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Product datasheet for RC206616L4V

Carbonic Anhydrase I (CA1) (NM_001738) Human Tagged ORF Clone Lentiviral Particle

Product data:

Product Type:	Lentiviral Particles
Product Name:	Carbonic Anhydrase I (CA1) (NM_001738) Human Tagged ORF Clone Lentiviral Particle
Symbol:	Carbonic Anhydrase I
Synonyms:	CA-I; CAB; Car1; HEL-S-11
Mammalian Cell Selection:	Puromycin
Vector:	pLenti-C-mGFP-P2A-Puro (PS100093)
Tag:	mGFP
ACCN:	NM_001738
ORF Size:	783 bp
ORF Nucleotide Sequence:	`The ORF insert of this clone is exactly the same as(RC206616).`
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:	NM_001738.1
RefSeq Size:	1319 bp
RefSeq ORF:	786 bp
Locus ID:	759
UniProt ID:	P00915
Cytogenetics:	8q21.2
Domains:	carb_anhydrase
Protein Families:	Druggable Genome

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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]