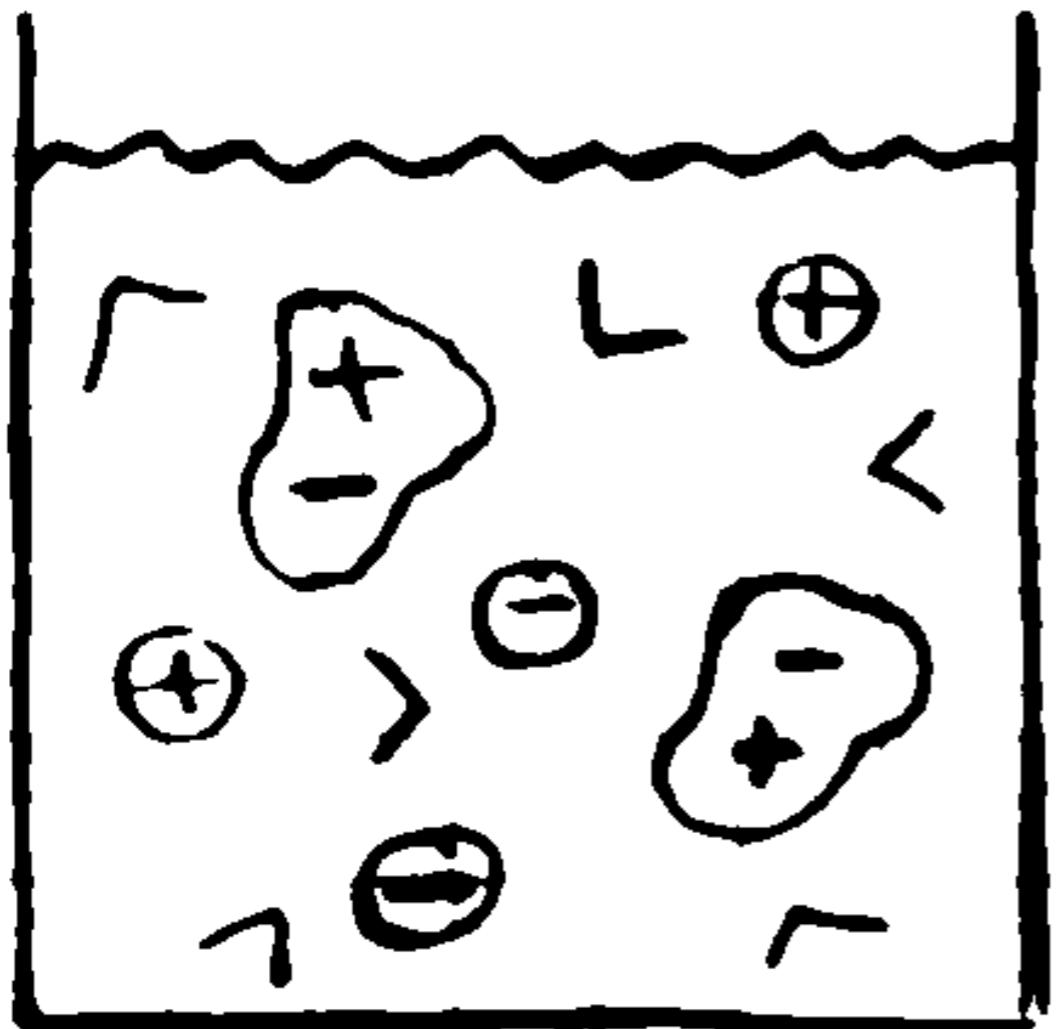


# Mesoscopic Simulations of Many-body Protein Interactions

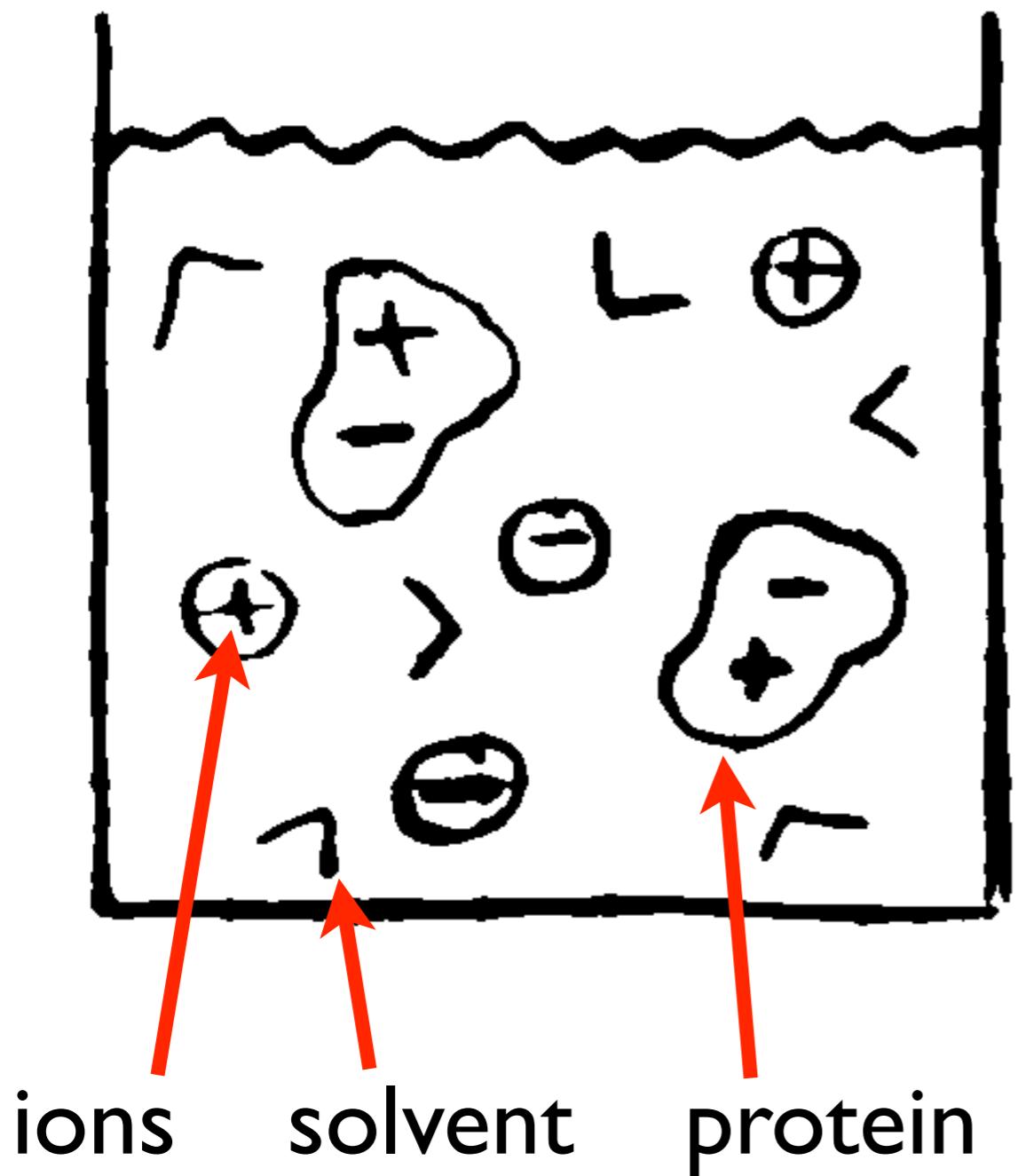
*NSC'09, October 2009*

*Mikael Lund*  
*Department of Theoretical Chemistry*  
*Lund University*

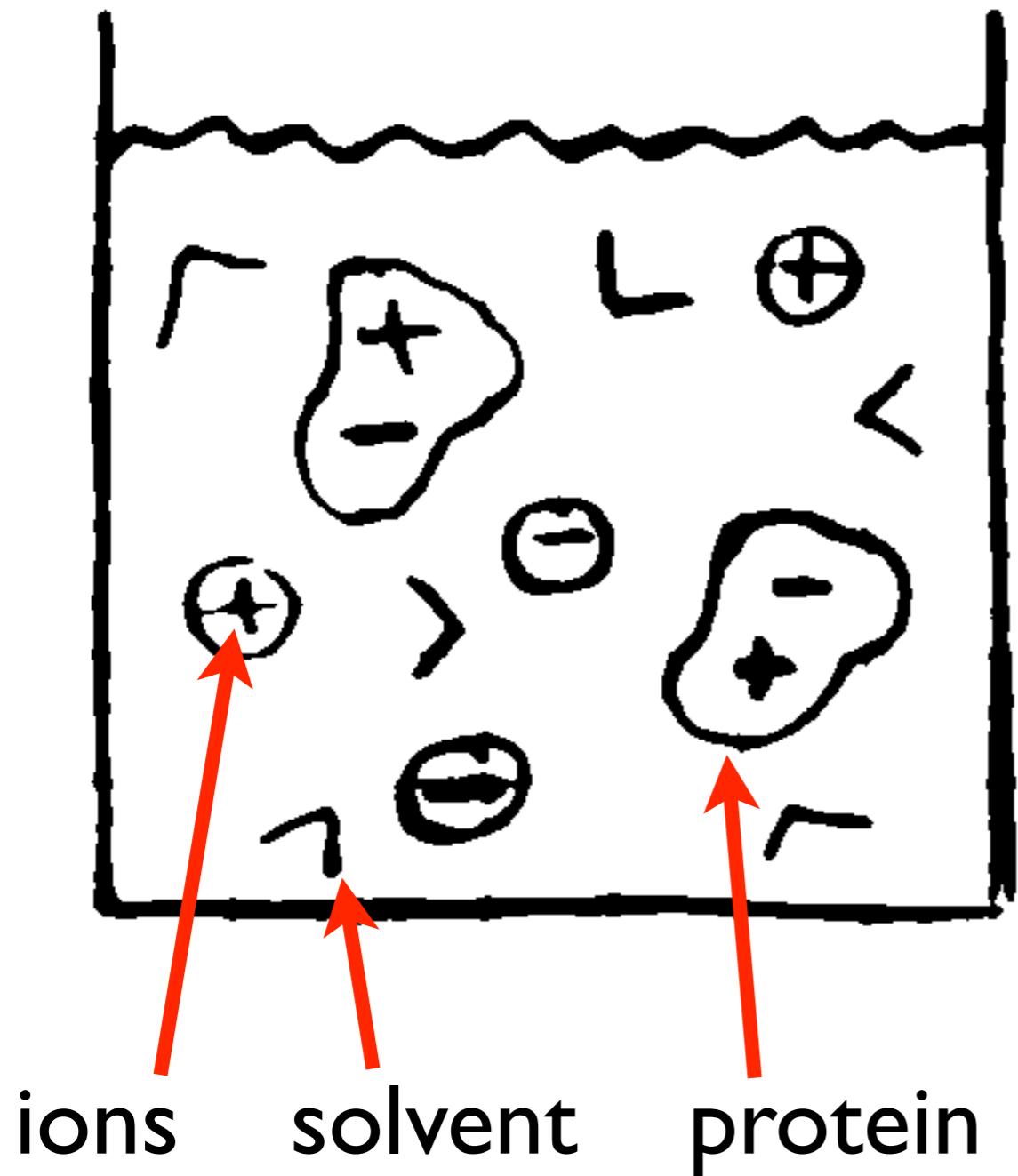
# Proteins in aqueous salt solutions



# Proteins in aqueous salt solutions

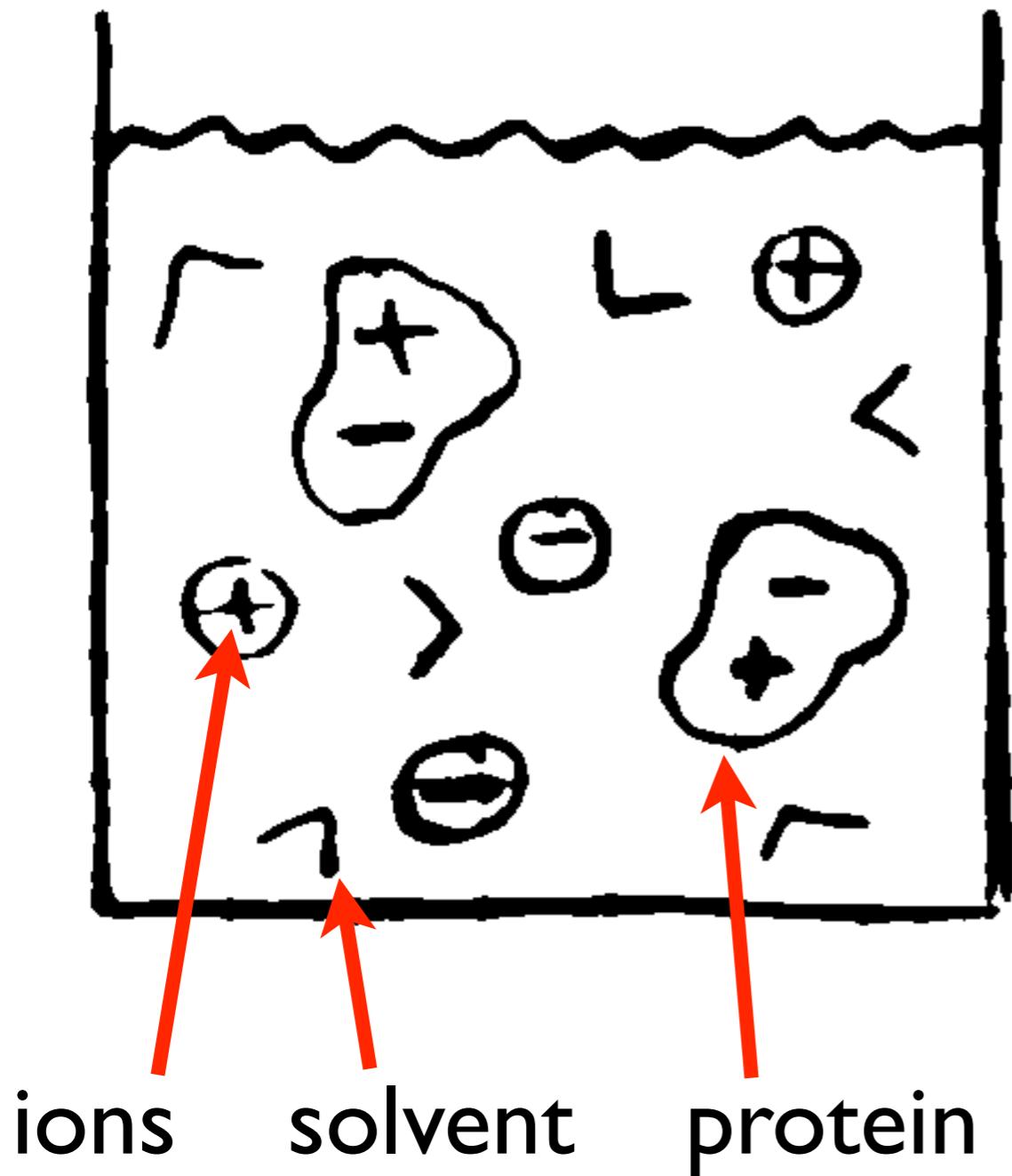


