



Cancer Genomics

EMBL CONFERENCE

We have moved our website to 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 The content below is no longer being updated.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! [#EMBLCanGen](#)

Day 1 - Monday 4 November 2019

Time	Speaker
11:00-13:00	Arrival / Registration with light refreshments Pre-conference workshop hosted by Samplix at 11:30-12:30 in Helix Seminar Room A
13:00-13:15	Opening remarks
13:15-16:30	Session 1: Cancer genetics and mutation Chairs: Catherine J. Wu & Jan Korbel
13:15-13:45	Somatic evolution in healthy and diseased bladder urothelium Inigo Martincorena, Wellcome Trust Sanger Institute, UK
13:45-14:00	A Pan-Cancer Analysis reveals Nonstop Mutations causing SMAD4 Tumor Suppressor Degradation Sven Diederichs, University of Freiburg, Germany

Time	Speaker
14:00-14:15	Large-scale analysis of liver cancer evolution in five species Duncan Odom, German Cancer Research Center, Germany
14:15-14:45	Full-length transcript isoforms associated with SF3B1 mutation in chronic lymphocytic leukemia Angela Brooks, University of California, Santa Cruz, USA
14:45-15:15	Coffee break
15:15-15:45	Understanding epitopes that drive T cell activation in cancer Matthew L. Meyerson, Dana-Farber Cancer Institute, USA
15:45-16:00	Comparison of somatic mutational processes across mammalian species Alex Cagan, Wellcome Sanger Institute, UK
16:00-16:15	Genotoxic pks+ E. coli induces a unique mutational signature in human colorectal cancer Axel Rosendahl Huber, Princess Máxima Center, The Netherlands
16:15-16:30	Oxidative DNA damage repair switches mutagenic outcomes in coding sequence dependent on the epigenome Anna Poetsch, St. Anna Children's Cancer Research Institute, Austria
16:30-17:00	Coffee break
17:00-18:00	Keynote: Hereditary predisposition to childhood cancer Stefan M. Pfister, Hopp Children's Cancer Center Heidelberg (KITZ), Germany
18:00-18:45	Digital poster presentations (Poster numbers 38, 45, 101, 107, 123, 124, 136, 137, 144, 146, 155, 157, 158) and Meet the speakers of Day 1 in the ATC Foyer
18:45-20:15	Dinner in the EMBL Canteen
20:15-22:00	After-dinner drinks in the ATC Rooftop Lounge

Day 2 - Tuesday 5 November 2019

Time	Speaker
09:00-12:15	Session 2: Cancer & microenvironment: immunogenomics & single cells Chairs: Elli Papaemmanuil & Peter Campbell

- 09:00-09:30 **Building personalized cancer vaccines**
Catherine J. Wu, Dana-Farber Cancer Institute, USA
- 09:30-09:45 **Single-cell transcriptomics predicts relapse in infants with acute lymphoblastic leukemia**
Frank Holstege, Princess Máxima Center for Pediatric Oncology, The Netherlands
- 09:45-10:00 **Computational study of the mechanisms of response to immunotherapy by transcriptomic analysis of the tumor immune microenvironment in melanoma**
Yamil Damian Mahmoud, Instituto de Biología y Medicina Experimental – CONICET, Argentina
- 10:00-10:30 **Tumor Genomic Profiling to Identify Therapeutic Biomarkers and Guide Clinical Care**
Michael F. Berger, Memorial Sloan Kettering Cancer Center, USA
- 10:30-11:00 Coffee break
- 11:00-11:30 **Somatic mutations in normal tissues**
Peter Campbell, Wellcome Trust Sanger Institute, UK
- 11:30-11:45 **Complex genomic rearrangements induced by ionizing radiation in normal cells**
Jeonghwan Youk, Korea Advanced Institute of Science and Technology (KAIST), Republic of Korea
- 11:45-12:00 **Lack of HLA affinity-based neoantigen depletion signals in the cancer genome when considering mutational sequence contexts**
Jimmy Van den Eynden, Ghent University, Belgium
- 12:00-12:15 **Life History of Normal Human Lymphocytes Revealed By Somatic Mutations**
Heather Machado, Wellcome Trust Sanger Institute, UK
- 12:15-13:45 **Lunch**
- 13:45-15:15 **Poster Session 1 (odd numbers)**
- 15:15-18:00 **Session 3: Cancer genome and epigenome**
Chairs: Núria López-Bigas & Matthew L. Meyerson
- 15:15-15:45 **Deciphering the evolutionary paths of tumor progression in Small Cell Lung Cancer**
Julie George, University of Cologne, Germany

