

STRUCTURAL BIOINFORMATICS POST-DOCTORAL POSITION AVAILABLE at the Institute of Biology and Chemistry of Proteins, (Lyon, France).

One post doctoral position is opened in LYON (France) for 2 years in the Bioinformatics and NMR Structural team of the Institute of Biology and Chemistry of Proteins (<http://www.ibcp.fr>).

“Impact of structural mutation on phenotype. Construction of 3D models analyzed by new structural bioinformatic tools and set up of a relational database. Application to proteins involved in human myopathies”.

Context :

Our bioinformatic group headed by Pr G. Deléage comprising 15 people (<http://pbil.ibcp.fr>) is involved for a long time in the development of methods and software/webware for protein function and structure prediction. In the field of protein sequence analysis, we provided to the biologist community ANTHEPROT (<http://antheprot-pbil.ibcp.fr>) and MPSA (<http://mpsa-pbil.ibcp.fr>) software and NPS@ Web server (<http://npsa-pbil.ibcp.fr>). The latter integrates in a user-friendly interface 48 analysis methods, 12 databases and it is connected to the SRS system. It performs more than 3000 analysis per day. For the protein structure prediction and analysis, we have developed the Geno3D (<http://geno3d-pbil.ibcp.fr>) and SuMo (<http://sumo-pbil.ibcp.fr>) Web servers which construct molecular models of protein using a molecular modeling under restraints protocol and search for known active sites. More recently we have also developed relational databases in particular in the Hepatitis C virus field with EC funds.

Tasks :

The successful candidate will develop new methods and tools for studying the impact of mutation at the 3D level on the phenotypic behavior of proteins involved into human myopathy. This work will be performed in collaboration with the group of O. Poch at IGBMC (Strasbourg, France) and thus implies several trips (Lyon – Strasbourg - Paris). The works will consists in i) the 3D modelling of protein of interest, ii) the building of a relational database to store the 3D information related to mutation, iii) the use of the developed tools to deduced generic rules that can be further tested on others proteins. The database will contain the proteins models and will be integrated with a Web server including tools to analyze structures and mutations. The Web server will be developed in close coordination with the PIG (Protein InvestiGator) Web server developed in the team by Dr E.Bettler. The successful candidate will also develop new algorithms to perform analysis and prediction of the structural impact of mutations. A knowledge of proteins involved in human myopathy will be positively considered..

Required qualifications :

Applicants are expected to have :

- a PhD in Bioinformatics or equivalent training with a good knowledge of biological macromolecule structures.
- an experience with Internet software development and relational database under the Linux operating system (Python, PostgreSQL).

Salary:

~1700 euros net of charge

Duration : 2-years, starting on January 2005

Contact:

We encourage candidates to send applications including a detailed *curriculum vitae*, statement of research interests and name of 2 referees. Applications and further inquiries should be sent to :

Dr. E. Bettler or G. Deléage
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