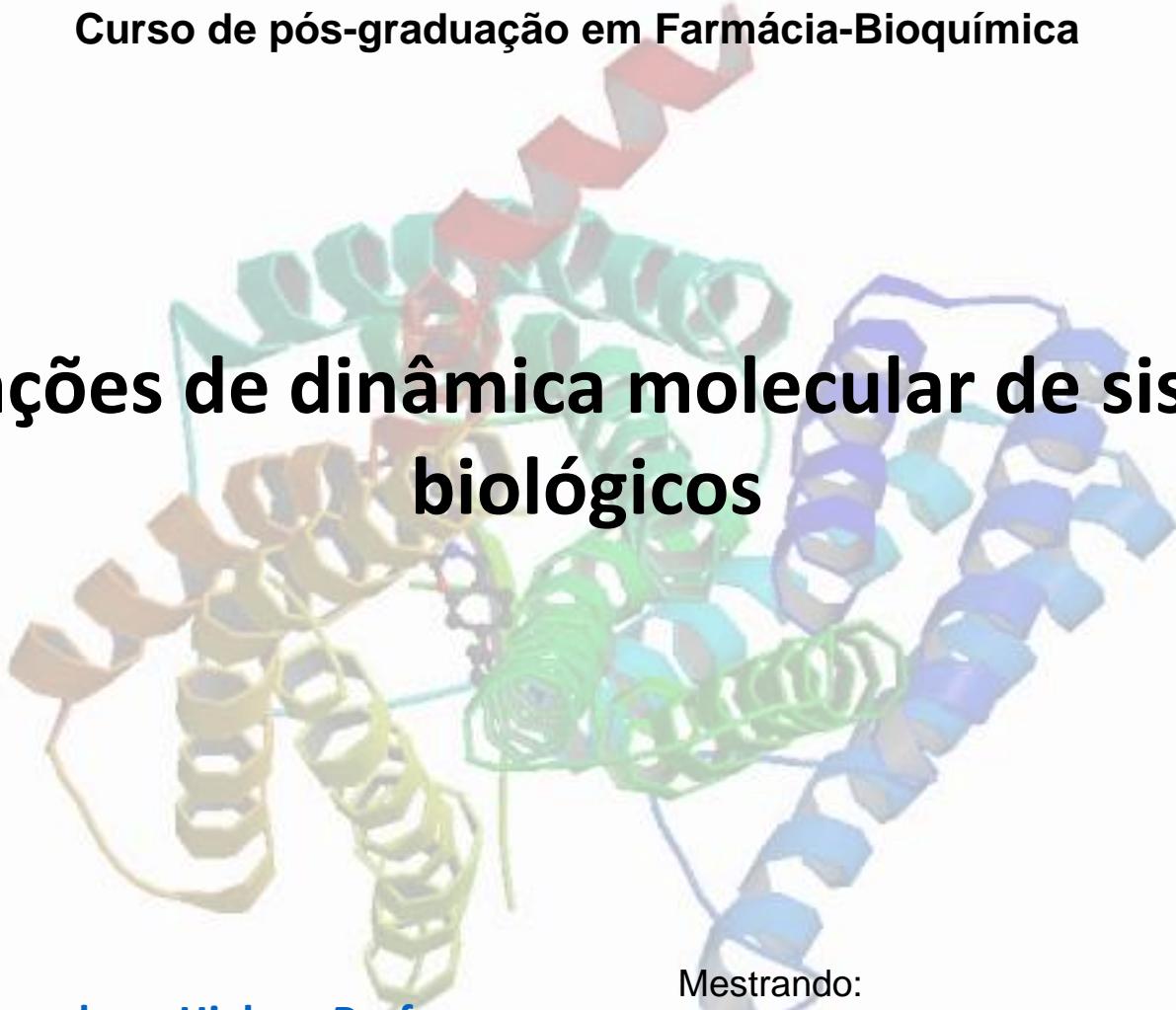




UNIVERSIDADE DE SÃO PAULO
FACULDADE DE CIÊNCIAS FARMACÊUTICAS
Curso de pós-graduação em Farmácia-Bioquímica



Simulações de dinâmica molecular de sistemas biológicos



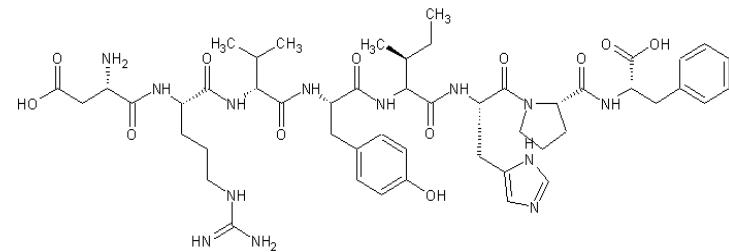
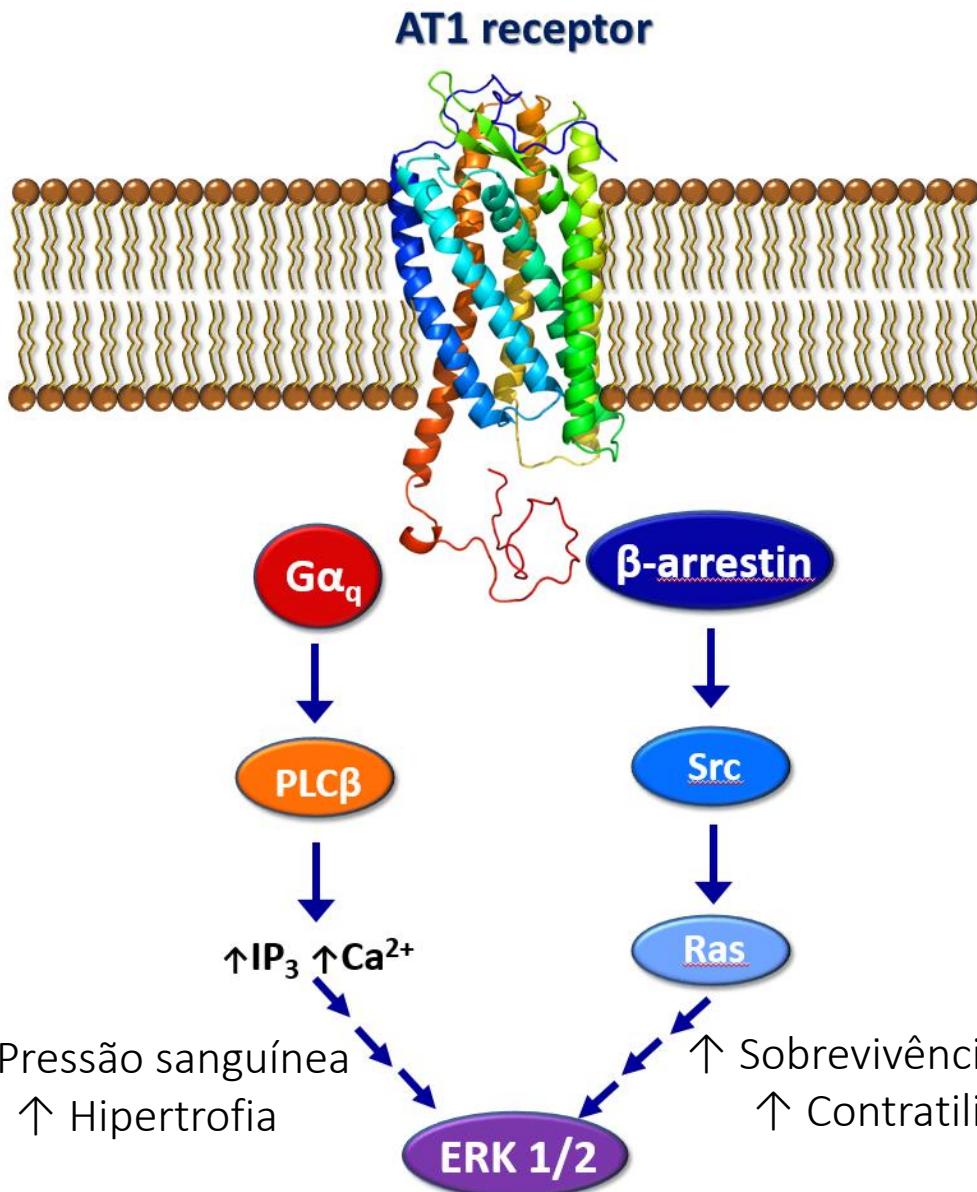
4º. Workshop de High Performance Computing – Convênio: USP – Rice University

