

## iSCMS Conference Program

### 10/4/2023 - BYU Conference Center

9:00 - 9:15 AM **Ryan Kelly** (Brigham Young University): Welcome/Logistics

#### Wednesday Session 1 (WS01). Chair: Jennifer Van Eyk (Cedars-Sinai)

9:15 - 9:45 **Keynote: Lingjun Li** (University of Wisconsin - Madison): *Enhancing single-cell mass spectrometry-based omics analysis via dual-polarity MALDI MS imaging and chemical tagging*

9:50 - 10:15 **Chris Rose** (Genentech): *Improved throughput of single cell proteomics with PairQuant intelligent data acquisition*

10:20 - 10:45 **Hua Tian** (The Pennsylvania State University): *Multimodal cryogenic SIMS imaging delineates spatial cellular pathways at 1 um resolution*

10:45 - 11:05 Break - Coffee and snacks in the exhibition hall

#### Wednesday Session 2 (WS02). Chair: Zhibo Yang (University of Oklahoma)

11:05 - 11:25 **Theodore Alexandrov** (European Molecular Biology Laboratory): *Spatial single-cell metabolomics*

11:30 - 11:50 **Vilmos Kertesz** (Oak Ridge National Laboratory): *Advancements of high throughput liquid capture single cell mass spectrometry*

12:00 - 2:00 Lunch Break/Poster Session - Stand by odd-numbered posters from 1:00 - 2:00

12:00 - 12:45 Luncheon Seminar with Boxed Lunch - Thermo Fisher Scientific

#### Wednesday Session 3 (WS03). Chair: Ying Zhu (Genentech)

2:00 - 2:25 Sciox-sponsored talk: **Jonathan Catrow** (University of Utah): *Toward single-cell metabolomics*. Coauthor: James Cox.

2:30 - 2:55 **Jonathan Sweedler** (University of Illinois Urbana-Champaign): *Increasing the throughput and molecular coverage of single cell mass spectrometry*

3:00 - 3:20 **Ingela Lanekoff** (Uppsala University): *Quantitative single-cell metabolomics using a tapered pneumatically assisted nano-DESI MS setup and automated data handling*

3:25 - 3:40 Break - Coffee and snacks in the exhibition hall

#### Wednesday Session 4 (WS04). Chair: Peter Nemes (University of Maryland)

3:40 - 4:05 **Alexey Nesvizhskii** (University of Michigan): *Analysis of low-input proteomics data using FragPipe computational platform*

4:10 - 4:30 **Frederik Haugaard Holck** (Evosep): *Enabling scalable single cell proteomics by utilizing unique analytical properties of the Evotip Pure*

4:35 - 5:00 **Zhibo Yang** (University of Oklahoma): *Single Cell Mass Spectrometry Metabolomics Studies of Cell Heterogeneity*

### 10/5/2023 - BYU Conference Center

9:00 - 9:10 AM Welcome/Logistics

#### Thursday Session 1 (TS01). Chair: Yu-Ju Chen (Institute of Chemistry, Academia Sinica)

9:10 - 9:40 **Keynote: Nikolai Slavov** (Northeastern University and Parallel Squared Technology Institute): *Biological and technological frontiers for single-cell proteomics*

9:45 - 10:05 **Carla Newman (GSK)**: *Single-cell analysis and its application in the pharmaceutical industry*

10:10 - 10:35 **Ying Zhu (Genentech)**: *Improving the throughput and resolution of spatial single cell proteomics*

10:40 - 11:00 Break - Coffee and snacks in the exhibition hall

**Thursday Session 2 (TS02). Chair: Yu (Tom) Gao** (University of Illinois Chicago)

- 11:00 - 11:25 **John Yates, III**, (Scripps Research Institute): TBD
- 11:30 - 11:55 **Olga Vitek** (Northeastern University): *Statistical considerations for quantitative single-cell proteomic experiments*
- 12:00 - 2:30 Lunch Break/Poster Session - Stand by even-numbered posters starting at 1:00  
Bruker Corp.-Sponsored Lunchtime Seminar (boxed lunch provided). Speakers: **Christoph Krisp** (Bruker) and **Jennifer Van Eyk** (Cedars-Sinai)
- 12:00 - 12:45

