1st European Top-Down Proteomics Symposium

Paris, February 12-14, 2019

ABSTRACT BOOK

WELCOME ADDRESS

Dear Delegates

On behalf of the Organizing and Scientific Committees, we are delighted to welcome delegates from all over the world to the 1st European Top-Down Proteomics Symposium, EuTDP2019.

Top-down proteomics is an emerging technology offering an unprecedented level of accuracy in detecting differentially modified intact proteins (proteoforms) or associated complexes. The term proteoform designates all of the different molecular forms in which the protein product of a single gene can be found, encompassing all forms of genetic variation, alternative splicing of RNA transcripts, and post-translational modifications (PTMs).

Over the last decade, significant progress has been made to advance top-down proteomics (both in denaturing and native conditions). As a result, interest in top-down proteomics has grown considerably, and a number of studies have already showcased the potential of this disruptive technique for the unraveling of disease mechanisms and discovery of new biomarkers.

The scientific committee has put together a truly unique program that addresses the different aspects of top-down proteomics: the latest developments in instrumentation, sample preparation (both in denaturing and native conditions), intact protein fractionation/separation, data analysis, as well as applications in life sciences and human health.

A series of state-of-the-art plenary lectures will be presented by internationally renowned scientists. This will be accompanied by sessions of oral presentations and posters. The associated exhibition will provide you with the latest information on a range of technologies and services to support for your research and development.

Additionally, we would like to thank all of our industrial sponsors: Bruker, ThermoFisher Scientific, Waters (our three Platinum sponsors) as well as Advion, Agilent, Expedeon, Merck, MSVision and CortecNet. We also wish to thank our Institutional sponsors: Institut Pasteur, Région Ile de France (DIM Analytics & DIM Elicit), the French Society for Mass Spectrometry, the Royal Society of Chemistry, Aviesan and the Eu FT-ICR MS network.

We would also like to acknowledge the Board Members of the Consortium for Top-Down Proteomics: J. Agar, P. Danis, Y. Ge, N. Kelleher, J. Loo, L. Pasa-Tolic, L. Smith and Y. Tsybin, for assisting with the organization and for leading round tables during the symposium.

The Institut Pasteur has become famous throughout the world as a symbol of Science and French culture. We are confident that this extraordinary location, steeped in history, will promote fruitful and creative scientific interactions during the meeting. We also hope it will prove to be an inspiring experience for you!

Thank you for your participation,
Best wishes,

Julia Chamot-Rooke
Institut Pasteur, CNRS, Paris, France

ORGANIZING COMMITTEE

Julia Chamot-Rooke	*Institut Pasteur, CNRS, Paris, France*
Paul Danis	*Consortium for Top-Down Proteomics*
Mathieu Dupré	*Institut Pasteur, CNRS, Paris, France*
Virginie Portelette	*Institut Pasteur, CNRS, Paris, France*
Martial Rey	*Institut Pasteur, CNRS, Paris, France*

SCIENTIFIC COMMITTEE

Julia Chamot-Rooke	*Institut Pasteur, CNRS, Paris, France*
Mathieu Dupré	*Institut Pasteur, CNRS, Paris, France*
Jared Shaw	*Pacific Northwest, National Laboratory, USA*
Joseph Loo	*University of California Los Angeles, USA*
Ljiljana Pasa-Tolic	*Pacific Northwest National Laboratories, USA*
Martial Rey	*Institut Pasteur, CNRS, Paris, France*

CONFIRMED SPEAKERS

Rodolphe Antoine	*University of Lyon, France*
Alain Beck	*Laboratoires Pierre Fabre, France*
Isabelle Fournier	*University of Lille, France*
Albert Heck	*Utrecht University, The Netherlands*
Amy Herr	*University of California Berkeley, USA*
Ole Jensen	*University of Southern Denmark, Denmark*
Neil Kelleher	*Northwestern University, USA*
Alexander Makarov	*Thermo Fisher Scientific, Germany*
Carol Robinson	*University of Oxford, United Kingdom*
Michal Sharon	*Weizmann Institute, Israel*
Yuri Van der Burgt	*Leiden University Medical Center, The Netherlands*
Vicki Wysocki	*Ohio State University, USA*

