

*Pseudomonas aeruginosa* is one of the most frequent cause of hospital acquired infections, particularly dangerous for patients of chirurgic, intensive care, transplantation and neonatal units since it could lead to systemic infections and consequently to death. In patients with genetically acquired cystic fibrosis *P. aeruginosa* causes chronical lung infection, which leads to life quality worsening and life span shortening. Infections caused by this bacterium are very difficult to eradicate due to the pathogen high resistance to many antibiotics and high adaptability to changing environmental conditions. Additionally, as a consequence of antibiotics and chemotherapeutics misuse highly resistant strains of *P. aeruginosa* become widely spread. Great adaptive capacity and high resistance to antibacterial therapies may cause future difficulties in eradication of this bacterium. Therefore, it is extremely important to search for novel targets for antibacterial therapy. Our preliminary findings indicate that the hypothetical PA2504 protein deserves special attention in this aspect.

The aim of this study is to determine biological function of this protein and to elucidate its role in complex with negative regulator of exotoxin A –the PtxS protein. Exotoxin A is the most prominent virulence factor of *P. aeruginosa*. Most probably, PA2504 may participate in the PtxS-PtxR regulatory circuit which also regulates glucose catabolism. Interestingly, the PA2504 protein is specific for *P. aeruginosa*. Although, proteins partially similar to PA2504 are present in other pathogenic bacteria there is no homology between PA2504 sequence and any proteins of nonpathogenic species. This observation suggest a special function of PA2504 in *P. aeruginosa* cells most probably connected to pathogenesis.

Over half of 5000 proteins encoded by the *P. aeruginosa* genome has no assigned function. Therefore, knowledge about the biology of this pathogen is very limited. Every new information about these proteins can bring new insight into processes related to virulence of this bacterium. Such knowledge can potentially be used to develop new antibacterial therapies.