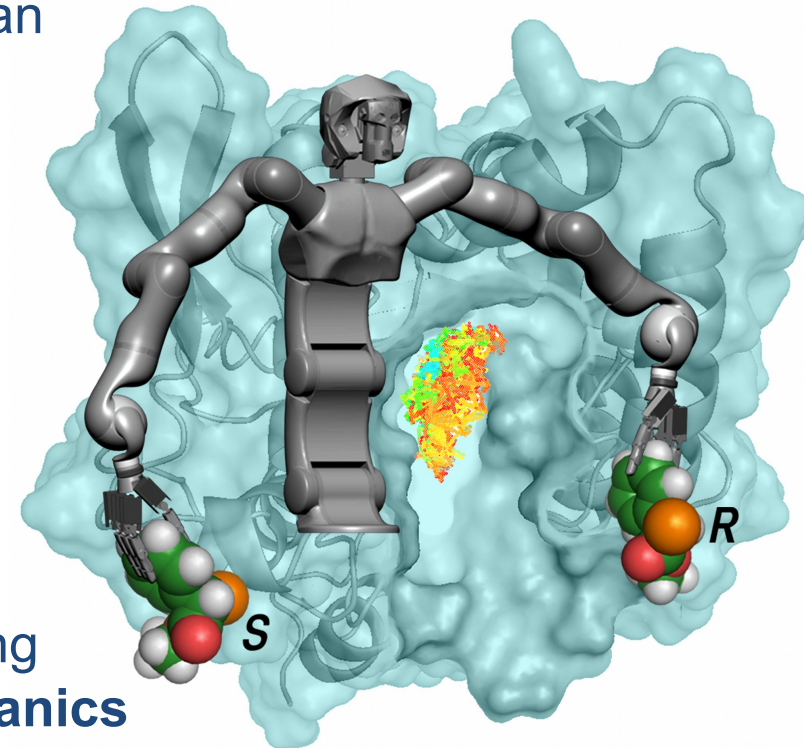


Molecular modeling methods for novel health and environmental applications

ALIVE axis

- > **Model-based computational methods** are an essential complement to experimentation for accelerating the **development of new technologies**
- > **Multidisciplinary approach:** collaboration between physicists, chemists, biologists and computer scientists
- > **Novel methods** based on multi-level modeling and efficient algorithms **inspired from mechanics and robotics**



