

## Product datasheet for **MC208833**

### **Klra2 (NM\_001170851) Mouse Untagged Clone**

#### Product data:

Product Type:	Expression Plasmids
Product Name:	Klra2 (NM_001170851) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Klra2
Synonyms:	Klra30; Ly49; Ly49b
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>MC208833 representing NM_001170851 Red=Cloning site Blue=ORF Orange=Stop codon

TTTGTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
GCC**CGATCGCC**

ATGAGTGAGCAGGAGGTCACTTACACAACCTCTGAGATTTTATAAGTCTTCAGGGTTCAGAACCCAGTGA  
GGCCTGAGGAGACTCAAAGGCCAGAGATGTGGCCACAGAGAGTGTTCAGTCCCCTGGAAGTTCATTGT  
GATAGTTCTTGAATCCTCTGTTTCTTCTGCTGGTAACTGTGGCAGTGTGGTGATACACATTTCCGG  
GATGGACAAGAGAAACATGAACAGGAGAAAACCTAAATAACCTCCGTCAGAGTACCAGGTCATGAAAA  
ATGACAGCTCCTTAATGGAAGAAATGTTAAGAAATAAGTCTTCAGAGTGAAGGCCCTCAATGATAGCCT  
GCACTACCTCAACAGAGAACAGAACAGATGCCTCAGGAAAACCAAGATTGTTTATAGATTGCTCACAGAAC  
AAAGGCAAGCAAGTGGAAGGATACTGGTTCTGCTGTGGCATGAAATGTTATTATTTTCATCATGGATGATA  
AAAAATTGAAAGGATGTAAACAGATCTGCCAGGCTTAACTTAACTCTTTGAAGACAAATGATGAGGA  
TGAATTGAAGTTCCTTAAATCCCAACTTCAAAGAAACACATACTGGATTGCACTGACACATCACGAAAGC  
AAAGAGGAATCGCAACAGATTGGTGATAGACCATCTAAACCGGCTCAAGAAGAGCAAAGTTTCATTGAAG  
ATTTATCCCTCTGCCATCTCATCCCTGTGGATTCTTTCCTGGTTCATCTTCTGACACAGATTGTCA  
TGTTTCAGCAGCAAGGAATTCAGTACCTAATAGAGAAAAGTGTGCATATCTAAATTCATTTTCTACAGAA  
GAGGATGACCGTGCTAGAAATCATGGTTGATTTGTGAAAAGAGATTGAATAAATCCCTATTCCAGGGA  
GCTGTGCCAAGGAAGAACTCAATCTGCTCTGCAGAGGGATGAAGATGAAAGT**TAA**

**ACGCGT**ACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:	SgfI-MluI
ACCN:	NM_001170851



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<b>Insert Size:</b>	966 bp
<b>OTI Disclaimer:</b>	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).
<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"> <li>1. Centrifuge at 5,000xg for 5min.</li> <li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>3. Close the tube and incubate for 10 minutes at room temperature.</li> <li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>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.</li> </ol>
<b>Note:</b>	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
<b>RefSeq:</b>	<a href="#">NM_001170851.1</a> , <a href="#">NP_001164322.1</a>
<b>RefSeq Size:</b>	1886 bp
<b>RefSeq ORF:</b>	966 bp
<b>Locus ID:</b>	16633
<b>Cytogenetics:</b>	6 63.44 cM
<b>Gene Summary:</b>	<p>The gene is a member of the large lectin-like type 2 transmembrane receptor family of the natural killer gene complex. The gene is located distantly telomeric to its family's gene cluster on chromosome 6. The gene differs from the other genes in its cluster as its promoter region contains long and short interspersed repetitive elements suggesting a possible rearrangement or gene conversion. It is unknown whether this gene's encoded protein is involved with natural killer cell differentiation as are its other family members. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jan 2010]</p> <p>Transcript Variant: This variant (1) represents the longer transcript and encodes the longer isoform (1). 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>