OPEN PHD POSITION FOR MARIE SKŁODOWSKA-CURIE INNOVATIVE TRAINING NETWORKS (MSCA-ITN) AT CSIC

**MSCA-ITN**
H2020-MSCA-ITN-2018 #813239

**PROJECT**
RNAct: Enabling proteins with RNA recognition motifs for synthetic biology and bio-analytics

**PhD SUPERVISOR(S)**
Guillermo Rodrigo

**SCIENTIFIC AREA**
Synthetic Biology

**HOST INSTITUTION**
Institute for Integrative Systems Biology (I2SysBio) Valencia area, Spain
CSIC (Spanish Research Council)

**DURATION**
3-4 years

**FIXED START DATE:**
Application deadline: **1 March 2019**
Start date: **1 September 2019**

**PLANNED SECONDMENT(S):**
Vrije University (Brussels, Belgium) and CNRS (Nancy, France)

**EMAIL OF THE PhD SUPERVISOR(S)**
guillermo.rodrigo@csic.es

**WEBSITE OF THE ITN-MSCA**
http://rnact.eu

**WEBSITE OF THE RESEARCH GROUP OR CENTRE/INSTITUTE**
http://biosysdesign.csic.es
**IDEAL CANDIDATES**

Students with Degree and Master in Biotechnology, Molecular Biology, or similar.

**DESIRABLE CANDIDATE REQUIREMENTS**

It is desirable some knowledge on Systems and Synthetic Biology.

**BENEFITS**

The Early Stage Researcher (doctoral student) contracted with this ITN project will take advantage of:

- a multidisciplinary environment in Systems and Synthetic Biology in Spain
- the resources available in the University (UPV) to conduct the PhD
- an international network of academic and industrial partners for traveling

**PhD PROJECT**

The student will work to develop synthetic circuits in bacteria based on post-transcriptional regulation, aimed at reprogramming the fadD regulation of the natural machinery. The focus will be on the Musashi RRM protein, where allosteric inhibition of RNA binding by a fatty acid can serve as a protein switch. First, the impact on the E. coli’s metabolic network by removal of the transcriptional repressor FadR will be evaluated. FadR controls the expression of fadD, an enzyme in charge of transporting and degrading fatty acids. We will then focus on the in silico re-engineering of the regulation of fadD at the post-transcriptional level by a new Musashi-like protein, and will define its desired new RNA-specificity. The performance of the new regulatory system will be tested in a ΔfadR background. We will analyze the allosteric communication pathways implicated in this regulation to identify its properties. It will be expected that by setting a synthetic regulation and comparing it to the wild-type system we will gain better understanding about the pathway, necessary otherwise for efficient genetic/metabolic engineering. Success in this area will provide circuits with a double level of regulation, both at the protein (RRM) and RNA (sRNA) levels, allowing combinatorial logic interactions. Quantitative assays will be implemented to monitor mRNA and protein expression levels and their control by binding of designed RBPs to cis-regulatory elements. The latter will be endogenous sequences but also modified RNA sequence motifs that match to designed RNA binding specificity developed and validated by other partners. The student will perform the molecular cloning necessary to implement genetically the circuits in bacteria (here, E. coli) to then perform the appropriate characterization experiments of the activity of the engineered systems.