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! #EMBLProteome

Day 1 - Wednesday 05 February 2020

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
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<tbody>
<tr>
<td>11:00-13:00</td>
<td>Arrival and Registration with light refreshments</td>
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<tr>
<td>11:45-12:45</td>
<td>Pre-conference workshop</td>
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<tr>
<td>13:00-13:30</td>
<td>Opening talk</td>
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<tr>
<td>13:00-13:30</td>
<td>The challenge of expanding the druggable proteome</td>
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<td>Adrian Carter, Boehringer Ingelheim, Germany</td>
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<td>13:30-15:00</td>
<td>Session 1: Illuminating the challenge and highlighting the opportunity for</td>
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<td>creating new medicines</td>
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<td>Chair: Adrian Carter</td>
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13:30-14:00
Illuminating the Druggable Genome with Informatics, Data Science and Machine Learning
Tudor Oprea - University of New Mexico, USA

14:00-14:30
Functionalization of the human protein-coding genome to discover medicines for neurodegenerative disease
Heiko Runz - Biogen, USA

14:30-15:00
Chemical probes and the chemical biology of cancer
Paul Workman - CRUK Cancer Therapeutics Unit, The Institute of Cancer Research, London, UK

15:00-15:30
Coffee break

15:30-17:45
Session 2: Illuminating the most promising proteins by virtue of druggability, human genetics and bioinformatics
Chair: Patrick Aloy

15:30-16:00
Computational identification of drug targets in cancer
Eytan Ruppin - National Cancer Institute, USA

16:00-16:15
Proteome-wide identification of new druggable targets for antibiotics
Stephan Hacker - Technical University of Munich, Germany

16:15-16:45
Target Tractability: Making full use of protein homology
Kristin Brown - GlaxoSmithKline, UK

16:45-17:15
Epigenetic variation across individuals to understand disease mechanisms
Judith Zaugg - EMBL Heidelberg, Germany

17:15-17:45
Extending the small molecule similarity principle to all levels of biology
Patrick Aloy - IRB Barcelona, Spain

17:45-18:35
Poster Session 1 (odd numbers)
with beer and snacks, ATC Helix A

18:35-19:30
Poster Session 2 (even numbers)
with beer and snacks, ATC Helix A

19:30-20:45
Dinner
EMBL Canteen

20:45-22:00
After Dinner Drinks
ATC Rooftop Lounge

20:00, 21:00, 22:00
Bus departure

Day 2 - Thursday 06 February 2020
<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
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<tr>
<td>09:00-12:30</td>
<td>Session 3: Interrogating the druggable proteome with chemical probes,</td>
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<td></td>
<td>imaging and sensor proteins, part 1</td>
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<td>Chair: Gerard Drewes</td>
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<td>09:00-09:30</td>
<td>Shaping biology by modulating access to chemical matter</td>
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<td></td>
<td>Giulio Superti-Furga - CeMM Research Centre for Molecular Medicine/</td>
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<td>Medical University of Vienna, Austria</td>
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<td>09:30-09:45</td>
<td>The target landscape of 1,200 kinase inhibitors</td>
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<td>Maria Reinecke - Technical University of Munich/ DKTK partner site</td>
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<td></td>
<td>Munich, Germany</td>
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<tr>
<td>09:45-10:00</td>
<td>Covalent inhibitors for 'undruggable' targets</td>
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<td>Nir London - The Weizman Institute of Science, Israel</td>
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<td>10:00-10:30</td>
<td>Targeting protein scaffolding function in kinases</td>
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<td>Stefan Knapp - Goethe University Frankfurt, Germany</td>
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<td>10:30-11:00</td>
<td>Coffee break</td>
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<tr>
<td>11:00-11:30</td>
<td>Exploring the druggable proteome by image-based phenotyping in cell</td>
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<td>lines and patient derived organoids</td>
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<td>Michael Boutros - German Cancer Research Centre/ Heidelberg University,</td>
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<td>Germany</td>
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<td>11:30-12:00</td>
<td>Mechanisms of intracellular DNA sensing through the cGAS-STING pathway</td>
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<td>Andrea Ablasser - EPFL, Switzerland</td>
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<td>12:00-12:15</td>
<td>Defining the human C2H2 zinc finger degrome targeted by thalidomide</td>
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<td>analogs through CRBN</td>
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<td>Georg Petzold - Friedrich Miescher Institute for Biomedical Research,</td>
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<td></td>
<td>Switzerland</td>
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<td>12:15-12:30</td>
<td>Stabilization of protein-protein interactions</td>
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<td>Pim de Vink - Eindhoven University of Technology, The Netherlands</td>
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<td>12:30-14:00</td>
<td>Lunch and meet the speakers</td>
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<td>14:00-14:00</td>
<td>Session 4: Interrogating the druggable proteome with chemical probes,</td>
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<td>imaging and sensor proteins, part 2</td>
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<td>Chair: Anke Müller-Fahrnow</td>
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<td>14:00-14:30</td>
<td>Tetrahydrobiopterin homeostasis</td>
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<td>Kai Johnsson - Max Planck Institute for Medical Research, Germany</td>
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Chemical physiology of natural products and antibody conjugates
14:30-15:00
Gonçalo Bernardes - University of Cambridge, UK and iMM Lisboa, Portugal