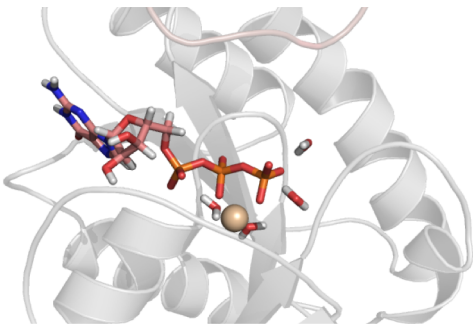
Novel Molecular Modeling Approaches

> Design
> Decision making

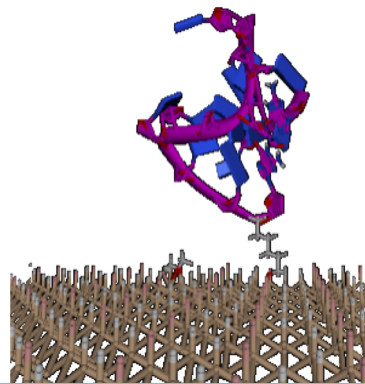
> Guide/control experiments

> Characterization
> Help understanding

> Health



> Bio/nano-technologies

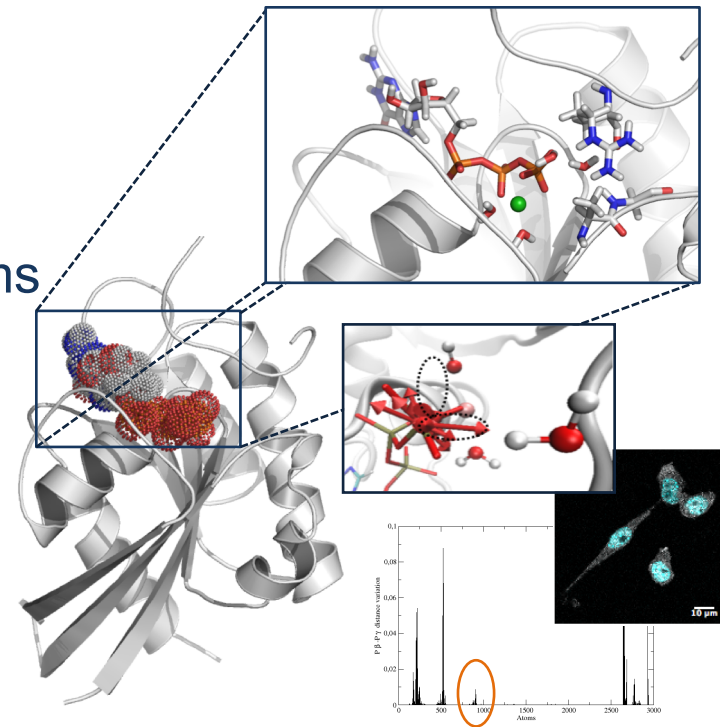


> Environment



- > **Software Development:**
- > Algorithmic modules : <http://projects.laas.fr/Psf-Amc>
- > Web servers : <http://moma.laas.fr> [Devaurs *et al.*, NAR, 2013]
- > Application programs : <https://homepages.laas.fr/mbrut/>

- > Molecular modeling for the understanding of **mechanisms of drug action and resistance**
- > **Goal:** modulate protein function
- > **Challenge:** multi-level/methods requirements
- > **Mechanobiology + quantum chemistry** algorithms to access both protein structure and activity
- > Applications: **cancer-type targeted therapies, drug resistance, drug receptors...**



[Brut et al., J Phys Chem B, 2011]

[Tichauer et al., Biophys J, 2018, *in revision*]

> **Collaborators:**



Funding:



- > Modeling/design of **antibodies for immunotherapy** and **cyclic peptides for inhibition of protein interactions**
- > **Goal:** enhance affinity/specificity/stability
- > **Challenge:** highly-flexible molecules
- > **Coupling efficient robotics-inspired exploration algorithms and molecular modeling tools**
- > Applications: *vaccines, diagnostic tests, caspase inhibition (apoptosis), ...*

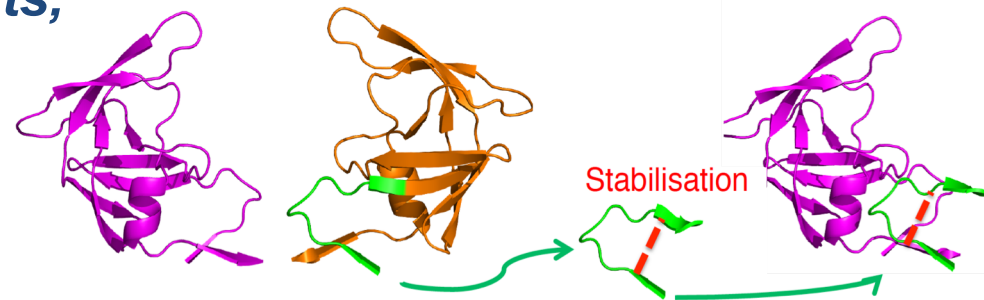
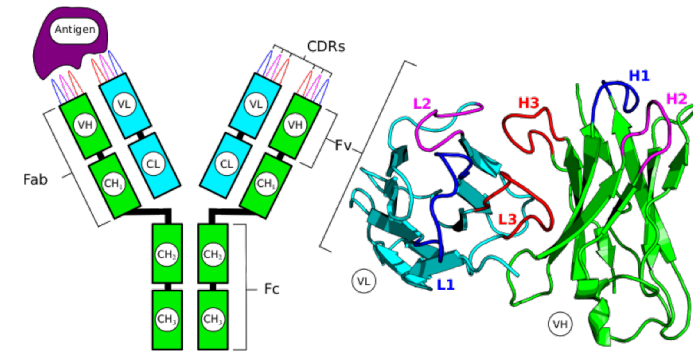
[Barozet et al., Immunol. Lett., 2018]

