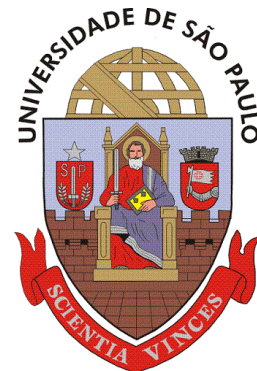
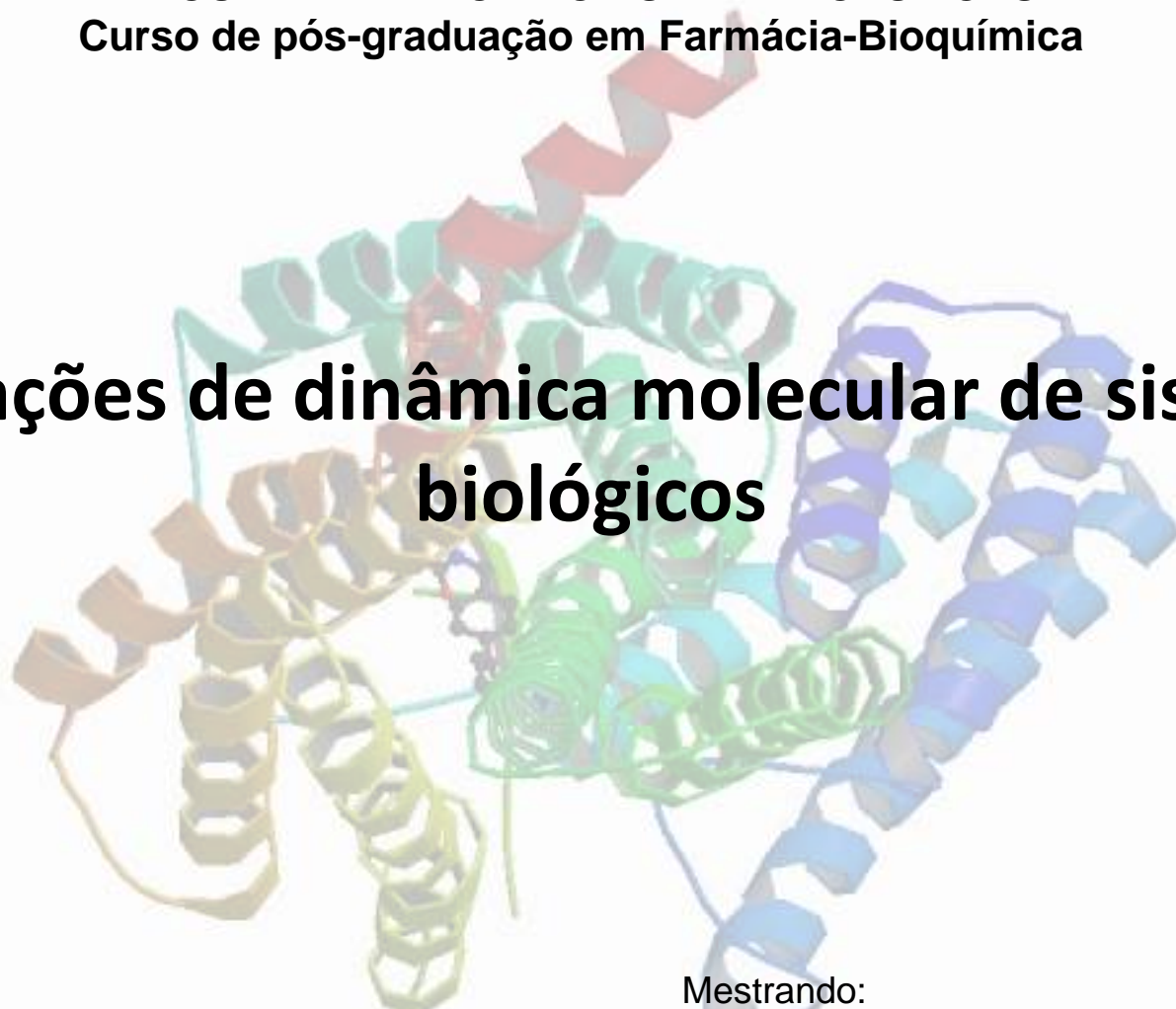




UNIVERSIDADE DE SÃO PAULO
FACULDADE DE CIÊNCIAS FARMACÊUTICAS
Curso de pós-graduação em Farmácia-Bioquímica



Simulações de dinâmica molecular de sistemas biológicos



4°. Workshop de High Performance Computing – Convênio: USP – Rice University

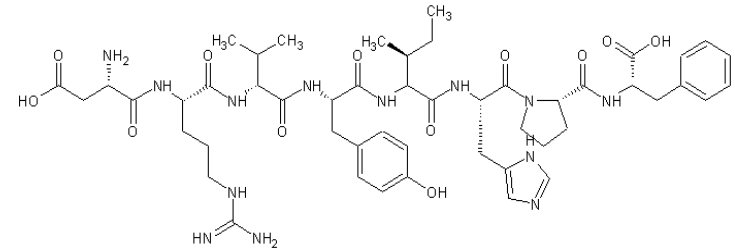
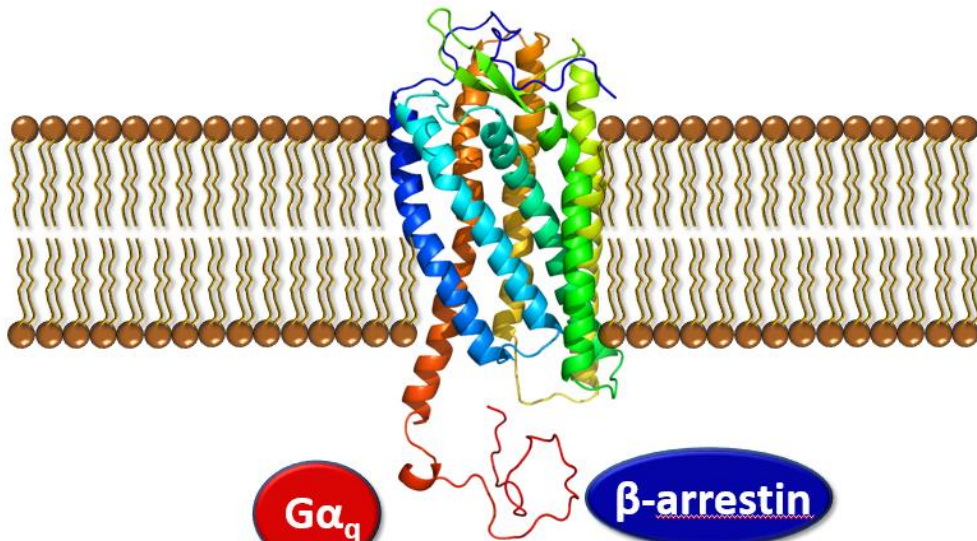
São Paulo, 17 de Outubro de 2016

