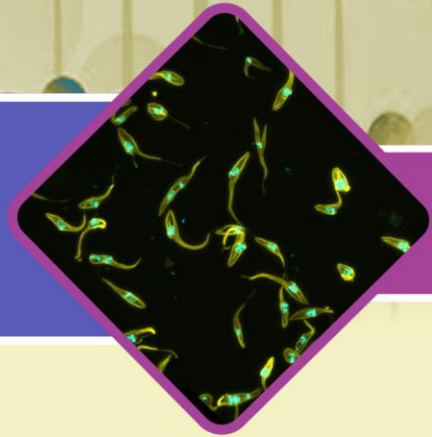


Webinar: “Model organisms for biotechnology development: application of x-omics data”



1-3-9-10-15
December 2020



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Our goal is to provide a state of the art of the available tools and biological models to overcome the overwhelming amount of existing data as we enter the 'post-genomic era'. Recently, 'genome-wide' expression profiling methods at the level of the transcriptome and proteome have come to the fore. Whilst over recent years there has been a tremendous drive to develop analytical technology and databases for 'transcriptomics' and 'proteomics', integrative analysis strategies for this omic data has yet to emerge. On the other hand, working on the hypothetical gene products from different genomes need to be validated in appropriate model organisms. We aim at describing several classical models as well as no that classical.

Speakers

- ◆ **Dr. Guillermo Alonso.** INGEBI-CONICET / FCEN-UBA, Argentina.
- ◆ **Dr. Francisco Velázquez Duarte.** iB3, FCEN-UBA / CONICET, Argentina.
- ◆ **Dra. Marcela Cucher.** IMPaM /UBA-CONICET, Argentina.
- ◆ **Dr. Malcolm Kennedy.** Glasgow University, UK.
- ◆ **Dra. Laura Kamenetzky.** iB3, FCEN-UBA / CONICET, Argentina.
- ◆ **Dra. Carolina Bagnato.** IEDS CNEA Bariloche / CONICET, Argentina.

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