São Paulo, 17 de Outubro de 2016

Mestrando:
Silvestre Massimo Modestia

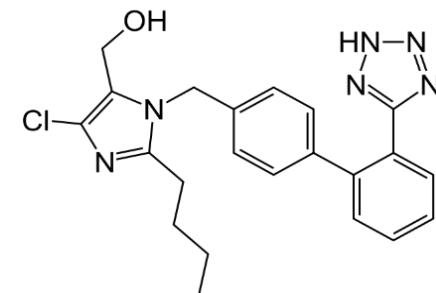
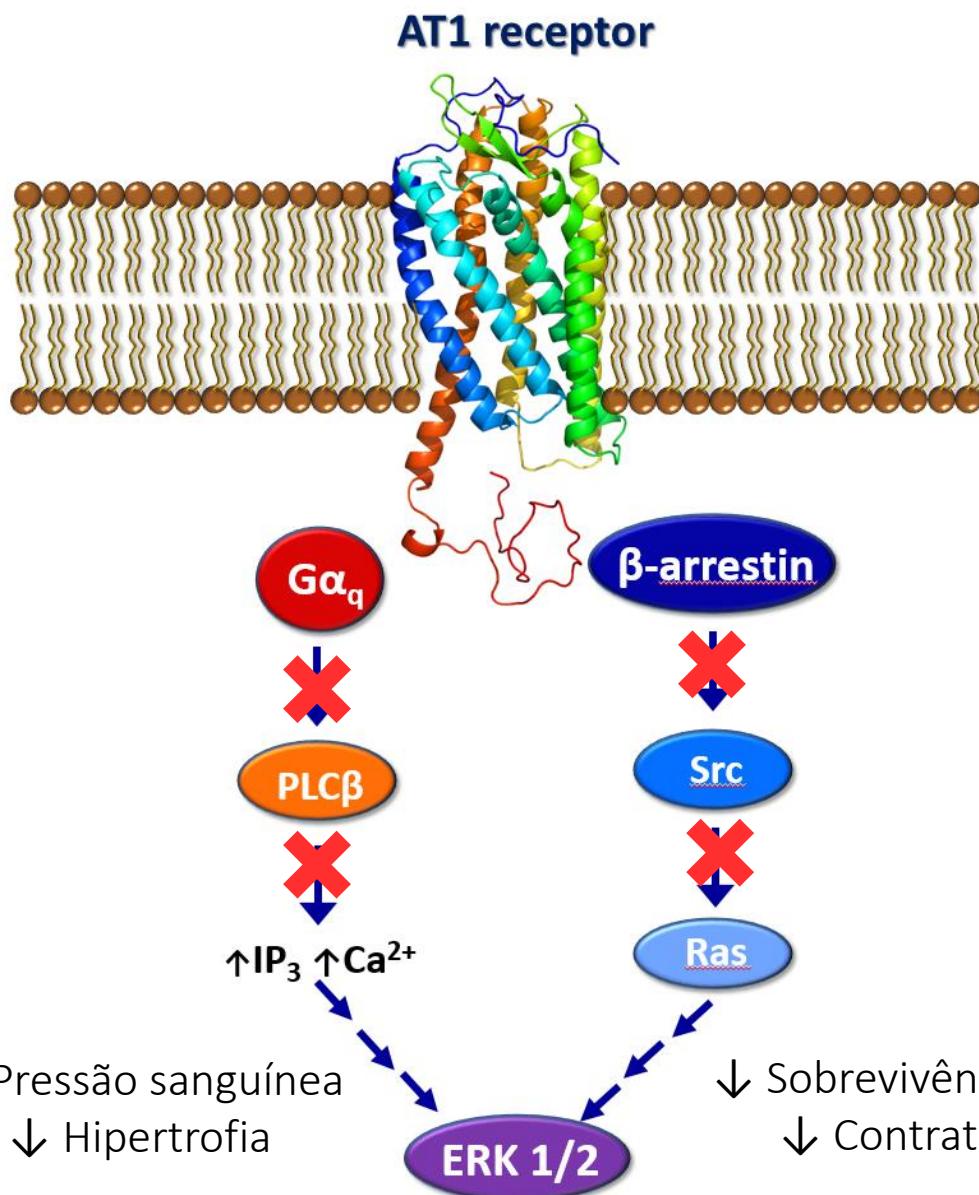
Orientadora:
Profa. Dra. Carlota de Oliveira Rangel-Yagui

