

# Dynamics of membrane bound peptides from NMR experiments and MD simulations

Ricky Nencini  
Supervisor: Samuli Ollila

Faculty of Science, University of Helsinki  
Institute of Biotechnology

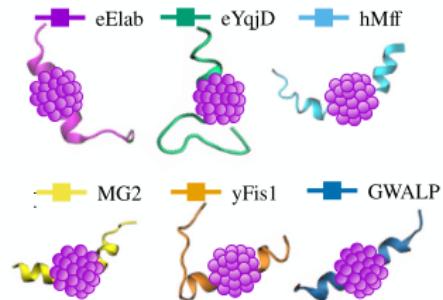
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*ricky.nencini@helsinki.fi*

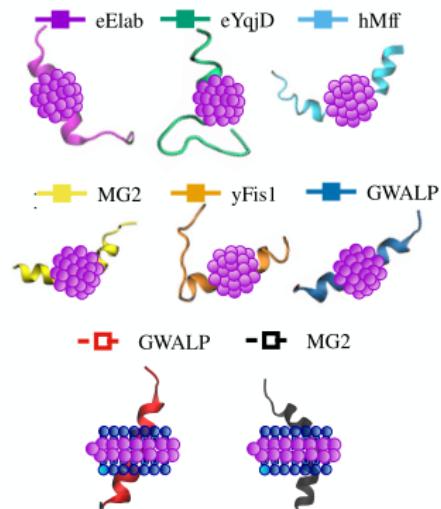
June 14, 2022

**Goal: What can we tell about membrane proteins based on differences in spin relaxation times?**

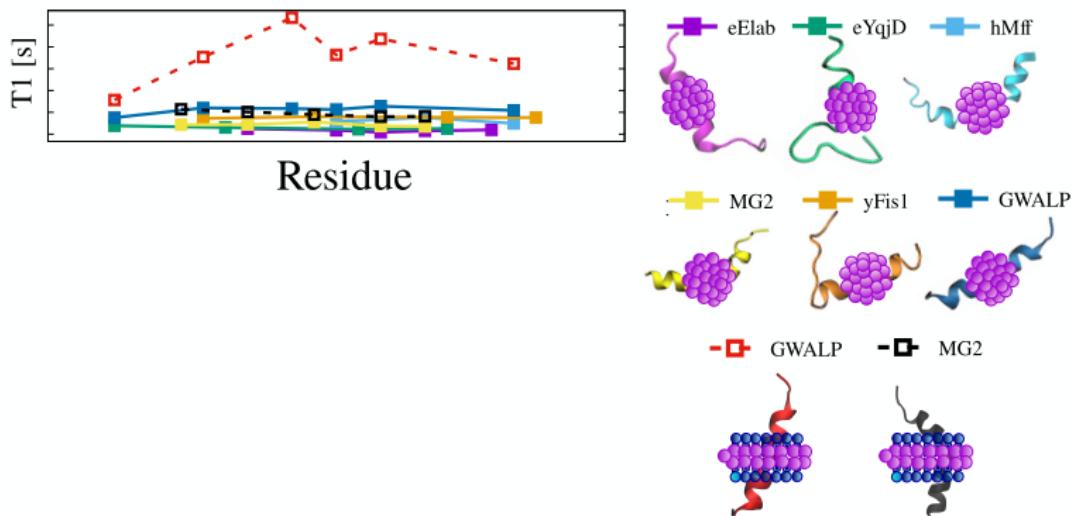
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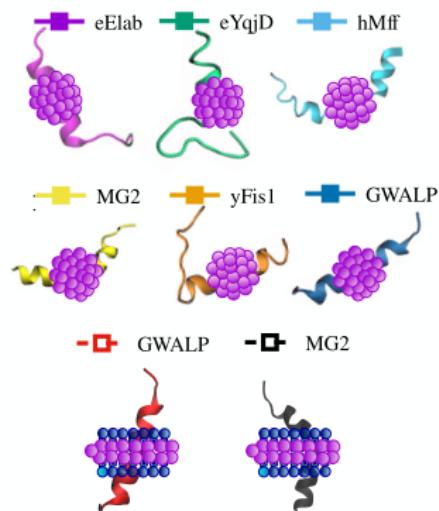
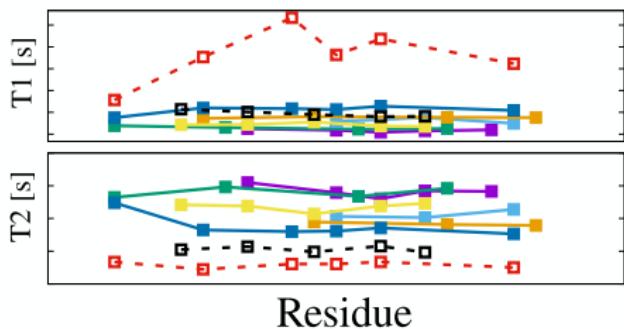
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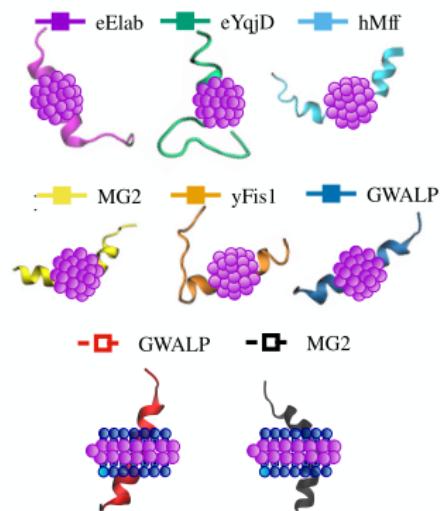
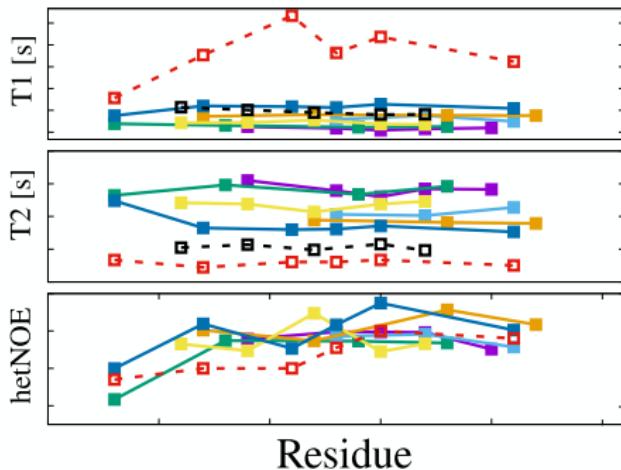
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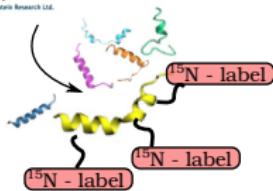
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# How do we actually do it?

PeptideSynthetics

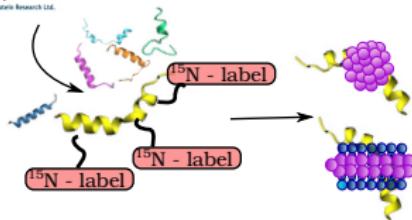
Peptide Protein Research Ltd.



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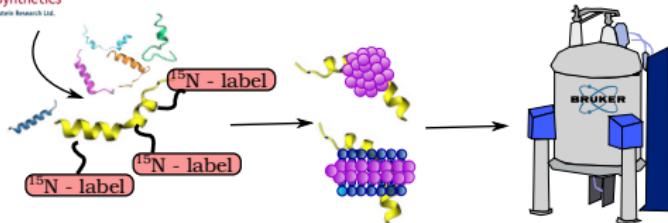
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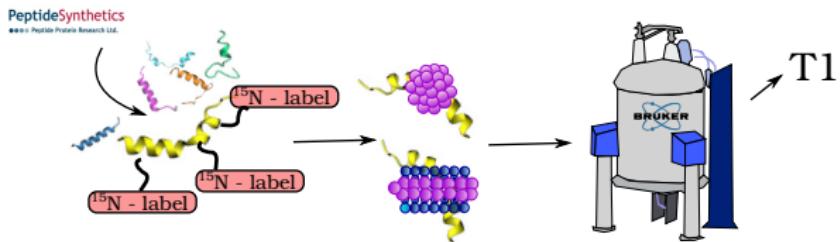
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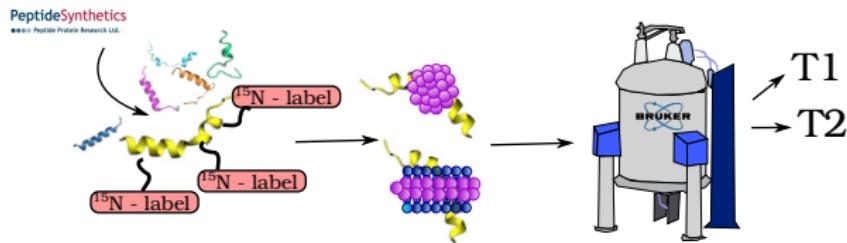
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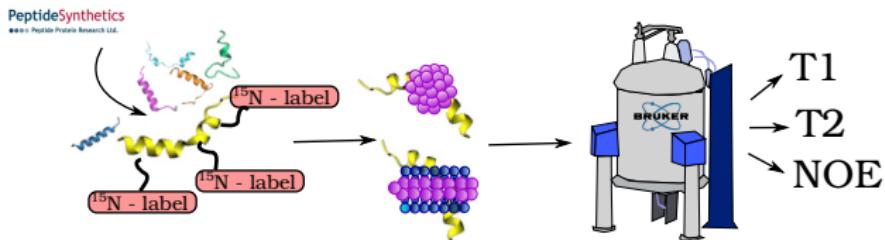
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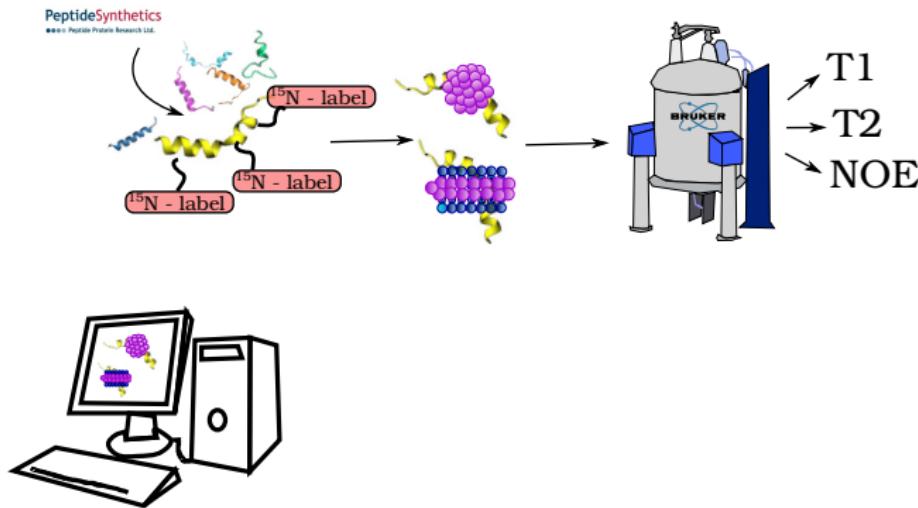
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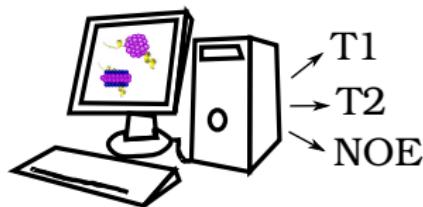
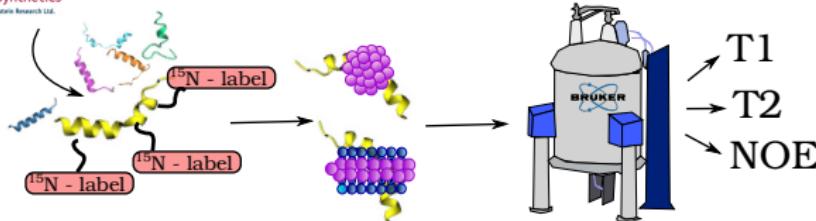


