PhD position on Palaeoproteomics for cultural heritage
- Proteins in figurative arts and artworks -
Marie Curie TEMPERA European Training Network

Title: *PhD candidate*
Tenure: *Three years*

One PhD position is available in the MSAP CNRS laboratory at the University of Lille in France (USR CNRS 3290 MSAP "Miniaturization for Synthesis, Analysis and Proteomics"), as part of the Marie Curie TEMPERA European Training Network.

Background

The position is part of the Marie Curie TEMPERA European Training Network (ETN) supported by the European Union's EU Framework Programme for Research and Innovation Horizon 2020, www.tempera-etn.eu.
TEMPERA ETN aims at providing international and interdisciplinary state-of-the-art doctoral training to prepare the next generation of specialists in mass spectrometry (MS)-based ancient protein residues analysis for biomolecular diagnostics and conservation of cultural heritage material. Europe's cultural heritage plays a fundamental role in European cultural integration and attracts millions of visitors each year. Most of the cultural heritage objects produced using biogenic materials are rich in protein residues. Proteomic analysis of cultural heritage will improve knowledge about production techniques and chemical preservation of cultural heritage materials, ultimately improving their safeguard and conservation. For the first time, TEMPERA brings together in a network the laboratories which have, largely in isolation, developed the techniques upon which ancient protein analysis is built.

Focus of the Project:

Proteins in figurative arts and artworks: from bottom up to top down approach

Objectives: (i) identification of proteins in paint binders and their biological origins for a better understanding of artworks, (ii) identification of protein chemical modifications (due to local environment, pollution, restoration treatments, conservation conditions, etc.) for a better knowledge of artwork conservation/degradation.

Expected Results: The impact of commonly used restoration tools will be defined at molecular level. Proteins truncations and chemical modifications will be determined. Identification of common and uncommon protein modifications, identification of biological species, study of proteins from unsequenced genomes will be massively improved.

The analysis of proteins in figurative arts includes (i) the identification of proteins and their biological origins for a better understanding of artworks, (ii) but also the identification of protein chemical modifications (due to local environment, pollution, restoration treatments, conservation conditions, etc.) for a better knowledge of artwork conservation/degradation. ESR1's activity will be divided in technical sessions (bottom up and top down experiments), visit of museums and their restoration/conservation sections and study of specific artworks. The interactions with museums, conservators and restorers will be done *via* (i) the LeadART network (resulting from JPI-JHEP project 2014-2018), and (ii) the NordART networkthat links research, museums (Louvre, Matisse museum, etc.) and archaeology in the North of France. The analytical sessions will include both bottom up and top down approaches. Bottom-up proteomics is the current proteomics mainstream. Particular focus will be given to sample preparation (according to the type of sample), analytical workflow adapted to the study of very small sample amounts (on-line nanoLC nanoESI-Orbitrap MS), instrument settings, and bioinformatic tools

(commercial softwares and custom-developed ones) used for protein identification, identification of common and uncommon protein modifications, identification of biological species, study of proteins from unsequenced genomes. The second part of the analytical session will focus on the top down approach (see Chem. Rev. 2016, 116, 2−79), using a high-resolution MS analyzer and the direct fragmentation of proteins without preliminary chemical or enzymatic hydrolysis. Particular cautions related to the sample preparation are needed and will be shown during ESR1's project (e.g. intact proteins extraction from their complex matrix). Top down experiments will be applied to the study of protein extracts from various ancient artworks using nanoLC nanoESI-Qh-FT-ICR MS including CID (Collision Induced Dissociation), ECD (Electron Capture Dissociation) and IRMPD (InfraRed MultiPhoton Dissociation) experiments. The impact of commonly used restoration tools will be studied at molecular level on model samples formulated in the lab with ancient recipes and on ancient samples restored/non restored in Partners'museums. Proteins truncations and chemical modifications will be studied.

The candidate will have to interact with restorers, conservators, art historians and archaeologists from the partners' museums and MSAP partners' laboratories.
The project will require careful development of activities for public engagement as well as writing scientific articles, papers, reports or books, as appropriate. The selected PhD candidate will also be required to attend network-wide workshop events and take active part to network-wide remote activities.

