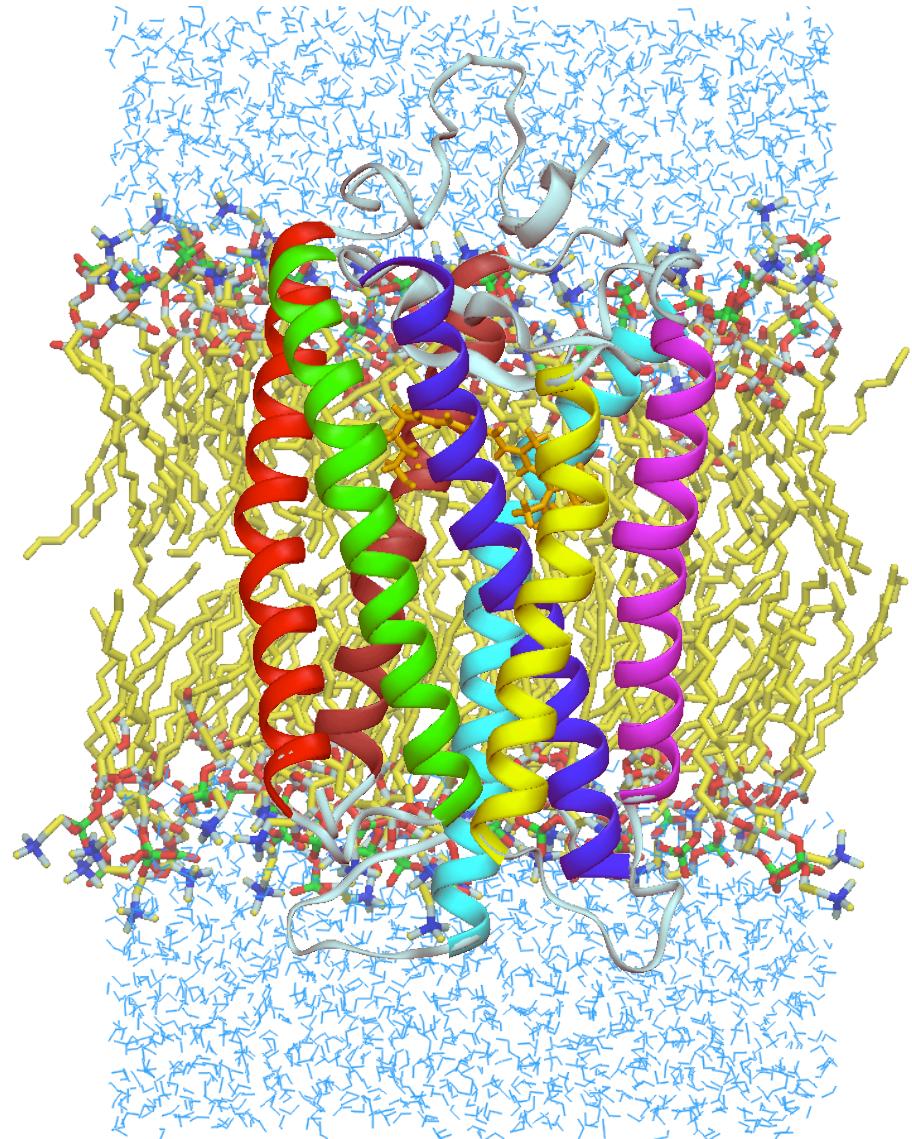
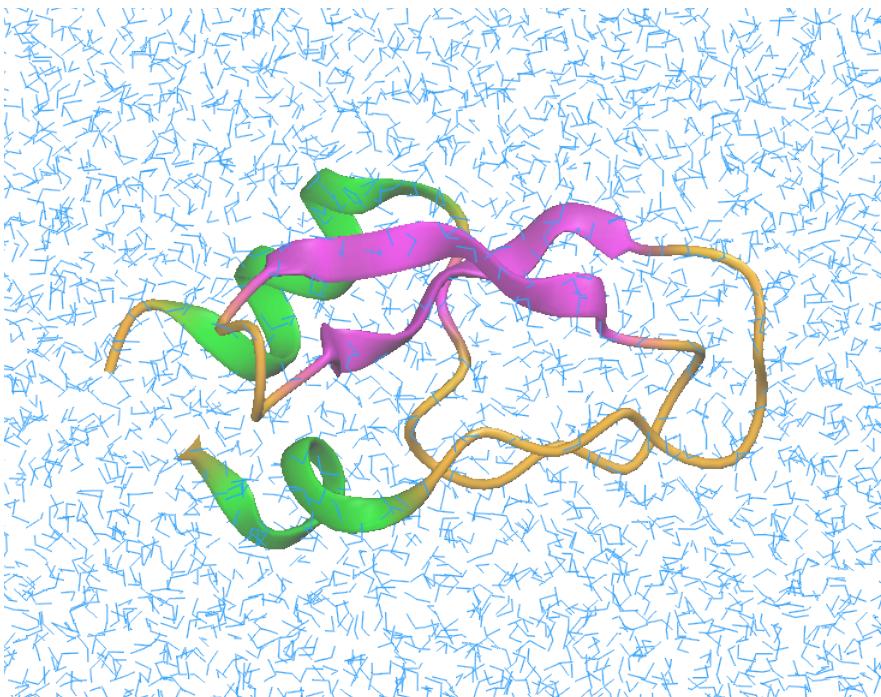


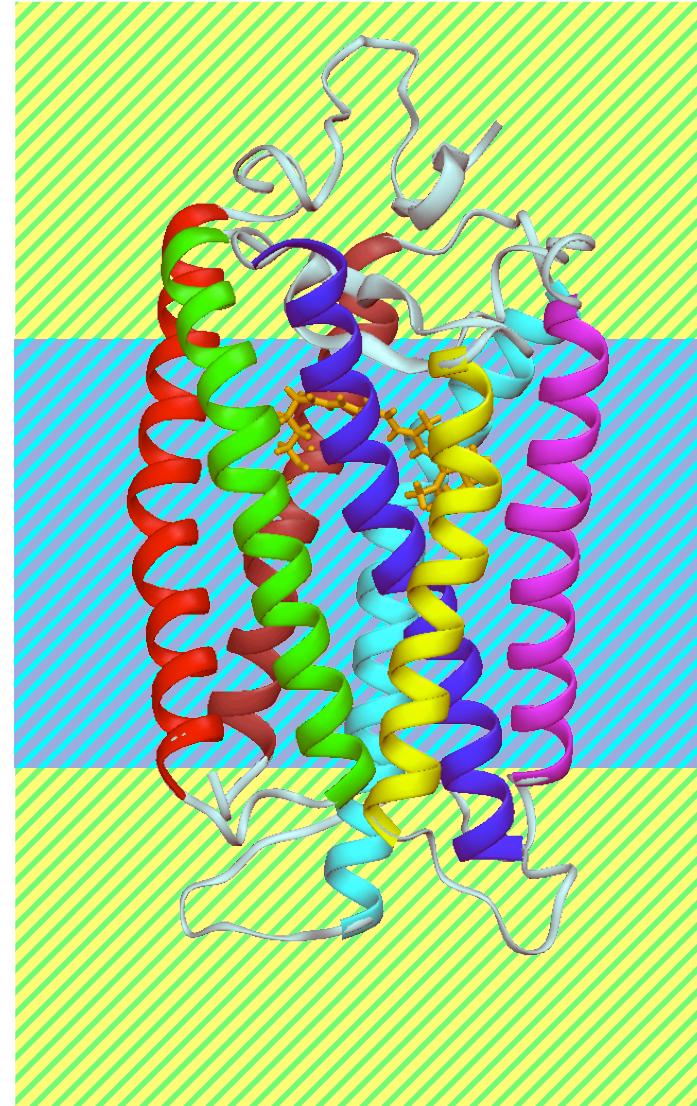
# **Implicit Solvent Models**

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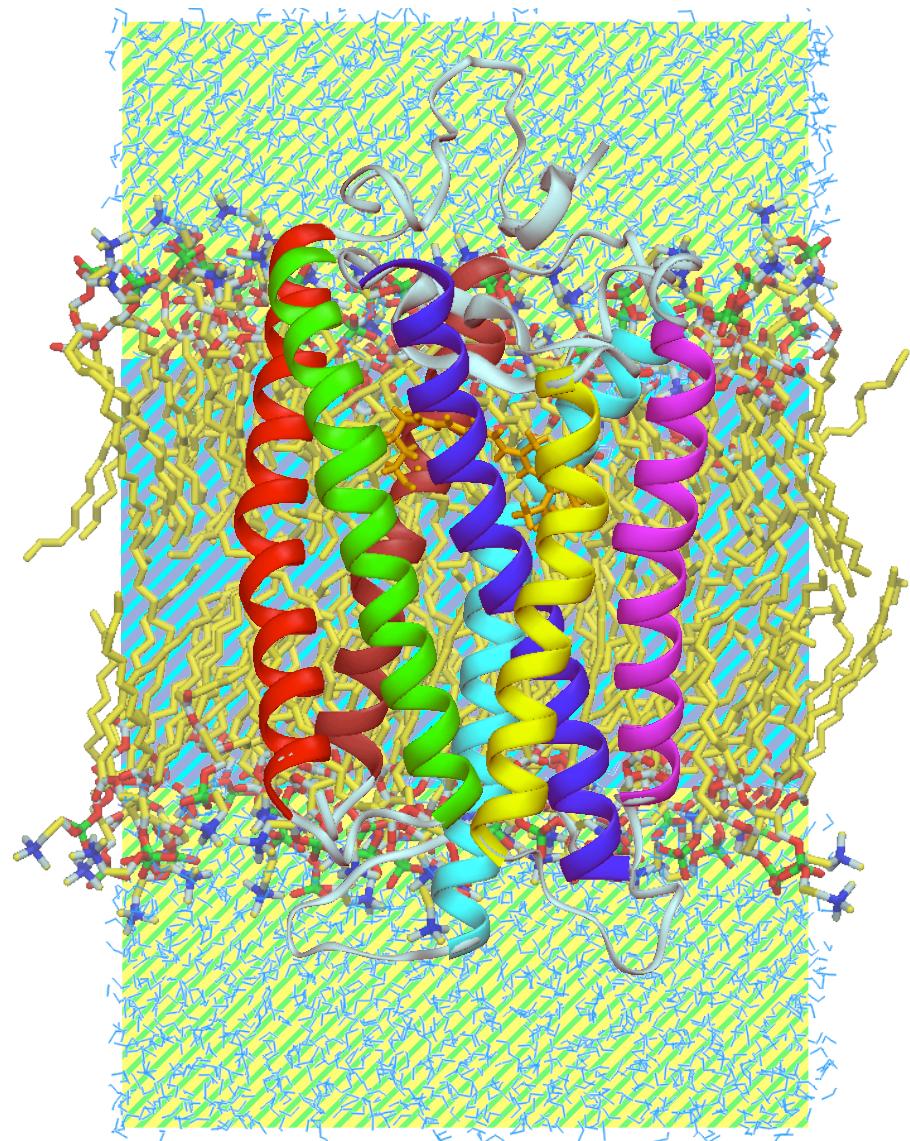
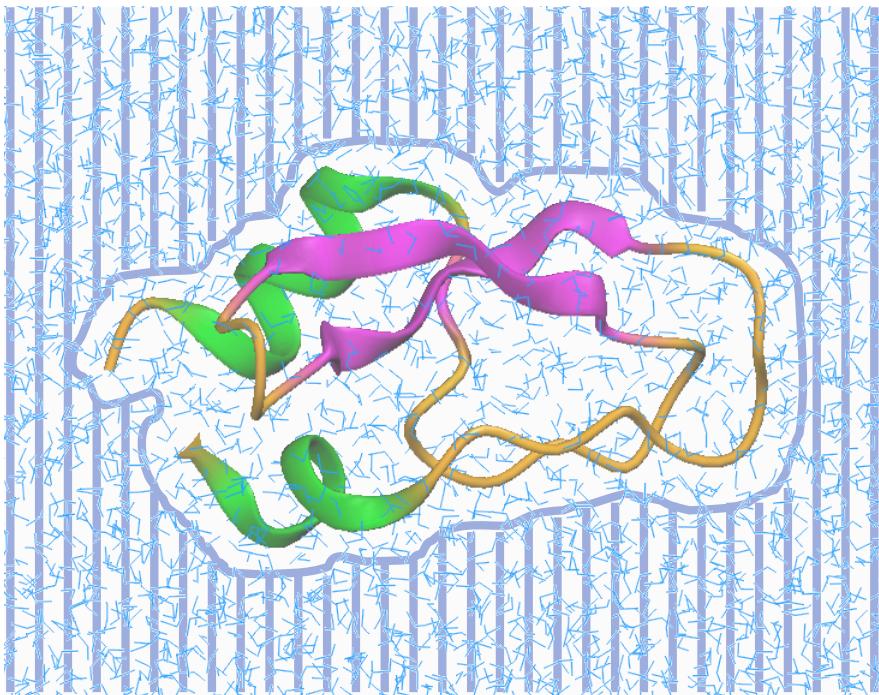
# *Explicit Solvent*



