

# “Bioinformatics applied to proteomics”

Thursday 8<sup>th</sup> September 2016

**Auditorium Fernand Gallais**  
**CNRS Campus, 205 route de Narbonne - Toulouse**

Nowadays mass spectrometry is routinely used for proteomic analysis in many laboratories. This has been accompanied by an increase in analysis throughput and depth, providing novel information on biological samples (identification and quantification of proteins, posttranslational modifications, protein-protein interactions, etc.) for entire proteomes. However, these insights could not be obtained without sophisticated bioinformatic tools, able to process and interpret the vast and complex datasets generated by mass spectrometers.

Whether one needs to answer a biological question (Veit Schwämmle), to improve the reliability and depth of results (Viktoria Dorfer), or even to take advantage of public data repositories (Marc Vaudel), we will see that these tools are constantly evolving to meet current and future challenges of the field.

## Scientific program:

**2 pm – 2:45 pm: Veit Schwämmle** (University of Southern Denmark, Odense)

*“The senile chromatin: age-dependent changes in the epigenome”*

**2:45 pm – 3:30 pm: Viktoria Dorfer** (University of Applied Sciences Upper Austria, Hagenberg Campus)

*“Analyzing high resolution tandem mass spectra using MS Amanda and ptmRS in Proteome Discoverer”*

**3:30 pm – 4:15 pm: Marc Vaudel** (University of Bergen, Norway)

*“Taking advantage of public proteomics data in your experiments”*

## References:

1. Schwämmle V *et al.*, *Level Analysis of Histone H3 Post-translational Modifications (PTMs) Reveals Features of PTM Crosstalk in Chromatin Regulation*, Mol Cell Proteomics, 2016.
2. Dorfer V *et al.*, *MS Amanda: a universal identification algorithm optimized for high accuracy tandem mass spectra*, J Proteome Res, 2014
3. Taus T *et al.*, *Universal and confident phosphorylation site localization using phosphoRS*, J Proteome Res, 2011
4. Vaudel M *et al.*, *Exploring the potential of public proteomics data*, Proteomics, 2016.

*Note for visitors: register at least 48h before the event by sending an email to [declaration\\_visite@ipbs.fr](mailto:declaration_visite@ipbs.fr)  
Please come with a valid identity card.*

**Contact: David Bouyssie:** [david.bouyssie@ipbs.fr](mailto:david.bouyssie@ipbs.fr)

Proteomics and Mass Spectrometry of Biomolecules lab and Proteomics Infrastructure of Toulouse.



Institut de Pharmacologie et de Biologie Structurale  
205 route de Narbonne, 31077 Toulouse Cedex 04