Mestrando:
Silvestre Massimo Modestia

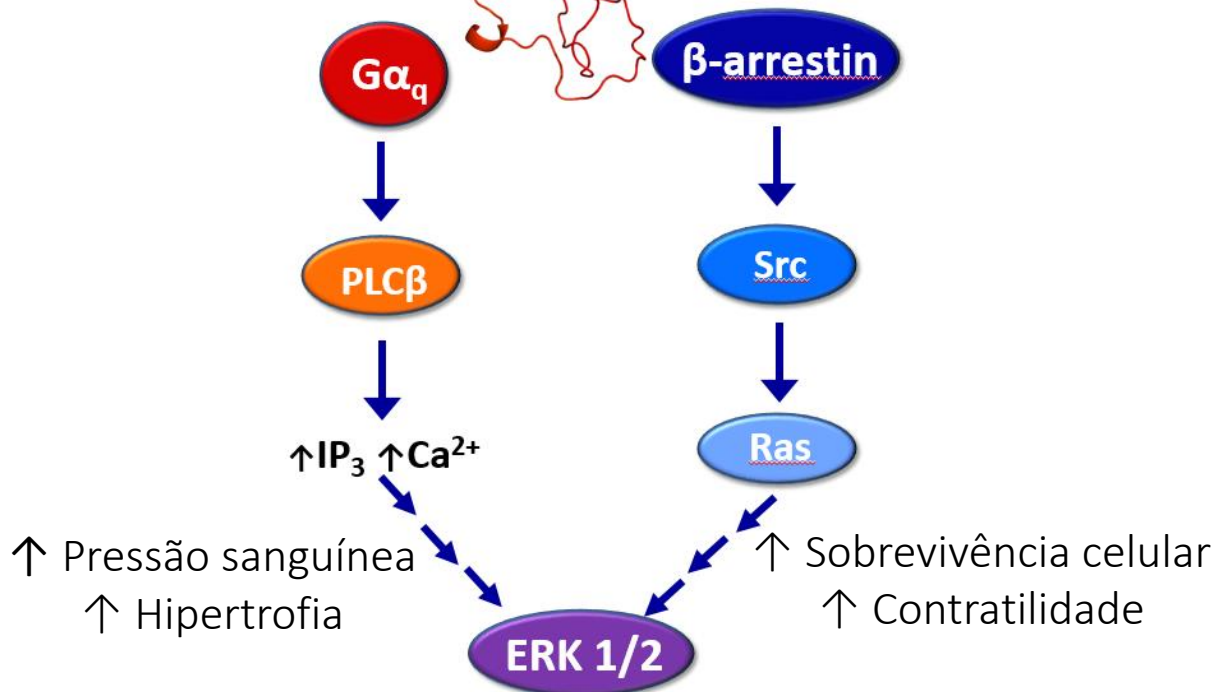
Orientadora:
Profa. Dra. Carlota de Oliveira Rangel-Yagui

Introdução

AT1 receptor

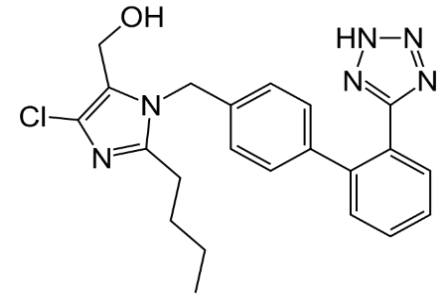
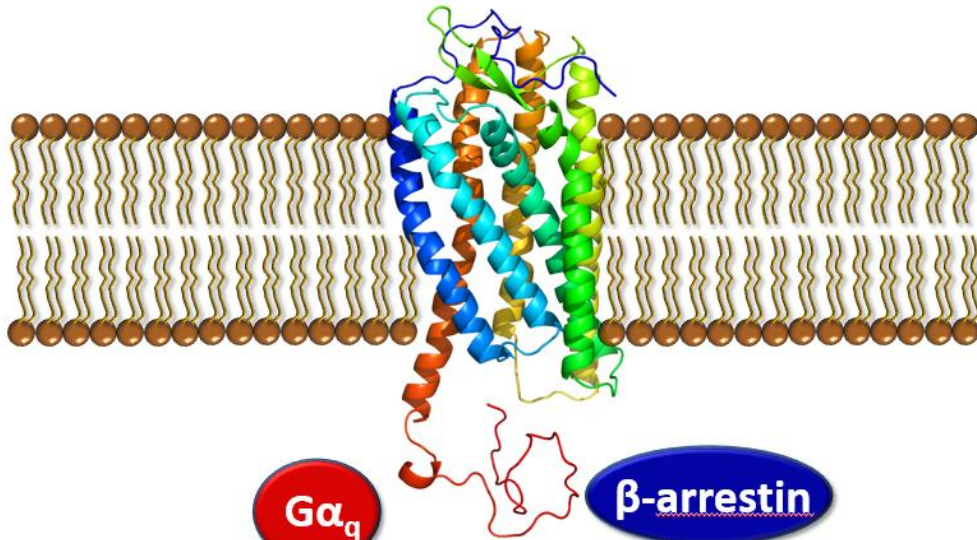


