2-YEAR POST-DOCTORAL POSITION: ABC-F PROTEINS FUNCTION IN CYANOBACTERIA AND CHLOROPLAST

Location: **Institut de Biologie Physico-Chimique, 75005, Paris**
Contact: Grégory Boël boel.lab@gmail.com

A two year postdoctoral position to start beginning of 2016 at the "Institut de Biologie Physico-Chimique" (IBPC) in the center of Paris. This fundamental research project will be conducted within a new team starting in September 2015 in the laboratory of "Expression Génétique Microbienne" (CNRS FRE3630). The project will investigate the function of a new class of protein translation factors belonging to the ABC-F protein family in cyanobacteria with the long-term objective of characterizing the function of the chloroplastic ABC-F in *Chlamydomonas*.

ABC (ATP-Binding Cassette) transporters represent the most common molecular architecture used to couple transmembrane transport to the hydrolysis of ATP. They belong to a larger superfamily of proteins containing homologous ABC ATPase domains, which includes numerous soluble-protein families that perform functions unrelated to transmembrane transport. ABC-F proteins comprise the most widespread family of soluble proteins within the ABC superfamily. Four representatives of this ABC-F family are present in *E. coli*, two in cyanobacteria, six in *Chlamydomonas* (including one chloroplastic), five in plants, and three in humans.

We have recently shown that EttA (energy-sensing translational throttle A), an *E. coli* ABC-F proteins, is a translation factor that gates ribosome entry into the elongation cycle in an ADP-to-ATP ratio-dependent manner (Boël, G., *et al.*, / Chen, B., *et al.*, *Nat Struct Mol Biol*, 2014. **21**(2)). Our results suggest that EttA maintains translation initiation complexes in a hibernating state when the ADP-to-ATP ratio is high. When ATP concentration increases, the binding of EttA-ATP promotes formation of the first peptide bond on the ribosome. Upon ATP hydrolysis, EttA is released from the ribosome, permitting entry into the elongation cycle. In conclusion, EttA provides a critical control on the commitment of energetic resources to protein synthesis.

The aims of the project are:

I. To use ABC-F mutations characterized in the *E. coli* system to test hypotheses about implication of the two *Synechocystis* ABC-F proteins in translation process.

II. To use the *E. coli* model to characterize key residues for EttA function.

III. To guide future *in vitro* biochemical studies establishing the mRNA sequences and structures targeted by the *E. coli* and *Synechocystis* ABC-F proteins using proteomics and RNAseq transcriptomics. Work under this aim will evaluate the hypothesis that the four *E. coli* and two *Synechocystis* paralogs regulate translation in a mechanistically equivalent manner but with varying specificity for different mRNAs.

IV. In collaboration with the laboratory of Molecular and Membrane Biology of the Chloroplast at the IBPC we will explore the function of the *Chlamydomonas* ABC-F present in the chloroplast. This investigation will be driven by the results obtained on the cyanobacteria ABC-Fs.

The ideal candidate should be familiar with bacterial genetic and molecular biology. Expertise in protein synthesis and RNA biochemistry is a plus.

The applicants should send their CV with full list of publications and 3 references that can be contacted to Grégory Boël at boel.lab@gmail.com.