




H2020 MSCA - ITN - 2017 - 766030

# C O N T R A

## Computational Oncology Training Alliance

### **ESR 2 - The mechanisms of coding and non-coding oncogenic alterations (including bioinformatics predictions and experimental validation; 70%/30%)**

Research project	The main aim of this project consists in identifying cellular pathways that become misregulated upon cancer driver coding and non-coding alterations, and which are ultimately responsible for tumourigenesis. It will be carried out at the interface between bioinformatics and wet-lab research. The project will start with bioinformatics analysis aimed at the identification of genes and other genomic regions with signals of positive selection (which are potentially drivers) across newly sequenced cohorts of tumours. The second stage of the project will consist in designing and carrying out experiments –and further bioinformatics analyses– to elucidate the mechanisms of tumourigenesis unleashed by somatic alterations of these elements. The analyses will include high throughput assays to probe the downstream transcriptional/translational alterations caused by somatic alterations of the drivers. Maps of altered transcriptome/proteome/signalosome upon alterations of different driver elements will thus be obtained across cancer types. Finally, we will design and carry out more bioinformatics analyses to determine the pathways that become mis-regulated upon alterations of the drivers under study. These analyses will tap on transcriptomic/proteomic data on the primary tumours in which the driver alterations were identified (in cases in which this is available) and on the experimental data generated during the second stage of the project.
Supervisor	<p>name      Nuria Lopez-Bigas</p> <p>e-mail     <a href="mailto:nuria.lopez@irbbarcelona.org">nuria.lopez@irbbarcelona.org</a></p> <p>website    <a href="https://bbglab.irbbarcelona.org/">https://bbglab.irbbarcelona.org/</a></p>
Host institution	<p>Institute for Research in Biomedicine, Spain</p> <p>Programme of Structural and Computational Biology</p> 
PhD program	PhD Program in Biomedicine, University Pompeu Fabra
Expected results	<ol style="list-style-type: none"> <li>1) List of experimentally validated cancer driver genomic regions across cancer types</li> <li>2) Mechanistic models of their involvement in tumourigenesis</li> </ol>
Planned secondments	<ol style="list-style-type: none"> <li>1) Merck (3 months) to learn methods of systems biology integrating somatic alterations and gene expression/protein activity analyses</li> <li>2) UVIGO/Posada (2 months) to learn on tumour growth modelling methods</li> <li>3) KCL/Cicarelli (2 months) to learn on tumour growth modelling methods</li> </ol>
Required profile	The candidate will have a demonstrated mixed background: i.e., comprising both wet-lab experience and bioinformatics expertise. Ideally, the applicant has received basic training in biology via a basic degree in biological or biomedical sciences, or related disciplines, and an MsC in bioinformatics. The candidate must have a i) solid biological background, ii) understanding of the basic concepts of cancer genomics and iii) the methodological basis of NGS technologies and their associated bioinformatics analysis.