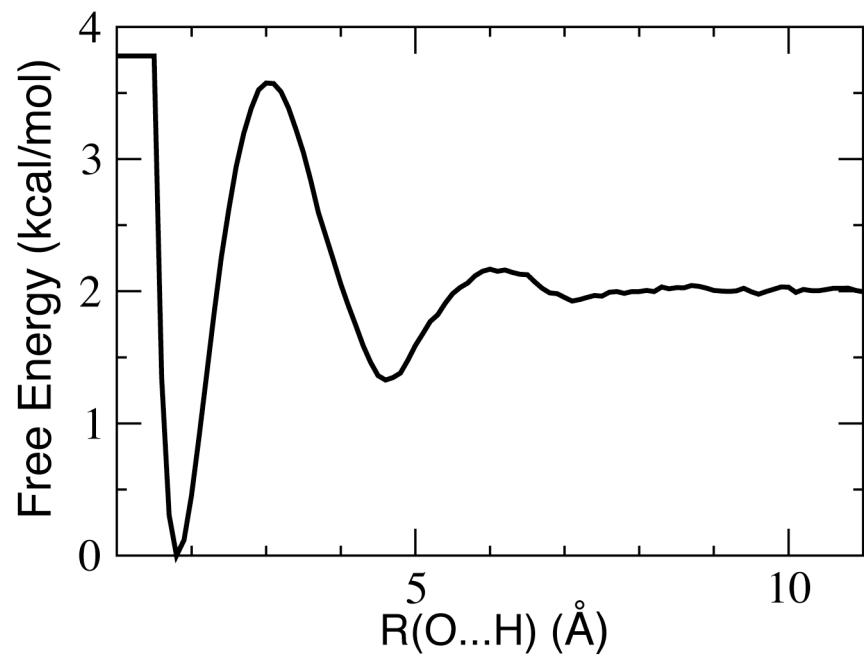
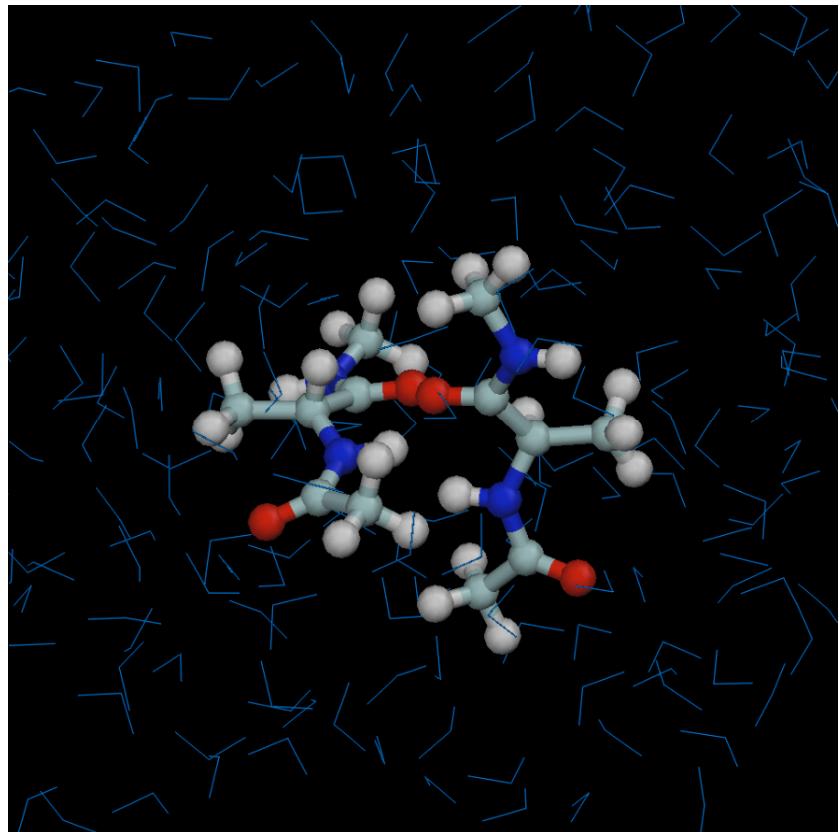
# *Implicit Solvent*



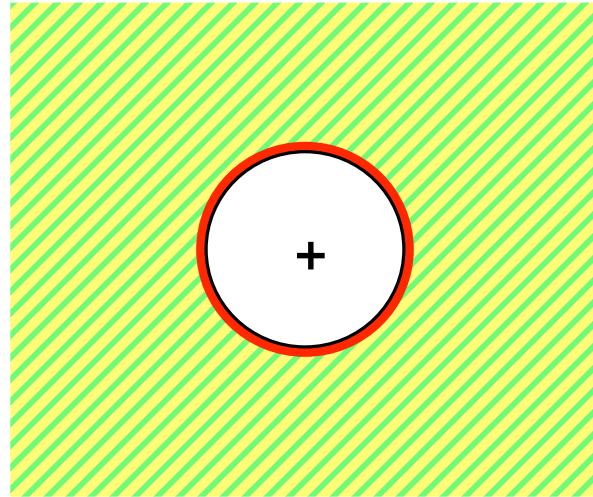
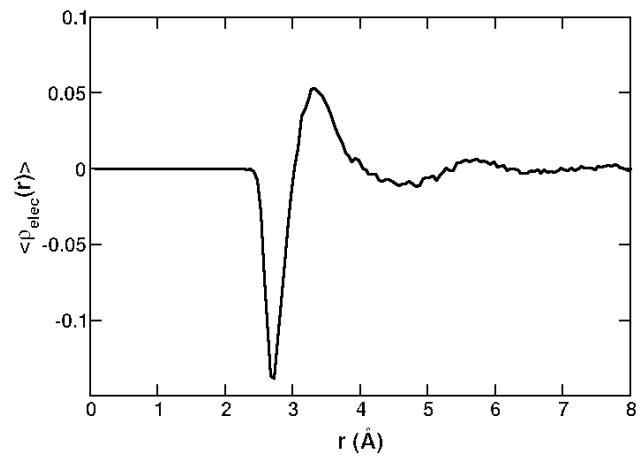
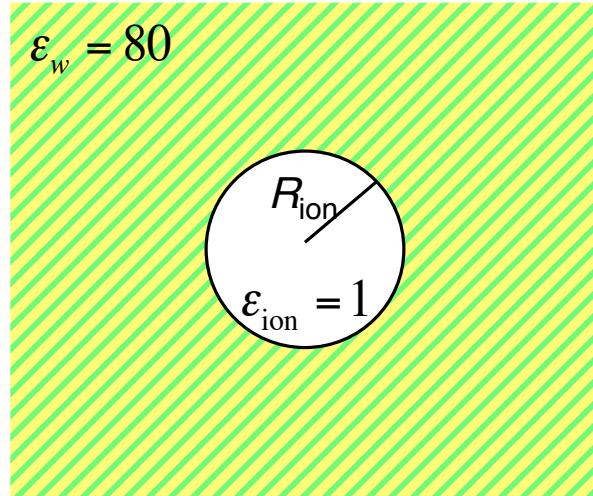
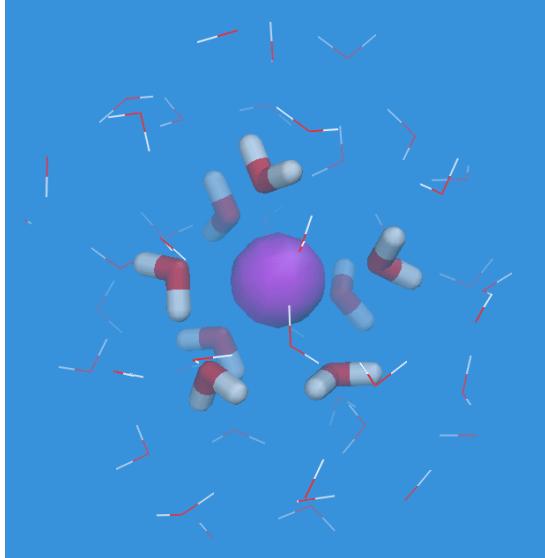
# *Simple & Efficient*