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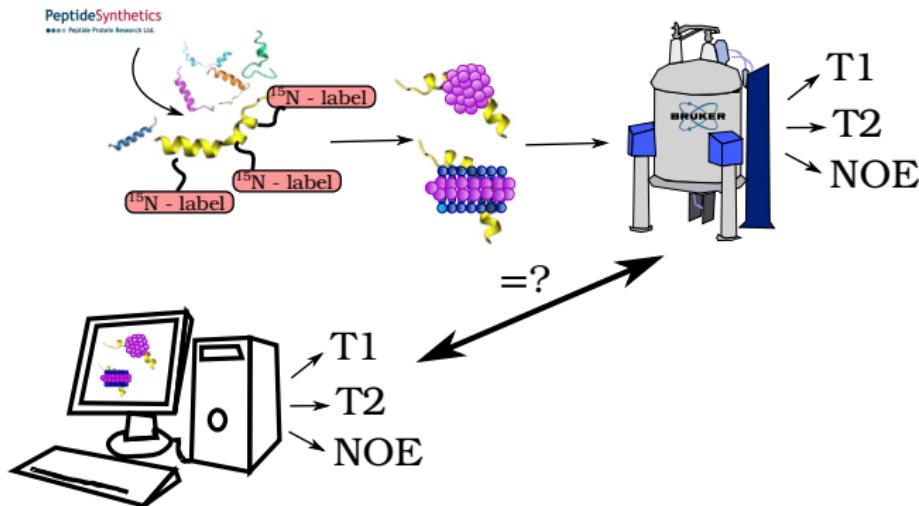


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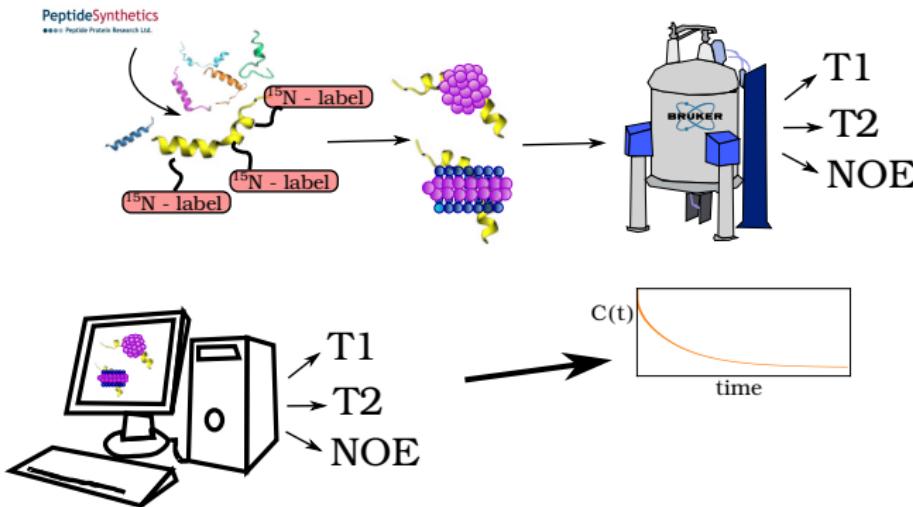
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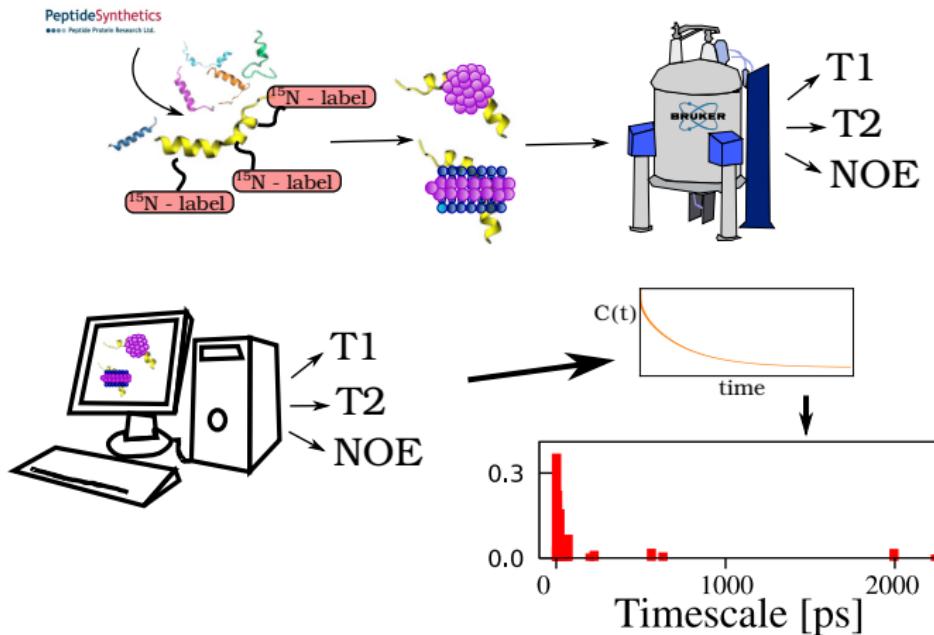
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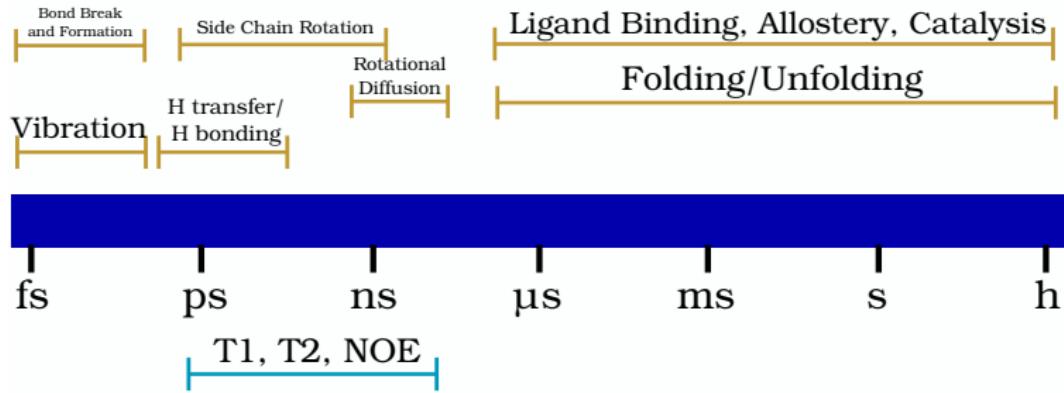


## **Succesfull case: TonB**

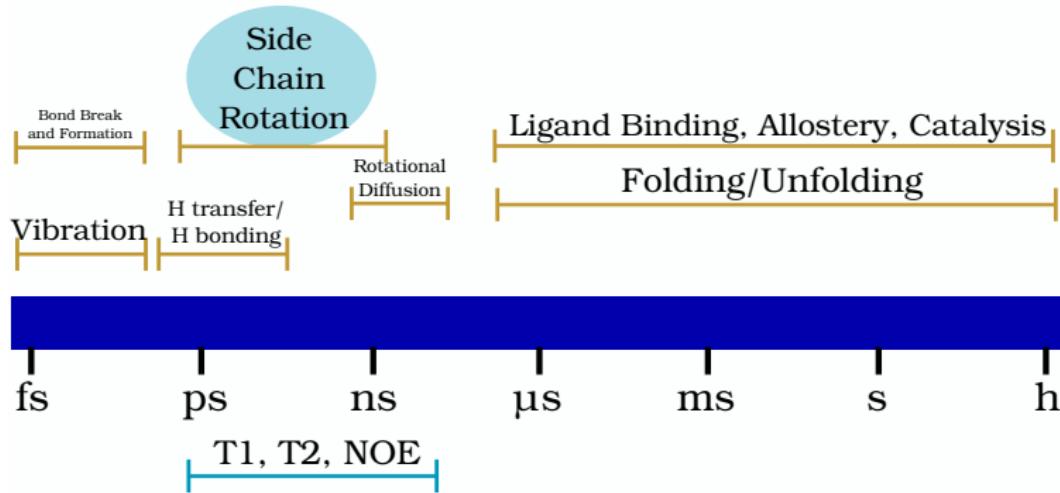
Yet to be done - Our approach shad a light on the conformational ensamble of the protein

# What do T1, T2 and NOE tell us?

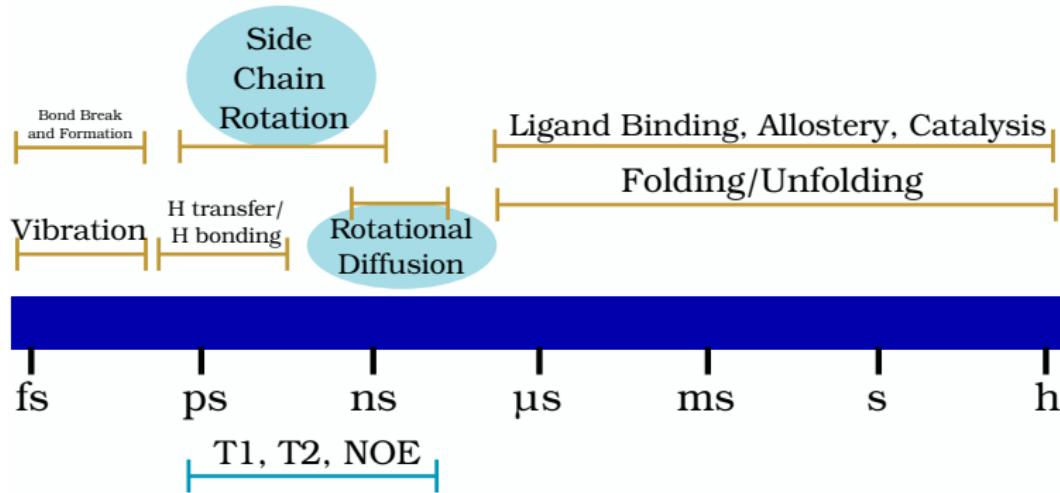
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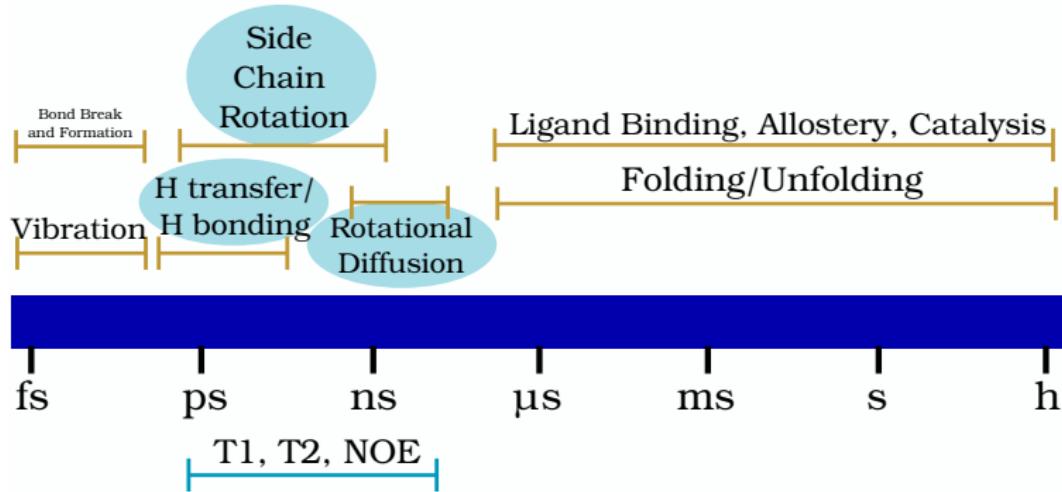
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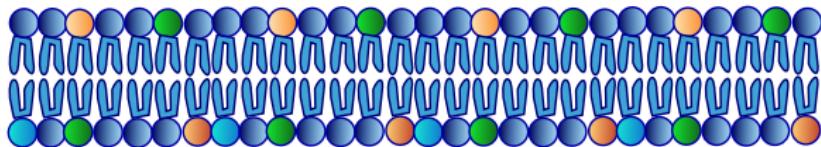
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# **What samples can be prepared?**

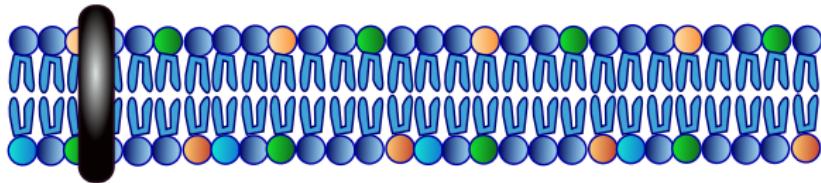
# What samples can be prepared?

