
PROGRAM SCHEDULE

All sessions and activities will be held at the Hotel Nikko San Francisco, unless noted otherwise.

SATURDAY, AUGUST 17

4:00 –
6:30 p.m. Registration open
Nikko Ballroom Foyer, 3rd Floor

SUNDAY, AUGUST 18

7:30 a.m. –
4:00 p.m. Registration open
Nikko Ballroom Foyer, 3rd Floor

8:00 a.m. Exhibitor Set-up
Nikko Ballroom Foyer, 3rd Floor

MINISYMPOSIUM ON DATA-INDEPENDENT ANALYSIS

Nikko Ballroom, 3rd Floor

Organizers: Robert Chalkley, University of California, San Francisco, CA, USA and Hannes Röst, University of Toronto, Canada

Plenary Session

8:30 **MS1** Improving the robustness, throughput and comprehensiveness of quantitative proteomics
Mike MacCoss, University of Washington, Seattle, WA, USA

Morning Session

Chair: Robert Chalkley, University of California, San Francisco, CA, USA

9:30 **MS2** Complex-centric proteome profiling by SEC-SWATH-MS
Isabell Bludau, ETH, Zurich, Switzerland

10:10 Coffee Break in foyer

10:50 **MS3** Aligning label-based discovery and global DIA validation proteomics to explore bacterial virulence phenotypes
Stuart Cordwell, University of Sydney, Australia

11:30 **MS4** Advanced algorithms to assess and improve quantitative suitability in large DIA datasets
Sebastian Vaca Jacome, Broad Institute of MIT and Harvard, Cambridge, MA, USA

12:10 Lunch on own
p.m.

Afternoon Session

Chair: Mike MacCoss, University of Washington, Seattle, WA, USA

1:40 **MS5** Parallel accumulation — serial fragmentation combined with data-independent acquisition (diaPASEF)
Florian Meier, Max Planck Institute of Biochemistry, Martinsried, Bavaria, Germany

2:20 **MS6** Mobi-DIK (Ion Mobility DIA Analysis Kit): Targeted analysis software for diaPASEF data improves proteome coverage
Hannes Röst, University of Toronto, Canada

3:00 **MS7** Applications of DIA for PTM research and specific DIA workflows
Birgit Schilling, Buck Institute for Research on Aging, Novato, CA, USA

3:40 **MS8** Peptide MS/MS prediction for DDA and DIA
Mathias Wilhelm, Technical University of Munich, Freising, Germany

4:00 **Poster Set-up – all authors to mount posters on boards**
Carmel and Monterey Rooms, 3rd Floor

4:00 –
6:00 **Exhibits Open**
p.m. *Nikko Ballroom Foyer, 3rd Floor*

6:00 **Opening Reception**
Golden Gate Room, 25th Floor

MONDAY, AUGUST 19

7:30 –
4:00 Registration open
p.m. *Nikko Ballroom Foyer, 3rd Floor*

8:00 –
1:00 **Exhibits Open**
p.m. *Nikko Ballroom Foyer, 3rd Floor*

SYMPOSIUM

Nikko Ballroom, 3rd Floor

8:15 **Introduction**
a.m. *A.L. Burlingame, Steven Carr, and Bernhard Kuster*

Plenary Session

Chair: A.L. Burlingame, University of California, San Francisco, CA, USA

- 8:30 1.1 The End of the End: High through-put discovery and analysis of deprotons
Stephen Elledge, Harvard Medical School, Cambridge, MA, USA

Morning Session

Chair: Bernhard Kuster, Technical University of Munich, München, Germany

- 9:30 1.2 Drug effects on protein stability and proteostasis
Marcus Bantscheff, Glaxo Smith Kline, Heidelberg, Germany
- 10:10 Coffee Break in foyer
- 10:30 1.3 Development, use, application of novel TIMS-Tof system
Matthias Mann, Max Planck Institute of Biochemistry, Martinsried, Germany
- 11:10 1.4 Lysine-targeted covalent inhibitors and chemoproteomic probes
Jack Taunton, University of California, San Francisco, CA, USA
- 11:50 1.5 Mapping proteolysis at the surface of living cells
Amy Weeks, University of California, San Francisco, CA, USA
- 12:30 Lunch on own
p.m.

