

Enolase-phosphatase E1

Cat. No. CBCRY26 Lot. No. (See product label)

SPECIFICATION

Product Overview

Source	E.coli
Background	Enolase-phosphatase E1 (MASA) is a bifunctional enzyme in the ubiquitous methionine salvage pathway that catalyzes the continuous reactions of 2,3-diketo-5-methylthio-1-phosphopentane to yield the acyl-reductone metabolite using Mg ²⁺ as cofactor. In this study, we have determined the crystal structure of MASA and its complex with a substrate analog to 1.7Å resolution by multi-wavelength anomalous diffraction and molecular replacement techniques, respectively.
Protein Classification	Hydrolase
Structure Weight	29316.11 Da
Polymer	1
Molecule	E-1 Enzyme
Chain Length	285 amino acids
PDB ID	1ZS9
MMDB ID	33918

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Method	X-Ray Diffraction
Resolution	1.7Å
Ligand Chemical Component	Selenomethionine
Reference	Wang, H., Pang, H., Bartlam, M., Rao, Z. (2005) Crystal Structure of Human E1 Enzyme and its Complex with a Substrate Analog Reveals the Mechanism of its Phosphatase/Enolase J.Mol.Biol. 348: 917-926

GENE INFORMATION

Gene Name	ENOPH1
Synonyms	DKFZp586M0524; E1; FLJ12594; MASA; MST145; E-1 enzyme; Enolase-phosphatase E1; MSTP145 protein; acireductone synthase; EC 3.1.3.77; 2,3-diketo-5-methylthio-1-phosphopentane phosphatase; MASA homolog
UniProt ID	Q9UHY7
Gene ID	58478
Chromosome Location	4q21.22
Function	magnesium ion binding; phosphor-glycolate phosphatase activity; acireductone synthase activity; metal ion binding; catalytic activity

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