

Product datasheet for **MC226400**

Klrk1 (NM_001286018) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Klrk1 (NM_001286018) Mouse Untagged Clone
Tag: Tag Free
Symbol: Klrk1
Synonyms: D6H12S2489E; NKG2-D; Nkg2d
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC226400 representing NM_001286018
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**GCGATCGCC**

ATGAGCAAATGCCATAATTACGACCTCAAGCCAGCAAAGTGGGATACTTCTCAAGAACAACAGAAACAAA
GATTAGCACTAACTACCAGTCAACCTGGAGAAAATGGTATCATAAGAGGAAGATACCTATAGAAAACT
CAAAATATCTCCAATGTTTCGTTGTTTCGAGTCCTTGCTATAGCCTTGGCAATTCGATTCACCTTAACACA
TTGATGTGGCTTGCCATTTTCAAAGAGAGCTTTTCAGCCAGTTATAATTATCTTGACAGTATTGTGCAACA
AGGAAGTCCCAGTTTCCTCAAGAGAGGGCTACTGTGGCCCATGCCCTAACAACTGGATATGTCACAGAAA
CAACTGTTACCAATTTTTAATGAAGAGAAAACCTGGAACCAGAGCCAAGCTTCCTGTTTGTCTCAAAAT
TCCAGCCTTCTGAAGATATACAGTAAAGAAGAACAGGATTTCTTAAAGCTGGTTAAGTCCTACTGGA
TGGGACTGGTCCAGATCCCAGCAAATGGCTCCTGGCAGTGGGAAGATGGCTCCTCTCTCATACAATCA
GTAACTCTGGTGGAAAATACCAAAGGATCCTGTGCTGTCTATGGCTCAAGCTTTAAGGCTTACACAGAA
GACTGTGCAAATCTAAACACGTACATCTGCATGAAAAGGGCGGT**TAA**

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
ACCN: NM_001286018
Insert Size: 678 bp



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| 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_001286018.1</u> , <u>NP_001272947.1</u> |
| RefSeq Size: | 3197 bp |
| RefSeq ORF: | 678 bp |
| Locus ID: | 27007 |
| Cytogenetics: | 6 63.44 cM |
| Gene Summary: | <p>Function as an activating and costimulatory receptor involved in immunosurveillance upon binding to various cellular stress-inducible ligands displayed at the surface of autologous tumor cells and virus-infected cells. Provides both stimulatory and costimulatory innate immune responses on activated killer (NK) cells, leading to cytotoxic activity. Acts as a costimulatory receptor for T-cell receptor (TCR) in CD8(+) T-cell-mediated adaptive immune responses by amplifying T-cell activation. Stimulates perforin-mediated elimination of ligand-expressing tumor cells. Signaling involves calcium influx, culminating in the expression of TNF-alpha. Participates in NK cell-mediated bone marrow graft rejection. May play a regulatory role in differentiation and survival of NK cells. Binds to ligands belonging to various subfamilies of MHC class I-related glycoproteins including RAET1A, RAET1B, RAET1C, RAET1D, RAET1E, H60 and MULT1.[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (3) differs in the 5' UTR and the 5' coding region and initiates translation at a downstream start codon, compared to variant 1. It encodes isoform c, which contains a distinct N-terminus and an additional internal in-frame segment, and is shorter, compared to isoform a. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.</p> |