# Proteins in aqueous salt solutions

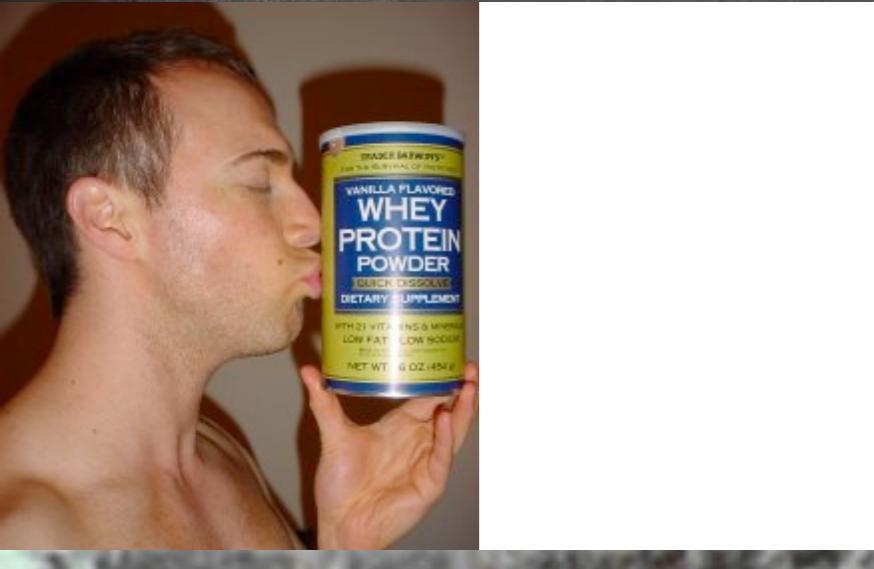


- Biological applications  
(strictly defined conditions)

# Proteins in aqueous salt solutions



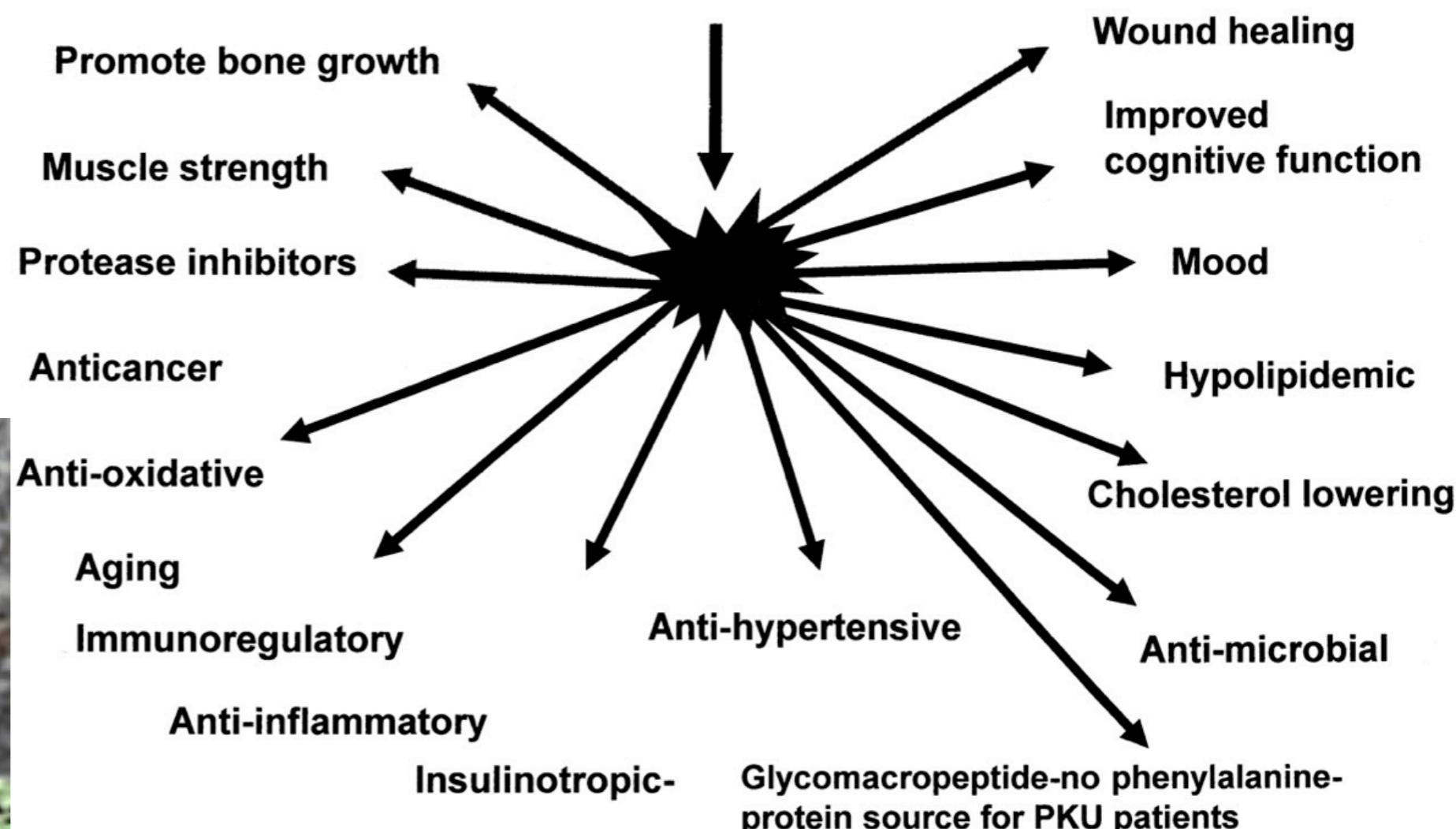
- Biological applications  
(strictly defined conditions)
- Technical applications  
(wider range of conditions)



