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Shedding Light on SARS-CoV-2 viral protein: Infrared Spectroscopy of the Receptor Binding Domain to Spike Protein

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Proteins, constituting the virus structure, cover a wide and diverse range of functions. Spike glycoprotein (S) of SARS-CoV-2 is a notable example. As the largest structural protein of the virus, the S protein plays a crucial role in attaching to the host receptor ACE2 through its receptor-binding domain (RBD) [1]. The functionalities of these membrane proteins, such as cellular targeting and recognition, transport, and communication are affected by viral and host factors, including immune evasion, conformational masking of binding domains, glycan shielding, as well as the extent of receptor binding affinity and specificity [1,2].
Understanding the secondary structure of the S protein is crucial for gaining insights into its functionality and into the mechanisms occurring in the viral process, and for addressing specific actions aimed at developing specific drugs, diagnostic tools, and prevention strategies. In this context, vibrational spectroscopy, including infrared (IR) spectroscopy, offers various advantages: it is label-free, fast, non-contact and non-destructive, and it allows multi-component assays. In addition, IR frequency region examines localized molecular vibrations of macromolecules, such as carbohydrates, lipids, DNA and RNA, proteins and their mechanisms of reactions, processes like folding, unfolding, and misfolding, and their secondary structures [3,4].
Here, we present an overview of our results obtained from a systematic and comparative study of SARS-CoV-2 viral protein, its individual protein domains, namely the RBD, S1, S2 regions, and S protein, as well as SARS-CoV-2 S1 variants at serological pH, by measuring the amide I absorption band (1600-1700 cm-1) using Attenuated Total Reflection Infrared (ATR-IR) spectroscopy [5-7]. The combination of experimental results with predictive and computational approaches, such as Define Secondary Structure of Proteins (DSSP) predictions, Molecular Dynamics (MD) simulations and protein Surface Polarity Calculations, provides a comprehensive understanding of the protein domains in terms of their secondary structure content, 3D conformation, and interaction with the solvent.

References
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Scholarship elegibility

no

Primary authors: D'ARCO, Annalisa (Sapienza University of Rome, Dept. of Physics); Dr MANCINI, Tiziana

(Sapienza University of Rome, Dept. of Physics); Dr MOSETTI, Rosanna (Sapienza University of Rome, Dept. of Physics); Dr BERTELÀ, Federica (Sapienza University of Rome, Dept. of Physics); Dr LUCHETTI, Nicole (Università Campus Bio-Medico di Roma); Prof. MINICOZZI, Velia (University of Rome Tor Vergata, Dept. of Physics); Prof. LUPI, Stefano (Sapienza University of Rome, Dept. of Physics)

Presenter: D'ARCO, Annalisa (Sapienza University of Rome, Dept. of Physics)

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