

Supervisor(s):

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Host laboratory:

IBS, <https://www.ibs.fr/>

Host group/team:

MEM: Methods and Electron Microscopy / AFM team

Title of the M2 research internship:

Atomic force microscopy topography and reconstruction of large biological complexes

Project summary:

With the recent revolution of Artificial Intelligence protein structure prediction (alpha-fold), there is not much doubt that very soon most of individual protein chains will have a D structure available. However, it is not yet the case for dimers, tetramers and oligomers of proteins. In case, we rely on integrative structural biology approaches that combine multiple technique toward a synergetic goal of determining the 3D structures of large protein assemblies. We participate in this effort by applying topographical information obtained from atomic force microscopy. We have a large experience in high-resolution AFM imaging combined with advanced image processing tools.

We have developed a computer pipeline that aims at building/selecting large protein assemblies. The internship will consist of applying this pipeline of two large multimeric assemblies: coagulation factors VIII and XIII. These two critical coagulation factors act at different levels in the coagulation cascade but their global and intact structure remains unknown. The candidate will pursue the refinement of the pipeline by defining a novel scoring energy function to select best assemblies.

Keywords:

coagulation factors, atomic force microscopy, protein assembly

Relevant publications of the team:

Chen SWW, Banneville A-S, Teulon JM, Timmins J and Pellequer JL (2020) Nanoscale surface structures of DNA bound to *Deinococcus radiodurans* HU unveiled by atomic force microscopy. *Nanoscale* 12: 22628-22638.

Singh S, Nazabal A, Kanniyappan S, Pellequer J-L, Wolberg AS, Imhof D, Oldenburg J and Biswas A (2019) The plasma Factor XIII heterotetrameric complex structure: unexpected unequal pairing within a symmetric complex. *Biomolecules* 9: 765.

Chaves RC, Dahmane S, Odorico M, Nicolaes GAF and Pellequer J-L (2014) Factor Va alternative conformation reconstruction using Atomic Force Microscopy. *Thromb. Haemost.* 112: 1167-1173.

Trinh M-H, Odorico M, Pique ME, Teulon J-M, Roberts VA, Ten Eyck LF, Getzoff ED, Parot P, Chen S-WW and Pellequer J-L (2012) Computational reconstruction of multidomain proteins using atomic force microscopy data. *Structure* 20: 113-120.