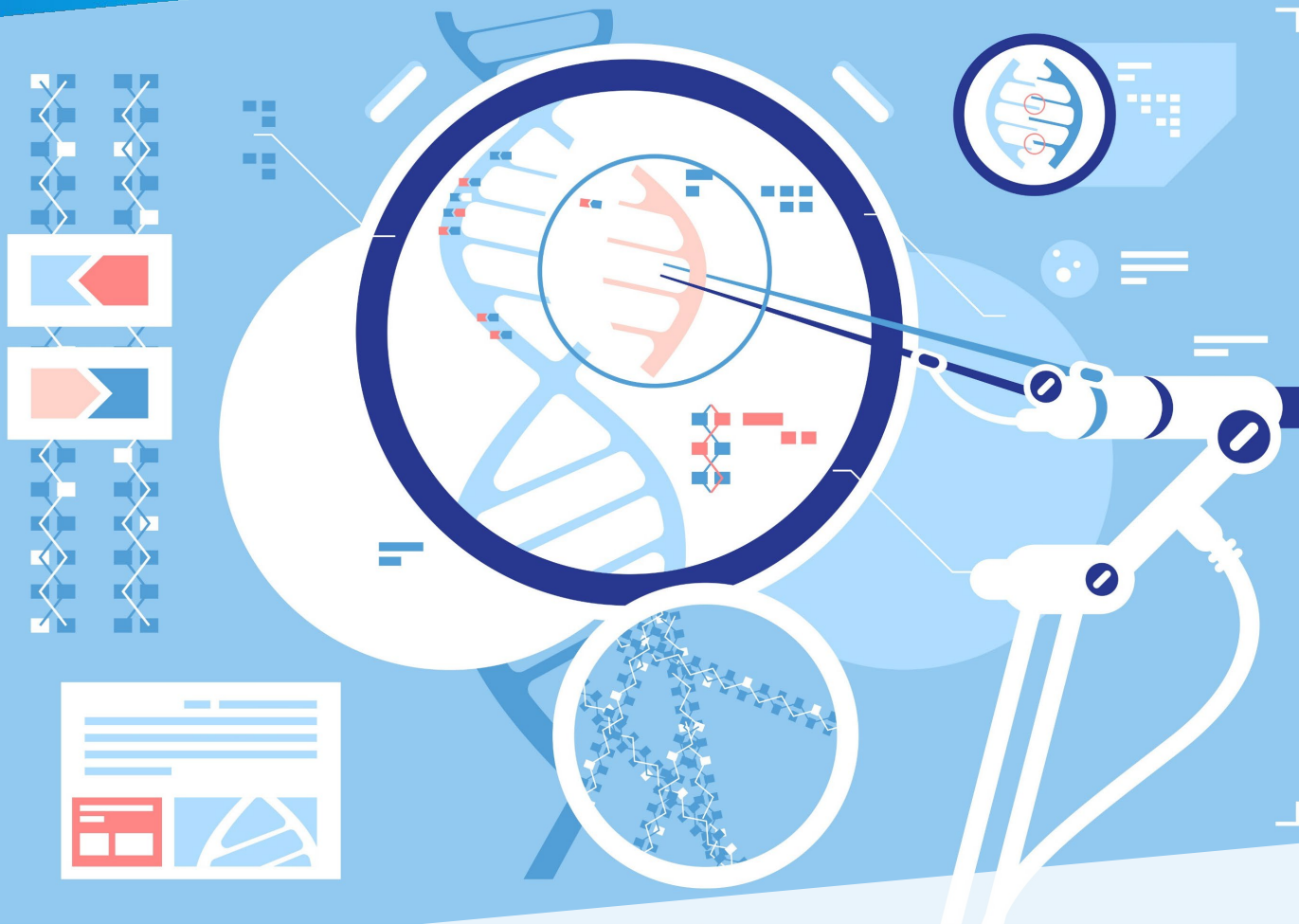# 1st European
Cancer Dependency
Map Symposium

8 May 2023
h 10:00 – 17:45

Human Technopole
Milan (IT)
+
Online

CONCEPT

COURSE OVERVIEW

The 1st European Cancer Dependency Map Symposium aims to present a general overview of the latest advances in the use of chemo-genomics and genome-editing screens for the discovery of new cancer vulnerabilities and therapeutic targets. The event will facilitate interactions among the participants, fostering the exchange of ideas with world-leading experts in the field and a line-up of renowned speakers who will present their most recent work and future projects.

