

HUMANITAS UNIVERSITY

Selection procedure for 1 Type B Research Fellowship in Life Sciences in compliance with art. 22 of Law 240/2010

Humanitas University invites applications for 1 position as Research Fellow in Life Sciences.

Research Program Title	“Deciphering the molecular and functional heterogeneity of myeloid cells in cancer.”
Tutor	Dott. Giulia SOLDA’
Scientific Area	05 - Biological Sciences
Gross amount of the fellowship	24.000 Euro
Duration of the fellowship	12 months
Objectives of the research	<p>Tumors exploit the plasticity of myeloid cells to reprogram their functions towards tumor promotion. Expansion of heterogeneous myeloid populations also contributes to anticancer therapy resistance. However, our knowledge on the actual heterogeneity of myeloid cells in tumors and their variability between patients and disease stages is still limited.</p> <p>Data in mice suggest that a population of monocyte precursors can be found before the occurrence of metastatic spread. This population has both proliferative and cell differentiation ability and, when transferred to tumor bearing mice, it favors metastatic dissemination to the lung. It is not entirely known if similar populations are present also in human patients.</p> <p>Objective of the research is to analyze human monocytes from the blood of tumor-bearing patients both by bulk RNA-seq and single-cell sequencing. In particular, we want to understand whether immune suppressive and pro-tumoral monocytes are distinct subsets in cancer-bearing hosts. In addition, we will analyze the ability of emerging gene signatures to discriminate cancer patients with poorer</p>

	disease outcome and at risk of developing metastatic disease.
Activities to be carried out	The Research Fellow will have to deal mainly with computational analyses of transcriptomic data (bulk RNAseq and single cell RNA sequencing) and epigenetics data (DNA methylation and CHIPseq).

The work place is in Pieve Emanuele - Milano.

A brief description of the project, activities to be carried out, mandatory requirements to take part into the selection process, information on the application procedure and on the selection criteria are presented in the following.

RESEARCH PROJECT:

Tumors exploit the plasticity of myeloid cells to reprogram their functions towards tumor promotion. Expansion of heterogeneous myeloid populations also contributes to anticancer therapy resistance. However, our knowledge on the actual heterogeneity of myeloid cells in tumors and their variability between patients and disease stages is still limited.

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Objective of the research is to analyze human monocytes from the blood of tumor-bearing patients both by bulk RNA-seq and single-cell sequencing. In particular, we want to understand whether immune suppressive and pro-tumoral monocytes are distinct subsets in cancer-bearing hosts. In addition, we will analyze the ability of emerging gene signatures to discriminate cancer patients with poorer disease outcome and at risk of developing metastatic disease.

ACTIVITIES TO BE CARRIED OUT:

The Research Fellow will have to deal mainly with computational analyses of transcriptomic data (bulk RNAseq and single cell RNA sequencing) and epigenetics data (DNA methylation and CHIPseq).

MANDATORY REQUIREMENTS:

In order to be considered for the post candidates must hold a Master's Degree in Biological Sciences, Molecular Biology, Biotechnology, Biomedical Engineering, Informatics, Physics or related disciplines.

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:

- knowledge of Biology and Molecular Genetics;
- Skills/Technical Abilities: Familiarity with Linux-based Operating system, bash scripting, R and/or Python;
- Previous experience with NGS data analyses (QC, alignment, differential gene expression, etc);
- Previous experience with single-cell sequencing data analysis would be preferred.

Possession of the following titles will be considered an advantage: PhD or a 2nd level University Master degree in Molecular Biology, Genetics, Biostatistics, Bioinformatics, Computational Biology, Data Science or related disciplines.

FURTHER INFORMATION:

For more details on the selection process please refer to the **Rectorate Decree n. 158/2020** (<http://www.hunimed.eu/it/lavora-con-noi/>) or send an inquiry to ufficiodocenti@hunimed.eu or telephone +39 02.8224.5642/5421.