HU
HUMANITAS
UNIVERSITY

Courtesy translation of D.R. n. 224/2024

For more details on the selection process, please refer to the Italian version of

D.R. n. 224/2024 available at http://www.hunimed.eu/it/lavora-con-noi/

SELECTION PROCEDURE FOR RESEARCH FELLOWSHIP

Research Program Title	**A mechanistic approach for personalized medicine in myeloid neoplasms**
Tutor	Prof. Matteo Giovanni Della Porta
Scientific Area	06 – Medical Sciences
Gross amount of the fellowship	35.000 Euro
Duration of the fellowship	24 months
Objectives of the research	Myeloid neoplasms (NM, including myelodysplastic syndromes, MDS and chronic myelomonocytic leukemia, CMML) occur in elderly people. The natural history of MN is highly heterogeneous and therefore a risk- adapted treatment strategy is mandatory. Several therapeutic strategies have been proposed for MN but only few survived the evidence-based criteria of efficacy. Overall, MN include patients with poor clinical outcome and significant unmet medical needs. Our working hypothesis is that a precise characterization of the genomic complexity of the malignant clone and of immune dysfunction in each patient (defined as "ecosystem") may significantly improve the prediction of disease evolution, of clinical outcome and of drug sensitivity, thus refining clinical management of these diseases.
Activities to be carried out	• We will study of comprehensive mechanisms of disease evolution and response to treatments by innovative single-cell sequencing methods that allow to provide multiomics analysis and can functionally dissect tumor

	• heterogeneity with the highest possible resolution (AIM1).
	• Moreover, we plan to apply modern bioinformatics techniques of bulk RNA-seq data deconvolution (trained on single cell experiments of AIM1) to identify distinct signatures ("ecosystems") in MN as a basis for next-generation prognostic/predictive tools (AIM2).
	• We hypothesize that the development and clonal evolution of MN requires for microbial-dependent inflammation.
	• Therefore, we will study relationships between gut/intratumoral microbiome with disease phenotype and genotype, clonal evolution and response to therapies, thus refining MN ecosystems provided by AIM2 (AIM3). Finally, we aim to identify targets for innovative treatments.
	• We will provide a framework for systematic identification of T cell antigens in MN by considering classical neoantigens originated from SNV and indels, but also non canonical antigens derived from gene fusions, splicing abnormalities, and reactivation of endogenous retroviruses.
Work place	PIEVE EMANUELE - Milan
Mandatory requirements	• Science, Technology, Engineering and Mathematics (STEM) MSc degree. • Science, Technology, Engineering and Mathematics (STEM) PhD. • 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. • Experience with textual data and NLP techniques and models (named entity recognition, document clustering, summarization, text classification, MLM, LLM, etc); • Experience in developing machine learning and deep learning techniques and algorithms (such as k-NN, Naive Bayes, Support Vector Machines, Random Forests, etc) in healthcare, also applied to time-series/longitudinal data; • Good knowledge of generative AI and LLM; • Experience in developing generative models (e.g. statistical, GAN, VAE, etc.) applied to medical data for synthetic data generation and digital twins; • Good knowledge of Computer Vision and/or NLP; • Understanding of data structures, data modeling and software architecture; • Experience in applied statistics skills, such as distributions, statistical testing, regression, etc; • Good scripting and programming skills; • Good proficiency in Python, R programming languages; • Experience with data science frameworks (e.g. tensorflow, pytorch, scikit learn, scipy, pandas, numpy) and visualization frameworks (e.g. plotly, seaborn, matplotlib); • Experience with cloud (GCP, AWS, Azure) and/or distributed computing;

	- Knowledge of database systems and data lakes, good knowledge of SQL; - Knowledge of MLOps practices, IT infrastructures, back end frontend development is appreciated; - Master (PhD would be a plus) in a STEM discipline; - Fluent in written and spoken English and Italian; - Excellent team-working capabilities even with colleagues from different research areas and backgrounds; - Strong self-motivation, commitment and proactive approach; - Ability to meet deadlines and work autonomously in rapidly changing environments; - Curiosity and ability of stepping outside your comfort zone.

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. 224/2024** (http://www.hunimed.eu/it/lavora-con-noi/) or send an inquiry to ufficiodocenti@hunimed.eu or telephone +39 02.8224.5642/5421.