Afternoon Session

Chair: Anne-Claude Gingras, Lunenfeld-Tanenbaum Research Institute, Toronto, Canada

- 2:00 1.6 Characterization and turnover of RNA-binding proteins: Novel insights into ribosome maintenance
Jeroen Krijgsveld, German Cancer Research Center, Heidelberg, Germany
- 2:40 1.7 Deciphering gene expression regulation in health and disease using integrative Omics approaches
Michiel Vermeulen, Radboud Institute for Molecular Life Sciences, Nijmegen, Netherlands
- 3:20 1.8 Protein interaction networks controlling gene expression programs and beyond
Jeffrey A. Ranish, Institute for Systems Biology, Seattle, WA, USA
- 4:00 **Poster Session A**
Carmel and Monterey Rooms, 3rd Floor
Co-Chairs: Robert Chalkley, University of California, San Francisco, CA, USA
Jason Maynard, University of California, San Francisco, CA, USA
- A.1 **Dynamic proteomic profiling of the Salmonella-host interplay reveals new modes of action for known and novel virulence factors**
Jennifer Geddes-McAlister*, Stefanie Vogt, Jennifer Rowland, Sarah Woodward, Arjun Sukumaran, Lilianne Gee, Baerbel Raupach, Brett Finlay, Felix Meissner
- A.2 **Identification of urine-derived diagnostic biomarkers for Tuberculosis**
Bridget Calder*

- A.3 Microscaled Proteogenomic Methods for Precision Oncology**
Shankha Satpathy*, Eric Jaehnig, Karsten Krug, Michael Gillette, Alexander Saltzman, Kimberly Holloway, Meenakshi Anurag, Chen Huang, Purba Singh, Beom-Jun Kim, Goerge Miles, Noel Namai, Anna Malovannaya, DR Mani, Chuck Perou, Bing Zhang, Steven Carr, Matthew Ellis
- A.4 Reduced proteasome activity in the aging brain results in ribosome stoichiometry loss and aggregation**
Joanna Kirkpatrick*, Erika Sacramento, Mariateresa Mazzetto, Simone Di Sanzo, Cinzia Caterino, Aleksandar Bartolome, Michele Sanguanini, Nikoletta Papaevgeniou, Maria Lefaki, Dorothee Childs, Eva Terzibasi-Tozzini, Natalie Romanov, Mario Baumgart, Wolfgang Huber, Niki Chondrogianni, Michele Vendruscolo, Alessandro Cellerino, Alessandro Ori
- A.5 Affinity Proteomics Reveals Assembly of PPP-type Phosphatase Holoenzyme by PPM1G-B56 δ**
Parveen Kumar*, Prajakta Tathe, Subbareddy Maddika
- A.6 Targeted Quantification of Incomplete Prohormone Processing Products in Type 1 Diabetes**
Yinyin Ye*, Adam Swensen, Lian Yi, Yuqian Gao, Emily Sims, Tujin Shi, Carla Greenbaum, Carmella Evans-Molina
- A.7 Novel methods and reagents for characterization of protein biotinylation sites by peptide-based immunoaffinity enrichment**
Matthew Stokes*, Yiying Zhu, Matthew Fry, Alissa Nelson, Jian Min Ren, Vicky Yang, Michael Palazzola, Charles Farnsworth, Kimberly Lee
- A.8 Exploring the glycosylation levels of snake venom proteins by mass spectrometry: microheterogeneity determination of sweet spots in toxins of Bothrops snake genus**
Débora Andrade Silva*, Lívia Rosa-Fernandes, Giuseppe Palmisano, Silvia Travaglia-Cardoso, Solange Toledo Serrano, Martin Larsen
- A.9 Expression of PNPLA3 I148M Variant Alters Lipid Droplet Proteome**
Mara Monetti*, Jeffrey Culver, Sharath Sasi, Liang Xue, Gregory Tesz, Collin Crowley, Trenton Ross, Thomas Magee, Melissa Miller, Bei Zhang, Kendra Bence
- A.10 Vascular Cell Surface Proteomics In Vivo**
Dirk Walther*, Elizabeth Gordon, Benjamin Smith, Thomas Cameron, Ru Wei, Peter Juhasz
- A.11 Application of 4C Proteomics and Interactomics in Study of PTM Proteins Involved in Regulation of Arabidopsis Flowering**
Ning Li*
- A.12 Characterization of Symptomatic Aortic Valve Stenosis Subtypes by DIA-MS Proteome Profiling**
Christof Lenz*, Lisa Neuenroth, Soeren Brandenburg, Stephan Lehnart, Henning Urlaub
- A.13 Cell-surface proteomic landscape of developing and mature olfactory projection neurons**
Jiefu Li*, Shuo Han, Hongjie Li, Namrata Udeshi, Tanya Svinkina, D. Mani, Chuanyun Xu, Ricardo Guajardo, Qijing Xie, Tongchao Li, Bing Wu, Anthony Xie, David Luginbuhl, Pornchai Kaewsapsak, Stephen Quake, Steven Carr, Alice Ting, Liqun Luo
- A.14 Breast cancer quantitative proteome and proteogenomic landscape**
Henrik Johansson*, Fabio Socciarelli, Nathaniel Vacanti, Mads Haugen, Yafeng Zhu, Ioannis Siavelis, Alejandro Fernandez-Woodbridge, Miriam Aure, Bengt Sennblad, Mattias Vesterlund, Rui Branca, Lukas Orre, Mikael Huss, Erik Fredlund, Elsa Beraki, Øystein Garred, Jorrit Boeke, Torill Sauer, Wei Zhao, Silje Nord, Elen Höglander, Daniel Jans, Hjalmar Brismar, Tonje Haukaas, Tone Bathen, Ellen Schlichting, Bjørn Naume, OSBREAC, Torben Luders, Elin Borgen, Vessela Kristensen, Hege Russnes, Ole Christian Lingjærde, Gordon Mills, Kristine Sahlberg, Anne-Lise Børresen-Dale, Janne Lehtiö