# *Competition: Not Simple!*



# Continuum Electrostatics



# Poisson-Boltzmann (PB) Equation

Poisson Equation :  $\nabla \cdot [\epsilon(\mathbf{r}) \nabla \phi(\mathbf{r})] = -4\pi \left[ \rho_{\text{prot}}(\mathbf{r}) + \sum_{\alpha} q_{\alpha} C_{\alpha}(\mathbf{r}) \right]$

non-linear PB Equation :  $\nabla \cdot [\epsilon(\mathbf{r}) \nabla \phi(\mathbf{r})] = -4\pi \left[ \rho_{\text{prot}}(\mathbf{r}) + \sum_{\alpha} q_{\alpha} C_{\alpha}^{\text{bulk}} \exp(-q_{\alpha} \phi(\mathbf{r}) / k_{\text{B}} T) \right]$

$$\downarrow \quad \exp(-x) \approx 1 - x$$

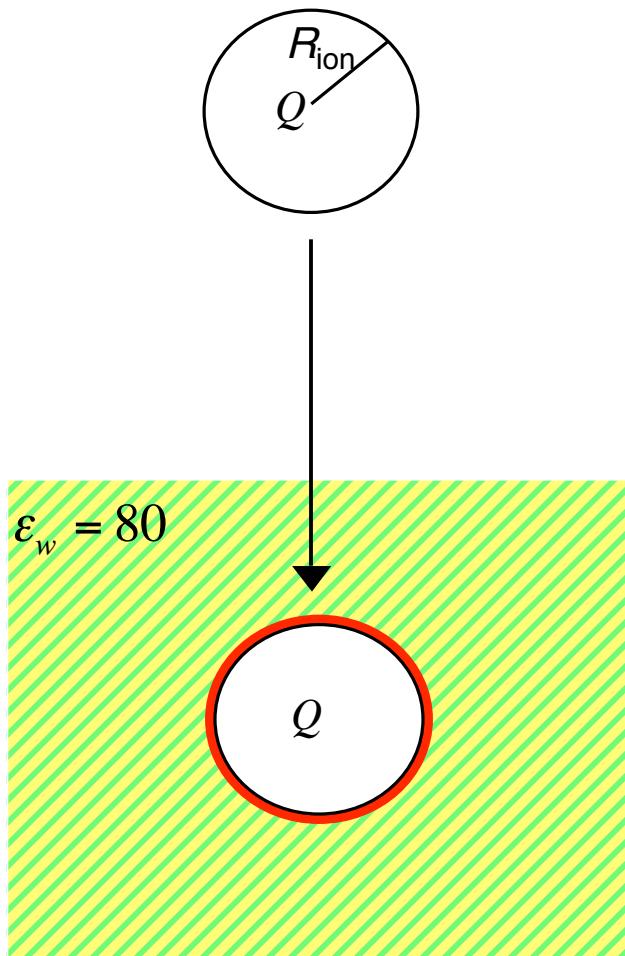
linearized PB Equation :  $\nabla \cdot [\epsilon(\mathbf{r}) \nabla \phi(\mathbf{r})] - \bar{\kappa}^2(\mathbf{r}) \phi(\mathbf{r}) = -4\pi \rho_{\text{prot}}(\mathbf{r})$

$$\bar{\kappa}^2(\mathbf{r}) = \frac{8\pi q_{\alpha}^2 C^{\text{bulk}}}{k_{\text{B}} T}$$

$$G_{\text{elec}} = \frac{1}{2} \sum q_i \phi(\mathbf{r}_i)$$

# Born Equation: Solvation Energy of Ion

$$\epsilon_p = 1$$

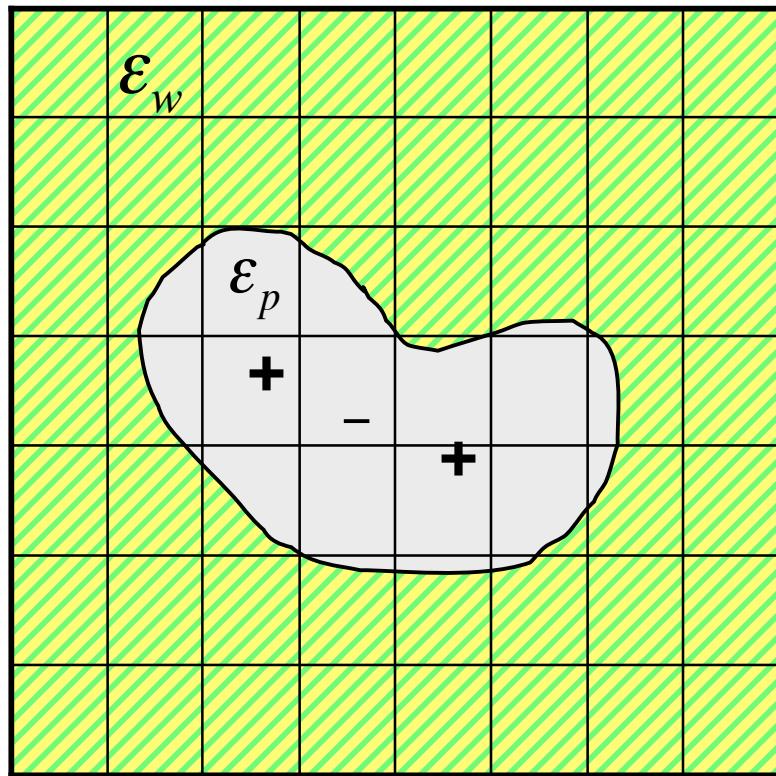


Reaction Field (Potential)

$$\begin{aligned}\Delta G_{\text{elec}} &= \frac{1}{2} Q \left[ \phi_s(\mathbf{r}_Q) - \phi_v(\mathbf{r}_Q) \right] \\ &= \frac{1}{2} \frac{Q^2}{R_{\text{ion}}} \left( \frac{1}{\epsilon_w} - \frac{1}{\epsilon_p} \right)\end{aligned}$$

$$R_{\text{ion}} \uparrow \implies \Delta G_{\text{elec}} \uparrow$$

# Finite-Difference PB Calculations



PB radii are very important  
Self-energy should be removed

$$\nabla \cdot [\epsilon(r) \nabla \phi(r)] - \bar{\kappa}^2(r) \phi(r) = -4\pi \rho_{\text{prot}}(r)$$

↓  
on 3d-grid

$$\begin{aligned} & \epsilon_x(i, j, k)[\phi(i+1, j, k) - \phi(i, j, k)] + \\ & \epsilon_x(i-1, j, k)[\phi(i-1, j, k) - \phi(i, j, k)] + \\ & \epsilon_y(i, j, k)[\phi(i, j+1, k) - \phi(i, j, k)] + \\ & \epsilon_y(i, j-1, k)[\phi(i, j-1, k) - \phi(i, j, k)] + \\ & \epsilon_z(i, j, k)[\phi(i, j, k+1) - \phi(i, j, k)] + \\ & \epsilon_z(i, j, k-1)[\phi(i, j, k-1) - \phi(i, j, k)] - \\ & \bar{\kappa}^2(i, j, k) \phi(i, j, k) h^2 = -4\pi \frac{q(i, j, k)}{h} \end{aligned}$$

Klapper et. al (1986) *Proteins* 1: 47  
Im et. al. (1998) *Comp. Phys. Comm.* 111: 59  
© Comp. Phys. Comm., 2006.

# *Applications of PB Calculations*

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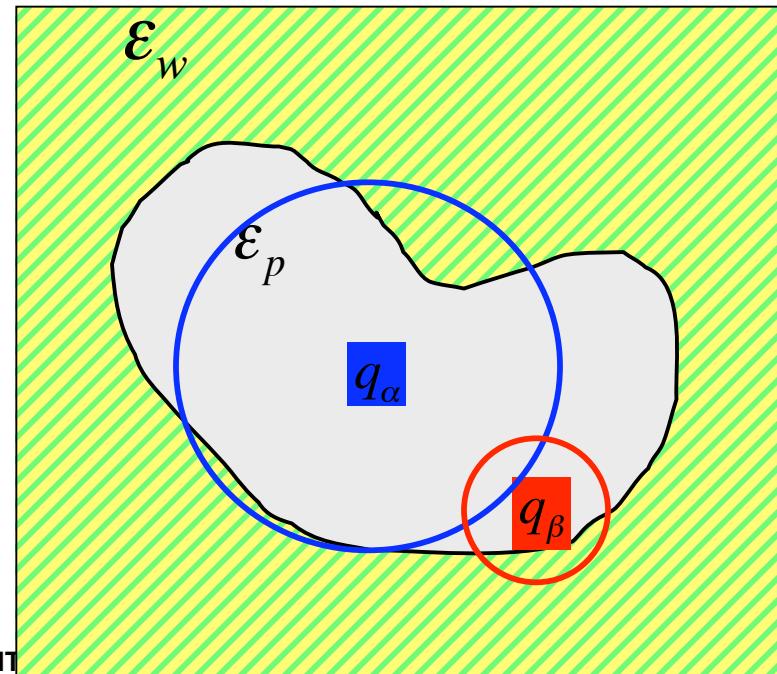
- Visualization of electrostatic potential of macromolecules
- Solvation free energy
- Protein-protein interactions in solution
- pKa shifts in specific residues in proteins
- Incorporation of transmembrane potential
- Electrostatic solvation forces

# Generalized Born (GB) Equation

$$\Delta G_{\text{elec}} \approx \frac{1}{2} \left( \frac{1}{\epsilon_w} - \frac{1}{\epsilon_p} \right) \sum_{\alpha\beta} \frac{q_\alpha q_\beta}{\sqrt{r_{\alpha\beta}^2 + R_\alpha^{\text{GB}} R_\beta^{\text{GB}}} \exp(-r_{\alpha\beta}^2 / 4R_\alpha^{\text{GB}} R_\beta^{\text{GB}})}$$

Still et. al. (1990) *J. Am. Chem. Soc.*

$$\Delta G_{\text{elec},\alpha} = \frac{1}{2} \left( \frac{1}{\epsilon_w} - \frac{1}{\epsilon_p} \right) \frac{q_\alpha^2}{R_\alpha^{\text{GB}}} , \quad R_\alpha^{\text{GB}} \uparrow \Rightarrow \Delta G_{\text{elec},\alpha} \uparrow$$



$$\Delta G_{\text{elec},\alpha} > \Delta G_{\text{elec},\beta}$$

$$R_\alpha^{\text{GB}} > R_\beta^{\text{GB}}$$

“The effective Born radius represents the distance between a particular atom and the effective spherical dielectric boundary.”

