



ALMA MATER STUDIORUM  
UNIVERSITÀ DI BOLOGNA

DIPARTIMENTO  
DI FARMACIA  
E BIOTECNOLOGIE

## AVVISO DI SEMINARIO

Il giorno **10 aprile 2026**  
alle ore **14.30**

### **Dr. Francesco Iorio**

Senior Research Group Leader presso Human Technopole, Milano  
(ospite della Prof.ssa A.M. Porcelli)

terrà un seminario in lingua inglese dal titolo:

# **Mining existing and newly designed CRISPR screens to map genomic, transcriptomic and phenotypic contexts of cancer dependencies**

*in presenza:*

**Aula A Farmacologia, Via Irnerio 48, Bologna**

*e in streaming:*

<https://teams.microsoft.com/l/meetup-join/19%3aN09c0NlyEssBnF70bCyDOQwkgDWm1qdd9f7F2nJV9fw1%40thread.tacv2/1631519544944?context=%7b%22id%22%3a%22e99647dc-1b08-454a-bf8c-699181b389ab%22%2c%22oid%22%3a%225a941351-ef41-4aa4-8771-fa50a6d62ca1%22%7d>

L'evento è organizzato nell'ambito del Corso di Dottorato in Biologia  
Cellulare e Molecolare

## **ABSTRACT**

Large-scale CRISPR screening efforts have enabled the systematic identification of genetic dependencies across diverse cancer models. However, most vulnerabilities are not universal, but arise within specific molecular or phenotypic contexts. Understanding these contexts is therefore essential to translate dependency maps into actionable therapeutic opportunities. I will present a set of complementary strategies to map the genomic, transcriptomic and phenotypic contexts that define cancer dependencies by mining both existing and newly designed CRISPR perturbation screens. First, I will describe a computational framework to identify mutation-specific vulnerabilities by leveraging large-scale CRISPR screening datasets, enabling high-resolution functional interpretation of variants of uncertain significance. Second, I will introduce DepSHOCK, an approach that combines computational modelling with targeted perturbation experiments to uncover transcriptional signatures predictive of cancer dependencies. Finally, I will discuss experimental strategies to identify vulnerabilities that emerge in drug-resistant states. Together, these approaches aim to move from cataloguing dependencies to systematically defining the contexts that make them actionable.

## **BIOGRAPHICAL SKETCH**

Francesco Iorio is a computational biologist and Senior Research Group Leader at the Human Technopole (Milan, Italy), where he leads a research group focusing on computational functional genomics of cancer. His lab generates large-scale perturbation data, including CRISPR screening and pharmacogenomic profiling, to uncover genetic interactions and context-specific vulnerabilities in cancer. His work integrates computational and experimental approaches to identify predictive biomarkers of therapeutic response and discover new targets for precision oncology. Francesco has contributed to several international initiatives in functional cancer genomics, including the Cancer Dependency Map, he is a founder of the nascent European PRECISE consortium, and is currently developing new strategies to systematically map and predict the molecular contexts of cancer dependencies.