Biology/Disease-HPP
Annual Report

Submitted at International HUPO, Adelaide
Fernando Corrales
on behalf of all members and liaisons of the B/D-HPP Executive committee

Sunday, September 15th
Overview

• Role
  • To support the use of state-of-the-art proteomic methods to characterize and quantify proteins for in-depth understanding of the molecular mechanisms of biological processes and disease across life sciences.

• Goals
  • Broaden the impact of proteomics in the broader community based on organ and disease areas.
  • Prioritize protein targets that are highly relevant to a particular field, deliver relevant quantitative assays for these selected targets and to disseminate and make publicly accessible the information and tools.
  • Contribute to the development of scientific sessions of International HUPO

• Organization
  • Fernando Corrales (chair) and Ileana Cristea (co-chair and incoming chair)
  • Jennifer Van Eyk (past-chair), Gil Omenn (Ex officio), Hui Zhang, Eric Deutsch, Pengyuan Yang, Tadashi Yamamoto, Sanjeeva Srivastava, Vera Ignjatovich, Ferdinando Cerciello (ECR representative), Paola Roncada.
  • 19 B/D-HPP initiatives with 4 closely related HPP resource pillars.
B/D HPP Initiatives. 2019 Questionnaire

- 18+1 B/D HPP active initiatives
- iMOP team in standby
- 17 B/D teams (83%, in green) + ECR submitted completed questionnaires
1. starting date of your B/D initiative and any additional information:
2. What are your main aims?
   2.a Brief statement:
   2.b Some of the current lines of work include (fill in for your initiative):
   2.c Main achievements in 2018
3. Any related documents you’d like to link?
   3.a Websites and links (fill in for your initiative):
   3.b Papers (fill in for your initiative):
      3.b.1 Total number of papers
      3.b.2 Papers published in collaboration within the initiative
      3.b.3 List Top 5 papers for 2018
   3.c Congresses in 2018? (Committees, lectures…)
      3.c.1 Participation in proteomics meetings in 2018?
      3.c.2 Participation in congresses organized by other biomedical or clinical associations
   3.d Other documents and tools (software, databases, etc.
4. Educational and dissemination activity (Courses, workshops, summer schools, etc) in 2018

• Updated information for each initiative: leadership, participation laboratories, main aims, plans and activity. Valuable information to keep updated the B/D HPP web page.
• 10 initiatives reported 382 published papers (160 authorships), of which 42 were collaborations (11 initiatives reported these collaborations).
• Participation in 82 international congresses, 49 in proteomics (14 teams) and 33 on other biomedical, clinical (11 teams) disciplines.
• Organisation of 28 educational and dissemination related activities (10 initiatives).
Identifying High-Priority Proteins Across the Human Diseasome Using Semantic Similarity.
Lau E¹, Venkatraman V², Thomas CT³, Wu JC¹, Van Eyk JE², Lam MPY³.

Systematic Protein Prioritization for Targeted Proteomics Studies through Literature Mining.
Yu KH¹,², Lee TM³, Wang CS³, Chen Yu³, Ré C⁵, Kou SC², Chiang JH⁴, Kohane IS¹, Snyder M⁷.

A Cloud-Based Metabolite and Chemical Prioritization System for the Biology/Disease-Driven Human Proteome Project.
Yu KH¹,², Lee TM³, Chen Yu³, Ré C⁵, Kou SC², Chiang JH⁴, Snyder M⁷, Kohane IS¹.

TDP-43 extracted from frontotemporal lobar degeneration subject brains displays distinct aggregate assemblies and neurotoxic effects reflecting disease progression rates.
Lafargue R¹, Manieles Z¹, Pérez-Barlanga M¹, Hruska-Plochan M¹, Gilhespy L¹, Hock EM¹, Wagner LP², Afrooz T¹, Boersena P², Barrettillo G³, Foti SC², Afi YI³, Issaou AM⁴, Al-Amoudi A³, Lewis A⁴, Stahlberg H⁴, Ravila J³, De Giorgi E¹, Ichas F¹, Bozard E¹, Pickolli F³, Lashley T⁶, Polymenidou M¹³.