**Agonista total
(Angiotensina II)**

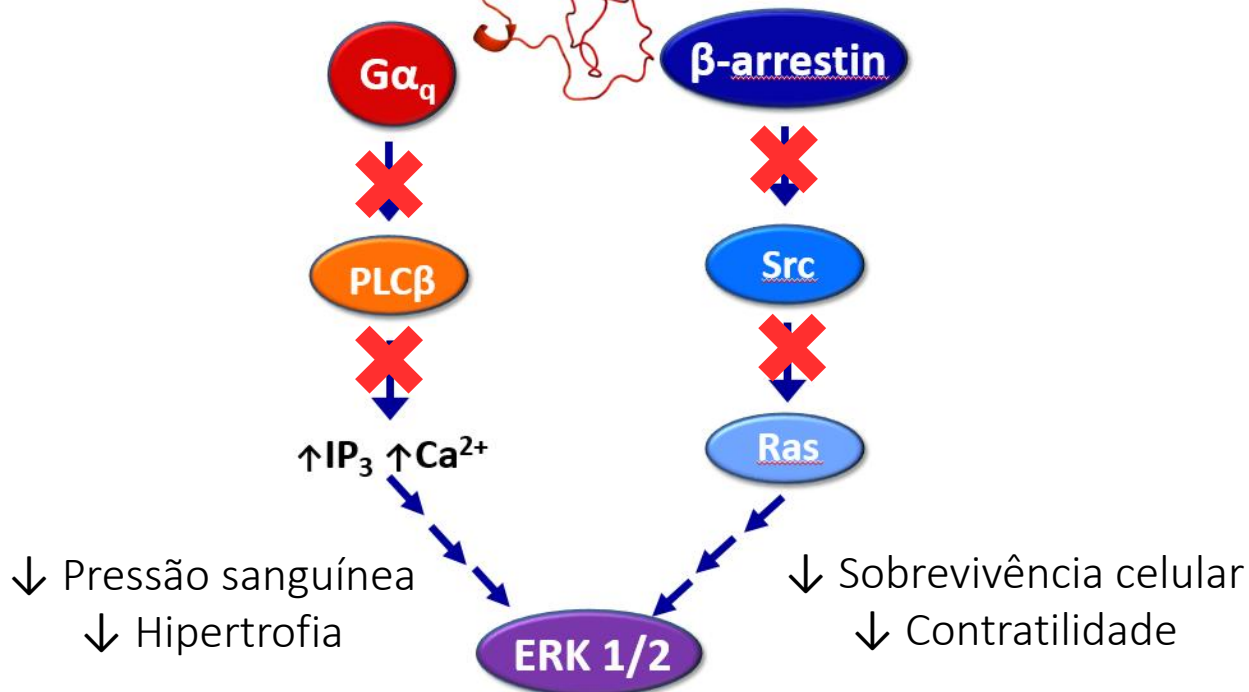


Introdução

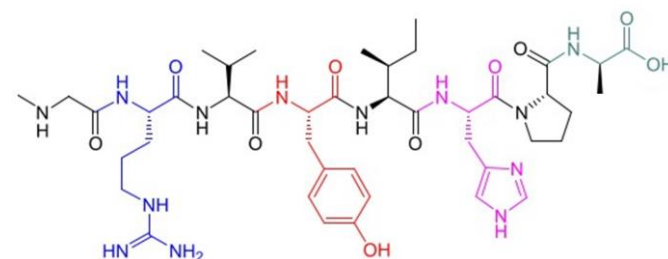
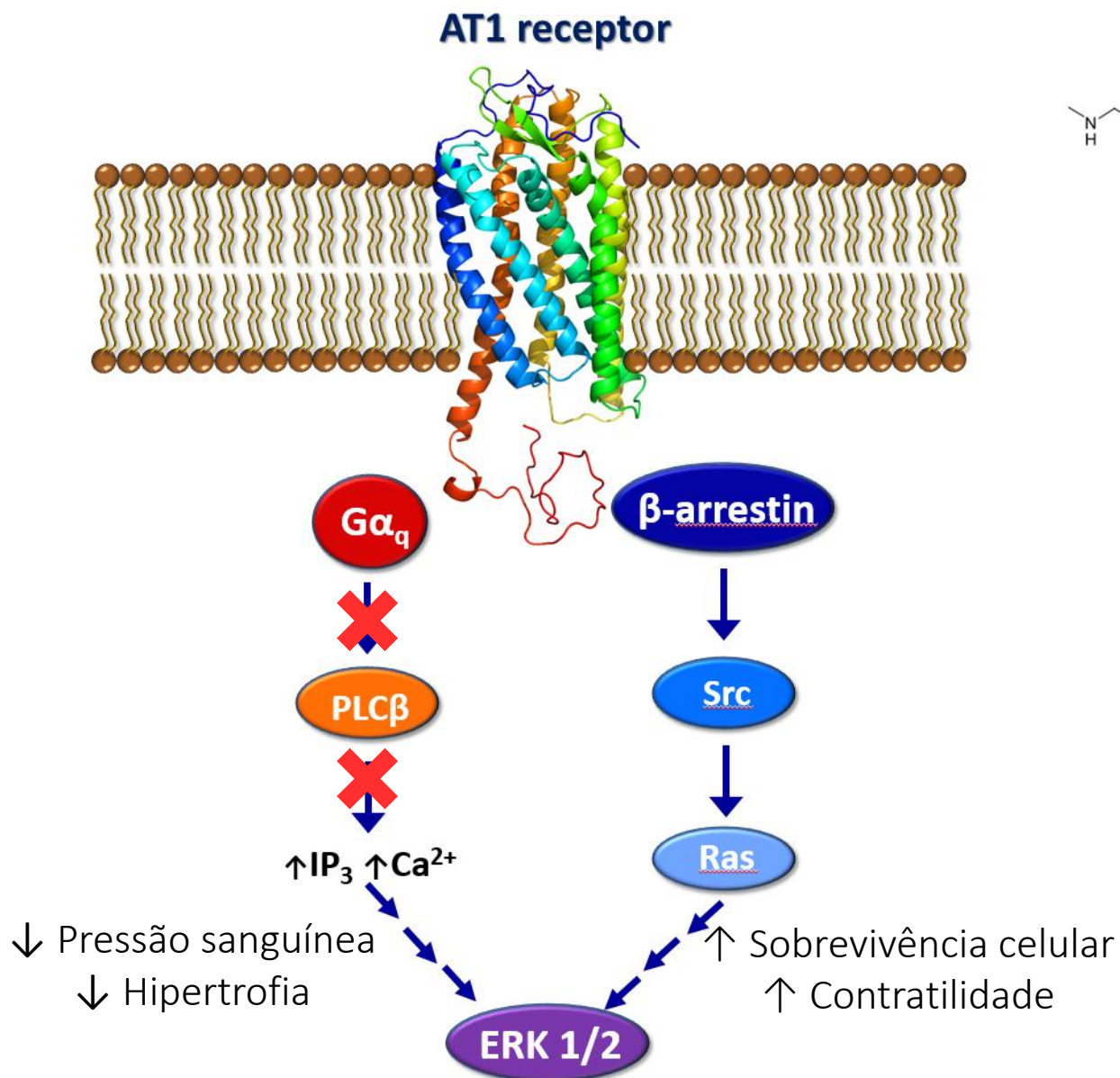
AT1 receptor



Antagonista
(Losartana)



Introdução



**Agonista enviado
(TRV27)**

Nova abordagem

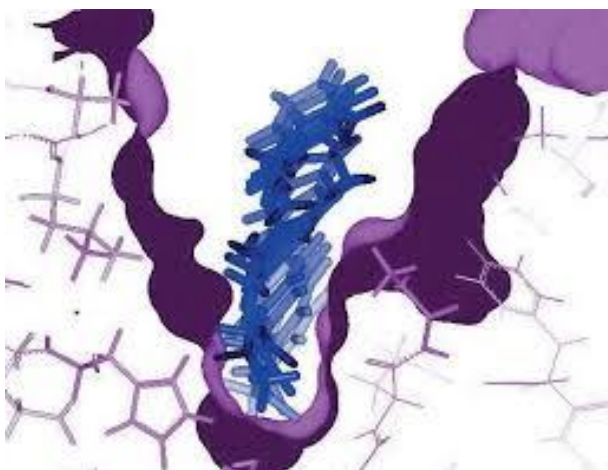
Introdução

Modelagem Molecular

Ancoramento Molecular (*docking*)

➤ Predição da conformação de um ligante no sitio de um receptor.

- Método de amostragem.
- Predição de afinidade.

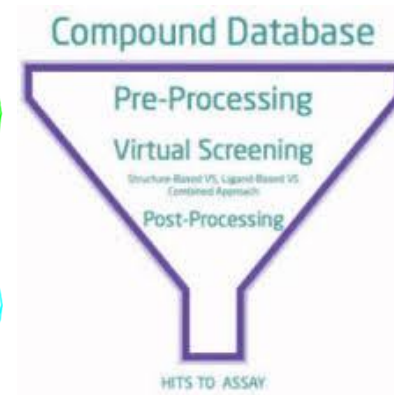
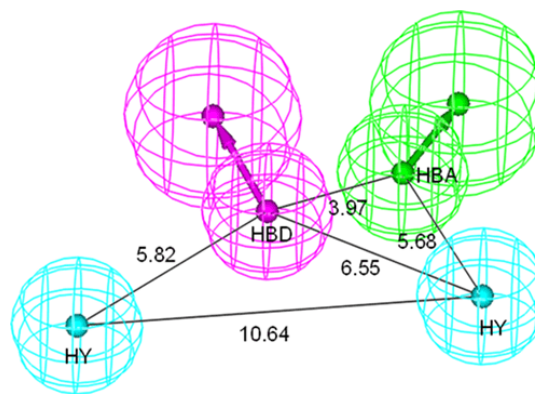


Dinâmica Molecular (DM)

➤ **Campo de força:** Conjunto de parâmetros e funções usadas para descrever a energia potencial de um sistema.

