

Product datasheet for **SC325695**

LDHA (NM_001135239) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	LDHA (NM_001135239) Human Untagged Clone
Tag:	Tag Free
Symbol:	LDHA
Synonyms:	GSD11; HEL-S-133P; LDHM; PIG19
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC325695 representing NM_001135239. Blue=Insert sequence Red=Cloning site Green=Tag(s)

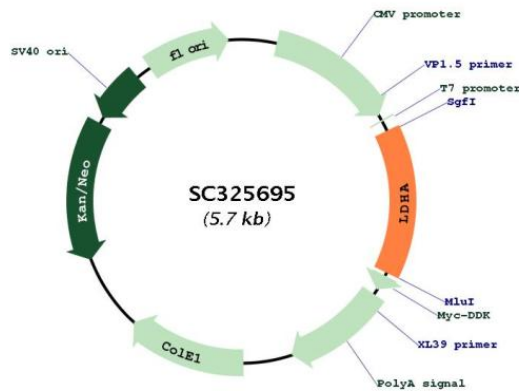
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GCTCGTTT TAGTGAACCGTCAGAATTTTGT AATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCC CGGATCGCC
ATGGCAACTCTAAAGGATCAGCTGATTTATAATCTTCTAAAGGAAGAACAGACCCCCAGAATAAGATT
ACAGTTGTTGGGGTTGGTGTCTGGCATGGCCTGTGCCATCAGTATCTTAATGAAGGACTTGGCAGAT
GAACTTGCTCTTGTGTATGTCATCGAAGACAAATTGAAGGGAGAGATGATGGATCTCCAACATGGCAGC
CTTTTCCTTAGAACACCAAAGATTGTCTCTGGCAAAGTGGATATCTTGACCTACGTGGCTTGAAGATA
AGTGGTTTTCCAAAAACCGTGTATTGGAAGCGGTTGCAATCTGGATTCAGCCCGATTCCGTTACCTA
ATGGGGAAAGGCTGGGAGTTCACCCATTAAGCTGTCATGGTGGTCTTGGGGAACATGGAGATTCC
AGTGTGCCTGTATGGAGTGAATGAATGTTGCTGGTGTCTCTGAAGACTCTGCACCCAGATTTAGGG
ACTGATAAAGATAAGGAACAGTGAAAGAGGTTACAAGCAGGTGGTTGAGAGTGCTTATGAGGTGATC
AACTCAAAGGCTACACATCCTGGGCTATTGGACTCTCTGTAGCAGATTTGGCAGAGAGTATAATGAAG
AATCTTAGCGGGTGCACCCAGTTCCACCATGATTAAGGGTCTTTACGGAATAAAGGATGATGTCTTC
CTTAGTGTCTTGCATTTTGGGACAGAATGGAATCTCAGACCTTGTGAAGGTGACTCTGACTTCTGAG
GAAGAGGCCCGTTTGAAGAAGAGTGCAGATACACTTTGGGGATCCAAAAGGAGCTGCAATTTAA
ACGGGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGCGC
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Restriction Sites: SgfI-MluI



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Plasmid Map:



ACCN: NM_001135239

Insert Size: 825 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).

OTI Annotation: This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

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_001135239.1](#)

RefSeq Size: 2052 bp

RefSeq ORF:	825 bp
Locus ID:	3939
UniProt ID:	P00338
Cytogenetics:	11p15.1
Protein Families:	Druggable Genome
Protein Pathways:	Cysteine and methionine metabolism, Glycolysis / Gluconeogenesis, Metabolic pathways, Propanoate metabolism, Pyruvate metabolism
MW:	30.2 kDa
Gene Summary:	<p>The protein encoded by this gene catalyzes the conversion of L-lactate and NAD to pyruvate and NADH in the final step of anaerobic glycolysis. The protein is found predominantly in muscle tissue and belongs to the lactate dehydrogenase family. Mutations in this gene have been linked to exertional myoglobinuria. Multiple transcript variants encoding different isoforms have been found for this gene. The human genome contains several non-transcribed pseudogenes of this gene. [provided by RefSeq, Sep 2008]</p> <p>Transcript Variant: This variant (2) lacks an in-frame exon in the central coding region, compared to variant 1. The resulting isoform (2) lacks a segment of the LDH domain but has the same N- and C-termini, 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>