

KEYNOTES



Andrea CARFI holds a Master of Science in Physics for University of Canterbury in UK, Laura degree (equivalent to Master of Science in Chemistry) from Pavia University, Italy, and a PhD in Biophysics from the Université Joseph Fourier in Grenoble, France. He also trained as a postdoctoral fellow in the laboratories of Prof. Stephen Harrison and Prof. Don Wiley at Boston Children's Hospital/Harvard. Dr. Carfi has more than 15 years of experience in drug discovery and vaccine development at Moderna, GSK, Novartis Vaccines and IRBM/Merck. Over the years he has covered roles of increasing responsibility with a focus on structural biology, antigen design, small molecule antivirals discovery and vaccines development. In particular, during the seven years at GSK and Novartis Vaccines, he led the US based Protein Biochemistry team and was responsible for the design, selection, characterization and early development of novel vaccine targets against

infectious diseases, including HIV. Some of these vaccine candidates are now in early and late stage clinical trials. He was also heading the Novartis Vaccines Antigen Design platform across the research sites of Cambridge, US and Siena, Italy. Dr. Carfi joined Moderna in 2017 as Head of Antigen Design and Selection and Project Leader for the CMV vaccine program now in a Phase 1 clinical trial and has become the Head of Research for Infectious Disease at Moderna since January 2019. He is currently leading Research for all Moderna Infectious Disease targets.

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DEVELOPMENT OF THE MODERNA MRNA VACCINE AGAINST COVID-19

ANDREA CARFI

Moderna, Cambridge, USA

The use of protein X-ray crystallography for structure-based design of small-molecule drugs is well-documented and includes several notable success stories. However, it is less well-known that structural biology has emerged as a major tool for the design of novel vaccine antigens. Over the years we have used crystallographic characterization of vaccine antigen structures, alone or in complexes with ligands, antibodies and receptors. The structural insights obtained via protein crystallography have been used to design novel optimized vaccine antigens and demonstrated the impact that antigen design can have on immunogenicity (both potency and breadth).

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