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

One post doctoral position is open in LYON (France) for 3 years in the Bioinformatics and NMR Structural team of the Institute of Biology and Chemistry of Proteins (http://ww.ibcp.fr).

"Development of structural bioinformatic tools to analyze viral resistance to treatment in the context of the european Hepatitis C Virus database"

Context :
Our group (http://pbil.ibcp.fr) is involved since 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's 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. The main biological thematic of the team is the Hepatitis C Virus (HCV) and we have developed the HCV DataBase (HCVDB: http://hepatitis.ibcp.fr). This database offers public access to all automatically annotated HCV sequences (genomes and proteins) by keyword queries with SRS or by standard biocomputing tools. The database is now part of two projects funded by the European community (HepCVax EC FP5 and viRgil EC FP6). Moreover, the team is the co-founder of the PBIL (http://pbil.univ-lyon1.fr) and "Pôle Rhône-Alpin de BioInformatique".

Tasks :
The successful candidate will develop the 3D european HCV database (3D-euHCVdb) in close coordination with euHCVdb currently developed in the team. The database will contain the 3D models of HCV proteins 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 any new algorithms to perform analysis and prediction of viral resistance to drugs.

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 (Java, Python, PostgreSQL).

Candidates with a background in structural Virology (especially in HCV) will be preferred.

Salary:
~1690 euros net of charge

Duration : 3-years, start on 1st november 2004

Contact:
We encourage candidates to send applications before Friday September 17th 2004, including a detailed *curriculum vitae*, statement of research interests and name of 2 referees. Applications and further inquiries should be sent to :

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