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- A.15 Native Mass Spectrometry Study on the Stoichiometry of Proteasome AAA+ ATPase Nucleotide Binding**
H. Ewa Witkowska*, Yadong Yu, Haichuan Liu, Zanlin Yu, Yifan Cheng
- A.16 Towards Elucidation of Muscle-Specific Receptor Tyrosine Kinase (MuSK) Signaling Pathway by Differential Agonists**
Hanna Budayeva*, Arundhati Sengupta Ghosh, Lilian Phu, Donald Kirkpatrick
- A.17 Multiplexed and Quantitative Assessment of the Cellular Reactive Cysteine in T cell activation**
Liang Xue*, Uthpala Seneviratne
- A.18 Enzyme toolkit for selective enrichment and analysis of mucin-domain glycoproteins**
Stacy Malaker*, Judy Shon, Kayvon Pedram, Nicholas Riley, Carolyn Bertozzi
- A.19 Functional Metabolomics uncovering the role of Trp–KYN–KA Axis in Intestinal Injury and Repair**
Di Wang*, Huimin Guo, Zunjian Zhang, Fengguo Xu
- A.20 Metabolic Control of OGT Interactome in Hepatocytes**
Krista Kaasik*, Chin Fen Teo, Robert Chalkey, Alma Burlingame
- A.21 Integrating Phosphoproteomics and Transcriptional Classifiers Reveals “Hidden Signaling” in Multiple Myeloma Including Differential KRAS and NRAS Mutant Effects**
Yu-Hsiu Lin*, Gregory Way, Benjamin Barwick, Margarette Mariano, Makeba Marcoulis, Ian Ferguson, Christoph Driessen, Lawrence Boise, Casey Greene, Arun Wiita
- A.22 Characterization of KRAS 4B C-Terminal Hypervariable Region using LC/MS**
James Wilkins*, A.L. Burlingame
- A.23 Rapid, Sensitive and Multiplexed Ubiquitylation Profiling in Cells and Tissues**
Deepak Mani*, Namrata Udeshi, Philipp Mertins, Shaunt Fereshetian, Jessica Gasser, Shankha Satpathy, Tanya Svinkina, Hasmik Keshishian, Benjamin Ebert, Steven Carr
- A.24 Characterization of a hybrid insulin peptide as an autoantigen in human type 1 diabetes**
Timothy Wiles*, Rocky Baker, Maki Nakayama, Thomas DeLong
- A.25 Improved reproducibility of enrichment and site-assignment of biotinylated peptides using new anti-biotin antibody and its use to investigate redox signaling**
Meagan Olive*, Namrata Udeshi, Samuel Myers, Steven Carr
- A.26 Proteome-wide analysis of protein stability in E. coli using pulse proteolysis**
Roman Körner*, Liang Zhao, Giulia Vecchi, Michele Vendruscolo, Manajit Hayer-Hartl, Ulrich Hartl
- A.27 The case for mass spectrometry-based proteomics and phospho-proteomics in personalized cancer medicine**
Sophia Doll*, Fabian Coscia, Alberto Santos, Philipp Nuhn, Philipp Geyer, Matthias Mann
- A.28 Characterization of the Sin3 HDAC complex interaction network**
Mark Adams*, Charles Banks, Janet Thornton, Cassandra Kempf, Sayem Miah, Laurence Florens, Michael Washburn
- A.29 Proteogenomics of melanoma cell lines and xenografts identifies amino acid variants with a potential to rewire signal transduction networks**
Marisa Schmitt*, Nicolas Nalpas, Tobias Sinnberg, Heike Niessner, Claus Garbe, Boris Macek
- A.30 Integration of the deep learning prediction tool Prosit into Skyline for high-accuracy, on-demand fragment intensity and iRT prediction**
Tobias Rohde*, Tobias Schmidt, Bernhard Kuster, Michael MacCoss, Mathias Wilhelm, Brendan MacLean

