



# Proteomics in Cell Biology and Disease Mechanisms

EMBL–WELLCOME GENOME CAMPUS CONFERENCE

WELLCOME GENOME CAMPUS  
CONNECTING  
SCIENCE  
ADVANCED  
COURSES+  
SCIENTIFIC  
CONFERENCES

**We have moved our website to [embl.org/events](https://embl.org/events). The content below is no longer being updated.**

## **EMBL Courses and Conferences during the Coronavirus pandemic**

With the onsite programme paused, many of our events are now being offered in virtual formats.

Registration is open as usual for many events, with back-up plans in place to move further courses and conferences online as necessary. Registration fees for any events affected by the COVID-19 disruption are fully refundable.

More information for participants of events at EMBL Heidelberg can be found [here](#).

## Programme

Got something to say? Tweet it! [#EWGProteomics](#)

### Day 1 - Thursday 7 March 2019

Time	Speaker
11:00 - 12:30	<b>Registration and light refreshments</b>
12:30 - 12:45	<b>Opening remarks</b>
	<b>Keynote Speaker</b>
12:45 - 13:30	<b>Ubiquitin Mediated Regulation of Transcription Factor Stability</b> <a href="#">Vishva Dixit</a> - <b>Genentech, USA</b>

Time	Speaker
13:30 - 16:30	<b>Session 1: Cell Biology</b> Chair: <a href="#">Michal Sharon</a> - <i>Weizmann Institute, Israel</i>
13:30 - 14:00	<b>MAPPING the degradation landscape via proteasomal profiling</b> <a href="#">Yifat Merbl</a> - <i>Weizmann Institute, Israel</i>
14:00 - 14:30	<b>Dissecting oncogenic EGF receptor signaling in-vivo by quantitative interaction proteomics and phosphoproteomics</b> <a href="#">Jesper Olsen</a> - <i>University of Copenhagen, Denmark</i>
14:30 - 15:00	<b>Coffee break and Meet the Speakers:</b> Vishva Dixit, Yifat Merbl
15:00 - 15:30	<b>Exploring proteome and organelle homeostasis mechanisms using quantitative proteomics</b> <a href="#">Wade Harper</a> - <i>Harvard Medical School, USA</i>
15:30 - 15:45	<b>Decoding Chromatin Modification States Using Chemical Biology and Computational Proteomics</b> Till Bartke - <i>Helmholtz Zentrum München, Germany</i>
15:45 - 16:00	<b>Quantitative analysis of murine T lymphocyte proteomes</b> Alejandro Brenes - <i>University of Dundee, United Kingdom</i>
16:00 - 16:15	<b>Decoding Proteostasis: Understanding how proteome foldedness changes under proteostasis stress</b> Dezerae Cox - <i>Bio21 Institute, University of Melbourne, Australia</i>
16:15 - 16:30	<b>The Solute Carrier Transporters Interactome</b> Alvaro Ingles Prieto - <i>CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences. Vienna, Austria</i>
16:30 - 17:15	<b>Flash talks (odd numbers 1 slide / 1 minute each)</b>
17:15 - 19:00	<b>Poster session 1 (odd numbers)</b>
19:00 - 21:00	<b>Dinner in the EMBL Canteen</b>
21:00 - 23:00	<b>After Dinner Drinks in the Rooftop Lounge</b>

## Day 2 - Friday 8 March 2019

Time	Speaker
09:00 - 12:00	<b>Session 2 - Structural Proteomics</b> Chair: <a href="#">Wade Harper</a> - <i>Harvard Medical School, USA</i>

- 09:00 - 09:30 **Rapid Investigation of Overproduced Proteins in Crude Samples**  
[Michal Sharon](#) - *Weizmann Institute, Israel*
- 09:30 - 10:00 **Structural proteomics of protein complexes**  
[Martin Beck](#) - *EMBL Heidelberg, Germany*
- 10:00 - 10:45 **Coffee Break and Meet the Speakers:** Wade Harper, Michal Sharon, Martin Beck
- 10:45 - 11:15 **The proteome in 3D**  
[Paola Picotti](#) - *ETH Zurich, Switzerland*
- 11:15 - 11:30 **Enumerating the site occupancy, complexity, and diversity of mucin type O glycosylation on CD43 using electron transfer dissociation (ETD) mass spectrometry**  
Vandita Dwivedi - *National Institute of Immunology, India*
- 11:30 - 11:45 **Cell Cycle Dependent Localization of Protocadherins**  
Nazli Ezgi Özkan Küçük - *Koç University, Turkey*
- 11:45 - 12:00 **Multilayered proteomic interaction analysis identifies cancer mutations that affect the composition and function of kinase complexes**  
Martin Mehnert - *ETH Zürich, Switzerland*
- 12:00 - 13:30 **Lunch**
- 13:30 - 16:30 **Session 3: Proteomics from lab to clinic**  
Chair: [Vishva Dixit](#) - **Genentech, USA**
- 13:30 - 14:00 **Microscaled methods for proteogenomic analysis of patient-derived tumors**  
[Steven Carr](#) - *Broad Institute, USA*
- 14:00 - 14:30 **Peroxisome remodeling en route to virus replication**  
[Ileana Cristea](#) - *Princeton University, USA*
- 14:30 - 15:00 **Novel MS scan modes applied to translational research**  
[Matthias Mann](#) - *Max Planck Institute of Biochemistry, Germany*
- 15:00 - 15:30 **Coffee Break and Meet the Speakers:** Steven Carr, Natalie Ahn, Paola Picotti
- 15:30 - 15:45 **Using Tandem Mass Tag Proteomics for the Detection of Changes in Phosphorylation State After Treatment with a Tyrosine Kinase Inhibitor, Dasatinib**  
David Galbraith - *Bristol Myers Squibb, United States of America*