Introdução



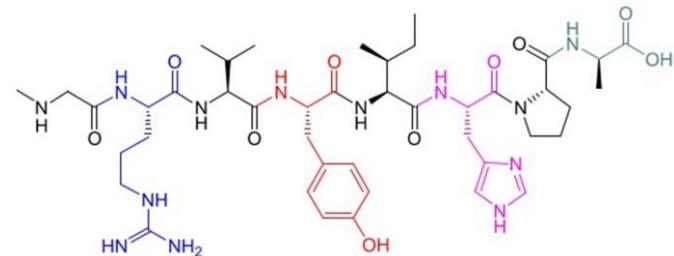
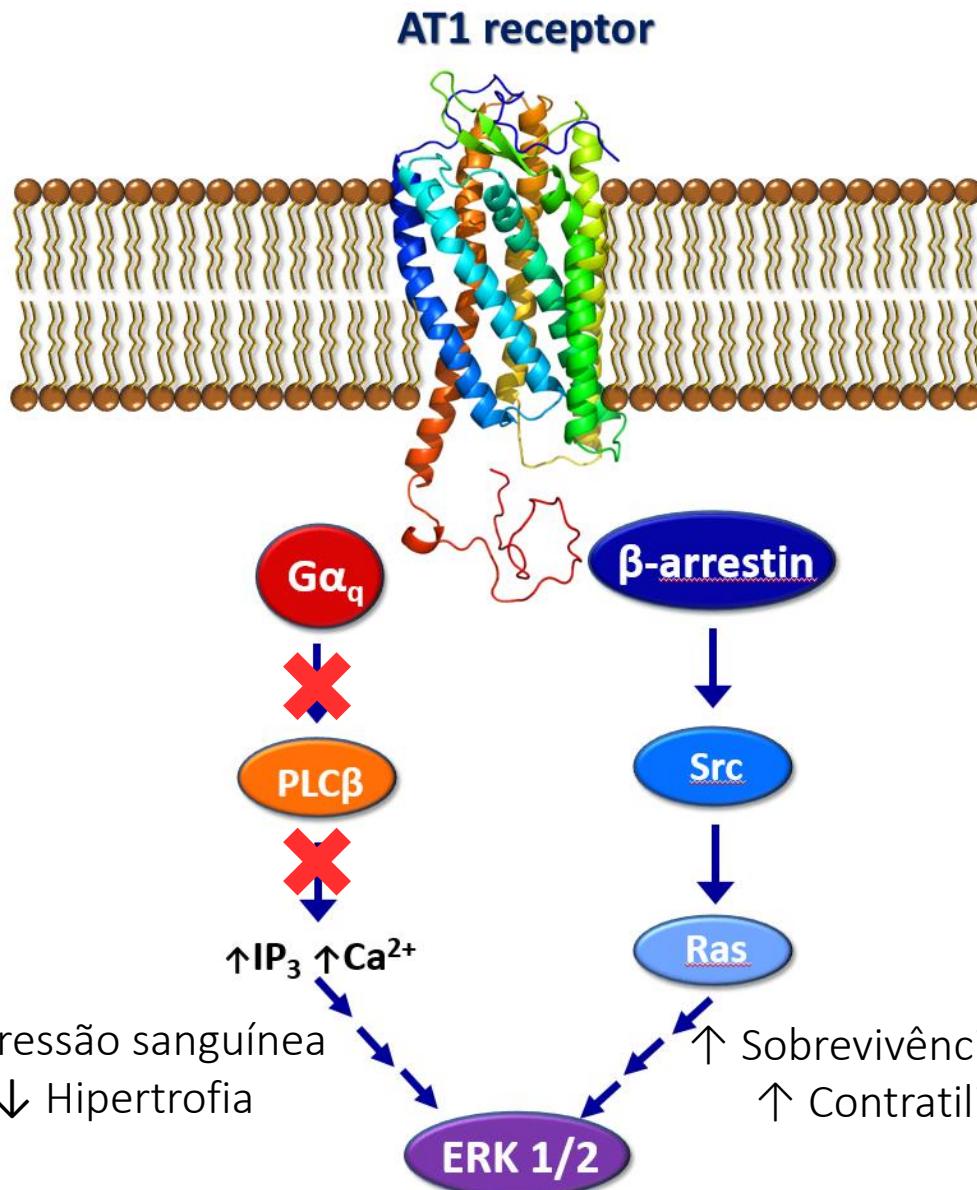
**Agonista total
(Angiotensina II)**

Introdução



**Antagonista
(Losartana)**

Introdução



**Agonista enviesado
(TRV27)**

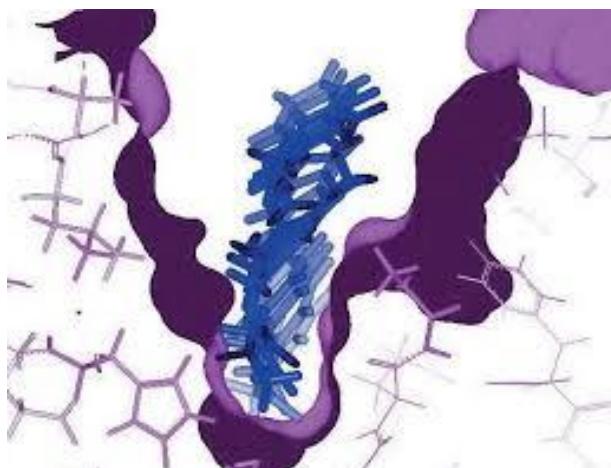
Nova abordagem

Introdução

Modelagem Molecular

Ancoramento Molecular (*docking*)

- Predição da conformação de um ligante no sitio de um receptor.
- Método de amostragem.
- Predição de afinidade.

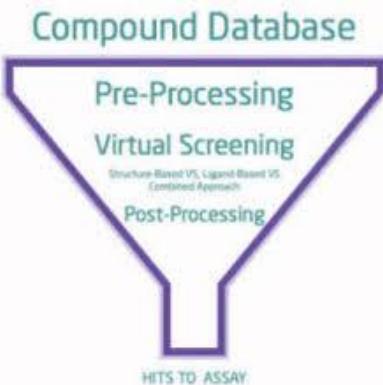
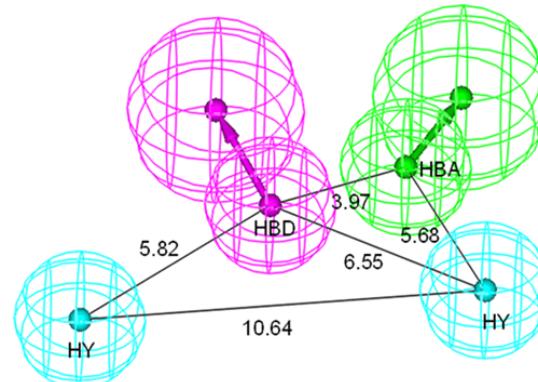


Dinâmica Molecular (DM)

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

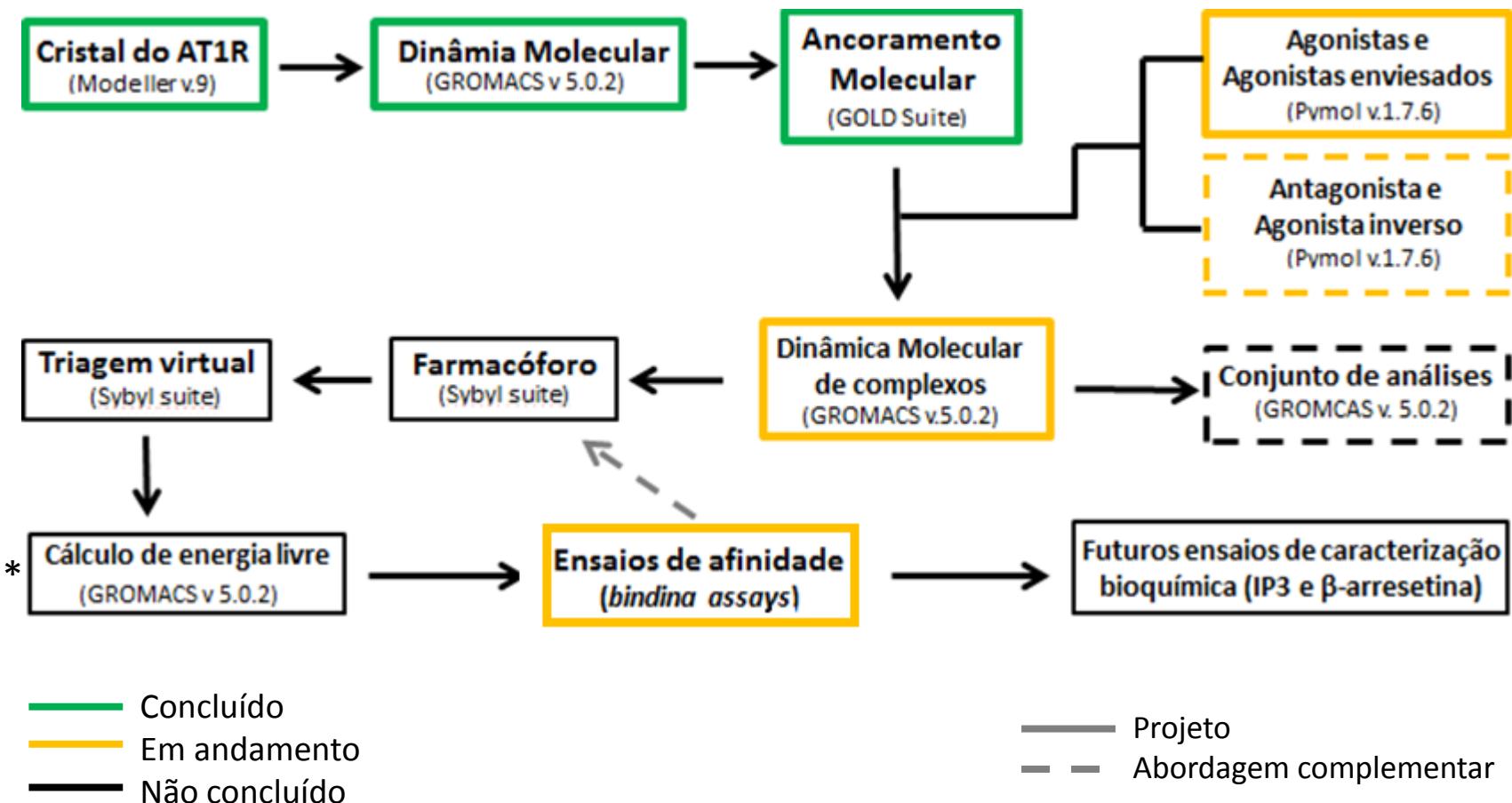
$$E_{\text{tot}} = E_{\text{str}} + E_{\text{bend}} + E_{\text{tors}} + E_{\text{vdW}} + E_{\text{elec}} + \dots$$