## Solid state NMR - lipid bilayer



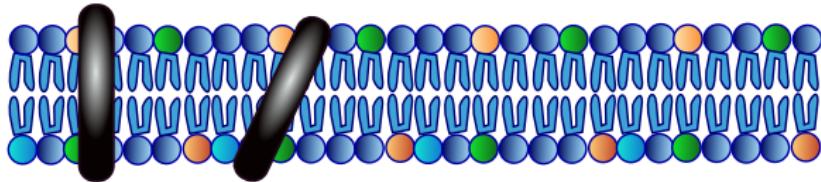
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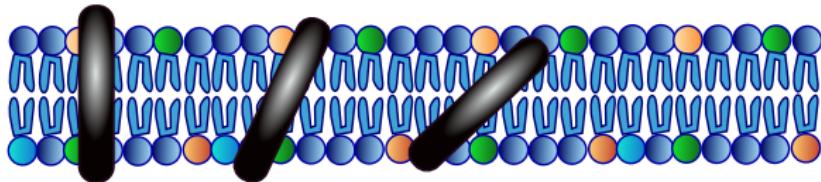
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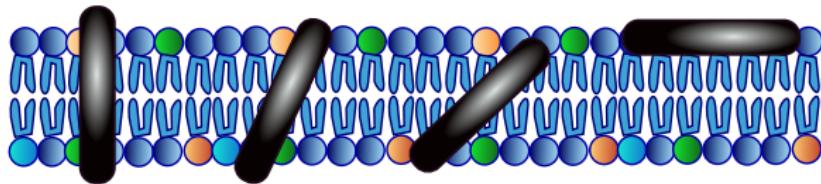
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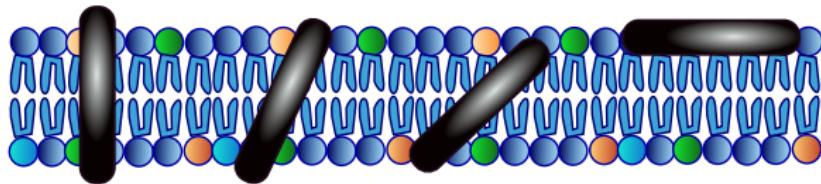
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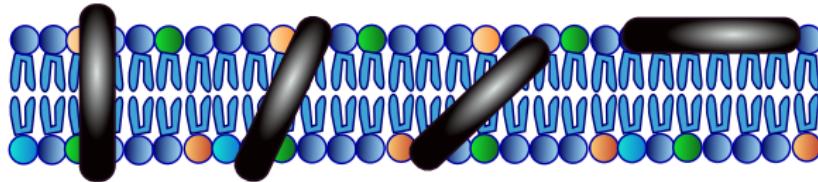
**Solid state NMR - lipid bilayer**



**Solution NMR**

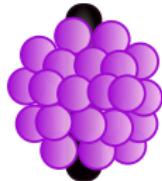
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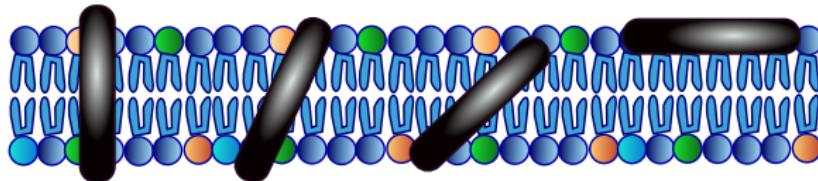
**Solution NMR**

**Micelle**



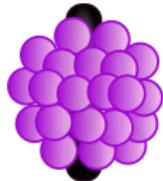
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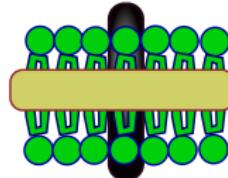


**Solution NMR**

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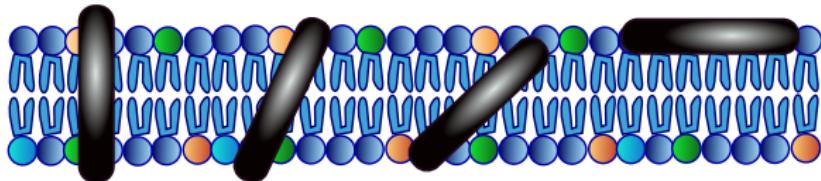


**Nanodisk**



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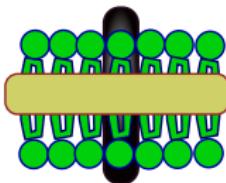


**Solution NMR**

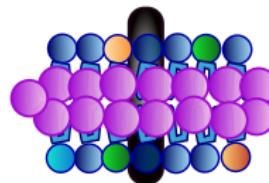
**Micelle**



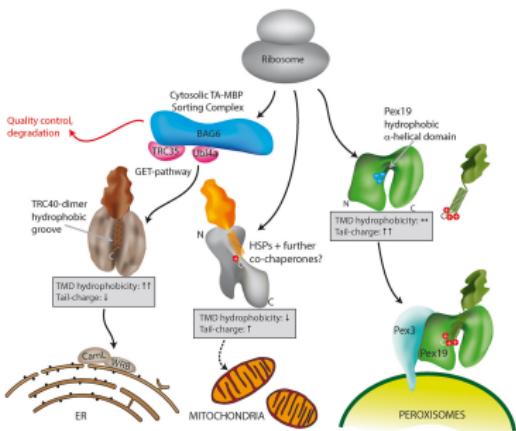
**Nanodisk**



**Bicelle**



# Case study: Tail anchored mitochondria targeted peptides to be developed



## Studied peptides

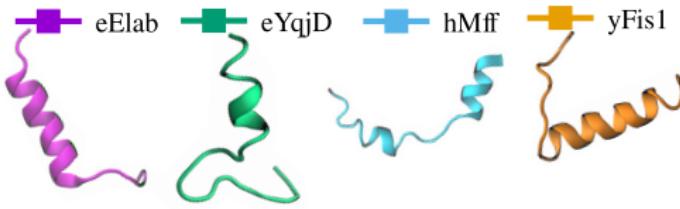
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E.coli - ElaB	PWQGIGVGAAVGLVLGLLLARR
E.coli - YqjD	WTGVGIGAAIGVVLGVLSSRR
human - Mff	AKREMVMISITVAFWLNSWLWFRR
yeast - Fis1	LKGVVVAGGVLAGAVAVASFFLRNKRR
Model - GWALP	Ac-GGALWLALALALALALWLAGA-NH-CH <sub>2</sub> -CH <sub>2</sub> OH
Model - Magainin 2	GIGKFLHSACKFGKAFVGEIMNS

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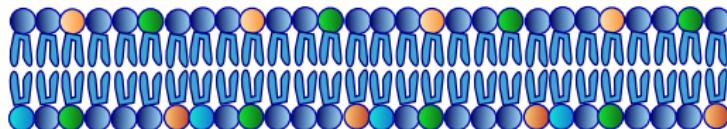
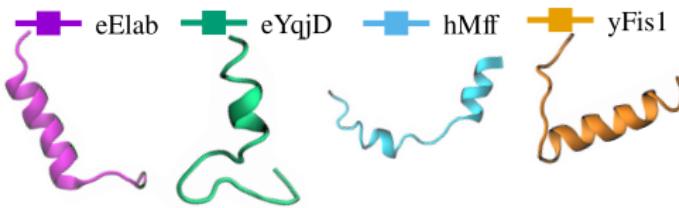
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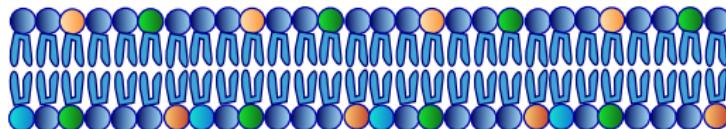
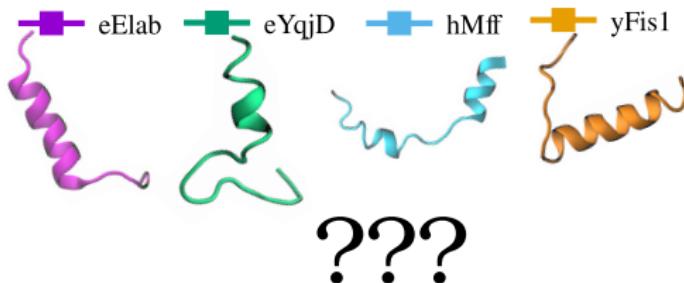
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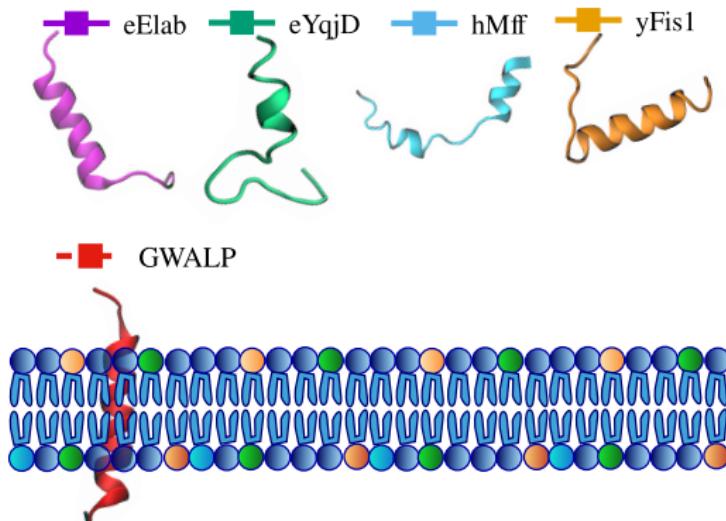
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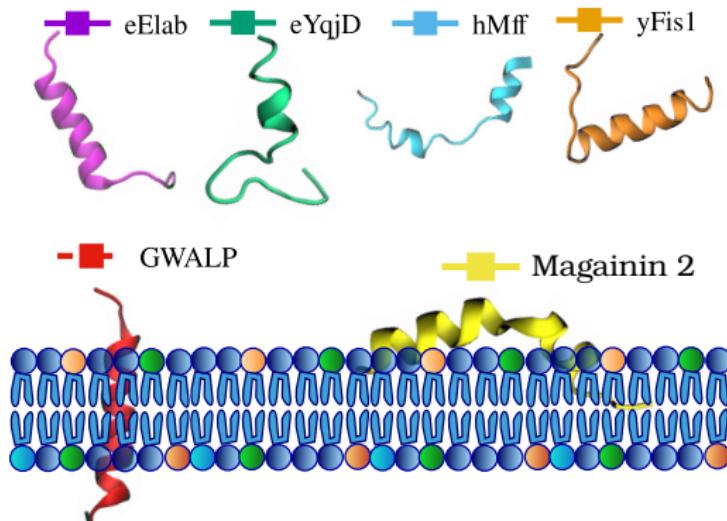
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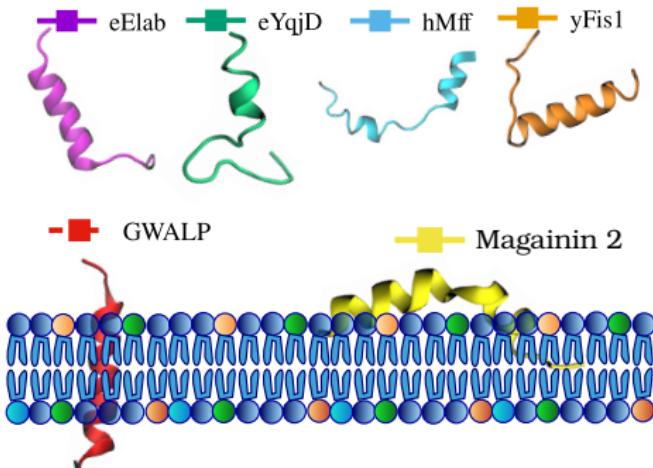
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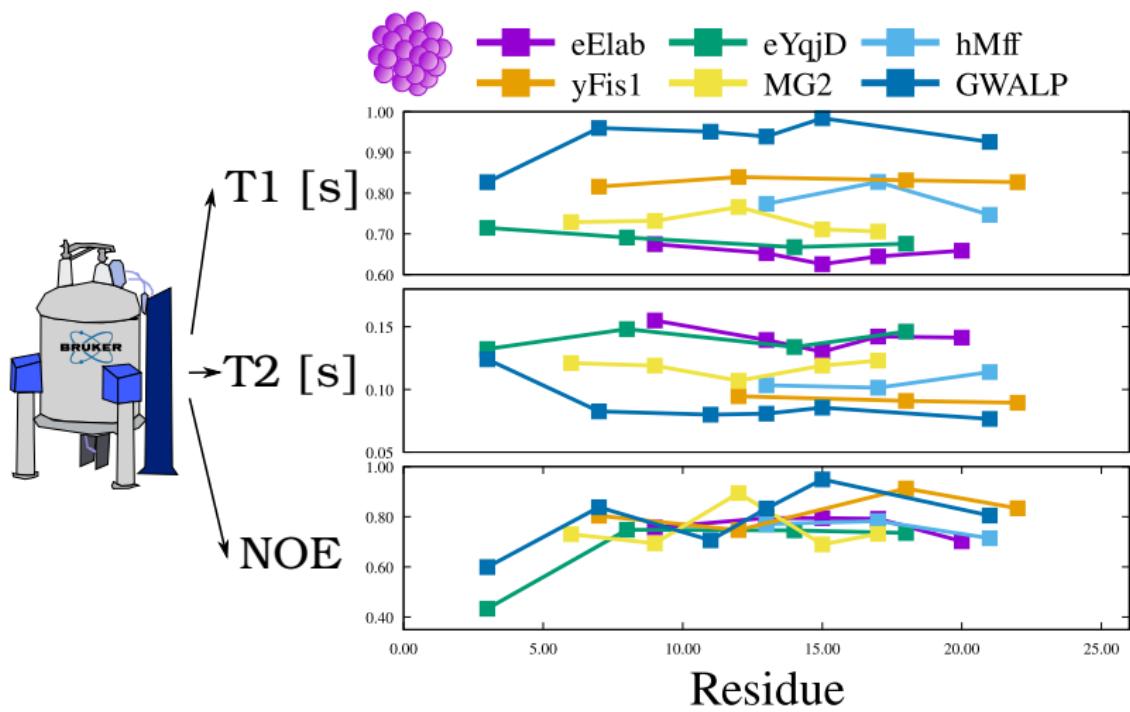
# Studied peptides

