1A, 5A, NE3A/ 2012G503, 2013G003

Crystal structure of L-serine 3-dehydrogenase complexed with NAD(P)$^+$ from *Pyrobaculum calidifontis*

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1 Introduction

L-Serine dehydrogenase (L-SerDH; EC 1.1.1.276) catalyzes the dehydrogenation of L-serine in the presence of NAD(P)$^+$. This enzyme catalyzes dehydrogenation at the β-carbon (C3) position of L-serine. The suspected product of the reaction is 2-aminomalonate semialdehyde, which nonenzymatically decomposes into 2-aminoacetaldehyde and CO_2.

Currently, no L-SerDH has been so far reported in archaea, the third domain of life, or in hyperthermophiles. Within the genomic sequence of an aerobic hyperthermophilic archaeon, *Pyrobaculum calidifontis*, we found a gene (open reading frame identification number Pcal_0699) whose predicted amino acid sequence exhibits 36% identity with that of *P. aeruginosa* L-SerDH. Moreover, we succeeded in the expression of the gene in *E. coli* and confirmed that the gene product surely exhibits L-SerDH activity [1]. The *P. calidifontis* enzyme is probably the most thermostable L-SerDH described to date, which makes this enzyme potentially useful for stereospecific synthesis of L-serine and measurement of L-serine in foods and in a variety of other environments. The structure information of this thermostable L-SerDH may be available for the development of its application. In this study, we expressed the gene, characterized the enzyme produced, and revealed that the enzyme is an extremely thermostable L-SerDH. We also determined the crystal structure of this enzyme at 2.0 Å resolution in the presence of NADP$^+$. This is the first description of the crystal structure of L-SerDH from archaea.

2 Experiment

Multiple-wavelength (0.9789, 0.9792, 0.9640 Å) data sets for *P. calidifontis* L-SerDH-NADP$^+$ were collected on the beamline 1A, 5A and NE3A at the Photon Factory. The data were processed using HKL2000 and the CCP4 program suite.

3 Results and Discussion

The structure of the NADP$^+$-bound *P. calidifontis* L-SerDH was determined using MAD and was refined at a resolution of 2.0 Å to a crystallographic *R*-factor of 22.7% and a free *R*-factor of 24.2%. The asymmetric unit consisted of one monomer with a solvent content of 58.7%, which corresponds to a Matthew's coefficient of 3.0 Å^{3}Da^{-1}. The final model was comprised of amino acid residues 1 to 207, 211 to 283, one NADP$^+$ coemzyme and 72 waters (Fig. 1, 2).

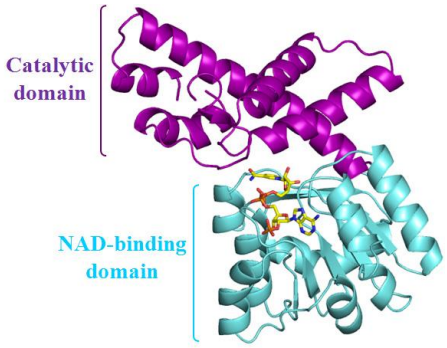

Fig.1 Overall structure of *P. calidifontis* L-SerDH. The figure shown is a ribbon representation of the *P. calidifontis* L-SerDH monomer. The NADP$^+$ binding and catalytic domains are shown in cyan and purple, respectively. NADP$^+$ (yellow) is shown as stick model.

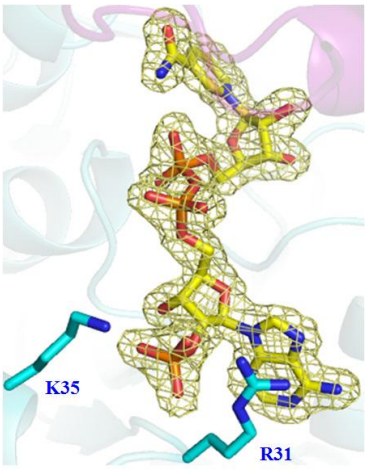

Fig.2 NADP$^+$ binding site of *P. calidifontis* L-SerDH**.** NADP$^+$-bound enzyme (cyan) and NADP$^+$ are shown. Residues that interact with NADP$^+$ are labeled. The final σ_A-weighted *Fo-Fc* omit electron density map for the NADP$^+$ is shown at the 2σ level.

Reference

[1] K. Yoneda *et al*., *Acta Crystallographica Section F.* (2013) **F69**, 134-136.

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