## Structural Vaccinology applications

Vaccine development has been traditionally a slow procedure. Over the past decade, starting from bacterial genomes, 'Reverse Vaccinology' (RV) introduced a new paradigm in vaccine development; this brought visible results in the field. 'Structural Vaccinology' (SV) presents a step further in streamlining antigen discovery and vaccine development, building on the RV principles, and complementing these with the power of 3D structural information and of computational biology. Focusing on the 3D structures of potential antigen (e.g. cell surface domains), and following their crystallographic analysis, we select epitopes within their (protein) antigens through computational and in vitro approaches. Thus, multiple epitopes (in the form of synthetic peptides) can be produced, *e.g.* to address different serovariants of a given pathogen, yielding a multivalent vaccine formulation, or to assemble immunodiagnostics. This approach requires synergistic scientific contributions, and may revolutionize the times and procedures associated with vaccine development.

Our expertise is in recombinant antigen production, crystal structure analyses, computational prediction of epitopes (within antigen 3D structures), experimental mapping of epitopes (possibly peptide synthesis).

We seek a broader collaboration that would include immunology, cell biology, animal models capabilities, synthetic chemistry to couple epitopes to suitable carriers for presentation, immunodiagnostic design, and experience with vaccine formulation.
Specific neglected disease pathogens must be targeted. Our previous experience concerned a tropical disease pathogen (Burkholderia pseudomallei) that is not included in the H2020 Health current call.

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- DeGregorio, e., Rappuoli, R. (2014) From empiricism to rational design: a personal perspective of the evolution of vaccine development. *Nature Rev. Immunol.* **14**, 505-514. doi:10.1038/nri3694
- Gourlay, L. J., … , Colombo, G., and Bolognesi, M. (2013) Exploiting the Burkholderia pseudomallei acute phase antigen BPSL2765 for structure-based epitope discovery/design in structural vaccinology. *Chemistry & biology* **20**, 1147-1156. doi: 10.1016/j.chembiol.2013.07.010