



Courtesy translation of D.R. n. 139/2024

For more details on the selection process, please refer to the Italian version of D.R. n. 139/2024 available at <http://www.hunimed.eu/it/lavora-con-noi/>

SELECTION PROCEDURE FOR RESEARCH FELLOWSHIP

Research Program Title	Characterization of a new in vitro model for GNAO1 encephalopathy based on human iPS cells and cortical organoids
Tutor	Prof.ssa Simona LODATO
Scientific Area	05 – Biological Sciences
Gross amount of the fellowship	30.000 Euro
Duration of the fellowship	12 months
Objectives of the research	<p>GNAO1 encephalopathy encompasses a group of rare disorders caused by heterozygous mutations in the GNAO1 gene, which encodes the α subunit of a heterotrimeric guanine nucleotide-binding protein (Go). This protein is one of the most abundant membrane proteins in the mammalian brain and plays critical roles in neurodevelopmental processes and synaptic transmission. Children affected by this condition exhibit a range of neurological symptoms, including developmental delay, hypotonia, epilepsy, and hyperkinetic movement disorders with life-threatening paroxysmal exacerbations. Currently, there are no curative treatments available, only symptomatic ones. Therefore, the aim of this study is to develop an appropriate system for modelling GNAO1-related disorders to provide insights into the pathophysiology of GNAO1 encephalopathy and aid in the development of novel therapeutic approaches for affected children.</p> <p>In our lab, we utilized the CRISPR-Cas9 genome editing system to create a collection of human induced pluripotent stem cell (iPSC) lines carrying various mutations</p>

	<p>representative of the clinical heterogeneity of this syndrome. We differentiated these GNAO1-mutated iPSCs into cortical neurons and generated cortical organoids. This project aims to study how alterations in Gao activity impact neurodevelopment by performing molecular, morphological, and functional analyses on cortical organoids, ultimately leading to psychomotor disorders. This innovative system will also lay the groundwork for future testing of new potential drugs and therapeutic approaches.</p>
<p>Activities to be carried out</p>	<ul style="list-style-type: none"> • Consolidated experience with: Pre-processing of scRNA-seq data (quality control, filtering, normalization, and integration); • Differential Gene Expression (DGE) Analysis (single cell and pseudobulk approached); • Inferring the developmental trajectory of cortical organoids (pseudotime); • Cell-to-Cell Communication Inference; • Cell Composition Analysis; • Visualization and Reporting; • Preferred experience with proteomic data and long read sequencing genomic analysis.
<p>Work place</p>	<p>PIEVE EMANUELE - Milan</p>
<p>Mandatory requirements</p>	<ul style="list-style-type: none"> • Degree in Biology, Biotechnology or Medicine and Surgery • PhD • Adequate scientific and professional background to carry out the research activity described in this call.
<p>Selection process</p>	<p>Application for admissions must be submitted at the following link: https://pica.cineca.it/humanitas No hard copy of the application must be sent by post. At first access, applicants need to register by clicking on “Register” and completing the requested data. If applicants already have LOGINMIUR credentials, they do not need to register again. They must access with their</p>

	<p>LOGINMIUR username and password in the relevant field LOGINMIUR.</p> <p>Applicants must enter all data necessary to produce the application and attach the required documents in PDF format.</p>
<p>Selection criteria</p>	<p>Selection criteria are predetermined by the Selection Committee. As part of the selection process, the Committee will evaluate the curriculum, titles and publications presented by the candidate and will consider, in particular:</p> <ul style="list-style-type: none"> • Proficient in writing complex scripts for data manipulation, automation, and bioinformatics pipeline development. • Experience using Bash for processing large datasets and integrating various bioinformatics tools. • Skilled in statistical analysis, data visualization, and bioinformatics packages such as Bioconductor (R). • Familiar with Python scripting and automation of bioinformatics workflows, with advanced knowledge of popular libraries such as Biopython, Pandas, and NumPy. • Competence in utilizing HPC resources for running large-scale bioinformatics analyses, including job scheduling, parallel processing, and optimizing workflows. • Strong experience in using Conda for package management and creating reproducible research environments. • A plus is the proficiency in version control using Git, Nextflow for workflow management, Docker/Singularity for containerization

FURTHER INFORMATION:

In the event of any conflict between Job Opening text and Italian D.R. text, the Italian version will prevail.

For more details on the selection process please refer to the **D.R. n. 139/2024** (<http://www.hunimed.eu/it/lavora-con-noi/>) or send an inquiry to ufficiodocenti@hunimed.eu or telephone +39 02.8224.5642/5421.