

Structural and unstructural biology of viral proteins

Center for Magnetic Resonance (CERM), University of Florence
Sesto Fiorentino (Florence), Italy

January 24-26 2012



“**Structural and Unstructural Biology of Viral Proteins**”, was held in the Center for Magnetic Resonance (CERM) - Florence, Italy 24-26 January 2012 in collaboration with BioNMR and INSTRUCT.

At the meeting scientists with different, complementary expertise gathered to discuss how modern methodologies can contribute to the high resolution characterization of viral proteins. This topic is central for the research activities of the IDPbyNMR Marie Curie Initial Training Network (www.idpbynmr.eu/) and shows strong synergy with the networking activities of the BioNMR project (www.bio-nmr.net) and of the European network of key structural biology infrastructure, INSTRUCT (www.structuralbiology.eu). In accord, the research areas covered range from the biochemical, biophysical and structural characterization of viral proteins, including intrinsically disordered ones, to the integrated approaches for their investigation and to their relevance in biomedical sciences.

The meeting was organized by the organizing committee

Isabella C. Felli (CERM)

Roberta Pierattelli (CERM)

Sonia Longhi (CNRS)

Peter Tompa (ENZIM)

In all, there were 54 participants at the meeting (see ITM_01_participants.pdf attached), who gave and listened to 18 40-min lectures (see ITM_01_program.pdf attached). Among the participants were representatives of the Marie Curie ITN IDPbyNMR, BioNMR network, INSTRUCT, students and leading figures of the viral research community. In the talks, the three organizations were introduced in detail, and many aspects of viral structural biology and NMR were covered:

- 1) In her introductory talk, Roberta Piratelli outlined the Marie Curie ITN IDPbyNMR.
- 2) Ivano Bertini outlined the concept of BioNMR, current developments and its access policy.
- 3) David Stuart talked about the European structural biology infrastructure network INSTRUCT.
- 4) Several talks covered basic biological/structural aspects of viruses (e.g. Dennis Bamford, Christian Cambillau).

- 5) Several talks addressed basic aspects of structural disorder (e.g. Vladimir Uversky, Peter Tompa)
- 6) Basic issues of approaching structural problems with NMR have been covered (e.g. Martin Blackledge)
- 7) Structural disorder in viral proteins in particular was also addressed (e.g. Norman Davey).

The program provided ample opportunity to exchange ideas about these problems, including the combination of diverse structural techniques to characterize the structure of viruses/viral proteins. The program also contained a round-table discussion on the last day, in which the idea was discussed at length that structural ensembles of disordered proteins should be presented to the public. Currently, disordered proteins can be best described by structural ensembles, which are usually 50-100 alternative structures that collectively fit experimental observations. Primary observation may come from NMR, SAXS, CD, MD simulations and others, and they collectively provide the best description of the protein. Protein Data Bank (PDB) does not accept these ensembles, and it was suggested and generally agreed upon that a novel database should be created for this purpose.