**Thursday Session 3 (TS03). Chair: Ingela Lanekoff** (Uppsala University)

- 2:30 - 2:55 **Peter Nemes** (University of Maryland, College Park): *Towards fast and deep single-cell 'omics by capillary electrophoresis mass spectrometry*
- 3:00 - 3:25 **Yu-Ju Chen** (Institute of Chemistry, Academia Sinica): *Nanoscale-to-Single Cell Phosphoproteomics by Chip-DIA Reveal Patient Heterogeneity and Therapeutic Opportunity*
- 3:30 - 3:55 **Yu (Tom) Gao** (University of Illinois Chicago): *Multimomics measurements of a single cell by LevCell*
- 4:00 - 4:15 Break - Coffee and snacks in the exhibition hall

**Thursday Session 4 (TS04). Chair: Vilmos Kertesz** (Oak Ridge National Laboratory)

- 4:15 - 4:35 **James Edwards** (Saint Louis University): *Single islet metabolomics*
- 4:40 - 5:00 **Jan Schwenzfeier** (University of Münster): *Investigation of THP-1 derived macrophage polarization using single-cell MALDI mass spectrometry imaging*

**10/6/2023 AM - BYU Conference Center**

- 9:00 - 9:10 Welcome/Logistics

**Friday Session 1 (FS01). Chair: Christopher Anderton** (Pacific Northwest National Laboratory)

- 9:10 - 9:40 Keynote: **Jennifer Van Eyk** (Cedars-Sinai): *iPSC verses tissue cardiomyocytes: are they the same?*
- 9:45 - 10:05 **Gioele La Manno** (École Polytechnique Fédérale de Lausanne): *A computational framework for the construction of MALDI imaging atlases*
- 10:10 - 10:35 **Julia Laskin** (Purdue University): *Ambient nano-DESI mass spectrometry imaging at the single-cell level*
- 10:40 - 10:55 Break - Coffee and snacks in the outdoor pavillion

**Friday Session 2 (FS02). Chair: Amanda Guise** (Biogen)

- 10:55 - 11:20 **Christopher Anderton** (Pacific Northwest National Laboratory): *Molecular cartography of the human kidney and lung, down to the single cell*
- 11:25 - 11:50 **Ben Orsburn** (Johns Hopkins University): *Single cell proteomics in the context of human pharmacology*
- 12:00 - 12:45 VICI - Sponsored Lunchtime Seminar

**10/6/2023 PM - BYU Aspen Grove Resort**

Early Career Summit and Conference Dinner

Transportation provided from the BYU Conference Center to Aspen Grove at 1:00

Free time at Aspen Grove (hiking, games, etc.)

**ECS Session 1 (ECS01). Chair: Hua Tian** (The Pennsylvania State University)

3:00 - 3:20	<b>Jared O. Kafader</b> (Northwestern University): <i>scPiMS: a novel strategy for profiling intact proteoform signals from single cells</i> . Coauthors: Pei Su, Stanislav Rubakhin, Michael A. R. Hollas, Ryan T. Fellers, Jonathan V. Sweedler, Neil L. Kelleher
3:20 - 3:40	<b>Pedro Aragón Fernández</b> (Technical University of Denmark): <i>Using next-generation LC-MS to disentangle an Acute Myeloid Leukemia hierarchy</i>
3:40 - 4:00	<b>Jake Penny</b> (University of Surrey): <i>Analyte transfer efficiency: a challenge of SEISMIC importance for single cell Omic LCMS</i>
4:00 - 4:20	<b>Stanislau Stanisheuski</b> (Oregon State University): <i>Single cell proteomics using thermal inkjet dispensing with impedance detection</i>
4:20 - 4:30	Short Break

### ECS Session 2 (ECS02). Chair: James Fulcher (Pacific Northwest National Laboratory)

4:30 - 4:50	<b>Amanda Guise</b> (Biogen): <i>TDP-43-stratified single-cell proteomic profiling of human spinal motor neurons in amyotrophic lateral sclerosis</i>
4:50 - 5:10	<b>Kyle Saunders</b> (University of Surrey): <i>Single cell lipidomics: robotic nanocapillary sampling coupled to highly sensitive micro-flow LC-MS/MS</i>
5:10 - 5:30	<b>Devon Kohler</b> (Northeastern University): <i>Single cell MS-based proteomics coupled with suitable experimental design enables the application of causal inference methods to observational experiments</i>
5:30 - 5:50	<b>Dong-Gi Mun</b> (Mayo Clinic): <i>Discovery of post-translationally modified and variant peptides in single cell proteomics experiments</i>
6:00 - 7:00	Conference Dinner - Onsite at Aspen Grove
7:00	Return to BYU Conference Center

