IN-SILICO CHARACTERIZATION OF A NOVEL DOMAIN OF THE CELL DIVISION PROTEIN AMIC

De Souza, R.F[1,2]. de Souza, S.J.[2] and Gueiros-Filho, F.J.[1]
[1]Departamento de Bioquímica – Instituto de Química - Universidade de São Paulo
[2]Ludwig Institute for Cancer Research – São Paulo Branch
Brasil

In *E. coli*, the last step of cell division involves the complete separation of the daughter cells, which is accomplished through the localized enzymatic activity of AmiC (N-acetilmuramoyl-L-alanine amidase), a periplasmic component of the septal ring. Bernhardt and de Boer (2003) showed that the proteins AmiC and AmiA are exported to the periplasm through the twin-arginine transport system and that AmiC depends on the protein FtsN and an N-terminal region of AmiC to properly localize to the septum. The N-terminal region is capable of localizing GFP fusions to the division septum without AmiC´s enzymatic domain, a property that prompted us to explore whether this region could be an autonomously evolved domain. Using a pipeline for intermediate sequence searches based on PSIBLAST, we demonstrate that the N-terminal region of AmiC is present in several periplasmic proteins of the PilQ and AmiC/B families and is widely distributed among Bacteria. Predictions of secondary structure and disordered regions for this family suggest their members are able to fold in a discrete and well defined ß-sheet rich conformation. We propose this family represents a previously uncharacterized protein domain, which we call tAMIC. Based on its role in *E. coli*, we suggest this domain is involved in protein-protein interactions in the bacterial periplasm.