Postdoctoral position in structural bioinformatics

The **Vrije Universiteit Brussel (VUB)**, in collaboration with the **Universiteit Gent (UG)**, is seeking candidates for a **postdoctoral position in structural bioinformatics**. The research project will investigate how sequence-based predictions of protein characteristics can be fully exploited on a large statistical scale to better understand their experimentally observed behavior, especially in relation to folding events, protein stability and post-translational modifications. It connects **structural bioinformatics** (Wim Vranken at the Structural Biology Brussels (SBB), VUB), **machine learning** (Tom Lenaerts at the Artificial Intelligence group (AI), VUB) and **proteomics** (Lennart Martens at the Computational Omics and Systems Biology Group, UG). The successful candidate will be mainly located at the (IB)^2 Interuniversity Institute of Bioinformatics in Brussels (http://ibsquare.be), an institute that brings together the science, engineering and medical faculties of VUB and the Université Libre de Bruxelles (ULB) in a collaborative and open atmosphere. The focus of the (IB)^2 is on interdisciplinary research, with expertise in machine learning, big data, rare diseases, oligenic disorders, network analysis, genome analysis, metagenomics and structural bioinformatics.

Research context: The interactions and function of proteins are determined by their dynamics and conformations. Proteins can adopt context-dependent and interchanging conformations, as illustrated by allosteric changes induced by binding events or by post-translational modifications. Local sequence-based interactions between amino acids have a large influence on these preferential conformations, even when long-range stabilizing interactions are present.

In this project, we investigate the influence of such local interactions on the behavior of proteins, from folded to intrinsically disordered. These analyses are possible through novel and unique tools and databases developed by our groups, such as DynaMine (http://dynamine.ibsquare.be), Start2Fold (http://start2fold.eu) and PepShell (http://compomics.github.io/projects/pepshell.html). The successful candidate will gather further relevant experimental data from public databases and literature and connect these data to results from sequence- and structure-based predictions in order to construct innovative computational approaches that can guide new experimental work in protein folding, stability and post-translational modifications.

Offer: A **full time postdoctoral position** for the duration of 3 years funded by the Research Foundation – Flanders (FWO), pending a review after the first 6 months.

Required:
- The candidate holds a PhD degree in Sciences, Bio-engineering Sciences, or a related field.
- Excellent programming and computer science skills, preferably in Python.
- Excellent communication skills in English: within the context of this project you will be interfacing with scientists of different backgrounds.
- Publication in peer-reviewed international scientific journals.
- The candidate is open to collaborative work between the research groups and willing to work in both Brussels and Gent, which are within easy reach by both car and public transport.

Desirable:
- Experience in the area of structural bioinformatics, with focus on the prediction and simulation of conformation and dynamics of proteins.
- Experience in protein folding, stability and/or post-translational modifications.

Contact: Please submit a 1) cover letter detailing your background and interest in this position, 2) a full C.V. and 3) at least two references (with name, email, address, phone number) via email to wvranken@vub.ac.be, or via mail to: Wim Vranken, Structural Biology Brussels, Pleinlaan 2, B-1050 Brussels, BELGIUM.

Application deadline: Please submit your application before the 5th of January 2016.