

Product datasheet for **SC334588**

KIR2DS4 (NM_001281972) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	KIR2DS4 (NM_001281972) Human Untagged Clone
Tag:	Tag Free
Symbol:	KIR2DS4
Synonyms:	CD158I; KIR-2DS4; KIR1D; KIR412; KKA3; NKAT-8; NKAT8
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>NCBI ORF sequence for NM_001281972, the custom clone sequence may differ by one or more nucleotides

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ATGTCGCTCATGGTCATCATCATGGCGTGTGTTGGGTTCTTCTTGCTGCAGGGGGCCTGGCCACAGGAGG
GAGTCCACAGAAAACCTTCTTCTGGCCCTCCCAGGTCACCTGGTAAAATCAGAAGAGACATCATCCT
GCAATGTTGGTCGGATGTCATGTTTGGCACTTCTTCTGCACAGAGAGGGGAAGTTTAAACAACACTTTG
CACCTCATTGGAGAGCACCATGATGGGGTTTCCAAGGCCAACTTCTCCATTGGTCCCATGATGCCTGTCC
TTGCAGGAACCTACAGATGCTACGGTCTGTTCTCTCACTCCCCATCAGTTGTCAGCTCCCAGTGACCC
TCTGGACATGGTATCATAGGTCTATATGAGAAACCTTCTCTCAGCCCAGCCGGGCCACGGTTCAG
GCAGGAGAGAATGTGACCTTGTCTGCAGCTCCATCTATCCAGGGAAGGGGAGGCCCATGAACGTAGGCT
CCCTGCAGTGCGCAGCATCAACGGAACATTCCAGGCCACTTCTCTGGGCCCTGCCACCCACGGAGGG
ACCTACAGATGCTTCGGCTCTTCCGTGACGCTCCCTACGAGTGGTCAAACCTCGAGTGATCCACTGCTTG
TTCCGTCACAGGTAACCCACAGACCTACATGTTCTGA
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Restriction Sites:	Sgfl-MluI
ACCN:	NM_001281972
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).
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:

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: [NM_001281972.1](#), [NP_001268901.1](#)

RefSeq Size: 1557 bp

RefSeq ORF: 669 bp

Locus ID: 3809

UniProt ID: [P43632](#)

Cytogenetics: 19q13.42

Protein Families: Transmembrane

Protein Pathways: Antigen processing and presentation, Natural killer cell mediated cytotoxicity

Gene Summary: Killer cell immunoglobulin-like receptors (KIRs) are transmembrane glycoproteins expressed by natural killer cells and subsets of T cells. The KIR genes are polymorphic and highly homologous and they are found in a cluster on chromosome 19q13.4 within the 1 Mb leukocyte receptor complex (LRC). The gene content of the KIR gene cluster varies among haplotypes, although several "framework" genes are found in all haplotypes (KIR3DL3, KIR3DP1, KIR3DL4, KIR3DL2). The KIR proteins are classified by the number of extracellular immunoglobulin domains (2D or 3D) and by whether they have a long (L) or short (S) cytoplasmic domain. KIR proteins with the long cytoplasmic domain transduce inhibitory signals upon ligand binding via an immune tyrosine-based inhibitory motif (ITIM), while KIR proteins with the short cytoplasmic domain lack the ITIM motif and instead associate with the TYRO protein tyrosine kinase binding protein to transduce activating signals. The ligands for several KIR proteins are subsets of HLA class I molecules; thus, KIR proteins are thought to play an important role in regulation of the immune response. [provided by RefSeq, Jul 2008] Transcript Variant: This variant (3) represents a 22nt deletion allele which also lacks a coding exon. The resulting protein (isoform 3) is frameshifted and lacks the C-terminal membrane binding domain found in the functional allele (KIR2DS4*001). 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.