# Enolase-phosphatase E1

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

## SPECIFICATION

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| **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 aci-reductone metabolite using Mg2+ as cofactor. In this study, we have determined the crystal structure of MASA and its complex with a substrate analog to 1.7A 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 |
| **Method** | X-Ray Diffraction |

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|---|---|
| **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

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| **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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