Driving scientific projects

1. HSLVU-INHIB - Le protéasome "bactérien" HslVU, cible thérapeutique potentielle pour lutter contre les protozoaires parasites

Andrey Kajava (coordinator and member of the infrastructure)

CRBM Montpellier, BONUS QUALITÉ-RECHERCHE, Université Montpellier 1 (2009-2010), and Grant of Programme Interdisciplinaire CNRS " Maladies Infectieuses Emergentes" 2009.

The project is aimed to analyse the known 3D structure of the HslVU proteasome, to identify pockets for binding of peptides and design peptide activators and inhibitors of HslVU proteasome of Leishmania. The goal is to develope efficient drugs against ***Leishmania*** and other parasites. This project implies developments to contribute to WP 3.3

2. HPASSB - High Performance Algorithms for Structural Systems Biology

David Ritchie (coordinator and member of the infrastructure)

Orpailleur-Nancy , ANR-08-CEXC-017-01

The objective of this project is to develop algorithms for protein-protein docking, based on shape analysis. The target programs are: HexServer, Eigenhex, KDD-Dock, PPI-Dock, and 3D-Blast projects.

3. DOVSA-Developing Novel Virtual Screening Algorithms(UE project)

David Ritchie (coordinator and member of the infrastructure)

Orpailleur-Nancy, FP7-People-2009-IEF-254128.

This Marie Curie grant is funding the DOVSA project. The proposal will allow large selections of potential compounds targeting disease-related proteins to be screened, and it will facilitate the introduction and take-up of novel shape-based screening approaches. This will benefit the pharmaceutical and biotechnology industries.

4. BREAKABOND- Design of protein-protein interaction inhibitors : application to nucleosome assembly chaperones.

Françoise Ochsenbein (coordinator) Raphaël Guerois (member of the infrastructure)

RPBS-Aplibio, ANR Jeunes chercheurs 2007-2010, ARC equipment 2009.
This project explores *in silico* design strategies to disrupt the formation of protein complexes using small cell-penetrating peptides. The part of the project
dedicated to molecular modelling aims at (i) extracting the binding epitopes involved in protein recognition (ii) stabilizing, (iii) tethering and (iv) optimizing the
interactions at the interface them so as to reach sufficient affinity. Starting from a 10µM initial hit, a 50 nM affine peptide has now been reached. The
development of automatic screening approach in WP 3.3 will help identifying suitable scaffolds to transfer these peptides into peptidomimetic compounds.

5. SM2PH-DB : From Structural Mutation to Pathology Phenotypes in Human databases

Gilbert Deléage (Coordinator)

PRABI-IBCP, Decrypthon grant, 2004-2007

The main objective of this project is to develop bioinformatic tools to understand the functional and structural impact of mutations in the Duchene myodystrophy. This Decrypthon grant is funding the MS2PHDB, MODEOME and MAGOS projects incorporated into the high- throughput annotation and structural modelling environment (3.1).

6. MAPREDUCE: Scalable data management for Map-Reduce-based data-intensive applications on cloud and hybrid infrastructures

Christophe Blanchet (coordinator), 2010-2014

PRABI-IBCP/BISI, ANR, programme Arpège

The main objective of this project is to explore advanced techniques for scalables, high-throughput, concurrency-optimized data and metadata management. This project is improving SuMo software to be incorporated into the high- throughput annotation and structural modelling environment (3.1).

7. Modeling of Biomolecules and their Interactions

Marie-Dominique Devignes (coordinator, member of the infrastructure)

ReNaBi-NE,LORIA -, CPER (50% Lorraine region, 50% INRIA).

This local research platform is developing interdisciplinary research activities in bioinformatics focusing on the introduction of knowledge-based approaches for the study of protein-protein and protein-ligand interactions. The proposal will help the LORIA platform to become fully connected to the ReNaBI network and infrastructure. It will help local researchers gain access to resources and expertise at regional and national levels. It will promote the introduction and coordination of bioinformatics resources in a consistent way. This program contributes to WP3.2 and WP3.3

8. DOCK - flexible Docking par des approches métaheuristiques parallèles hybrides.

E-G Talbi (coordinator and member of the infrastructure)
INRIA- DOLPHIN - Lille, ANR Calcul sur Grilles, 2007-2010
The three imperative research directions in present day's molecular modelling: (1) the search for mathematical models of maximum simplicity that nevertheless provide a relevant description of molecular behaviour, (2) the development of powerful distributed optimization algorithms for sampling the molecular energy surface for stable, populated conformations, and (3) deploying those intrinsic distributed algorithms on computational Grids. This approach will be generalized to include intermolecular degrees of freedom, turning it into a flexible docking procedure. Developments will contribute to WP 3.3.