Proteomic Architecture of Human Coronary and Aortic Atherosclerosis.
Herrington DM¹, Mao C², Parker SJ³, Fu Z⁴, Yu G⁵, Chen L⁵, Venkatraman V³, Fu Y⁶, Wang Y⁵, Howard TD⁵, Jun G⁷, Zhao CR⁵, Liu Y⁷, Saylor G⁸, Stivia WR³, Athas GB¹⁰, Troxclair D¹⁰, Hixson JE¹, Vander Heide RS¹⁰, Wang Y⁵, Van Eyk JE².

Orchestration of protein acetylation as a toggle for cellular defense and virus replication.
Murray LA¹, Sheng X¹, Cristea IM².


Germline Duplication of SNORA18L5 Increases Risk for HBV-related Hepatocellular Carcinoma by Altering Localization of Ribosomal Proteins and Decreasing Levels of p53.
Cao F¹, Yang A², Wang B³, Xia X¹, Zhai Y¹, Li Y¹, Yang F¹, Cui Y¹, Xie W¹, Liu Y⁶, Liu T⁶, Jia W¹, Jiang Z⁵, Li Z⁵, Han Y¹, Gao C¹, Song G¹⁰, Xie B¹, Zhang L¹, Zhang H¹, Zhang J¹, Shen X², Yuan Y¹, Yu E³, Wang Y⁴, Xu B³, Ma Y⁴, Mo Z¹², Yu W¹³, He F¹⁴, Zhou G¹⁵.

Orchestrating protein acetylation as a toggle for cellular defense and virus replication.
Murray LA¹, Sheng X¹, Cristea IM².
6. Are you currently doing research on popular/priority proteins?
Yes: Brief description
If not, would you be willing to?

- Protein lists available from peptide atlas
- Four published tools for selecting popular proteins from the literature

Data-Driven Approach To Determine Popular Proteins for Targeted Proteomics Translation of Six Organ Systems.
Lam MP, Venkatraman V1, Xing Y, Lau E, Cao Q2, Ng DC, Su AI3, Ge J2, Van Eyk JE1, Ping P.

Systematic Protein Prioritization for Targeted Proteomics Studies through Literature Mining.
Yu KH, Lee TM, Wang CS, Chen YJ, Ré C, Kou SC, Chiang JH, Kohane IS, Snyder M.

Identifying High-Priority Proteins Across the Human Diseasome Using Semantic Similarity.
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A Cloud-Based Metabolite and Chemical Prioritization System for the Biology/Disease-Driven Human Proteome Project.
Yu KH, Lee TM, Chen YJ, Ré C, Kou SC, Chiang JH, Snyder M, Kohane IS.
Yes, we systematically derived popular and relevant proteins from >20,000 terms from 4 ontology databases (DOID, HPO, PW, BTO). We developed the PubPular web app and are continuing to improve the speed, capacity, and functions.

**Extreme conditions**
Identification of protein expression changes caused by spaceflight.
A SRM method has been developed to quantify proteins in blood. We are currently standardizing the method that has been previously adapted to perform the quantitative measurements in DBS.

**EyeOme**
We already established a list of popular proteins in eye research

**FAN**
tropomyosin

**HBPP**
Implementation of MS-based assays for alpha synuclein quantification.
Identification of proteins in human brain and blood plasma that still have no evidence at proteins level (MPs) according to UniProt
Association of 14-3-3 signaling proteins and schizophrenia during early neurodevelopment using cerebral organoids
Protein interactome of hnRNP in the context of schizophrenia using cross-linking

**HPPP**
Collected of proteins measurable by both MS and affinity assays in 2017

**HLPP**
We have identified One Carbon Metabolism (1CM) enzymes as “popular proteins” associated with the progression of chronic liver injury and hepatocellular carcinoma. A SRM method has been developed and the hypothesis has been validated in mouse liver. We are currently standardizing the method to perform the quantitative measurements in humans.

**RAD**
A manuscript has been submitted reporting high priority proteins in rheumatic and autoimmune diseases (PubPular and PURPOSE).