**beta-lactoglobulin (65%)  
alpha-lactalbumin (25%)  
Serum albumin (8%)**



## Whey proteins

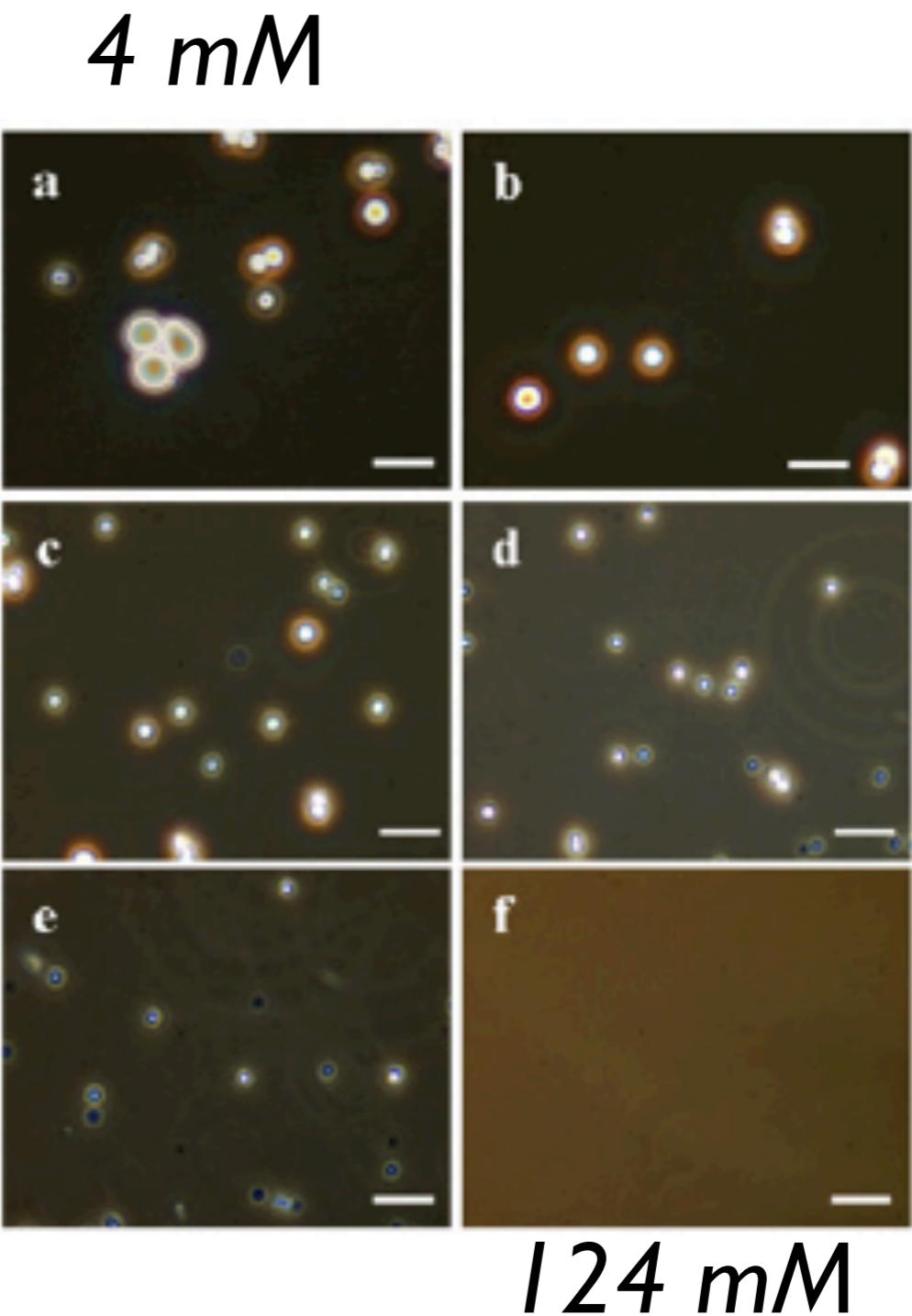


# Milk↔Egg Interactions!

# Milk↔Egg Interactions!

*M. Nigen et al. / Food Hydrocolloids 23 (2009) 510–518*

I:I mixture of lysozyme and  
α-lactalbumin in salt  
solutions

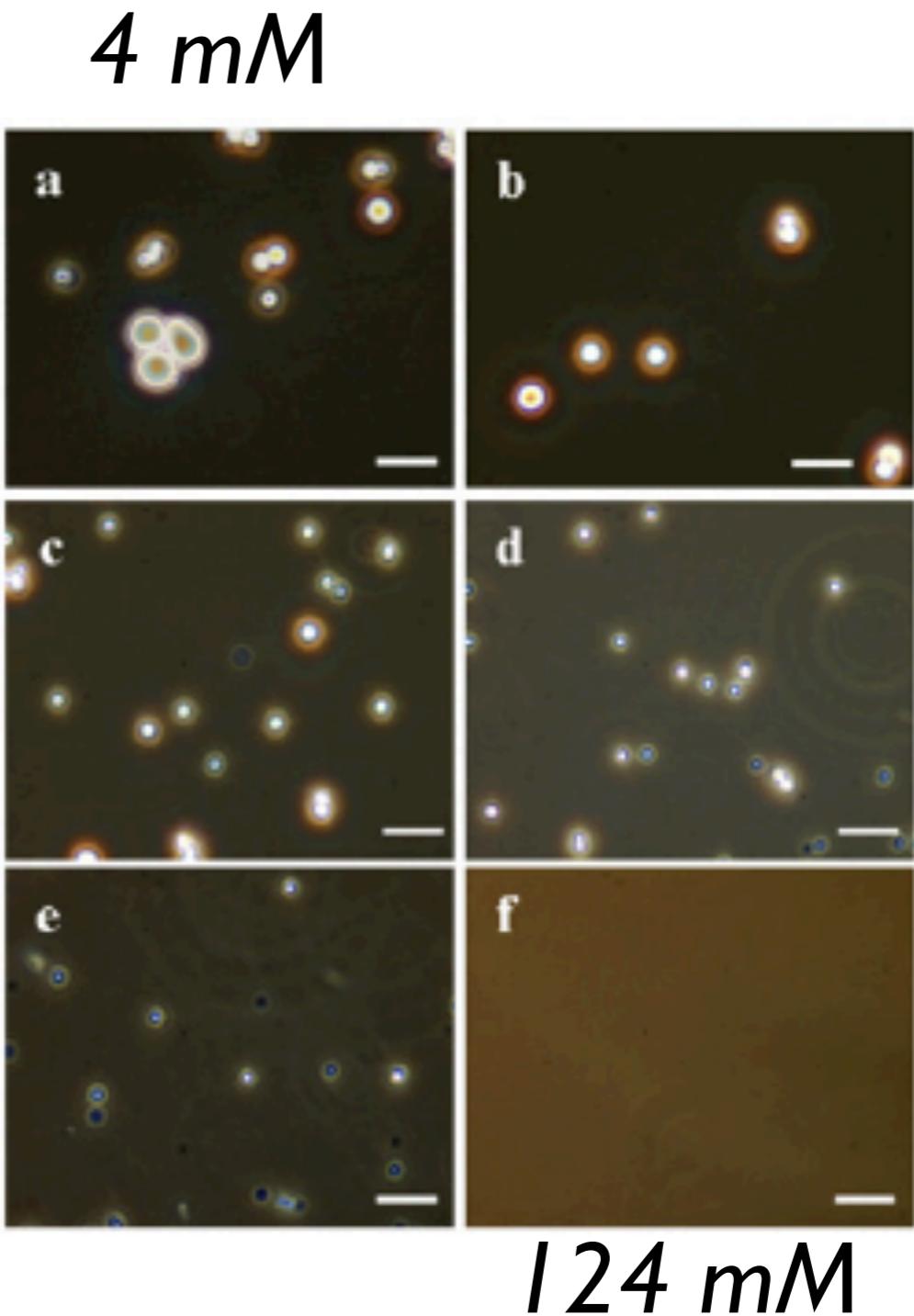


# Milk↔Egg Interactions!

*M. Nigen et al. / Food Hydrocolloids 23 (2009) 510–518*

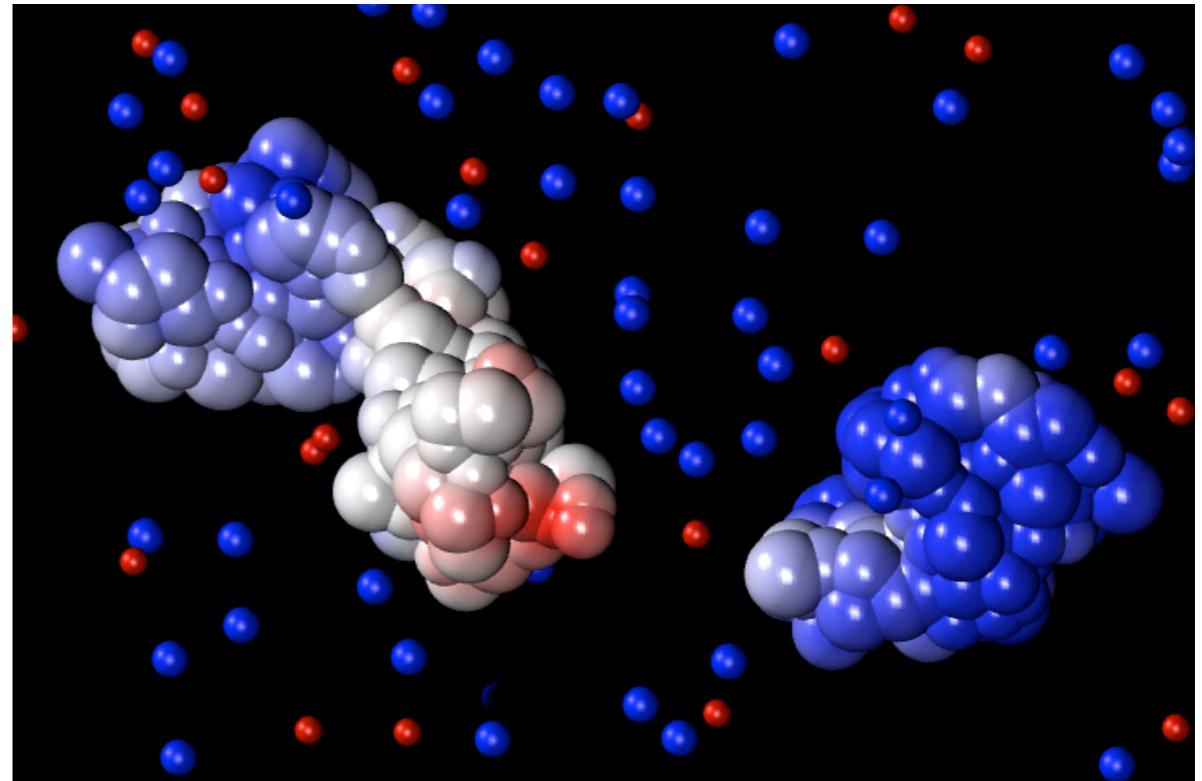
I:I mixture of lysozyme and  
α-lactalbumin in salt  
solutions

Rich salt and pH specific  
behavior.



