

From targeted proteomics to deep proteome quantification

Preliminary Program

November 23, 2017, Institut Curie, Amphiteater BDD, 11-15, rue Pierre et Marie Curie, Paris

Contact : dps2017@curie.fr

09.30 - 09.45 *Welcome coffee*

09.45 – 09.50 Introduction

Session I **Session Introduction to SRM/PRM/DIA**

09.50 - 10.50 An introduction into targeted proteomics: From SRM to DIA/SWATH **Christina Ludwig** (BayBioMS)

10.50 – 11.20 Performance comparisons of targeted quantification methods. **Christine Carapito** (IPHC)

11.20 - 11.40 Speeding up Biomarker Discovery: Advanced Targeted Proteomics Workflow with High Resolution Accurate Mass (HRAM) MS. **Sebastien Gallien** (Thermo Fisher Scientific)

11.40 – 12.10 Quantitative profiling of post-translational modifications in complex samples by Parallel reaction monitoring (PRM)-based targeted mass spectrometry **Nathalie Selevsek** (FGCZ)

12.10 - 13.30 *Lunch*

Session II

13.30 - 14.00 SWATH/DIA data analysis: basics and latest developments **Ludovic Gillet** (ETH Zurich)

14.00 - 14.30 “DDA vs. DIA: considerations from a core facility perspective” **Francis Impens** (VIB)

14.30 - 14.50 How to have your cake and eat it too: Hybrid spectral library generation strategies with Spectronaut Pulsar **Lukas Reiter** (Biognosys)

14.50 - 15.10 *coffee break, poster* **Quentin Enjalbert** (ANAQUANT)

Discussion **Round table**

16.00 *End of the meeting*

