

# URGENT

**Lecturer / PostDoc (ATER) position**

**ATER 12 months (renewable 1 time)**

**Biochemist – Structural biologist**

The unit of **Microbiologie Structurale** at the **Institut Pasteur (Paris)** recruits a **Lecturer & Researcher PostDoc position (ATER)** (teaching in French). The position is full time for 1 year renewable one time.

Candidate profile : section **64, 65**

The candidate must have a PhD in biochemistry – structural biology.

Deadline: **May 4th, 2021 at 4 pm (UTC+1 time).**

To postulate, candidates have to fill the documents on « Galaxie » (module ALTAÏR) :  
<https://galaxie.enseignementsup-recherche.gouv.fr/documentation/web/altair-cand>

Please contact **Stéphanie Petrella** asap to have more information:  
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## ATER PROFILE

**Sections/discipline** : section 64, 65 (Biochemistry / Structural Biology / Bacteriology)

**Profile** : Biochemist and structural biologist. Experience in **cryo-electron microscopy** will be a plus. The candidate will have an integrated knowledge of bacteriology, biochemistry and molecular biology.

**Location** : **Institut Pasteur** – 25 rue du Dr Roux – 75015 Paris for the research activity.  
**Université de Paris** -75013 Paris for teaching activity.

**Teaching profile:** All teaching will be in French. Several teaching profiles are offered and the recruited candidate will join the teaching team in place, position of **150 hours / year**. The different teaching profiles are available on the Galaxie website.

**Research profile:** Our research unit has a solid knowledge in structural studies by protein crystallography and X-ray diffraction, recently extended to **cryo-electron microscopy**. In addition, structural investigation is now combined with *in vivo* studies. ***Corynebacterium glutamicum*** is used as a model organism for investigating *M. tuberculosis* and Actinobacteria in general. Indeed, during the last 4 years, a collection of conditional mutants on several kinases and proteins involved in cell division of *C. glutamicum* have been built, and cell imaging tools have been developed.

The Unit, headed by P. Alzari, has 4 principal investigators on complementary subjects: M. Bellinzoni (metabolism of Actinobacteria, drug design), AM. Wehenkel (cell division of Actinobacteria), S. Petrella (resistance to antibiotics, DNA gyrase) and F. Gubellini (structural biology of large membrane complexes). We benefit from the assistance of M. Martinez (lab manager, protein biochemistry and bacterial genetics) and M. Ben Assaya (technical support in production recombinant proteins and bacterial genetics, corresponding CHSCT). The Unit is also composed of 5 doctoral students. Our synergy in the Unit creates a strong experimental dynamism favouring advances in all the experimental subjects.

It is within this very broad framework and complementary environment that the research program of the recruited ATER will take place. The research project will focus on structural studies of bacterial proteins already in progress in the Unit, mainly by **cryo-electron microscopy**. The laureate will join the team's efforts to advance the various projects centered around the Unit's 3 main areas of research: 1- the study of metabolism in Actinobacteria; 2- the study of super-complexes essential in the cell division of Actinobacteria; 3- the study of DNA gyrase from ***Mycobacterium tuberculosis***.

The expected results will increase the fundamental knowledge on the link between bacterial metabolism and cell division. Ultimately this will allow the identification of new antibacterial targets. A direct medical application will be the development of new inhibitors against the ***M. tuberculosis* DNA gyrase**, an important therapeutic target.

Various electron microscopes are accessible on the IP campus: two T12 microscopes for screening, one F20 equipped with a Falcon 2 camera, two Glacios (Falcon 2) and one Titan Krios (Falcon 3) supporting results in **high-resolution cryo-EM**.

5 recent Unit publications:

**Giganti D**, Albesa-Jové D, Urresti S, Rodrigo-Unzueta A, Martínez MA, Comino N, **Barilone N**, **Bellinzoni M**, Chenal A, Guerin ME, **Alzari PM** (2015) Secondary structure reshuffling modulates glycosyltransferase function at the membrane. ***Nat Chem Biol*** 11: 16-18. doi: 10.1038/nchembio.1694.

**Lisa MN**, Gil M, **André-Leroux G**, **Barilone N**, Durán R, Biondi RM, **Alzari PM** (2015) Molecular basis of the activity and the regulation of the eukaryotic-like S/T protein kinase PknG from *Mycobacterium tuberculosis*. ***Structure*** 23: 1039-1048. doi:

10.1016/j.str.2015.04.001. *Preview by* Reckel S, Hantschel O (2015) Kinase regulation in *Mycobacterium tuberculosis*: Variations on a theme. *Structure* 23: 975-976. doi: 10.1016/j.str.2015.05.005.

**Petrella S**, Capton E, Raynal B, Giffard C, Thureau A, Bonneté F, **Alzari PM**, Aubry A, **Mayer C** (2019) Overall structures of *Mycobacterium tuberculosis* DNA gyrase reveal the role of a Corynebacteriales GyrB-specific insert in ATPase activity. *Structure* 27: 579-589. doi: 10.1016/j.str.2019.01.004.

**Wagner T**, **André-Leroux G**, Hindie V, Barilone N, Lisa MN, Hoos S, Raynal B, **Vulliez-Le Normand B**, O'Hare HM, **Bellinzoni M**, **Alzari PM** (2019) Structural insights into the functional versatility of an FHA domain protein in mycobacterial signaling. *Sci Signal* 12: eaav9504. doi: 10.1126/scisignal.aav9504.

**Sogues A**, **Martinez M**, **Gaday Q**, **Ben-Assaya M**, Graña M, Voegele A, VanNieuwenhze M, England P, Haouz A, Chenal A, Trépout S, Duran R, **Wehenkel AM**, **Alzari PM** (2020) Essential dynamic interdependence of FtsZ and SepF for Z-ring and septum formation in *Corynebacterium glutamicum*. *Nat Comm* 11: 1641. doi: 10.1038/s41467-020-15490-8.

**Laboratory name** : Unité de Microbiologie Structurale – Institut Pasteur – CNRS UMR 3528 - Université de Paris.

**Research keywords** : **cryo-electron microscopy**, single particle analysis, cryo-electron tomography, *Corynebacterium glutamicum*, Actinobacteria, *Mycobacterium tuberculosis*, cell division, bacterial metabolism, DNA gyrase, bioinformatics.

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