# Model

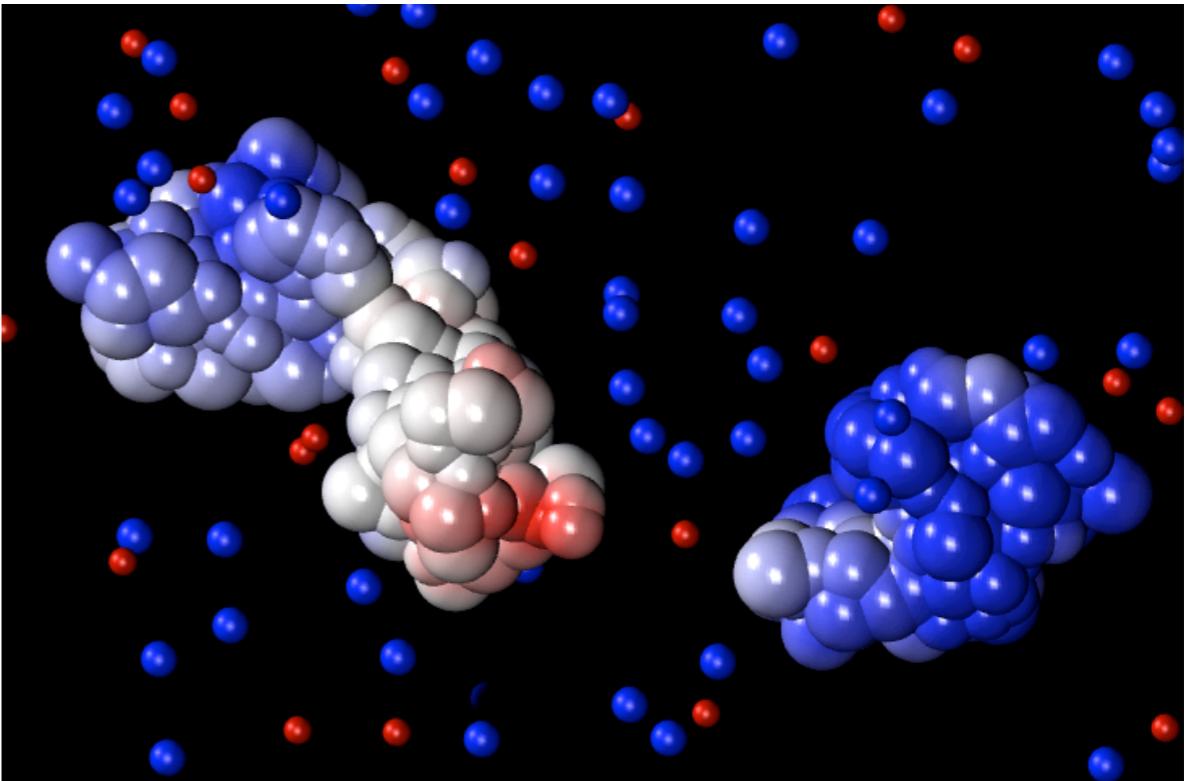
- Two (or more) proteins:  
lys &  $\alpha$ Lac.
- Explicit salt
- Continuum solvent
- Metropolis MC, NVT



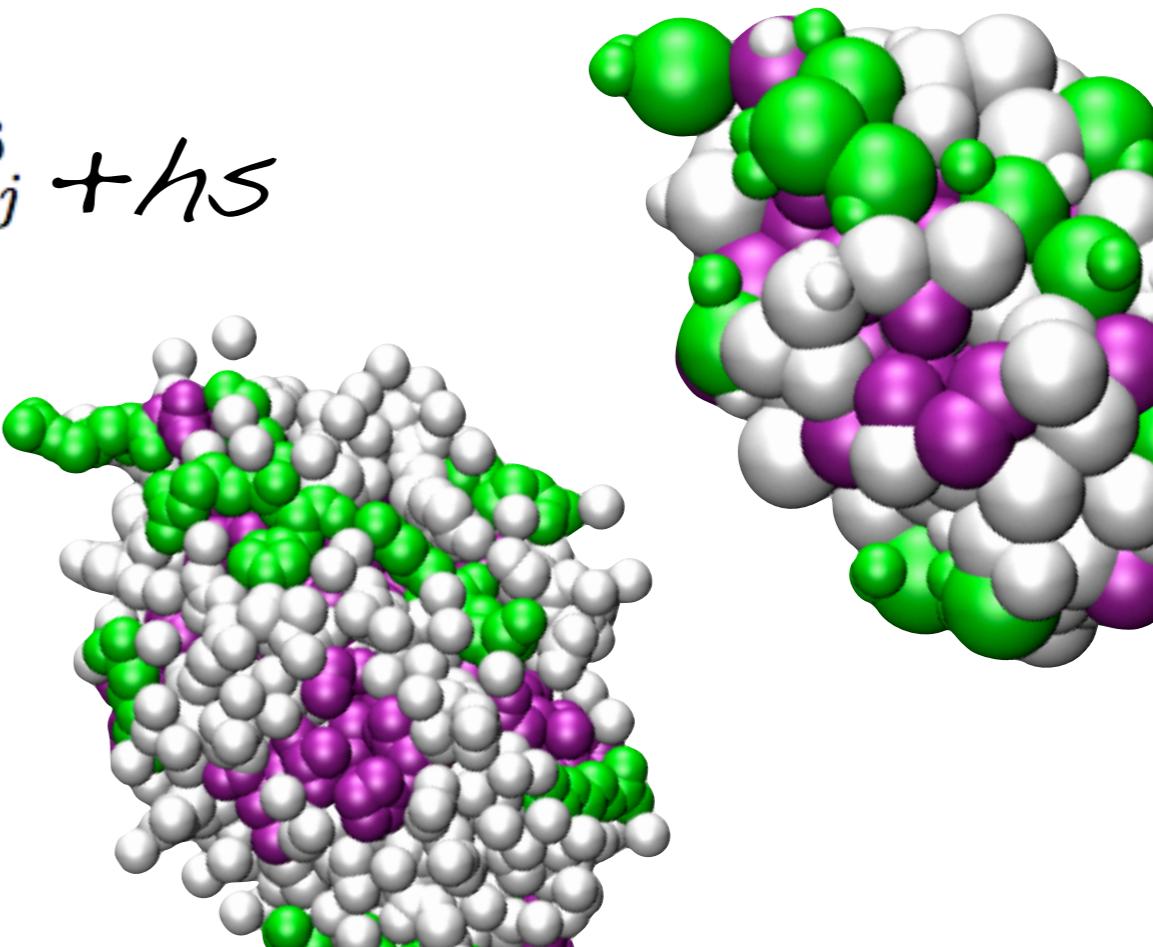
$$U = \sum_{i \neq j}^{N_{\text{all}}} \frac{e^2 q_i q_j}{4\pi\epsilon_0\epsilon_r r_{ij}} - \sum_i^{N_a} \sum_j^{N_b} C_{\text{vdW}} kT / r_{ij}^6 + h\varsigma$$

# Model

- Two (or more) proteins:  
lys &  $\alpha$ Lac.
- Explicit salt
- Continuum solvent
- Metropolis MC, NVT

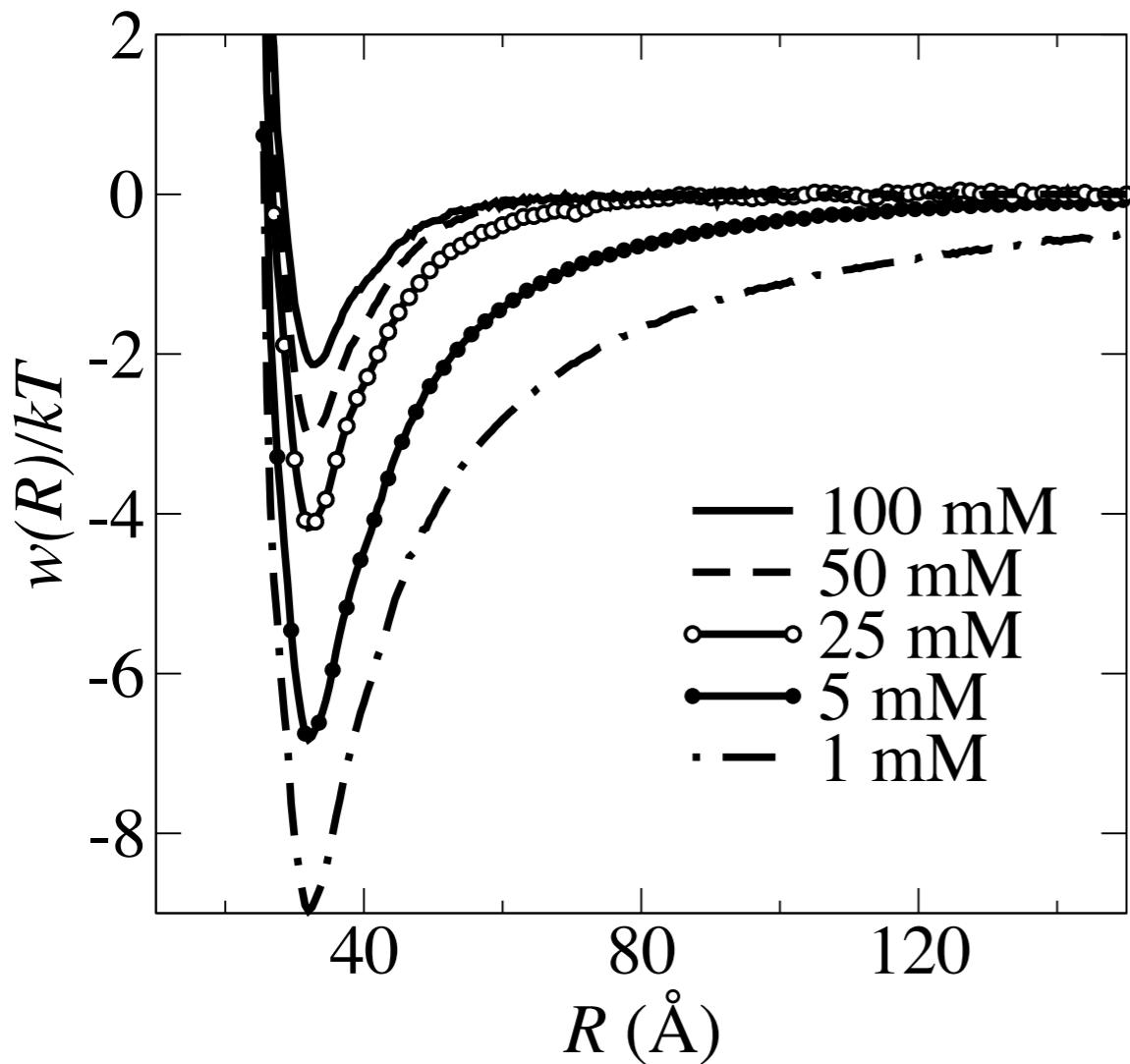


$$U = \sum_{i \neq j}^{N_{\text{all}}} \frac{e^2 q_i q_j}{4\pi\epsilon_0\epsilon_r r_{ij}} - \sum_i^{N_a} \sum_j^{N_b} C_{\text{vdW}} kT / r_{ij}^6 + hS$$