# Calculation of Effective Born Radii

- Continuum electrostatics

$$\Delta G_{\text{elec},\alpha} = \frac{1}{8\pi} \int \frac{D^2(\mathbf{r})}{\epsilon(\mathbf{r})} d\mathbf{r} = \frac{1}{8\pi\epsilon_w} \int D^2(\mathbf{r}) d\mathbf{r} + \frac{1}{8\pi} \left( \frac{1}{\epsilon_p} - \frac{1}{\epsilon_w} \right)_{\text{solute}} \int D^2(\mathbf{r}) d\mathbf{r}$$

- Coulomb Field Approximation (CFA)

$$\Delta G_{\text{elec},\alpha} \approx \Delta G_{\text{elec},\alpha}^0 = -\frac{q_\alpha^2}{2} \left( \frac{1}{\epsilon_p} - \frac{1}{\epsilon_w} \right) \left( \frac{1}{\eta_\alpha} - \frac{1}{4\pi} \int_{r>\eta_\alpha} d\mathbf{r} \frac{v(\mathbf{r};\{\mathbf{r}_\alpha\})}{|\mathbf{r} - \mathbf{r}_\alpha|^4} \right)$$

volume function

Pairwise Summation  
GenBorn

Volume Integration  
GBMV and GBSW

$$\frac{1}{R_\alpha^{\text{GB}}} = \frac{1}{R_\alpha + P_1} + \sum_{\text{bonds}} \frac{P_2 V_\beta}{r_{\alpha\beta}^4} + \sum_{\text{angles}} \frac{P_3 V_\beta}{r_{\alpha\beta}^4} + \sum_{\text{non-bonded}} \frac{P_4 V_\beta CCF}{r_{\alpha\beta}^4}$$

Dominy and Brooks (1999) *J. Phys. Chem. B* 103:3765  
Lee et. al. (2002) *J. Chem. Phys.* 116:10606  
Im et. al. (2003) *J. Comput. Chem.* 24:1691  
© 2006 Pil Im , 2006.

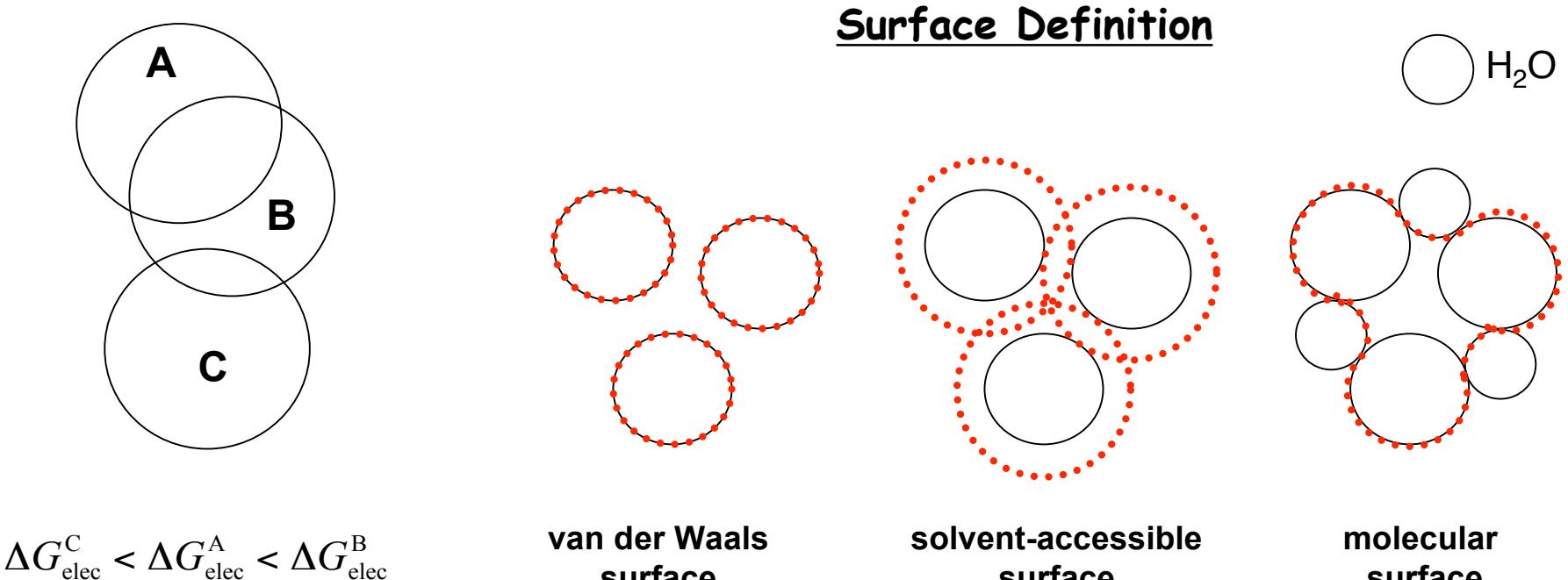
# The Generalized Born Zoo

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Name	Year	Authors	Program	Calculation of Born radii	CFA Corr.	Dielectric Boundary
GB GB/SA	1990	Still, Tempczyk, Hawley, Hendrickson	Macromodel	FDPB	Yes	Molecular surface
GB	1995	Hawkins, Cramer, Truhlar	Amber, Tinker	Pairwise descreening	No	Overlapping spheres
ACE	1996/ 2001	Schaefer, Karplus	CHARMM	Pairwise sum of atomic volumes	No	Overlapping Gaussians
GB	1997	Qiu, Shenkin, Hollinger, Still	Macromodel,Tinker	Pairwise sum of atomic volumes	No	Overlapping spheres
S-GB	1998	Ghosh, Rapp, Friesner	Impact	Surface integral formulation	Yes	Overlapping spheres
GenBorn	1999	Dominy, Brooks	CHARMM	Pairwise sum of atomic volumes	No	Overlapping spheres
GBMV	2002/ 2003	Lee, Salsbury, Feig, Brooks	CHARMM	Numerical integration	Yes	Molecular surface
GBSW	2003	Im, Lee, Brooks	CHARMM	Numerical integration	Yes	Overlapping spheres + smooth boundary
AGB	2004	Gallicchio, Levy	Impact	Pairwise descreening	No	Overlapping spheres
GB	2004	Onufriev, Case	Amber	Pairwise descreening, radius rescaling	No	Molecular surface

# *Dielectric Boundary: A Key Concept*

In continuum dielectric solvent models, the extent of solvent-exposure of each atom at the dielectric boundary dictates all of the electrostatic and most of nonpolar solvation energetics.



Input radii are very important.

# GBMV vs. GBSW

- Correction term

$$\Delta G_{\text{elec},\alpha} \approx -a_0 \Delta G_{\text{elec},\alpha}^0 + a_1 \Delta G_{\text{elec},\alpha}^1$$

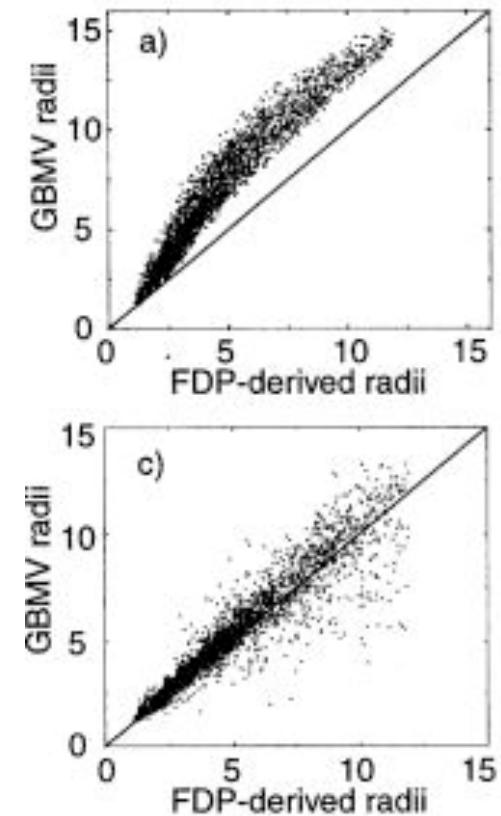
$$\Delta G_{\text{elec},\alpha}^0 = -\frac{q_\alpha^2}{2} \left( \frac{1}{\varepsilon_p} - \frac{1}{\varepsilon_w} \right) \left( \frac{1}{\eta_\alpha} - \frac{1}{4\pi} \int_{r>\eta_\alpha} d\mathbf{r} \frac{v(\mathbf{r}; \{\mathbf{r}_\alpha\})}{|\mathbf{r} - \mathbf{r}_\alpha|^4} \right)$$

$$\Delta G_{\text{elec},\alpha}^1 = -\frac{q_\alpha^2}{2} \left( \frac{1}{\varepsilon_p} - \frac{1}{\varepsilon_w} \right) \sqrt{\frac{1}{2\eta_\alpha^2} - \frac{1}{4\pi} \int_{r>\eta_\alpha} d\mathbf{r} \frac{v(\mathbf{r}; \{\mathbf{r}_\alpha\})}{|\mathbf{r} - \mathbf{r}_\alpha|^5}}$$

- Target Surface

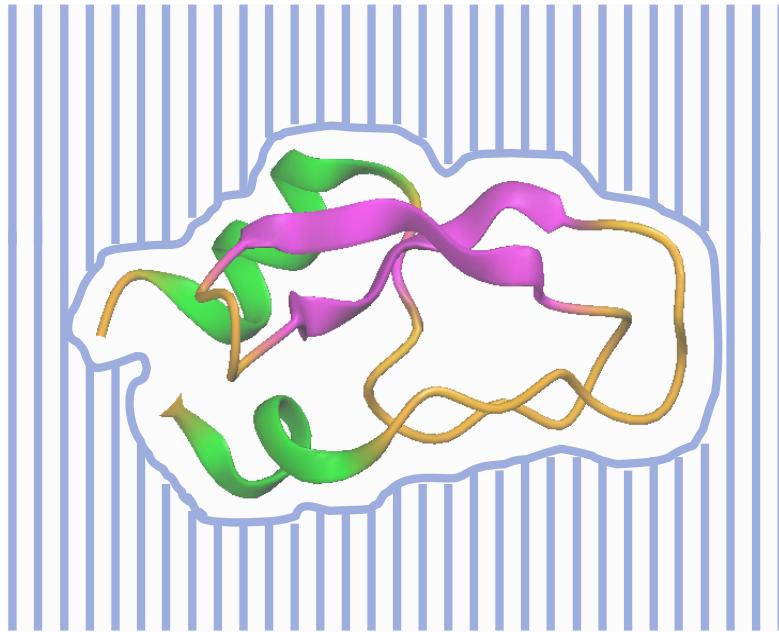
**GBSW**: van der Waals smoothed surface

**GBMV**: molecular surface



Lee, Salsbury, and Brooks (2002) *J. Chem. Phys.* 116:10606  
Lee, Feig, Salsbury, and Brooks (2003) *J. Comput. Chem.* 24:1348  
Im, Lee, and Brooks (2003) *J. Comput. Chem.* 24:1691  
© Wonpil Im , 2006.