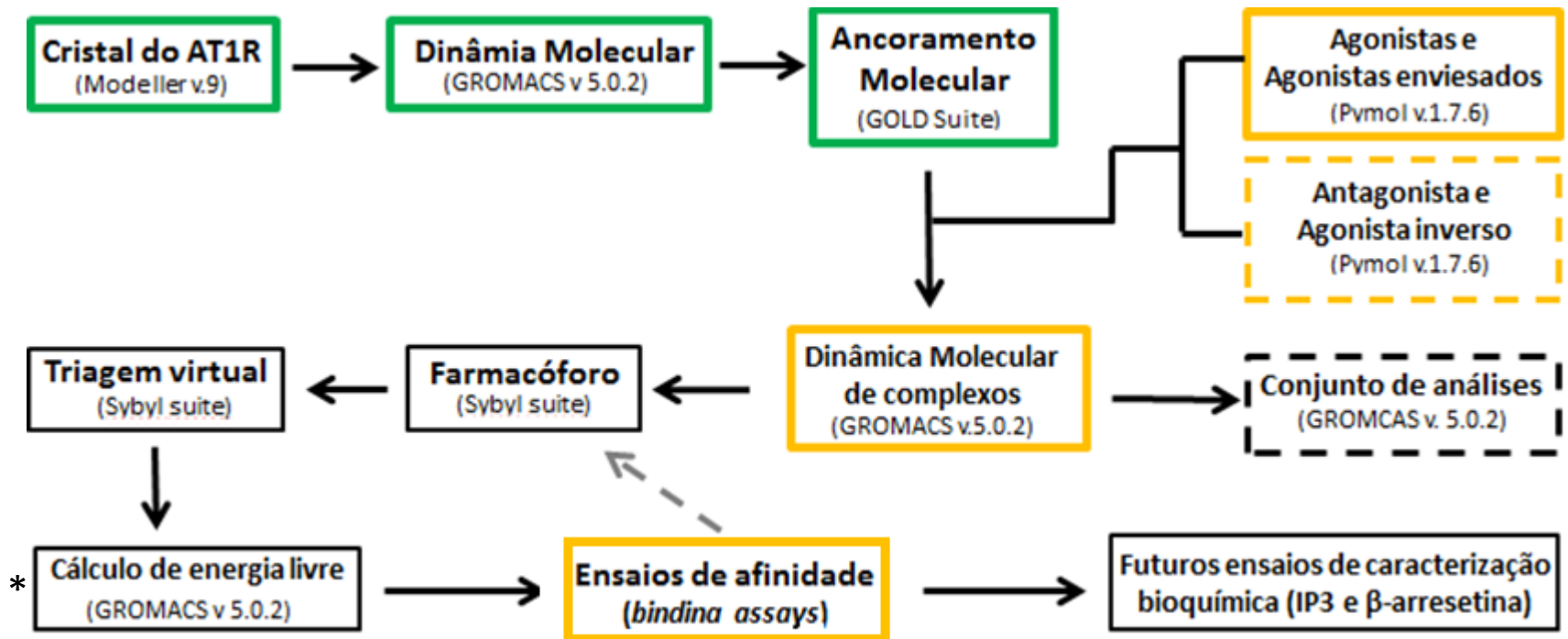
$$E_{\text{tot}} = E_{\text{str}} + E_{\text{bend}} + E_{\text{tors}} + E_{\text{vdW}} + E_{\text{elec}} + \dots$$

Farmacóforo e Triagem virtual



Objetivo

Planejamento de ligantes não peptídicos com atividade agonista enviesada para o receptor AT1.



— Concluído
— Em andamento
— Não concluído

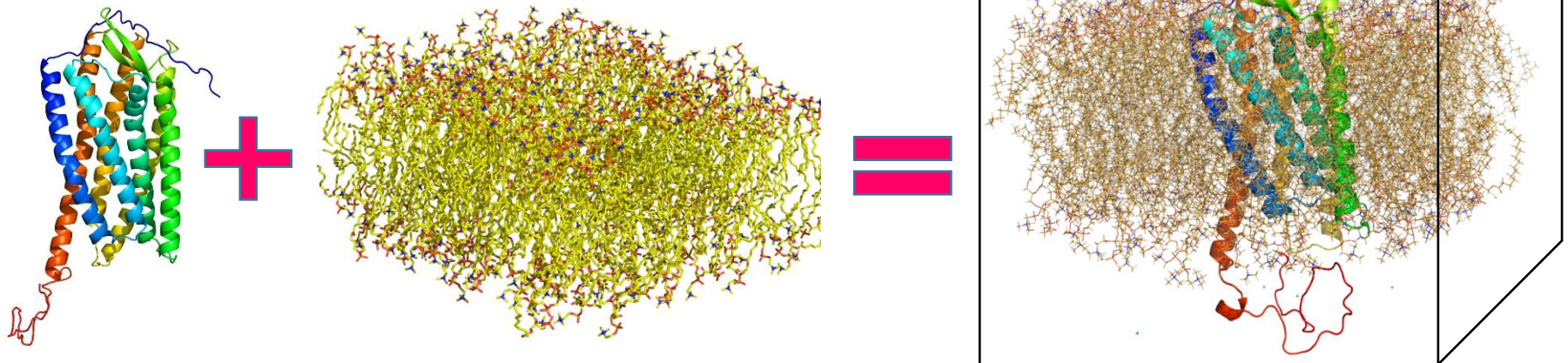
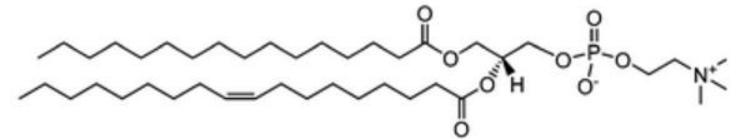
— Projeto
- - Abordagem complementar

Metodologia

Dinâmica molecular (DM)

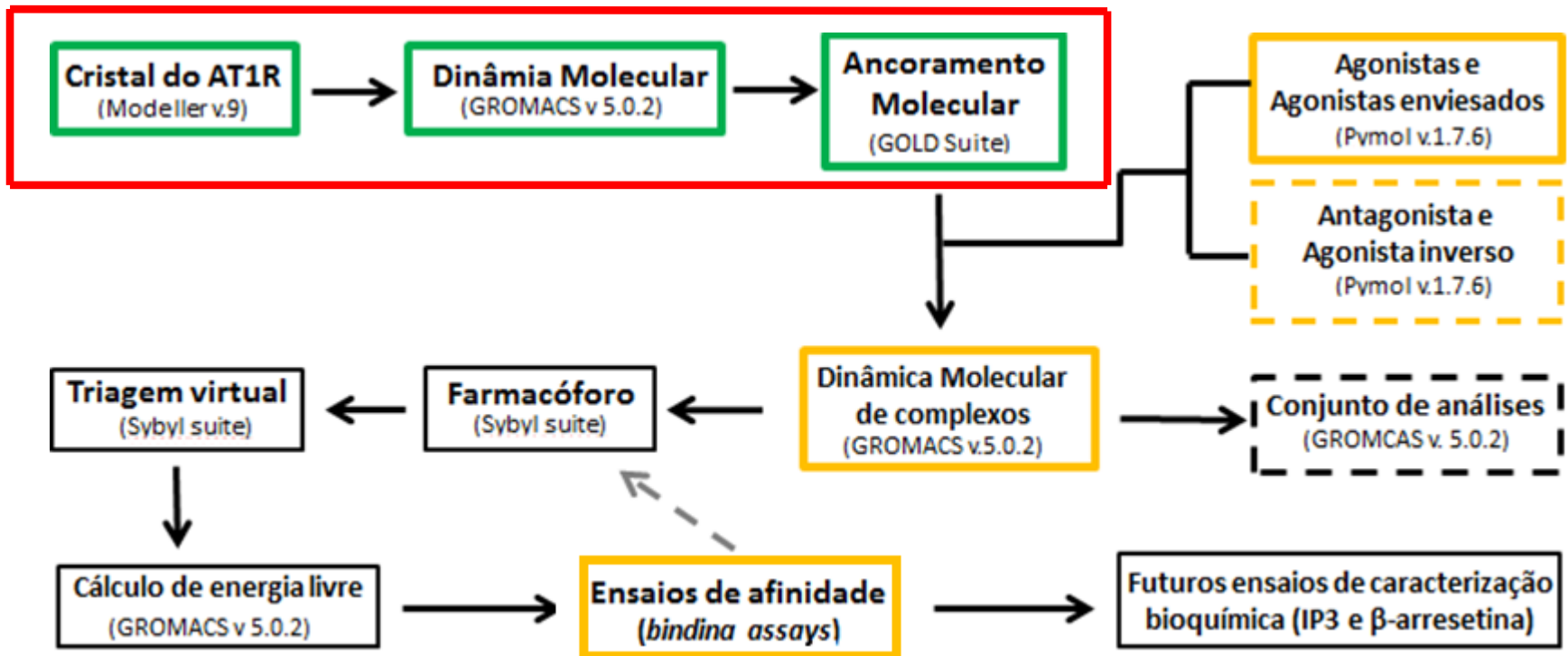
- GROMACS v. 5.0.5 (Abraham *et al.*, 2015).
- CHARMM36 (Best *et al.*, 2012).
- *High Performance Computing*, HPC-USP.
- Bicamada de POPC (Klauda *et al.*, 2010).
- InflateGRO (Kandt *et al.*, 2007).
- 10 simulação de 200 ns = 2 μ s.