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- A.31 Exploring mechanisms of immune suppression promoted by cancer-associated fibroblasts in lung squamous cell carcinoma**
Carlo Ramil*, Handan Xiang, Josephine Hai, Chunsheng Zhang, Huijun Wang, Amanda Watkins, Roshi Afshar, Peter Georgiev, Xuelei Song, Dongyu Sun, Andrey Loboda, Yanlin Jia, Lily Moy, Philip Brandish, An Chi
- A.32 Changes in prooncogenic and immune response proteins during development of cervical cancer through quantitative proteomics**
Jose Hernandez-Hernandez*, Gonzalo Soto-Fuenzalida, Rosa Lopez-Sanchez, Sergio Encarnacion-Guevara, Juan Martinez-Ledesma, Rocio Ortiz-Lopez, Luis Villela-Martinez, Victor Treviño-Alvarado
- A.33 Elucidating Changes in O-GlcNAcylation in Pancreatic Cancer**
Talieh Zomorrodinia*, Jason Maynard, Krista Kaasik, Alma Burlingame
- A.34 In vivo investigation of kigelia africana leaf as possible therapeutic option for gastric ulcer disease**
Oladayo Apalowo*, Babatunde Adekola, Funke Asaolu, Vincent Oriyomi, Gbenga Ogunleye, Oladayo Areola, Olusegun Babalola
- A.35 Formation of N-GlcNAc proteins is upregulated upon inhibition of proteasome activity in Ngly1-KO cells**
Jason Maynard*, Haruhiko Fujihira, Gabby Dolgonos, Tadashi Suzuki, Alma Burlingame
- A.36 Unbiased Proteomics and Network Propagation Reveals Cancer Drug Targets**
Mehdi Bouhaddou*, Neil Bhola, Rachel O'Keefe, Margaret Soucheray, Hua Li, Tian Zhu, Kelechi Nwachuku, Toni Brand, Gordon Mills, Dan Johnson, Danielle Swaney, Jennifer Grandis, Nevan Krogan
- A.37 Tuning residence time with lysine-targeted, reversible covalent probes**
Tangpo Yang*, Adolfo Cuesta, Xiaobo Wan, Jack Taunton
- A.38 Characterizing and Targeting the Hypoxic T Cell Surfaceome to Promote Immune Function in Cancer**
James Byrnes*, Lisa Kirkemo, Amy Weeks, James Wells
- A.39 Twins Labeling Derivatization-based LC-MS/MS Strategy for absolute quantification of modified metabolites**
Wei Li*, Zunjian Zhang, Fengguo Xu
- A.40 A Chemoproteomics Workflow for the Global Analysis of Acyl-CoA Signaling Networks**
Michaela Levy*, David Montgomery, Mihaela Sardu, Abigail Thorpe, Steve Fox, Qishan Lin, Thorkell Andresson, Laurence Florens, Michael Washburn, Jordan Meier
- A.41 Proteomics insights into the role of PknG in mycobacterial physiology and pathogenesis**
Rosario Durán*, Analía Lima, Magdalena Gil, Bernardina Rivera, Jessica Rossello, Annemarie Wehenkel, María Lisa, Pedro Alzari
- A.42 Pushing the limits: Boosting sensitivity of PRM assays for the detection of very low abundant proteins in complex samples**
Alexander Schmidt*, Emmanuelle Lezan, Erik Ahrné, Thomas Bock
- A.43 Discovery of a common target of natural products through combination of chemical genomics and proteomics**
Haijun Guo, Yang Yang, Jieren Deng, Mankin Wong, Qian Zhao
- A.44 Developing a reversible covalent protein/ peptide capture technology for low abundance proteomics**
Brendan M. Floyd, Cecil J. Howard II, Jagannath Swaminathan, James L. Reuther, Edward M. Marcotte, Eric V. Anslyn

TUESDAY, AUGUST 20

8:00 –
1:00 **Exhibits Open**
p.m. *Nikko Ballroom Foyer, 3rd Floor*

SYMPOSIUM

Nikko Ballroom, 3rd Floor

8:30 **Flash Talks: Poster presenters will be invited to give 1 min. “flash” talks on**
a.m. **their work.**

Chair: Angus Lamond School of Life Sciences, University of Dundee, Dundee, Scotland

10:10 Coffee Break in foyer
a.m.

