



## WE ARE HIRING A DEVELOPER IN COMPUTATIONAL BIOPHYSICS

### **JOB DESCRIPTION**

Sibylla Biotech is looking for an outstanding and highly-motivated developer in computational biophysics to join its multidisciplinary team located in Trento (Italy). The company, Sibylla, is the exclusive licensee of an innovative technology named Pharmacological Protein Inactivation by Folding Intermediate Targeting (PPI-FIT) which enables the identification of small molecules that promote the degradation of a target protein by interfering with its folding pathway. Such a new technology paves the way for selectively degrading previously undruggable proteins. The application of our computational platform allows us to characterize previously unexplored protein conformations (folding intermediates) that can be exploited as new drug targets. The computational methods developed by Sibylla Biotech have recently been used to design new pharmacological strategies for prion diseases [Spagnolli et al. 2021] and for COVID-19 [Massignan et al. 2021].

### **YOUR ROLE**

You will take part in the development of computational methods for the simulations and characterization of protein folding pathways at atomic-level of resolution. You will work closely with the internal software development team to improve Sibylla's computational platform.

Your tasks will primarily include:

- design and programming of enhanced sampling algorithms to study protein folding;
- design and programming of clustering schemes;
- refinement, improvement, and maintenance of the production pipeline;
- participation in scientific meetings for the dedicated tasks.

### **IDEAL CANDIDATE**

The ideal candidate should hold a Master's degree in physics, chemistry, engineering, computer science or computational biology. A PhD in related fields is desirable but not mandatory. The requirements for eligibility are:

- deep knowledge in programming. Python is mandatory, experience with C/C++ and web development is welcomed;
- deep knowledge of algorithms and data structure;
- experience in working with the UNIX environment;
- experience with molecular dynamics simulations software (e.g., Gromacs, NAMD, Amber...);
- basic knowledge in biophysics.

Fluency in English, high predisposition to problem-solving, marked enthusiasm for research, and willingness to work in a team are also mandatory.

**WHAT WE OFFER**

You will be part of a highly cross-disciplinary environment. Scientists in our company come from diversified scientific areas, such as theoretical physics, computer science, medicinal chemistry, and biology. You will have opportunities to break new grounds. Our company is fast-growing, which means there will be excellent opportunities for promotions. You will be given responsibilities and we will fully support your professional growth, always giving extreme importance to your personal needs. Last but not least, we also offer a competitive salary. Sibylla Biotech is an equal opportunity employer, freedom from discrimination is a fundamental human right.

Start of the activities: July - September 2022.

**HOW TO APPLY**

Interested applicants should submit a cover letter including research accomplishments and interests, CV, and contact information of at least two professional references to [hiring@sibyllabiotech.it](mailto: hiring@sibyllabiotech.it), specifying 'Developer in computational biophysics' in the mail object.