WELCOME MESSAGE

Dear AOHUPO community and friends,

Warm wishes to you and everyone around you for a safe, healthy and better 2021!

On behalf of the Asia Oceania Human Proteome Organization (AOHUPO), it is my great pleasure and honor to welcome you to "The 1st AOHUPO Online Educational Series 2021" that will be held on 3 consecutive Saturday mornings (27 Feb, 6 March, and 13 March 2021) at online virtual meeting.

The main aim of AOHUPO is to promote and coordinate the activities of the regional proteomics community and indeed it has firmly established the tradition of organizing a highly successful biannual conference being hosted by different countries in the AO region. The COVID-19 pandemic has become a global health issue and has had major impacts on education and social interactions. Therefore, AOHUPO Council has decided to launch a new online education program, called "AOHUPO Online Educational Series" to support learning and to continue our communications during the pandemic.

The theme of the 1st AOHUPO Online Educational Series 2021 is "Next Generation Proteomics in Precision Oncology: Concepts, Technologies and Challenges". The organizing committee led by Drs. Terence Poon (Vice-President of AOHUPO, University of Macau, Macau) and Teck Yew Low (Secretary General of AOHUPO, National University of Malaysia, Malaysia) would like to focus on the recent proteogenomic studies of precision oncology. We invite 6 eminent speakers to address their recent researches in proteogenomics toward precision medicine and appreciate for their excellent contributions to the 1st AOHUPO Online Educational Series. I also appreciate the strong support by Dr. Chuxia Deng, Faculty of Health Sciences, University of Macau and sponsors who have greatly contributed to prepare this meaningful online education program with fruitful outcomes.

Finally, I wish all of you will actively participate the programs of this meeting for 3 consecutive Saturday mornings (27 Feb, 6 March, and 13 March 2021) and enjoy exciting science.

Thank you for your attention and I look forward to the days we can meet in person again!

With best wishes,

Ho Jeong KWON,
President of AOHUPO,
Professor, Yonsei University, Korea

1st AOHUPO Online Educational Series Organizing Committee 2021

Chair	Terence C.W. Poon	Faculty of Health Sciences, University of Macau Vice-President, AOHUPO
Co-Chair	Ho Jeong Kwon	Yonsei University, Korea President, AOHUPO
Secretary General	Teck Yew Low	National University of Malaysia, Malaysia Secretary General, AOHUPO
Committee member	Maxey Chung	National University of Singapore, Singapore Past-President, AOHUPO
Committee member	Stuart Cordwell	University of Sydney, Australia Vice-President, AOHUPO
Committee member	Yasushi Ishihama	Kyoto University, Japan President, Japanese Proteomics Society (JPS)
Committee member	Yu-Ju Chen	Academia Sinica, Taiwan President, Human Proteome Organization (HUPO)
Committee member	Je-Yoel Cho	College of Veterinary Medicine Seoul National University, Korea President, Korean Human Proteome Organization (KHUPO)

REGISTRATION

REGISTRATION METHOD

1. Fill in the registration form which is available at the AOHUPO website, www.aohupo.org;

2. Email the filled form to the organizing committee at AOHUPO2001@gmail.com

Registration Fee: Free

Registration Deadline: 22 February 2021

Maximum number of participants: 250

Contact Email: AOHUPO2001@gmail.com

PROGRAM [to be updated]