Palmitoil-oleil-fosfatidilcolina (POPC)



Resultados Parciais

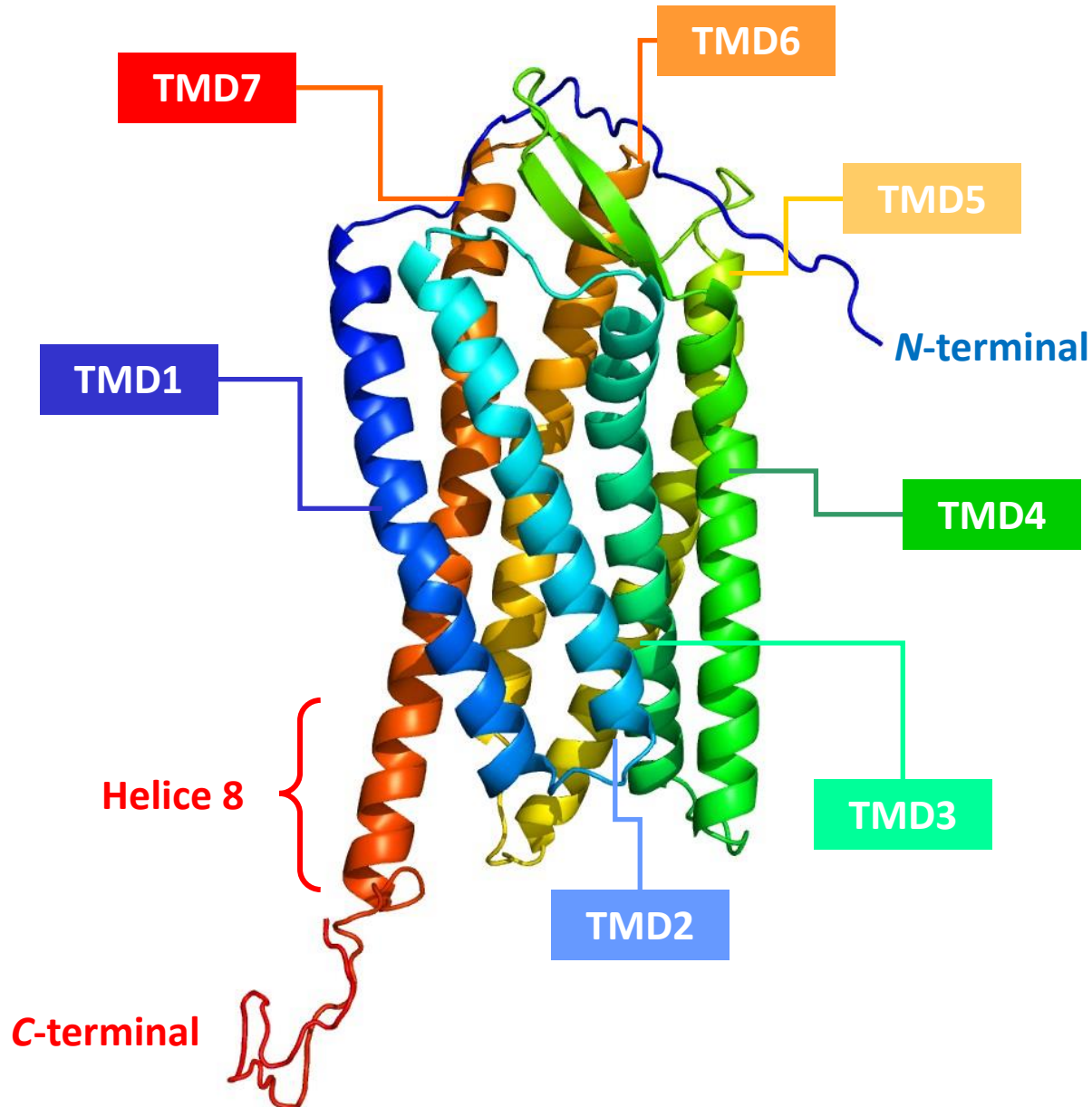
Resultados Computacionais



- Concluído
- Em andamento
- Não concluído

- Projeto
- Abordagem complementar

Estrutura do receptor completo



Resultados Parciais

Dinâmica Molecular

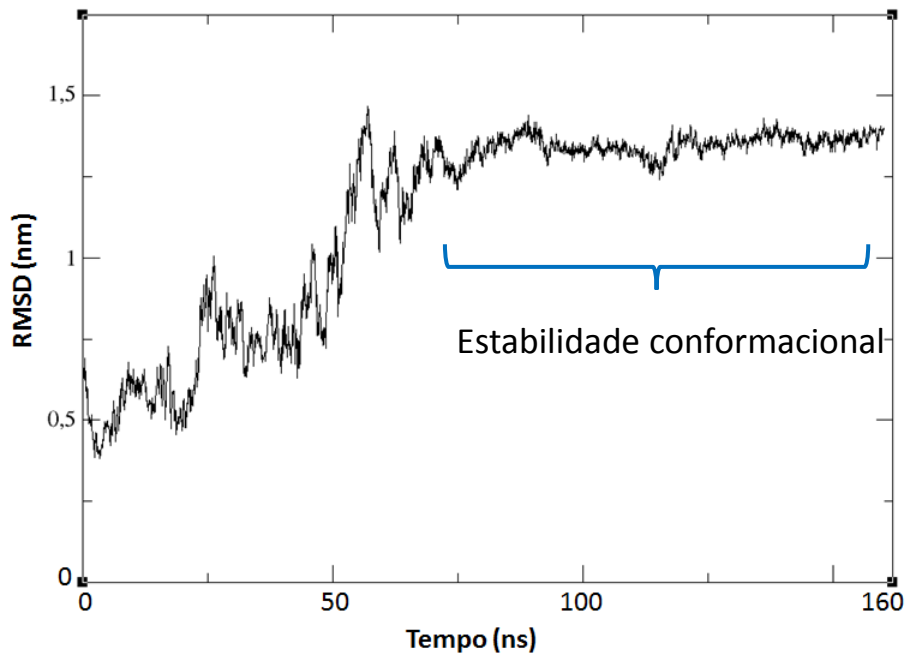
$$RMSD(t) = \sqrt{\frac{1}{N} \sum_{i=1}^N (x_i(t) - x_i(0))^2}$$

