The Crystal Structure of L-proline Dehydrogenase in a Hyperthermophilic Archaeon

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Two different type of archaeal L-proline dehydrogenase (PDH) was found in *P. horikoshii* OT-3. PDH1 formed an operon that consisted of two consecutive genes, PH1363 and PH1364 and the molecular masses of α and β subunit were determined to be about 56 and 43kDa, respectively. The native molecular mass of PDH1 is 440kDa with ($\alpha\beta4$ hetero-octamer.

We have purified recombinant PDH1, crystallized and determined the crystal structure of PDH1 from *P. horikoshii* at 2.8Å resolution. The structure revealed that β subunit, which bears PDH activity, was similar to monomeric sarcosine oxidase. FAD was bound in the β subunit non-covalently. The α subunit contains a dinucleotide fold domain with unexpected ATP, a central domain, a N-terminal domain and Cys-clustered domain. Furthermore FMN is bound between α and β subunits. The structure of α and β subunit is totally different except the dinucleotide domain, but it is suggested that each structure diverged from common ancestral flavoenzyme formed a complex to make a new electron transport pathway.

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