### 10/7/2023 - BYU Benson Building

Hands-on workshop for single-cell proteomics

9:00 - 12:00	Lab Session 1
12:00 - 1:30	Lunch at Brick Oven Pizza
1:30 - 4:30	Lab Session 2

### Poster Presentations - Odd numbers present on 10/4/2023 and even numbers present on 10/5/23

- Remco van Soest** (SCIEX USA): *Data-independent acquisition (DIA) performance on proteomic samples using a Zeno trap*. Coauthors: Patrick Pribil, Ihor Batruch
- Ximena Sanchez-Avila** (Brigham Young University) *Easy and Accessible Workflow for Label-Free Single-Cell Proteomics*. Coauthors: Ximena Sanchez-Avila, Thy Truong, Xiaofeng Xie, Kei G. I. Webber, S. Madisyn Johnston, Hsien-Jung L. Lin, Nathaniel B. Axtell, Veronica Puig-Sanvicens, Ryan T. Kelly
- Alyssa Nitz** (Brigham Young University) *How many proteins is enough? The race for utility in single-cell proteomics*. Coauthors: Jose Humberto Giraldez Chavez, Samuel H. Payne
- Gangsoo Jung** (Bertis, Inc.): *Spatial proteomic approaches for triple-negative breast cancer on single-cell resolution*. Coauthors: Jung yong Eum, Sunghyun Huh, Yourae Shin, Amos C. Lee, Sumin Lee, Sunghoon Kwon and Un-Beom Kang
- Xiaofeng Xie** (Brigham Young University): *MS Connect: Open platform for automated backup, processing and visualization of MS-based omics data*. Coauthors: Thy Truong, Kei G. I. Webber, Yiran Liang, S. Madisyn Johnston, Samuel H. Payne, Ryan T. Kelly
- Merin Rixen** (University of California Los Angeles): *Unraveling the Proteomic Dynamics of Actin Mesh Regulation through Single-Cell Analysis*. Coauthors: Margot Quinlan, Rachel R. Ogorzalek Loo, Joseph A. Loo
- Siqi Huang** (Brigham Young University): *A Novel Design for Cheap Robust Pre-Formed Step Gradient LC System*. Coauthors: Kei Webber, Thy Truong, Xiaofeng Xie and Ryan T. Kelly
- Gul Muneer** (Institute of Chemistry, Academica Sinica): *Streamlined Chip-DIA Platform for Nanoscale-to-Single-Cell Phosphoproteomics*. Coauthors: Sofani Gebreyesus, Ciao-Syuan Chen, Tzu-Tsung Lee, Fengchao Yu, Chih-An Lin, Min-Shu Hsieh, Alexey I. Nesvizhskii, Chao-Chi Ho, Sung-Liang Yu, Hsiung-Lin Tu and Yu-Ju Chen

