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Product datasheet for SC335805

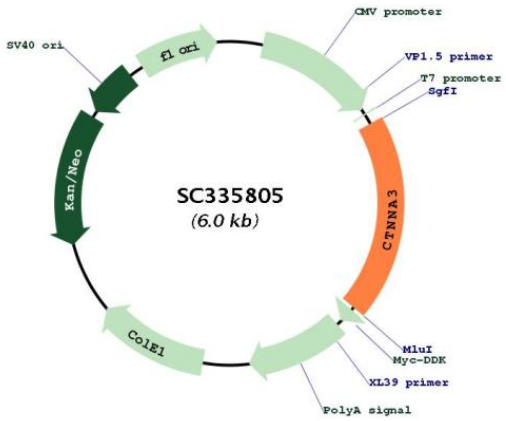
CTNNA3 (NM_001291133) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	CTNNA3 (NM_001291133) Human Untagged Clone
Tag:	Tag Free
Symbol:	CTNNA3
Synonyms:	ARVD13; VR22
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC335805 representing NM_001291133. Blue=Insert sequence Red=Cloning site Green=Tag(s) GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGAAATCAACGCAAAGGAGAGAGAAACAAGGCAGCATGTCAGCTGAAACACCAATCACATTGAATATC GATCCTCAGGATCTGCAGGTCCAAACATTCACCGTGGAGAAGCTACTGGAGCCTCTCATAATCCAGGTT ACCACACTTGTAAACTGTCCCCAGAACCCTTCCAGCAGGAAAAAAGGACGTTCGAAAAGAGCCAGTGTC CTTCTAGCTTCTGTGGAGGAAGCAACTTGGAATTTATTAGACAAGGGAGAGAAGATTGCCCAGGAAGCT ACAGTTTTAAAGGATGAGCTTACGGCTTCACTTGAGGAAGTTCGCAAAGAAAGTGAAGCTCTGAAAGTA TCAGCTGAGAGATTTACAGATGACCCCTGTTTTCTCCCAAAAAGGGAGGCTGTGGTTCAAGCTGCCCGT GCCTTGCTGGCTGCGGTGACGAGACTCCTTATCCTTGCGGACATGATTGATGTCATGTGCCTCTTGCAA CATGTGTCAGCTTTTCAAAGGACATTTGAGTCTCTCAAAAATGTTGCCAACAAATCTGACCTCCAGAAA ACCTACCAGAAGCTTGGGAAGGAGCTGGAAAATTTGGATTATTTAGCCTTCAAACGTCAGCAGGACTTA AAATCTCCAAATCAGAGAGATGAAATTGCAGGAGCCCGAGCTTCACTGAAGGAGAACTCTCCCCTCTTG CATTCAATTTGTTCAGCTTGTTTGGAGCATTCTGATGTTGCTTCCCTCAAAGCAAGCAAGGACACAGTT TGTGAAGAAATTCAGAATGCTCTCAATGTAATTTCAAATGCTTCACAAGGGATCCAGAATATGACAACC CCACCAGAACCTCAGGCAGCAACCCTGGGAAGTGCCCTTGATGAGCTGGAGAATTTAATTGTCCTGAAT CCACTCACAGTAACTGAGGAGGAAATACGACCATCACTAGAGAAACGCCTTGAAGCCATTATCAGTGGG GCTGCTCTGCTGGCGGATTCTTCATGTACGAGGGACTTACACCGAGAGCGGATTATCGCAGAATGCAAC GCCATTCGCCAGGCTCTTCAGGATCTGCTTTCAGAGTACATGAACAACCTCTGTAATCAAAAGTCTGAC CTGGGCCTCACTGGAGTAAAAATCAAATTGTTGGAGGAATGCATTATTTTCTGGAGTCTCTAG ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
Restriction Sites:	SgfI-MluI

View online »

Plasmid Map:



ACCN:	NM_001291133
Insert Size:	1167 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).
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_001291133.1
RefSeq Size:	2790 bp
RefSeq ORF:	1167 bp
Locus ID:	29119
Cytogenetics:	10q21.3
Protein Pathways:	Adherens junction, Arrhythmogenic right ventricular cardiomyopathy (ARVC), Endometrial cancer, Leukocyte transendothelial migration, Pathways in cancer, Tight junction
MW:	43 kDa

Gene Summary: This gene encodes a protein that belongs to the vinculin/alpha-catenin family. The encoded protein plays a role in cell-cell adhesion in muscle cells. Mutations in this gene are associated with arrhythmogenic right ventricular dysplasia, familial 13. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Mar 2014]
Transcript Variant: This variant (3) has multiple differences compared to variant 1. These differences result in distinct 5' and 3' UTRs and cause translation initiation at an alternate start codon compared to variant 1. The encoded protein (isoform b) has a longer N-terminus, a distinct C-terminus, and is shorter compared to 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. The intron between the last two exons of the source sequence is in a repeat-rich region and appears to be an artifact. This intron was replaced by genomic sequence to merge the two exons into one long exon.