Morning Session

Chair: Don Kirkpatrick, Genentech, Inc.

- 10:30 **2.1** The growing molecular complexity of ribosome biology
Maria Barna, Stanford University, Stanford, CA, USA
- 11:10 **2.2** Deciphering cellular organization using protein thermal stability and solubility
Mikhail M. Savitski, European Molecular Biology Laboratory, Heidelberg, Germany
- 11:50 **2.3** A proteomics view of mTOR signaling in humans
Anne-Claude Gingras, Lunenfeld–Tanenbaum Research Institute, Toronto, Canada
- 12:30 Lunch on own
p.m.

Afternoon Session

Chair: Bernhard Kuster, Technical University of Munich, München, Germany

- 2:30 **2.4** New Ub profiling approaches and applications
Namrata Udeshi, Broad Institute of MIT and Harvard, Cambridge, MA, USA
- 3:10 **2.5** Proteomic exploration of lysine acetylation signaling
Chuna Choudhary, University of Copenhagen, Copenhagen, Denmark
- 3:50 **2.6** Characterization of complexes and organelles
Kathryn Lilley, University of Cambridge, United Kingdom
- 4:30 **Poster Session B**
Carmel and Monterey Rooms, 3rd Floor

Chairs: Michael Trnka, University of California, San Francisco, CA, USA and Nancy Phillips, University of California, San Francisco, CA, USA

- B.1 Identification and Quantification Method for UCN2 by LC/MS/MS from Plasma/Serum from Mouse Disease Models**
Shakey Quazi*, Wei Zheng, Olivier Bezy
- B.2 Integrating de novo sequencing with sequence database and spectral library search for in-depth analysis of DIA data with PEAKS**
Paul Shan*, Xin Chen, Clark Chen, Julia Hopkins
- B.3 High-Throughput PEAKS Workflow for Large Scale Quantitative Proteomics using PEAKS Online X**
Jonathan Krieger*, Julia Hopkins, Lei Xin, Baozhen Shan
- B.4 TAILS identifies candidate substrates and biomarkers of ADAMTS7, a therapeutic protease target in coronary artery disease**
Charlie Mundorff*, Daniel Lai, Nadine Elowe, Hasmik Keshishian, Alessandro Arduini, Bryan MacDonald, Steven Carr
- B.5 Role of the Particle for Arrangement of Quaternary structure (PAQosome) in assembly/maturation of human protein complexes and networks**
Benoit Coulombe*, Philippe Cloutier, Maxime Pinard, Christian Poitras, Marie-Soleil Gauthier
- B.6 Comprehensive Comparative Immunopeptidome Analysis of I-Ab-bound peptides from Thymus, Splenic B cells and Dendritic cells in C57BL/6 mice**
Padma Nanaware*, J. Mauricio Calvo-Calle, Liying Lu, Mollie Jurewicz, Laura Santambrogio, Lawrence Stern
- B.7 Diversity of the MHC-II immunopeptidome is modulated by the non-classical MHC proteins HLA-DM and HLA-DO and controls thymic selection of CD4+ and regulatory T cells**
Lawrence Stern*, Padma Nanaware, Mollie Jurewicz, John Leszyk, Scott Shaffer
- B.8 Size exclusion chromatography-based proteomics to identify novel components of the HSP90-dependent proteome following pharmacologic inhibition in colon cancer cells**
Rahul Samant*, Silvia Aires-Batista, Bugra Ozer, Mark Larance, Craig McAndrew, Alexia Hervieu-Vilches, Bissan Al-Lazikani, Paul Clarke, Angus Lamond, Paul Workman
- B.9 Disruption-Compensation (DisCo) analysis of RNA polymerase II Protein Interactome**
Katlyn Burriss*, Guihong Qi, Whitney Smith-Kinnaman, Amber Mosley
- B.10 Plasma proteome profiling to detect and avoid sample-related biases in biomarker studies**
Philipp Geyer*, Matthias Mann, Lesca Holdt
- B.11 Production and Generation of Proteogenomics Databases using PyPGATK**
Husen Umer*, Yafeng Zhu, Enrique Audain, Janne Lehtiö, Rui Branca, Yasset Perez-Riverol
- B.12 Multi-omic profiling reveals differential kinase activity in neuronal differentiation**
Dmitry Kuchenov*, Fima Zaltsman, Jeremy Willsey, Ruth Huttenhain, Nevan Krogan
- B.13 A novel HLA-peptide profiling workflow called MAPTACTM (Mono-Allelic-Purification-with-Tagged-Allele-Constructs) leverages mass spectrometry to improve neoantigen prediction**
Lia Serrano*, Dominik Barthelme, Rob Oslund, Amanda Creech, Tyler Colson, Scott Goulding, Daniel Rothenberg, Chris McGann, Ying Ting, Yusuf Nasrullah, Janani Sridar, Dewi Harjanto, Matt Malloy, Christina Kuksin, Joel Greshock, Terri Addona, Michael Rooney, Jennifer Abelin
- B.14 Selective capture and release of nascent proteins for translome profiling**
Nancy Phillips*, Craig Forester, Bala Vinaithirthan, Juan Osés-Prieto, Robert Chalkley, Alma Burlingame