# Continuum Electrostatics



$$\begin{aligned}W &= U_{\text{MM}} + \Delta G_{\text{solv}} \\&= U_{\text{MM}} + \Delta G_{\text{elec}} + \Delta G_{\text{np}} \\ \Delta G_{\text{np}} &= \gamma \cdot S\end{aligned}$$

**Continuum Electrostatics :**

Protein/solvent system is divided into an interior **low dielectric** ( $\epsilon_p$ ) and an exterior **high dielectric** ( $\epsilon_w$ ) region

- Poisson-Boltzmann (PB):  $\nabla \cdot [\epsilon(\mathbf{r}) \nabla \phi(\mathbf{r})] - \kappa^2(\mathbf{r}) \phi(\mathbf{r}) = -4\pi \rho_{\text{prot}}(\mathbf{r})$

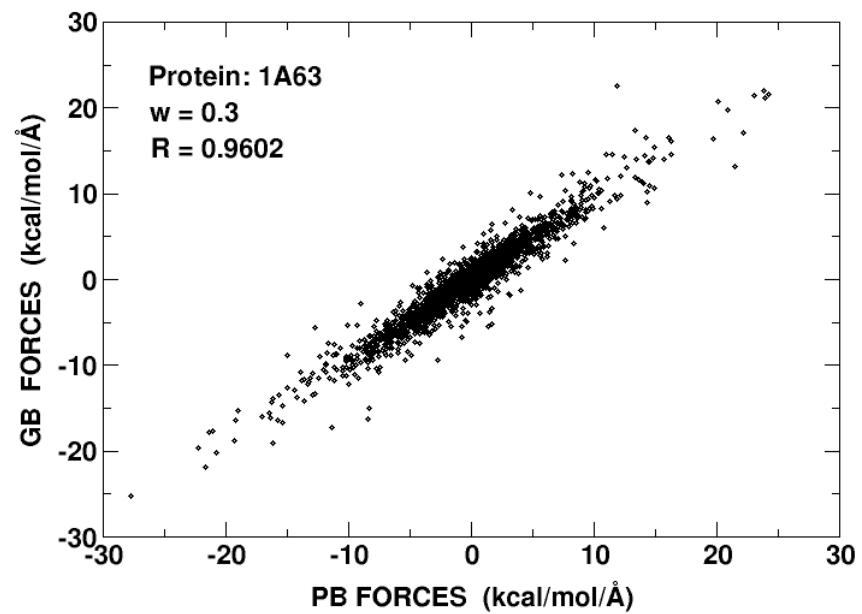
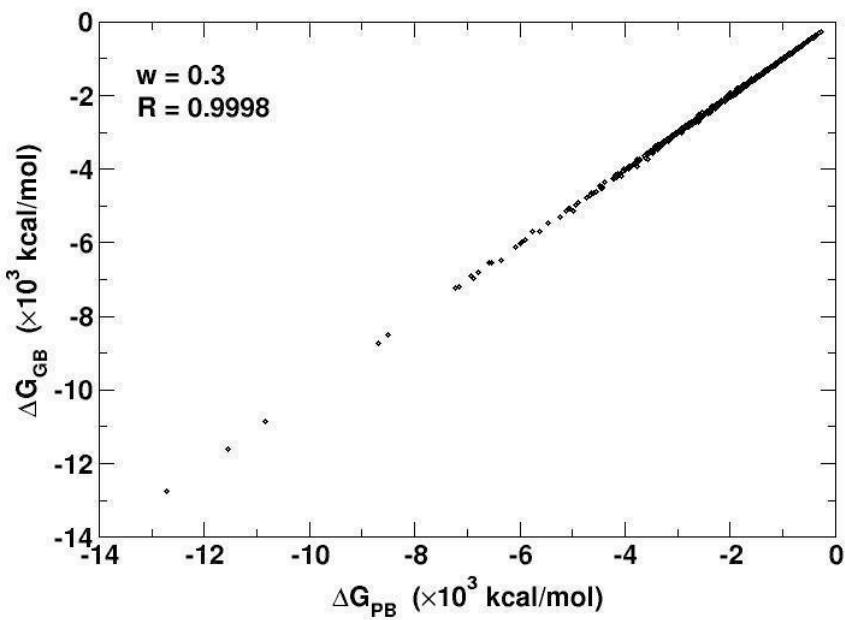
$$\Delta G_{\text{elec}} = \frac{1}{2} \sum q_i \phi(\mathbf{r}_i)$$

- Generalized Born (GB)

$$\Delta G_{\text{elec}} \approx \frac{1}{2} \left( \frac{1}{\epsilon_w} - \frac{1}{\epsilon_p} \right) \sum_{\alpha\beta} \frac{q_\alpha q_\beta}{\sqrt{r_{\alpha\beta}^2 + R_\alpha^{\text{GB}} R_\beta^{\text{GB}}} \exp(-r_{\alpha\beta}^2 / 4R_\alpha^{\text{GB}} R_\beta^{\text{GB}})}$$

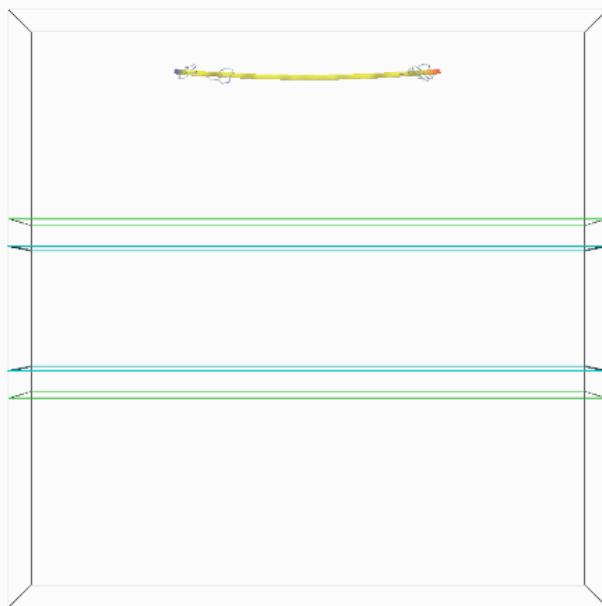
❤ Please, be careful with nonbond options  
© MMTSB/CTBP Summer Workshop, 2008

# PB Forces vs. GB Forces



# Membrane GB models : GBSWmemb

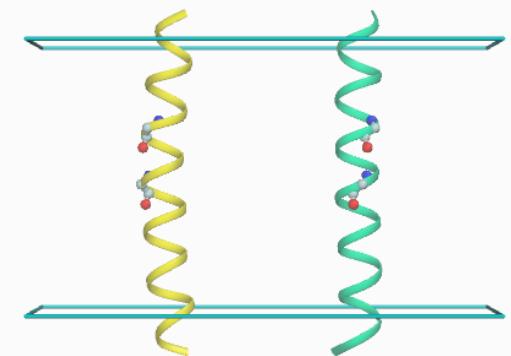
## *Insertion, Folding, and Assembly of Membrane Proteins/Peptides*



Im & Brooks (2005)  
*Proc. Natl. Acad. Sci.* 102:6771

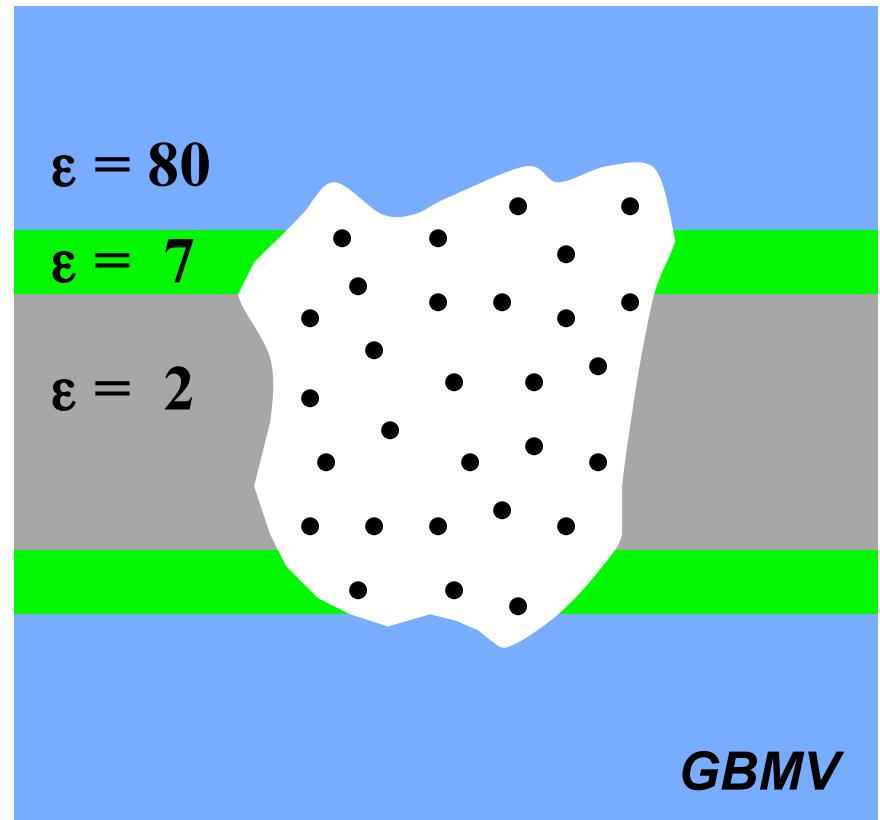
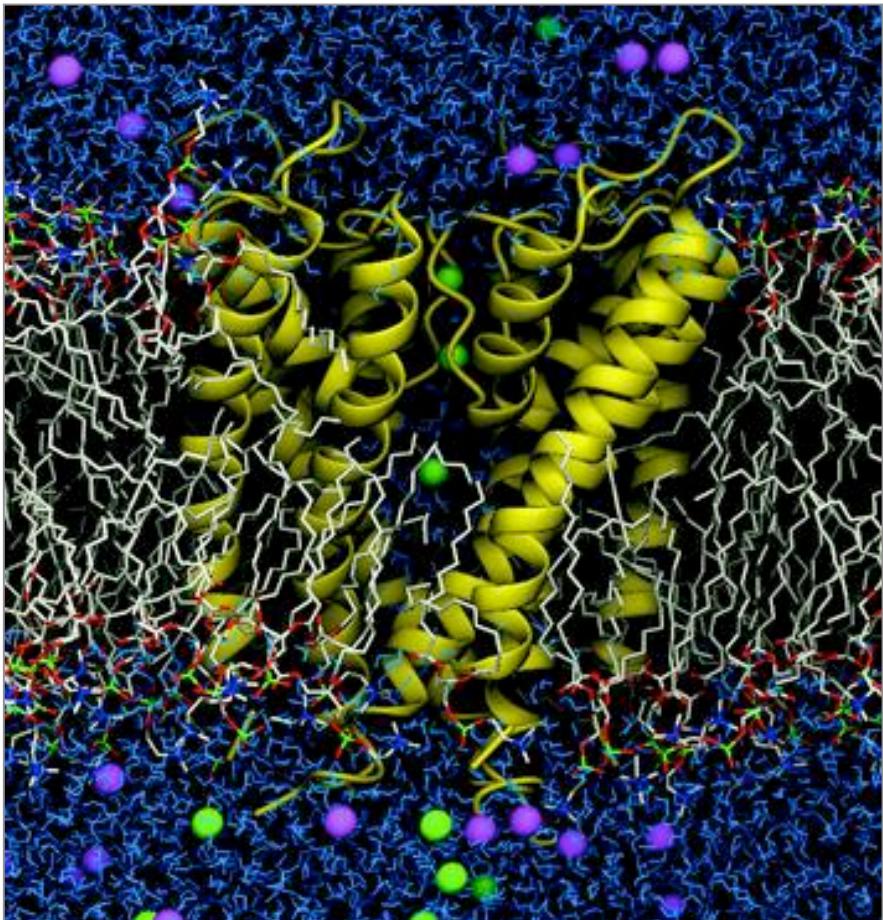


