Courtesy translation of D.R. n. 267/2023

For more details on the selection process, please refer to the Italian version of D.R. n. 267 /2023 available at http://www.hunimed.eu/it/lavora-con-noi/

SELECTION PROCEDURE FOR RESEARCH FELLOWSHIP

Research Program Title	**Bioinformatic analysis for translational research in head and neck and hematological cancers**
Tutor	Prof. Paolo BOSSI, prof. Carmelo CRLO-STELLA
Scientific Area	05 – Biological Sciences
Gross amount of the fellowship	20.000 Euro
Duration of the fellowship	12 months
Objectives of the research	The project aims to identify biomolecular correlates in head-and-neck and haematological tumors, with prognostic and/or predictive value. In particular, the following tumors and settings will be studied: head-neck neoplasms subjected to immunotherapeutic treatment; hematological neoplasms in immunotherapeutic treatment. The analyses carried out will be aimed at defining the impact of tumor gene expression and gene mutation profile on the prognosis of patients. Bioinformatics analyses will allow to correlate the raw data obtained from the analyses with known prognostic factors and to place such analyses in the context of multiparametric evaluations with radiomic and clinical data.
Activities to be carried out	• Collaborate and interact with multi-disciplinary team of scientists and engineers. • Develop new bioinformatics processes and use computational tools to extract actionable information from sequencing data. • Analyze complex genomic datasets to generate biological insights in the context of cancer detection and progression.

	• Perform end-to-end analyses that include data gathering, processing, analysis, and presentation of results. • Work closely with Data Scientists and Genomic Scientists to improve our bioinformatics and machine learning model. • Document code, results and details of the approaches in a thorough and systematic way in order to promote knowledge sharing and cod
Work place	PIEVE EMANUELE - Milan
Mandatory requirements	• Bioinformatics Master degree or related disciplines; • Adequate scientific and professional background to carry out the research activity described in this call.
Selection process	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 LOGINMIUR username and password in the relevant field LOGINMIUR. Applicants must enter all data necessary to produce the application and attach the required documents in PDF format.
Selection criteria	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. • 1 years experience in NGS data analysis, including sequencing quality analysis. • 1 year experience in analysis methods for bulk, and genomics data, including statistical analysis methods. • Proficiency with bash scripting, R and Python.

	• Experience with large public consortia data sets (e.g., TCGA). • Highly motivated, independent self-starter with sense of ownership and time management skills. • Strong interpersonal and communication skills to collaborate effectively with other cross-functional team members. • Strong analytical and problem-solving skills. • Must enjoy and work effectively in a fast-paced environment.

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. 267/2023** (http://www.hunimed.eu/it/lavora-con-noi/) or send an inquiry to ufficiodocenti@hunimed.eu or telephone +39 02.8224.5642/5421.