- Thy Truong** (Brigham Young University): *Data-Dependent Acquisition with Precursor Coisolation Improves Proteome Coverage and Measurement Throughput for Label-Free Single-Cell Proteomics*. Coauthors: Kei G. I. Webber, S. Madisyn Johnston, Yiran Liang, Alissia Nydegger, Xiaofeng Xie, Tsz-Ming Tsang, Dasun N. Jayatunge, Joshua L. Andersen and Ryan T. Kelly
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- Steven M. Yannone** (Cinder Biological, Inc.): *From Volcanoes to the Bench: Advantages of Novel Hyperthermoacidic Archaeal Proteases for Proteomics Workflows*.
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- Liang Chen** (Pacific Northwest National Laboratory): *Toward spatially-resolved proteome mapping of senescent cells and their tissue microenvironment at single-cell resolution*. Coauthors: Yumi Kwon, Andrey V. Liyu, Julia Unsworth, Lye Meng Markillie, Sarah M. Williams, Dehong Hu, Megan K. Rugland, Ying Zhu and Ljiljana Paša-Tolić
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- Yumi Kwon** (Pacific Northwest National Laboratory): *mTIFF: multiplexed transferring identification based on FAIMS filtering enhances throughput of single-cell proteomics*. Coauthors: Fengchao Yu, James M. Fulcher, Sarah M. Williams, Ljiljana Paša-Tolić, Alexey I. Nesvizhskii and Ying Zhu
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- Rahul Deshpande** (Thermo Fisher Scientific): *Nano-LC-MS based lipidomics for single cell applications*. Coauthors: Susan Bird and Bashar Amer
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- Hua Zhang** (University of Wisconsin): *Single-cell analysis enabled by dual-polarity ionization and ion mobility-mass spectrometry imaging*. Coauthors: Yuan Liu, Lauren Fields, Xudong Shi, Penghsuan Huang, Haiyan Lu, Andrew J. Schneider, Luigi Puglielli, Nathan V. Welham and Lingjun Li
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- Ruiqi Jian** (Stanford University): *Mass spectrometry-based single cell proteomics*. Coauthors: Lihua Jiang, Tiffany Trinh, Chenchen Zhu and Michael Snyder
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- Lizhou Ai** (Cedars-Sinai Medical Center): *Understanding iPSC-derived cardiomyocyte heterogeneity using single cell proteomics*. Coauthors: Aleksandra Binek, Ali Haghani, Simion Kreimer and Jennifer Van Eyk
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- Christoph Krisp** (Bruker Corporation): *Single cell proteome analysis with Ultra-high sensitivity on the timsTOF Ultra*. Coauthors: Anjali Seth, David Hartlmayer, Guilhem Tourniaire, Markus Lubeck and Gary Kruppa
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- Christoph Krisp** (Bruker Corporation): *Single cell proteome analysis with Ultra-high sensitivity on the timsTOF Ultra*. Coauthors: Anjali Seth, David Hartlmayer, Guilhem Tourniaire, Markus Lubeck and Gary Kruppa
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- Deepti Bhusal** (University of Oklahoma): *Developing cell quenching method to facilitate single cell mass spectrometry metabolomics studies*. Coauthors: Shakya Wije Munige, Zongkai Peng and Zhibo Yang
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- Fernanda Salvato** (Thermo Fisher Scientific): *Label-free DIA-based workflow for single-cell proteomic analysis on an Orbitrap Ascend mass spectrometer*. Coauthors: Bernard Delanghe, Santosh Renuse, Sally Webb and Amirmansoor Hakimi
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- Bernard Delanghe** (Thermo Fisher Scientific): *Sensitive and robust high-throughput workflow for qualitative and quantitative single-cell/single cell like analysis*. Coauthors: Tabiwang N. Arrey, Fernanda Salvato, Santosh Renuse, Jeff Op De Beeck and Nicolaie Eugen Damoc
- 21
- Bernard Delanghe** (Thermo Fisher Scientific): *A high-sensitivity low-nano flow LC-MS configuration for high-throughput sample-limited proteomics*. Coauthors: Runsheng Zheng, Manuel Matzinger, Rupert Mayer, Santosh Renuse, Fernanda Salvato and Karl Mechtler
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- James Fulcher** (Pacific Northwest National Laboratory): *CoRegR: A tool for identifying functional protein networks within single-cell proteomics data*. Coauthors: David J. Degnan, Kyle Nadeau, Lyle Meng Markillie, Hugh D. Mitchell, Sarah M. Williams, Kristin M. Engbrecht, Ronald J. Moore, William B. Chrisler, Joshua Cantlon-Bruce, Johannes W. Bagnoli, Anjali Seth, Ljiljana Paša-Tolić and Ying Zhu
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- Cory Matsumoto** (University of Illinois at Chicago): *Automated Containerless Cell Processing System for Single Cell Proteomics and Multiomics Analyses*. Coauthors: Xinhao Shao, Marko Bogosavljevic, Ziwei Zhang, Liang Chen, Jose Hernandez, Yu Gao
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- Timothy Licknack** (Arizona State University): *Generating a spatial map of protein localization in the ciliate *Paramecium tetraurelia**. Coauthors: Jeremy Wideman, Michael Lynch and Timothy Karr
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- Michael Ho** (University of California, Santa Barbara): *Using microfluidic single cell device for high throughput single cell mass spectrometry metabolomics studies*. Coauthors: yungpeng Lan and Zhibo Yang
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- Melinna Tra Nguyen** (University of California, Santa Barbara): *Investigating metabolomics features in the invasion of primary/metastatic melanoma cells using single cell mass spectrometry*. Coauthors: Tra D. Nguyen and Zhibo Yang
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- Xiaofeng Xie** (Brigham Young University): *Robust multi-column nanoLC platform for single-cell/low-input proteome profiling with 100% duty cycle*. Coauthors: Thy Truong, S. Madisyn Johnston, Kei G. I. Webber and Ryan T. Kelly
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- Andikan Nwosu** (Brigham Young University): *Towards single bacterium proteomics: isolating and dispensing single bacterial cells using the cellenONE with microLIFE software*. Coauthors: Cecile Thion, S. Madisyn Johnston, Xiaofeng Xie, Thy Truong, Joshua Cantlon and Ryan T. Kelly
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