Im & Brooks (2004)  
*J. Mol. Biol.* 337:515



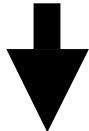
Im, Feig, and Brooks (2003)  
*Biophys. J.* 85:2900

# GBMV Membrane



# *GB for Heterogeneous Environments*

$$\Delta G_{elst} = -166 \left(1 - \frac{1}{\varepsilon}\right) \sum_i \sum_j \frac{q_i q_j}{\sqrt{r_{ij} + \alpha_i \alpha_j \exp(-r_{ij}^2 / F \alpha_i \alpha_j)}}$$

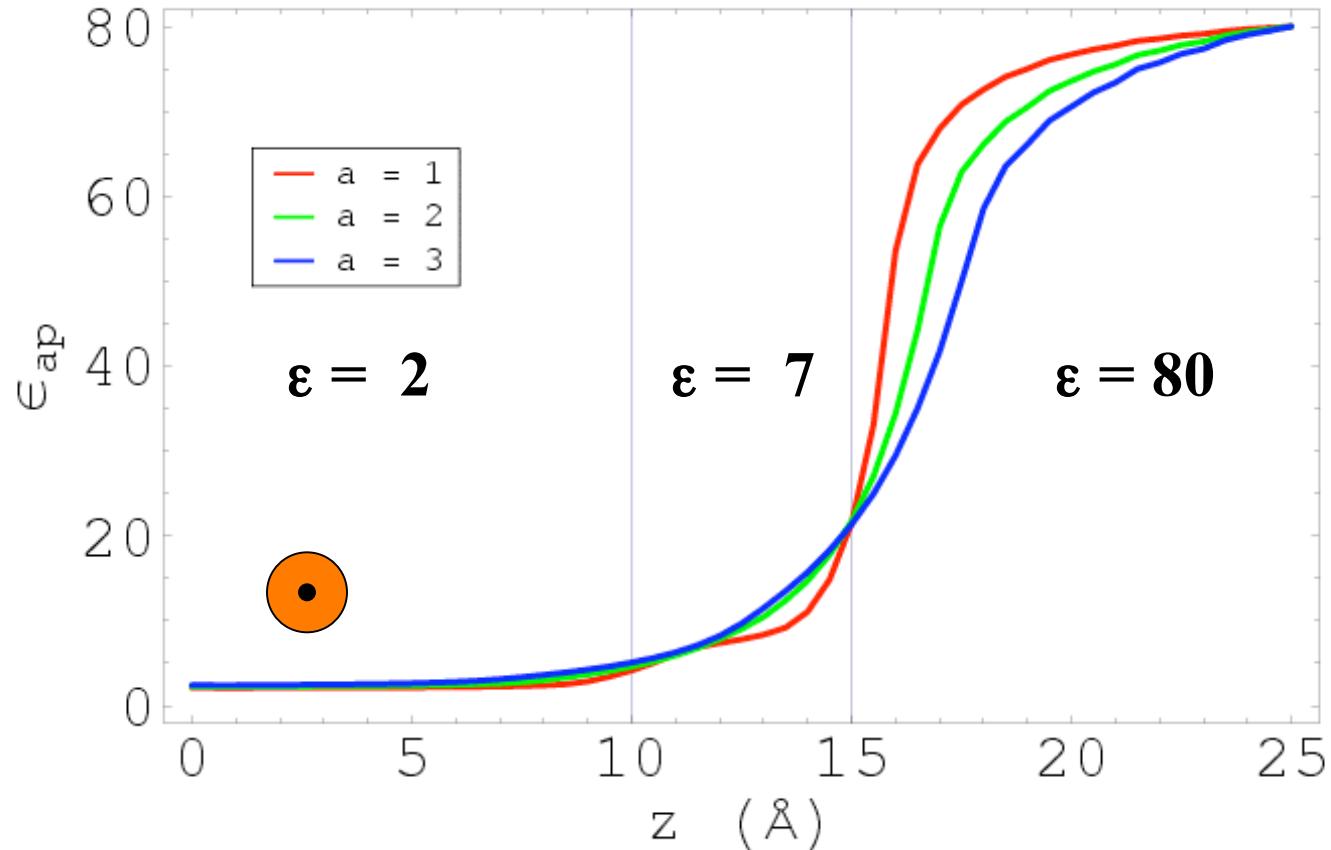


$$\Delta G_{elst} = -166 \sum_i \sum_j \left(1 - \frac{1}{\varepsilon_{ij}}\right) \frac{q_i q_j}{\sqrt{r_{ij} + \alpha_i(\varepsilon_i) \alpha_j(\varepsilon_j) \exp(-r_{ij}^2 / F \alpha_i(\varepsilon_i) \alpha_j(\varepsilon_j))}}$$

$$\varepsilon_{ij} = \frac{\varepsilon_i + \varepsilon_j}{2}$$

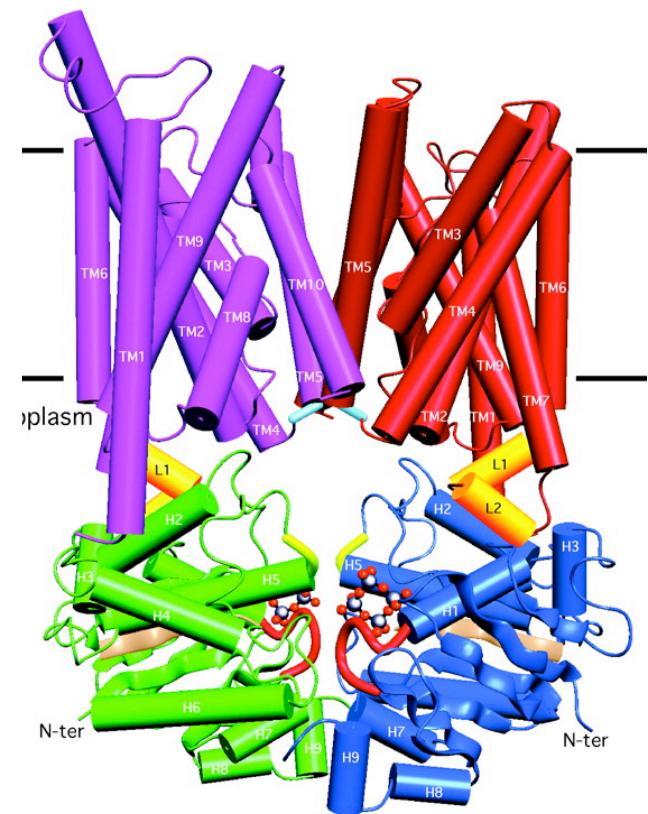
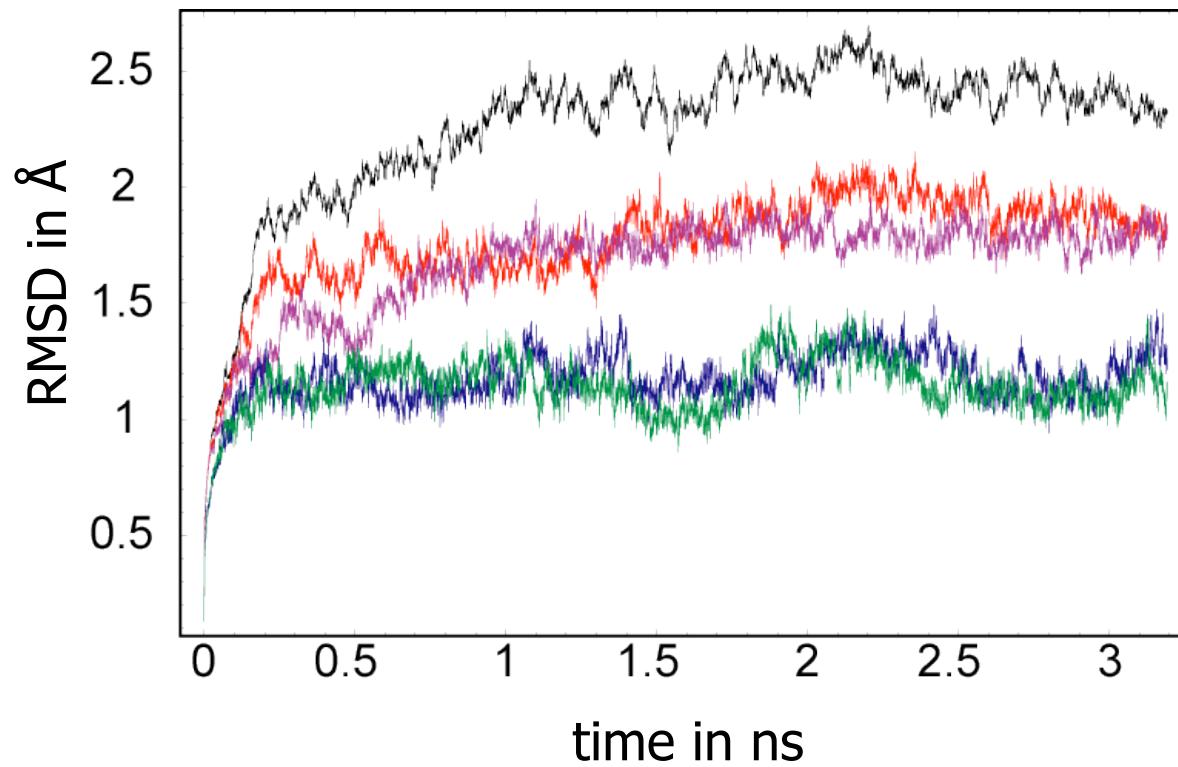
$$\varepsilon_i = \varepsilon_{eff}(z_i)$$

