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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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