

Join us in Cambridge, Massachusetts for the
12th Symposium for Structural Proteomics
October 28th-30th, 2024



The Symposium for Structural Proteomics (SSP) will be held in the United States for the first time, at the world-renowned Broad Institute of MIT & Harvard in Cambridge, MA.

SSP 2024 will bring together leaders in structural mass spectrometry, cryo-electron microscopy, computational structure prediction, and integrative modeling.

Structural proteomics has reached an inflection point in the last few years, with major advances in all of these areas, and we invite you to become part of the conversation of where (and how) this field goes forward.

The Organizers



Francis O'Reilly

National Cancer
Institute, NIH

USA

Malvina Papanastasiou

Broad Institute of MIT &
Harvard

USA

Stephen Fried

Johns Hopkins
University

USA

The Final Schedule for #SSP2024 has now been set!

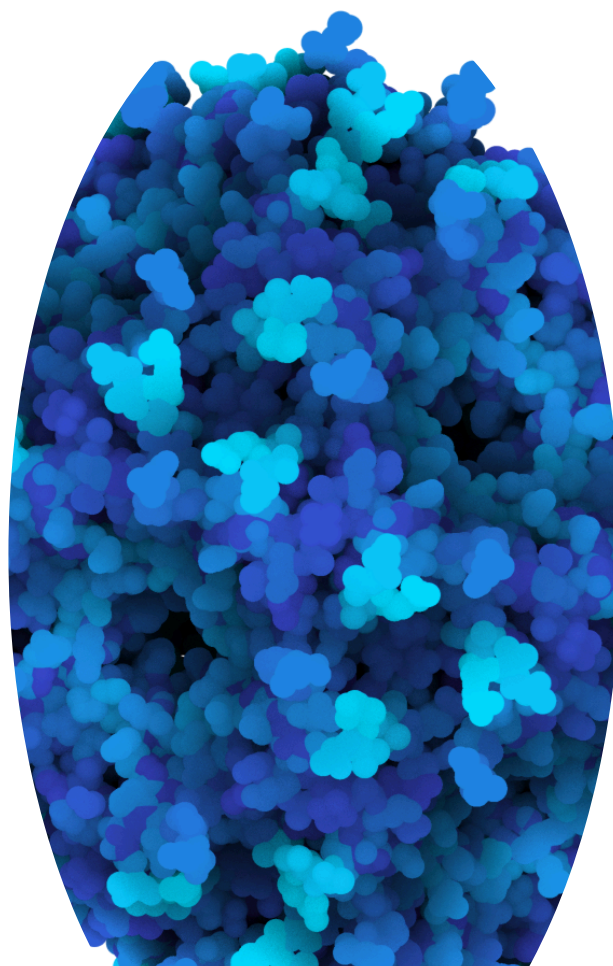
Monday, 28 October 2024	
Orals, Keynotes, Workshops & Sponsor Talks take place in the Auditorium	
9:00-9:05	Opening Remarks from the organizers
9:05-10:35	Session 1: Crosslinking MS (Chair: David Schriemer, University of Calgary) <ul style="list-style-type: none">Lan Huang (University of California at Irvine) "Advancing MS-cleavable Cross-linking Mass Spectrometry for Comprehensive Mapping of Protein-Protein Interactions"Richard Scheltema (University of Liverpool)TBDJames Bruce (University of Washington) "Cellular interactome dynamics in phenotypic and functional comparisons"Juri Rappsilber (Technische Universität Berlin) "Connecting Crosslinking Mass Spectrometry to Global Repositories"<i>Selected talk (10 min):</i> Miguel Gonzalez Lozano (Harvard University) "EndoMAP, a Structural Protein Complex Landscape of the Human Endosomes"
10:35-11:05	Coffee Break
11:05-12:35	Session 2: Labeling Approaches (Chair: Shaunak Reval, Broad Institute) <ul style="list-style-type: none">Sheena D'Arcy (University of Texas at Dallas) "Regulation of Protein Complexes by Disordered Domains"Ben Walters (Genentech) "Exploring dynamic pockets: HDX-Driven MD Simulations for Structure-Based Drug Design"Gabriel Rocklin (University of Chicago) "Learning the determinants of protein energy landscapes from large-scale experiments"Thomas Wales (Northeastern University) "Exploring the conformational preferences of the Tec-family tyrosine kinase BTK with HDX MS"<i>Selected talk (10 min):</i> Darragh O'Brien (University of Oxford) "Next Generation Therapeutics for Parkinson's Disease - Structural Premise of Selective Deubiquitinase USP30 Inhibition by Small-Molecule Benzotriazolones"
12:35-13:30	Lunch with Sponsor Talk (Chair: Malvina Papanastasiou, Broad Institute)
13:05-13:35	<ul style="list-style-type: none">Mike Graig (Bruker, Gold Sponsor Talk) "Who's next door? Current and future tools to explore your atomic neighborhood"
13:35-13:45	Short break
13:45-15:30	Session 3: Interactome Mapping (Chair: Namrata Udeshi, Broad Institute) <ul style="list-style-type: none">Fan Liu (FMP Berlin, Berlin University Medicine) MCP Award presented by Steven A. Carr (Broad Institute) "Building structural and spatial interactomes by cross-linking mass spectrometry"Ilaria Piazza (Max Delbrück Center for Molecular Medicine) "Protein structures in context with proteome-wide biophysics"Jiefu Li (HHMI, Janelia Research Campus) "Membrane signaling in the brain: from interactome mapping to in vivo mechanistic discoveries"Norman Davey (The Institute of Cancer Research, London) "Towards a functional map of the intrinsically disordered proteome"<i>Selected talk (10 min):</i> Audrey Kishishita (UCSF) "Probing the structural surfaceome of myeloma models to identify tumor-specific protein conformations"
15:30-16:10	Coffee Break
16:10-17:20	Keynote session (Presented by Stephen Fried, Johns Hopkins University) <ul style="list-style-type: none">Rosa Viner (Thermo, Platinum Sponsor Talk) "Bound Together for Structural Biology: Mass Spectrometry and Cryo-EM"Keynote: Nevan Krogan (UCSF, Gladstone Institutes) "Using Systems Approaches to Understand Mechanisms in Infectious Disease"
17:20-17:35	Transfer to 2 nd floor & poster setup
17:35-19:30 (2 nd floor)	Poster session & Reception

