INTERNSHIP PROPOSAL

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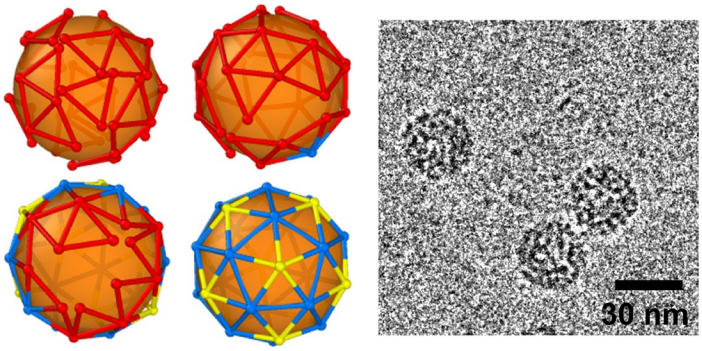
Virus self-assembly dynamics in crowded environment

Viruses are amazing biological agents in which hundreds of molecular blocks integrate with atomic precision into the final structure. Their regularity is all the more remarkable because for many viruses it occurs **spontaneously**, in an efficient self-assembly process, whether in the host cell or in a test tube. Remarkably, many viruses are assembled in a **crowded intracellular environment** (up to 30% of the volume fraction in the cytosol), with a low error rate, despite numerous non-specific interactions with cellular components.

The objective of the internship will be to elucidate and model **the self-assembly of a simple icosahedral virus** in an environment mimicking the cytosol. Cytosol depletion forces will be simulated by the presence of model polymers at different volume fractions. Dynamics will be measured by time-resolved light scattering and fluorimetry, and kinetic data will be modeled using codes in Matlab.

In the case of a continuation in PhD, the aim will be to finalize the study on the role of crowding but also to extend towards the reconstitution of the translation machinery in order to gain a physical understanding of **viral assembly in non-equilibrium cellular conditions**. Experimental campaigns at large-scale facilities (X-ray and neutron scattering, X-ray imaging) will be conducted in France or abroad. The nanometer-scale structures will be resolved by cryo-transmission electron microscopy and image analysis (class average). The project will be carried out in collaboration with biologists at the Institute of Biology and Chemistry of Proteins (Lyon), biophysicists at the University of California Los Angeles and theoreticians at the University of California Riversides.

The candidate must have a background in **soft condensed matter or biological physics** with an interest in modeling.



Left: Numerical simulations illustrating the self-organization of a viral capsid around an electrostatic core. Right: Cryo-electron microscopy image of viruses assembled in vitro.

To learn more:
M. Chevreuil *et al.*, *Nat. Commun.* **9** (2018) 3071 (doi.org/10.1038/s41467-018-05426-8)
G. Tresset *et al.*, *Reflets de la Physique* **52** (2017) 22-26 (doi.org/10.1051/refdp/201752022)