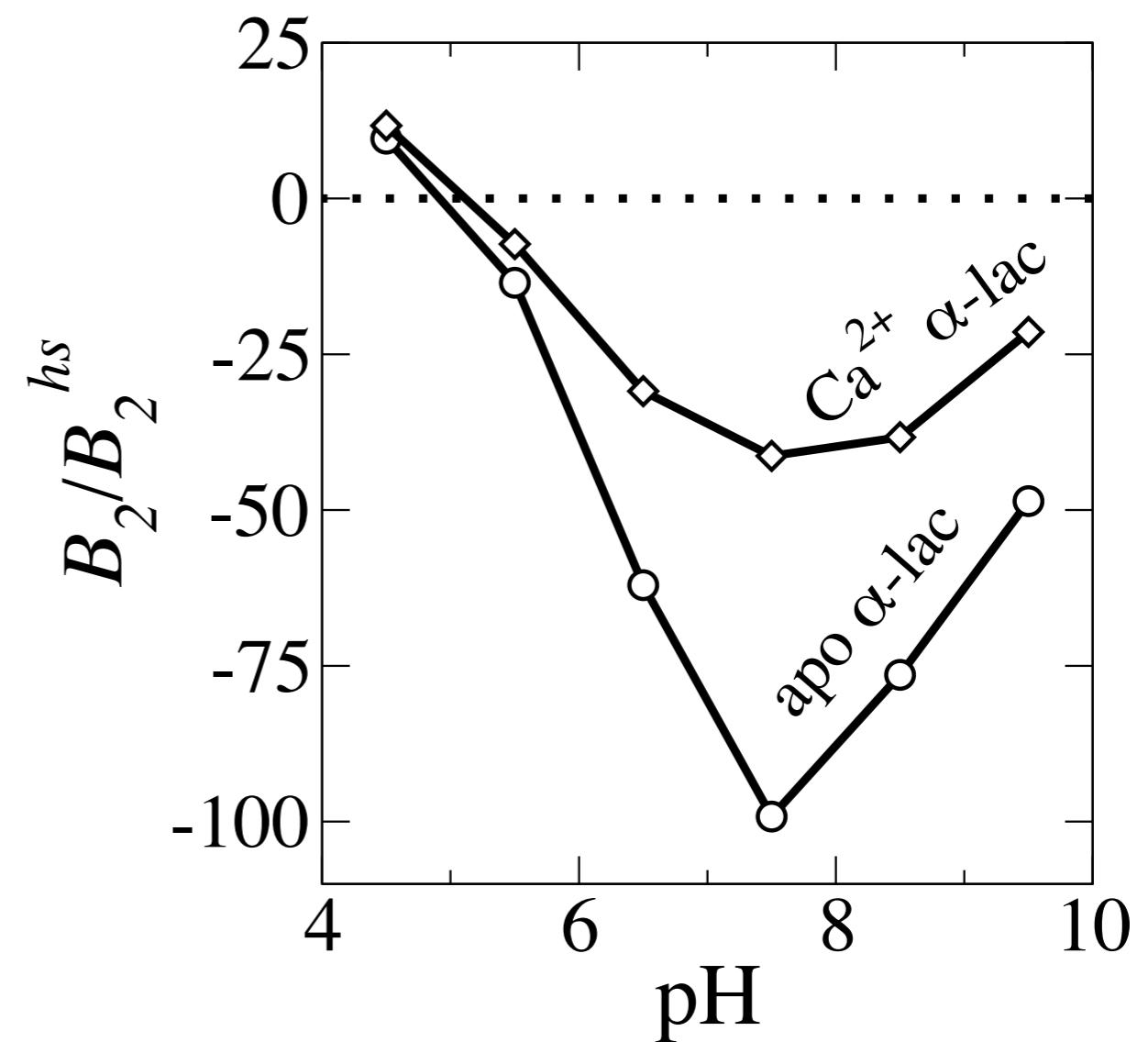
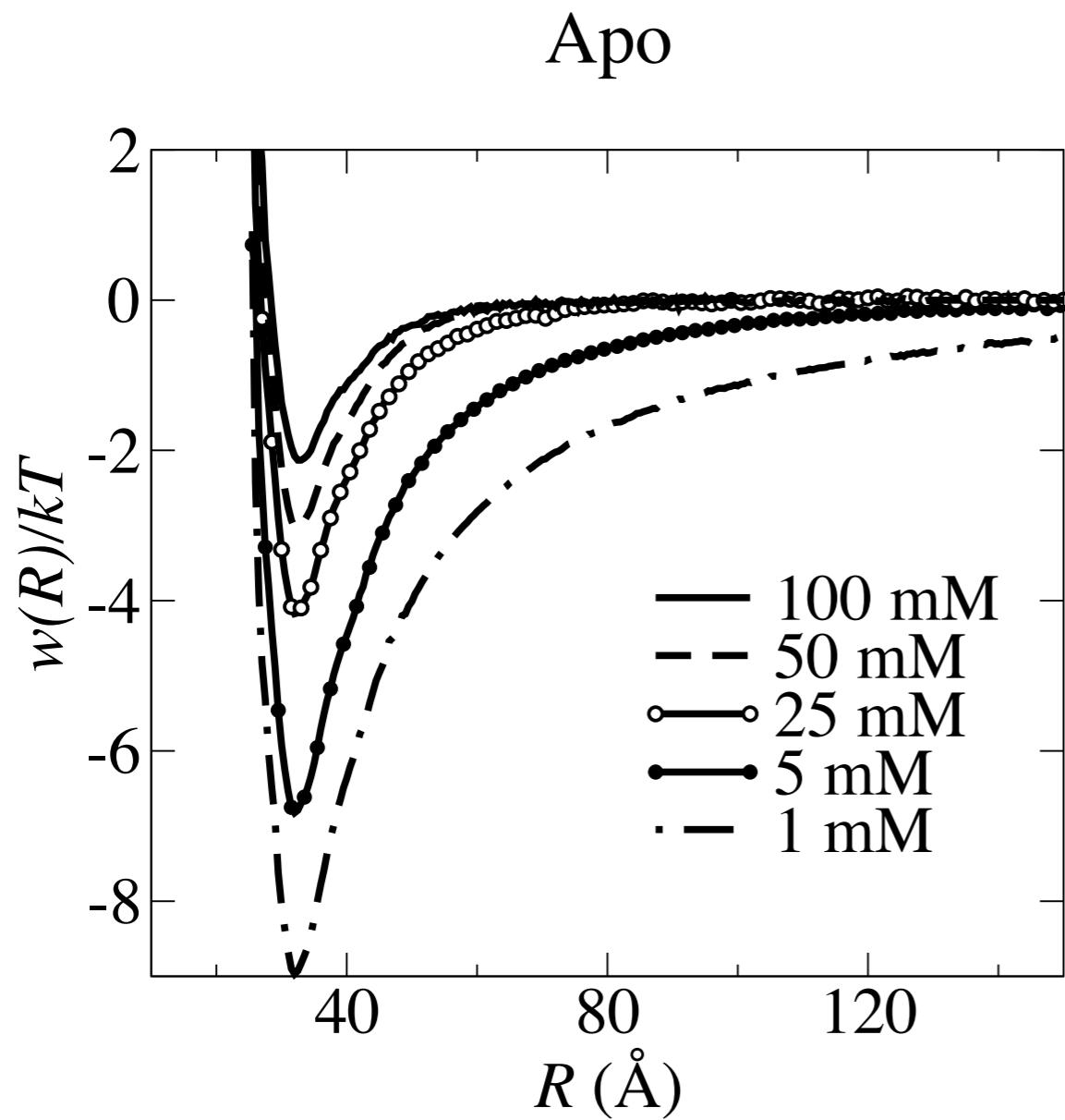


