

# **Computational design of vaccine antigens for pandemic preparedness**

**Professor Bruno Correia** - Ecole polytechnique fédérale de Lausanne

Protein design has sparked hopes in the field of vaccinology, in particular, to elicit targeted neutralizing antibody (nAb) responses. Although many potent nAbs have been identified and structurally characterized in complex with their target antigens, the design of immunogens that elicit precise antibody responses remains a major challenge. Thus, one of the central goals for vaccine development is to elicit antibody responses with precisely defined epitope specificities.

The difficulty in developing immunogens that drive the induction of antibodies specific for a restricted subset of epitopes on a single protein, and consequently the fine specificity of the B cell response following immunization continues to be a critical barrier to rational vaccine design. To address these limitations, we used a newly developed computational method to engineer epitope-focused immunogens of the Respiratory Syncytial Virus. This approach enables to target specific epitopes for vaccine and therapeutic antibody development.

In the next stage of our work, we will bring these technologies for use in pathogens with pandemic potential (e.g. Influenza and Coronavirus) in an attempt to target highly conserved regions of these pathogens that may afford broad protection. In a long-term perspective such technologies may enable the development of improved vaccines tailored to personalized immunological profiles.