

## ***30 months Engineer Assistant position available at I2BC, Gif Sur Yvette (20 km from Paris- FRANCE)***

***A 30 months engineer assistant position is available at the beginning of December 2018 /January 2019 to study the multifaceted functions of protein acetyltransferases in plant stress response and regulation of metabolism in the group of “Protein Maturation Cell Fate and Therapeutics” at the I2BC in Gif Sur Yvette (<https://www.i2bc.paris-saclay.fr/spip.php?article1>).***

### **Background**

Protein modifications are emerging as key players for controlling countless essential cellular processes. In principle, all proteins of any living organism undergo to co- and/or post-translational modifications which define protein life and function. Each modification converts one protein species into another that is a functionally distinct species. Among protein modifications, N-terminal protein acetylation (NTA) is one of the most common protein modifications as it occurs on more than 80% of eukaryotic proteins. NTA was initially considered only co-translational, but modification has now been documented also to occur post-translationally after removal of transit peptides from imported proteins in organelles (chloroplast and mitochondria). Despite it has been shown that this modification is involved in a number of crucial cellular processes, controlling in specific proteins half-life, membrane and compartment localization, protein-protein interaction, protein folding, protein aggregation, many questions about this modification and the enzymes involved (Nats) remain to elucidate.

### **Project**

In the course of a recent international financed project, bringing together five recognized European groups (ERACAPS KATNAT), we have started a study which overarching aim is to provide a mechanistic understanding of protein acetylation in plants, with a particular focus on investigating the enzymes that catalyze this modification and its role on proteostasis, photosynthesis and metabolism. For this project we are looking for an Engineer Assistant with expertise in protein biochemistry and enzymology, mass spectrometry targeted techniques, enrichment of post-translational modification. Experience in computational proteomics will be appreciated. The selected person will be trained to use our in-house pipelines/methods for the proteomics N-terminal characterization and quantification, NAT enzymatic evaluation and partners sample analyses by MS. The successful candidate should be able to perform the experiments, analyze and interpret the emerging data. The ideal candidate is expected to be highly motivated and capable to have a strong relational and organizational sense. Fluency in English is preferred.

For further information please contact: Carmela GIGLIONE: [carmela.giglione@i2bc.paris-saclay.fr](mailto:carmela.giglione@i2bc.paris-saclay.fr)

Carmela Giglione PhD  
Protein Maturation, Cell fate and Therapeutics  
Institute for Integrative Biology of the Cell (I2BC)  
CNRS UMR9198, Bâtiment 21, 1 avenue de la Terrasse  
F-91198 Gif-sur-Yvette cedex, France  
E-mail: [carmela.giglione@i2bc.paris-saclay.fr](mailto:carmela.giglione@i2bc.paris-saclay.fr)

Tel: 01 69 82 46 44

<http://www.i2bc.paris-saclay.fr/spip.php?article130>

To apply it is required:

- A CV
- Full Contact details of at least two references

### Selected Publications of the group:

Castrec B, et al (2018) Structural and genomic decoding of human and plant myristoylomes reveals a definitive recognition pattern. *Nat Chem Biol* 14: June 11, DOI: 10.1038/s41589-018-0077-5

Majeran W, et al (2018) Targeted profiling of *A. thaliana* sub-proteomes illuminates new co- and post-translationally N-terminal Myristoylated proteins. *Plant Cell* 30: 543–562

Bienvenut WV, Giglione C, Meinnel T (2015) Proteome-wide analysis of the amino terminal status of *Escherichia coli* proteins at the steady-state and upon deacetylation inhibition. *Proteomics* 15: 2503-18

Bienvenut WV, Giglione C, Meinnel T (2017) SILProNAQ: A Convenient Approach for Proteome-Wide Analysis of Protein N-Termini and N-Terminal Acetylation Quantitation. *Methods Mol Biol* 1574: 17-34

Bienvenut WV, et al (2017) EnCOUNTER: a parsing tool to uncover the mature N-terminus of organelle-targeted proteins in complex samples. *BMC Bioinformatics* 18: 182

Linster E., et al (2015) Downregulation of N-terminal acetylation triggers ABA-mediated drought responses in *Arabidopsis*. *Nat Commun* 6: 7640

Xu F., et al (2015) Two N-terminal acetyltransferases antagonistically regulate the stability of a nod-like receptor in *Arabidopsis*. *Plant Cell* 27: 1547-62

Dinh, T.V et al (2015) Molecular identification and functional characterization of the first N<sup>ε</sup>-acetyltransferase in plastids by a global acetylome profiling test, *Proteomics*, 15, 2426-2435

Bienvenut, W.V., et al (2012) Comparative large-scale characterisation of plant vs. mammal proteins reveals similar and idiosyncratic N-alpha acetylation features. *Mol. Cell. Proteomics*, 11: M111 015131