Environment

The MSAP laboratory is a CNRS laboratory located at the University of Sciences and Technologies of Lille. It is specialized in "omics" developments and flow chemistry. MSAP integrates a mass spectrometry/omics platform developing cutting-edge technologies and offering services in different domains (biology, chemistry, medicine, plant science, environment, cultural heritage) on sample preparation (in-gel/ offgel separation); targeted and non-targeted quantitative proteomics including relative quantification with (Stable Isotope Labeling) or without labeling (Label Free Quantification) or absolute quantification, accurate proteins characterization by top-down analysis including post-translational modifications and exact molecular mass determination. MSAP is equipped with 8 state of the art mass spectrometers including high resolution (2 nanoESI-Orbitraps) and very high resolution mass spectrometers (nanoESI-FT-ICR MS 9.4 T equipped with IRMPD and ECD).
MSAP is a major international player in proteomics applied to Cultural Heritage samples. The group proposed the first applications of bottom up proteomics applied to artworks and more recently the first application of top down and native protein analysis from Cultural Heritage samples (Chem. Rev. 2016, 116, 2−79). MSAP is also head of several cross-disciplinary projects and networks such as the european LeadART network (11 european partners including research laboratories and museums such as Rijksmuseum, Amsterdam), regional NordART network (links research, museums and archaeology in the North of France) and international long-term partnerships (e.g. Metropolitan Museum of Art, New York).

Qualifications

Essential Experience and Skills

Essential skills and experience include:

- Chemistry or biochemistry background
- Demonstrated knowledge of analytical chemistry, in particular, mass spectrometry techniques (theoretical and experimental).
- Demonstrated knowledge of protein (bio)chemistry and understanding of processes of protein degradation, both spontaneous and enzymatic.
- Knowledge of, and demonstrated experience in designing, implementing, and optimising: (i) analytical methods for protein characterisation, (ii) biochemical methodologies for sample preparation for protein analysis.
- Demonstrated experience in tandem MS-based proteomics data generation and analysis is a valued plus.

- Demonstrated experience in interpretation and analysis of MS/MS data, protein sequence reconstruction and statistical validation of the results is a valued plus.
- Ability to comfortably work in a highly interdisciplinary environment with colleagues with different scientific backgrounds.

Experience in detection and identification of protein residues from cultural heritage by proteomics is a valued plus.
Knowledge of use and conservation of proteinaceous materials in art and archaeology is a valued plus.
Demonstrated experience in development and delivery of public outreach initiatives is a valued plus.
Candidates will be expected to closely interact with other PhD candidates and supervisors within the TEMPERA ETN network and with other members of the local scientific community in Lille and MSAP international partners.

Desired Experience and Skills

- As MSAP and TEMPERA are highly international research environments, good communication skills in written and oral English is required.
- Integrity, motivation, and good collaboration skills.
- Experience bioinformatic manipulation and statistical analysis of large molecular datasets is a valued plus.

Elegibility:

TEMPERA is a Marie Curie European Training Network. PhD candidates within the the TEMPERA ETN program are expected to fulfil the conditions for international mobility. Namely, researchers are required to undertake trans-national mobility (i.e., move from one country to another) when taking up the appointment. At the time of recruitment by the University of Lille, candidates must not have resided or carried out their main activity (work, studies, etc.) in France for more than 12 months in the 3 years immediately prior to their recruitment. Short stays, such as holidays, are not taken into account. The applicant must also fulfil the criteria of an Early Stage Researcher. Specifically, at time of recruitment the researcher must be in the first 4 years (full-time equivalent research experience) of his/her research career and must not have been awarded a doctoral degree.

Place of employment and work

The successful applicant will mainly be based at the MSAP laboratory in the University of Lille 1 Sciences and Technologies (Villeneuve d'Ascq). Secondments to other institutions within the TEMPERA consortium are a mandatory part of the successful researcher's employment. Accordingly, the selected PhD candidate is expected to spend time, for no more than 11 months, studying and performing interdisciplinary research at a different TEMPERA institution.

Required documents for application, deadline, agenda and contact

The required documents have to be sent by e-mail to Pr Caroline Tokarski (supervisor of the PhD): Caroline.Tokarski@univ-lille1.fr

Submission deadline: 15 July 2017
Results of candidate selection: 17 July 2017
PhD starting: 1st September 2017

The candidates will have to provide the following documents and information:
(*reminder: candidates must not have resided or carried out their main activity (work, studies, etc.) in France for more than 12 months in the 3 years immediately prior to their recruitment*)

Personal data:

- First name:
- Last name:
- Private address:
- Postal code:
- City:
- Country:
- Telephone:
- E-mail:
- Year of birth:
- Gender:
- Citizenship:

Degree

- Degree names:
- Dates of obtained degree:
- Institution:
- Country:
- Level: Master/Bachelor:
- Title of Master thesis:
- Status of thesis: Approved/Pre-Approved/Pending:
- Name of the Master thesis supervisor:
- Other relevant education:
- Which year did you finish other relevant education:

Additional merits

- Participated in research and academic work: Yes/No (to be detailed in CV)
- Completed prize Master thesis: Yes/No (to be detailed in CV)
- Other prices/awards: Yes/No (to be detailed in CV)
- Completed study abroad: Yes/No (to be detailed in CV)

Please include the following files (Word or PDF files)

- Cover Letter
- CV
- Diploma and transcripts of records
- List of publications
- Other information to consider