ROUNDTABLES AND MODERATORS (CTDP)

Sample preparation, intact protein separation, instrumentation, data analysis

Ljiljana Pasa-Tolic	*Pacific Northwest, National Laboratory, USA*
Jared Shaw	*Pacific Northwest, National Laboratory, USA*

Industrial and regulatory applications (i.e. antibody and biologics analysis)

Yury Tsybin	*Spectroswiss, Switzerland*
Alain Beck	*Laboratoires Pierre Fabre, France*

Future directions of top-down proteomics

Neil Kelleher	*Northwestern University, USA*
Joseph Loo	*University of California Los Angeles, USA*

CTDP Board of Directors

CTDP
Consortium for Top-Down Proteomics
Bringing Proteoforms to Life℠

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Eastwoods Consulting
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Pre-cut sheets of Western blotting transfer membrane offer convenience, but are more expensive per use, and are not adaptable when a different size is needed. Standard rolls of membrane are more flexible, but plan for extra bench time with ruler and scissors to cut to the size needed for your gel. Over time, this handling leads to costly membrane waste and occasional visualization of your lab mate's thumb print on your blot...

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European Network of Fourier Transform Ion Cyclotron Resonance Mass Spectrometry Centers

EU FT-ICR MS

A Horizon 2020 INFRAIA Project for Starting Communities (2018-2021)

The EU FT-ICR MS project aims at establishing a European wide network of Fourier Transform Ion Cyclotron Resonance (FT-ICR) mass spectrometry (MS) centers in association with an instrument manufacturer and a SME software company. Mass spectrometry (MS) has become the most ubiquitous analytical techniques in use today, providing more information on the composition and the structure of a substance – from a smaller amount of sample than any other technique. This EU project promotes the use and development of high end FT-ICR MS through TransNational Access (TNA), dedicated training and education, open data & e-infrastructure program as well as joint research activities and networking.

Transnational access

Education & training

Joint research activities

- Organic chemistry
- IR spectroscopy of ions in the gas phase
- Imaging
- Bioorganic & Bioinorganic
- Medicine
- Nanoparticles
- Physical chemistry

EU FT-ICR MS

First European FT-ICR MS network

Academic & Industrials free access

- Lipidomics
- Petroleum & bio-oil
- Environment
- Glycomics
- Structural biology
- Cultural heritage
- Proteomics

This project has re funding from the European Union's Horizon 2020 research and innovation Programme under grant agreement No. 731077

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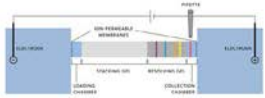
FEATURES

- Intact protein molecular weight fractionation, isolation, and purification
- Liquid-phase recovery without band or spot cutting
- Broad mass range fractionation up to 500 kDa
- Up to eight samples processed in parallel
- Programmable fractionation for isolating and purifying targeted proteins
- High protein recovery (>80%)
- High reproducibility (<15% CV)
- Sampling unbiased by hydrophobicity, pI
- High loading capacity (>5X more than a 1D gel)
- Proteins are recovered intact, for complete characterization

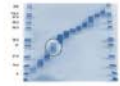
GELFrEE® is Gel Elution Liquid Fraction Entrapment Electrophoresis. It enables molecular weight-based fractionation of intact proteins into liquid-phase fractions and bypasses both the low recovery of proteins and extensive workup steps before mass spectrometry.

How does it work?

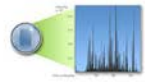
GELFrEE® 8100 has eight channels. Each channel consists of a precision-cast gel column with a sample loading chamber at the front and a fraction collection chamber at the end. One to eight channels can be used at any one time. Samples are pipetted into the sample loading chamber, electric current is applied and charged molecules in each channel migrate along the column gel. Eluting proteins are trapped in a defined liquid volume. At pre-defined intervals, the instrument automatically pauses for easy removal of the liquid fraction with a pipette. For collection of the next size-based fraction, the sequence is restarted and the process continued.



