

# Master project 2020-2021

## Personal Information

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## Project

## Computational genomics

### Project Title:

Identification of domain-specific adaptations for protein synthesis

### Keywords:

Protein synthesis, proteome diversity, transfer RNA, modified bases, evolution

### Summary:

We have developed tools to detect and analyze protein sequences that are impossible to synthesize for some organisms. Those species that can make these proteins do so thanks to special adaptations ('upgrades') of the protein synthesis machinery. Now we want to further develop and use these tools to map the global proteome landscape and identify all possible protein sequences possibly unique to some group of species thanks to the existence of 'upgrades'. We offer one or two paid (modestly) positions to carry out these analyses. We look for candidates interested in evolution, biochemistry, and confident in the use of R.

### References:

References: 1. The mitochondrial tRNA conundrum. (2020) Ribas de Pouplana L. Nat Rev Mol Cell Biol. doi: 10.1038/s41580-020-0220-5. 2. Differential expression of human tRNA genes drives the abundance of tRNA-derived fragments. (2019) Torres AG, Reina O, Stephan-Otto Attolini C, Ribas de Pouplana L. Proc Natl Acad Sci U S A. 116(17):8451-8456. 3. The Expansion of Inosine at the Wobble Position of tRNAs, and Its Role in the Evolution of Proteomes. (2019) Rafels-Ybern A, Torres AG, Camacho N, Herencia-Ropero A, Roura Frigolé H, Wulff TF, Raboteq M, Bordons A, Grau-Bové X, Ruiz-Trillo I, Ribas de Pouplana L. Mol Biol Evol. 36(4):650-662. 4. Codon adaptation to tRNAs with Inosine modification at position 34 is widespread among Eukaryotes and present in two Bacterial phyla. (2018) Rafels-Ybern A, Torres AG, Grau-Bové X, Ruiz-Trillo I, Ribas de Pouplana L. RNA Biol. 2018;15(4-5):500-507.

### Expected skills:

R. Desirable but not essential: Python, and experience in phylogenetic analysis.

### Possibility of funding:

Yes

**Possible continuity with PhD: :**

To be discussed

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