

# **Product datasheet for MC228110**

# Camk2d (NM\_001293663) Mouse Untagged Clone

## **Product data:**

**Product Type:** Expression Plasmids

**Product Name:** Camk2d (NM\_001293663) Mouse Untagged Clone

Tag: Tag Free Symbol: Camk2d

**Synonyms:** 2810011D23Rik; 8030469K03Rik; CaMK II; [d]-CaMKII

Mammalian Cell Neomycin

Selection:

Vector:pCMV6-Entry (PS100001)E. coli Selection:Kanamycin (25 ug/mL)

#### OriGene Technologies, Inc.

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Fully Sequenced ORF: >MC228110 representing NM\_001293663

Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC

ATGGCTTCGACCACCACCTGCACCCGGTTCACCGACGAGTATCAGCTCTTTGAGGAGCTCGGAAAGGGGG CGTTCTCAGTGGTGAGAAGATGTATGAAAATCCCTACTGGACAAGAGTATGCTGCCAAAATTATCAACAC CAAAAAGCTTTCTGCTAGGGACCATCAGAAACTGGAAAGGGAAGCTAGAATCTGCCGTCTCTTGAAGCAC CCCAATATTGTGAGACTTCACGACAGTATATCGGAGGAGGGCTTCCATTACTTGGTGTTTTGACTTAGTGA CTGGTGGCGAACTGTTTGAAGACATAGTGGCAAGAGAATATTACAGTGAAGCTGATGCCAGTCATTGTAT ACAACAGATTCTAGAGAGTGTAAATCATTGTCACCTAAATGGCATAGTTCACAGGGACCTGAAGCCTGAG AATTTGCTTTTAGCTAGCAAGTCCAAAGGAGCAGCTGTGAAGCTGGCAGACTTCGGCTTAGCCATAGAAG TTCAAGGCGACCAGCAGGCATGGTTTGGTTTTGCTGGCACACCTGGGTATCTTTCTCCAGAAGTCCTGCG TAAAGATCCTTATGGAAAACCAGTGGATATGTGGGCATGCGGTGTCATCCTCTACATCTTGCTGGTGGGA TACCCACCCTTCTGGGATGAAGATCAGCATAGACTGTATCAGCAGATCAAGGCCGGAGCTTACGATTTTC CGTCACCAGAATGGGATACAGTGACACCTGAAGCCAAAGACCTCATCAACAAAATGCTGACCATCAACCC TGCCAAACGTATCACAGCCTCTGAGGCCCTGAAACACCCATGGATCTGTCAACGCTCTACTGTTGCCTCC ATGATGCACAGGCAGGAGACTGTAGACTGCTTGAAGAAATTTAATGCTAGACGGAAACTGAAGGGCGCCA TCTTGACAACTATGCTGGCTACGAGAAATTTTTCAGCAGCCAAGAGTTTATTGAAGAAACCAGATGGGGT AAAGATAAACAACAAAGCCAACGTGGTAACCAGCCCCAAAGAAAATATTCCTACCCCGGCGCTGGAGCCC CAAACTACTGTAATCCACAACCCTGACGGAAACAAGGAGTCAACTGAGAGCTCAAACACCACCATTGAGG ATGAAGACGTGAAAGCACGAAAACAGGAGATCATCAAAGTCACTGAGCAACTGATTGAAGCTATCAACAA TGGGGACTTTGAGGCTTACACAAAAATCTGTGATCCAGGCCTCACTGCCTTTGAACCTGAAGCATTGGGC AACTTAGTGGAAGGGATGGACTTTCACAGATTCTACTTTGAAAATGCTTTGTCCAAAAGCAATAAACCAA TCCACACGATCATCCTCAACCCACACGTTCACCTGGTAGGGGATGACGCAGCCTGCATCGCATACATTCG CGCCGTGATGGGAAGTGGCAGAATGTTCACTTTCACCGTTCGGGGTCCCCCACAGTACCCATCAACTAA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATTACAAGGATGACGACGATAAGGTTTAA

**Restriction Sites:** Sgfl-Mlul

**ACCN:** NM\_001293663

**Insert Size:** 1539 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.

**Note:** Plasmids are not sterile. For experiments where strict sterility is required, filtration with

0.22um filter is required.

**RefSeq:** <u>NM 001293663.1</u>, <u>NP 001280592.1</u>

 RefSeq Size:
 5615 bp

 RefSeq ORF:
 1539 bp

 Locus ID:
 108058

 UniProt ID:
 Q6PHZ2

Cytogenetics: 3 G1



### **Gene Summary:**

Calcium/calmodulin-dependent protein kinase involved in the regulation of Ca(2+) homeostatis and excitation-contraction coupling (ECC) in heart by targeting ion channels, transporters and accessory proteins involved in Ca(2+) influx into the myocyte, Ca(2+) release from the sarcoplasmic reticulum (SR), SR Ca(2+) uptake and Na(+) and K(+) channel transport. Targets also transcription factors and signaling molecules to regulate heart function. In its activated form, is involved in the pathogenesis of dilated cardiomyopathy and heart failure. Contributes to cardiac decompensation and heart failure by regulating SR Ca(2+) release via direct phosphorylation of RYR2 Ca(2+) channel on 'Ser-2808'. In the nucleus, phosphorylates the MEF2 repressor HDAC4, promoting its nuclear export and binding to 14-3-3 protein, and expression of MEF2 and genes involved in the hypertrophic program. Is essential for left ventricular remodeling responses to myocardial infarction. In pathological myocardial remodeling acts downstream of the beta adrenergic receptor signaling cascade to regulate key proteins involved in ECC. Regulates Ca(2+) influx to myocytes by binding and phosphorylating the L-type Ca(2+) channel subunit beta-2 CACNB2. In addition to Ca(2+) channels, can target and regulate the cardiac sarcolemmal Na(+) channel Nav1.5/SCN5A and the K+ channel Kv4.3/KCND3, which contribute to arrhythmogenesis in heart failure. Phosphorylates phospholamban (PLN/PLB), an endogenous inhibitor of SERCA2A/ATP2A2, contributing to the enhancement of SR Ca(2+) uptake that may be important in frequencydependent acceleration of relaxation (FDAR) and maintenance of contractile function during acidosis. May participate in the modulation of skeletal muscle function in response to exercise, by regulating SR Ca(2+) transport through phosphorylation of PLN/PLB and triadin, a ryanodine receptor-coupling factor.[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (4) lacks an alternate exon and contains an alternate exon but maintains the reading frame compared to variant 1. The encoded isoform (4) is the same length as isoform 1, but contains a distinct internal segment. 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.