

AVAILABLE POSITIONS

Principal Investigator	Lorenzo Calviello
Institute of Affiliation	Human Technopole

PROJECT 1 INFO	
Title of the proposed project:	<i>De novo</i> discovery from RNA to Protein in patient-derived cancer models (experimental)
Short description of the project	The prospective PhD student will plan and perform the experimental assays for high-resolution transcriptomics (including long-read sequencing), translation and proteomics, supported by a Senior Technician and the excellent Genomics and Proteomics facilities at HT, who have already extensive experience with these assays and familiarity with the project goals. Moreover, the candidate will develop proteomics assays, such as immunopeptidomics and surface proteomics, to probe the potential of detected novel ORFs as neoantigens for targeted immunotherapy. In addition, building on already available engineered cell lines in the lab, the student will focus on designing RNA-based perturbation screens, targeting high-priority <i>de novo</i> identified regions. Desired skills include: foundations on gene regulation, experience with protein and nucleic acids biochemistry, knowledge of -omics technologies, cell culture, excellent communication skills. This project is funded by AIRC.
Main research area for the project	Cancer proteogenomics towards personalized medicine
Second research area for the project	Computational methods for cancer integrative -omics
3 key words for the project	Proteogenomics, cancer neoantigens, dark proteome

PROJECT 2 INFO	
Title of the proposed project:	<i>De novo</i> discovery from RNA to Protein in patient-derived cancer models (computational)
Short description of the project	The PhD candidate will expand our <i>de novo</i> discovery pipeline from RNA to protein, improving on algorithms and software we have previously developed in the past years. Importantly, the student will integrate our strategy with sequence and structural variants detected at the DNA level, to quantify its impact on RNA and ORF discovery, and identify patient-specific transcripts and protein variant, including their potential for immunogenicity towards developing personalized therapy solutions. In addition, the candidate will develop methodologies to test for the specificity of detected RNAs and proteins, by leveraging on re-analysis of large public datasets (e.g. GTEx, TCGA, CPTAC). Desired skills will include: robust foundations on gene regulation, experience with R/Python programming, applied knowledge of statistical learning concepts, good knowledge of functional

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LAB INFO	
Main topic/s of the lab	Computational Biology, Translation, Transcriptomics, Proteogenomics,
Short description of the lab activity	The Calviello Group is a multidisciplinary research group in the Genomics Research Centre – Functional Genomics Programme, adjunct with the Computational Biology Research Centre at the Human Technopole. The group studies post-transcriptional gene regulation, employing computational and experimental methods revolving around the -omics of translation, a fundamental process which dictates the functions of transcribed genome, and impacts the cytoplasmic fate of mRNAs and proteins.
Recent bibliography	https://scholar.google.co.uk/citations?hl=en&user=p2emIPUAAAJ
Lab website link	https://humantechnopole.it/en/research-groups/calviello-group/
Social media links	https://x.com/translatomics