Updated on January 30, 2021

MC & Moderator: Terence POON **Vice-President of AOHUPO** **University of Macau, Macau**	**27 Feb 2021, Day 1 (Saturday)**	**6 March 2021, Day 2 (Saturday)**	**13 March 2021, Day 3 (Saturday)**
8:30AM – 9:20AM (GMT+8)	8:30AM – 8:45AM Opening Speech (15 min speech) Ho Jeong Kwon President of AOHUPO Professor, Yonsei University, Korea	8:30AM – 9:20AM ***Plenary Lecture 2*** Proteogenomic study of Non-smoking Lung Cancer in East Asia [Talk Title to be Confirmed] Yu-Ju Chen President, HUPO Acting Director, Institute of Chemistry, Academia Sinica, Taiwan	8:30AM – 9:20AM ***Plenary Lecture 3*** Proteogenomic study of Endometrial Carcinoma [Talk Title to be Confirmed] David Fenyo Professor, Department of Biochemistry and Molecular Pharmacology, Institute for Systems Genetics, NYU School of Medicine, USA
	8:45AM – 9:05AM Opening Speech (10 min speech) Chuxia Deng Dean, Faculty of Health Sciences University of Macau, Macau		
9:20AM – 10:10AM (GMT+8)	9:05AM – 10:10AM ***Plenary Lecture 1*** Overview of Next Generation Proteomics in Precision Oncology AND Integrative Proteomics Study of Lung Adenocarcinoma [Talk Title to be Confirmed] Fuchu He Professor, Beijing Institute of LifeOmics Director, State Key Laboratory of Proteomics, China	9:20AM – 10:10AM ***Plenary Lecture (Technology) 2*** Tools/Application in Proteogenomics for Precision Oncology [Talk Title to be Confirmed] Bing Zhang Professor, Lester and Sue Smith Breast Center Baylor College of Medicine, USA	9:20AM – 10:10AM ***Plenary Lecture (Technology) 3*** [Speaker & Title to be Confirmed]
10:10AM – 11:00AM (GMT+8)	10:10AM – 11:00AM ***Plenary Lecture (Technology) 1*** Practical Tips & Challenges in Integrated Proteogenomic Data Analysis of Lung Adenocarcinoma Minjia Tan Professor, State Key Laboratory of Drug Research Shanghai Institute of Materia Medica Chinese Academy of Sciences, China	Technological Advances for Clinical/Disease Proteomics [Parallel sections for diff vendors, to be confirmed]	Closing Speeches

"DAY 1" Plenary Speaker: Fuchu He, Ph.D.

Resource

Integrative Proteomic Characterization of Human Lung Adenocarcinoma

Jun-Yu Xu [1, 11], Chunchao Zhang [2, 11], Xiang Wang [3, 11], Linhui Zhai [1, 11], Yiming Ma [4, 11], Yousheng Mao [5], Kun Qian [6], Changqing Sun [7], Zhiwei Liu [1, 8], Shangwen Jiang [1], Minghui Wang [3], Lin Feng [3], Lei Zhao [1], Ping Liu [1], Bo Wang [4], Xin Zhao [6], Hui Xie [7], Xiaoyun Yang [4], Liyuan Zhao [4], Yafei Chang [4], Jingya Jia [4], Xijun Wang [3], Yimin Zhang [4], Yaru Wang [3], Yikun Yang [5], Zhixiang Wu [1], Longhai Yang [5], Bin Liu [1], Teng Zhao [6], Shengguo Ren [9], Aihua Sun [2], Yang Zhao [2], Wantao Ying [2], Fei Wang [9], Guangshun Wang [10], Yi Zhang [6], Shujun Cheng [3], Jun Qin [2], Xiaohong Qian [2], Yi Wang [2 ✉], Jing Li [4 ✉], Fuchu He [2 ✉], Ting Xiao [3 ✉], Minjia Tan [1, 8, 12 ✉]

[1] State Key Laboratory of Drug Research, Shan Sciences, Shanghai 201203, China
[2] State Key Laboratory of Proteomics, Beijing Sciences (Beijing), Beijing Institute of Lifeom
[3] State Key Laboratory of Molecular Oncology, Center/National Clinical Research Center for Sciences and Peking Union Medical College,
[4] Department of Bioinformatics and Biostatist Tong University, Shanghai 200240, China
[5] Department of Thoracic Surgery, National Ca Cancer/Cancer Hospital, Chinese Academy o 100021, China
[6] Department of Thoracic Surgery, Xuanwu Ho
[7] Department of Oncology, Tianjin Baodi Hosp
[8] University of the Chinese Academy of Scienc
[9] Shanghai Key Laboratory of Intelligent Inforr Technology, Fudan University, Shanghai 200
[10] Department of Oncology, Baodi Clinical Coll

Proteomics identifies new therapeutic targets of early-stage hepatocellular carcinoma

Ying Jiang, Aihua Sun, Yang Zhao, Wantao Ying, Huichuan Sun, Xinrong Yang, Baocai Xing, Wei Sun, Liangliang Ren, Bo Hu, Chaoying Li, Li Zhang, Guangrong Qin, Menghuan Zhang, Ning Chen, Manli Zhang, Yin Huang, Jinan Zhou, Yan Zhao, Mingwei Liu, Xiaodong Zhu, Yang Qiu, Yanjun Sun, Cheng Huang, Meng Yan, Mingchao Wang, Wei Liu, Fang Tian, Huali Xu, Jian Zhou, Zhenyu Wu, Tieliu Shi, Weimin Zhu, Jun Qin, Lu Xie, Jia Fan ✉, Xiaohong Qian ✉, Fuchu He ✉ & Chinese Human Proteome Project (CNHPP) Consortium -Show fewer authors