		Hydrophobic	Acid	Basic	Neutral
E.coli - ElaB	PWQGIGVGAAGVLVLGLLLARR	63.64%	0.0%	9.09%	27.27%
E.coli - YqjD	WTGVGIGAAIGVVLGVLLSRR	57.14%	0.0%	9.52%	33.33%
human - Mff	AKREMVMISITVAFWLLNSWLWFRR	60.00%	4.0%	16.00%	20.00%
yeast - Fis1	LKGVVVAGGVLAGAVAVASFFLRRKRR	59.26%	0.0%	18.52%	22.22%
Model - GWALP	Ac-GGALWLALALALALALALWLAGA-NH-CH <sub>2</sub> -CH <sub>2</sub> OH	100.00%	0.0%	0.00%	0.00%
Model - Magainin 2	GIGKFLHSAAKKFGKAFVGCEIMNS	43.48%	4.4%	21.74%	30.43%

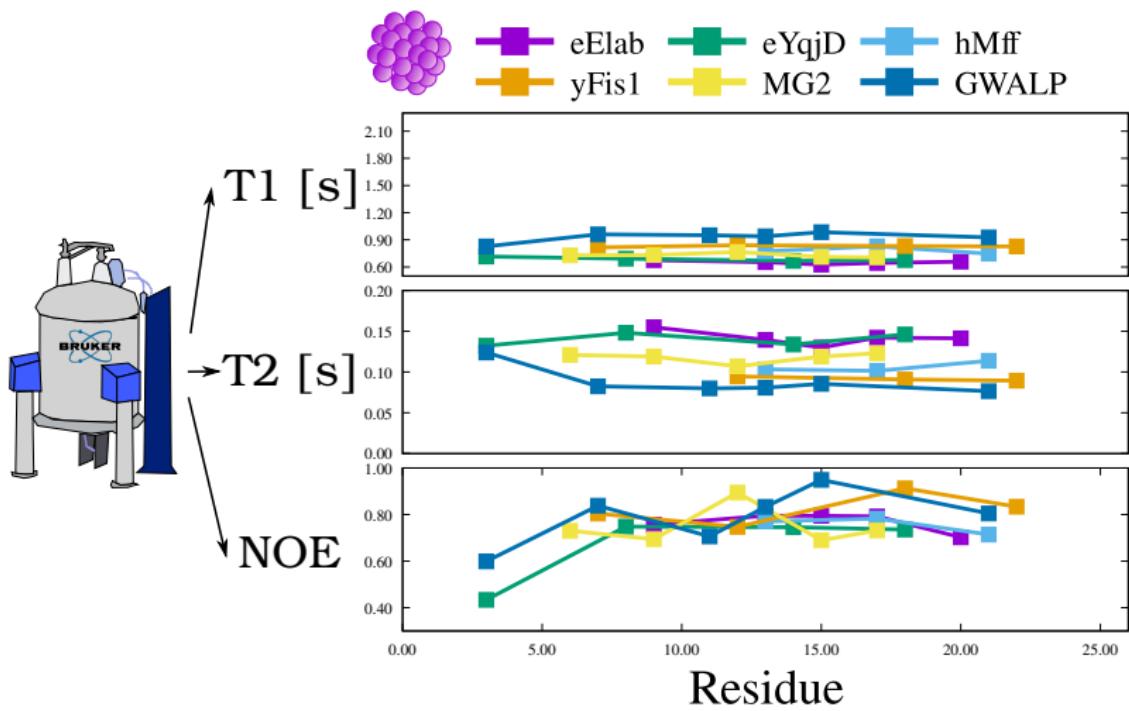
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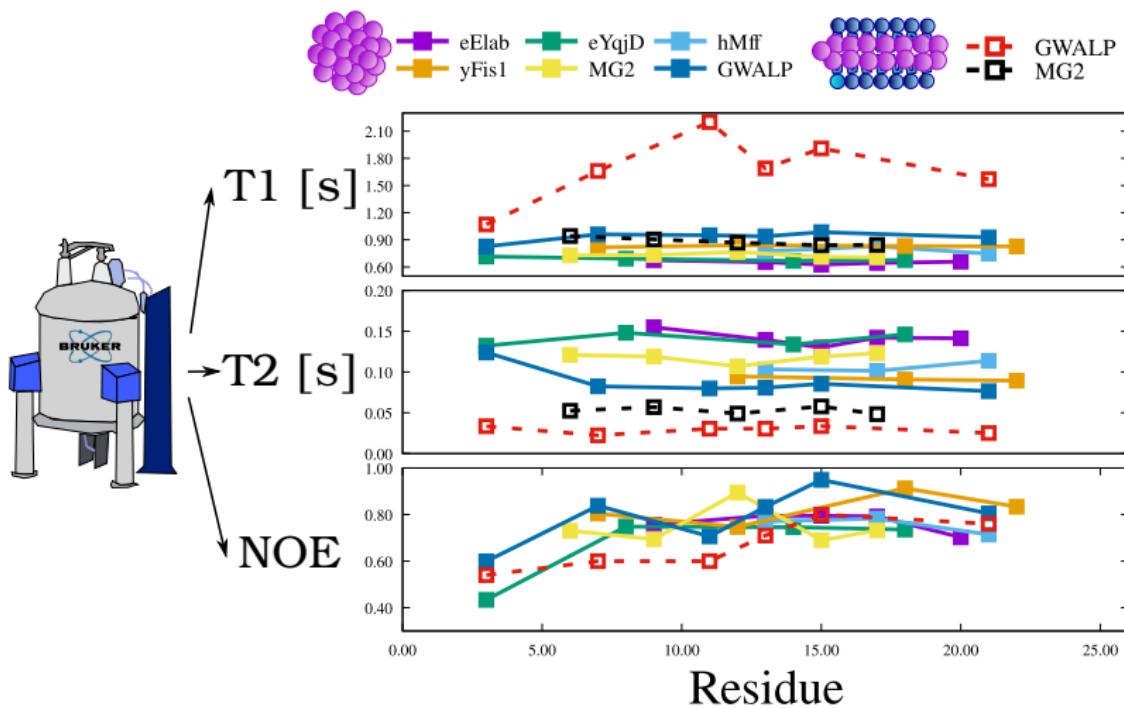
# Results



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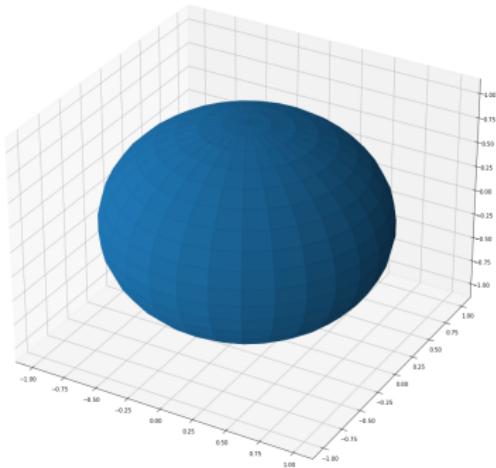


# Results



# How can we interpret experimental NMR spin relaxation times?

To be developed or deleted, comment on what people do otherwise...



# How can we interpret experimental NMR spin relaxation times?

## Redfield equations

$$\frac{1}{T_1} = \frac{d_{\text{NH}}^2}{20} [J(\omega_H - \omega_N) + 3J(\omega_N) + 6J(\omega_H + \omega_N)]$$

$$\frac{1}{T_2} = \frac{1}{2} \frac{d_{\text{NH}}^2}{20} [4J(0) + J(\omega_H - \omega_N) + 3J(\omega_N) + 3J(\omega_H) + 6J(\omega_H + \omega_N)]$$

$$\text{NOE} = 1 + \frac{d_{\text{NH}}^2}{20} [J(\omega_H + 6J(\omega_H + \omega_N))] \frac{\gamma_H T_1}{\gamma_N}$$

# How can we interpret experimental NMR spin relaxation times?

## Redfield equations

Dipolar coupling constant

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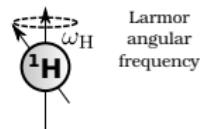
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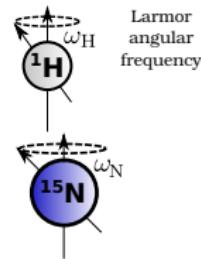
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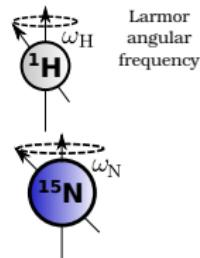
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Dipolar coupling constant



## spectral density

$$J(\omega) = 2 \int_0^\infty C(t) \cos(\omega t) dt$$

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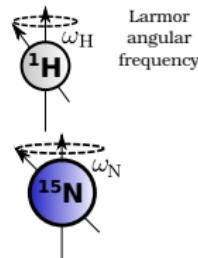
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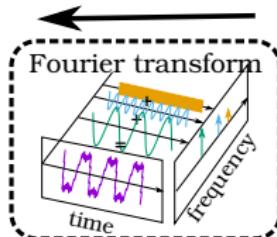
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$$J(\omega) = 2 \int_0^\infty C(t) \cos(\omega t) dt$$



# How can we interpret experimental NMR spin relaxation times?

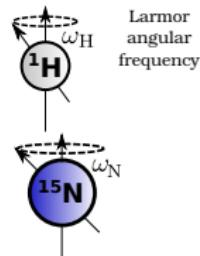
## Redfield equations

$$\frac{1}{T_1} = \frac{d_{\text{NH}}^2}{20} [J(\omega_H - \omega_N) + 3J(\omega_N) + 6J(\omega_H + \omega_N)]$$

