

## Post-doctoral position in Structural Bioinformatics

**Organisation/Company:** Commissariat à l'Énergie Atomique et aux Énergies Alternatives (CEA) – Laboratory of Biocatalysis and Synthetic Metabolism (LBMS) and Laboratory of Bioinformatics Analyses for Genomics and Metabolism (LABGeM)

**Research Field:** structural bioinformatics, molecular modeling, comparative genomics, biocatalysis

**Profile:** First stage researcher (Post Doc)

**Application Deadline:** November 30, 2019

**Location:** France > Evry > Genoscope

**Type of contract:** temporary (CEA contract) - 24 months

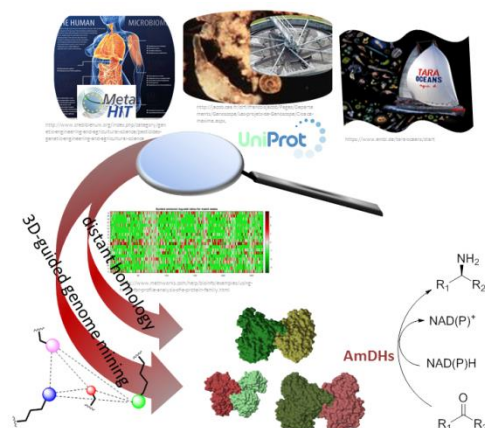
**Starting date:** April 2020

### Job description

The successful candidate will be a key member of a research project, MODAMDH, funded by the French Research Agency (ANR) and carried out in the Research Unit of Genoscope (CEA, CNRS, Paris-Saclay Univ., UMR8030). From its inception, Genoscope has been at the forefront of large-scale sequence-based science. Today, our institute performs biological and bioengineering research with applications in environment, healthcare and alternative energy. The Genoscope encompasses multidisciplinary team of ~100 staff with postdocs and engineers having expertise in genomics, bioinformatics, microbiology, biochemistry and biocatalysis.

The MODAMDH project aims at finding new amine dehydrogenases among biodiversity. It will be carried out by innovative approaches based on distant homology and 3D modeling of enzymes to mine massive (meta)genomic data. This project involved the biocatalysis (LBMS) and bioinformatics (LABGeM) teams of the Genoscope in collaboration with the York Structural Biology Laboratory (York, UK).

The candidate will be in charge of conducting bioinformatics analysis using cutting-edge methods in structural bioinformatics and sequence analysis. Large amount of candidate enzymes will be experimentally screened and selected hits will be characterized for biocatalysis application by a PhD student involved in this project. In addition, structural determination of the enzymes will be performed with another PhD student of the York laboratory.



### Qualifications

- PhD degree in bioinformatics or structural biology (a first experience in molecular modeling is essential)
- Technical skills:
  - o molecular modeling (*ab initio*/homology modeling, ligand docking, structural motifs)
  - o analysis of massive (meta)genomics data sets (comparative and functional genomics)
  - o programming skills and High-Throughput Computing
- Employability skills: strong communication and organizational skills, ability to work in a team-oriented environment, autonomy, good english skills are required and notions of french would be a plus.

### Publications of interest

Bastard K et al. Revealing the hidden functional diversity of an enzyme family. Nat Chem Biol. 2014 Jan;10(1):42-9. doi: 10.1038/nchembio.1387

de Melo-Minardi RC, Bastard K et al. Identification of subfamily-specific sites based on active sites modeling and clustering. *Bioinformatics*. 2010 Dec 15;26(24):3075-82. doi: 10.1093/bioinformatics/btq595

Mayol et al. A family of native amine dehydrogenases for the asymmetric reductive amination of ketones. *Nat. Catal*. 2019 Mar; 2:324–333. doi: 10.1038/s41929-019-0249-z

### **Contact details**

<https://bit.ly/2Zs2QEG>

Interested candidates should send their CV, statement of research interests, and contact information of at least 2 references to Carine Vergne-Vaxelaire ([carine.vergne@genoscope.cns.fr](mailto:carine.vergne@genoscope.cns.fr)) and David Vallenet ([vallenet@genoscope.cns.fr](mailto:vallenet@genoscope.cns.fr)).