Abstract

Hepatocellular carcinoma is the third leading cause of deaths from cancer worldwide. Infection with the hepatitis B virus is one of the leading risk factors for developing hepatocellular carcinoma, particularly in East Asia[1]. Although surgical treatment may be effective in the early stages, the five-year overall rate of survival after developing this cancer is only 50–70%[2]. Here, using proteomic and phospho-proteomic profiling, we characterize 110 paired tumour and non-tumour tissues of clinical early-stage hepatocellular carcinoma related to hepatitis B virus infection. Our quantitative proteomic data highlight heterogeneity in early-stage hepatocellular carcinoma: we used this to stratify the cohort into the subtypes S-I, S-II and S-III, each of which has a different clinical outcome. S-III, which is characterized by disrupted cholesterol homeostasis, is associated with the lowest overall rate of survival and the greatest risk of a poor prognosis after first-line surgery. The knockdown of sterol O-acyltransferase 1 (SOAT1)−high expression of which is a signature specific to the S-III subtype−alters the distribution of cellular cholesterol, and effectively

Fuchu He, Ph.D.
Professor, Beijing Institute of LifeOmics, China
Director, State Key Laboratory of Proteomics, China
President, National Center for Protein Sciences, Beijing
President, Beijing Proteome Research Center, China
Member of CAS and TWAS

Dr. He is the leading scientist studying proteomics in China. He was the founder of CNHUPO and among the first group of people who founded HUPO in 2001. He was the first Chinese scientist who led an international consortium-Human Liver Proteome Project (HLPP), and the founder of Beijing Proteome Research Center, Phoenix Center (proteomics) and Institutes of Biomedical Sciences Fudan University. As the chief scientist, he has been propelling HLPP to the China Human Proteome Project (CNHPP), to create an encyclopedia of proteins in the human body under physiological and pathological conditions. Recently, his team stratified early hepatocarcinoma (HCC) into 3 proteomic subtypes with different clinical outcome. Some drug targetable proteins have been demonstrated useful in identifying patients with HCC who could potentially benefit from targeted treatment in further clinical trials. These studies demonstrated the proteomic analysis as an independent powerful tool in cancer molecular subtyping, indicating that the era of "Proteome Driven Precision Medicine (PDPM)" is coming.

"DAY 1" Plenary Speaker (Technology): Minjia Tan, Ph.D.

Resource

Integrative Proteomic Characterization of Human Lung Adenocarcinoma

Jun-Yu Xu [1, 11], Chunchao Zhang [2, 11], Xiang Wang [3, 11], Linhui Zhai [1, 11], Yiming Ma [4, 11], Yousheng Mao [5], Kun Qian [6], Changqing Sun [7], Zhiwei Liu [1, 8], Shangwen Jiang [1], Minghui Wang [3], Lin Feng [3], Lei Zhao [1], Ping Liu [1], Bo Wang [4], Xin Zhao [6], Hui Xie [7], Xiaoyun Yang [4], Liyuan Zhao [4], Yafei Chang [4], Jingya Jia [4], Xijun Wang [3], Yimin Zhang [4], Yaru Wang [3], Yikun Yang [5], Zhixiang Wu [1], Longhai Yang [5], Bin Liu [1], Teng Zhao [6], Shengguo Ren [9], Aihua Sun [2], Yang Zhao [2], Wantao Ying [2], Fei Wang [9], Guangshun Wang [10], Yi Zhang [6], Shujun Cheng [3], Jun Qin [2], Xiaohong Qian [2], Yi Wang [2 ⚲ ✉], Jing Li [4 ⚲ ✉], Fuchu He [2 ⚲ ✉], Ting Xiao [3 ⚲ ✉], Minjia Tan [1, 8, 12 ⚲ ✉]

[1] State Key Laboratory of Drug Research, Shanghai Institute of Materia Medica, Chinese Academy of Sciences, Shanghai 201203, China

[2] State Key Laboratory of Proteomics, Beijing Proteome Research Center, National Center for Protein Sciences (Beijing), Beijing Institute of Lifeomics, Beijing 102206, China

[3] State Key Laboratory of Molecular Oncology, Department of Etiology and Carcinogenesis, National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing 100021, China

