

Product datasheet for **SC337626**

CD56 (NCAM1) (NM_001242607) Human Untagged Clone

Product data:

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| Product Type: | Expression Plasmids |
| Product Name: | CD56 (NCAM1) (NM_001242607) Human Untagged Clone |
| Tag: | Tag Free |
| Symbol: | CD56 |
| Synonyms: | CD56; MSK39; NCAM |
| Mammalian Cell Selection: | Neomycin |
| Vector: | pCMV6-Entry (PS100001) |
| E. coli Selection: | Kanamycin (25 ug/mL) |



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Fully Sequenced ORF: >NCBI ORF sequence for NM_001242607, the custom clone sequence may differ by one or more nucleotides

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ATGCTGCAAACCTAAGGATCTCATCTGGACTTTGTTTTCTCTGGAACTGCAGTTTCTCTGCAGGTGGATA
TTGTTCCAGCCAGGGGAGATCAGCGTTGGAGAGTCCAATTCTTCTTATGCCAAGTGGCAGGAGATGC
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GCTCATGTTCAAGAATGCGCCAACCCACAGGAGTTCCGGGAGGGGAAGATGCCGTGATTGTGTGTGAT
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GCTCTCTCCGAGTGGAAACCAGAGATCAGGCTCCCGTCTGGCAGTGACCACGTGATGCTGAAGTCCCTG
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CTGACGGAGCCGAGAAGGGCCCGTAGAAGCAAAGCCAGAGTGCCAGGAGACAGAAACGAGCCAGCGC
CAGCCGAAGTCAAGACGGTCCCCAATGACGCCACACAGACAAAGGAGAACGAGAGCAAAGCATGA
    
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Restriction Sites: SgfI-MluI

ACCN: NM_001242607

OTI Disclaimer: Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).

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| Components: | The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water). |
| Reconstitution Method: | <ol style="list-style-type: none">1. Centrifuge at 5,000xg for 5min.2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.3. Close the tube and incubate for 10 minutes at room temperature.4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C. |
| RefSeq: | <u>NM_001242607.1, NP_001229536.1</u> |
| RefSeq Size: | 6070 bp |
| RefSeq ORF: | 2655 bp |
| Locus ID: | 4684 |
| Cytogenetics: | 11q23.2 |
| Protein Families: | Druggable Genome, ES Cell Differentiation/IPS, Transmembrane |
| Protein Pathways: | Cell adhesion molecules (CAMs), Prion diseases |
| Gene Summary: | <p>This gene encodes a cell adhesion protein which is a member of the immunoglobulin superfamily. The encoded protein is involved in cell-to-cell interactions as well as cell-matrix interactions during development and differentiation. The encoded protein plays a role in the development of the nervous system by regulating neurogenesis, neurite outgrowth, and cell migration. This protein is also involved in the expansion of T lymphocytes, B lymphocytes and natural killer (NK) cells which play an important role in immune surveillance. This protein plays a role in signal transduction by interacting with fibroblast growth factor receptors, N-cadherin and other components of the extracellular matrix and by triggering signalling cascades involving FYN-focal adhesion kinase (FAK), mitogen-activated protein kinase (MAPK), and phosphatidylinositol 3-kinase (PI3K). One prominent isoform of this gene, cell surface molecule CD56, plays a role in several myeloproliferative disorders such as acute myeloid leukemia and differential expression of this gene is associated with differential disease progression. For example, increased expression of CD56 is correlated with lower survival in acute myeloid leukemia patients whereas increased severity of COVID-19 is correlated with decreased abundance of CD56-expressing NK cells in peripheral blood. Alternative splicing results in multiple transcript variants encoding distinct protein isoforms. [provided by RefSeq, Aug 2020]</p> <p>Transcript Variant: This variant (5) represents the longest transcript and encodes the longest protein (isoform 5). Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.</p> |