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- B.15 Targeting a subset of the membrane proteome - the proteolipids that extract into chloroform, the proteolipidome**
Julian Whitelegge*
- B.16 Allosteric HSP70 inhibitors overcome proteasome inhibitor resistance by perturbing mitochondrial proteostasis**
Arun Wiita*, Ian Ferguson, Christine Lam, Sami Toumivaara, Margarette Mariano, Paul Phojanakong, Donghui Wang, Hao Shao, Byron Hann, Jason Gestwicki
- B.17 Comparative Proteomic in Multiple Brain Regions of the Naked Mole-Rats and Mice**
Thu Nguyen*, Emily Vice, Melissa Pergande, Vince Amoroso, Thomas Park, Stephanie Cologna
- B.18 Development and Application of a Targeted immuno-MRM-MS Assay to Identify the Mechanism of Activity and Resistance to Thalidomide Analogs**
Michael Burgess*, Adam Sperling, Hasmik Keshishian, Eric Kuhn, Steven Carr, Benjamin Ebert
- B.19 ITRAQ Proteomic Profiling of Tissue Interstitial Fluid from Paired High Grade Serous Ovarian Cancer and Fallopian Tube Samples Reveals Novel Biomarker Candidates**
Shayan Avanesian*, Eric Kuhn, Karsten Krug, Yi Feng, Alexandra Cocco, Sho Sato, Yiling Liu, Paul Ippoliti, Marilyn Mitchell, Lauren Schwartz, Daniele Moreira, Kai Doberstein, Michael Birrer, DR Mani, Steven Skates, Steven Carr, Ronny Drapkin, Michael Gillette
- B.20 Application of Quantitative Phosphoproteomics in the Study of Plant Mechanosignaling**
Zhu Yang*, Ning Li
- B.21 Deep Label-Free Quant: Deciphering the MS1 Hieroglyph with IT and AI**
David Chiang*, Patrick Chu, Brian Chiang
- B.22 Quantitative proteomics of MPK4 phosphorylation dynamics and interacting proteins**
Sixue Chen*, Tong Zhang, Chuwei Lin, Jacqueline Schneider, Tianyi Ma, Sisi Geng, Sheldon Lawrence, Craig Dufresne, Alice Harmon
- B.23 Composition of the myddosome during the innate immune response**
Joseph Gillen*, Aleksandra Nita-Lazar
- B.24 Thermal profiling as a novel tool to analyze the impacts of missense mutants on the proteome**
Sarah Peck Justice*, Quihong Qi, H.R. Sagara Wijeratne, Jose Victorino, Aruna Wijeratne, Amber Mosley
- B.25 Quantitative Proteomic Analysis to Identify Developmentally Regulated Proteins in Leishmania Major Isolate**
Nasrin Amiri-Dashatan*, Nayebali Ahmadi
- B.26 SC-514 Loaded PLGA Particle Formed by Single Emulsion Method**
Toluleke Famuyiwa*
- B.27 Purification and Proteomic Analysis of the Golgi Outpost – an Organelle that Nucleates Microtubules in Oligodendrocytes**
Meng-meng Fu*, Thomas MacAlear, Juan Oses-Prieto, Huy Nguyen, Alex Valenzuela, Rebecca Shi, Ting-Ting Wang, Alma Burlingame, Susanne Bechstedt, Ben Barres
- B.28 Autoimmune regulator dependent alterations in proteome profiles in spermatogonial cells**
Pradeep Kumar*, Karthika Radhakrishnan, Kongattu Bhagya, Anil TR Kumar, Anandavally Devi, Sengottian Jeeva
- B.29 Molecular bases of ferroptosis induction by endoperoxides**
Juan Oses-Prieto*, Ying-Chu Chen, Al Burlingame, Adam Renslo
- B.30 Systematic identification of fat-derived secreted factors acting on the brain**
Pierre Jean-Beltran*, Lucy Liu, Tess Branon, Alice Ting, Norbert Perrimon, Steven Carr