15:45 - 16:00	<b>Plasma proteome profiling to detect and avoid sample related biases in biomarker studies</b> Philipp Geyer - <i>Max Planck Institute of Biochemistry, Germany</i>
16:00 - 16:15	<b>Deep Phosphoproteomics Profiling of 20 Breast Cancer Cell Lines Reveals Distinct Molecular Signaling of Triple negative Breast Cancer</b> Alexander Högberg - <i>University of Copenhagen, Denmark</i>
16:15 - 16:30	<b>Opposing effects of cancer type specific SPOP mutants</b> Namrata Udeshi - <i>Broad Institute of MIT and Harvard, United States of America</i>
16:30 - 17:15	<b>Flash talks (even numbers - 1 slide / 1 minute each)</b>
17:15 - 19:00	<b>Poster session 2 (even numbers)</b>
19:00 - 21:00	<b>Conference Dinner in the EMBL canteen</b>
21:00 - 00:00	<b>Conference Party in the ATC Rooftop Lounge</b>

## Day 3 - Saturday 9 March 2019

Time	Speaker
<b>09:00 - 12:15</b>	<b>Session 4 - Cell signalling</b> Chair: <a href="#">Steven Carr</a> - <i>Broad Institute, USA</i>
09:00 - 09:30	<b>Measurements of protein motions by proteomics: The allosteric activation of ERK2 by phosphorylation</b> <a href="#">Natalie Ahn</a> - <i>University of Colorado, Boulder, USA</i>
09:30 - 10:00	<b>Unconventional Serine Ubiquitination: finding substrates, ligases and deubiquitinases</b> <a href="#">Ivan Dikic</a> - <i>Goethe University Frankfurt, Germany</i>
10:00 - 10:30	<b>New technologies to interrogate the dynamics and function of the phosphoproteome</b> <a href="#">Judith Villen</a> - <i>University of Washington, USA</i>
10:30 - 11:00	<b>Coffee break and Meet the Speakers:</b> Ivan Dikic, Angus Lamond, Brenda Schulman
11:00 - 11:15	<b>Deep proteome profiling of breast cancer cells unraveled subtype specific pathway dysregulations</b> Asfa Alli Shaik - <i>Institute of Molecular and Cell Biology, Singapore</i>

- Proteome wide profiling of lysine deacetylase complexes with chemical probes**  
11:15 - 11:30  
Iris Finkemeier - *University of Muenster, Germany*
- A Precise and Sensitive LRRK2 Kinase Activity Assay by Targeted LC MS/MS Analysis of its Substrate Phosphorylation Stoichiometry**  
11:30 - 11:45  
Ozge Karayel - *Max Planck Institute of Biochemistry, Germany*
- Targeting the evolution of persistent clones in Jak2 mutated neoplasms**  
11:45 - 12:00  
Ashok Kumar Jayavelu - *Max Planck Institute of Biochemistry, Germany*
- Mining and integration of multi species proteomics data with the Biological Knowledge Graph**  
12:00 - 12:15  
Alberto Santos - *University of Copenhagen, Denmark*
- Lunch**  
12:15 - 13:30
- Session 5 - Integrated Proteomics**  
13:30 - 14:30  
Chair: Judit Villen - *University of Washington, United States of America*
- Deep Proteomes, iPS cells & Data Mountains**  
13:30 - 14:00  
[Angus Lamond](#) - *University of Dundee, UK*
- Functional relevance of eukaryotic protein phosphorylation**  
14:00 - 14:30  
[Pedro Beltrao](#) - *EMBL-EBI, UK*
- Poster Prize**  
14:30 - 14:40
- Keynote Speaker**  
14:40 - 15:25  
**Integrative studies of Ubiquitin Signaling**  
[Brenda Schulman](#) - *Max Planck Institute of Biochemistry, Germany*
- Closing Remarks**  
15:25 - 15:30
- Departure**  
15:45