

## Product datasheet for **MC208248**

### Cd247 (NM\_001113393) Mouse Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	Cd247 (NM_001113393) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Cd247
Synonyms:	4930549J05Rik; A430104F18Rik; AW552088; Cd3; Cd3-eta; Cd3-zeta; Cd3h; Cd3z; Cd3zeta; T3z; Tcrk
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin
Fully Sequenced ORF:	>MC208248 representing NM_001113393 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
GCC**CGATCGCC**

ATGAAGTGGAAAGTGTCTGTTCTCGCTGCATCCTCCACGTGCGGTTCCAGGAGCAGAGGCACAGAGCT  
TTGGTCTGCTGGATCCCAAACCTGCTACTTGCTAGATGGAATCCTCTTCATCTACGGAGTCATCATCAC  
AGCCCTGTACCTGAGAGCAAAATTCAGCAGGAGTGCAGAGACTGCTGCCAACCTGCAGGACCCCAACCAG  
CTCTACAATGAGCTCAATCTAGGGCGAAGAGAGGAATATGACGTCTTGGAGAAGAAGCGGGCTCGGGATC  
CAGAGATGGGAGGCAAACAGAGGAGGAGGAACCCCGGAAGGCGTATACAATGCACTGCAGAAAGACAA  
GATGGCAGAAGCCTACAGTGAGATCGGCACAAAAGGCGAGAGGCGGAGAGGCAAGGGGCACGATGGCCTT  
TACCAGGACAGCCACTTCCAAGCAGTGCAGTTCGGGAACAGAAGAGAGAGAAGGTTTCAGAACTCACAA  
GGACCCTTGGGTTAAGAGCCCGCCCAAAGCCTGCCGACATAAGAAGCCTCTTAGCCTCCAGCAGCCGT  
ATCCTAA

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites:	Sgfl-Mlul
ACCN:	NM_001113393
Insert Size:	567 bp



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<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>RefSeq:</b>	<u>NM_001113393.2, NP_001106864.2</u>
<b>RefSeq Size:</b>	2804 bp
<b>RefSeq ORF:</b>	567 bp
<b>Locus ID:</b>	12503
<b>Cytogenetics:</b>	1 73.14 cM
<b>Gene Summary:</b>	<p>Part of the TCR-CD3 complex present on T-lymphocyte cell surface that plays an essential role in adaptive immune response. When antigen presenting cells (APCs) activate T-cell receptor (TCR), TCR-mediated signals are transmitted across the cell membrane by the CD3 chains CD3D, CD3E, CD3G and CD3Z. All CD3 chains contain immunoreceptor tyrosine-based activation motifs (ITAMs) in their cytoplasmic domain. Upon TCR engagement, these motifs become phosphorylated by Src family protein tyrosine kinases LCK and FYN, resulting in the activation of downstream signaling pathways. CD3Z ITAMs phosphorylation creates multiple docking sites for the protein kinase ZAP70 leading to ZAP70 phosphorylation and its conversion into a catalytically active enzyme. Plays an important role in intrathymic T-cell differentiation. Additionally, participates in the activity-dependent synapse formation of retinal ganglion cells (RGCs) in both the retina and dorsal lateral geniculate nucleus (dLGN). [UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (theta) uses an alternate in-frame splice site in the central coding region, and has alternate exon structure in the 3' coding region and 3' UTR, compared to variant zeta. The resulting isoform (theta) has a distinct C-terminus and is longer than isoform zeta. Sequence Note: This RefSeq record was created from 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>