

## POST-DOCTORAL FELLOWSHIP

Instituto de Biofísica, Universidade Federal do Rio de Janeiro.  
Laboratório de Genômica Estrutural  
Head: Prof Ronaldo Mohana-Borges

## Biochemical and mechanistic dissection of interferon response inhibition in human respiratory syncytial virus

*Directors/Supervisors: Dr. Gonzalo de Prat Gay and Ronaldo Mohana Borges*

The human respiratory syncytial virus (RSV) is the main etiological agent for lower respiratory tract disease worldwide, with particular impact in developing countries, in terms of both morbidity and mortality. In spite of this, there are neither vaccines nor antivirals available. A member of the non-segmented single-stranded RNA viruses (Mononegavirales), RSV belongs to the paramixoviridae family, which includes other widespread pathogens such as measles and mumps, among others. It shares several common gene products with paramixoviridae and other distant families, which include fusion, entry, matrix, RNA dependent polymerase, nucleocapsid, and a phosphoprotein polymerase cofactor. However, RSV codes for two proteins found only in this virus (non-structural proteins NS1 and NS2 with no sequence homologs in databases). The general aim of this project is to investigate the key molecular-biochemical mechanisms in which these unique proteins participate, as a way to expose specific targets for therapeutic and protective intervention. NS1 and NS2 interfere with signaling pathways by binding to a large ( $\geq 200$ ) number of putative targets. By applying a rational biochemical proteomic approach using the pure proteins, we aim at identifying a discrete number of high affinity bona fide targets from extracts of infected and uninfected cells under highly controlled conditions. We intend to pursue a possible interaction between the two proteins which is not known at the present, and we expect to obtain a hierarchy of targets that can bind either or both proteins. An important goal is a biophysical and structural characterization of the two proteins for which there is no structure and scarce biophysical information. In addition, NS1 is the most abundant protein in early infection, we want to confirm the presence of large oligomeric forms (NS1SOs), which we previously described to be formed in a quasi-spontaneous manner in solution, in cells. We will carry out immunofluorescence analysis for the localization of both proteins engineered variants in different situations (infected, non-infected and transfected cells), and in the particular case of NS1, we will aim at determining the presence of the oligomeric forms and their differential localization. A multidisciplinary and collaborative project, it covers disciplines from biophysics, molecular biology, and proteomics. Background in at least one of these areas is expected. The ongoing nature of the project and the stimulating environment anticipates scientific productivity, training in a wide range of techniques, and collaboration with other groups.

*-Duration:* one year, renewable for more two years

*Salary:* R\$ 4.100,00

*-Opening/Starting date:* Position open until filled. Starting preferably from September 2014, or when candidate is selected.

*-Send CV along with a letter of presentation,* either Portuguese or English, stating the interest in the project, and the name of two references to **gpg@leloir.org.ar**. For group's publications see Google Scholar or PubMed.