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## Kinetic study of proline dehydrogenase from *saccharomyces cerevisiae* (yeast)

Proline dehydrogenase is the first enzyme in the proline catabolic pathway which converts proline to $\Delta^1$-pyrroline-5-carboxylate (P5C). Function of this enzyme is very important in regulating proline levels in all organisms. Proline plays a central role in metabolism and is recognized as an important amino acid in bioenergetics, osmoprotectant, cellular redox control, apoptosis and cancer.

In bacteria, proline dehydrogenase is a part of a multifunctional enzyme called proline utilization A (PutA). PutA consists of a proline dehydrogenase domain and a $\Delta^1$-pyrroline-5-carboxylate dehydrogenase domain which catalyze the two step conversion of proline to glutamate. In addition to its enzymatic activities PutA is an autorepressor of *PutA* gene. In contrast, eukaryotic proline dehydrogenase is a monofunctional enzyme.

Although prokaryotic Proline dehydrogenase (PutA) is exclusively studied, little information is known for the eukaryotic enzyme. Therefore, our goal was to purify and characterize the eukaryotic proline dehydrogenase. In our work, we have over-expressed the eukaryotic proline dehydrogenase of yeast (Put1p) in *E .coli* and successfully purified the enzyme. Kinetic study of the purified enzyme revealed a $K_M$ of 35.7mM and that D-proline is a mix type inhibitor of proline dehydrogenase. Kinetic analysis of the purified enzyme will be discussed.

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