

OriGene Technologies, Inc.

9620 Medical Center Drive, Ste 200 Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com CN: techsupport@origene.cn

Product datasheet for SC204643

Carbonic Anhydrase I (CA1) (NM_001128830) Human 3' UTR Clone

Product data:

Product Type:	3' UTR Clones
Product Name:	Carbonic Anhydrase I (CA1) (NM_001128830) Human 3' UTR Clone
Vector:	pMirTarget (PS100062)
Symbol:	CA1
Synonyms:	CA-I; CAB; Car1; HEL-S-11
ACCN:	NM_001128830
Insert Size:	982 bp
Insert Sequence:	<pre>>SC204643 3'UTR clone of NM_001128830 The sequence shown below is from the reference sequence of NM_001128830. The complete sequence of this clone may contain minor differences, such as SNPs. Blue=Stop Codon Red=Cloning site GGCAAGTTGGACGCCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG TAACAATTGGCAGAGCTCAGAATTCAAGCGATCGCC AAGGGCAGAACAGTGAGAGCTCATTTTGATGATATTGAGAAGAAACTTGTCCTTCCT</pre>
	ACGCGTAAGCGGCCGCGGCATCTAGATTCGAAGAAAATGACCGACC
Restriction Sites:	Sgfl-Mlul



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OTI Disclaimer:	Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).
Components:	The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.
RefSeq:	<u>NM 001128830.4</u>
Summary:	Carbonic anhydrases (CAs) are a large family of zinc metalloenzymes that catalyze the reversible hydration of carbon dioxide. They participate in a variety of biological processes, including respiration, calcification, acid-base balance, bone resorption, and the formation of aqueous humor, cerebrospinal fluid, saliva and gastric acid. They show extensive diversity in tissue distribution and in their subcellular localization. This CA1 gene is closely linked to the CA2 and CA3 genes on chromosome 8. It encodes a cytosolic protein that is found at the highest level in erythrocytes. Allelic variants of this gene have been described in some populations. Alternative splicing and the use of alternative promoters results in multiple transcript variants. [provided by RefSeq, Nov 2016]
Locus ID:	759
MW:	38.4

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