Thandeeswaran Murugesan, Karuppuswamy Velliayadevar, Murugesh Easwaran, Kiran K.G., Ayub Nawaz K.A., Mahendran Ramasamy, Palaniswamy Muthusamy and Angayarkanni Jayaraman*

Molecular architecture of pterin deaminase from Saccharomyces cerevisiae NCIM 3458

https://doi.org/10.1515/pterid-2017-0011

Received June 20, 2017; accepted August 16, 2017; previously published online October 14, 2017

Abstract: As early as 1974, reports have confirmed the anticancer activity of pterin deaminase isolated from fungi. The enzyme has also been reported in bacteria, fungi and slime mold genera, but the enzyme characterization was effetely done. The present study attempted to purify and characterize pterin deaminase enzyme from Saccharomyces cerevisiae NCIM 3458. The protein was extracted from the extracellular extract by using the ethanol precipitation method. Partial purification of pterin deaminase enzyme was achieved by ion exchange chromatography (Hi-Trap QFF) by fast protein liquid chromatography (AKTA purifier). The molecular weight of the protein was apparently determined by SDS-PAGE, and the presence of pterin deaminase was confirmed by activity staining. The purified enzyme was further biochemically characterized. Molecular docking studies showed higher binding affinity towards folic acid interaction. The structural characterization of this protein may open the windows for new drug targets for cancer therapy.

Keywords: enzyme activity; optimization; protein structure; pterin deaminase; *Saccharomyces cerevisiae*.

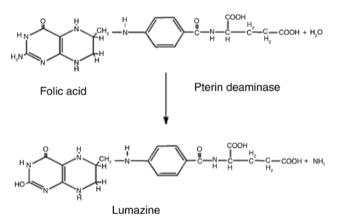
Introduction

Pteridine research has been renowned as eminent for scores of natal process [1]. It also acts as essential cofactors

University, Coimbatore 641021, Tamilnadu, India

in the process of cell metabolism and has turned into a focal point of cancer screening research because of reported varying pteridine levels in cancers [2]. In the pathway of pteridines, one of the most momentous uncharted enzymes was pterin deaminase. Most of the studies have focused only on the pteridines and its derivatives, whereas the studies on pterin deaminase are countable. Pterin deaminase is an enzyme belonging to the family of hydrolases, acting on carbon-nitrogen bonds other than peptide bonds. The reaction took place as follows [3].

2-amino-4-hydroxypteridine + $H_2 0 \Longrightarrow$ 2,4-dihydroxypteridine + NH_2



The pterin deaminases were disseminated as intracellular, membrane-bound or extracellular enzyme in a spacious variety of prokaryotic and eukaryotic sources [4]. The first report on the intracellular pterin deaminase was isolated from the bacterium Alcaligenes metalcaligenes by Levenberg and Hayaishi in 1959 [5]. However, extracellular pterin deaminase was reported in eukaryotic organisms such as Aspergillus sp., Mucor sp., Rhizopus sp. and Penicillium sp. [6–8]. Rembold and Simmersbach [9] revealed that the pterin deaminase present in rat liver showed the highest substrate specificity. Besides this report in mammalian system, there are no other research findings in mammalian pterin deaminase. The 3D structure of the pterin deaminase enzyme is not available in the database plow at present. This uncharacteristic pterin deaminase is lighting an interest in developmental and neuronal biologist. The structure

^{*}Corresponding author: Angayarkanni Jayaraman, Cancer Therapeutics Lab, Department of Microbial Biotechnology, Bharathiar University, Coimbatore 641046, Tamilnadu, India, E-mail: angaibiotech@buc.edu.in

Thandeeswaran Murugesan, Karuppuswamy Velliayadevar, Kiran K.G., Ayub Nawaz K.A. and Mahendran Ramasamy: Cancer Therapeutics Lab, Department of Microbial Biotechnology, Bharathiar University, Coimbatore 641046, Tamilnadu, India Murugesh Easwaran: Department of Bioinformatics, Bharathiar University, Coimbatore 641046, Tamilnadu, India Palaniswamy Muthusamy: Department of Microbiology, Karpagam