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- B.31 Improved HLA peptide sequencing accuracy and sensitivity via optimized scoring of database search results and de novo interpretations**
Karl Clauser*, Susan Klaeger, Tamara Ouspenskaia, Travis Law, Derin Keskin, Siranush Sarkizova, Nir Hacohen, Catherine Wu, Steven Carr
- B.32 Plasma proteome profiling discovers potential biomarkers of non-alcoholic fatty liver disease**
Rajat Gupta*, Lili Niu, Philipp Geyer, Nicolai J Albrechtsen, Lise Gluud, Alberto Santos, Sophia Doll, Jens Holst, Filip Knop, Tina Vilsbøll, Anders Junker, Stephan Sachs, Kerstin Stemmer, Timo Müller, Matthias Tschöp, Susanna Hofmann, Matthias Mann
- B.33 Discovery of Mitochondrial Protease ClpP as a Target for the Anticancer Compounds ONC201 and Related Analogs**
Lee Graves*, Paul Graves, Lucas Aponte-Collazo, Emily Fennell, Adam Graves, Andrew Hale, Nedyalka Dicheva, Laura Herring, Thomas Gilbert, Michael East, Ian McDonald, Matthew Lockett, Hani Ashamalla, Nathaniel Moorman, Donald Karanewsky, Edwin Iwanowicz, Ekhsan Holmuhamedov
- B.34 Functional Versatility of Mycobacterium marinum Type III Polyketide Synthases**
Priti Saxena*, Amreesh Parvez, Samir Giri, Gorkha Giri, Monika Kumari, Renu Bisht
- B.35 Characterizing and Targeting the Cell Surface Proteome of Hypoxic Pancreatic Cancer**
Lisa Kirkemo*, James Wells
- B.36 Automated Quality Assessment of Chromatographic Peaks in Targeted Proteomics Data using Machine Learning**
Shadi Eshghi*, Erick Velasquez, W. Rodney Mathews
- B.37 Application of TurboID-mediated proximity labeling for mapping a GSK3 kinase signaling network in Arabidopsis**
Chuan-Chih Hsu*, Chan Ho Park, Tae-Wuk Kim, Jia-Ying Zhu, Yu-Chun Hsiao, Tess Branon, Alice Ting, Shou-Ling Xu, Zhi-Yong Wang
- B.38 MHC-TreASUre_Hunt: a computational pipeline for the identification of MHC-I peptides from mass spectrometry**
Eric Wilson*, Melissa Wilson, Karen Anderson
- B.39 Identification of spatiotemporally resolved GPCR protein interaction networks regulating receptor function**
Ruth Huttenhain*, Braden Lobingier, Jiewei Xu, Brian Shoichet, Mark Von Zastrow, Nevan Krogan
- B.40 Accelerating DIA Studies to Extend Workflow Utility, Using Fast Microflow LC Gradients**
Loren Olson*, Christie Hunter, Nick Morrice
- B.41 eIF4E selective control for metabolic fitness and healthspan**
Haojun Yang*, Crystal Conn, Kenji Ikeda, Juan Osés-Prieto, Supna Nair, Matt Parker, Patrick Ventura, Saul Villeda, Shingo Kajimura, Alma Burlingame, Davide Ruggero
- B.42 Profiling of phosphorylation sites of Arabidopsis microsomes with PolyMAC-Ti nanoparticle bead enrichment and mass spectrometry**
Ing-Feng Chang*, Tsung-Ju Hsieh, Man-Hsuan Lee, Pei-Yuan Chen
- B.43 Characterizing the role of ribosomal protein phosphorylation in control of gene regulation and cell fate**
Victoria Hung*, Juan A. Osés-Prieto, Steven M. Moss, Jack Stevenson, Kevan M. Shokat, Alma L. Burlingame, Maria Barna
- B.44 HYPERsol: flash-frozen results from archival FFPE samples for clinical proteomics**
Dylan M. Marchione, Ilyana Ilieva, Benjamin A. Garcia, Darryl J. Pappin, John B. Wojcik, John P. Wilson*

B.45 Tag-free rapid enrichment of ribosome-associated proteins across cell types, tissues, and species.