The event will feature a series of talks, a roundtable discussion and a poster session for participants, covering the latest discoveries and future challenges in the area of cancer dependencies.

TARGET AUDIENCE

Open to the national and international community of scientists working in the fields of computational genomics, pharmacogenomics, and therapeutic target discovery.
The Symposium will be of interest to scientists at different levels, from PhD students to more senior researchers.

symposium

FACULTY

SCIENTIFIC ORGANISERS

FRANCESCO IORIO
Research Group Leader,
HT Computational Biology Research
Centre

PEDRO BELTRAO
Research Group Leader, Institute of
Molecular Systems Biology, ETH Zurich,
Switzerland

ISIDRO CORTES-CIRIANO
Research Group Leader, EMBL-European
Bioinformatics Institute, Cambridge, UK

MATHEW GARNETT
Research Group Leader, Wellcome
Sanger Institute, Cambridge, UK

EVANGELIA PETSALAKI
Research Group Leader,
EMBL-European Bioinformatics Institute,
Cambridge, UK

SPEAKERS

IAIN MATTAJ
Former HT Director

NURIA LOPEZ-BIGAS
Research Group Leader, Institute for
Research in Biomedicine (IRB), Spain

SUMANA SHARMA
Sir Henry Wellcome Postdoctoral Fellow,
MRC Weatherall Institute of Molecular
Medicine (WIMM), UK

CHRIS TAPE
Research Group Leader, University College
London (UCL), UK

JOLANDA VAN LEEUWEN
Research Group Leader, Center for
Integrative Genomics (CIG), Switzerland

FRANCISCA (PAQUITA) VAZQUEZ
Director of the Cancer Dependency Map
Project (DepMap) at the Broad Institute, USA

symposium

PROGRAMME

10.00 – 11.00   **REGISTRATION AND WELCOME COFFEE**

11.00 – 11.15   **INTRODUCTION**
FRANCESCO IORIO (HT)

11.15 – 11.30   **OPENING REMARKS**
IAIN MATTAJ (Former HT Director)

SESSION 1, chaired by Isidro CORTES-CIRIANO

11.30 – 12.30   "Building a cancer dependency map to accelerate precision cancer medicine"
MATHEW GARNETT (Wellcome Sanger Institute)
FRANCISCA (PAQUITA) VAZQUEZ (Broad Institute)
An overview on the ongoing expansion of DepMap, highlighting the efforts to enable the scientific community, and the focus on identifying new targets for precision cancer therapy, to advance the field of precision cancer medicine.

12.30 – 13.00   "Understanding context-dependent gene essentiality through genetic suppression analysis"
JOLANDA VAN LEEUWEN (CIG)
Genes that are required for cellular viability are often highly conserved across eukaryotes, but in some cases, genomic mutations have the potential to bypass their requirement. It will be presented how genetic variants can suppress the lethality of essential gene mutants.

13.00 – 14.30   BUFFET LUNCH & POSTER SESSION

SESSION 2, chaired by Evangelia PETSALAKI

14.30 – 15.00   "Application of CRISPR-based approaches to study cellular signalling processes"
SUMANA SHARMA (WIMM)
A discussion on using CRISPR-based screening approaches to unravel the complex process of cellular signalling, from the point of receptor identification to intracellular signalling pathways, with a particular emphasis on signalling mediated by inhibitory immune checkpoints.

PROGRAMME

15.00 – 15.30   "Single-cell signalling analysis of tumour microenvironment organoids"
CHRIS TAPE (UCL)
A talk on single-cell analysis of drug-response mechanisms in patient-derived organoids (PDOs) and cancer associated fibroblasts (CAFs). It will be shown that CAFs alter PDO drug sensitivity by cell-fate plasticity switching and mechanistic insights can drive rational drug re-sensitisation.

15.30 – 16.00   "In silico saturation mutagenesis of cancer and clonal hematopoiesis genes"
NURIA LOPEZ-BIGAS (IRB)
Most mutations identified in tumors in cancer genes are mutations of unknown significance. In this talks, machine learning models, BoostDM, inspired in evolutionary biology to effectively identify driver mutations in each gene and cancer type will be discussed. With those models, in silico saturation mutagenesis is performed to outline blueprints of potential driver mutations in cancer genes.

16.00 – 16.30   COFFEE BREAK

16.30 – 17.30   **ROUNDTABLE DISCUSSION**
Cancer DepMap: Key aspects, emerging technologies, academic and industrial perspectives
Moderated by Mathew GARNETT

17.30 – 17.45   **WRAP UP**
By Pedro BELTRAO