# Interaction free energy

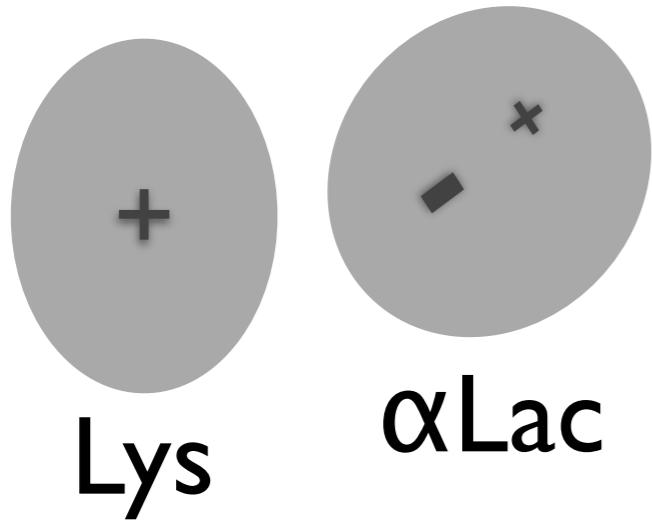
Apo



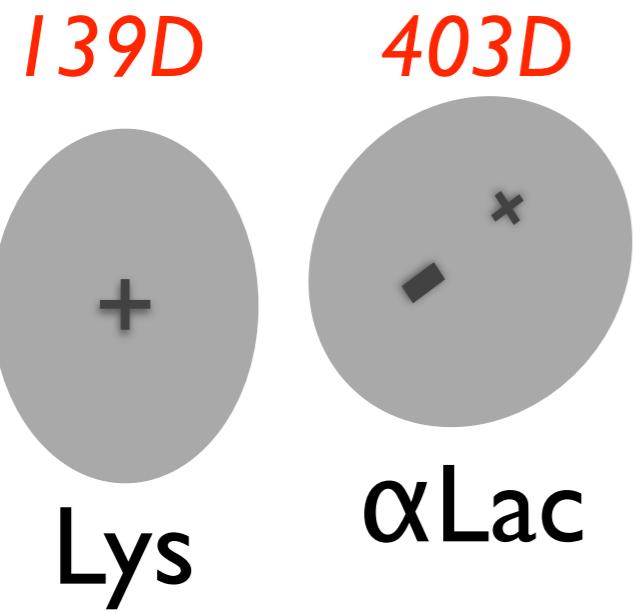
# Interaction free energy



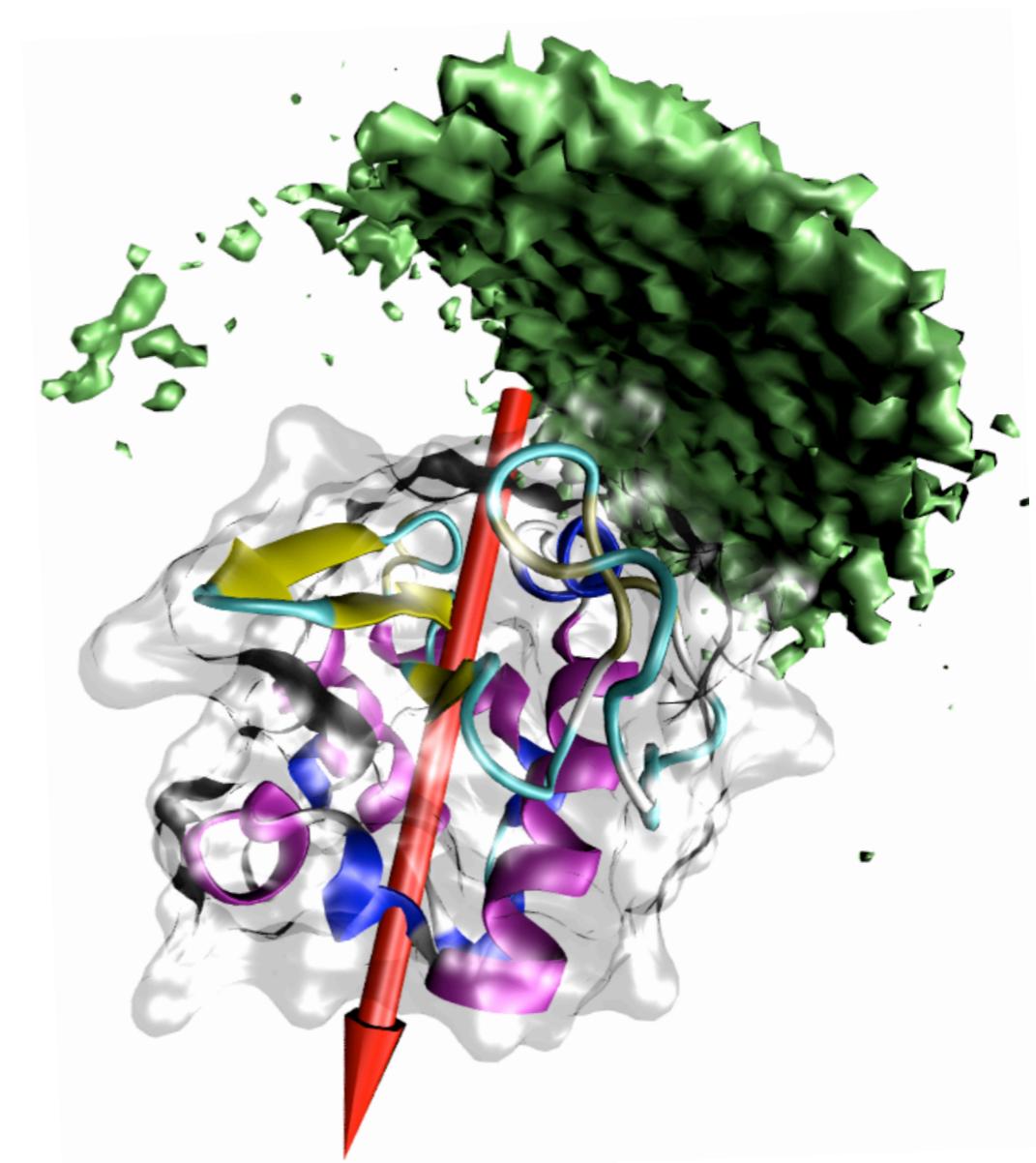
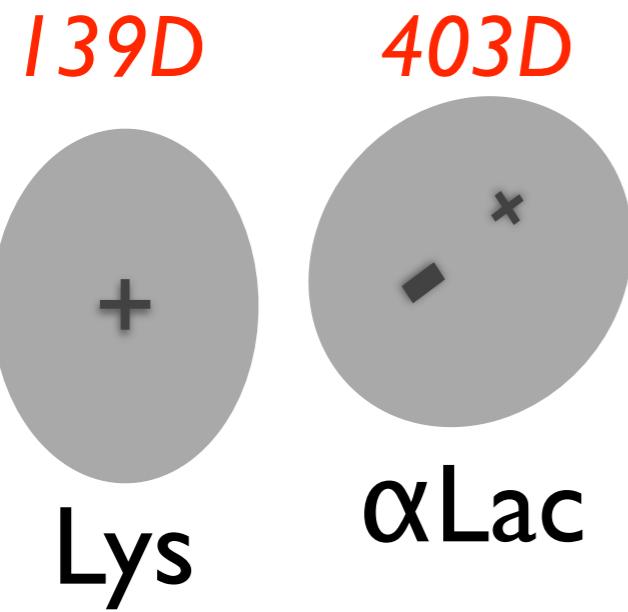
# Alignment



# Alignment



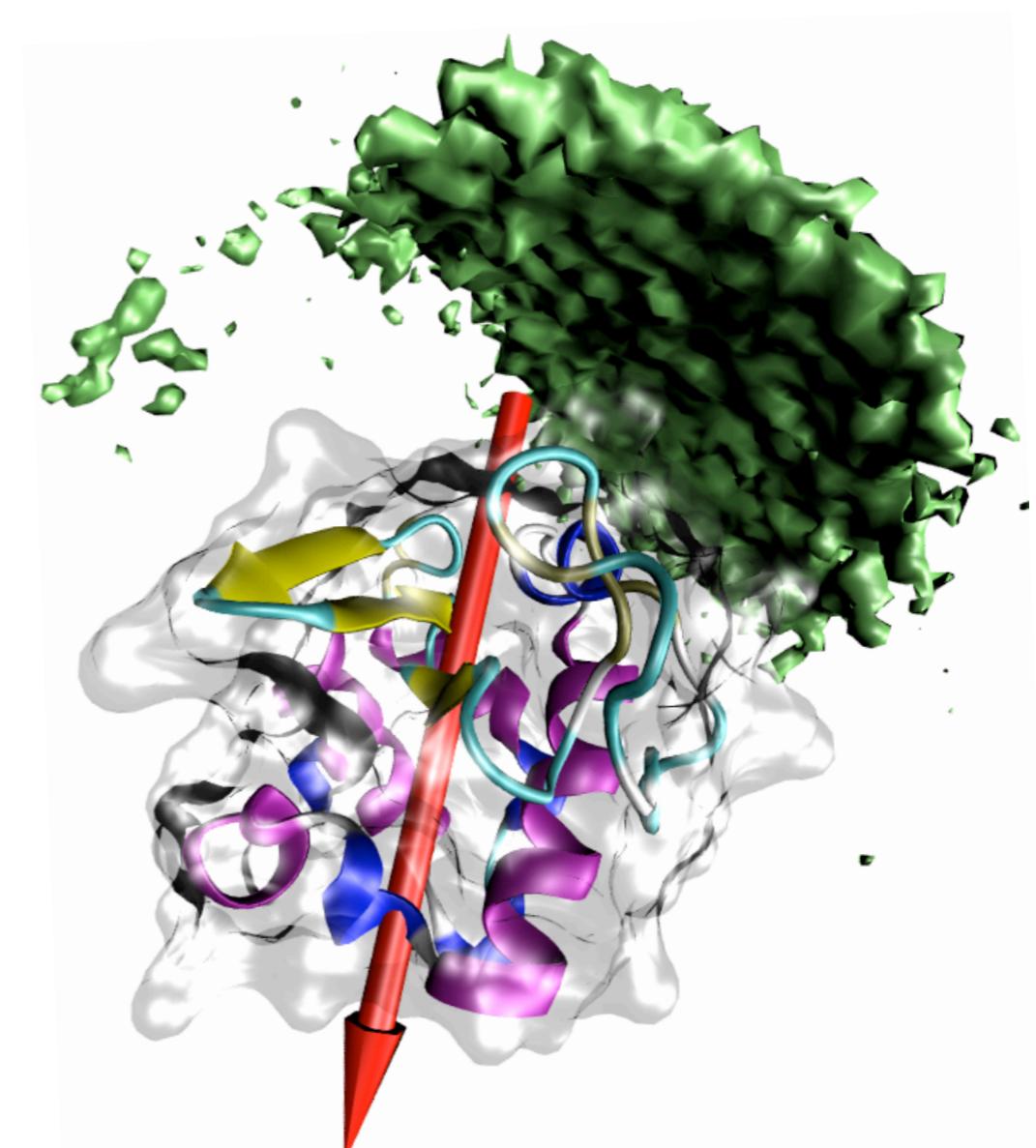
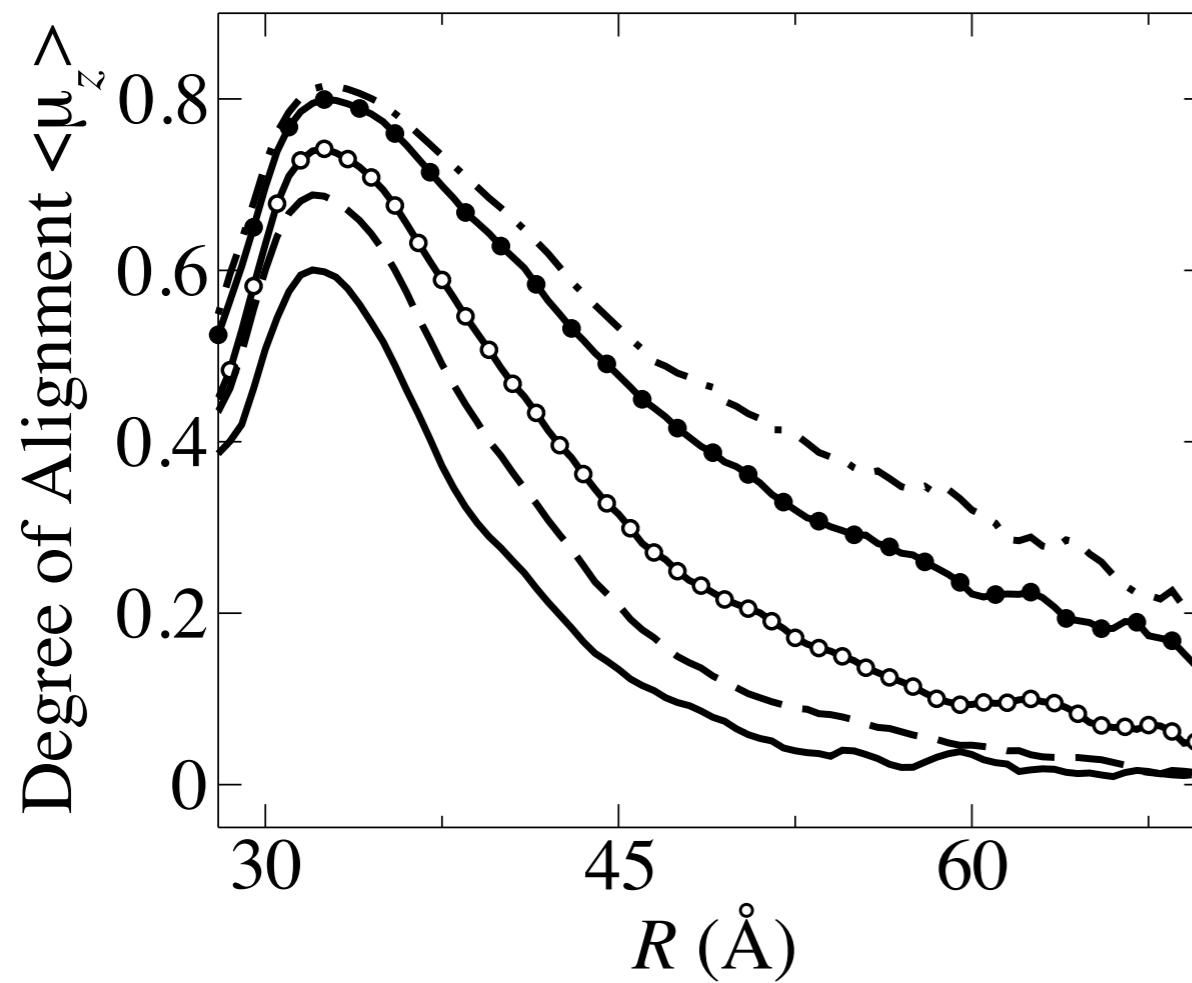
# Alignment