[4] Department of Bioinformatics and Biostatistics, School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, Shanghai 200240, China

[5] Department of Thoracic Surgery, National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing 100021, China

[6] Department of Thoracic Surgery, Xuanwu Hospital, Capital Medical University, Beijing 100053, China

[7] Department of Oncology, Tianjin Baodi Hospital, Tianjin 301800, China

[8] University of the Chinese Academy of Sciences, Beijing, China

[9] Shanghai Key Laboratory of Intelligent Information Processing, School of Computer Science and Technology, Fudan University, Shanghai 200433, China

[10] Department of Oncology, Baodi Clinical College of Tianjin Medical University, Tianjin 301800, China

Minjia Tan, Ph.D.
Professor, Shanghai Institute of Materia Medica
Chinese Academy of Sciences
University of the Chinese Academy of Sciences,
Beijing, China

Dr. Tan's current research interest is mainly focused on developing novel mass spectrometry-based chemical proteomics technologies to characterize protein post-translational modifications (PTMs) and to identity molecular mechanisms and sensitive/resistant biomarkers of molecularly targeted therapy in precision medicine. By integrating proteomics, biochemistry, bioinformatics technology, Dr. Tan's study significantly increased new histone epigenetic marks, and identified lysine crotonylation, succinylation, malonylation, and glutarylation as new types of protein modification pathways, which are important for cellular energy metabolism and epigenetic regulation. These works expanded the protein lysine acylation landscape in cellular physiology.

"DAY 2" Plenary Speaker: Yu-Ju Chen, Ph.D.

Resource

Proteogenomics of Non-smoking Lung Cancer in East Asia Delineates Molecular Signatures of Pathogenesis and Progression

Yi-Ju Chen [1, 24], Theodoros I. Roumeliotis [2, 24], Ya-Hsuan Chang [3, 24], Ching-Tai Chen [4, 25], Chia-Li Han [5, 25], Miao-Hsia Lin [1, 25], Huei-Wen Chen [6], Gee-Chen Chang [7, 8], Yih-Leong Chang [9], Chen-Tu Wu [9], Mong-Wei Lin [10], Min-Shu Hsieh [9], Yu-Tai Wang [11], Yet-Ran Chen [12], Inge Jonassen [13], Fatemeh Zamanzad Ghavidel [13], Ze-Shiang Lin [14], Kuen-Tyng Lin [1], Ching-Wen Chen [14], Pei-Yuan Sheu [14], Chen-Ting Hung [14], Ke-Chieh Huang [1], Hao-Chin Yang [1], Pei-Yi Lin [1], Ta-Chi Yen [1], Yi-Wei Lin [10], Jen-Hung Wang [4], Lovely Raghav [3, 15], Chien-Yu Lin [3], Yan-Si Chen [3], Pei-Shan Wu [1], Chi-Ting Lai [1], Shao-Hsing Weng [1], Kang-Yi Su [14, 16], Wei-Hung Chang [12], Pang-Yan Tsai [14], Ana I. Robles [17], Henry Rodriguez [17], Yi-Jing Hsiao [14], Wen-Hsin Chang [18], Ting-Yi Sung [4], Jin-Shing Chen [19], Sung-Liang Yu [14, 16], Jyoti S. Choudhary [2], Hsuan-Yu Chen [3, 20], Pan-Chyr Yang [21, 22], Yu-Ju Chen [1, 23, 26]

1 Institute of Chemistry, Academia Sinica, Taipei, Taiwan
2 Functional Proteomics Group, Chester Beatty Laboratories, The Institute of Cancer Research, London SW3 6JB, UK
3 Institute of Statistical Science, Academia Sinica, Taipei, Taiwan
4 Institute of Information Science, Academia Sinica, Taipei, Taiwan
5 Master Program in Clinical Pharmacogenomics and Pharmacoproteomics, College of Pharmacy, Taipei Medical University, Taipei, Taiwan
6 Graduate Institute of Toxicology, College of Medicine, National Taiwan University, Taipei, Taiwan
7 Division of Chest Medicine, Department of Internal Medicine, Taichung Veterans General Hospital, Taichung, Taiwan
8 Faculty of Medicine, School of Medicine, National Yang-Ming University, Taipei, Taiwan
9 Department of Pathology, National Taiwan University Hospital and National Taiwan University College of Medicine, Taipei, Taiwan
10 Division of Thoracic Surgery, Department of Surgery, National Taiwan University Hospital, Taipei, Taiwan
11 National Applied Research Laboratories, National Center for High-performance Computing, Hsinchu, Taiwan
12 Agricultural Biotechnology Research Center, Academia Sinica, Taipei, Taiwan
13 Computational Biology Unit (CBU), Informatics Department, University of Bergen, Bergen, Norway
14 Department of Clinical Laboratory Sciences and Medical Biotechnology, College of Medicine, National Taiwan University, Taipei, Taiwan
15 Institute of Bioinformatics and Systems Biology, National Chiao Tung University, Bioinformatics Program,

Yu-Ju Chen, Ph.D.