[Jusot et al., JCIM, *submitted*]

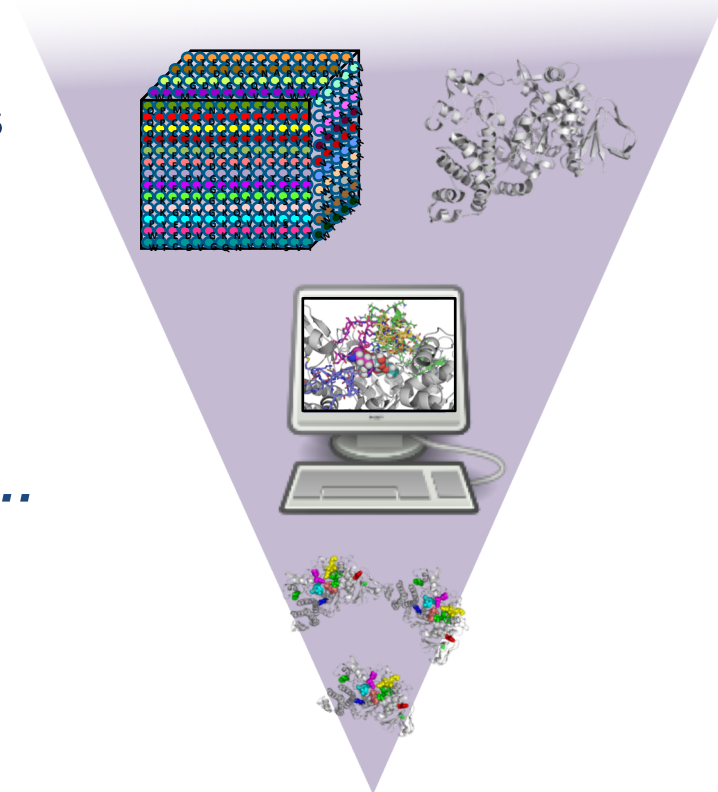
- > **Collaborators:**



- Funding:**



- > **Enzyme design** for diverse applications in biotechnologies
- > **Goal:** produce new enzymes with new functions or improved properties with respect to natural proteins
- > **Challenge:** huge number of possible sequences
- > **Computation Protein Design (CPD)** algorithms reduce the time and cost of developments
- > Applications: ***eco-friendly bioprocesses, valorization of renewable carbon resources, ...***
- > Software prototype : ***CUSTOZYME***



[Lafaquière et al., ChemBioChem, 2009]

[Molloy et al., IJRR, 2018]

> **Collaborators:**



Funding:



- > **Design and functionalization of DNA** for biological sensing and imaging applications
- > **Goal:** integrate active functions into nanodevices
- > **Challenge:** bio / non-bio interface
- > **Sequence design + molecular dynamics** algorithms to predict sensor structure and properties
- > Applications: **DNA-based sensors, quantum dots for medical imaging**

[Trapaidze et al., APL, 2015]
 [Brut et al., APL, 2012]

> **Collaborators:**

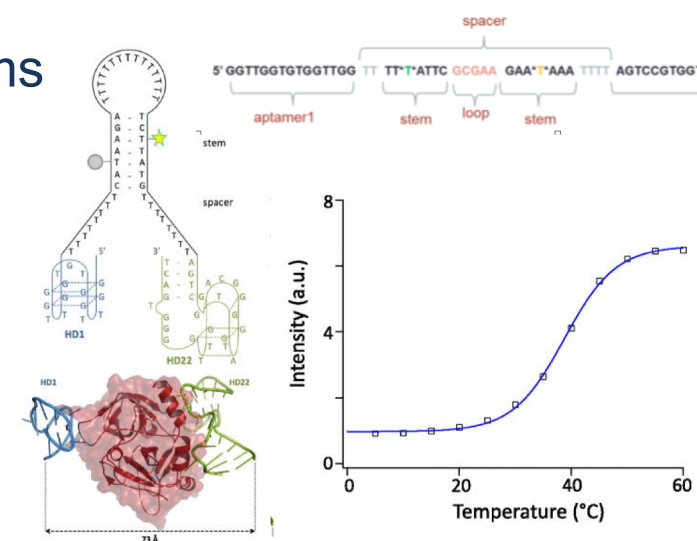


Funding:

