



# Research engineer Structural Bioinformatics

2-year contract



## Context:

The [Protein-Interaction-Evolution \(PIE\) Cross-Disiplinary Project](#) aims to explore the role of protein-protein interactions in the evolution of biodiversity. By examining different levels of biological organization, the project seeks to understand how molecular interactions emerge, change, and diverge over the course of evolution, ultimately contributing to the remarkable diversification of life and the emergence of new species.

This project involves three different laboratories in Lille ([UGSF](#), [EEP](#) and [CRISTAL](#)) and the [Bilille bioinformatics and biostatistics platform](#), and is shared into 4 interconnected work packages. Work Package 4 is focused on the development of bioinformatics tools. In particular, WP4.1 is dedicated to the setup of methods for protein structure prediction.

In this context, the Bilille platform is hiring a research engineer for 2 years at the University of Lille, who will be supervised by the UGSF team that was at the origin of the MassiveFold software.

## Main activities:

- Generating predicted structures of many protein complexes on a GPU cluster with MassiveFold (AlphaFold2/ColabFold/AlphaFold3)
- Evaluating, adapting, and developing scoring functions to:
  - 1) estimate the quality of a structure prediction
  - 2) estimate the veracity of a predicted interaction (e.g. in PPI screening)
- Implementing relevant scoring functions in MassiveFold
- Developing a web server for MassiveFold and relevant scoring functions
- Analysing generated predictions (interfaces, conservation, key residues...)

## Associated activities:

- Ensuring support to users in utilizing MassiveFold (command line and web server)
- Getting involved in training connected to the main activities (at local and national levels with the IFB)
- Participating in the writing of publications

## Expected skills:

- Solid knowledge of structural modeling (AlphaFold, Pymol, scoring methods...)
- Solid programming skills in a Linux environment (Python, bash)
- Good practices in reproducibility (Git, Conda), knowledge of Docker and NextFlow would be appreciated
- Very good knowledge of web programming
- Being able to interact with people of diverse profiles (bioinformaticians, biostatisticians, biologists, biochemists)
- Technical English (B2)

## Specificities of the position:

You will work in the CNRS building on the Haute Borne campus in Villeneuve d'Ascq, next to Lille, where the UGSF team is located, as well as in a Bilille-associated office on one of the three university campuses, in order to facilitate exchange with the other Bilille-engineers.

**Degree required:** master, engineer or PhD in bioinformatics, computer science or biochemistry with solid skills in structural bioinformatics and programming.

**Contract:** 2-year contract, starting November 2025 at the earliest.

**Salary:** in function of experience, following the University salary grid.

**Application deadline:** Applications will be accepted until the position is filled.

**Contact :** Applications have to be sent to [bilille@univ-lille.fr](mailto:bilille@univ-lille.fr) and [guillaume.brybaert@univ-lille.fr](mailto:guillaume.brybaert@univ-lille.fr). The file should contain: **CV, letter of motivation and at least one letter or name of a reference.**