

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:	<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_004092.2 , NP_004083.2
RefSeq Size:	1326 bp
RefSeq ORF:	873 bp
Locus ID:	1892
UniProt ID:	P30084
Cytogenetics:	10q26.3
Domains:	ECH
Protein Pathways:	beta-Alanine metabolism, Butanoate metabolism, Fatty acid elongation in mitochondria, Fatty acid metabolism, Limonene and pinene degradation, Lysine degradation, Metabolic pathways, Propanoate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation
Gene Summary:	The protein encoded by this gene functions in the second step of the mitochondrial fatty acid beta-oxidation pathway. It catalyzes the hydration of 2-trans-enoyl-coenzyme A (CoA) intermediates to L-3-hydroxyacyl-CoAs. The gene product is a member of the hydratase/isomerase superfamily. It localizes to the mitochondrial matrix. Transcript variants utilizing alternative transcription initiation sites have been described in the literature. [provided by RefSeq, Jul 2008]