

Product datasheet for RC225351L3V

OriGene Technologies, Inc.

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Carbonic Anhydrase I (CA1) (NM_001128831) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type: Lentiviral Particles

Symbol: Carbonic Anhydrase I

Synonyms: CA-I; CAB; Carl; HEL-S-11

Mammalian Cell Puromycin

Selection:

Vector: pLenti-C-Myc-DDK-P2A-Puro (PS100092)

Tag: Myc-DDK

ACCN: NM_001128831

ORF Size: 783 bp

ORF Nucleotide Sequence: The ORF insert of this clone is exactly the same as(RC225351).

OTI Disclaimer: The molecular sequence of this clone aligns with the gene accession number as a point of

reference only. However, individual transcript sequences of the same gene can differ through naturally occurring variations (e.g. polymorphisms), each with its own valid existence. This clone is substantially in agreement with the reference, but a complete review of all prevailing

variants is recommended prior to use. More info

OTI Annotation: This clone was engineered to express the complete ORF with an expression tag. Expression

varies depending on the nature of the gene.

RefSeq: <u>NM_001128831.1</u>

RefSeq Size: 1265 bp

RefSeq ORF: 786 bp

Locus ID: 759

UniProt ID: <u>P00915</u>

Cytogenetics: 8q21.2





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Protein Families: Druggable Genome

Protein Pathways: Nitrogen metabolism

MW: 28.9 kDa

Gene 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]