

A position is open in the Mass Spectrometry Unit (MSU) at Department of Experimental Oncology (DEO) a leading cancer research institution located in the south area of Milan (<https://www.research.ieo.it>, <https://www.ieo.it/>).

The Unit provide MS-based proteomics analysis for DEO scientists, including protein identification, protein expression profile either in Label-Free or label-Based methods (SILAC, TMT), interaction proteomics (AP-MS, proximity labelling), mass mapping and PTMs characterisation. The unit is equipped with state-of-art of Orbitrap-Hybrid mass spectrometers. The instruments are operating in bottom-up LC-MS workflows (DDA, DIA) and are coupled to a variety of nano-flow chromatography systems (nLC-1200, Neo Vanquish and Evosep-one). The unit also makes use of an 1680 HPLC (Agilent) for offline peptide fractionation (RP-HpH, SCX). Recently, we implemented Quantitative Proteomics Made Simple (QProMS), a user-friendly, search engine-agnostic data analysis and visualisation pipeline. QProMS guides the user through data analysis and statistical testing in a graphical interface. Statistical tests rely on established R functions and are compatible with all types of label-free quantification experiments (<https://bioserver.ieo.it/shiny/app/qproms>).

**We are looking for a motivated, enthusiastic person to work on sample preparation protocols optimization and to operate LC-MS equipment as well as to run proteomics data analysis pipelines.**

**Key responsibilities are:**

- Operate and maintain Unit equipment.
- Reliably document all procedures along QC standards.
- Closely collaborate with research groups to plan experiments, communicate results, and provide analytical support.
- Introduce, train and supervise users to sample preparation, equipment operations and provide evaluation support.
- Implement rules/guidelines/SOPs.

**Requirements**

The ideal candidate has an advanced degree (M.Sc. or Ph.D.) in Chemistry, Biochemistry, Biology or a similar field. Practical experience in the operation of MS equipment and basic knowledge of proteomics data analysis tools (i.e MaxQuant/Perseus, Proteome Discoverer, Skyline, MaxQuant, Msfragger and DIA-NN). A proactive approach to collaborations and a demonstrated ability to work in a team environment it is strongly preferable.

Contract and salary conditions will be discussed based on candidate profile.

Potential applicants are encouraged to contact Dr. Alessandro Cuomo (Head of the Unit) a CV with a CV with at list one referee to [alessandro.cumo@ieo.it](mailto:alessandro.cumo@ieo.it)