MARIE SKŁODOWSKA-CURIE POSTDOCTORAL FELLOWSHIPS 2021

EXPRESSION OF INTEREST FOR HOSTING MARIE CURIE FELLOWS

HOST INSTITUTION

NOVA University Lisbon | School of Science and Technology
UCIBIO – Applied Molecular Biosciences Unit

RESEARCH GROUP AND URL

Computational Multi-Omics Group
https://comics.dcv.fct.unl.pt/

SUPERVISOR (NAME AND E-MAIL)

Ana Rita Grosso
argrosso@fct.unl.pt

SHORT CV OF THE SUPERVISOR

Ana Rita Grosso is the Lab Leader of the Computational Multi-Omics Lab at the Applied Molecular Biosciences Unit (UCIBIO)/ NOVA School of Science and technology at the NOVA University Lisbon, Portugal. Her main mission is to decipher pathological conditions using computational multi-omics approaches, identifying molecular events to be further used as biomarkers and therapeutic targets.
Ana Rita Grosso gathered a PhD in Biomedical Sciences, under supervision of Simon Tavaré (Cambridge Univ., UK) and Maria Carmo-Fonseca (IMM/FMUL). In 2018, Ana Rita Grosso moved to UCIBIO/FCT-NOVA to foster her scientific independence and consolidate her research group, currently composed of: 1 Senior Researcher, 2 PostDocs, 3 PhD-students, 1 junior Bioinformatician and 1 MSc Student. To date, she published 42 papers **(1560 citations**) and won in highly competitive schemes: 2 Research Contracts; 6 Projects Grants (2 as PI, 1 as Co-PI and 5 as Researcher Core CV) as well as 2 Pfizer Awards for Basic Research. Additionally, she has been teaching specialized MSc courses in Genomics and Computational Biology fields in NOVA School of Science and technology.

5 SELECTED PUBLICATIONS

- Andrade J, Shi C, Costa ASH, Choi J, Kim J, Doddaballapur A, Sugino T, Ong YT, Castro M, Zimmermann B, Kaulich M, Guenther S, Wilhelm K, Kubota Y, Braun T, Koh GY, **Grosso AR**, Frezza C, Potente M (2021) "*Control of endothelial quiescence by FOXO-regulated metabolites*", ***Nat Cell Biol***, 23(4): 413-423.

- Povoa V, Almeida CR, Maia-Gil M, Sobral D, Domingues M, Martinez-Lopez M, Fuzeta MA, Silva C, **Grosso AR**, Fior R (2021) Innate immune evasion revealed in a colorectal zebrafish xenograft model, ***Nature Communications***, 12(1156).

- Mancio-Silva L, Slavic K, Ruivo MG, **Grosso AR**, Modrzynska KK, Vera IM, Sales-dias J, Gomes AR, Macpherson CR, Crozet P, Adamo M, Baena-gonzalez E, Tewari R, Llinás M, Billker O, Mota MM. (2017) *Nutrient sensing modulates malaria parasite virulence*. ***Nature***. 547:213-216.

- Nojima T, Gomes T, **Grosso AR**, Kimura H, Dye M , Dhir S, Carmo-fonseca M, Proudfoot N . (2015) *Mammalian NET-Seq Reveals Genome-wide Nascent Transcription Coupled to RNA Processing*. ***Cell***. 2015;161:526-40.

- **Grosso AR**, Leite AP, Carvalho S, Matos MR, Martins FB, Vítor AC, Desterro JM, Carmo-fonseca M, de Almeida SF. (2015) *Pervasive Transcription Read-Through promotes aberrant expression of oncogenes and RNA chimeras in renal carcinoma*. ***eLife***. 2015;4:e09214.

PROJECT TITLE AND SHORT DESCRIPTION

Unveiling the complexity of cell biology and underlying disregulation of diseases by deciphering multi-omics data

A wide range of diseases, from cancer to age-related disorders, are associated with an increase in transcriptional noise and expression of many aberrant mRNAs. While it is clear that the regulation of epigenome and transcriptome networks is a crucial component of a healthy cell, it is relatively unknown the molecular mechanisms underlying its misregulation for many diseases. Therefore, we aim to decipher pathological conditions using multi-omics approaches, identifying molecular events to be further used as biomarkers and therapeutic targets. Here, we will integrate multi-omics profiles and apply machine learning approaches to identify the mechanisms underlying several diseases. These studies will reveal the interplay between the (epi)genome and transcriptome that may determine cell fate and disease onset.

SCIENTIFIC AREA WHERE THE PROJECT FITS BEST*

Life Sciences (LIF)