# *Effective Dielectric Constant*

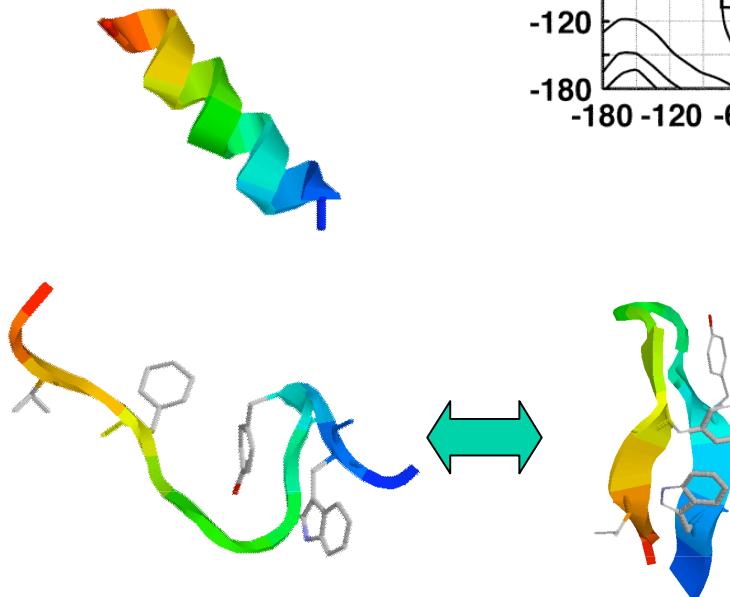
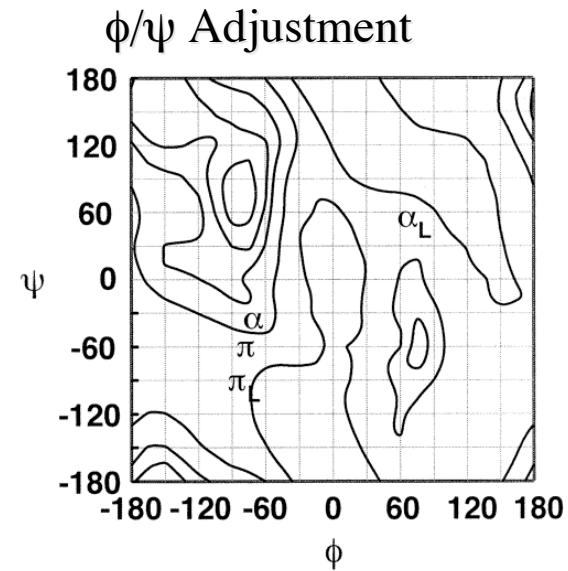
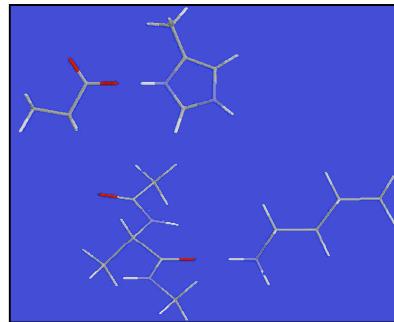
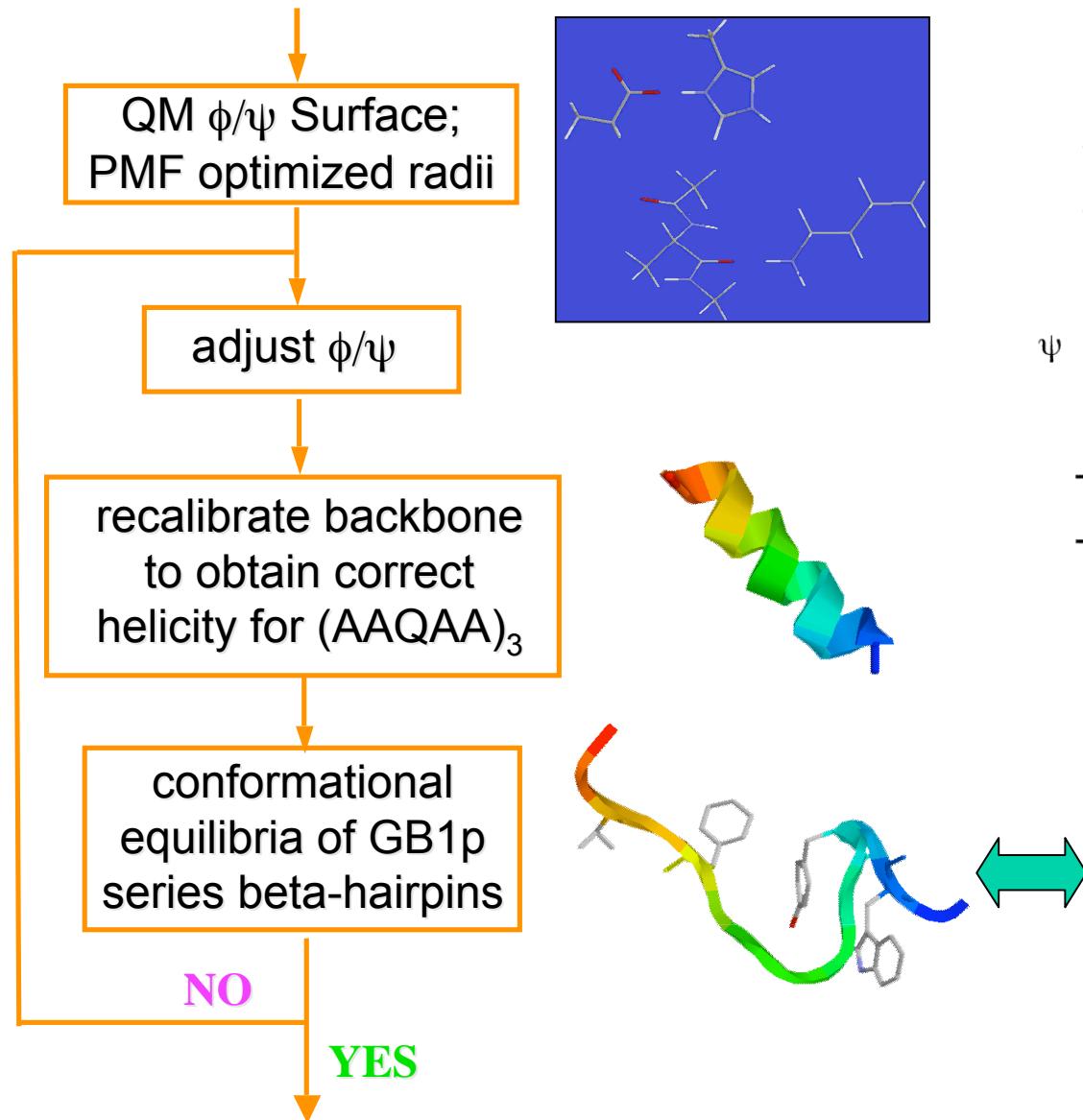


$$\Delta G_{elst}(PB) = -166 \left( 1 - \frac{1}{\epsilon_{eff}(z)} \right) \frac{q^2}{a}$$

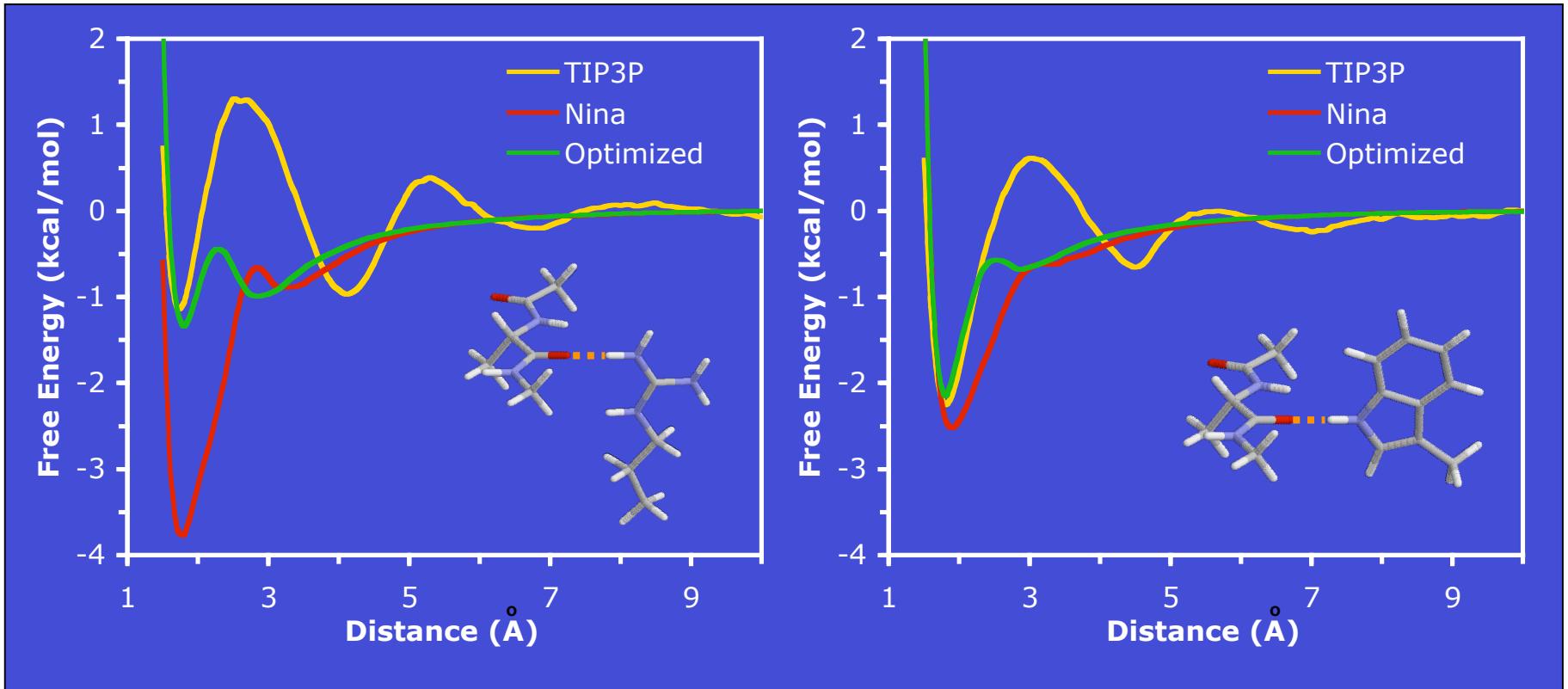
# *Simulations of Membrane Proteins: $B_{12}$ Transporter ButCD*