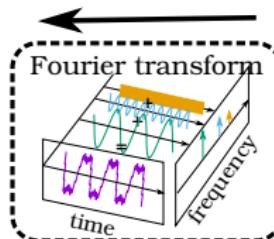
$$\frac{1}{T_2} = \frac{1}{2} \frac{d_{\text{NH}}^2}{20} [4J(0) + J(\omega_H - \omega_N) + 3J(\omega_N) + 3J(\omega_H) + 6J(\omega_H + \omega_N)]$$

$$\text{NOE} = 1 + \frac{d_{\text{NH}}^2}{20} [J(\omega_H + 6J(\omega_H + \omega_N))] \frac{\gamma_H T_1}{\gamma_N}$$

Dipolar coupling constant



spectral density  
 $J(\omega) = 2 \int_0^\infty C(t) \cos(\omega t) dt$



second-order rotational correlation function of N-H bond vector

$$C(t) = \left\langle \frac{3}{2} \cos^2 \theta_{t'+t} - \frac{1}{2} \right\rangle_{t'}$$

# How can we interpret experimental NMR spin relaxation times?

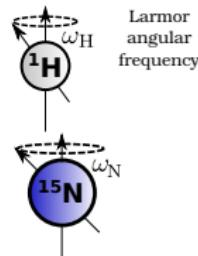
## Redfield equations

$$\frac{1}{T_1} = \frac{d_{\text{NH}}^2}{20} [J(\omega_H - \omega_N) + 3J(\omega_N) + 6J(\omega_H + \omega_N)]$$

$$\frac{1}{T_2} = \frac{1}{2} \frac{d_{\text{NH}}^2}{20} [4J(0) + J(\omega_H - \omega_N) + 3J(\omega_N) + 3J(\omega_H) + 6J(\omega_H + \omega_N)]$$

$$\text{NOE} = 1 + \frac{d_{\text{NH}}^2}{20} [J(\omega_H + 6J(\omega_H + \omega_N))] \frac{\gamma_H T_1}{\gamma_N}$$

Dipolar coupling constant



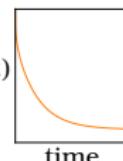
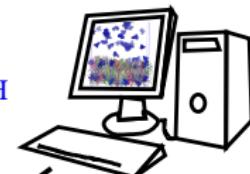
Larmor angular frequency

spectral density  
 $J(\omega) = 2 \int_0^\infty C(t) \cos(\omega t) dt$

Fourier transform

second-order rotational correlation function of N-H bond vector

$$C(t) = \left\langle \frac{3}{2} \cos^2 \theta_{t'+t} - \frac{1}{2} \right\rangle_{t'}$$

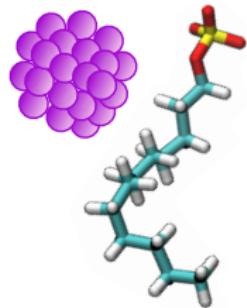


# Results

# Empty SDS micelles

SDS

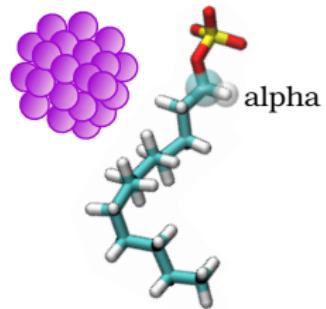
sodium dodecyl sulfate



# Empty SDS micelles

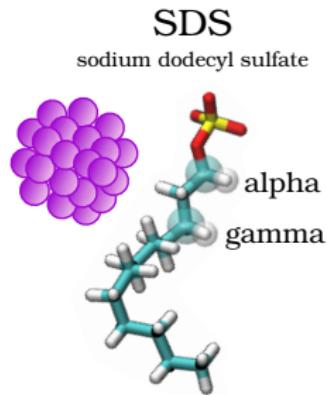
SDS

sodium dodecyl sulfate

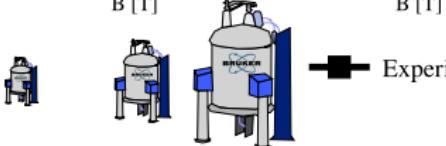
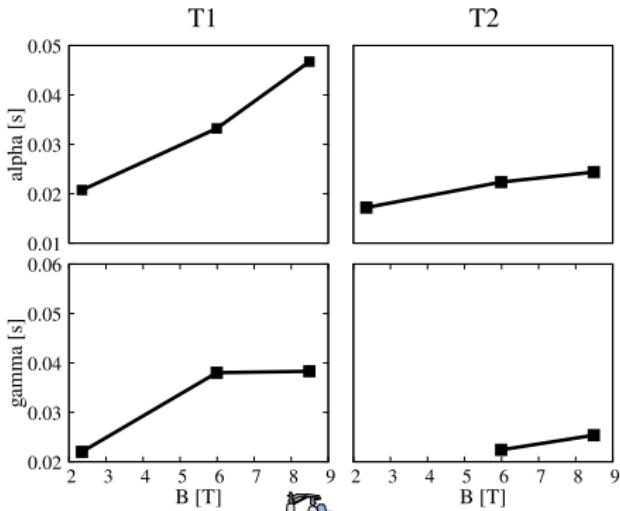
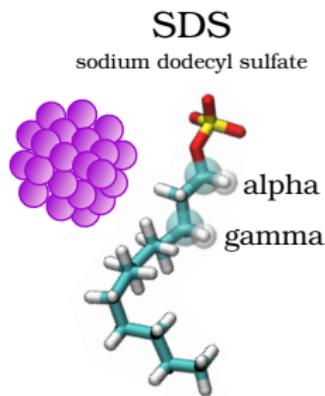


alpha

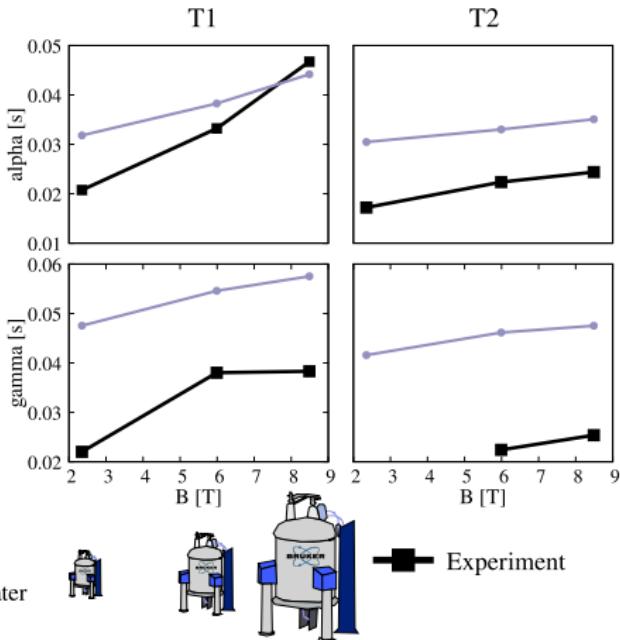
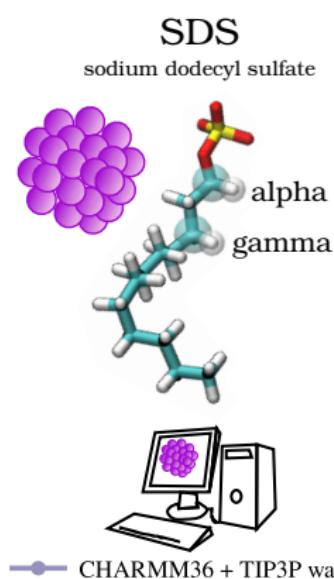
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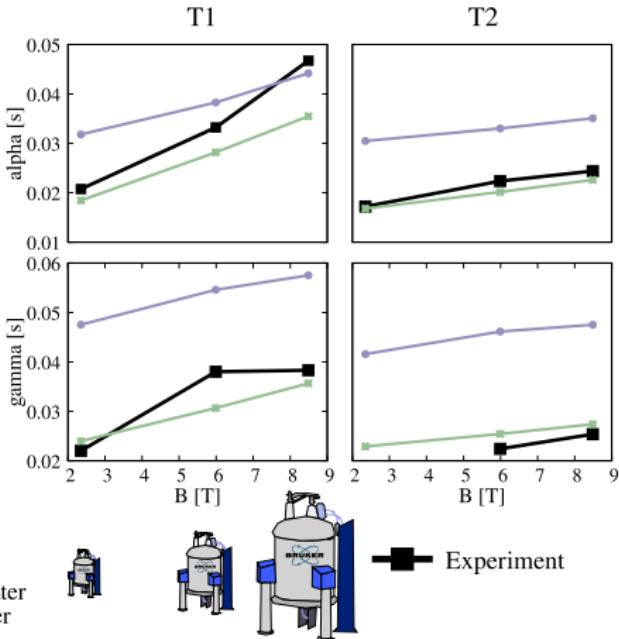
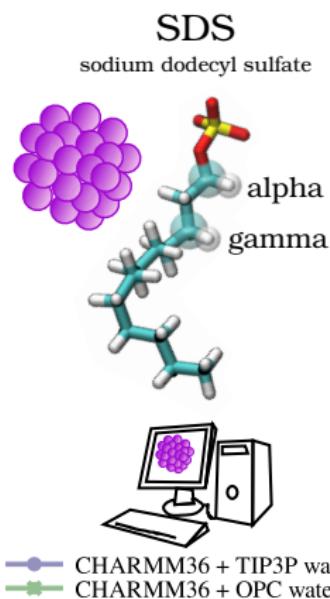
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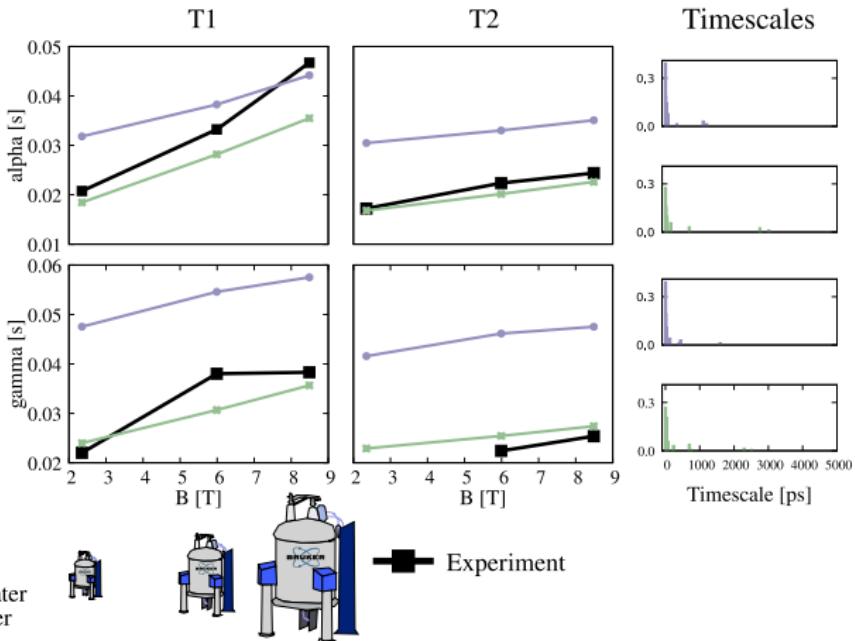
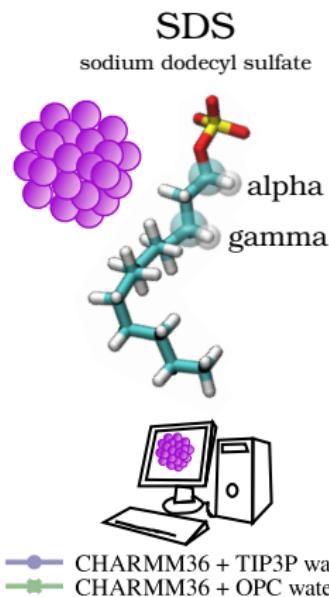
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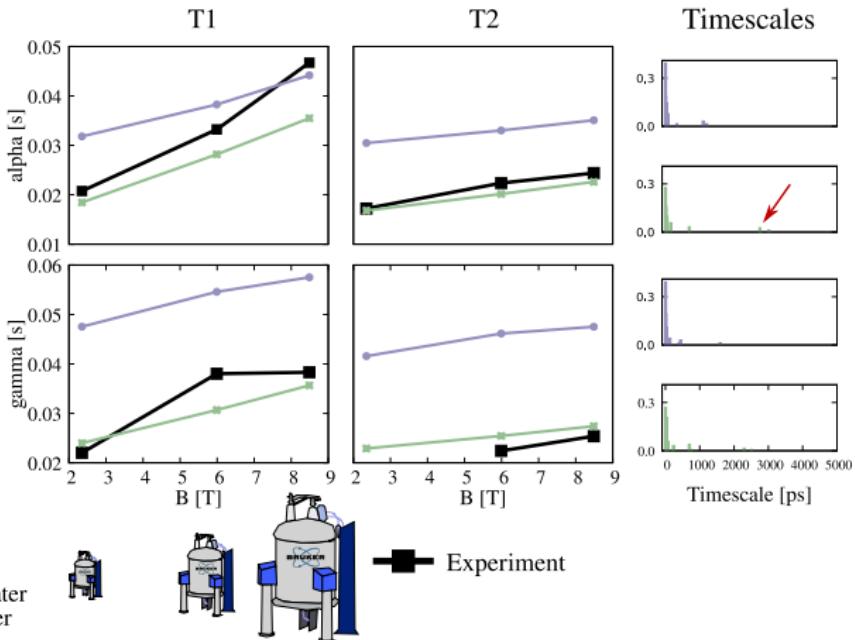
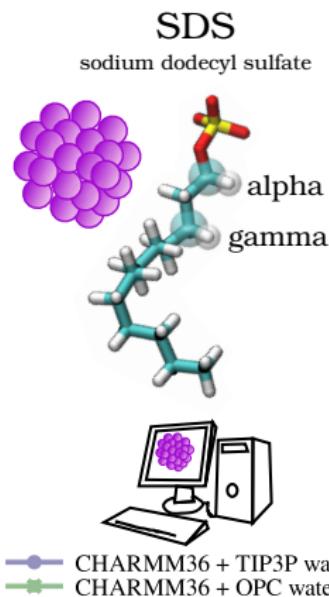
# Empty SDS micelles



