

## Product datasheet for **SC329619**

### ALDH7A1 (NM\_001201377) Human Untagged Clone

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** ALDH7A1 (NM\_001201377) Human Untagged Clone  
**Tag:** Tag Free  
**Symbol:** ALDH7A1  
**Synonyms:** ATQ1; EPD; PDE  
**Vector:** pCMV6-Entry (PS100001)  
**Fully Sequenced ORF:** >SC329619 representing NM\_001201377.  
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

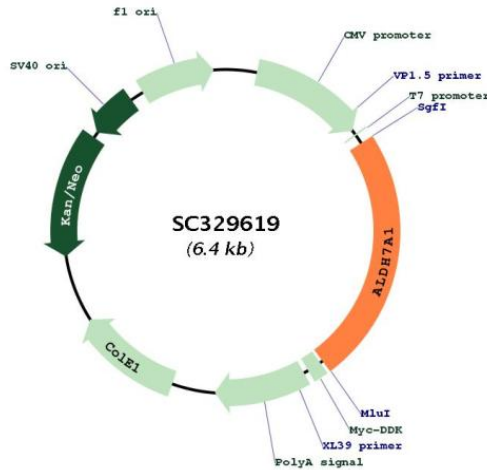
```

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GGAATCAAGTTTCAGTAA
  
```

**Restriction Sites:** SgfI-MluI



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**Plasmid Map:**


**ACCN:** NM\_001201377

**Insert Size:** 1536 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\\_001201377.1](#)

**RefSeq Size:** 4953 bp

**RefSeq ORF:** 1536 bp

**Locus ID:** 501

**UniProt ID:** [P49419](#)

**Cytogenetics:** 5q23.2

<b>Protein Families:</b>	Druggable Genome
<b>Protein Pathways:</b>	Arginine and proline metabolism, Ascorbate and aldarate metabolism, beta-Alanine metabolism, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Limonene and pinene degradation, Lysine degradation, Metabolic pathways, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation
<b>MW:</b>	55.4 kDa
<b>Gene Summary:</b>	<p>The protein encoded by this gene is a member of subfamily 7 in the aldehyde dehydrogenase gene family. These enzymes are thought to play a major role in the detoxification of aldehydes generated by alcohol metabolism and lipid peroxidation. This particular member has homology to a previously described protein from the green garden pea, the 26g pea turgor protein. It is also involved in lysine catabolism that is known to occur in the mitochondrial matrix. Recent reports show that this protein is found both in the cytosol and the mitochondria, and the two forms likely arise from the use of alternative translation initiation sites. An additional variant encoding a different isoform has also been found for this gene. Mutations in this gene are associated with pyridoxine-dependent epilepsy. Several related pseudogenes have also been identified. [provided by RefSeq, Jan 2011]</p> <p>Transcript Variant: This variant (1) encodes two isoforms resulting from the use of alternative in-frame translation initiation codons. The longer isoform (1) is derived from an upstream AUG (at nt 193-195), while the shorter isoform (2) is derived from a downstream AUG (at nt 277-279). This RefSeq represents the shorter isoform, which is found in the cytosol (PMIDs: 20207735 and 19885858). Sequence Note: This Refseq, containing three potential in-frame translation initiation codons (all with weak Kozak signals), is annotated with a CDS starting from a downstream start codon (at nt 277-279), which results in a shorter, soluble isoform that is localized in the cytosol (PMIDs: 20207735 and 19885858). A longer isoform, resulting from the use of an upstream start codon (at nt 193-195) and localized in the mitochondria, is represented in a separate RefSeq (NM_001182.4). The use of another upstream start codon (at nt 112-114) that is present in only a subset of higher mammals, would increase the protein length by another 27 aa. This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The extent of this transcript is supported by transcript alignments.</p>