Acting Director

Institute of Chemistry

Academia Sinica

Taipei, Taiwan

President, HUPO

Dr. Chen obtained her B.S. in chemistry from National Taiwan University (1992) and Ph.D. degree from Iowa State University (1997). After postdoctoral research work at the Ames Laboratory, Department of Energy, USA [1997] and National Tsing Hua University [1999], Dr. Chen joined the Institute of Chemistry of Academia Sinica and was promoted to research fellow (2010). Since 2013, she has been the Director for the Institute of Chemistry at Academia Sinica. She also currently holds con-current adjunct professorships at few universities.

Her research focuses on methodology development of mass spectrometry-based proteomics by integrating novel nanomaterial, advanced mass spectrometry and bioinformatics. In particular, she is interested in applying these tools to delineate the membrane proteome and post-translation modificome on cancer and stem cell biology. She has received domestic and international awards including Outstanding Young Investigator Award from Chinese Chemical Society (2006), Distinguished Young Chemists Award from Federation of Asian Chemical Societies (2007), Mr. Wu Ta-you Memorial Award from National Science Council (2008), and Research Award for Junior Research Investigators from Academia Sinica (2008), the first award for outstanding scholar of Taiwan Society for Mass Spectrometry (2011), outstanding young scholar, 13th Shu-Mu Foundation of Chemistry (2012), and the outstanding research award from National Science Council (2013). She has been the Council Member of "International Mass Spectrometry Foundation". She has been the President of the Taiwan Proteomics Society, President of Taiwan Society for Mass Spectrometry. She has been the Vice-President of Asia Oceania Human Proteome Organization (AOHUPO). Currently, she is the President of Human Proteome Organization (HUPO)

She is acting as Senior Editor of "Proteomics" and editorial board member of the European Journal of Mass Spectrometry. Dr. Chen has published more than 140 articles including *Nat. Commun.*, *Cancer Cell*, *Mol. & Cell. Proteom.*, *Anal. Chem.*, *J. Am. Chem. Soc.*, and *Proc. Natl. Acad. Sci.*, and 5 patents.

Cell

Volume 177, Issue 4, 2 May 2019, Pages 1035-1049.e19

CellPress

Resource

Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities

Suhas Vasaikar [1, 2, 14], Chen Huang [1, 2, 14], Xiaojing Wang [1, 2, 12, 14], Vladislav A. Petyuk [3, 14], Sara R. Savage [4, 14], Bo Wen [1, 2], Yongchao Dou [1, 2], Yun Zhang [1], Zhiao Shi [1, 2], Osama A. Arshad [3], Marina A. Gritsenko [3], Lisa J. Zimmerman [5], Jason E. McDermott [3], Therese R. Clauss [3], Ronald J. Moore [3], Rui Zhao [3], Matthew E. Monroe [3], Yi-Ting Wang [3], Matthew C. Chambers [5], Robbert J.C. Slebos [5], Ken S. Lau [6], Qianxing Mo [7, 13], Li Ding [8], Matthew Ellis [1, 7], Mathangi Thiagarajan [9], Christopher R. Kinsinger [10], Henry Rodriguez [10], Richard D. Smith [3], Karin D. Rodland [3, 11, 15] ✉, Daniel C. Liebler [5, 15] ✉, Tao Liu [3, 15] ✉, Bing Zhang [1, 2, 7, 15, 16] ✉