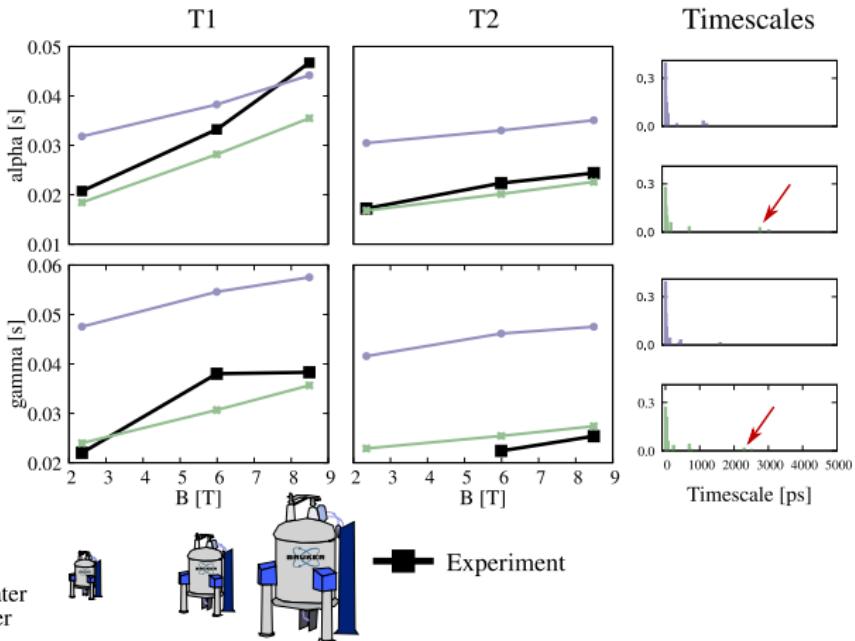
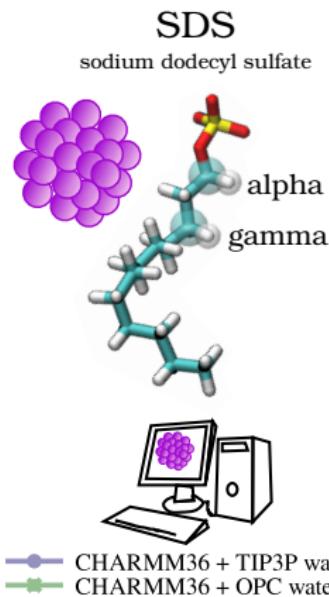
# Empty SDS micelles



# Empty SDS micelles

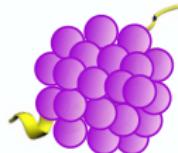


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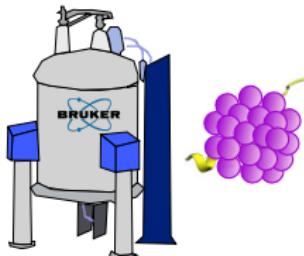
# Optimization of simulations

■ Magainin 2

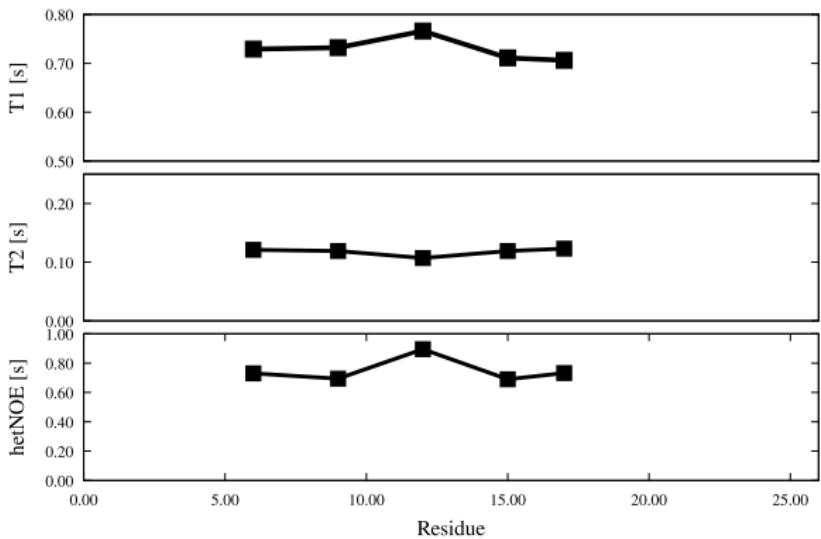


# Optimization of simulations

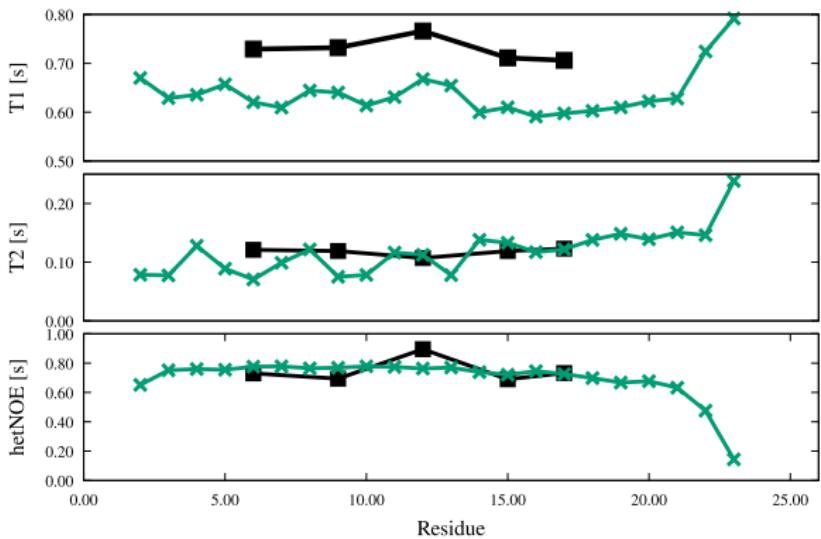
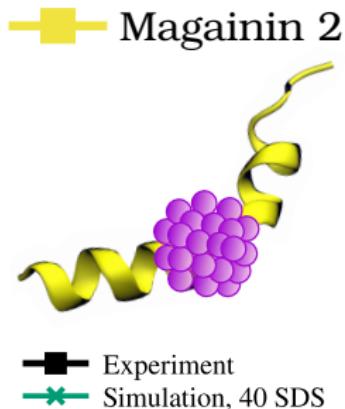
■ Magainin 2



■ Experiment

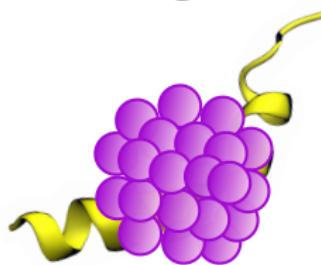


# Optimization of simulations

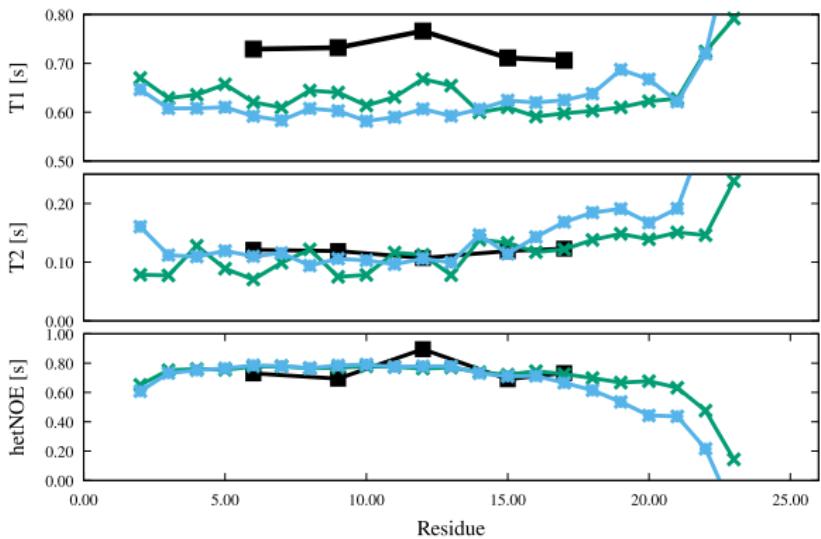


# Optimization of simulations

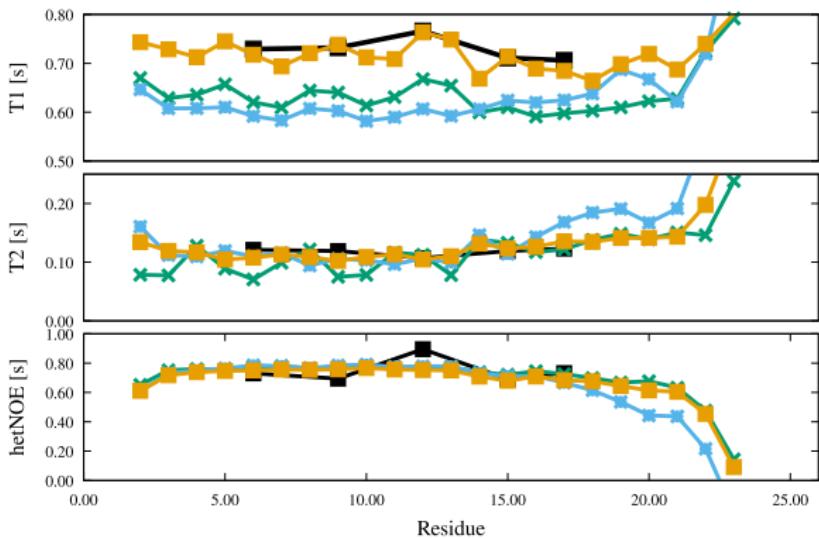
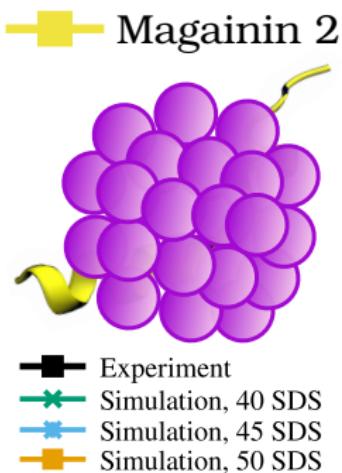
Magainin 2