Farmacóforo e Triagem virtual



Objetivo

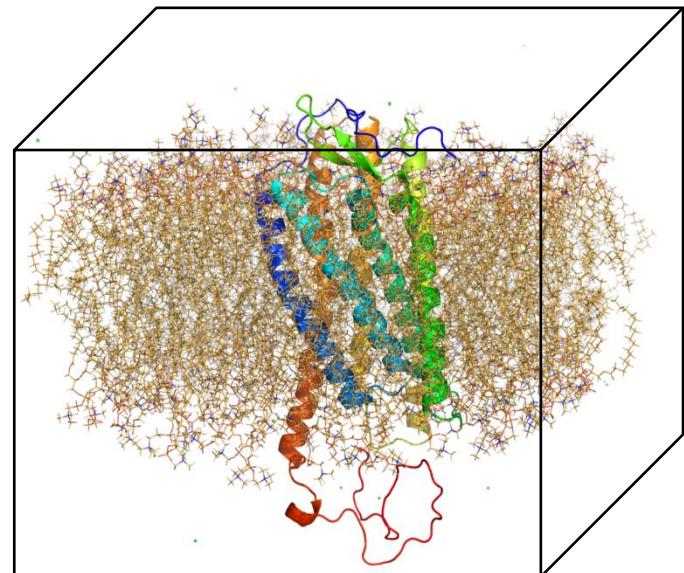
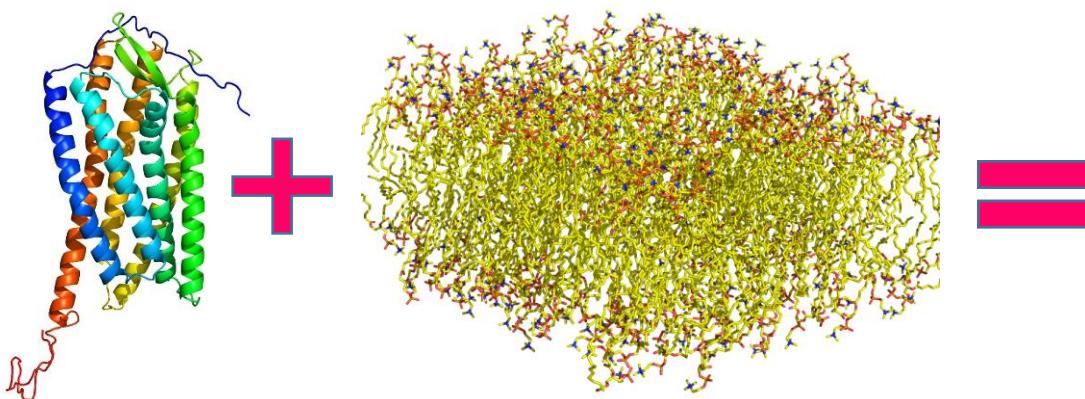
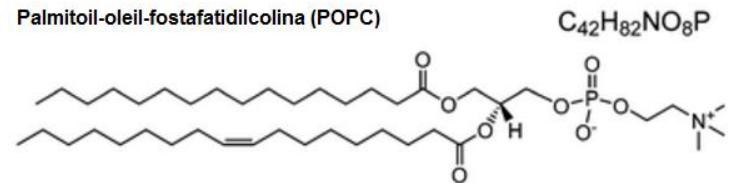
Planejamento de ligantes não peptídicos com atividade agonista enviesada para o receptor AT1.



Metodologia

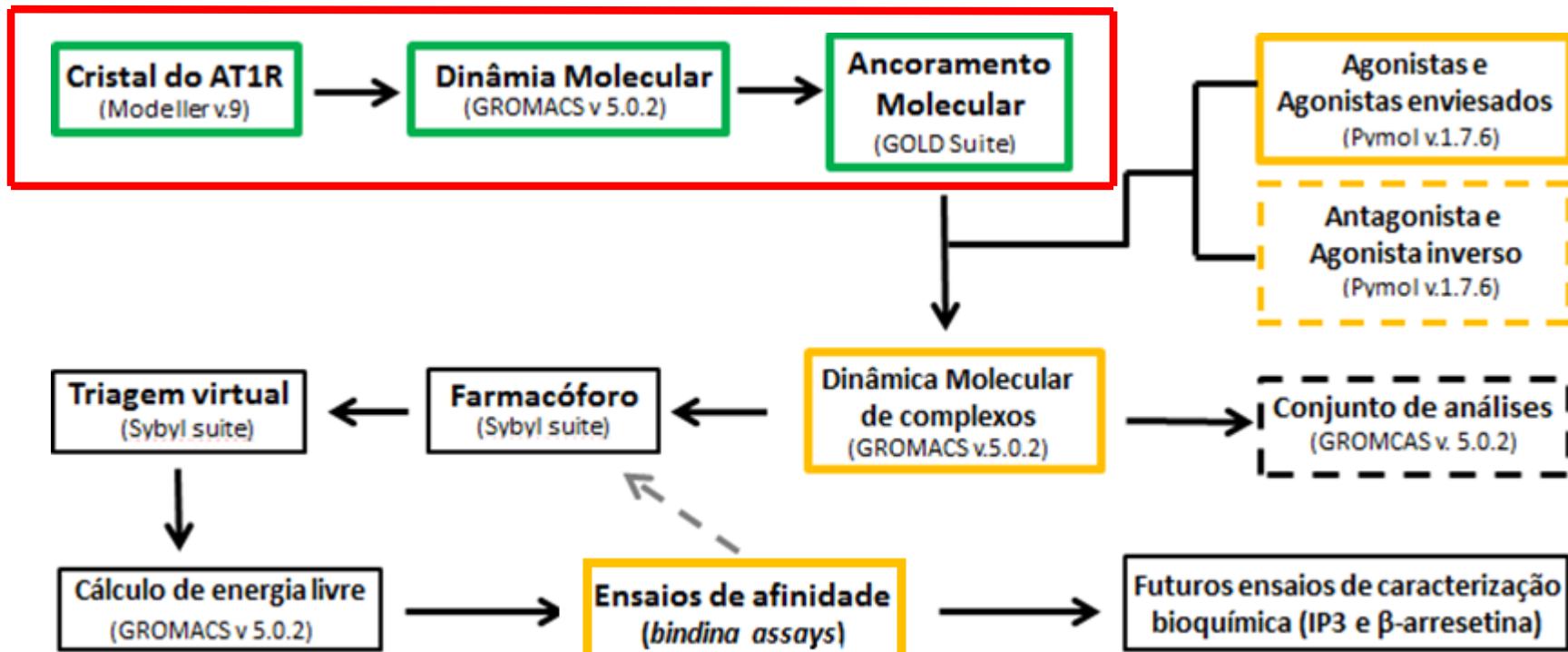
Dinâmica molecular (DM)

