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X-Ray Crystallography for Vaccine Development Against Emerging Pathogens

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Structural vaccinology is a rational-based approach to design immunogenic antigens aimed at generating an effective vaccine. It combines experimental methods like X-ray crystallography, molecular biology, electron microscopy and mass spectrometry, with computational methods like molecular modelling and epitope prediction [1-4].

The first step of this approach is the three-dimensional structure determination of the antigen using structural biology tools such as X-ray crystallography, cryo-electron microscopy, nuclear magnetic resonance or computational approaches. Key to vaccine development is the knowledge of the exact regions of an antigen that are recognized and bound by antibodies. This knowledge may be acquired using experimental methods named as “epitope mapping”, which makes use of x-ray crystallography, NMR and more recently cryo-EM. These methods provide the whole set of information needed to engineer new constructs with better properties in terms of elicitation of the immune response, stability in solution and ease of production [5]. Using this approach, we have currently identified and developed several vaccine antigens against difficult emerging pathogens. These studies are being implemented through an integrative effort of Partners of the Marie Skłodowska-Curie Action BactiVax - Anti-Bacterial Innovative Vaccines.

References

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Primary author: Dr BERISIO, Rita (CNR - Istituto di Biostrutture e Bioimmagini)

Co-authors: Dr KRAMARSKA, Eliza (CNR - Istituto di Biostrutture e Bioimmagini); Dr SQUEGLIA, Flavia (CNR - Istituto di Biostrutture e Bioimmagini); Dr RUGGIERO, Alessia (CNR - Istituto di Biostrutture e Bioimmagini)

Presenter: Dr BERISIO, Rita (CNR - Istituto di Biostrutture e Bioimmagini)

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