In silico characterization of a potential Zn2+ ABC transporter

Suraj Kumar Mandal1, Shankar Prasad Kanaujia1
1Department Of Biosciences And Bioengineering, Indian Institute Of Technology Guw, Guwahati, India
E-mail: surajkmandal@iitg.ernet.in

Metalloproteins, the most diverse classes of proteins, require metal ions (Mn2+, Zn2+, Ni2+, Fe2+/3+, etc.) for their regulatory, catalytic and/or structural activities making them inevitable for survival of an organism. One of the most efficient systems of acquiring metal ions inside a bacterial cell is the ATP-binding cassette (ABC) transporters, which are further classified into importers and exporters. Structurally, ABC importers comprises of a transmembrane domain, a nucleotide binding domain and a substrate binding protein (SBP) for substrate acquisition. Being specific to prokaryotes and often accountable for their pathogenicity, SBPs are recognized as potential drug targets. In this study, TTHA0596, a SBP from Thermus thermophilus HB8 is characterized using in silico approaches. Homology search and phylogenetic tree analysis exhibit that TTHA0596 is similar to a group of Zn2+/Mn2+ binding SBPs. Furthermore, TTHA0596 protein attains an unusual structural prototype similar to that of cluster A-I SBPs. Akin to Zn2+ binding SBPs, binding pocket of TTHA0596 is constituted of three histidine residues (His52, His123 and His185). However, the presence of an aspartate (Asp259) and absence of the histidine-rich loop, an attribute of Zn2+ binding SBPs, indicates its possible affinity towards Mn2+ ion. This further led us to identify a subdivision within the Zn2+ binding SBPs, group I display affinity for both Zn2+ and Mn2+ ions, while group II are highly specific towards Zn2+ ion. Our analysis concludes that TTHA0596 protein belongs to group I Zn2+ binding SBPs and thus bear a tendency to bind both Zn2+ and Mn2+ ions.


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