Courtesy translation of D.R. n. 179/2023

For more details on the selection process, please refer to the Italian version of D.R. n. 179/2023 available at http://www.hunimed.eu/it/lavora-con-noi/

SELECTION PROCEDURE FOR RESEARCH FELLOWSHIPS

Research Program Title	**Dissecting the genetic architecture of COVID-19 severity and bacterial coinfections.**
Tutor	Prof.ssa Rosanna ASSELTA
Scientific Area	05 – Biological Sciences
Gross amount of the fellowship	25.000,00 Euro
Duration of the fellowship	19
Objectives of the research	Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the etiologic agent of the coronavirus disease 2019 (COVID-19) pandemic. Clinical manifestations of the disease range from an asymptomatic condition to life-threatening events and death, with more severe courses being associated with age, male sex, and comorbidities. In addition, a key role seems to be played by the concomitant occurence of microbial co-infections, which are associated with higher mortality rates. Importantly, besides these risk factors, intrinsic characteristics of the virus as well as genetic factors of the host are expected to account for COVID-19 clinical heterogeneity. Here, we plan to investigate whether genetic factors play a role in modulating susceptibility to SARS-CoV-2 infection and severity of clinical manifestations, with a special enphasis in exploring the contribution of variants in the predisposition to microbial co-infections. We will perform a genome-wide association study (GWAS) on a cohort of patients collected in one of the most affected area in Italy (Milano, Monza, Bergamo). We plan to adopt a GWAS study design, which is a robust tool for deciphering genetic predisposition, and allows, using imputation, to capture the great majority of genetic variability. In addition,

	we plan to perform exome sequencing, for collecting data on rare variants possibly associated with the investigated phenotypes. We plan to stratify patients based on severity of symptoms, age, sex, co-infection status . Importantly, clinical and genetic data will be analyzed together using an unbiased approach (based on machine learning) to identify combinations of variables able to predict different outcomes. This study has the potential to identify genetic variants: 1) predisposing to increased susceptibility to SARS-CoV2 infection; 2) explaining different outcomes in affected; and 3) predisposing patients to co-infections, thus determining more severe outcomes.
Activities to be carried out	• Usage of DNA databases (Genome Browser, 1000Genomes, HapMap, dbSNP, GnomAD) • Bioinformatic analyses of nucleotide sequences (exome, genome) (alignment, filtering, annotation, and variant calling using specific pipelines and software, such as BWA, Samtools, Annovar, FastQC, Galaxy) • In-silico analysis of the effect of mutations (using programs such as Polyphen, Sift, Mutation taster, Condel, NNSPLICE, Human Splicing Variation, NetGene2) • GWAS data QC, imputation, association analyses • Haplotype analysis • XWAS analysis • Integration of genetic and clinical data by machine learning
Work place	PIEVE EMANUELE - Milan
Mandatory requirements	• Degree in Biology/Biotechnology, Bioinformatics (and related degrees), Engineering, Physics, Statistics • 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: Having a PhD degree and experience in the use of R, Bash, SAS, Python and programming languages will be preferential selection criteria, together with fluent knowledge of English

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. 179/2023** (http://www.hunimed.eu/it/lavora-con-noi/) or send an inquiry to ufficiodocenti@hunimed.eu or telephone +39 02.8224.5642/5421.