

MS05-2-1 Crystallographic structures of aIF5B from *Pyrococcus abyssi* in its GDP and GTP-bound forms
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Abstract

e/aIF5B is a eukaryotic and archaeal translational GTPase involved in the late steps of translation initiation. After start codon recognition on the small ribosomal subunit and *e*/aIF2 release, *e*/aIF5B-GTP binds the initiator tRNA and catalyzes the joining of the large ribosomal subunit to form a ribosome competent for elongation. *e*/aIF5B is then released in a GDP-bound form. Despite their central role, the mechanisms of GTP-dependent conformational switching is still debated. Here, we present two crystal structures of aIF5B from the hyperthermophilic archeon *Pyrococcus abyssi*. The structure of the full-length protein bound to GDP was refined 2.9 Å resolution. The structure of a C-terminally truncated form of the protein bound to GTP was refined to 1.7 Å resolution. In this structure, one magnesium ion and one sodium ion are tightly bound to the nucleotide. Comparison of both structures highlights the conformational changes associated to the binding of the nucleotides. As for all translational GTPases, the GDP/GTP binding is controlled by the OFF/ON movements of two switch regions. However, other specific regions of aIF5B change their conformation during the GTP/GDP transition. The movement of these regions could be involved in the mechanism of action of the factor on the ribosome.