

Unzipping the Secrets of Transcription Regulation: How Intrinsically Disordered Regions Guide Transcription Factor Target Search

Dr. Ariel Kaplan

Faculty of Biology - Israel Institute of Technology

- **Miércoles 19 de Agosto a las 13 horas**
- **Aula: RFP 3er piso DQIAQF/INQUIMAE**
- **Streaming por el canal de YouTube del DQIAyQF**

Resumen

Transcription factors recognize specific DNA motifs, yet these motifs are typically short, degenerate, and vastly overrepresented in the genome. Recognition by a structured DNA-binding domain alone is therefore insufficient to explain how transcription factors efficiently locate and selectively occupy their functional regulatory targets.

In this seminar, I will present our recent work on Msn2, a master regulator of the environmental stress response in budding yeast. Using single-molecule optical-tweezers assays, we dissected the contribution of Msn2's extensive intrinsically disordered regions to its interactions with DNA. We find that these regions promote an initial, charge-mediated association with nonspecific DNA and facilitate one-dimensional exploration toward the target motif. Remarkably, both the initial association and subsequent scanning are sensitive to promoter-derived DNA sequences, demonstrating that Msn2–DNA interactions alone can generate promoter selectivity, even in the absence of chromatin or additional cofactors. Together, these results support a model in which intrinsically disordered regions shape the kinetics and spatial organization of transcription-factor target search, providing an additional layer of specificity in gene regulation.