**HID**
Bioinformatics studies based on GO terms related with infectious diseases and using PubPular and PURPOSE software
• Collaborations already ongoing, mostly between national teams.
• Data sharing (12 teams) under collaboration if not published. Routine investigations on special sample/conditions may be a good source for searching MPs.
• Sample sharing (9 teams) depending on availability and always under collaboration.
• Sample analysis (9 teams), according to capacity. Validation and functional experiments (in combination with the availability of rare samples).
• Functional annotation of PE1 (9 teams), PE2 (8 teams) and non PE1-PE2 (5 teams)
• Work on PTMs (9 teams): P, U, M, A, CIT, OX, DEAM, GLYCO.
• Development of targeted assays for disease associated proteins.

How interaction across teams should be structured?
10. Would your initiative be willing to prepare a data-driven manuscript based around your initiative for the **HPP special issue** in *Journal of Proteome Research*? Manuscripts are due by 31 May 2019

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11. Would your initiative participate in the upcoming HUPO Congress to be held in Adelaide (Australia) in 15-19 Sept 2019? If YES, then address these questions:

- The Annual HUPO World Congress includes six sessions dedicated to the HPP. Would your initiative be willing to participate in the coordination of one of these sessions? [This is urgent, as the Local Organizing Committee is determined to finalize the program very soon.]
- Would your initiative participate in the HPP precongress workshop (Sunday HPP workshop)?
- Would your initiative participate in the HPP post-congress workshop (Thursday HPP workshop)?

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B/D-HPP contribution of HUPOST

2019
September – Interview with Ruedi Aebersold (Vera Ignjatovic)
August - Sample menu for BD-HPP at Orlando 2018 (Vera Ignjatovic)
July – Affinity proteomics workshop summary (Jochen Schwenk)
June – Pathology Pillar update (Ed Nice)
May - Prioritizing popular proteins - summary of the best currently available tools (Kun-Hsing Yu and Maggie Lam)
April – ECR Report (Ferdinando Cerciello on behalf of the ECR)
March – Update on the Human Glycoproteomics Initiative (HGI) (Morten Thaysen-Andersen and Nicky Parker)
February - Q&A with Gil Omenn - HPP Immediate Past Chair (Vera Ignjatovic)
Jan - Q&A with Vera Ignjatovic, new B/D-HPP HUPOST coordinator (Michelle Hill)

2018
December – NextGen Human Proteome Project (Michelle Hill)
November –1st HIPP Summer School on Immunopeptidomics (Miguel Marcilla).
Supportive programing for Annual HUPO meeting

Adelaide 2019

Sunday: HPP Investigators Meeting
Sunday: Early Career Mentoring day
Monday – Wednesday: HPP Scientific Track: 6 sessions
ECR manuscript competition
Clinical Scientist Travel Awardee round table

Thursday: HPP Strategic Workshop

Bioinformatics Hub

Clinical Scientist Travel Award and Workshop
The Clinical Scientist Travel Award is to foster outreach into the clinical scientist.

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<td>Li Qing Kay</td>
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<td>Noguchi Rei</td>
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<td>Kassem Iris</td>
<td>USA</td>
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<td>Tu Ngoc Nguyen</td>
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<td>Soren Naaby-Hansen</td>
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ECR Manuscript Competition

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<td>Maggie Lam</td>
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<td>Ankit Sinha</td>
<td>Germany</td>
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<tr>
<td>Eneko Villanueva</td>
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HPP 1: Towards the complete cardiac proteome and beyond

Peipei Ping and Ying Ge

- Chamber and cell type specific views of the human heart glycoproteome and glycome in health and disease - Rebekah L Gundry
- Delving Deeper into the Cardiac Proteome – Analyzing the Heart “Modificome” - Melanie Y White
- Proteomic profiling of plasma lipoprotein particles as a tool to identify novel subtypes - Stefan Lehr
- Relating high density lipoprotein (HDL) particle composition to clinical signaling capacity - Sandra Goetze
- Cross-species tissue proteomics analyses in cardiovascular disease: unraveling Ariadne’s thread - Merika Mokuw
- An anatomically resolved human heart transcriptome and proteome landscapes reveal molecular signatures and disease-relevant pathways of end-stage dilated cardiomyopathy - Ling Lin

