ID

VP006_BIOTEC

Visiting Professor Program
Academic Year 2024/2025

TEACHING COMMITMENT: 16 hours

COURSE TITLE
Mass Spectrometry-Based Palaeoproteomic Analysis of Ancient Proteins

TEACHING PERIOD
1st term

SCIENTIFIC AREA
Analytical Chemistry

LANGUAGE USED TO TEACH
English

COURSE SUMMARY
This course will provide you with a detailed introduction to the methods used for mass spectrometry (MS)-based ancient protein sequencing, i.e. palaeoproteomics. The course will focus on the most advanced methodologies and applications of palaeoproteomics to palaeontology, palaeoprimatology and palaeoanthropology. A series of lectures will present: (i) the history of this research field, (ii) the most advanced technologies and methodologies it relies on, and (iii) the most impressive scientific achievements it accomplished.

LEARNING OBJECTIVES
The teaching offers as principal objective the learning of the principles of the bioanalytical chemistry analysis of ancient proteins as biomolecules.

In particular the objectives to be reached are: knowledge of sampling and extractive procedures of proteins from biological samples; knowledge of MS analysis used in the ancient paleoproteomics fields; knowledgo of the most popular free database for proteins identification.

VISITING PROFESSOR PROFILE

The VP should have a deep knowledge of the use of mass spectrometry (MS) and high-resolution MS to sequence ancient protein residues recovered from paleontological and cultural heritage materials. The use of separation techniques such as LC and GC for the characterization of biomolecules is also appreciated.

The VP should be actively involved in methodological development to push reliable recovery of ancient proteins further back in time, to minimise starting sample quantities and to improve data analysis and interpretation. Such expertise should be supported by several coherent publications in high-impact factor scientific journals.

CONTACT REFERENT

Federica Dal Bello

federica.dalbello@unito.it