

PhD Student Recruitment

Histone Post-Translational Modifications (PTMs) regulate chromatin functions. Misregulation of histone PTMs and their regulators is associated with cancer, among other human diseases. Hundreds of histone PTMs have been identified in the eukaryotic cell. A small subset of them are very well characterized from model organisms to human cells, however, the function of many others and how they are regulated in a context-specific manner remains a mystery. Until now, **systematic functional studies** were not possible due to methodological limitations. We are going to tackle this question using a new approach based on reverse genetics, chemical genomics and computational analysis. Are you interested in joining our group?

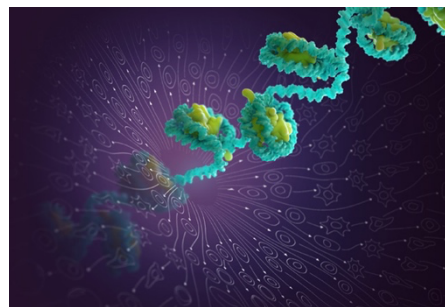
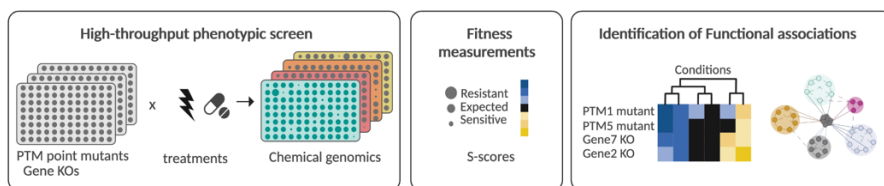


Image: Campbell Medical Illustration

We combine cutting-edge **high-throughput methodologies based on reverse genetics, chemical genomics and computational analysis** with classical **molecular biology** techniques using *S. cerevisiae* as a model organism. We collaborate with international groups, which offers the possibility of short research visits during the PhD. Our group is based at the Functional Biology and Genomics Institute (IBFG) in Salamanca, Spain. IBFG is a joint centre between the Spanish Research Council (CSIC) and the University of Salamanca.



Candidate requirements:

- Degree in Bioscience (Biology, Biotechnology, Biochemistry, Pharmacy, etc)
- Official Master in Bioscience
- Previous Research Experience
- Team player and good communication skills

It will be positively valued:

- Experience working with yeast
- Fluent in English
- High grades in Bs (to apply for competitive national and regional calls >8/10)
- Experience in Bioinformatics (R language or Python)

Are you interested? Send us a Motivation letter, CV and 2 Reference letters to cristina.vieitez@usal.es

More info:

- **Lab Website** <https://sites.google.com/view/cristinavieitezlab/home>
- **Viéitez C, et al. High-throughput functional characterization of protein phosphorylation sites in yeast, *Nature Biotechnology*, 2022.**
- **Viéitez C, et al. A genetic analysis reveals novel histone residues required for transcriptional reprogramming upon stress, *Nucleic Acids Res*, 2020.**