCCAACCTGCCATCA

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).



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## CSRP2BP (KAT14) (NM\_020536) Human 3' UTR Clone - SC211161

**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 020536.7</u>

**Summary:** CSRP2 is a protein containing two LIM domains, which are double zinc finger motifs found in

proteins of diverse function. CSRP2 and some related proteins are thought to act as protein adapters, bridging two or more proteins to form a larger protein complex. The protein

encoded by this gene binds to one of the LIM domains of CSRP2 and contains an

acetyltransferase domain. Although the encoded protein has been detected in the cytoplasm,

it is predominantly a nuclear protein. Alternatively spliced transcript variants have been

described. [provided by RefSeq, Jun 2011]

**Locus ID:** 57325 **MW:** 22.8