COMPUTER-AIDED IDENTIFICATION OF POTENTIAL DRUG TARGETS AND VACCINE CANDIDATES IN BACTERIAL PROTEOMES

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Proteome-wide scanning for proteins with specific characteristics has become a common strategy for the identification of novel targets for biomedical applications. In this context, our group is combining experimental and computational approaches to the analysis of proteomes for the identification of new vaccine candidates and anti-bacterial targets in pathogenic bacteria. At the experimental level, we base our work on the comparison of strains with distinct phenotypes (virulent vs. non-virulent, resistant vs. non-resistant) and the serologic recognition of antigens. At the computational level, we scan the proteomes of the pathogens of interest for proteins with predifined characteristics that are assumed relevant to immunogenicity and/or therapeutic targeting. This work is being performed within a number of collaborative projects that I will introduce in my talk, covering both experimental and computational aspects of our research.