- 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.



Resultados Parciais

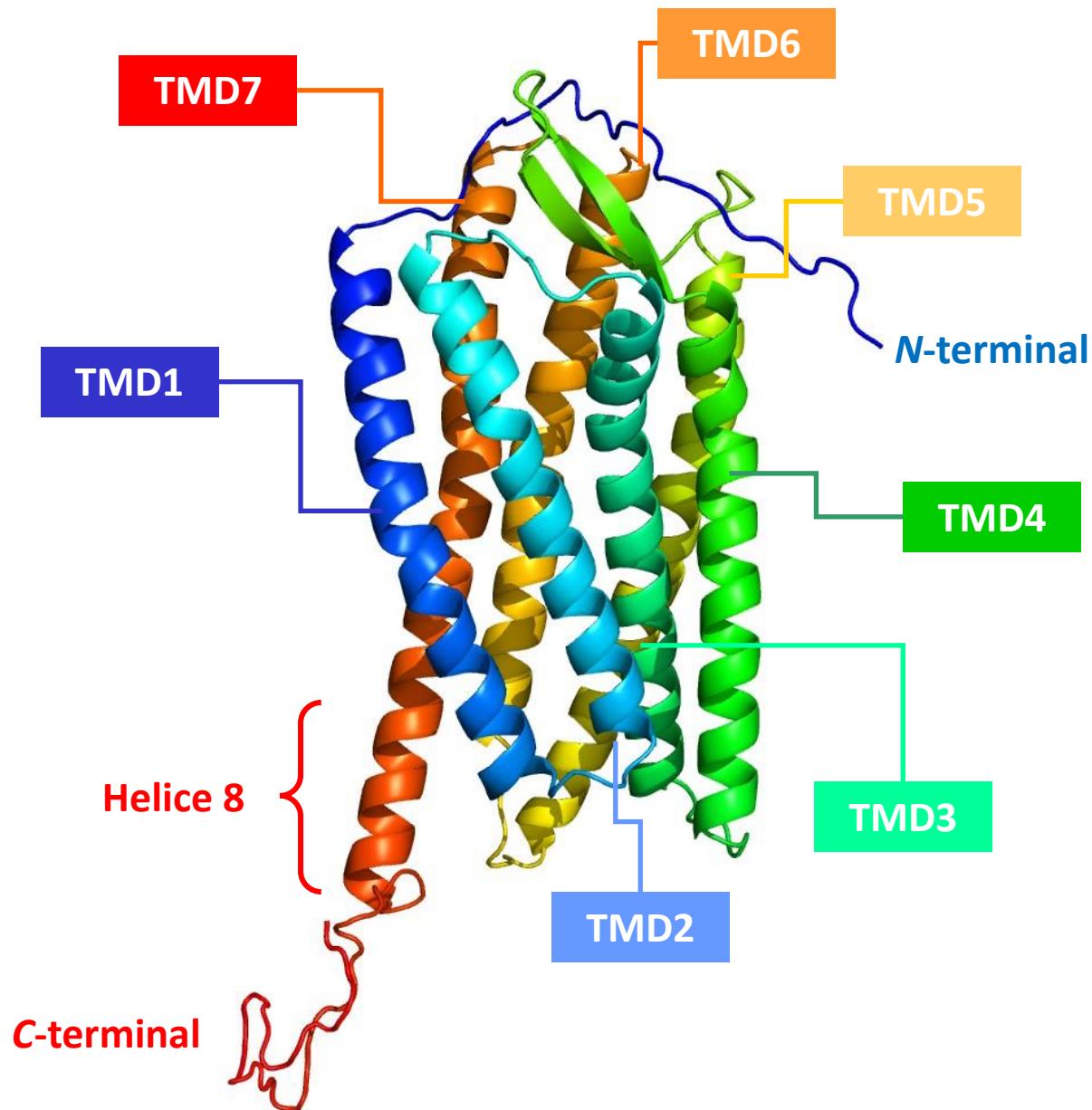
Resultados Computacionais



— 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

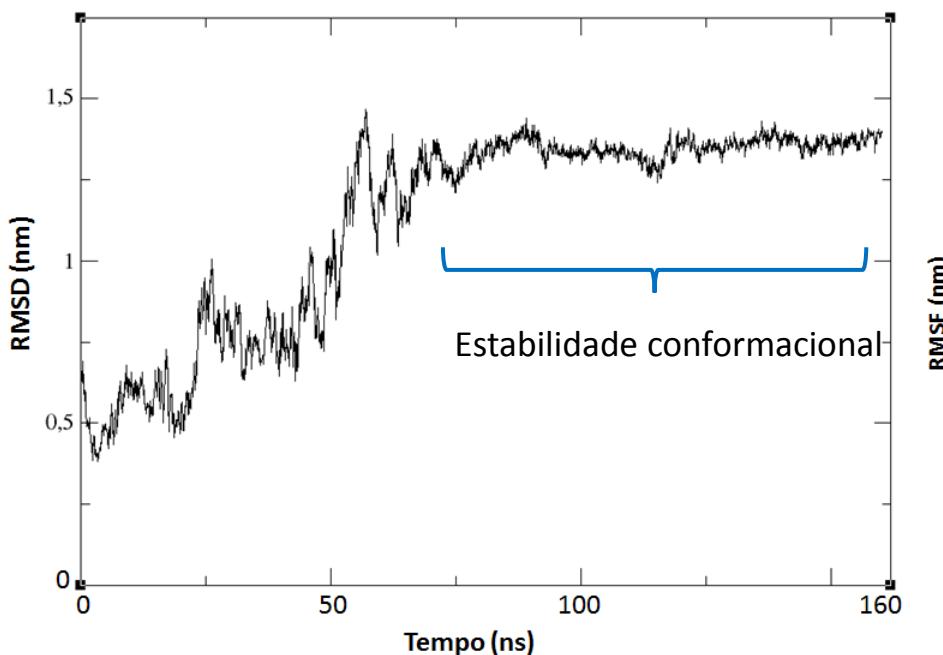
i = posição atômica

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

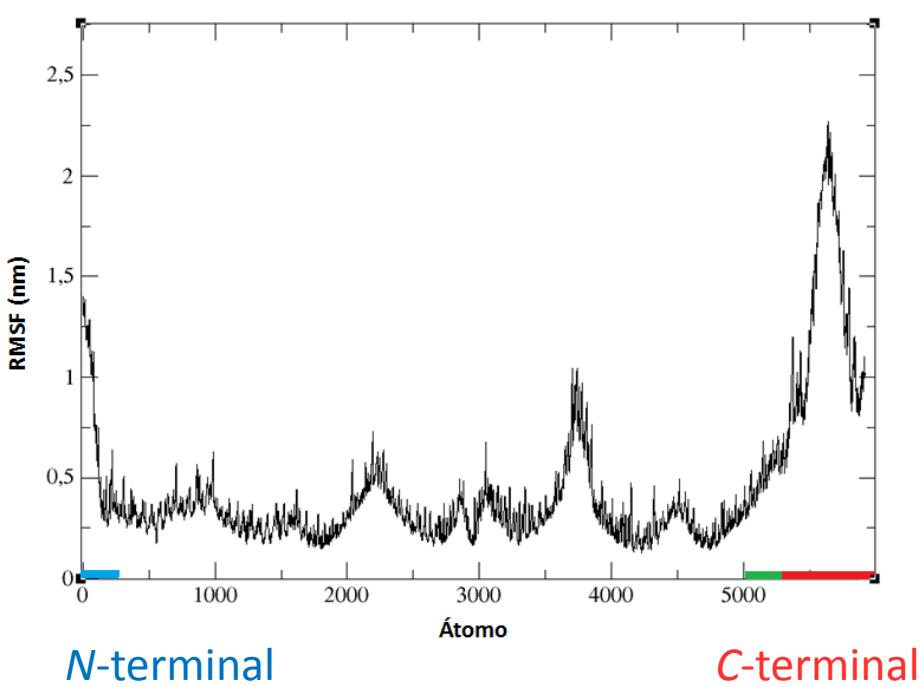
T = Número de frames

i = posição atômica

Gráfico de desvio quadrático médio das posições atômicas
(RMSD)

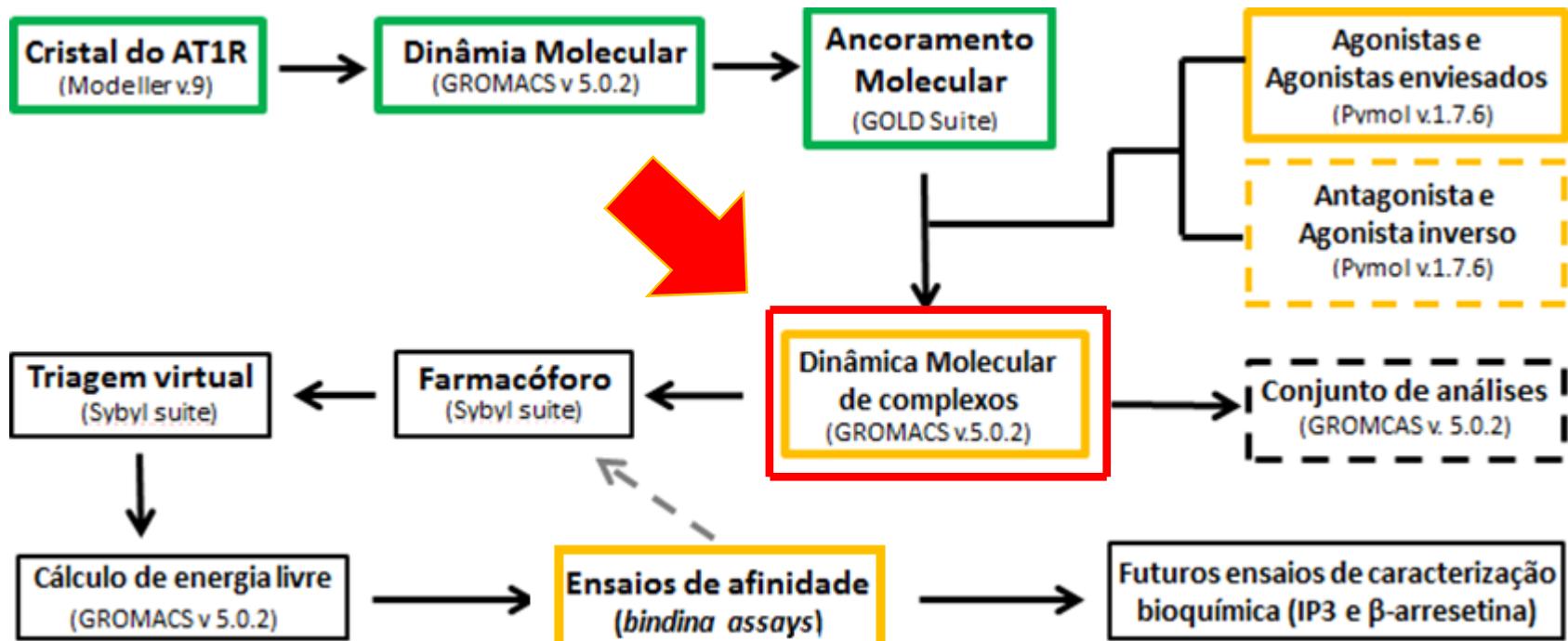


Flutuação do Desvio Quadrático Médio (RMSF)



