

Poster Presentation

MS001.P06

Structure of ATP-binding protein exhibiting a novel terminal domain

Hema M. K.¹, Lokanath N. K.¹, Pampa K. J.²

¹Department of Studies in Physics, University of Mysore, Manasagangotri, Mysuru, India, ²Department of Studies in Biotechnology, University of Mysore, Manasagangotri, Mysuru, India
E-mail: hema@physics.uni-mysore.ac.in

The ATP binding cassette (ABC) transporters, represent one of the largest superfamilies of primary transporters, which are very essential for various biological functions. The crystal structure of ATP-binding protein from *Pyrococcus horikoshii* has been determined at 2.1 Å resolution. The crystal structure revealed that the protomer has three distinct domains (Large, small and terminal domains). The large domain consists of two thick arms, which resembles 'L' shape. The phosphate binding loop is present in the large domain. ATP molecule is located at the active site interacting with residues at the large domain. Novel terminal domain is observed. The catalytic residues Ser41, Gly 42, Lys45, Thr47, Asp167 are highly conserved. The invariant residue ASP167 interacts with the γ -phosphate of ATP molecule. The residues involved in the dimer interface and the structural feature responsible for thermostability are evaluated. The crystal structure of multiple sugar binding transport ATP-binding protein from *Pyrococcus horikoshii* has been compared with the previously reported crystal structure of ATP-binding subunit of ABC transporter from *Salmonella typhimurium*.

[1] Tam, R. & Saier. M. H. (1993). *Microbiological reviews*, 57, 320-346

[2] Laemmli, U.K. (1970). *Nature*, 227, 680-685

Keywords: [ABC transporters](#), [Pyrococcus horikoshii](#), [protomer](#)