- Experiment
- Simulation, 40 SDS
- Simulation, 45 SDS

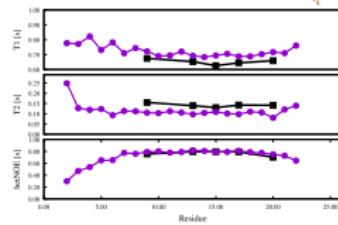
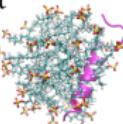


# Optimization of simulations



■ Experiment

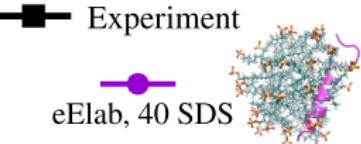
eElab, 40 SDS



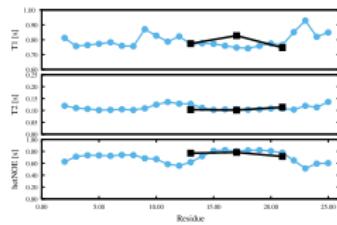
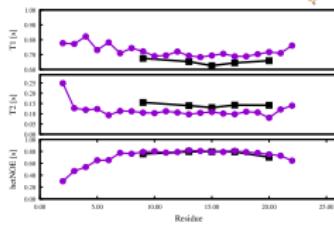
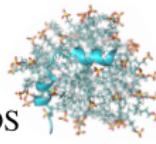
■ Experiment



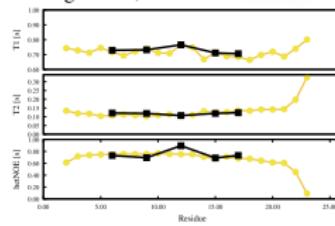
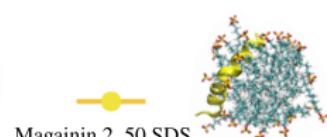
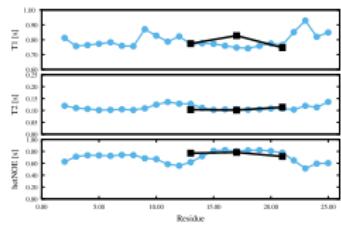
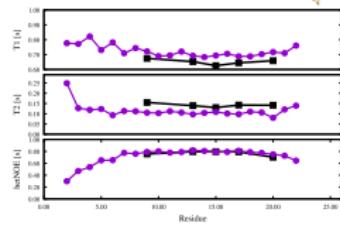
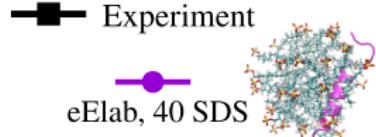
eElab, 40 SDS



hMff, 50 SDS



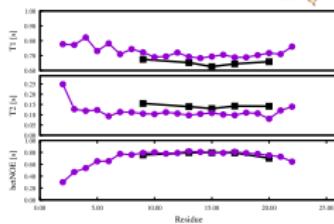
■ Experiment



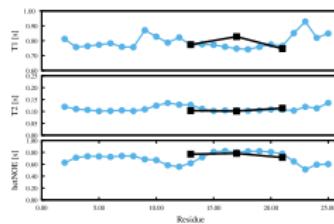
■ Experiment



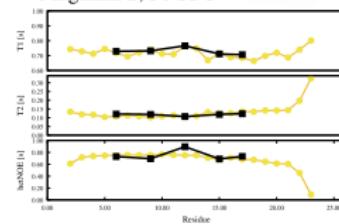
eElab, 40 SDS



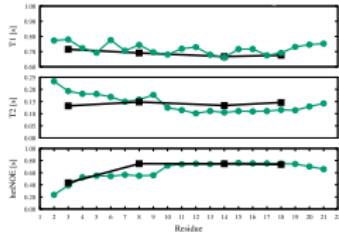
hMff, 50 SDS



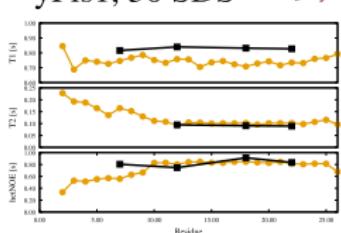
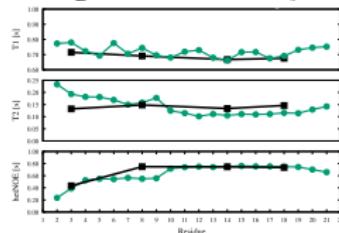
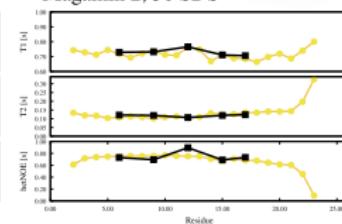
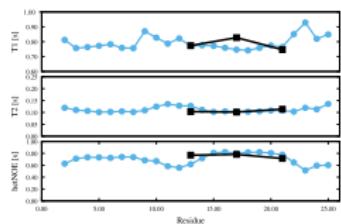
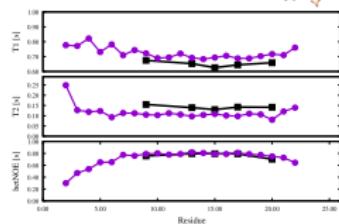
Magainin 2, 50 SDS



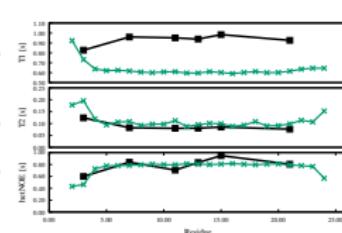
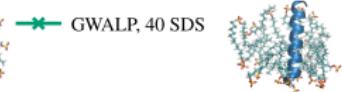
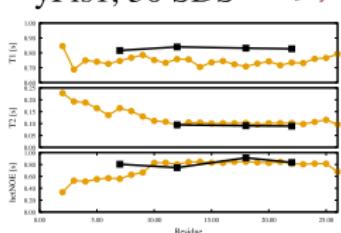
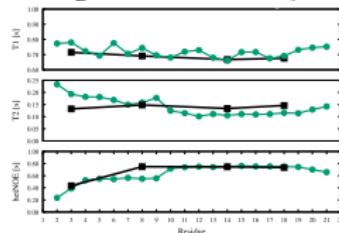
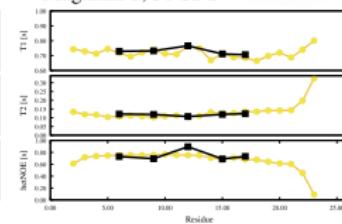
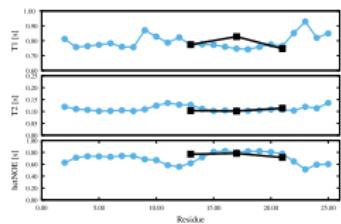
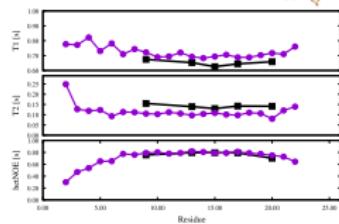
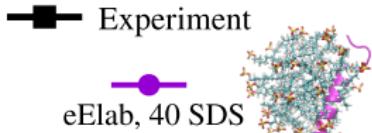
eYqjD, 50 SDS



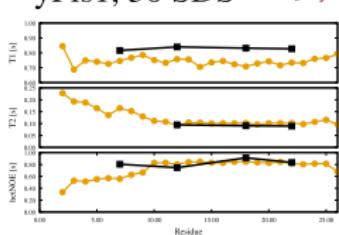
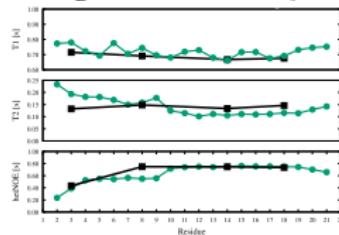
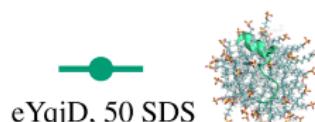
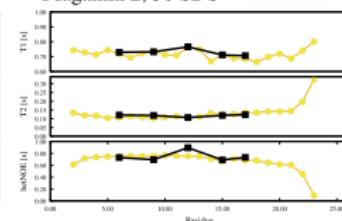
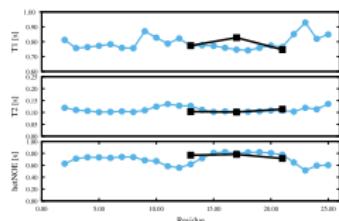
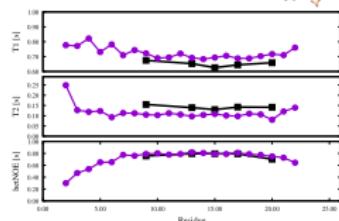
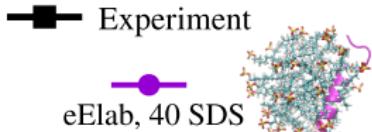
■ Experiment



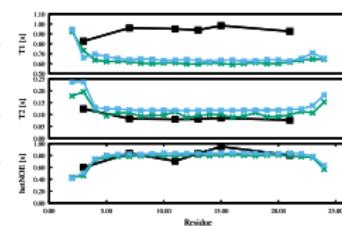
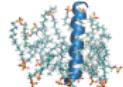
■ Experiment



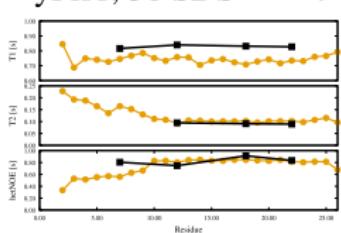
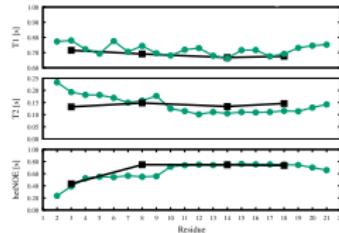
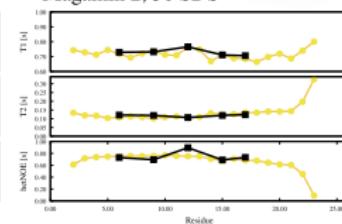
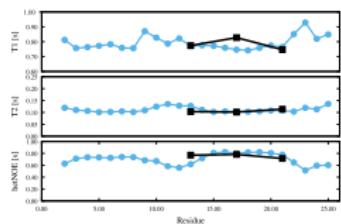
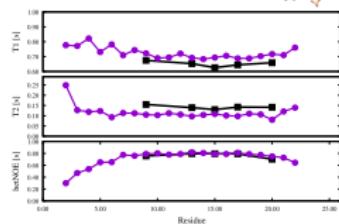
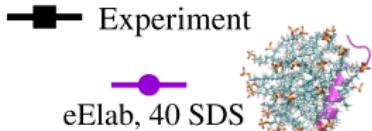
■ Experiment



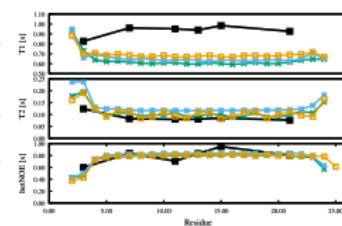
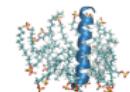
GWALP, 40 SDS  
GWALP 45 SDS