Resultados Parciais

Resultados Computacionais

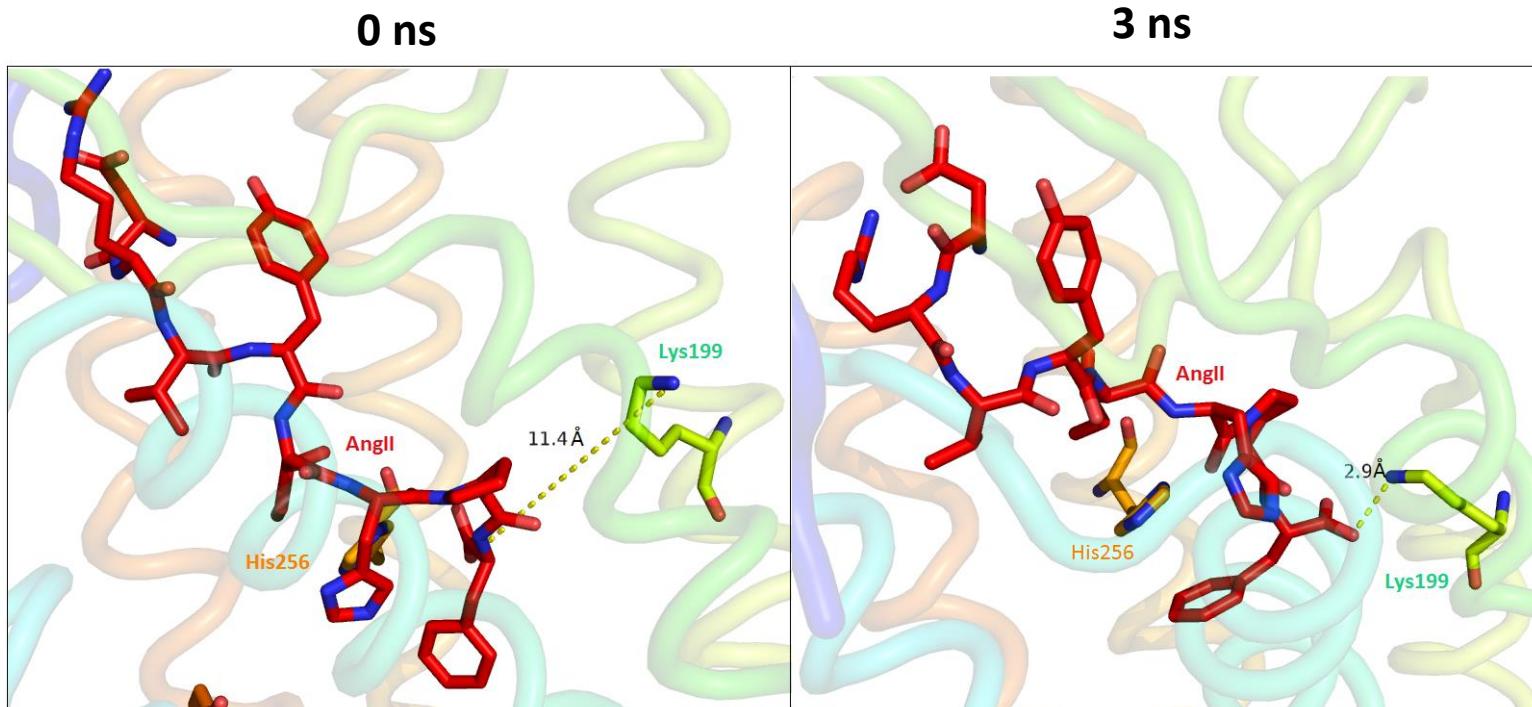


— Concluído
— Em andamento
— Não concluído

— Projeto
— Abordagem complementar

Resultados Parciais

Simulated Annealling

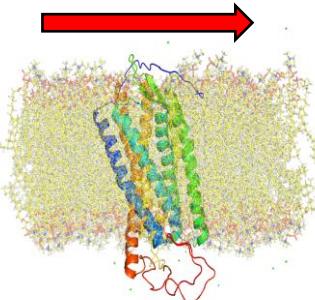


Tempo (ps)	0	200	400	500	600	700	800	900	1000	1200
Temperatura (K)	310	600	700	800	700	600	500	450	400	310