N = Número de átomos i = posição atômica

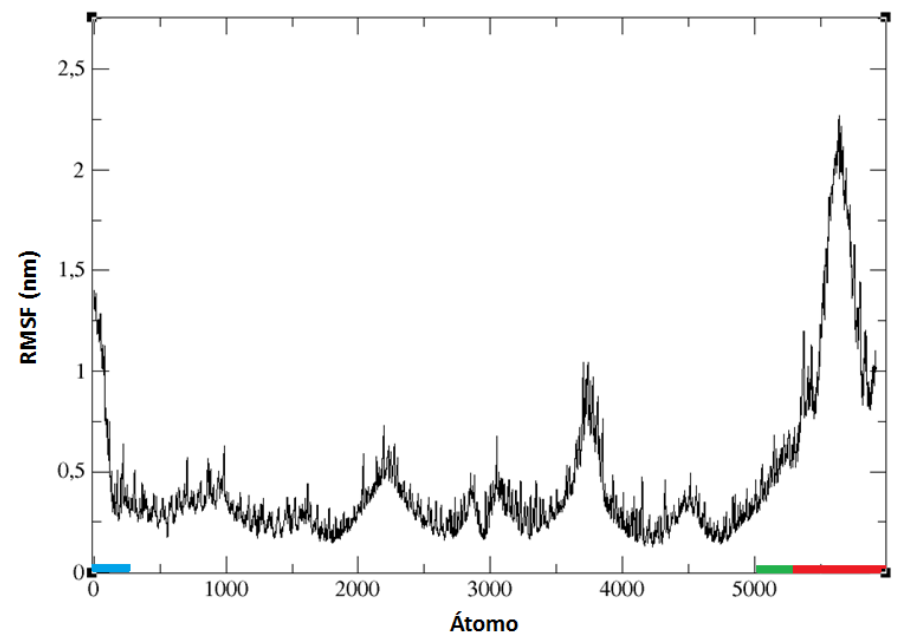
$$RMSF(i) = \sqrt{\frac{1}{T} \sum_{t=1}^T (x_i(t) - \bar{x}_i)^2}$$

T = Número de frames i = posição atômica

**Gráfico de desvio quadrático médio das posições atômicas
(RMSD)**



Flutuação do Desvio Quadrático Médio (RMSF)

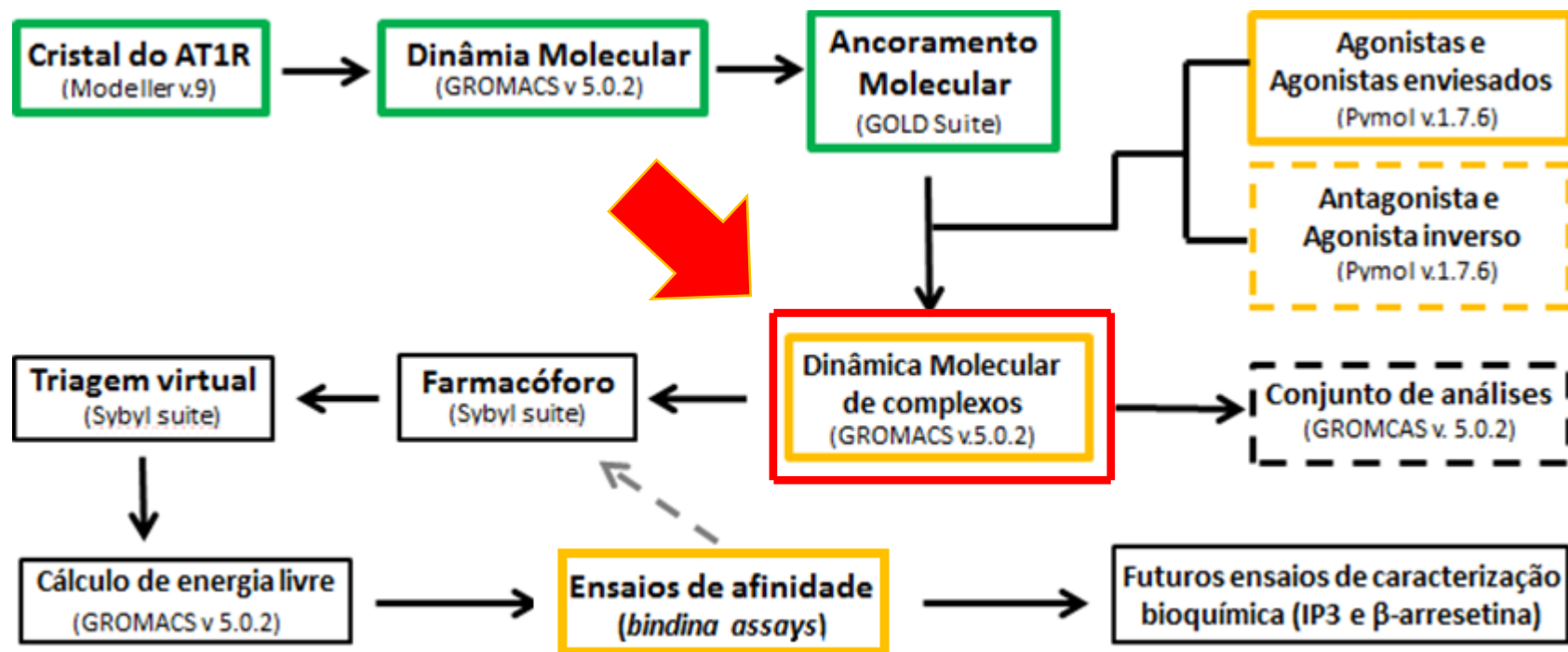


N-terminal

C-terminal

Resultados Parciais

Resultados Computacionais



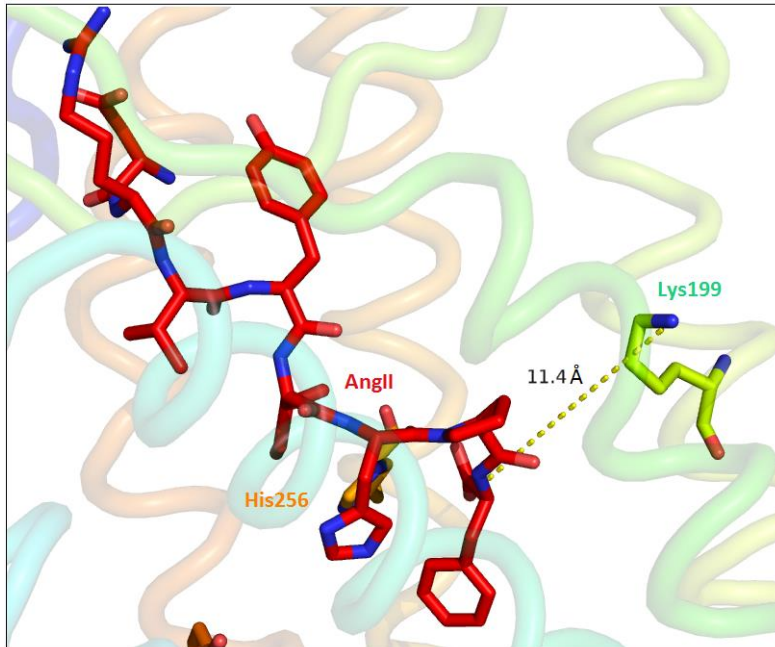
— Concluído
— Em andamento
— Não concluído