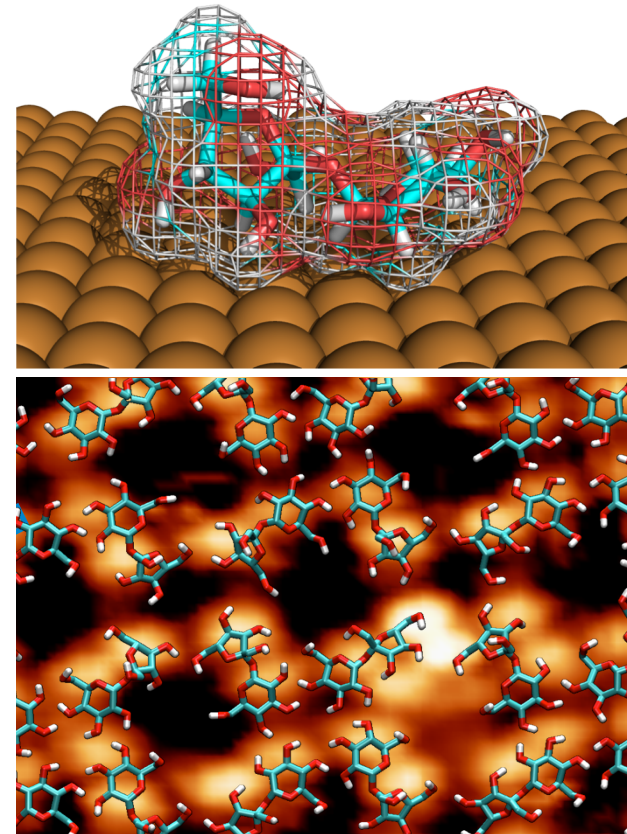


```

./Optim_spacer
Choose Input file (0) or Interactive input (1) : 1
Sequence of the first aptamer (use capitals) :GGTTGGTGGTTGG
Sequence of the second aptamer (use capitals) :AGTCCGTGATAGGGCAGTTGGGGTGACT
Number of bases in each stem strand : 8
Number of bases without complementary in each stem strand : 6
Number of bases in the loop : 8
Number of I spacers on apta1 : 0
Number of T spacers on apta2 : 0
DNA concentration (in M) : 0.001
Na concentration (in M) : 0.15
Sort solutions by free energy (0) or melting temperature (1): 1
generated file:
-----
Sequence | dH (kcal/mol) | dS (cal/K.mol) | dG37°C (kcal/mol) | Tm
-----
CATCGCAAAAAAAAAATCGCGATG -63.100002 -166.300003 -8.842521
CGAAGCTTAAAAAAAAAAGCTTCG -60.000000 -160.199997 -7.602521
CGAAGCTTAAAAAAAAAAGCTTCG -60.000000 -160.199997 -7.602521
GCCGAGATAAAAAAAAAATCTTCGC -59.700005 -159.599991 -7.502521
GCCGAGATAAAAAAAAAATCTTCGC -59.700005 -159.599991 -7.502521
GCCGAGATAAAAAAAAAATCTTCGC -59.700005 -159.599991 -7.502521
    
```



- > Modeling **biomolecules on surfaces**
- > **Goal:** Predict structural and kinetic properties of complex molecular systems
- > **Challenge:** bio/non-bio interface, weak interactions
- > **Synergistic coupling of experimental techniques and multi-model computational methods**
- > Applications: *implants (biocompatibility), physical scaffolding, pharmaceutical applications, imaging, ...*



[Abb et al., *in preparation*]

[A. Hémerlyck et al. APS, 2017]

> **Collaborators:**

IR CP Institut de Recherche de Chimie Paris



MAX-PLANCK-GESELLSCHAFT



CEMES



Toulouse

Funding:



Université de Toulouse

- > Efficient tools to accelerate the development of new technologies
- > Reinforce collaborations with experimentalists and technologists at LAAS
- > Open to new external collaborations in different application domains