Outros projetos

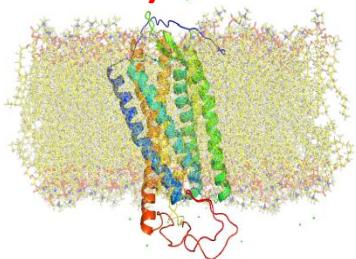
Força

Shear stress

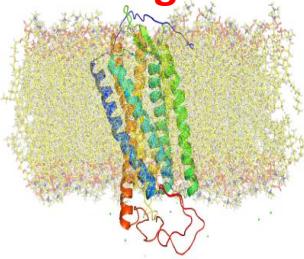


Ligantes

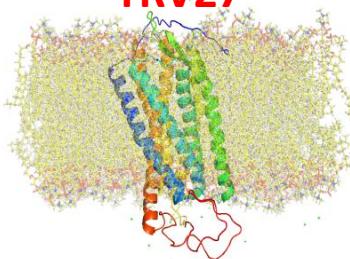
∅



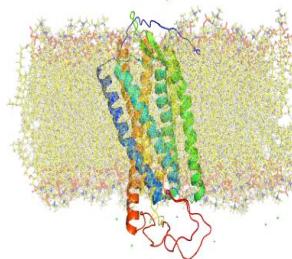
AngII



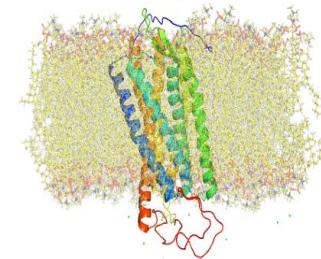
TRV27



Losartana

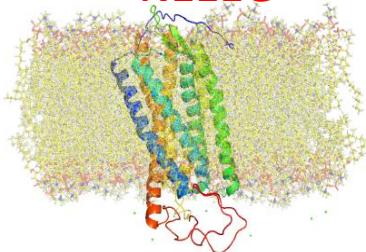


Olmesartana

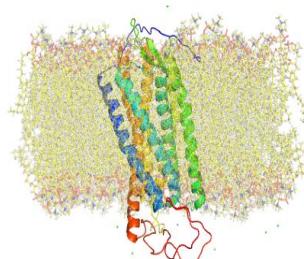


Mutantes

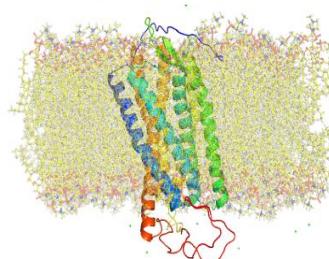
N111G



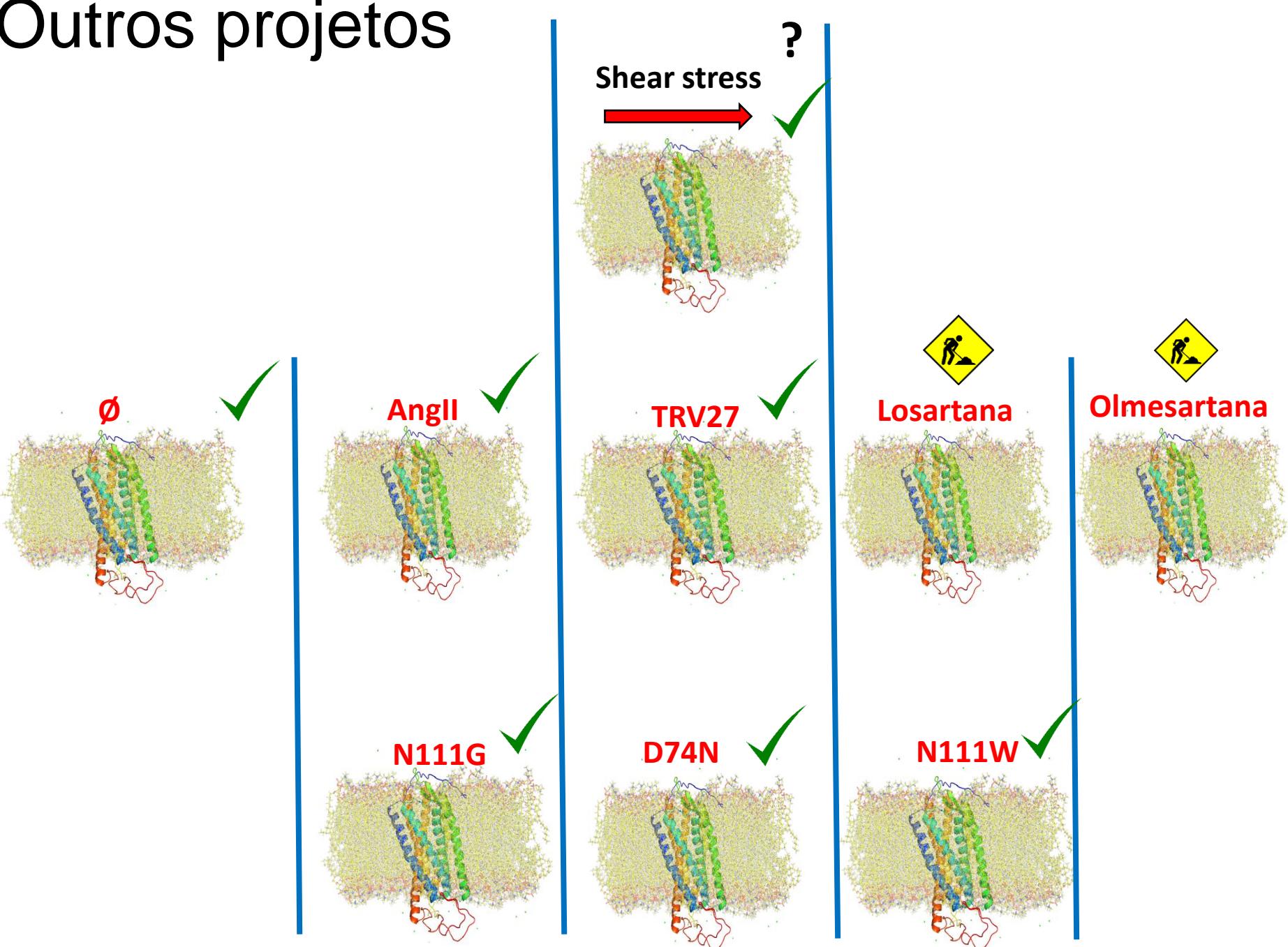
D74N



N111W



Outros projetos



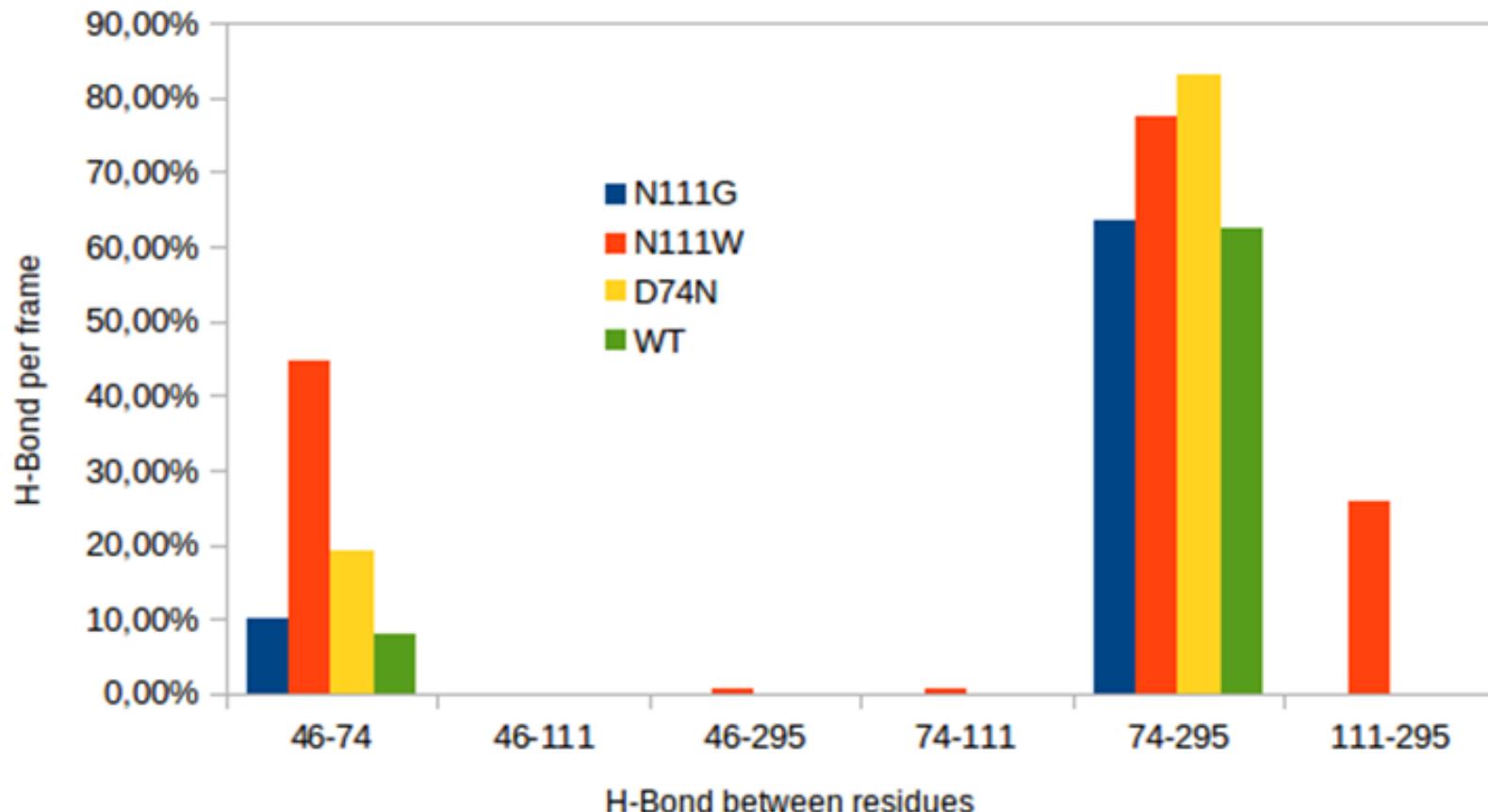
Resultados Parciais

N111G – Constitutivamente ativo

N111W – Inativo

D74N – Ativo para via da β -arrestina apenas