HPP 2: Rheumatic and Autoimmune Disorders

Cristina Ruiz and Alex J Rai

- Clinical evaluation of a multiplexed protein panel to discriminate patients with psoriatic arthritis from those with rheumatoid arthritis - Stephen R Pennington
- Affinity proteomics for array based profiling of autoantibody repertoires - Peter Nilsson
- Allelic association with ankylosing spondylitis fails to correlate with HLA-B27 homodimer formation - Ralf B Schittenhelm
- Development of an autoantigen microarray for the screening of novel autoantibodies in psoriatic arthritis - Tianfu Wu
- HLA-B27 Immunoproteome: Understanding the connection between Salmonella typhimurium infection and ankylosing spondylitis - Terry C.C Lim Kam Sian
- ThyroProt: a robust protein classification system for thyroid disease based on deep learning of proteome data - Yoating Sun

Pathology and the Cancer Proteome: Towards Precision Medicine

Daniel Chan and Hui Zhang

- Proteome-Based Diagnostics: The Next Revolution in Medicine and Pathology - Michael H. Roehr
- Enabling Precision Medicine for Alzheimer’s Disease through Biofluid-Based Biomarkers - Daniil Li
- Heterogeneity study of pancreatic tumor tissue: Proteomic characterization of tumor cells obtained by laser microdissection (LMD), coring, and bulk sampling techniques. - Qing Kay Li
- Intra- and inter-individual variation in the proteome of high-grade serous ovarian cancer - Rosemary Balleine
- Proteomic Tissue Biomarkers for Early Prediction of Prostate Cancer Progression - Jacob Kagan
- Oxygen-sensitive interactions between glycolytic enzymes and a cancer-testis antigen established signaling scaffold are regulated by lysine acetylation - Soren Neaby Hansen

HPP 3: Plasma, Pediatrics and Proteomics

Jochen Schwenk

- Systems-level analysis of immune development early in life - Petter Brodin
- Temporal profiles of plasma proteome during childhood development and natural progression of Type 1 Diabetes - Qibin Zhang
- Orthogonal validation of Duchenne Muscular Dystrophy biomarkers using targeted proteomics - Cristina Al-Khalili Szigayto
- Mass spectrometry workflow for characterization of plasma proteome changes related to ageing - Valentina Silino
- The sweet separation between bacterial and viral infections by glycopeptide profiling - Esther Willems
- A comprehensive proteomic analysis of medulloblastoma subtypes reveals mechanistic insights of Group 3 tumors - Sanjeeda Srivastava

HPP 4: High Connectivity: Neuroproteomics at the Interface of Bench and Bedside

Oliver Schubert and Katrin Marcus

- The use of proteomics to identify blood-based protein changes in childhood that are associated with increased risk for later psychosis - Melanie Foecking
- Comparative glycoproteomic analyses of cerebrospinal fluids reveal novel molecular players in Alzheimer’s disease - Lingju Li
- Autoantibody Profiling of Schizophrenia and related Psychotic Disorders in the Australian National Survey of High Impact Psychosis (SHIP) - K. Oliver Schubert
- Human brain proteome draft atlas to understand biological function and reference for brain tumour investigations - Sanjeeda Srivastava
- Proteomic and bioenergetic analyses demonstrate synaptic mitochondrial alterations due to age-related pathologic tau accumulation - Kelly L Staub
- A Proteome Atlas of Senescence-Associated Secretomes for Aging Biomarker Development - Nathan Basisty

HPP 5: Moving proteomics into pharmaceutical discovery and application

Jenifer Van Eyk and Ferdinando Cerciello

- Proteome Landscape of Early Stage Hepatocellular Carcinoma Identifies Proteomic Subtypes and New Therapeutic Targets - YING JIANG
- Venoms to Drugs - Paul Alewood
- Unveiling protein targets involved in haptogenesis in allergic contact dermatitis via high resolution mass spectrometry - Wint Wint Phoo
- Reverse chemical proteomics identifies unanticipated human target of anti-malarial drug, Artesunate, for drug repositioning - Sung Min Cho
- Proteome profiling of multiple sclerosis cerebrospinal fluid by data independent acquisition reveals changes in protein involved in adaptive immunity - David R. Spiliarich
- Thermostable potassium channel-inhibiting neurotoxins in processed scorpion medicinal material revealed by proteomic analysis: Implications of its pharmaceutical basis in traditional Chinese medicine - Xiaolu Zhao