— Projeto
- - Abordagem complementar

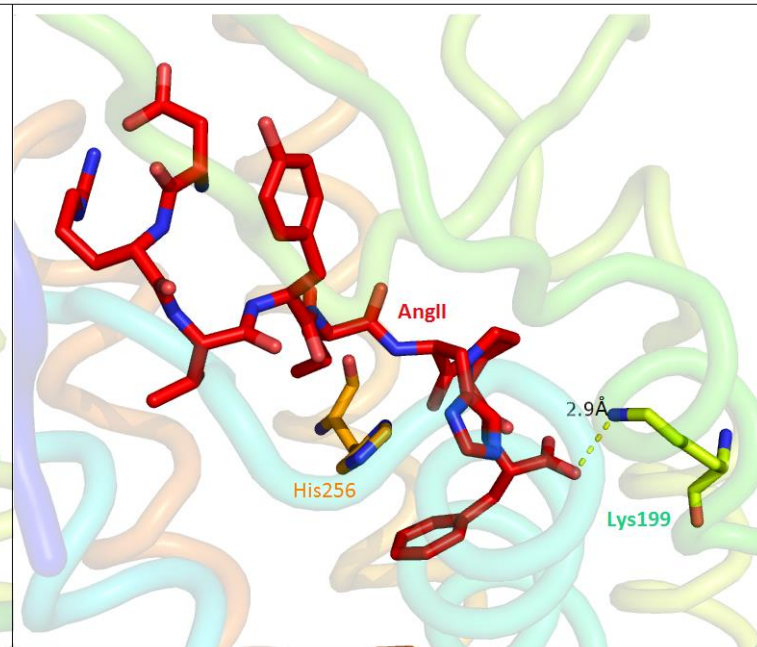
Resultados Parciais

Simulated Annealing

0 ns



3 ns

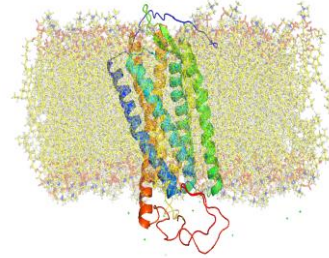


Tempo (ps)	0	200	400	500	600	700	800	900	1000	1200
Temperatura (K)	310	600	700	800	700	600	500	450	400	310

Outros projetos

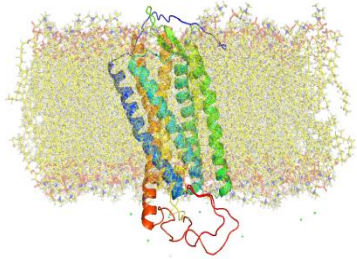
Força

Shear stress

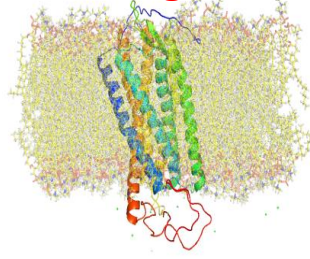


Ligantes

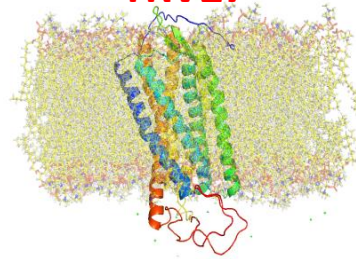
∅



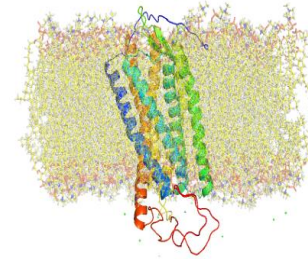
AngII



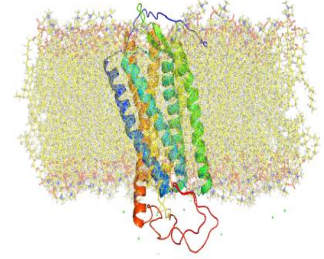
TRV27



Losartana

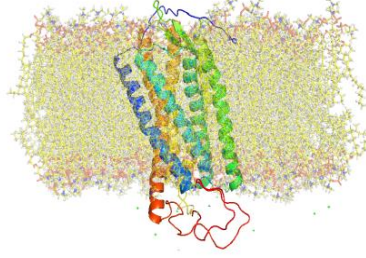


Olmesartana

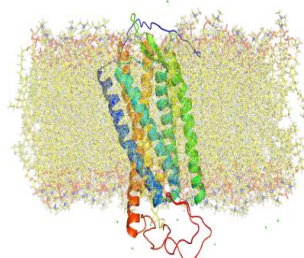


Mutantes

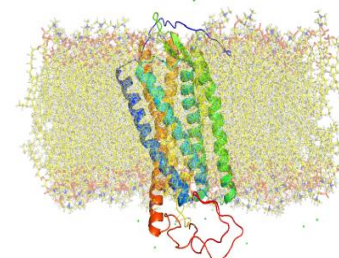
N111G



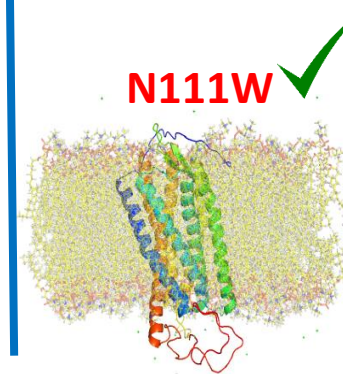
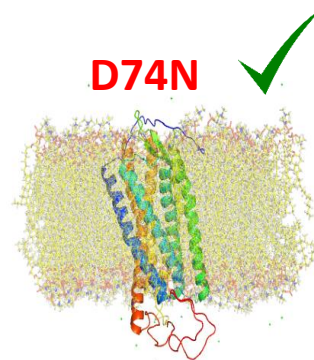
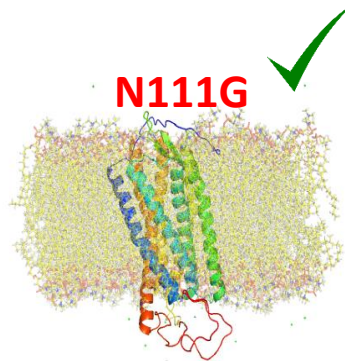
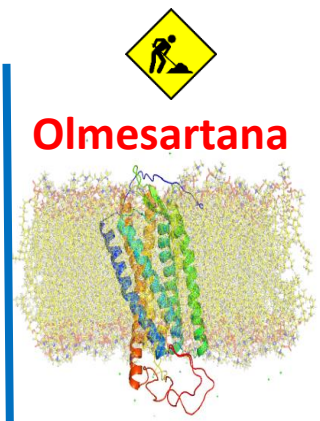
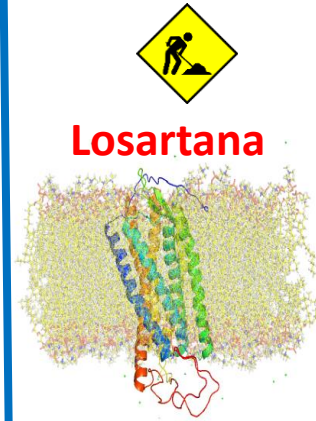
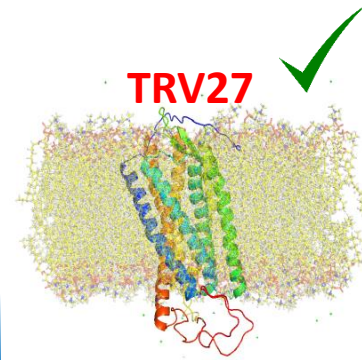
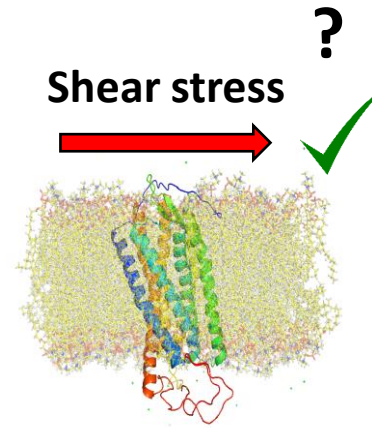
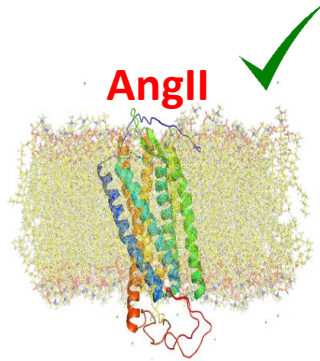
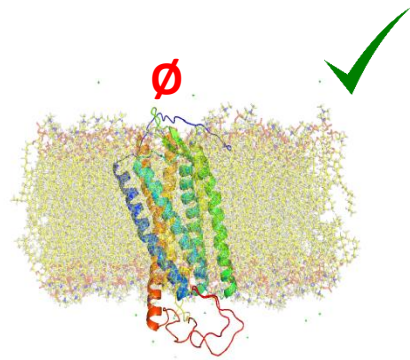
D74N