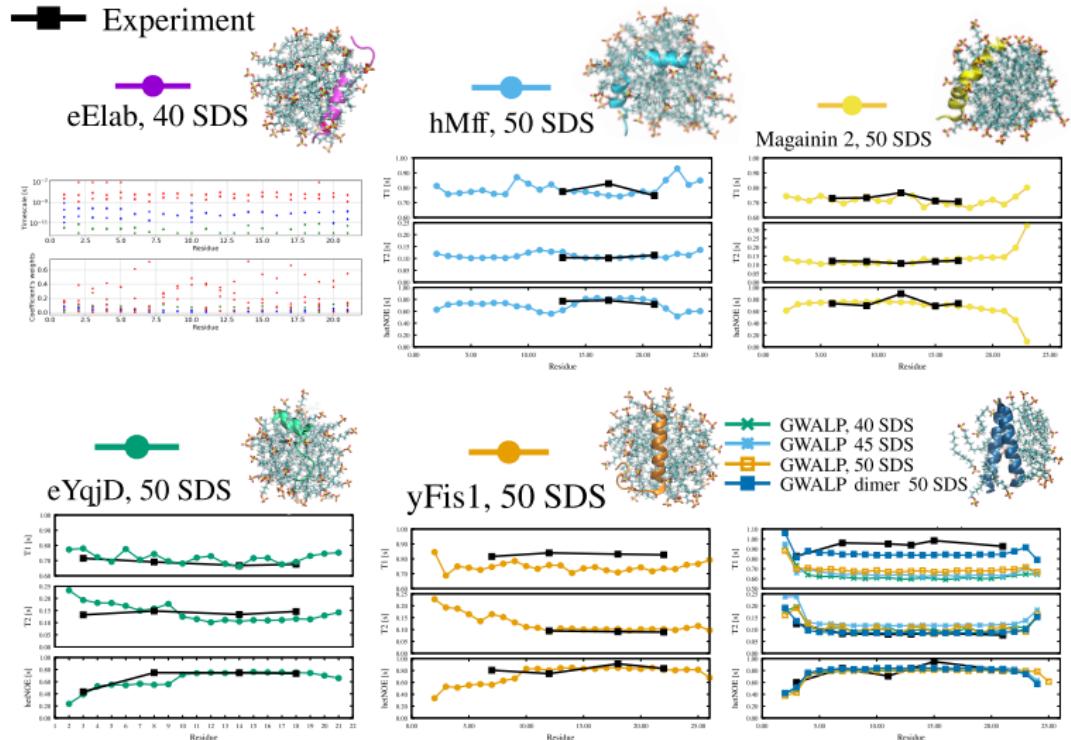


■ Experiment



GWALP, 40 SDS  
GWALP 45 SDS  
GWALP, 50 SDS

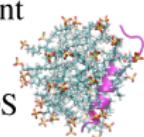




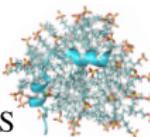
Experiment



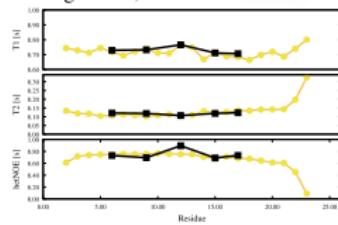
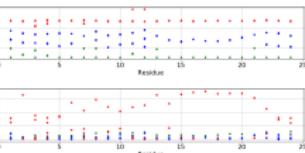
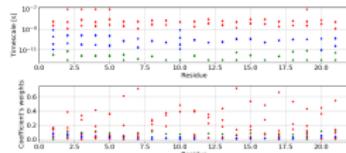
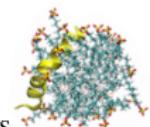
eElab, 40 SDS



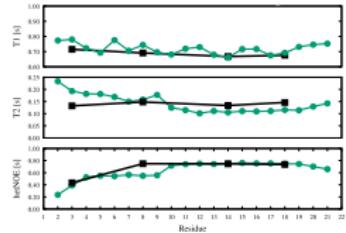
hMff, 50 SDS



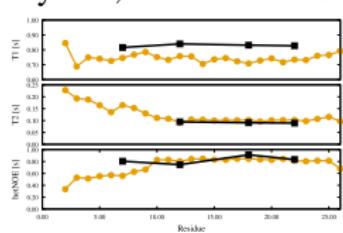
Magainin 2, 50 SDS



eYqjD, 50 SDS



yFis1, 50 SDS

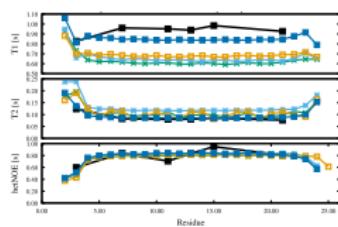
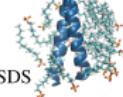


GWALP, 40 SDS

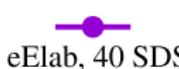
GWALP, 45 SDS

GWALP, 50 SDS

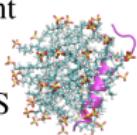
GWALP dimer 50 SDS



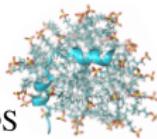
■ Experiment



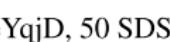
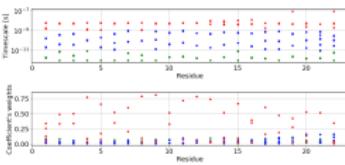
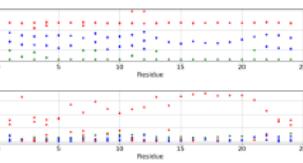
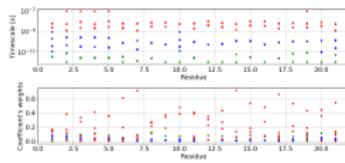
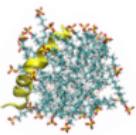
eElab, 40 SDS



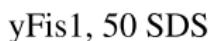
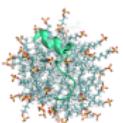
hMff, 50 SDS



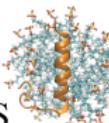
Magainin 2, 50 SDS



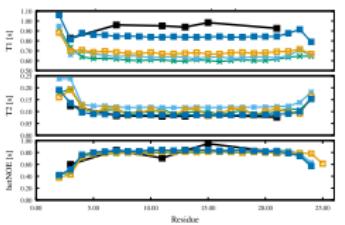
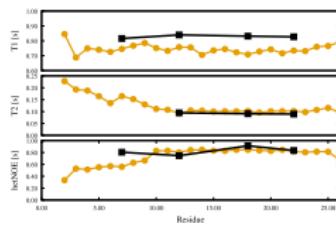
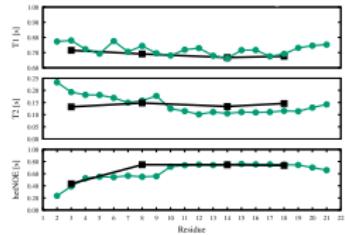
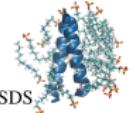
eYqjD, 50 SDS



yFis1, 50 SDS



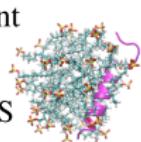
GWALP, 40 SDS  
GWALP 45 SDS  
GWALP, 50 SDS  
GWALP dimer 50 SDS



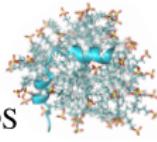
Experiment



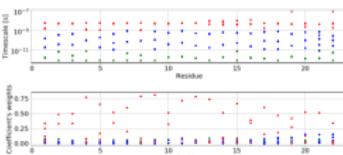
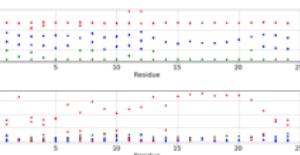
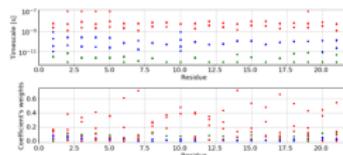
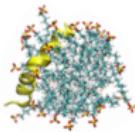
eElab, 40 SDS



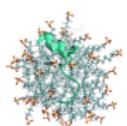
hMff, 50 SDS



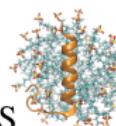
Magainin 2, 50 SDS



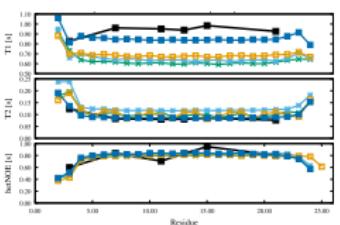
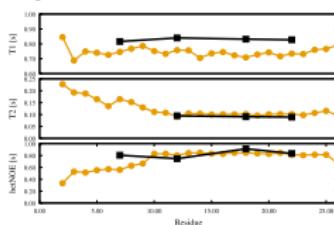
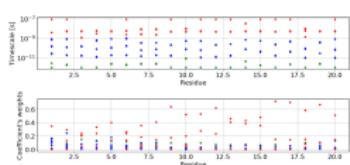
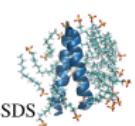
eYqjD, 50 SDS



yFis1, 50 SDS



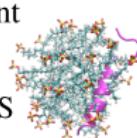
GWALP, 40 SDS  
GWALP 45 SDS  
GWALP, 50 SDS  
GWALP dimer 50 SDS



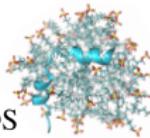
Experiment



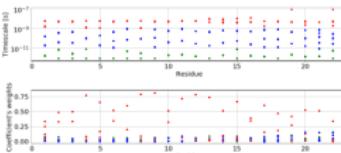
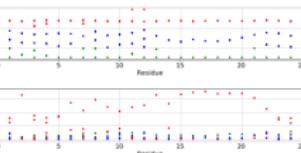
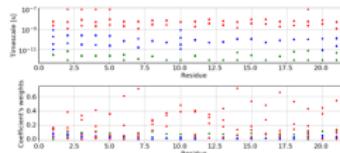
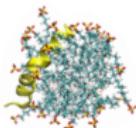
eElab, 40 SDS



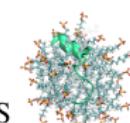
hMff, 50 SDS



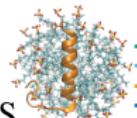
Magainin 2, 50 SDS



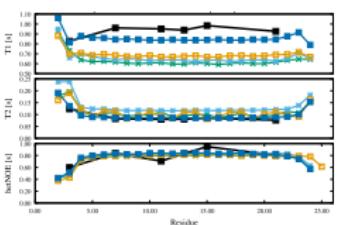
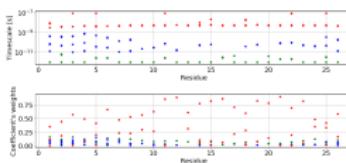
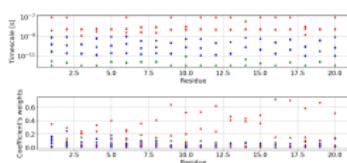
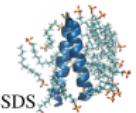
eYqjD, 50 SDS



yFis1, 50 SDS



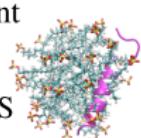
GWALP, 40 SDS  
GWALP 45 SDS  
GWALP, 50 SDS  
GWALP dimer 50 SDS



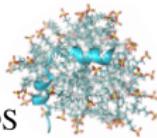
Experiment



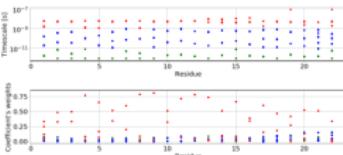
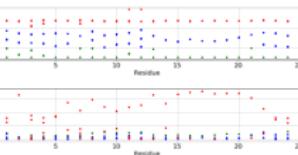
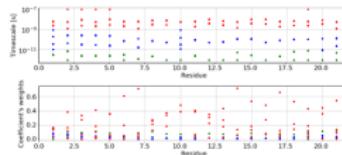
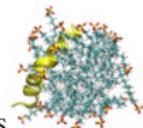
eElab, 40 SDS



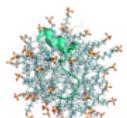
hMff, 50 SDS



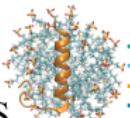
Magainin 2, 50 SDS



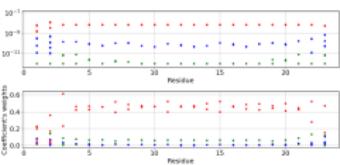
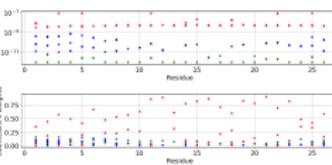
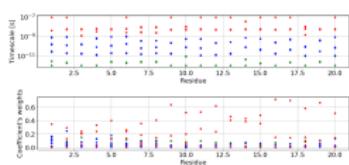
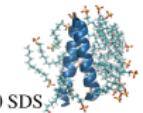
eYqjD, 50 SDS



yFis1, 50 SDS



GWALP, 40 SDS  
GWALP 45 SDS  
GWALP, 50 SDS  
GWALP dimer 50 SDS



## Results in Micelles

Empty bicelles work with CHARMM36 and  
OPC water

Optimization of micelle size  
GWALP fits better as dimer

to be developed

## **Results in Micelles**

We can get time scales

Comment on helicity??

to be developed

# Acknowledgments

to be developed