Collecting a fraction from a single tube gel



1D gel of S. cerevisiae fractions prepared using the GELFrEE® System.
A 200µg aliquot of yeast was fractionated into 12 fractions using the Gelfree® 8100 system. 1D gel analysis with silver staining was used to visualize the results.



Basepeak chromatogram of digested fraction from GELFREE® System.
A yeast sample, S. cerevisiae, was fractionated into 12 fractions. The resulting fractions were acetone precipitated to remove SDS, digested using trypsin, and analysed using nanoLC-MS/MS.

GELFrEE® 8100 Sample Specifications

- Max sample load volume: 150 µl
- Fixed fraction volume of 150 µl
- Protein load ≤ 500 µg (≤ 3.3 mg/ml)
- Conductance ≤ 2 mS/cm
- pH 8.4 ± 1.0

In proteomics mass spectrometry analysis, protein mixtures are so complex that the low abundant proteins, the main ones of interest, are lost among the highly abundant signals. Excising protein bands from preparative slab gels can result in little or no protein. Hence, effective fractionation of complex samples for in-depth proteomic analysis by mass spectrometry is critical.

Molecular weight protein fractionation

Up to eight samples are run in parallel using a programmable control module. The system separates proteins by their molecular weight. GELFrEE® 8100 provides robust fractionation over the mass range 3.5 kDa – 500 kDa.

✔ User friendly touch-screen interface

✔ High reproducibility and high recovery

✔ Convenient ready-to-use cartridge kits

✔ 8 lane high throughput cartridges

GELFREE® 8100 CARTRIDGE SPECIFICATIONS

% Polyacrylamide	mW Range	Optimum mW Range	average Fraction Width
5%	3.5 - 500 kDa	75 - 500 kDa	40 kDa
8%	3.5 - 150 kDa	35 - 150 kDa	10 kDa
10%	3.5 - 100 kDa	15 - 100 kDa	7 kDa
12%	3.5 - 60 kDa	10 - 50 kDa	4 kDa

Applications

- Simplify and reduce the dynamic range of complex protein mixtures for bottom-up discovery proteomics using LC-MS/MS
- Fractionate and recover proteins intact for top-down proteomics
- Isolate and enrich user-selected molecular weight fractions for targeted protein quantification using LC-MS/MS
- Isolate intact proteins to analyse variants, post-translational modifications and alterations
- Separate protein pull-down components for target protein purification
- Separation, isolation and intact recovery of antibodies for in-depth characterisation

Bottom-up proteomics

Broad fractionation for increased coverage. Reduced complexity. Gain molecular weight information to distinguish peptides from multiple gene products.

Top-down proteomics

Intact protein fractionation and isolation. Analyse post-translational modifications, variants and alterations. Native electrophoresis is in development.

Pharma

Characterise bio-therapeutic degradation products. Separate protein pull-down components for target protein purification. Characterise antibodies.

Ordering Information

CAT. NO.	DESCRIPTION	CAT. NO.	DESCRIPTION
48100	GELFrEE® 8100 Fractionation System + Cartridges		
42104	5% Tris Acetate - Cartridge kit	42105	10% Tris Acetate - Cartridge kit
42103	8% Tris Acetate - Cartridge kit	42102	12% Tris Acetate - Cartridge kit

