

Crystal structure of YlqF, a circularly permuted GTPase

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The YlqF GTPase subfamily members are broadly conserved in eukaryotes, archaea, and bacteria, and include the stem cell regulator nucleostemin. In *Bacillus subtilis*, YlqF participates in the late step of 50S ribosomal subunit assembly and is targeted to premature 50S subunit lacking ribosomal proteins L16 and L27 to assemble functional 50S subunit through a GTPase activity-dependent conformational change of 23S rRNA. Since there has been no report of the structure of YlqF family GTPase, we have determined the crystal structure of YlqF from *Thermotoga maritima* in complex with a non-hydrolyzable GTP analog, GTP, and GDP. YlqF is a circularly permuted GTPase. It is composed of two domains: an N-terminal G domain and a C-terminal basic α -helical bundle domain. The guanidine nucleotide binding site of the proteins is highly electropositive. The switch-I and II regions of the G domain are displaced from their expected positions, possibly due to the circular permutation of the protein. Mg^{2+} is missing in all three structures, and binding of Mg^{2+} and activation of the protein seemed to require ordering of the switch regions upon binding with the ribosomal subunit.