Tuesday, 29 October 2024	
9:00-10:30	Session 4: Computational Approaches (Chair: Andrea Graziadei, Human Technopole) <ul style="list-style-type: none">Karen Manalastas-Cantos (Leibniz-Institut für Virologie, Hamburg) "Crosslinks complement structure prediction to capture protein dynamics and interactions"Ellen Zhong (Princeton University) "Visualizing heterogeneous molecular landscapes inside the cell with cryoDRGN-ET"Emmanuel Levy (University of Geneva) "From sequence to structure, from structure to biology - On homo-oligomers and co-translational assembly"Haiyuan Yu (Cornell University) "Constructing a comprehensive 3D structurally-resolved human interactome at the whole proteome level"<i>Selected Talk (10 min):</i> Andrew Savinov (MIT) "High-throughput computational discovery of inhibitory protein fragments with AlphaFold"
10:30-11:00	Coffee Break
11:00-12:00	Technical Session 1 (Chair: Andrea Graziadei, Human Technopole) <ul style="list-style-type: none">Brinda Vallat (RCSB Protein Data Bank, Rutgers University) "PDB-Dev: A prototype system for archiving integrative structures"Weijing Liu (Thermo, Platinum Sponsor Talk) "Targeted Protein Degradation- Screening molecular glues by Native MS"
12:00-12:15	Transfer to 2 nd floor & poster setup
12:15-14:15 (2 nd floor)	Poster session & Lunch
14:15-14:30	Transfer to the Lobby
14:30-16:00	Session 5: Intact & Top-down MS (Chair: Fanny Caroline Liu, Florida State University) <ul style="list-style-type: none">Vicki Wysocki (Georgia Institute of Technology) "Native MS of glycoproteins and AAVs by electron capture charge reduction and/or surface induced dissociation"Dimitris Papanastasiou (Fasmatech) "A new adaptation of the Omnitrap platform integrated into a trapped ion mobility time-of-flight mass spectrometer"Michael Marty (University of Arizona) "Alanine Scanning to Define Membrane Protein-Lipid Interaction Sites Using Native Mass Spectrometry"Stephan Rauschenbach (Oxford University) "Atomic resolution molecular imaging by scanning probe and electron microscopy based on soft-landing electrospray ion beam deposition"<i>Selected talk (10 min):</i> Kallioi Gupta (Yale University) "A nanoscale spatially resolved macromolecular cartography of the cellular membrane"
16:00-16:30	Coffee Break
16:30-17:15	Technical Session 2 (Chair: Francis O'Reilly, NCI-NIH) <ul style="list-style-type: none">Juri Rappsilber (Technische Universität Berlin) "FDR estimation in crosslinking mass spectrometry"Poster Awards (sponsored by Nature Methods & JPR) Presented by Allison Doerr (Nature Methods)
17:15-17:30	Short Break
17:30-18:20	Keynote session (Presented by Malvina Papanastasiou, Broad Institute) <ul style="list-style-type: none">Keynote: Vamsi Mootha (MGH, HMS, HHMI, Broad Institute) "The mitochondrial proteome and human disease"
18:30-20:30	SSP2024 Reception