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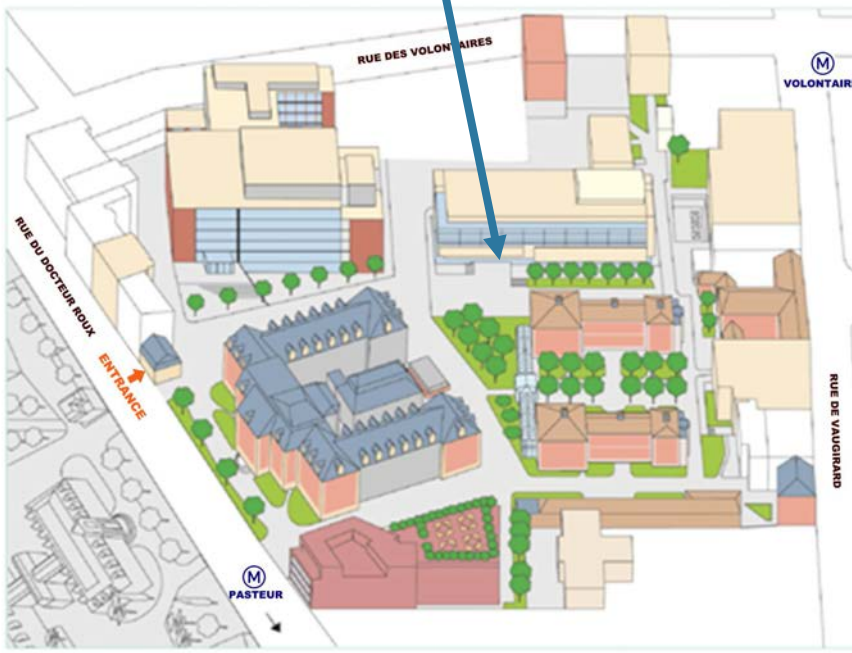
TABLE OF CONTENTS

Summary **Page**

MAP OF THE CAMPUS

Scientific Information
Center Auditorium (CIS)

Hall of CIS : *Welcome Desk, Posters and Sponsors exhibitions, Cocktail, Lunches and Coffee breaks*



GENERAL INFORMATION

On the Institut Pasteur campus, the "Plan Vigipirate Attentats" is on, so please make sure to have an official ID or passport to enter the campus.

If your registration is fully covered, you will receive your complete congress kit including your badge, the certificate of attendance, the conference programme. Please wear your badge at all time. Do not forget your badge for the Dinner Cruise it will be asked at the entrance of the Boat.

If registration was not fully covered, please come directly to the registration desk "on site payment". We accept payment by cash or credit card (Visa or Mastercard).

REGISTRATION

Registration desk opens at 9 am on February 12th, 2019 in the hall of the CIS Auditorium.

- Opening hours other days: 8:15 am - 9:30 am.
- Congress staff assistance also during coffee breaks, lunches and cocktails.
- A cloakroom is available on registration level. We ask you not to leave any personnal belongings unattented in the auditorium.

GENERAL INFORMATION

PLENARY SESSIONS

Scientific sessions are taking place in the auditorium of the CIS.
Coffee-breaks, lunch and cocktail will be served in the hall of the CIS.
Access to lunch is limited to participants who are registered.
All attendees are invited to the Symposium cocktail that will be held on February 12, from 7 to 9 pm in the hall of the CIS auditorium.
For the cruise dinner, all participants are expected to be at the gate of the boat at 8 pm at the latest Wednesday 13th February. See next page for the map to get there.

POSTER SESSIONS

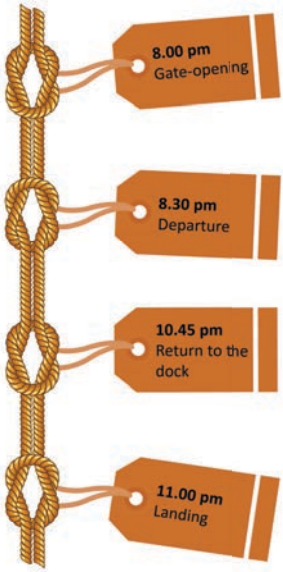
All selected posters will be displayed throughout the conference. All posters have to be in place before the coffee-break of Tuesday 12th February and should be kept at least until the last coffee-break Thursday 14th February.

Check the matching number on the board to display your poster in the right place. Magnets are available at the welcome desk to fix your poster.

SOCIAL PROGRAMME

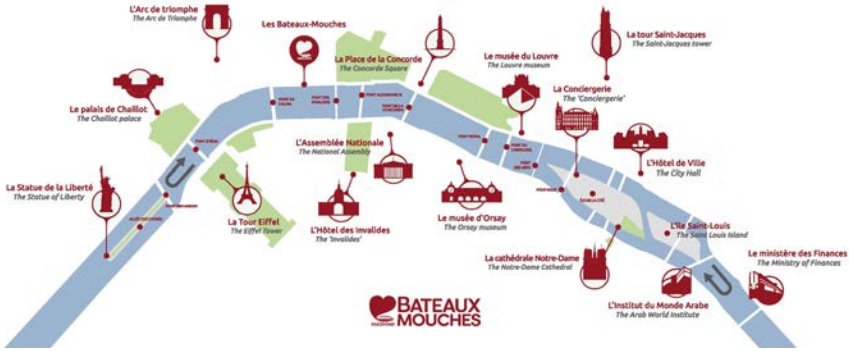
Cruise Dinner on the Seine River

Wednesday 13th February 8-11 pm



Le Jean-Bruel

Picture credits : Bateaux-Mouches



HOW TO GET THERE ?

