

Product datasheet for **SC331965**

Aldolase (ALDOA) (NM_001243177) Human Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Aldolase (ALDOA) (NM_001243177) Human Untagged Clone
Tag: Tag Free
Symbol: Aldolase
Synonyms: ALDA; GSD12; HEL-S-87p
Vector: pCMV6-Entry (PS100001)
Fully Sequenced ORF: >SC331965 representing NM_001243177.
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

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ATGGCAAGGCGCAAGCCAGAAGGGTCCAGCTTCAACATGACCCACCTGTCCATGGCTATGGCCTTTTCC
TTTCCCCAGTTGCCAGTGGGCACTCCACCCTCAGCTGGGCAACACCCAGCACCAGACAGAGTTAGGA
AAGGAAGTTGCTACTACCAGCACCATGCCCTACCAATATCCAGCACTGACCCGGAGCAGAAGAAGGAG
CTGTCTGACATCGCTCACCGCATCGTGGCACCTGGCAAGGGCATCCTGGTGCAGATGAGTCCACTGGG
AGCATTGCCAAGCGGCTGCAGTCCATTGGCACCGAGAACACCGAGGAGAACCAGCGCTTCTACCGCCAG
CTGCTGCTGACAGCTGACGACCGGTGAACCCCTGCATTGGGGGTGCATCCTCTCCATGAGACTC
TACCAGAAGGCGGATGATGGGCGTCCCTTCCCCAAGTTATCAAATCCAAGGGCGGTGTTGTGGGCATC
AAGGTAGACAAGGGCGTGGTCCCCTGGCAGGGACAAATGGCGAGACTACCACCAAGGGTTGGATGGG
CTGTCTGAGCGCTGTGCCAGTACAAGAAGGACGGAGCTGACTTCGCCAAGTGGCGTTGTGTGCTGAAG
ATTGGGGAACACACCCCTCAGCCCTCGCCATCATGGAAAATGCCAATGTTCTGGCCGTTATGCCAGT
ATCTGCCAGCAGAATGGCATTGTGCCATCGTGGAGCCTGAGATCCTCCCTGATGGGGACCATGACTTG
AAGCGTGCCAGTATGTGACCGAGAAGGTGCTGGCTGTGTCTACAAGGCTCTGAGTGACCACCACATC
TACCTGGAAGGCACCTTGCTGAAGCCCAACATGGTCACCCAGGCCATGCTTGCAGTCAAGATTTTCT
CATGAGGAGATTGCCATGGCGACCGTACAGCGCTGCGCCGCACAGTGCCCCCGCTGTCACTGGGATC
ACCTTCTGTCTGGAGGCCAGAGTGAGGAGGAGGCGTCCATCAACCTCAATGCCATTAACAAGTGCCCC
CTGCTGAAGCCCTGGGCCCTGACCTTCTCTACGGCCGAGCCCTGCAGGCCTCTGCCCTGAAGGCCTGG
GGCGGGAAGAAGGAGAACCTGAAGGCTGCGCAGGAGGAGTATGTCAAGCGAGCCCTGGCCAACAGCCTT
GCCTGTCAAGGAAAGTACTCCGAGCGGTGAGGCTGGGGCTGCTGCCAGCGAGTCCCTCTCTGCTCT
AACCACGCCTATAA
  
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Restriction Sites: SgfI-MluI
ACCN: NM_001243177
Insert Size: 1257 bp



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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:	<ol style="list-style-type: none">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_001243177.1
RefSeq Size:	1751 bp
RefSeq ORF:	1257 bp
Locus ID:	226
UniProt ID:	P04075
Cytogenetics:	16p11.2
Protein Families:	Druggable Genome
Protein Pathways:	Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Metabolic pathways, Pentose phosphate pathway
MW:	45.3 kDa
Gene Summary:	<p>This gene encodes a member of the class I fructose-bisphosphate aldolase protein family. The encoded protein is a glycolytic enzyme that catalyzes the reversible conversion of fructose-1,6-bisphosphate to glyceraldehyde 3-phosphate and dihydroxyacetone phosphate. Three aldolase isozymes (A, B, and C), encoded by three different genes, are differentially expressed during development. Mutations in this gene have been associated with Glycogen Storage Disease XII, an autosomal recessive disorder associated with hemolytic anemia. Disruption of this gene also plays a role in the progression of multiple types of cancers. Related pseudogenes have been identified on chromosomes 3 and 10. [provided by RefSeq, Sep 2017]</p> <p>Transcript Variant: This variant (6) differs in the 5' UTR and 5' coding region, and uses an alternate start codon, compared to variant 1. The resulting isoform (2) is longer at the N-terminus, compared to isoform 1. 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.</p>