

Product datasheet for MC229422

Plcb2 (NM_001290790) Mouse Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Plcb2 (NM_001290790) Mouse Untagged Clone
Tag: Tag Free
Symbol: Plcb2
Synonyms: AI550384; B230205M18Rik; B230399N12
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >MC229422 representing NM_001290790
 Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
 GCC**CGGATCGCC**

ATGCTTTGCTCAACCCTGTTCTATTGCCCCCTAACGTGAAGGCATATCTGAGCCAAGGGGAGCGCTTCA
 TCAAGTGGGACGATGAACTTCAATAGCCTCTCCTGTTATCCTCCGTGTGGATCCCAAGGGCTATTACTT
 ATACTGGACATATCAAAATCAGAGCCAGAACTCCGGGAGGTCTTCAACATGGACTTTCCAGACAACCAC
 TTCTGCTGAAAACACTCACAGTGGTGTCCGGCCCTGACATGGTGGACCTCACCTTCTACAACCTTTGCT
 CTTACAAGGAGAACGTAGGCAAGGACTGGGCTGAGGACGTGCTAGCTCTCGCAAACACCCGATGACAGT
 CAATGCTCCTCGAAGCACATTTCCTGGACAAGATCCTGGTGAAGCTTAAGATGCAGCTCAACCCTGAAGGG
 AAGATCCCGTGAAGAATTTTTCCAGATGTTTCTGCTGATCGAAAACGGGTGGAAGCTGCCCTCGGTG
 CTTGTCACCTTGCAAAAGGCAAAAATGATGCTATCAACCAGAGGACTTCCCAGAATCCGTGTACAAGAG
 CTTCTCATGAGCCTCTGTCTCGGCCAGAAATCGACGAGATCTCACTTCTACCACTCTAAAGCTAAG
 CCCTACATGACCAAGGAACACCTGACCAAATTCATCAATCAGAAGCAGCGAGACCCTCGACTCAACTCCT
 TGCTGTTCCACAGCCCGGCCAGCAAGTCAAGTGCTCATTGACAAGTACGAACCCAGCGGCATCAA
 TGTGACAGAGGGCCAGCTGTACCAGAGGGGATGGTCTGGTTTCTGTGGACCAGAGAACAGTGTGCTG
 GCCCAGATACACTGCTGATCCACCAAGACATGACACAACCCTGAATCACTATTTTCATCAACTCCTCAC
 ACAACACCTACCTGACAGCCGGCCAGTTCTCAGGCCTTTCCTCGGCTGAGATGTACCGCCAGGTGCTGCT
 GTCTGGCTGCCGGTGTGTAGAGTTAGACTGTTGGAAGGGCAAGCCCCCTGACGAAGAGGCCATTATCACC
 CACGGCTTACCATGACCACAGATATCTGTTCGAAGGAAGCAATTGAAGCCATTGCAGAAAGTGCCTTTA
 AGACCTCCCGTATCCTGTCATCCTATCATTTGAAAACCATGTAGACTCACCCCGCAACAGGCTAAGAT
 GGCTGAGTACTGCAGGAGCATGTTTGGAGAGACCTTGCTCACAGATCCCCTGGAAAATTTCCCTCTGAAA
 CCTGGCATCCCTCTGCCAGCCCGAGGACCTCCGGGCAAGATCCTCATTAAAGAATAAGAAGAACCAGT
 TTTCTGGCCAGCATCCCCAGCAAGAAGCCTGGTGGGGTGGCTGAGGGCAGCCTCCCGTCTAGTGTCCC
 TGTAGAAGAGGACACGGGTGGACTGCTGAGGACCGGACTGAGGTGGAGGAGGAGGAGGTGGTGAAGAG
 GAGGAAGAGGAGGAGTCAGGAAACCTGGATGAAGAAGAAATTAAGAAGATGCAGTCGGATGAGGGCACAG



