

Product datasheet for SC208305

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CLEC12A (NM_138337) Human 3' UTR Clone

Product data:

Product Type: 3' UTR Clones

Product Name: CLEC12A (NM 138337) Human 3' UTR Clone

Vector: pMirTarget (PS100062)

Symbol: CLEC12A

Synonyms: CD371; CLL-1; CLL1; DCAL-2; MICL

ACCN: NM_138337

Insert Size: 599 bp

The sequence shown below is from the reference sequence of NM_138337. The complete

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

Blue=Stop Codon Red=Cloning site

GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG

TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC

AAATTATTTTTAAGTAAAAGCCAATAAACAAAAACGAAAAGGCAA

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.





CLEC12A (NM_138337) Human 3' UTR Clone - SC208305

RefSeq: <u>NM 138337.6</u>

Summary: This gene encodes a member of the C-type lectin/C-type lectin-like domain (CTL/CTLD)

superfamily. Members of this family share a common protein fold and have diverse functions, such as cell adhesion, cell-cell signaling, glycoprotein turnover, and roles in inflammation and immune response. The protein encoded by this gene is a negative regulator of granulocyte and monocyte function. Several alternatively spliced transcript variants of this gene have been described, but the full-length nature of some of these variants has not been determined. This gene is closely linked to other CTL/CTLD superfamily members in the natural killer gene complex region on chromosome 12p13. [provided by RefSeq, May 2011]

Locus ID: 160364 **MW:** 22.6