

RPBS PLATFORM

IT resource platform for Structural Biology

SCIENTIFIC EXPERTISE

- Analysis and structural prediction of proteins and small compounds scaffold
- 7 associated laboratories
- Member of bioinformatics networks (APLIBIO, IFB and IBiSA)
- Partner of the national project MobyLe

APPLICATIONS

- Sectors: pharmaceuticals, medicine, health

TRACK RECORD

- >10 industrial partnerships

PUBLICATIONS

Shen Y & al. *J. Chem. Theor. Comput.* 10:4745-4758 (2014)

Labbé C & al. *Nucleic Acids Res.* 43(W1):W448-54 (2015)

Guyon F & al. *Nucleic Acids Res.* pii: gkv492. (2015)

CONTACT

Mail : bd-services@idfinnov.com

Phone : +33(0)1.80.05.65.01

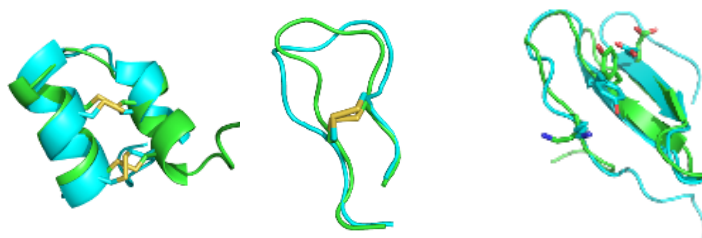
- Structural Bioinformatics
- Prediction of protein conformation
- Structure-based peptide design
- SLiMs

SERVICE DESCRIPTION

The platform results of the joint effort of several academic research teams in Paris. Their objectives, since the launch of the project in 2003, were to promote a common resource around Structural Biology problematics. Through the specific expertise of the founders of the platform, the core of the analysis conducted on the platform concerns small endogenous peptides (hormones, neuropeptides) or small exogenous compounds (such as toxins or antimicrobial peptides). However, they are not limitative and may be extended to other applications.

The main covered themes are:

- Analysis and modeling of protein's structures and functions,
- Structure and toxicity of small compounds for therapeutic use,
- Identification and study of interaction partners (protein-protein, protein-drug).



PEP-FOLD: prediction of de novo peptide structure

OFFER

- Secured access via a dedicated web portal MobyLe@RPBS
- > 30 programs and software for analysis, modeling, measuring the toxicity and study of interactions
- Advice to biologists.
- Training in structural biology methods
- Tutorials
- 3D printing services