

Product datasheet for **MC226494**

Cd63 (NM_001282966) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Cd63 (NM_001282966) Mouse Untagged Clone
Tag: Tag Free
Symbol: Cd63
Synonyms: C75951; ME491; Tspan30
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC226494 representing NM_001282966
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**GCGATCGCC**

ATGGCGGTGGAAGGAGGAATGAAGTGTGTCAAGTTTTTGTCTACGTTCTCCTGCTGGCCTTCTGCGCT
GTGCAGTGGGATTGATCGCCATTGGTGTAGCGTTTCAAGTGTCTTGAAGCAGGCCATTACCCATGAGAC
TACTGCTGGCTCGCTGTTGCCTGTGGTCATCATTGCAGTGGTGCCTTCTCTTCTGCTGGCCTTTGTG
GGCTGCTGTGGGGCTGCAAGGAGAACTACTGTCTCATGATTACATTTGCCATCTTCTGCTCTTATCA
TGCTTGTGGAGGTGGCTGTGGCCATTGCTGGCTATGTGTTTAGAGACCAGGTGAAGTCAGAGTTAATAA
AAGCTTCCAGCAGCAGATGCAGAATTACCTTAAAGACAACAAAACAGCCACTATTTGGACAAATTGCAG
AAAGAAAATAACTGCTGTGGAGCTTCTAACTACACAGACTGGGAAAACATCCCGGCATGGCCAAGGACA
GAGTCCCCGATTCTTGTGCATCAACATAACTGTGGGCTGTGGGAATGATTTCAAGGAATCCACTATCCA
TACCCAGGGCTGCGTGGAGACTATAGCAATATGGCTAAGGAAGAACATACTGCTGGTGGCTGCAGCGCC
CTGGGCATTGCTTTTGTGGAGTCTTGGGAATTATCTTCTCCTGCTGTCTGGTGAAGAGTATTCAAGTG
GCTATGAAGTAATG**TAG**

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: Sgfl-Mlul
ACCN: NM_001282966
Insert Size: 717 bp



[View online »](#)

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).
OTI Annotation:	Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
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_001282966.1</u> , <u>NP_001269895.1</u>
RefSeq Size:	999 bp
RefSeq ORF:	717 bp
Locus ID:	12512
UniProt ID:	<u>P41731</u>
Cytogenetics:	10 77.19 cM
Gene Summary:	<p>Functions as cell surface receptor for TIMP1 and plays a role in the activation of cellular signaling cascades. Plays a role in the activation of ITGB1 and integrin signaling, leading to the activation of AKT, FAK/PTK2 and MAP kinases. Promotes cell survival, reorganization of the actin cytoskeleton, cell adhesion, spreading and migration, via its role in the activation of AKT and FAK/PTK2. Plays a role in VEGFA signaling via its role in regulating the internalization of KDR/VEGFR2. Plays a role in intracellular vesicular transport processes, and is required for normal trafficking of the PMEL luminal domain that is essential for the development and maturation of melanocytes. Plays a role in the adhesion of leukocytes onto endothelial cells via its role in the regulation of SELP trafficking. May play a role in mast cell degranulation in response to Ms4a2/FceRI stimulation, but not in mast cell degranulation in response to other stimuli.[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (3) has an alternate 5' UTR exon, compared to variant 1. Variants 1, 2 and 3 encode the same protein. 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>