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Crystallization and preliminary X-ray crystallographic analysis of Quinolinate phosphoribosyltransferase of *Helicobacter pylori*

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The quinolinic acid(QA) phosphoribosyltransferase (PRTase) (EC 2.4.2.19), is a key enzyme involved in NAD^+ biosynthesis in prokaryotes and eukaryotes. The QAPRTase produces nicotinic acid mononucleotide (NAMN) from QA and 5-phosphoribosyl-1-pyrophosphate (PRPP). For this reaction, the QA is decarboxylated (Fig.1). Produced NAMN is used to a synthesis of nicotinate adenine dinucleotide(NAD^+).

The QAPRTase is a type II PRTase and only known example of that. The type II PRTase has two domains. One is N-terminal four stranded β-sandwich domain and the other is a C-terminal α/β barrel domain. The three dimensional structures of QAPRTase from *Mycobacterium tuberculosis* and *Salmonella typhimurium* have been reported in complex with their substrates(QA, NAMN) and substrate analogs(PA, PRPCP).

However, Many QAPRTases have dimeric state in *Escherichia coli*, *Salmonella typhimurium*, *Mycobacterium tuberculosis*, and caster bean. But some hexameric QAPRTases have been reported from other sources such as hog, rat and human. The enzyme exists as a dimer and a hexamer depending on the source. The protein sequence identity between *Hp*-QAPRTase and other QAPRTase is about 30%; *Mycobacterium tuberculosis* (34%), *Salmonella typhimurium* (32%), *Escherichia coli* (32%), *Mus musculus* (33%), human (29%) and so on (BLAST). Most QAPRTases have similar sequence identity with QAPRTase of *Helicobacter pylori*. The *Hp*-QAPRTase has been purified as a hexamer during size exclusion chromatography in physiological condition.

This report describes the characteristics of *Hp*-QAPRTase and the crystal structure of *Hp*-QAPRTase in complex with quinolinic acid (QA), nicotinic acid mononucleotide (NAMN) and analogue of quinolinic acid, phthalic acid (PA).