

## Product datasheet for SC204190

## OriGene Technologies, Inc.

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## Macrophage Inflammatory Protein 1 beta (CCL4L2) (NM 001001435) Human 3' UTR Clone

**Product data:** 

**Product Type:** 3' UTR Clones

Product Name: Macrophage Inflammatory Protein 1 beta (CCL4L2) (NM 001001435) Human 3' UTR Clone

**Vector:** pMirTarget (PS100062)

Symbol: CCL4L1

Synonyms: AT744.2; CCL4L; LAG-1; LAG1; SCYA4L

**ACCN:** NM\_001001435

**Insert Size:** 349 bp

Insert Sequence: >SC204190 3'UTR clone of NM\_001001435

The sequence shown below is from the reference sequence of NM\_001001435. The complete

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

AAAA

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:** NM 001001435.2





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**Summary:** 

This gene is one of several cytokine genes that are clustered on the q-arm of chromosome 17. Cytokines are a family of secreted proteins that function in inflammatory and immunoregulatory processes. The protein encoded by this family member is similar to the chemokine (C-C motif) ligand 4 product, which inhibits HIV entry by binding to the cellular receptor CCR5. The copy number of this gene varies among individuals, where most individuals have one to five copies. This gene copy contains a non-consensus splice acceptor site at the 3' terminal exon found in other highly similar gene copies, and it thus uses other alternative splice sites for the 3' terminal exon, resulting in multiple transcript variants. [provided by RefSeq, Apr 2014]

**Locus ID:** 9560 **MW:** 12.7