BIOPHYSICS WEEK EBSA LECTURE

Single particle cryo-electron microscopy: A method of choice for solving large and heterogeneous molecular complexes

Dr. Yaser Hashem, Université de Bordeaux, EBSA Young Investigator Award 2021

Friday, March 26th 15:00

Functions of biomolecules are directly tied to their structures. Methods such X-ray crystallography and nuclear magnetic resonance (NMR) can offer an atomic view on biomolecules. However, solving structures of increasingly large molecules is not possible with NMR and becomes very challenging with X-ray crystallography, especially when the structures exhibit intrinsic structural heterogeneity, rendering them difficult to crystallize. In addition, the quality and validity of X-ray structures may be compromised by artifacts related to crystal packing and the use of different crystallization agents that do not exist in living cells.

Today, single-particle cryogenic electron microscopy (cryo-EM) became incontestably the way to go in solving the structures of various molecular complexes and nanomachines, especially when the size surpasses several hundred kilo Daltons. Historically, the development of cryo-EM was linked to several molecules such as the ribosomes, which were used to develop, benchmark and test the technique. Indeed, the ribosome provided a sturdy large nano object that is abundant and easy to obtain from most cells. However, it was rather surprising to slowly realize, step by step, the paramount number of different complexes and the incalculable multiplicity of conformations, orientations and shapes that this central molecule can adopt on its long path of mRNA translation into proteins.

Here, after an introduction on cryo-EM general principles, I will present few molecular stories from the book of mRNA translation where the technique has proven to be the best storyteller.

EBSA
Biophysics in Europe