Clinical Proteomic Tumor Analysis Consortium

Akhilesh Pandey, Amanda Paulovich, Andrew Hoofnagle, D.R. Mani, Daniel W. Chan, David F. Ransohoff, David Fenyo, David L. Tabb, Douglas A. Levine, Emily S. Boja, Eric Kuhn, Forest M. White, Gordon A. Whiteley, Heng Zhu, Hui Zhang, Ie-Ming Shih, Jasmin Bavarva, Jeffrey Whiteaker, Karen A. Ketchum, Karl R. Clauser, Kelly Ruggles, Kimberly Elburn, Linda Hannick, Mark Watson, Mauricio Oberti, Mehdi Mesri, Melinda E. Sanders, Melissa Borucki, Michael A. Gillette, Michael Snyder, Nathan J. Edwards, Negin Vatanian, Paul A. Rudnick, Peter B. McGarvey, Philip Mertins, R. Reid Townsend, Ratna R. Thangudu, Robert C. Rivers, Samuel H. Payne, Sherri R. Davies, Shuang Cai, Stephen E. Stein, Steven A. Carr, Steven J. Skates, Subha Madhavan, Tara Hiltke, Xian Chen, Yingming Zhao, Yue Wang, Zhen Zhang

[1] Lester and Sue Smith Breast Center, Baylor College of Medicine, Houston, TX 77030, USA
[2] Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX 77030, USA
[3] Biological Sciences Division, Pacific Northwest National Laboratory, Richland, WA 99352, USA
[4] Department of Biomedical Informatics, Vanderbilt University Medical Center, Nashville, TN 37232, USA
[5] Department of Biochemistry, Vanderbilt University, Nashville, TN 37232, USA
[6] Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN 37232, USA
[7] Dan L Duncan Comprehensive Cancer Center, Baylor College of Medicine, Houston, TX 77030, USA
[8] The McDonnell Genome Institute, Washington University in St. Louis, Forest Park Avenue, Campus Box 8501, St. Louis, MO 63108, USA
[9] Leidos Biomedical Research Inc., Frederick National Laboratory for Cancer Research, Frederick, MD 21702, USA
[10] Office of Cancer Clinical Proteomics Research, National Cancer Institute, Bethesda, MD 20892, USA
[11] Department of Cell, Developmental, and Cancer Biology, Oregon Health & Science University, Portland, OR 97221, USA

Bing Zhang, Ph.D., McNair Scholar
Professor
Department of Molecular and Human Genetics
the Lester and Sue Smith Breast Center
Baylor College of Medicine, USA
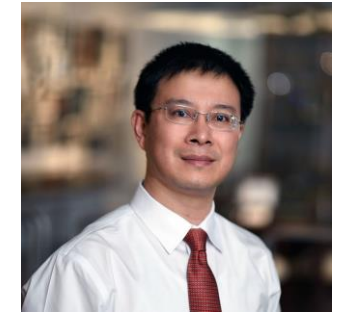
Dr. Zhang received his Ph.D. degree in Molecular Genetics from the Chinese Academy of Sciences followed by a postdoctoral training in bioinformatics at the Oak Ridge National Laboratory. Before joining Baylor College of Medicine in August 2016, he had been a faculty member in the Department of Biomedical Informatics at the Vanderbilt University for 10 years.

During his tenure at Vanderbilt, Dr. Zhang has established an internationally recognized research program in cancer proteogenomics, focusing on integrating genomic and proteomic data to better understand cancer biology. Innovative bioinformatics methods and tools developed by his group enabled the first integrative proteogenomic characterization of human cancer, which was published in Nature. This landmark study demonstrated that integrated proteogenomic analysis provides functional context to interpret genomic abnormalities, and that proteogenomics holds great potential to enable new advances in cancer biology, diagnostics and therapeutics.

Dr. Zhang has more than 70 publications in the areas of bioinformatics, proteomics and cancer systems biology. He has served as principal investigator, bioinformatics director, or co-investigator on more than 10 federal grants. He serves frequently as program committee member in international conferences and as reviewer for NIH study sections. He also serves on the editorial board of multiple journals including Molecular & Cellular Proteomics and Clinical Proteomics. He has been honored with local, national and international awards in recognition of his research activities, including an award from the National Library of Medicine (NLM) for Innovative Uses of NLM Information. Dr. Zhang is a funded scholar of the Cancer Prevention and Research Institute of Texas.

The long-term goal of Zhang's research is to use proteogenomics and multi-omics data to better understand cancer biology and to improve cancer care.

"DAY 3" Plenary Speaker: David Fenyo, Ph.D.

