Methods to tackle chromatin architecture and function

Dates and times

From *20th* to *24th* January 2025, 14:00 – 17:00 (**GMT+1**)
Farbiomot classroom Via F. Selmi 3, Bologna
Microsoft Teams link:
https://teams.microsoft.com/l/meetup-join/19%3ameeting_MDNiNWI2M2UtYjliZi00OWQyLWIwOWMtYWQwMDM5MzMzNmVj%40thread.v2/0?context=%7b%22Tid%22%3a%22e99647dc-1b08-454a-bf8c-699181b389ab%22%2c%22Oid%22%3a%2266e8e709-3392-4f2b-b89a-e65e01243114%22%7d

Learning outcomes and Course contents

This course will provide the basic concepts behind different methods to analyse the chromatin architecture and function.
Specifically, the student will learn how to fully set up and analyse experiments aimed to study chromatin conformation, function and interaction.

The course will go deeper into chromatin-related techniques such as:

- *Chromosome Conformation Capture (3C)*
- *Chromatin-IP (Ch-IP)*
- *Ch-IP related methodologies (CUT&RUN and EXO-Ch-IP)*
- *Nuclease-deficient CAS9 applications*

Teaching methods

The PhD student will learn how to use key publicly available software to fully design all the necessary experimental steps. The course will consist of both theoretical lessons and practical exercises.

Assessment methods

Multiple-choice test

How to attend

The course is specifically designed for first-year PhD students. While it is highly recommended to attend during the first year, it is not mandatory.
Students interested in attending the course are kindly requested to register by sending an email with the subject line 'Methods to tackle chromatin architecture and function' to giorgio.milazzo@unibo.it, indicating whether they plan to attend in person or online, no later than Wednesday, January 15, 2025, to allow for the organization of the classroom (physical + virtual Teams) based on the number of participants. It is highly recommended to attend the classes in person unless there are proven reasons that prevent it.