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**Structure of GTP Dependent Phosphoenolpyruvate Carboxykinase (PCK) from *Corynebacterium glutamicum*.** Lata Prasad, Sanjukta Aich, Fumie Imabayashi, Louis Delbaere, Biochemistry, Univ. of Saskatchewan, 107 Wiggins Road, Saskatoon Sk S7H 5J7, CANADA.

Substrate free structure of GTP-dependent phosphoenolpyruvate carboxykinase (PCK) from gram positive bacterium *Corynebacterium glutamicum* has been solved from 2.1 Å resolution data. Initial phasing of the diffracted data has been obtained by PHASER program using 1KHF (human cytosolic PCK structure) as a starting model. It shows a P2 (1) symmetry with  $a=72.336$ ,  $b=118.055$ ,  $c=152.931$ ,  $\beta=96.443$  and have 4 molecules in each asymmetric unit. PCK is one of the key enzymes in the gluconeogenesis process which controls the blood sugar level during fasting in mammals. All the eukaryotic mammalian PCKs are GTP-specific though eukaryotic archaea species show mostly ATP specificities. Bacterial PCKs can be ATP-or GTP-specific but all plant PCKs are ATP-specific. Alignment of PCK enzymes shows that the ATP- and GTP- specific binding sites are somewhat conserved based on the nucleotide binding specificities with few exceptions which do not have any clear ATP- or GTP-specific binding sites. Phylogenetic studies have been performed to understand the evolutionary relationship of various PCKs from different sources. This research was funded by a CIHR grant to L.T.J.D.