Cell

Volume 180, Issue 4, 20 February 2020, Pages 729-748.e26

CellPress

Resource

Proteogenomic Characterization of Endometrial Carcinoma

Yongchao Dou [1, 2, 3, 32], Emily A. Kawaler [4, 5, 32], Daniel Cui Zhou [6, 7, 32], Marina A. Gritsenko [8, 32], Chen Huang [1, 2, 3], Lili Blumenberg [9], Alla Karpova [6, 7], Vladislav A. Petyuk [8], Sara R. Savage [1, 2, 3], Shankha Satpathy [10], Wenke Liu [4, 5], Yige Wu [6, 7], Chia-Feng Tsai [8], Bo Wen [1, 2, 3], Zhi Li [4, 5], Song Cao [6, 7], Jamie Moon [8], Zhiao Shi [1, 2, 3], MacIntosh Cornwell [4, 5], Matthew A. Wyczalkowski [6, 7], Rosalie K. Chu [8], Suhas Vasaikar [11], Hua Zhou [4, 5], Qingsong Gao [6, 7], Ronald J. Moore [8], Kai Li [1, 2, 3], Sunantha Sethuraman [6, 7], Matthew E. Monroe [8], Rui Zhao [8], David Heiman [10], Karsten Krug [10], Karl Clauser [10], Ramani Kothadia [10], Yosef Maruvka [10], Alexander R. Pico [12], Amanda E. Oliphant [13], Emily L. Hoskins [13], Samuel L. Pugh [13], Sean J.I. Beecroft [13], David W. Adams [13], Jonathan C. Jarman [13], Andy Kong [14], Hui-Yin Chang [14], Boris Reva [15], Yuxing Liao [1, 2, 3], Dmitry Rykunov [15], Antonio Colaprico [16, 17], Xi Steven Chen [16, 17], Andrzej Czekański [18, 19], Marcin Jędryka [18, 19], Rafał Matkowski [18, 19], Maciej Wiznerowicz [20, 21, 22], Tara Hiltke [23], Emily Boja [23], Christopher R. Kinsinger [23], Mehdi Mesri [23], Ana I. Robles [23], Henry Rodriguez [23], David Mutch [24], Katherine Fuh [24], Matthew J. Ellis [1, 2, 3], Deborah DeLair [25], Mathangi Thiagarajan [26], D.R. Mani [10], Gad Getz [10], Michael Noble [10], Alexey I. Nesvizhskii [14, 27], Pei Wang [15], Matthew L. Anderson [28], Douglas A. Levine [29], Richard D. Smith [8], Samuel H. Payne [13], Kelly V. Ruggles [9], Karin D. Rodland [30, 31] ✉, Li Ding [6, 7] ✉, Bing Zhang [1, 2, 3] ✉, Tao Liu [8] ✉, David Fenyö [4, 5, 33] ✉

the Clinical Proteomic Tumor Analysis Consortium

Anupriya Agarwal, Meenakshi Anurag, Dmitry Avtonomov, Chet Birger, Michael J. Birrer, Simina M. Boca, William E. Bocik, Uma Borate, Melissa Borucki, Meghan C.

David Fenyo, Ph.D.
Professor
Department of Biochemistry and
Molecular Pharmacology
Institute for Systems Genetics
NYU School of Medicine, USA

David Fenyö is a Professor in the Department of Biochemistry and Molecular Pharmacology at NYU Langone Medical Center, and the Director for the Ph.D. program in biomedical informatics. David heads the NYU Laboratory of Computational Proteomics focusing on the development of methods to identify, characterize and quantify proteins and in the integration of data from multiple modalities including mass spectrometry, sequencing and microscopy.

David studied engineering physics, with a focus on mathematical and numerical methods, at Uppsala University in Sweden. After receiving an M.Sc. in 1987, he joined the laboratory of Dr. Bo Sundqvist at Uppsala University, and studied the mechanisms of ion–solid interaction both experimentally, theoretically and using molecular dynamics and Monte Carlo simulations. For this work, he received a Ph.D. in Physics in 1991.

He then went on to complete his postdoctoral work at Rockefeller University with Brian Chait where he developed algorithms to analyze proteomics data obtained using mass spectrometry, laid a statistical foundation to protein identification, and applied modeling and simulations to optimize proteomics experimental design and study replication in yeast.

In 1997, David co-founded the bioinformatics start-up ProteoMetrics, LLC, and served as the President of the company until 2002 during which he developed software systems for automated analysis of large-scale proteomics data. Subsequently, he served as the Director of Proteomics at Genomic Solutions, and as Staff Scientist and Product Manager at Amersham Biosciences and GE Healthcare before returning to academia.