# Alignment

139D      403D  
Lys       $\alpha$ Lac

Apo  $\alpha$ -lactalbumin

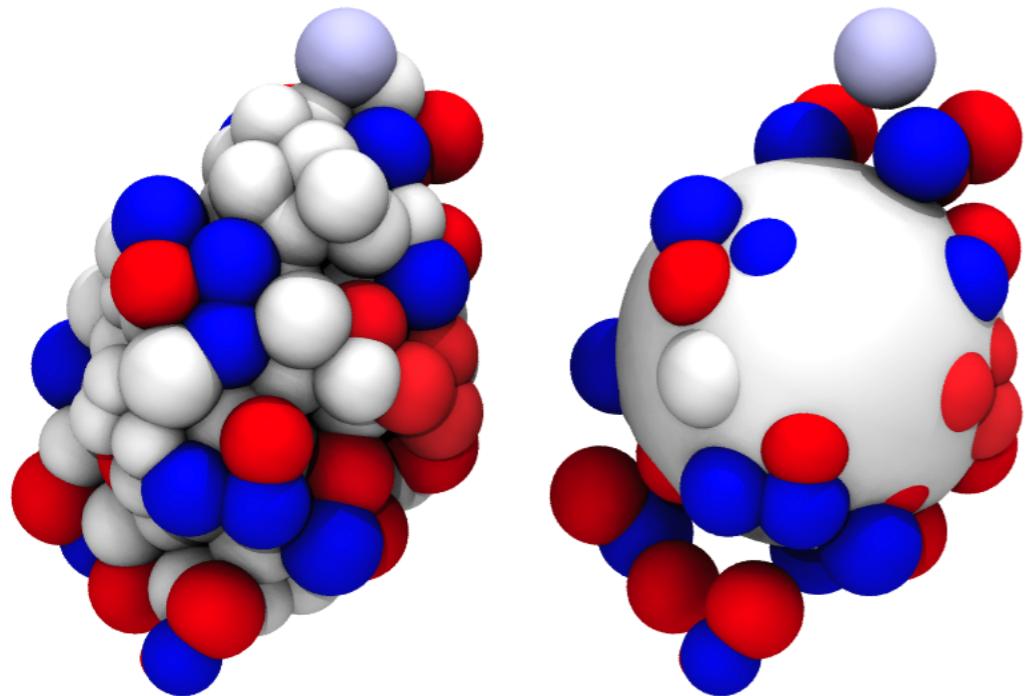


# More coarse graining

- explicit to implicit salt (DH level)
- More protein simplifications

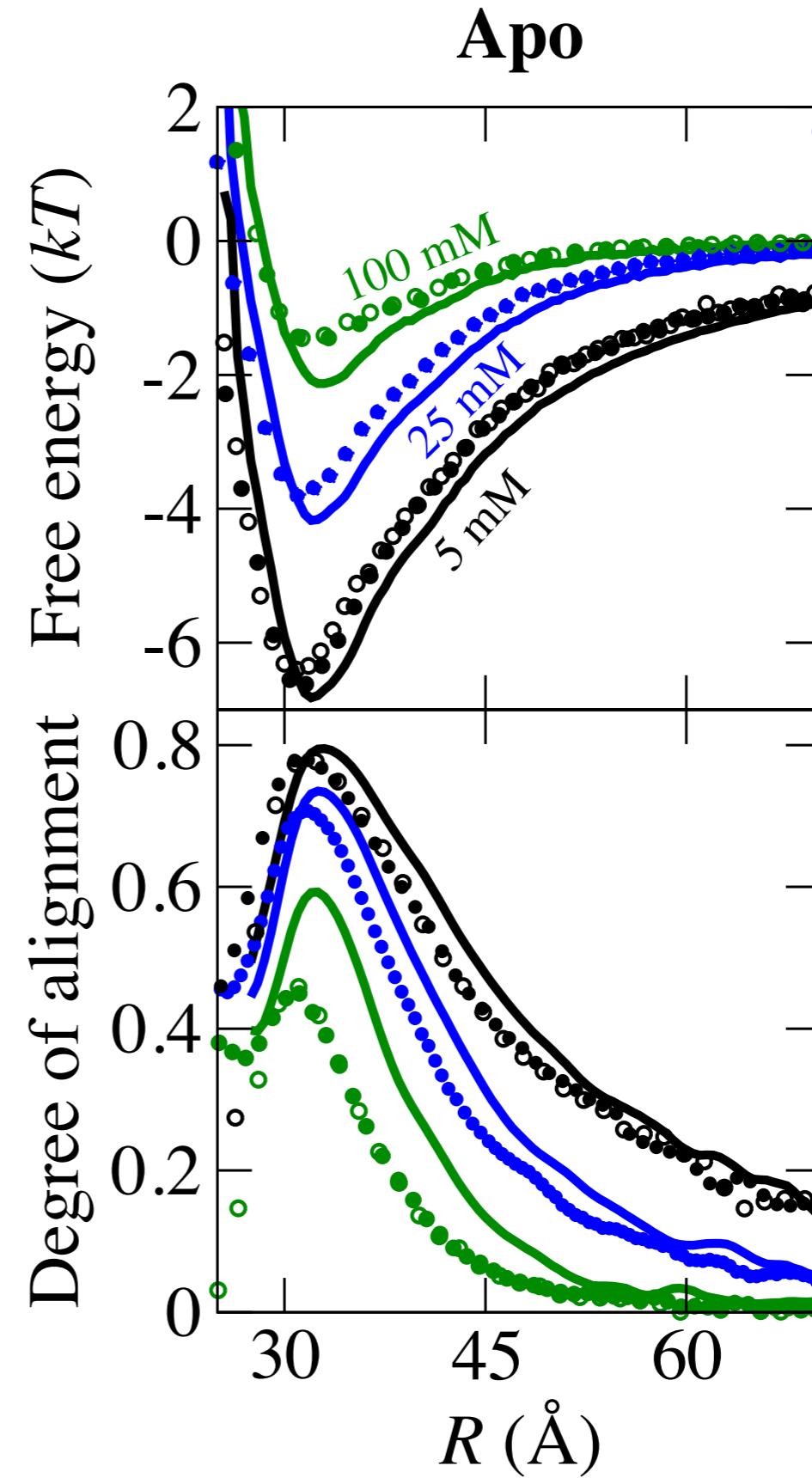
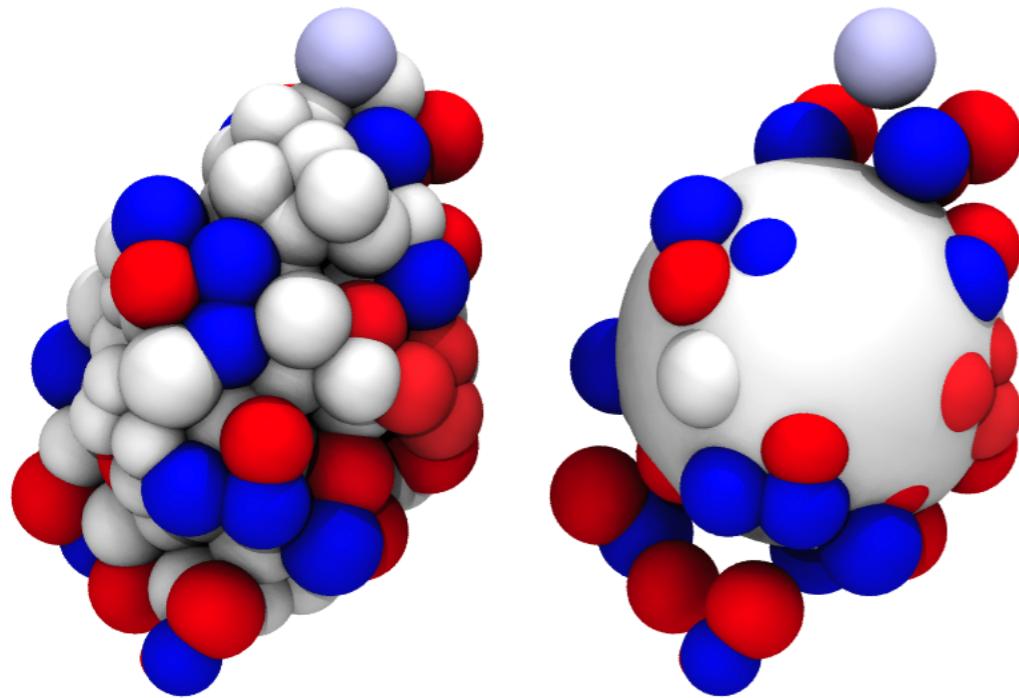
# More coarse graining

