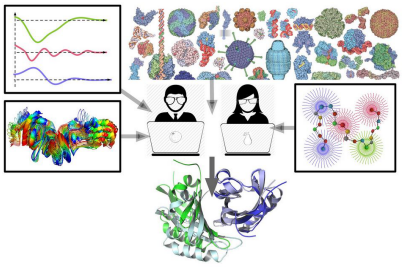

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Structural diversity and odd functions in RNA viruses.

In the recent years a massive amount of raw viral genomic data has been produced and released in sequenced databases, leading to the paradoxical situation of generating the Domain of Unknown Function (DUF), the number one domain in knowledge databases. Together with bio-informatics prediction, the knowledge of the three-dimensional structures of DUF proteins is the key to unveil the full potential of viral genomic information. At the dawn of the century, cutting-edge research in structural biology moved in two distinct directions: either tightly focused long-term research in individual laboratories, or large consortia of structural biologists developing strategies to determine new protein structures rapidly. On one hand, the latter succeeded in producing large numbers of homologous proteins, and generated advances in light sources, detectors, new algorithms and methods which benefit the entire community, however failed to unravel accurate structures for most viral DUF. On the other hand, the anticipated results that a small number of viral systems, studied in depth, would provide insights across the field of biology with the aid of genome-based comparative structural analysis, moved slower than expected. This was firstly due to the intrinsic complexity and plasticity of the viral models and the challenging molecular ensembles that need to be generated and stabilized prior to study. Secondly, a large part of the viral genome space falls under the category of the viral Dark Proteome (24% proteins & 25% of domains), for which very few new folds are unraveled and a lack of diversity in the known fold.
In the last decade viral human disease emerging from unforeseen viral family (Nidovirales, Mononegavirales, Bunyavirales, Flaviviridae) has stressed the critical necessity to solve the actual structure, to enlighten structural and functional oddities.

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