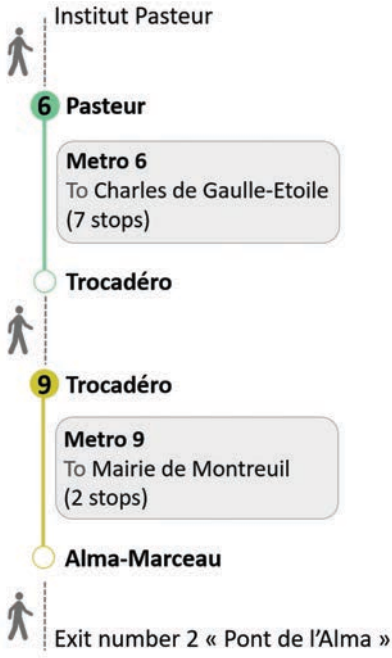
- **By taxi or Uber :**

  Bateaux-Mouches
  Port de la Conférence (Pont de l'Alma)
  75008 PARIS

- **By public transportation (metro) :**

  Approx. 35 min (from Institut Pasteur)

  Take metro line 6 to "Charles de Gaulle-Etoile"
  Change at the station Trocadéro for the line 9 to "Montreuil"
  Stop at the station Alma-Marceau, exit number 2 "Pont de l'Alma"



Picture credits : Institut Pasteur / Thomas LANG 2017

Institut Pasteur

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tdp2019@conferences-pasteur.org

SCIENTIFIC PROGRAMME

FEBRUARY 12TH, 2019

1 Opening of the 1st EuTDP Symposium — 11 am - 3.40 pm

11 am **Registration and installation of posters**

1.45 pm **Welcome and Opening**
Julia Chamot-Rooke
Institut Pasteur, Paris, France

1 — 2 pm **Opening Lecture: Profiling cellular-to-molecular diversity using electrophoretic cytometry**
Amy Herr
University of California Berkeley, United States

2 — 2.50 pm **Leveraging proteoforms and a growing community to determine the composition of the human proteome**
Neil Kelleher
Northwestern University, United States

3 — 3.20 pm **The Top-Down Community**
Paul Danis[2], Julia Chamot-Rooke[1]
[1]Institut Pasteur, France [2]Eastwoods Consulting, United States

3.40 pm **COFFEE BREAK**

2 Instrumentation and analytical strategies — 4.10 pm - 7 pm

Chair: Jared Shaw

4 — 4.10 pm **Advances in Orbitrap mass spectrometry for top-down analysis**
Alexander Makarov
Thermo Fisher Scientific, Bremen, Germany

5 — 4.40 pm **Enhancing middle-down and top-down protein and PTM characterization by mass spectrometry and new computational tools**
Ole Jensen
University of Southern Denmark, Denmark

6 — 5.10 pm **Chromatographic strategies for top-down mass spectrometry of integral membrane proteins**
Julian Whitelegge
University of California Los Angeles, United States

7 5.30 pm	**Development of Liquid Extraction Surface Analysis Mass Spectrometry for Top-Down Protein Identification of ESKAPE Pathogens Growing on *in vitro* 3D Skin Models** Jana Havlikova *University of Birmingham, United Kingdom*
5.50 pm	**And now a word from our sponsors!**
8 6 pm	**Round table: Sample preparation, intact protein separation, instrumentation, data analysis** Ljiljana Pasa-Tolic, Jared Shaw *Pacific Northwest National Laboratories, United States*

