Molecular functions of the most conserved ABC-protein within ribosome recycling

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The twin ATPase ABCE1 is one of the most conserved proteins within evolution, ubiquitous in eukaryota and archaea. ABCE1 is an essential, multi-domain enzyme which belongs to the ATP-binding cassette subfamily E of ATPases. It consists of two head-to-tail oriented nucleotide-binding domains (NBDs) and it harbors a unique N-terminal region coordinating two FeS clusters. ABCE1 was originally found as the RNase L inhibitor in the innate immune system of higher vertebrates and subsequently identified as an essential factor for HIV-1 RNA/gag capsid assembly. Further it interacts with a number of translation factors and co-localizes with ribosomal subunits, pointing to a much more fundamental role during translation.

We have recently revealed the essential function of ABCE1 in ribosome recycling in archaea, using *Sulfolobus solfataricus* as a model organism. The archaeal system resembles a minimalistic version of the eukaryotic process and serves therefore as an ideal model for functional and structural analysis. Based on this system we analyzed the structural organization of the FeS clusters by EPR spectroscopy and determined the x-ray structure of ABCE1 at 2.0 Å resolution. We further demonstrated that ABCE1 possesses an energy dependent ribosome dissociation activity, enabled via a conformational switch of both NBDs upon ATP binding and hydrolysis. The activity is synergistically enhanced by the archaeal release factor 1, which forms a stable binary complex with ABCE1.