INSTITUTO DE INGENIERÍA
BIOLÓGICA Y MÉDICA
PONTIFICIA UNIVERSIDAD CATÓLICA DE CHILE

IIBM Seminar

"Study of the Protein-DNA recognition process from different perspectives through interdisciplinary approaches"

Francisco Melo
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School of Biological Sciences, Pontificia Universidad Católica de Chile

Wednesday 31th August 2022 - 13:00 Hrs - Lunch included
Hybrid Seminar – Classroom to be announced
Zoom link: Contact **secretariaiibm@uc.cl**

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"Study of the Protein-DNA recognition process from different perspectives through interdisciplinary approaches“

Abstract: "The specific protein-DNA molecular interactions events constitute the basis of key cell processes such as regulation of gene expression, DNA packing, DNA replication, DNA recombination and DNA repair. The detailed understanding of the molecular recognition process that mediates the selectivity of protein-DNA binding is one of the most interesting present challenges in structural and molecular biology. Known genomes encode from hundreds to several thousands transcription factors, which orchestrate the gene expression in cells and constitute the direct link between genotype and phenotype in living systems.

In this presentation I will focus on describing some advances of the current knowledge in the important field of molecular recognition between proteins and DNA from an interdisciplinary perspective. To achieve that we combine the use of bioinformatics and computational biology tools with experimental molecular biology, structural biology and microbiology approaches.

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We gathered large, relevant and new functional data in vitro, in vivo and in silico, using an innovative experimental design based on a particular transcription factor (called MarA) that exhibits a highly complex DNA binding mode for which, despite significant research carried out worldwide to date, their DNA binding specificity determinants at the molecular level are still unknown.

We expect that through a carefully-designed in vivo directed co-evolution experimental setup we will be able to collect valuable information that is not available in the evolutionary record currently known and present in public databases for this model transcription factor."