15:45-16:00	Epigenetic and transcriptional reprogramming underlies lung adenocarcinoma histological intra-tumor heterogeneity and microenvironment composition Giovanni Ciriello, University of Lausanne, Switzerland
16:00-16:15	Reconstructing shattered chromosomes in oesophageal adenocarcinomas Jannat Ijaz, Wellcome Sanger Institute, UK
16:15-16:45	Genomic Alterations Across Molecular Subtypes of Mantle Cell Lymphoma Elías Campo, Hospital Clinic of the University of Barcelona, Spain
16:45-17:15	Coffee break & Meet the speakers of Day 2
17:15-17:30	Aberrant integration of Hepatitis B virus DNA promotes restructuring of hepatocellular carcinoma genome Eva Alvarez, CIMUS, University of Santiago de Compostela, Spain
17:30-18:00	Decoding pancreatic cancer through large scale cohort and single cell sequencing Sean Grimmond, The University of Melbourne, Australia
18:00-19:00	Keynote: Partnering with patients to accelerate cancer genomics and precision medicine Nikhil Wagle, Dana-Farber Cancer Institute, USA
19:00-19:15	Apéritif in the ATC Foyer
19:15-21:15	Conference Dinner in the EMBL Canteen
21:15-00:00	Conference Party with DJ in the ATC Foyer

Day 3 - Wednesday 6 November 2019

Time	Speaker
09:00-12:00	Session 4: Drivers of cancer and genome-wide functional screens Chairs: Angela Brooks & Peter J.M. Valk
09:00-09:30	Accelerating prediction of tumor vulnerabilities using precision functional genomics Jesse S. Boehm, Broad Institute, USA
09:30-09:45	The U1 Spliceosomal RNA is Recurrently Mutated in Multiple Cancers Shimin Shuai, Ontario Institute for Cancer Research, Canada

09:45-10:00	Functional genomic studies of cancer immune evasion using in vitro and in vivo CRISPR/Cas9 genetic screens Dimitrios Garyfallos, University of Cambridge, UK
10:00-10:30	The mutational footprints of cancer therapies Núria López-Bigas, ICREA, Institute for Research in Biomedicine, Spain
10:30-11:00	Coffee break
11:00-11:30	Jan Korbel, EMBL Heidelberg, Germany
11:30-11:45	Uncovering the role of the disruption of ubiquitin mediated proteolysis in tumorigenesis Francisco Martinez-Jimenez, IRB, Spain
11:45-12:00	Elevated pyrimidine dimer formation at distinct genomic bases underlies promoter mutation hotspots in UV-exposed cancers Kerryn Elliott, University of Gothenburg, Sweden
12:00-13:30	Lunch
13:30-15:00	Poster Session 2 (even numbers)
15:00-17:00	Session 5: Cancer genome medicine Chair: Jesse S. Boehm
15:00-15:30	Mathew Garnett, Wellcome Trust Sanger Institute, UK
15:30-15:45	The Evolutionary Dynamics and Fitness Landscape of Clonal Haematopoiesis Jamie Blundell, University of Cambridge, UK
15:45-16:00	CRUK Grand Challenge Mutographs: Mutation signature analysis of Oesophageal Squamous Cell Carcinoma (ESCC) from high incidence regions Sarah Moody, Wellcome Sanger Institute, UK
16:00-16:30	Oncologic therapy shapes the fitness landscape of clonal hematopoiesis Elli Papaemmanuil, Memorial Sloan Kettering Cancer Center, USA
16:30-17:00	NGS-based molecular minimal residual disease detection in acute myeloid leukemia Peter J.M. Valk, Erasmus University Medical Center, The Netherlands
17:00-17:15	Closing remarks and poster prize
17:30	Bus departures downtown and to Frankfurt Airport (airport shuttle tickets for sale at registration desk)

