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Product datasheet for SC329386

CACNA1A (NM_001174080) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	CACNA1A (NM_001174080) Human Untagged Clone
Tag:	Tag Free
Symbol:	CACNA1A
Synonyms:	APCA; BI; CACNL1A4; CAV2.1; DEE42; EA2; EIEE42; FHM; HPCA; MHP; MHP1; SCA6
Mammalian Cell Selection:	None
Vector:	pCMV6-XL5
E. coli Selection:	Ampicillin (100 ug/mL)

Fully Sequenced ORF:

>NCBI ORF sequence for NM_001174080, the custom clone sequence may differ by one or more nucleotides

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ATGGCCCGCTTCGGAGACGAGATGCCGGCCCGCTACGGGGGAGGAGGCTCCGGGGCAGCC
GCCGGGGTGGTCGTGGGCAGCGGAGGCGGGCGAGGAGCCGGGGGCAGCCGGCAGGGCGGG
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CACCGGCAGTAG

Restriction Sites: Please inquire

ACCN: NM_001174080

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: This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

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_001174080.1, NP_001167551.1
RefSeq Size:	8632 bp
RefSeq ORF:	6792 bp
Locus ID:	773
UniProt ID:	O00555
Cytogenetics:	19p13.13
Protein Families:	Druggable Genome, Ion Channels: Calcium, Transmembrane
Protein Pathways:	Calcium signaling pathway, Long-term depression, MAPK signaling pathway, Taste transduction, Type II diabetes mellitus
Gene Summary:	Voltage-dependent calcium channels mediate the entry of calcium ions into excitable cells, and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, and gene expression. Calcium channels are multisubunit complexes composed of alpha-1, beta, alpha-2/delta, and gamma subunits. The channel activity is directed by the pore-forming alpha-1 subunit, whereas, the others act as auxiliary subunits regulating this activity. The distinctive properties of the calcium channel types are related primarily to the expression of a variety of alpha-1 isoforms, alpha-1A, B, C, D, E, and S. This gene encodes the alpha-1A subunit, which is predominantly expressed in neuronal tissue. Mutations in this gene are associated with 2 neurologic disorders, familial hemiplegic migraine and episodic ataxia 2. This gene also exhibits polymorphic variation due to (CAG)n-repeats. Multiple transcript variants encoding different isoforms have been found for this gene. In one set of transcript variants, the (CAG)n-repeats occur in the 3' UTR, and are not associated with any disease. But in another set of variants, an insertion extends the coding region to include the (CAG)n-repeats which encode a polyglutamine tract. Expansion of the (CAG)n-repeats from the normal 4-18 to 21-33 in the coding region is associated with spinocerebellar ataxia 6. [provided by RefSeq, Jul 2016] Transcript Variant: This variant (5) uses two alternate splice sites, compared to variant 2. The resulting isoform (5) lacks an internal 3-aa segment and has a shorter and distinct C-terminus that does not include the polyglutamine tract, compared to isoform 2. 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.