



In silico Structure Analysis of *Acinetobacter baumannii* Outer Membrane Protein, BtuB, as a Potential vaccine candidate

Parisa Ghasemi^{1*}, Fatemeh Sefid² ¹Department of Biology,Tarbiat Modares University, Tehran, Iran ²Department of Biology,Shahed University, Tehran-Qom Express Way, Iran *parisa.ghasemi@modares.ac.ir

Abstract: Acinetobacter baumannii is a Gram-negative aerobic bacterium, This is recognized as a notorious opportunistic pathogen mainly prevalent in hospital settings. A. baumannii's ability to adapt and survive in a range of environments has been a key feature for its persistence and success as an opportunistic pathogen. Gram-negative bacteria possess specialized active transport systems that function to transport organometallic cofactors or carriers, such as cobalamins, siderophores, and porphyrins, across their outer membranes. Cobalamins bind to BtuB with nanomolar affinity.BtuB is a β -barrel membrane protein that facilitates transport of cobalamin (vitamin B12) from the extracellular medium across the outer membrane of Escherichia coli. It is thought that binding of B12 to BtuB alters the conformation of its periplasm-exposed N-terminal residues (the TonB box), which enables subsequent binding of a TonB protein and leads to eventual uptake of B12 into the cytoplasm.

Here we describe the topology and 3D structure of a novel antigen which was discovered by mining the bacterial genome and that is very effective in inducing bactericidal antibodies. This antigen is a very good candidate for inclusion in universal vaccines against *Acinetobacter baumannii*.

Keywords: Acinetobacter baumannii, BtuB; 3D structure

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