9. SensingWithArf (ANR) (Coord. B. Antonny, IPMC) 2008:

Sensing lipid membranes with Arf dependent molecular machineries. This ANR funds the Heliquest server.

10. FRAGSCREEN (ANR) (Coord. J.-F. Guichou, CBS) ANR-07-JC-JC-0046-01,

Fragment-based Hit Hunting : development of in silico and experimental fragment screenings with the objective to Integrate cheminformatics and molecular modeling
activities in experimental studies performed by X-ray crystallography and NMR. This ANR funds the e-LEA3D server.

Collaboration and service

1. **PROTEUS**

T. Simonson (coordinator), J.F. Gibrat (partner, member of the infrastructure).

ANR grant 2007-2010

This project aims at detecting "remote" homologs, i.e., homologous proteins whose sequences have undergone many mutations, insertions and deletions. Such proteins have sequences that are no longer sufficiently similar to be detected as homologs by sequence comparison methods. The purpose of the project is to use fold recognition and inverse folding methods to analyse "orphan" protein sequences in bacterial genomes. Orphan protein sequences are those sequences in sequenced genomes that apparently do not look similar to any known protein (this represents between 20 to 40% of the total number of genome protein sequences depending on the bacterial species analyzed).

2. BOND

J Samitier (coordinator, Barcelona University) J.F. Gibrat (partner, member of the infrastructure)

European grant 2009-2011

The Bond project proposes a new bioelectronic nose based on olfactory receptors in order to mimic the animal nose. For this aim, micro/nano, bio and information technologies will converge to develop an integrated bioelectronic analytical nanoplatform based on olfactory receptors for odour detection. More precisely our task is to identify the olfactory receptor(s) relevant to detect an odorant of interest (ORMODEL tool)

3. TB-Hits - Relationships between horizontal transfers and virulence in tubercle bacilli: Searching for new drug targets to fight tuberculosis.

P. Deschavanne (coordinator, member of the infrastructure)
RPBS-aplibio, ANR MIE 2009-2013.
The TB-Hit ANR project (coord. P. Deschavanne, Mti - RPBS) addresses the emergence of multidrug-resistant and extensively drug-resistant forms of Tuberculosis.
The aim of this project is to identify new mycobacterial genes/proteins involved in the development of tuberculosis using new approaches: *i.e.* genes acquired by
horizontal transfer, to put in evidence their polymorphisms and to study their functions in order to propose targets, candidates to the conception of new specific drugs.
In this project RPBS is in charge for 3D characterization of candidate targets.

4. HPGenVar - Homologous recombination and genetic variability in Helicobacter pylori

P. Radicella (coordinator) Raphaël Guerois (partner 1, member of the infrastructure)
RPBS-Aplibio, ANR 2009-2013.
This project aims at analyzing the origins of the high genetic variability in Helicobacter pylori genome. At the root of this plasticity, the genes encoding the DNA repair
machineries have themselves extensively diverged. Sequence analysis coupled to structure prediction of the diverged genes can thus provide important hints about the
impact of the variability into the pathogen cellular functions. The platform will be useful to analyze remote homologies, perform structure prediction to improve the
annotation of rapidly diverging sequences as found in the H. pylori.

5. Protein structure based strategies for antigen discovery and vaccine development against malaria and other pathogens

G. Corradin (coordinator) A. Kajava (partner, member of the infrastructure).
ReNaBi-GS (CRBM). This project is linked to the European patent application 05018052.0 “Antigenic peptides and their use”Inventors: G. Corradin and A.V. Kajava
and its US application IB2006/002232 Inventors: G. Corradin A. Jafarshad, P. Druilhe and A.V. Kajava .
Ongoing activity on clinical tests of some vaccine candidates is supported by a grant of European Malaria Vaccine Initiative (2009-2010) (Coordinator G. Corradin).
Bioinformatics part of this work consists of analysis of the P. falciparum genome in order to select appropriate peptides of the parasite proteins for further experimental
tests. It is related to WP 3.3.2.

6. CRAZYPOLYSACCHARIDES

William Helbert (coodinator; CNRS Roscoff); B. Henrissat (partner, member of the infrastructure)
ReNaBi-GS ANR Chimie et Procédés pour le Développement Durable 2008-2011.
Screening of carbohydrate-active enzymes on a collection of polysaccharides with known and unknown structures to identify novel sugar-cleaving enzymes.

7. E-TRICEL

Pedro Coutinho (coordinator; AFMB Marseille); B. Henrissat (partner, member of the infrastructure)
ANR Programme National de Recherche sur les Bioénergies Dec 2008 - Nov 2012
Exploring enzymatic diversity to complement the secretome of Trichoderma reesei to improve lignocellulose saccharification.