“Proteomics of Protein Misfolding Diseases”
B/D HPP Working Group

Chairs: Melinda Rezeli (Lund University, Sweden) and Paola Picotti (ETH Zurich, Switzerland)

Protein aggregation diseases (PAD), exemplified by Parkinson’s or Alzheimer’s disease and systemic amyloidoses, are characterized by an abnormal deposition of protein aggregates of regular three-dimensional structure (amyloid). The B/D PAD working group aims at developing proteomics assays for proteins that are relevant to the study, diagnosis and therapy of protein aggregation diseases. These assays are tested and refined on a set of relevant patient samples (for clinical applications) and on samples from model organisms and cell culture (for basic research). Besides developing assays for measuring protein abundances, a peculiarity of our initiative is that it will attempt also the development of proteomics assays for “aberrant protein conformations”, those typically generated in PADs. In this workshop of the PAD working group we will present the current status of the project, summarize the assays for PAD targets developed and validated so far and discuss future directions.

Program

7.30-7.40 Introduction (M. Rezeli)

7.40-8.00 **Melinda Rezeli** (Lund University)
“ TBA ”

8.00-8.20 **Yuehan Feng** (ETH Zurich, Switzerland)
“Probing the conformational changes of amyloidogenic proteins in biological samples

8.20-8.40 **Bouke Hazenberg** (University of Groningen, Netherlands) –
“The relevance of typing amyloidosis correctly”

8.40-9.00 **Paul Boersema** (ETH Zurich, Switzerland)
“Targeted proteomic assays for the diagnosis and subtyping of systemic amyloidoses”

9.00 Wrap-up (M. Rezeli)