Within our control? Leveraging precision electrophile signaling toward drug discovery
15:00-15:30
Yimon Aye - EPFL, Switzerland

Understanding cellular phenotypes; from screens to probes towards clinical candidates
15:30-16:00
Marcus Bauser - Bayer AG, Germany

Coffee break
16:00-16:30

Session 5: Interrogating the druggable proteome with phenotypic screens
16:30-19:00
Chair: Herbert Waldmann

Towards improved biophysical models of protein folding to identify disease-causing mutations and rescue by small molecules
16:30-16:45
Amelie Stein - University of Copenhagen, Denmark

Using metabolic fingerprints to rationally design combination therapies
16:45-17:00
Mattia Zampieri - ETH Zürich, Switzerland

Pseudo Natural Products
17:00-17:30
Herbert Waldmann - Max Planck Institute of Molecular Physiology, Germany

A systems approach to functional precision medicine by deep learning and multi-OMICs
17:30-18:00
Berend Snijder - ETH Zürich, Switzerland

Advances in phenotypic and pathway profiling: Elucidating novel target biology and drug mechanism-of-action under appropriate biological context
18:00-18:30
Neil Carragher - The University of Edinburgh, UK

Conference Dinner
18:45-20:30
EMBL Canteen

After Dinner Drinks, live music
20:30-23:00
ATC Rooftop Lounge

Bus departure
20:00, 21:30, 23:00
Session 6: New engineering approaches for expanding the druggable proteome  
Chair: Stefan Knapp  
09:00-10:45

Mapping genetic networks using functional and chemical genomics  
Brenda Andrews - University of Toronto, Canada  
09:00-09:30

Biophysical screening of combinatorial libraries to target protein-protein interactions with covalent agents  
Maurizio Pellecchia - University of California, Riverside, USA  
09:30-10:00

NanoBRET cellular target engagement assays are versatile in enabling drug screening for various proteins – the SGC experience  
Benedict Berger - Structural Genomics Consortium, Goethe University Frankfurt, Germany  
10:00-10:15

Chemical biology at the interface of discovery to deliver novel to targets to the Drug Discovery Pipeline  
Christine Donahue - GlaxoSmithKline, USA  
10:15-10:45

Coffee break  
10:45-11:15

Session 7: New engineering approaches for breaking the druggability barrier  
Chair: Katrin Rittinger  
11:15-13:15

Targeting the active site of E3 ligases with chemical tools  
Katrin Rittinger - The Francis Crick Institute, UK  
11:15-11:45

Structure based PROTAC design to expand the druggable proteome  
Alessio Ciulli - University of Dundee, UK  
11:45-12:15

Chemical probes in target discovery  
Paul Brennan - University of Oxford, UK  
12:15-12:45

Identification of microbiome-encoded enzymes involved in drug metabolism  
Michael Zimmermann - EMBL Heidelberg, Germany  
12:45-13:15

Closing remarks and Poster Prize  
13:15-13:30

End of conference  
Packed lunch and departure  
13:30-14:00

Bus departure all stops downtown  
14:00

Bus to Frankfurt Intl. Airport  
14:10