27th HUPO Brain Proteome Project Workshop

May 9th – 10th, 2017
Ruhr-University Bochum, Germany

This workshop will provide a forum for researchers to meet and discuss the latest developments in neuroproteomic research to better understand brain function and dysfunction.

All participants will have the opportunity to present their work in short presentations.

Young scientists are very welcome!

General information:
Registration fee: 120 €
Number of participants: max. 50

The HUPO Human Brain Proteome Project (HBPP):

Mission: Create and harbour a broad and global network of neuroproteomic researchers with a focus of attracting young researchers.

Steering Commitee:
Lea Grinberg, UCSF, USA & Brazilian Brain Bank, Sao Paulo, Brazil
Katrin Marcus, Medizinisches Proteom-Center, Bochum, Germany
Helmut E. Meyer, ISAS, Dortmund, Germany
Peter Nilsson, KTH- Royal Institute of Technology, Stockholm, Sweden
Daniel Martins-de-Souza, University of Campinas, São Paulo
Young Mok Park, Korean Basic Science Institute, Daejon, Korea
Oliver Schubert, Unversity of Adelaide, Australia
Charlotte Teunissen, VU University Medical Center Amsterdam, The Netherlands

Local organizers:
Katrin Marcus & Caroline May , Medizinisches Proteom-Center, Bochum, Germany

www.hbpp.org

HBPP

27th HBPP Workshop Program

Tuesday, May 9th

9.00 – 9.30	**Arrival & Registration & Coffee**
	Welcome
	Session 1: Schizophrenia & Psychiatric disorders **Chair: Oliver K. Schubert**
9.45 – 10.00	Oliver K. Schubert: Integrated proteomic approaches for personalized psychiatry
10.00 – 10.15	Juliana S. Cassoli: Ion mobility-enhanced data independent acquisitions to unravel effects of antipsychotics on oligodendrocytes and their relation to schizophrenia
10.15 – 10.30	Caroline Brandão-Teles: Employing phosphoproteomics to shed light in the molecular effects of antipsychotics on cultured oligodendrocytes: insights in schizophrenia
10.30 – 10.45	Veronica M. Saia-Cereda: The proteome of schizophrenia: the role of signaling pathways on the communication of neurons-astrocytes
10.45 – 11.00	Rita Marreiros: Functional proteomics identifies novel candidate proteins involved in schizophrenia and other chronic mental illnesses
11.00 – 11.15	David Just: Towards understanding psychiatric illness with affinity proteomics
	Session 2: Movement disorders **Chair: Caroline May**
11.15 – 11.30	Enrique Santamaría-Martínez: Olfactory bulb proteomics unveils a Lewy-type alpha synucleinopathy stage-dependent proteostasis imbalance in Parkinson´s disease
11.30 – 11.45	Simone Steinbach: Which proteins are responsible for the selective neuronal vulnerability in Parkinson's disease?
11.45 – 12.00	Steffen Kösters: Proteome characterization of human neuromelanin granules and neurons in the context of dementia with Lewy bodies
12.00 - 13.30	**Lunch**

Session 3: Spinal cord injury & Trauma
Chair: Charlotte Teunissen

13.30 – 13.45   Jean-Charles Sanchez:
Cerebrovascular disorders: Diagnostic biomarkers associated to treatment issues

13.45 – 14.00   Michel Salzet:
Shedding new light on spinal cord injury

14.00 – 14.15   Mélodie-Anne Karnoub:
Acute inflammatory response after spinal cord injury

14.15 – 14.30   Zahra Lahouby:
Involvement of the Fc gamma receptors in the neuroimmunomodulation following the spinal cord injury

14.30 – 14.45   Robert Kumsta:
Proteomics of the human stress response

14.45 – 15.00   Johannes Zang:
A Proteomics approach to childhood maltreatment

15.00 – 15.15   Elisa Pin:
Profiling the saliva autoantibody repertoire of young American football and lacrosse players to identify early biomarkers for traumatic brain injury (TBI)

15.15 – 15.45   **Coffee break**

Session 4: Myelin proteomics & Autoimmunity
Chair: Peter Nilsson

15.45 – 16.00   Olaf Jahn:
Myelin: A proteomic challenge

16.00 – 16.15   Hauke Werner:
Myelin proteomics: novel myelin proteins and their relevance for myelin structure and brain function

16.15 – 16.30   Peter Nilsson:
Profiling the autoantibody repertoire in ALS

16.30 – 18.00   **MPC lab tour (optional)**

18.00 –   **Dinner & Pub & Mingle**

Wednesday, May 10th

Session 5: Alzheimer's disease & Dementias
Chair: Helmut E. Meyer

9.00 – 9.15

Helmut E. Meyer:
Biomarkers of ageing associated dysfunctions and neurodegenerative diseases

9.15 – 9.30

Gerd Schmitz:
Platelet Extracellular Vesicles (PL-EVs) are carriers of proteins involved in vascular and neurodegenerative diseases

9.30 – 9.45

Klaus Gerwert:
Alzheimer's disease diagnosis by immuno-infrared-spectroscopy

9.45 – 10.00

Claudia Fredolini:
Verification of biomarkers associated to Alzheimer's disease in CSF by mass spectrometry based quantification

10.00 – 10.15

Mercedes Lachén-Montes:
Olfactory proteomics reveals a chronological perturbation of survival routes and a dysruption of Prohibitin complex during Alzheimer's disease progression

10.15 – 10.30

Charlotte Teunissen:
Difference in overall blood protein profile in frontotemporal dementia compared to controls identified by aptamer based proteomics

10.30 – 11.00   **Coffee break**

11.00 – 11.45   **Session 6: Cancers of the CNS**
Chair: Katrin Marcus

11.00 – 11.15

Manuel Fuentes:
 CSF analysis for protein biomarker identification in patients with CNS Lymphoma

11.15 – 11.30

Isabelle Fournier:
Can MALDI MS imaging bridged to spatially resolved microproteomics bring new insights to glioma classification?

11.30 – 11.45

Andrea Gonzáles-Morales:
Spatial and temporal proteome dynamics of glioma cells during oncolytic adenovirus DNX-2401 infection

12.00 – 13.00	**Lunch**

Session 7: New approaches & Bioinformatics
Chair: Martin Eisenacher

13:00 – 13.15	Evelina Sjöstedt: Searching for missing protein in the Hypothalamus-Pituitary pathways
13.15 – 13.30	Lukas Schilde: Expanding the CSF proteome: A useful tool for protein biomarker studies
13.30 – 13.45	Peter Verhaert: Mass spectrometry histochemistry of neuropeptides on FFPE tissue
13.45 – 14.00	Patrick Öckl: Is there a benefit of using winged stable-isotope labeled (WiSIL) peptides in CSF MRM analyses?
14.00 – 14.15	Martin Eisenacher: PIA – Protein Inference Algorithm: a flexible tool for differentiating sequence isoforms in bottom-up Proteomics
14.15 – 14.30	Michael Turewicz: Differential co-expression network analysis in quantitative proteomics
14.30 – 14.45	Julian Uszkoreit: A modular cascaded identification workflow for mass spectrometric metaproteomics
14.45 – 16.00	**General discussion & Concluding remarks**