

Research Topics

PhD Programme in Biosciences



DIPARTIMENTO DI BIOLOGIA
UNIVERSITÀ DEGLI STUDI DI PADOVA

Research Topics XL cycle Further PhD Scholarships 2024-2025

Below are the descriptions of all projects considered as priorities for the XL cycle. Candidates are encouraged to identify at least one project of interest and mention it in the research statement to be uploaded with their application. For further details regarding the required documents for the application, please refer to the FAQ section available on the PhD Programme's website (please note that in this call there are not "Funded by University Scholarships" or Positions without scholarship).

Curriculum Cell Biology and Physiology

Seeding and Sorting of intramitochondrial protein aggregates*

Contact: Prof. Luca Scorrano, e-mail: luca.scorrano@unipd.it

(1)

Exploring the factors controlling unfolded mitochondrial protein aggregates (UMPA) seeding. The PhD student will focus on the mitochondrial dynamics associated with UMPA formation. This involves investigating how mitochondrial fission and fusion impact UMPA seeding within different mitochondrial compartments. Utilizing advanced microscopy techniques, such as AiryScan, the PhD student will assess protein aggregates and employ genetic approaches to modulate key mitochondrial dynamics genes, exploring their influence on UMPA accumulation and its effects on cellular function.

(2)

Exploring the factors controlling unfolded mitochondrial protein aggregates (UMPA) seeding. The PhD student will investigate the cellular fate of UMPA-loaded mitochondria. The PhD student will apply high-resolution imaging and molecular tools to explore the sorting and degradation pathways UMPA follows across mitochondrial subcompartments. This role also includes manipulating disposal mechanisms to observe the broader impact of UMPA on cellular health, providing insights into mitochondrial quality control and potential therapeutic targets.

* In your research statement please specify if you are interested in project 1, 2 or both.

Transcriptome analysis of marine sentinel organisms in response to environmental pollutants and extreme conditions.

Contact: Prof. Cristiano De Pittà, e-mail: cristiano.depitta@unipd.it

In recent years, "omics" approaches (genomics and transcriptomics), based in particular on gene expression data produced by microarrays and Next Generation Sequencing (NGS) techniques, have represented a very powerful tool for deciphering the molecular mechanisms underlying the response and the adaptation of marine organisms to environmental changes, defining new metrics that integrate gene expression profiles with traditional chemical and biochemical measurements. Recently, research has also highlighted the role of microRNAs (miRNAs) in response to environmental stress. Evidence shows that miRNA expression profiles can change rapidly following stressful events, positioning them as promising candidates for environmental biomarkers. This project aims to utilize sentinel organisms, specifically *M. galloprovincialis* and *E. superba*, to define gene and miRNA expression signatures in specimens collected or transplanted at various time points (ranging from a few days to several weeks) in different environments: the Venice lagoon in Italy and regions of the Southern Ocean subjected to varying levels of anthropogenic and industrial pollution, as well as extreme environmental conditions due to climate change (Antarctic region). We plan to identify specific gene and miRNA transcriptional signatures associated with these different gradients.

Curriculum Genetics, Genomics and Bioinformatics

Development of a toolbox to untangle virus-host interactions on ribosomes.

Contact: Dr. Umberto Rosani, e-mail: umberto.rosani@unipd.it

High throughput sequencing and metagenomics have deepened our understanding of viruses in nature, yet linking viruses to their hosts remains a challenge, hindering our knowledge and biotechnological applications. The goal of the recently financed VirHoX European project (2025-2029) is to "hack" the ribosome, in order to map virus-host associations by developing an innovative technology able to operate at metagenomic level. Functional testing of engineered enzymes will be pursued as well as development of high-throughput sequencing protocols covering a range of model and non-model biological systems. The PhD fellow will be part, together with other junior researchers, of this project from its beginnings, being a central actor of the planned research. The PhD candidate will become part of the VirHoX Consortium, which includes academic and industrial experts in microbiology, protein engineering, gene editing and viral genomics/transcriptomics from Italy, France, Austria, Germany and Norway.