

# POSTDOCTORAL POSITION TO STUDY THE EVOLUTION OF THE YEAST TRANSCRIPTOME USING LONG READS

(Ref. 2218 - ALBÀ)

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## OFFERS:

We offer a 2 year postdoctoral position to investigate the evolutionary dynamics of the yeast transcriptome using Nanopore direct RNA reads. The project will focus on the identification of transcript isoforms, with a special focus on transcription termination and alternative polyadenylation events in *Saccharomyces cerevisiae* and related species. The researcher will be part of the Evolutionary Genomics team led by Mar Albà at IMIM-PRBB ([evolutionarygenomics.imim.es](http://evolutionarygenomics.imim.es)). She/he will have access to state-of-the-art computational resources and a wide range of training opportunities. The position is funded by Agencia Estatal de Investigación (Spanish Government) project PID2021-122726NB-I00. Gross salary 30.951,44 - 33.899,38 Eur per year depending on experience. Flexible starting date.

## Requirements of the candidates:

- ✓ Research experience in comparative genomics and transcriptomics
- ✓ Expertise in at least one programming language
- ✓ Expertise in a programmatic statistics language (ideally R)
- ✓ Interest in developing new code to analyze RNA-seq long read data
- ✓ Interest in molecular evolution
- ✓ Excellent verbal and written communication skills in English

## Project:

Many genes contains alternative termination and polyadenylation sites, which can produce transcripts with different 3'UTRs and sometimes also affect the coding sequence. Alternative transcription termination impacts post-transcriptional regulation of gene expression and generates transcript and protein diversity upon which natural selection can act, shaping the evolution of genes. In this project we will investigate alternative transcriptional termination in different yeast species using Nanopore native RNA sequencing data. We will identify complete single mRNA molecules, including isoforms showing differences in exon composition and/or the 3'UTR region, obtaining a unique view into the transcriptional diversity of the species. The

effects at the level of translation of early transcription termination events will be investigated using Ribo-Seq data from the same species. Furthermore, by using similar data from different *Saccharomyces* yeasts we will be able to identify conserved as well as species-specific events, obtaining a picture of the evolutionary dynamics of alternative transcription termination in this eukaryotic model system.

Related Publications:

Montañés, J.C., Huertas, M., Moro, S.G., Blevins, W.R., Carmona, M., Ayté, J., Hidalgo, E., Albà, M.M. (2022). Native RNA sequencing in fission yeast reveals frequent alternative splicing isoforms. *Genome Research*, 32:1215-1227.

Blevins, W.R., Ruiz-Orera, J., Messeguer, X., Blasco-Moreno, B., Villanueva-Cañas, J.L., Espinar, L., Díez, J., Carey, L.B., Albà, M.M. (2021). Uncovering de novo gene birth in yeast using deep transcriptomics. *Nature Communications*, vol. 12: 604.

**For more information and to submit your curriculum vitae**, please contact Mar Albà ([malba@imim.es](mailto:malba@imim.es)). Include a CV and a motivation letter, together with the name of two contacts for references.