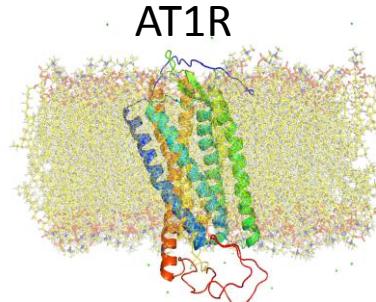
WT – *Wild type* (sem mutação)



Uso e performance - Lince

Sistema completo – AT1R + Membrana + água e íons

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

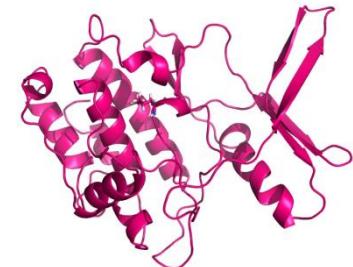
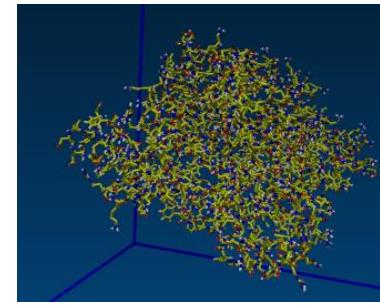


5 gb gerados para
cada 100 ns simulados

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

Outros projetos

```
[smmodestia@lince:/scratch/smmodestia/Lince]$ du -h
588K  ./charmm36.ff
13G   ./2WID
330G  ./ASNase
66G   ./MYLK/P1588L
134G  ./MYLK
982G  .
```



Em torno de 1 terabyte ocupado no momento!

2WID

MYLK

Agradecimentos

HPC - High Performance Computing