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CAGGCCTGGAGGTGACAGCTTATGAGGAAATGTCCAGCCTTGTC AATTATATCCAGCCCACCAAGTTTAT
 CTCCTTCGAGTTCTCTGCACAGAAGAACAAGTTACGTTGTCTCTTCCTTCACGGAGCTCAAGGCCTAC
 GAGCTGCTCTCCAAGGCCTCCATGCAGTTTGTGGACTATAATAAACGCCAGATGAGCCGTGTGTACCCCA
 AGGGCACACGCATGGACTCTTCCAACACATGCCCCAGATGTTCTGGAATGCTGGATGTCAGATGGTTGC
 CCTCAATTTCCAGACAATGGACCTGCCATGCAGCAGAACATGGCACTGTTTGAGTTCAACGGGCAGAGT
 GGCTACCTCTAAAGCAGAGTTCATGCGCAGACTGGACAAGCAGTTCAACCCCTTCTCAGTGGACCGCA
 TTGATGTGGTGGTAGCCACCACCCTTCCATTACGATCATCTCTGGGCAGTTCCCTGTGTCAGAGCCAGTGT
 ACGCACCTATGTGGAAGTGGAACTGTTTGGCCTCCAGGGGACCCCAAGAGGCGGTATCGAACCAAGCTG
 TCACCTACTGCTAACTCCATCAATCCTGTCTGGAAGAGGAACCCCTTTATCTTTGAGAAGATCTTGATGC
 CTGAGCTGGCCTCCCTCAGGATAGCTGTGATGGAAGAAGGCAGCAAATTTCTTGACACCCGCATCATCCC
 CATCAATGCCTTACATTCTGGATACCACCATCTGTGCCTGCGCAGTGAGAGCAACATGGCCCTTACCATG
 CCAGCTCTCTTTGTCTTCTGGAGATGAAGGACTACATACCTGACACCTGGGCAGATCTTACAGTAGCCC
 TTGCCAACCCATCAAGTACTTCAATGCCAGGATAAGAAGTCCGTGAAGCTCAAAGGAGTGACAGGAAG
 TCTGCCGAGAACTCTCTCTGGGACACCTGTTGCCAGTCAGTCCAATGGGGCGCCAGTCTCGGCAGGC
 AATGGGTCAACAGCGCCTGGGACCAAGGCCACGGGGGAAGAAGCTACGAAAGAAGTGACAGAGCCACAGA
 CCGCCAGCTTGAAGAGTTGCGGGAAGTGAAGGGCGTGGTGAAGTGCAGCGAAGACATGAGAAGGAGCT
 TCGAGAGTTGGAGCGCCGTGGAGCCCGCGCTGGGAGGAACTGCTGCAGCGTGGCGCCGCACAGCTGGCG
 GAGCTCCAGACCCAGGCAGCAGGCTGCAAGCTCCGCCAGGCAAGGGCTCCCGCAAGAAGAGGACCTGC
 CCTGTGAGGAGACCGTCTGTGGCGCTAGCGAGCCACGACCGGGCGGACCCGCGCTGCAGGAGCTGAA
 GGACAGGCTGGAGCAGGAGCTGCAGCAGCAAGGCGAGGAGCAGTACCGTCCGTCTCAAGCGCAAGGAG
 CAGCAGTGACCGAGCAAATCGCCAAGATGATGGAGCTGGCCAGAGAGAAACAGGCTGCTGAACTCAAGA
 CCTTCAAGGAGACCTCAGAACTGACACCAAAGAAATGAAGAAAAACTGGAGGCCAAGAGGCTGGAACG
 GATCCAAGCCATGACCAAGGTCACCACAGACAAGGTGGCCAGGAGAGGCTCAAGAGAGAAATTAACAAC
 TCCACATCCAGGAAGTGGTCCAGGCTGTCAAGCAGATGACAGAGACCCTGGAGCGTCAACAGGAGAAGC
 TGAAGAGAGGCAGACAGCCTGCCTGGAGCAGATCCAGGCAATGGAAGCAGTTCCAGGAGAAGGCGCT
 GGCAGAGTATGAGGCCAAGATGAAGGGCCTGGAGGCTGAAGTAAAGGAGTCGGTGCGGCCCTACTTCAAG
 GACTGTTCCCCACCGAAGCAGAAGACAAGCCTGAGAGGTCCTGTGAGGCCTCTGAGGAGTCGTGTCCAC
 AGGAACCACTTGTGAGCAAGGCAGACACTCAGGAGAGCCGCTCTGA

ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
 ACAAGGATGACGACGATAAGGTTTAA

- Restriction Sites:** SgfI-MluI
- ACCN:** NM_001290790
- Insert Size:** 3477 bp
- 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:

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_001290790.1](#), [NP_001277719.1](#)

RefSeq Size: 5091 bp

RefSeq ORF: 3477 bp

Locus ID: 18796

UniProt ID: [A3KGF7](#)

Cytogenetics: 2 59.43 cM

Gene Summary: The production of the second messenger molecules diacylglycerol (DAG) and inositol 1,4,5-trisphosphate (IP3) is mediated by activated phosphatidylinositol-specific phospholipase C enzymes. This protein may be involved in the transduction of bitter taste stimuli (By similarity).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (2) lacks an alternate in-frame exon in the 5' coding region, compared to variant 1, resulting in an isoform (b) that is shorter than isoform a. 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.