

Poster Presentation

MS69.P09

Crystal Structure of the Carbon-Phosphorus Lyase Complex from Escherichia coli

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Phosphorus is an essential element for all living cells and is usually taken up in the form of phosphate. A number of microorganisms, however, are capable of extracting phosphorous from organic phosphonate compounds, which are characterized by a stable carbon-phosphorus (C-P) bond (1). The metabolic pathway responsible for phosphonate degradation is still poorly understood, but the process is known to involve two reactions before the actual C-P bond cleavage, which has been proposed to take place via a radical mechanism. A key component in the process is C-P lyase, an enzyme encoded by *phnJ* within the *phn* operon (2). To get a better insight into the mechanism of this complex degradation pathway, we have determined the crystal structure of the core of a multi-subunit enzymatic complex including the C-P lyase component with a total molecular mass of 220 kDa (3). The structure reveals the overall architecture of the C-P lyase and has important implications for our understanding of enzyme mechanism and catalysis.

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Keywords: C-P lyase, phosphonate degradation, *phn* operon