- explicit to implicit salt (DH level)
- More protein simplifications



# More coarse graining

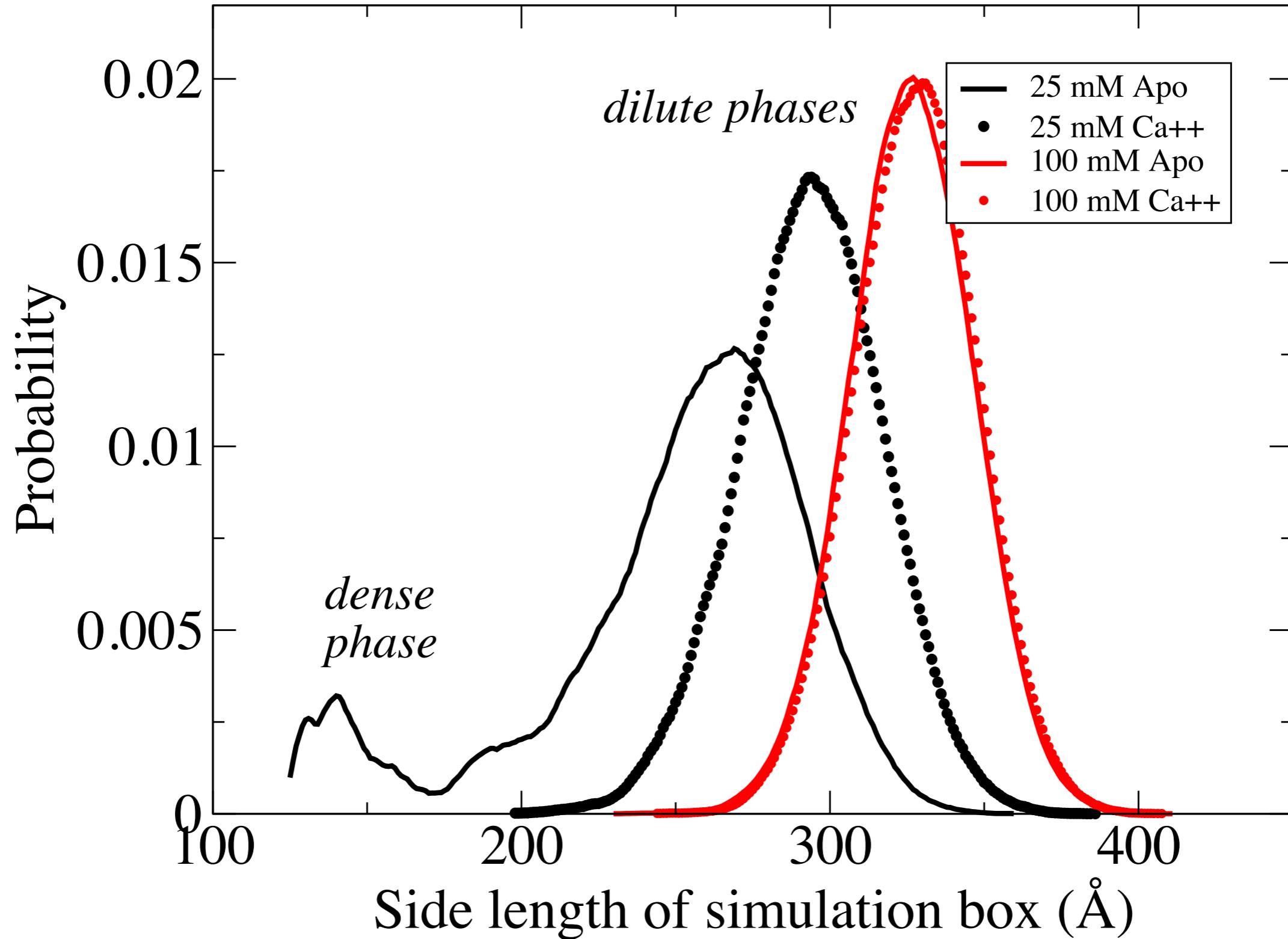
- explicit to implicit salt (DH level)
- More protein simplifications



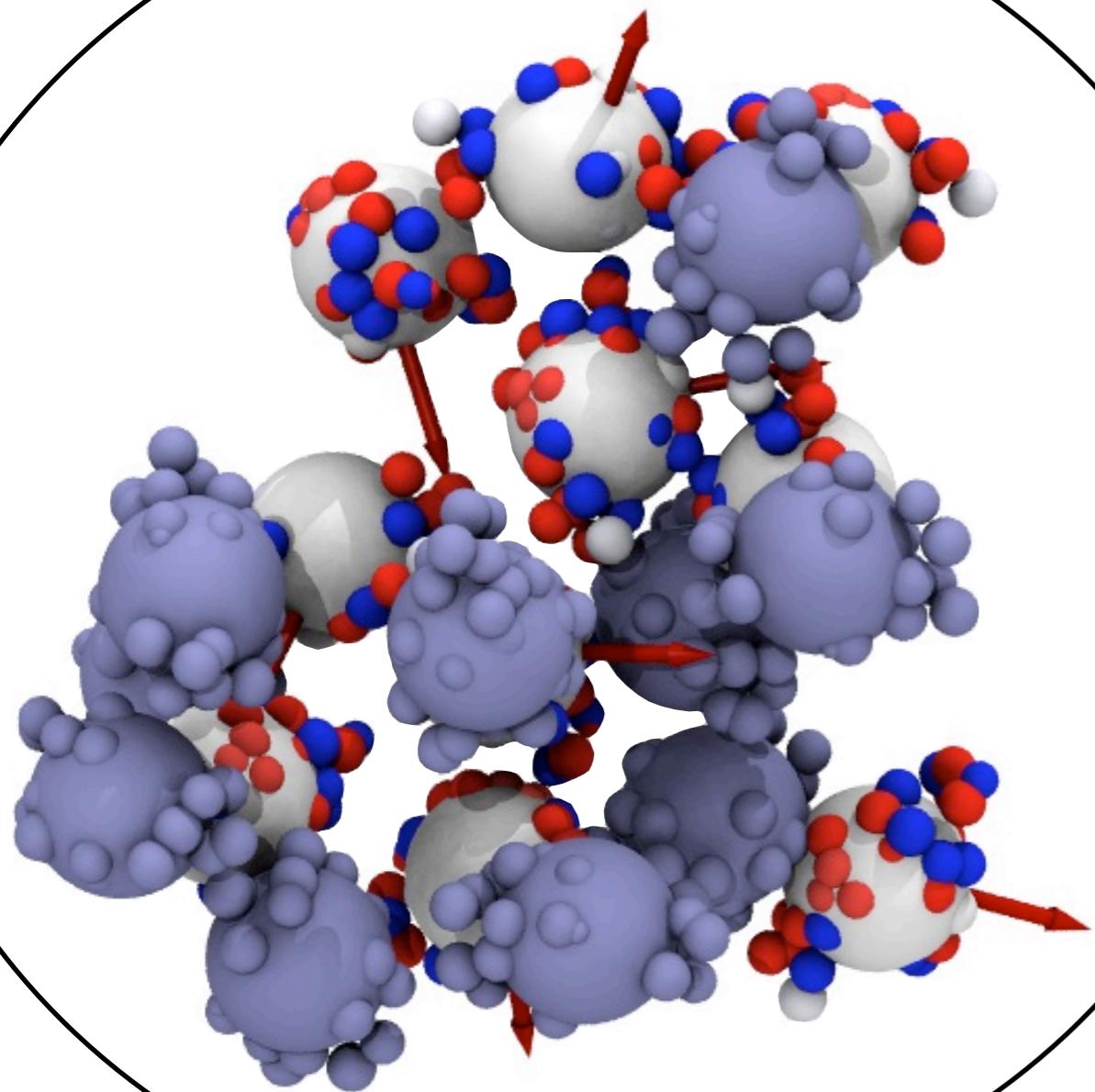
# Many proteins

- 40 proteins
- NVT to NPT ensemble

# Many proteins



# proteins



P

0.005

*dense  
phase*

100

200

300

400

Side length of simulation box ( $\text{\AA}$ )

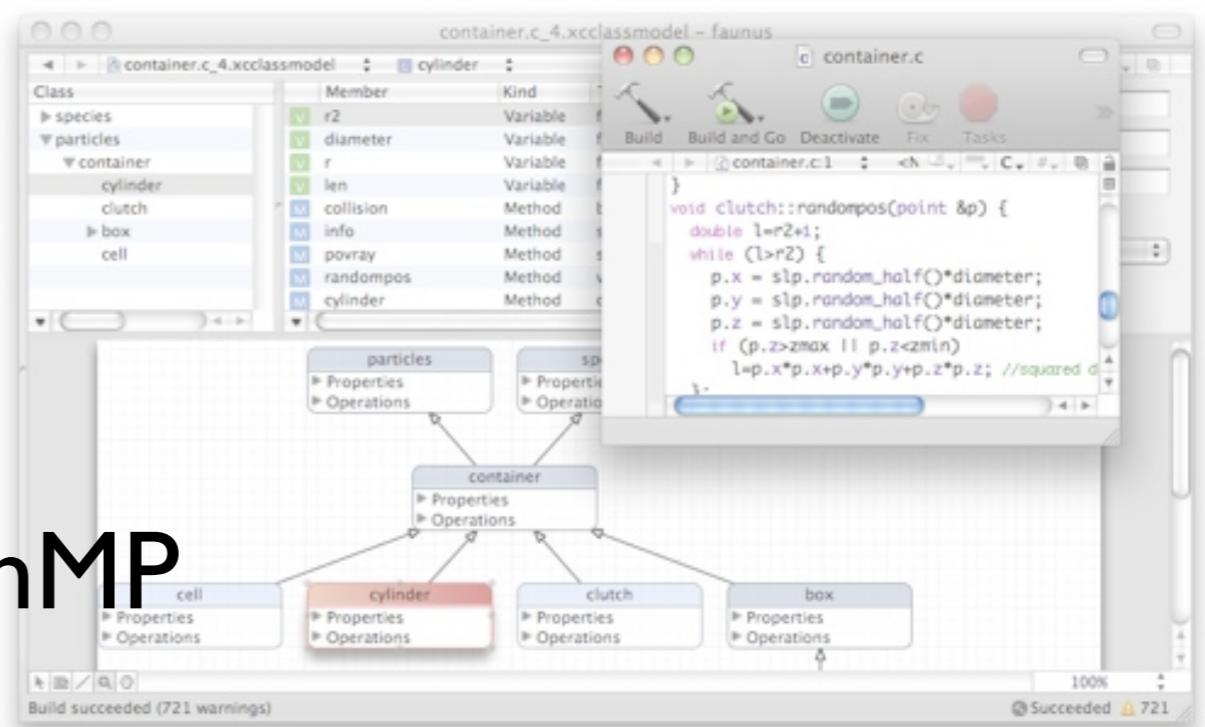
*dense phases*

- 25 mM Apo
- 25 mM Ca<sup>++</sup>
- 100 mM Apo
- 100 mM Ca<sup>++</sup>



<http://faunus.sourceforge.net>

- Object oriented C++ class library
- Python bindings
- Gromacs trajectories, OpenBabel, CMake, OpenMP parallelization, Doxygen
- Open Sourced - GPL.



# Thanks to:

- Anil Kurut, Istanbul University
- Björn Persson, Lund University
- The OMM Linnaeus Center of Excellence,  
Lund University.