

Recombinant Human ACAD8, T7-tagged

Cat. No. ACAD8-26H Lot. No. (See product label)

SPECIFICATION

Product Overview	Recombinant Human Acyl-Coenzyme A Dehydrogenase 8 produced in <i>E. Coli</i> is a non-glycosylated, polypeptide chain containing amino acids 1-415 and having a total molecular mass of 47.7 kda. ACAD8 contains T7 tag at the N-terminus. ACAD-8 is purified by proprietary chromatographic techniques.
Species	Human
Source	E.coli
ProteinLength	1-415 a.a.
Description	Acyl CoA dehydrogenase is the enzyme used to catalyze the first step of β -oxidation in Fatty acid metabolism. Acyl-coenzyme A (CoA) dehydrogenases (ACADs) are a family of mitochondrial enzymes that catalyze the first dehydrogenation step in the β -oxidation of fatty acyl-CoA derivatives. Several human ACADs exist and all ACADs catalyze the same initial dehydrogenation of the substrate at the beta-carbon atom and require electron transfer flavoprotein as an electron acceptor. The predicted 415-amino acid ACAD8 protein contains many of the residues conserved in most other ACADs, including an active site glutamic acid residue and residues important for tetramer formation.
Physical Appearance	Sterile Filtered clear solution.
Purity	Greater than 95.0% as determined by SDS-PAGE.

Tel: 1-631-559-9269 1-516-512-3133

Email: info@creative-biomart.com Fax: 1-631-938-8127

45-1 Ramsey Road, Shirley, NY 11967, USA

Formulation	Acyl-Coenzyme A Dehydrogenase 8 at a concentration of 0.1 mg/ml in 10 mM Tris, pH 8.0, 0.1% Triton X-100, 0.002% NaN ₃ , 10 mM DTT.
Applications	• ELISA • MS • Inhibition Assays • Western Blotting
Stability	ACAD8 although stable at 14°C for 1 week, should be stored desiccated below -18°C. For long term storage it is recommended to add a carrier protein (0.1% HSA or BSA). Please prevent freeze-thaw cycles.

GENE INFORMATION

Gene Name	ACAD8 acyl-Coenzyme A dehydrogenase family, member 8 [Homo sapiens]
Synonyms	ACAD8; acyl-Coenzyme A dehydrogenase family, member 8; ACAD-8; FLJ22590; Isobutyryl-CoA dehydrogenase, mitochondrial; Acyl-CoA dehydrogenase family member 8; Activator-recruited cofactor 42 kDa component; ARC42
Gene ID	27034
mRNA Refseq	NM_014384
Protein Refseq	NP_055199
UniProt ID	Q9UKU7
Chromosome Location	11q25
MIM	604773
Pathway	Metabolic pathways; Valine, leucine and isoleucine degradation; Metabolism of amino

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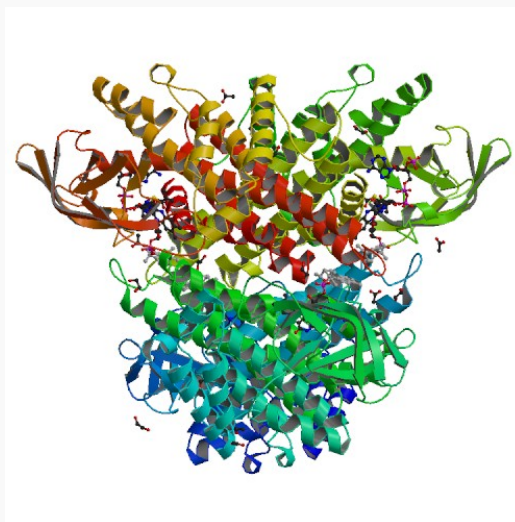
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acids

Function

FAD binding; acyl-CoA dehydrogenase activity

PDB rendering based
on 1rx0.



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