TO MAGNIFICO RETTORE OF UNIVERSITA' DEGLI STUDI DI MILANO **ID CODE __6266___**

I the undersigned asks to participate in the public selection, for qualifications and examinations, for the awarding of a type B fellowship at **Dipartimento di.** **Department of Oncology and Hemato-Oncology**

Scientist- in – charge: **______Pier Guiseppe pelicci____**

Iman Nazari

CURRICULUM VITAE

PERSONAL INFORMATION

Surname	Nazari
Name	Iman

PRESENT OCCUPATION

Appointment	Structure
Post-doc	Dpt of Experimental Oncology, European Institute of Oncology (IEO)- Milano, Italy

EDUCATION AND TRAINING

Degree	Course of studies	University	year of achievement of the degree
Degree			
Specialization			
PhD	System Medicine	University Milano	2023
Master	Master of engineering	Chonbuk National University	2019
Degree of medical specialization			
Degree of European specialization			
Other			

REGISTRATION IN PROFESSIONAL ASSOCIATIONS

Date of registration	Association	City

FOREIGN LANGUAGES

Languages	level of knowledge
English	Flounet

AWARDS, ACKNOWLEDGEMENTS, SCHOLARSHIPS

Year	Description of award
2021	FIEO scholarship
2022-2023	IEO scholarship

TRAINING OR RESEARCH ACTIVITY

Integrative computational analyses of single-cell/single-molecule transcriptional and mutational profiling of AML samples

Objective: integrative analysis of mutational and transcriptional profile setting up a method to overcome the coverage bias of the high-throughput short-read single cell in Acute myeloid leukemia (AML) from patients. AML is an aggressive cancer originating from hematopoietic stem cells, exhibits substantial intra-tumoral heterogeneity impacting disease development, prognosis, and treatment response. However, understanding the interplay between various layers of heterogeneity at the single-cell level remains limited due to technological constraints. To address this, we developed a novel high-throughput multi-omics approach, Single Cell and Molecule sequencing (SCM-seq). This method integrates droplet-based single-cell RNA sequencing with Nanopore single-molecule sequencing, allowing comprehensive profiling of the tumor ecosystem in AML.

SCM-seq was employed to analyze AML samples with SRSF2 spliceosome-factor gene mutations, elucidating the relationship between genetic complexity and transcriptional heterogeneity in malignant and immune compartments. The results confirmed the efficacy of SCM-seq in achieving high-throughput multi-omic profiling at the single-cell level and reconstructing sample complexity. Analyses of expression profiles using reference datasets enabled the identification of malignant and microenvironment compartments within AML samples. Long-read analyses of mutated gene transcripts facilitated the sensitive identification of mutations at the individual cell level.

Role of p21 in the immune response against breast cancer.

Objective: RNA Sequencing and analysis of WT and p21-/- CD11B+ cells. We characterized WT and p21-/- cellular subpopulations and identify transcribed genes that distinguish different subpopulations, with particular emphasis to the antigen presentation machinery and also integrate these data with bulk RNA sequencing data.

PROJECT ACTIVITY

Year	Project
2020-2023	Integrative computational analyses of single-cell/single-molecule transcriptional and mutational profiling to understand the Myelodysplastic syndrome (MDS) to secondary acute myeloid leukemia (sAML) evolution system
2020	Role of p21 in the immune response against breast cancer

PATENTS

CONGRESSES AND SEMINARS

Date	Title	Place

PUBLICATIONS

Books
“Barcode demultiplexing of nanopore sequencing raw signals by unsupervised machine learning” 2023
”Single-Cell Technologies to Decipher the Immune Microenvironment in Myeloid Neoplasms: Perspectives and Opportunities” 2022
“i6mA-DNC: Prediction of DNA N6-Methyladenosine sites in rice genome based on dinucleotide representation using deep learning” 2020
”4mCCNN: Identification of N4-Methylcytosine Sites in Prokaryotes Using Convolutional Neural Network” 2019
”iN6-Methyl (5-step): Identifying RNA N6-methyladenosine sites using deep learning mode via Chou’s 5-step rules and Chou’s general PseKNC” 2019
“Branch Point Selection in RNA Splicing Using Deep Learning” 2018

Articles in reviews

Congress proceedings

OTHER INFORMATION

Declarations given in the present curriculum must be considered released according to art. 46 and 47 of DPR n. 445/2000.

The present curriculum does not contain confidential and legal information according to art. 4, paragraph 1, points d) and e) of D.Lgs. 30.06.2003 n. 196.

Please note that CV WILL BE PUBLISHED on the University website and It is recommended that personal and sensitive data should not be included. This template is realized to satisfy the need of publication without personal and sensitive data.

Please DO NOT SIGN this form.

Place and date: ___Milan ______, ____19/01/2024__________