Dr. Fenyő is a member of the Editorial Advisory Boards of Molecular and Cellular Proteomics, Journal of Proteomics, Proteome Science and mSystems. He serves on the scientific advisory boards of The Global Proteome Machine, BC Proteome Network, Proteome Software, Protein Metrics and Denator AB. He is also a member of the board of directors for US Human Proteome Organization (USHUPO) and serves as the treasurer.
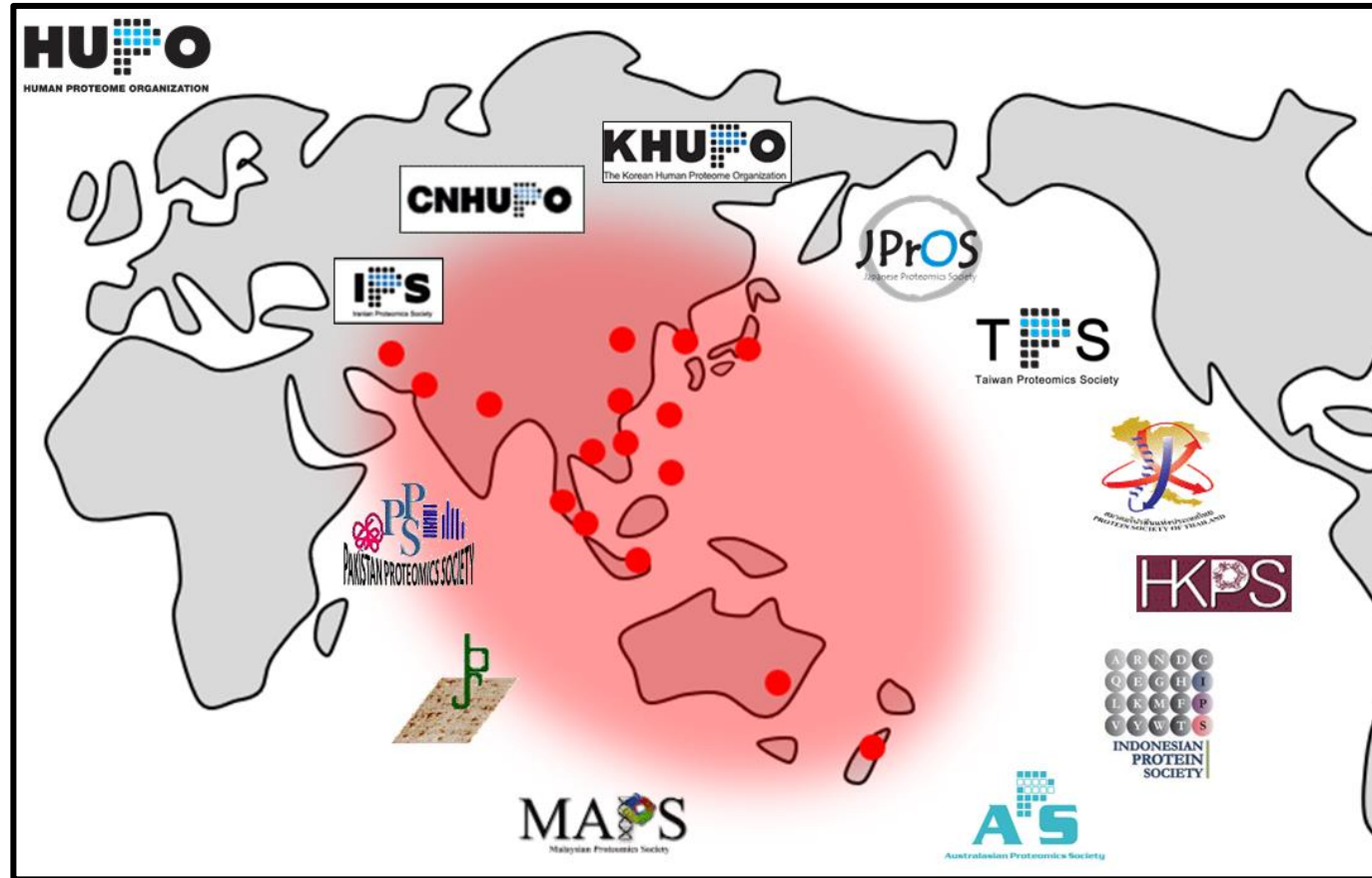
(Ref) *Mol Cell Proteomics*, 2021, DOI:https://doi.org/10.1016/j.mcpro.2021.100048

* AOHUPO website: www.aohupo.org
* Email: AOHUPO2001@gmail.com