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The structural approach to vaccine development against ESKAPE pathogens

ESKAPE group includes pathogens with extreme capacities to develop antibiotic resistance, which makes them insusceptible to conventional treatments. Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter sp. are members of this unglorious group. These bacteria are leading etiological agents of dangerous hospital-related nosocomial infections and pose a serious risk to immunocompromised patients [1]. In 2017, the World Health Organisation highlighted five out of six ESKAPE bacteria as the highest threat to human health [2]. Under the framework of the Marie Skłodowska-Curie Action BactiVax - Anti-Bacterial Innovative Vaccines, we are investigating new strategies to combat these pathogens through the development of novel, effective vaccines. These strategies allow to produce long-lasting immunity in a pre-infected patients and prevent the life-threatening conditions. Importantly, introduction of a successful way to protect from diseases will help to stop antibiotics administration, thus limiting the resistance problem [3]. AdcA is a surface exposed, metal-binding lipoprotein from the ABC-transporter family of E. faecium. The protein is a key component in a zinc homeostasis and is an essential molecule for bacterial survival. Also, it is able to induce an immune response in mice [4]. We adopt a structural vaccinology approach to develop enhanced AdcA based vaccine antigens against E.faecium. Moreover, we detected possible cross-reactivity due to conservancy of zinc-binding protein in S.aureus and confirmed activity of our antigen in staphylococci.

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