Teodorus Theo Susanto*, Victoria Hung, Kotaro Fujii, Maria Barna

6:00 **Poster Dismantle – all authors to remove posters from boards**
Carmel and Monterey Rooms, 3rd Floor

WEDNESDAY, AUGUST 21

8:00 –
1:00 **Exhibits Open**
p.m. *Nikko Ballroom Foyer, 3rd Floor*

SYMPOSIUM

Nikko Ballroom, 3rd Floor

Plenary Session

Chair: Steven Carr, Broad Institute of MIT and Harvard, Cambridge, MA, USA

8:30 **3.1** Proteogenomics-based diagnostics for cancer
Matthew Ellis, Baylor College of Medicine, Houston, TX, USA

Morning Session

Chair: Bernhard Kuster, Technical University of Munich, München, Germany

9:30 **3.2** Proteins to pathways: Functional insights from comprehensive proteomics and phosphoproteomics
Karin Rodland, Pacific Northwest National Laboratory, Richland, WA, USA

10:10 Coffee Break in foyer

10:30 **3.3** Non MS-based techniques for proteomic profiling of large human cohorts: Trust . . . but verify
Robert Gerszten, Beth Israel Deaconess Medical Center, Boston, MA, USA

Plenary Session

11:10 **3.4** Proteogenomic analyses of lung adenocarcinoma
Michael Gillette, Broad Institute of MIT and Harvard, Cambridge, MA, USA

12:10 Lunch on own

Afternoon Session

Chair: Nicholas Hertz, Mitokinin

1:20 **3.5** The human iPS cell proteome in health and disease
Angus Lamond, University of Dundee, United Kingdom

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- 2:00 **3.6** Modulating nerve growth through RNA-protein interactions
Jeff Twiss, University of South Carolina, Columbia, SC, USA
- 2:40 **3.7** Mapping axon initial segment structure and function by multiplexed proximity
biotinylation
Brian Lim, Baylor College of Medicine, Houston, TX, USA
- 6:00
p.m. Reception & Dinner at the General's House at Fort Mason Center for Arts & Culture
Advance ticket purchase required

THURSDAY, AUGUST 22

SYMPOSIUM

Nikko Ballroom, 3rd Floor

Morning Session

Chair: Steven Carr, Broad Institute of MIT and Harvard, Cambridge, MA, USA

- 8:30 **4.1** Cancer proteomics—connecting genotype with molecular phenotype
Janne Lehtiö, Karolinska Institute, Stockholm, Sweden
- 9:10 **4.2** A link between gut infection, autoimmunity and Parkinson's disease
Michel Desjardins, University of Montreal, Quebec, Canada
- 9:50 **4.3** Identification of mechanisms of activity and resistance to thalidomide analogs with a
targeted quantitative immuno-mass spectrometry assay
Adam Sperling, Dana-Farber Cancer Institute, Boston, MA, USA
- 10:30 Coffee Break in foyer
- 11:00 **4.4** Crosslinking mass spectrometry and single particle cryoEM describe the structure of
a novel translocon in complex with the ribosome
Michael Trnka, University of California, San Francisco, CA, USA
- 11:40 Lunch on own

Afternoon Session

Chair: Pierre Thibault, University of Montreal, Quebec, Canada

- 1:40 **4.5** Systematic profiling of HLA class I immunopeptidome improves neoantigen binding
prediction
Susan Klaeger, Broad Institute of MIT and Harvard, Boston, MA, USA
- 2:20 **4.6** Ribo-seq predicted novel unannotated open reading frames contribute peptides to
the MHC class I immunopeptidome
Tamara Ouspenskaia, Broad Institute of MIT and Harvard, Boston, MA, USA

3:00 **4.7** The genomic dark matter is a major source of targetable tumor-specific antigens
Pierre Thibault, University of Montreal, Quebec, Canada

Plenary Session

Chair: Pierre Thibault, University of Montreal, Quebec, Canada

3:40 **4.8** Proteogenomics and immunopeptidomics for the development of personalized cancer immunotherapy
Michal Bassani-Sternberg, Ludwig Cancer Center, Lausanne, Switzerland
Molecular and Cellular Proteomics Lecturer

4:40 Closing Remarks

5:00 Adjourn