N111W

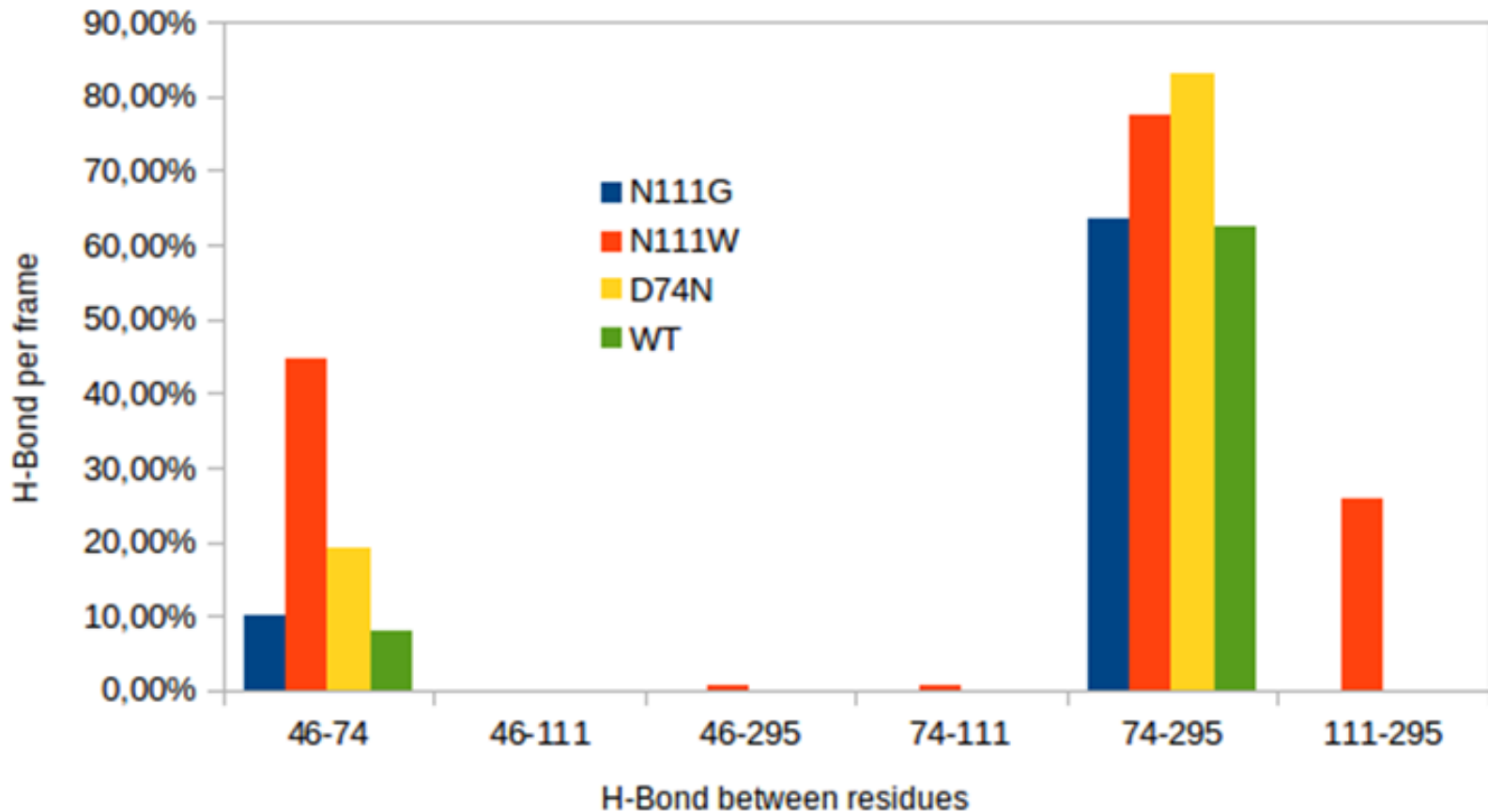


Outros projetos



Resultados Parciais

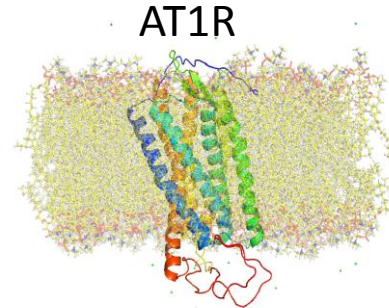
- N111G** – Constitutivamente ativo
- N111W** – Inativo
- D74N** – Ativo para via da β -arrestina apenas
- WT** – *Wild type* (sem mutação)



Uso e performance - Lince

Sistema completo – AT1R + Membrana + água e íons

```
Time:      Core t (s)   Wall t (s)      (%)
          5192111.308   325972.223      1592.8
                   3d18h32:52
Performance: (ns/day)   (hour/ns)
            26.505      0.905
```

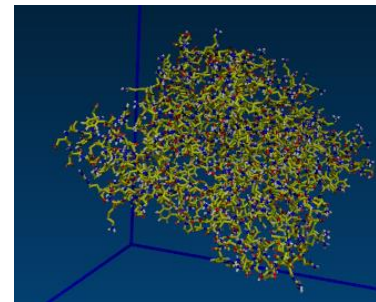


5 gb gerados para
cada 100 ns simulados

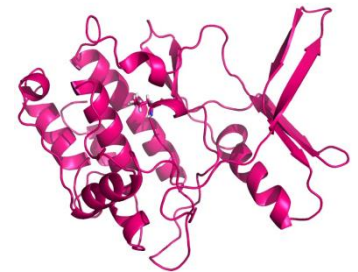
Projeto AT1R – 500 gb utilizados até agora (sem as análises)

Outros projetos

```
[smmodestia@lince:/scratch/smmodestia/Lince]$ du -h
588K    ./charm36.ff
13G     ./2WID
330G    ./ASNase
66G     ./MYLK/P1588L
134G    ./MYLK
982G    .
```



2WID



MYLK

Em torno de 1 terabyte ocupado no momento!

Agradecimentos

HPC - High Performance Computing