Wednesday, 30 October 2024	
9:00-10:30	Session 6: Structural Biology (Chair: Stephen Fried, Johns Hopkins University) <ul style="list-style-type: none"> Edward Huttlin (Harvard University) "Unraveling Protein Function through Proteome-scale AP-MS Interaction Mapping and Structural Prediction" Katja Luck (Institute of Molecular Biology, Mainz) "Integrative approaches to map protein interaction interfaces at scale" Naoko Mizuno (NHLBI-NIH) "Visual structure mining by cryo-ET" Keren Lasker (The Scripps Research Institute) "A Multi-Scale Model of PopZ Condensation" <i>Selected talk (10 min):</i> Yuqi Tang (Johns Hopkins University) "Unraveling structural biology within glycolytic bodies using XL-MS"
10:30-11:00	Coffee Break
11:00-11:45	Session 7: Structural Biology (Chair: Francis O'Reilly, NCI-NIH) <ul style="list-style-type: none"> Manuel Leonetti (Chan Zuckerberg Biohub) "OpenCell: Intracellular cartography of the human proteome" Vladimir Svetlov (New York University) "Integrated XLMS+cryo-EM pipeline for structural interrogation of bacterial transcription in vivo"
11:45-12:35	Keynote session (Presented by Francis O'Reilly, NCI-NIH) <ul style="list-style-type: none"> Keynote: Ed Marcotte (University of Texas at Austin) "Protein complexes across deep evolutionary time"
12:35-12:45	Closing remarks from the organizers

SSP 2024 Topics Include

- Crosslinking mass spectrometry
- Labeling Approaches (HDX, FPOP)
- Protein Interactome Mapping
- Computational Approaches in Structural Proteomics
- Intact and Top-Down Mass Spectrometry



- Integrative Structural Biology
- Emerging Methods



Speakers

Join us for keynote addresses from:



Nevan Krogan

University of California, San Francisco, Gladstone Institutes
USA



Vamsi Mootha

Mass General Hospital, Harvard Medical School, HHMI, Broad Institute of MIT & Harvard
USA



Lori Passmore

MRC Laboratory of Molecular Biology
UK

With plenary addresses from:



James Bruce

University of Washington



Norman Davey

The Institute of Cancer Research, London



Lan Huang

University of California, Irvine

USA



Edward Huttlin

Harvard Medical
School

USA

UK



Lisa Jones

University of California, San
Diego

USA

USA



Emmanuel Levy

University of Geneva
Switzerland



Jiefu Li

HHMI, Janelia
Research Campus

USA



Fan Liu

Leibniz-Forschungsinstitut
für Molekulare
Pharmakologie (FMP),
Berlin

Germany



Edward Marcotte

University of Texas at
Austin
USA



Michael Marty

University of Arizona
USA



Naoko Mizuno

NHLBI, National Institutes
of Health



**Dimitris
Papanastasiou**

Fasmatech - A Bruker
Company

USA

Greece



Ilaria Piazza

Max Delbrück Center,
Berlin

Germany



Juri Rappsilber

Technische Universität
Berlin

Germany



**Stephan
Rauschenbach**

Oxford University

UK



Gabriel Rocklin

Northwestern
University

USA



Richard Scheltema

Liverpool University

UK



Maya Topf

CSSB, Hamburg

Germany



Thomas Wales

Northeastern
University

USA



Benjamin Walters

Genentech

USA



Vicky Wysocki

The Ohio State
University

USA



Haiyuan Yu

Cornell University

USA



Ellen Zhong

Princeton University

USA



Manuel Leonetti

Chan Zuckerberg
Biohub

USA

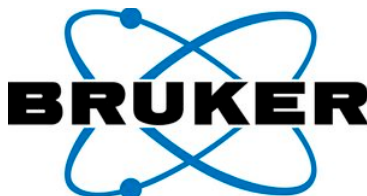
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