7 pm - 9 pm **APÉRO POSTER**

FEBRUARY 13TH, 2019

3 Human Health — 9 am - 2 pm

Chair: Yury Tsybin

9 9 am
A wealth of proteoforms exposed and quantified by hybrid mass spectrometry approaches
Albert Heck
Utrecht University, The Netherlands

10 9.50 am
Cutting-edge mass spectrometry methods for the multi-level structural characterization of Antibodies and Antibody Drug Conjugates
Alain Beck
Laboratoires Pierre Fabre, France

11 10.20 am
Sequence validation of three human IgG1 antibodies by Mass Spectrometry during an inter-Laboratory Study
Detlev Suckau
Bruker Daltonik, Bremen, Germany

10.40 am **COFFEE BREAK**

12 11.10 am
Round table: Industrial and regulatory applications (i.e. antibody and biologics analysis)
Yury Tsybin[1], Alain Beck[2]
[1]Spectroswiss, Switzerland [2]Laboratoires Pierre Fabre, France

12.10 pm **LUNCH & POSTER**

4 Proteoform-centric Bioinformatics — 2 pm - 4 pm

Chair: Ljiljana Pasa-Tolic

13 2 pm
Implications of proteoforms in clinical chemistry (glyco)proteomics
Yuri Van Der Burgt
Leiden University Medical Center, The Netherlands

14 2.30 pm
UniProt protein resource and the proteoform atlas: linking proteoforms with the UniProt Knowledgebase
Emanuele Alpi
European Bioinformatics Institute (EMBL-EBI), United Kingdom

15 2.50 pm **A proteoform centric paradigm for pathway and biological network analysis**
Luis Francisco Hernández Sánchez
University of Bergen, Norway

3.10 pm **And now a word from our sponsors!**

3.20 pm **COFFEE BREAK**

5 Technological Developments — 4 pm - 11 pm

Chair: Neil Kelleher

16 4 pm **Bridged MS Imaging of Proteins and Top-Down Spatially-Resolved Proteomics Strategy to better Characterize Tumor Microenvironment**
Isabelle Fournier
University of Lille, France

17 4.30 pm **An isotope depletion strategy for improved top-down fragmentation analysis**
Kelly Gallagher
University of Edinburgh, United Kingdom

18 4.50 pm **Tandem Mass Spectrometry using Electron Capture Dissociation for the Structural Characterization of Intact Proteins**
Jonathan Williams
Waters Corporation, Wilmslow, United Kingdom

5.10 pm **And now a word from our sponsors!**

19 5.20 pm **Round table: Future directions of top-down proteomics**
Joseph Loo[1], Neil Kelleher[2]
[1]*University of California, United States* [2]*Northwestern University, United States*

8 pm - 11 pm **CRUISE DINNER ON THE SEINE RIVER**

FEBRUARY 14TH, 2019

6 Native Top-Down and Beyond… 9 am - 1.15 pm

Chairs: Julia Chamot-Rooke & Joseph Loo

20 9 am **Native MS Coupled to Surface Collisions for "Complex-Down" Dissociation**
Vicki Wysocki
Ohio State University, United States

21 9.50 am **In-depth Investigation of recombinant proteins in crude samples**
Michal Sharon
Weizmann Institute of Science, Israel

22 10.20 am **Fast-photochemical Oxidation of Proteins and Top-down Mass Spectrometry**
Petr Novak
Institute of Microbiology, Czech Republic

10.40 am **And now a word from our sponsors!**

10.50 am COFFEE BREAK

23 11.20 am **Mass and charge distributions of entire amyloid fibers by charge detection mass spectrometry: mapping heterogeneity, polymorphism and co-aggregation**
Rodolphe Antoine
University of Lyon, France

24 11.50 am **Nanomechanical resonators based neutral MS of viral capsids above 100 MDa**
Christophe Masselon
CEA Grenoble, France

25 12.10 pm **Closing lecture: Membrane Proteins – the Lipid Connection**
Carol Robinson
University of Oxford, United Kingdom

1 pm **Final remarks**
Julia Chamot-Rooke[1], Paul Danis[2],
[1]Institut Pasteur, France [2]Eastwoods Consulting, United States