# Recent Optimization for GBSW



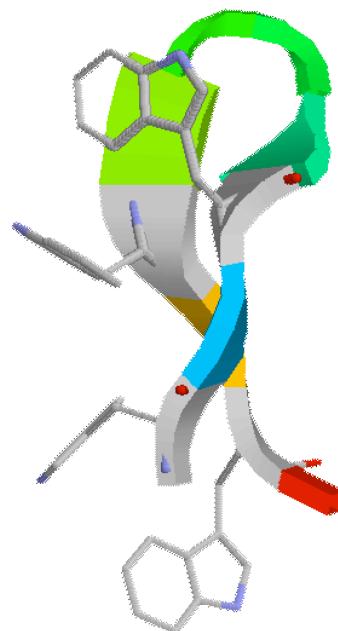
# Pair-wise Interactions



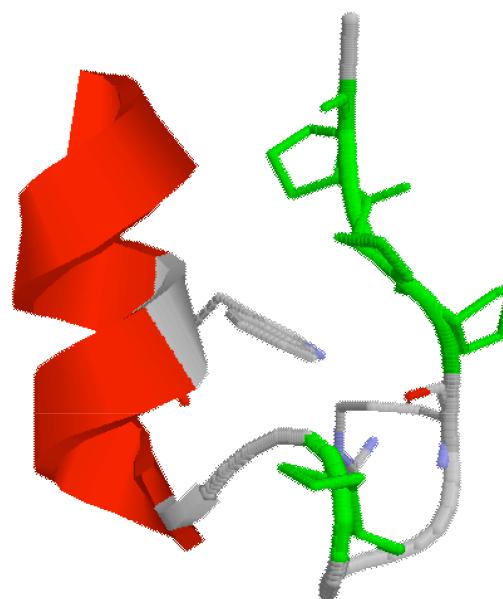
- Hydrogen bonding is often over-stabilized with the original Nina radii;
- Agreement with explicit solvent is significantly improved after direct optimization of the pair-wise interactions.

# *Trpzip2 and Trp-Cage*

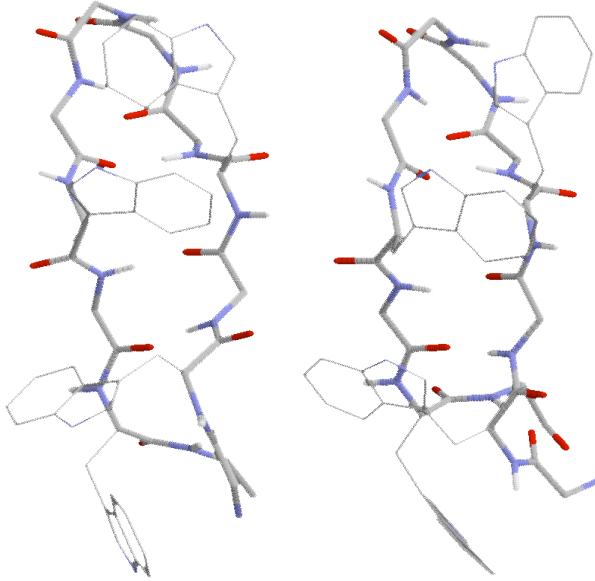
SWTWE NGKWT WK



NLYIQ WLKDQ GPSSG RPPPS



# Folding of Trpzip2

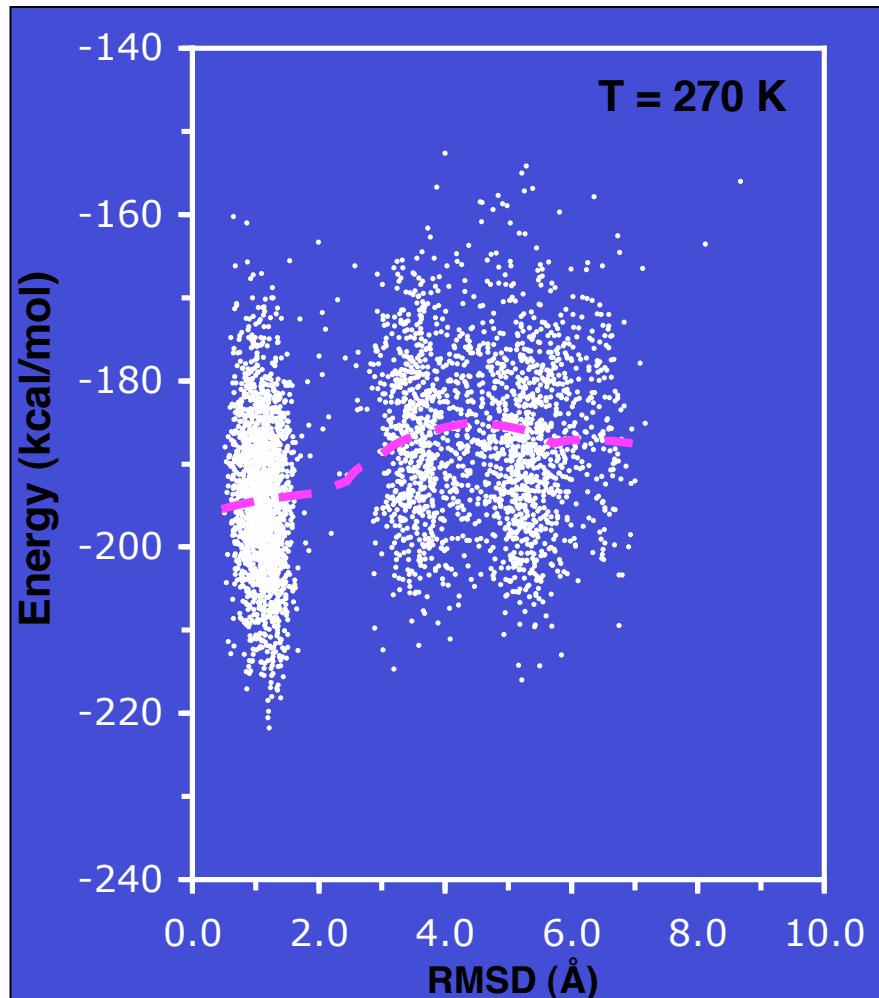


PDB: 1le1      54%, 1.0 Å

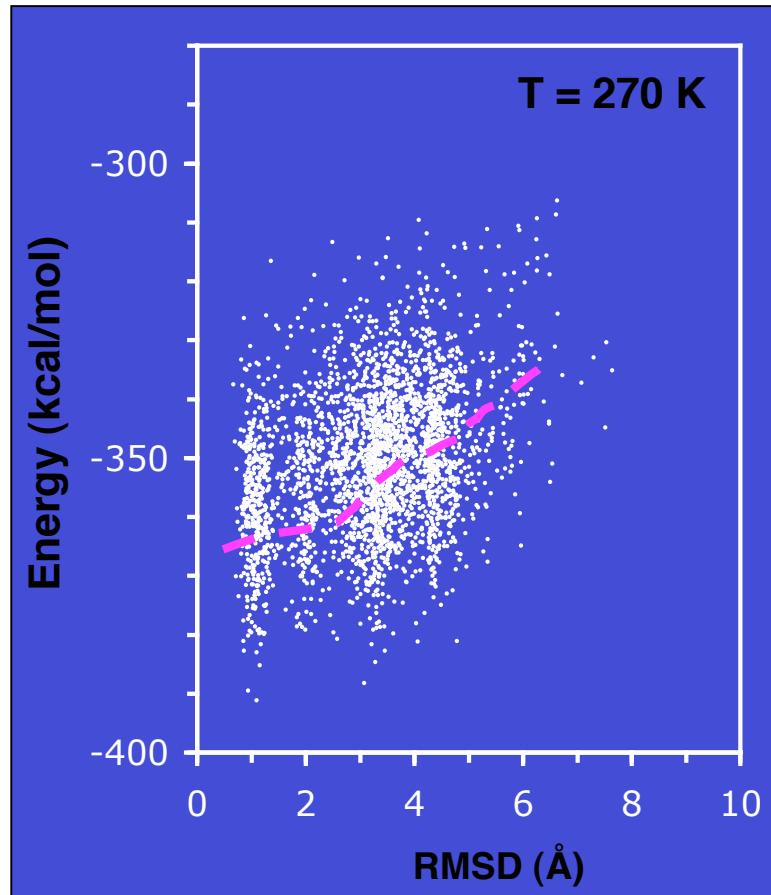
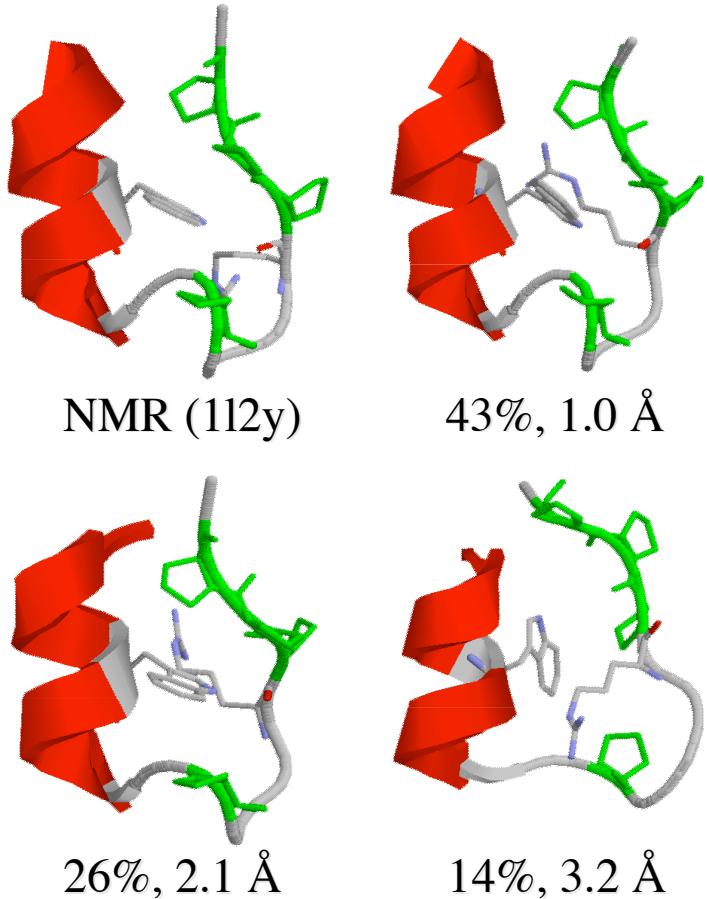
## Simulation details:

40 ns REX-MD with 16 replicas @ 270-550K;  
CHARMM22/CMAP<sup>GBSW</sup>/GBSW;

The population shown is computed from  
clustering the last 10 ns of the lowest  
temperature ensemble.



# Folding of Trp-Cage



## Simulation details:

30 ns REX-MD with 16 replicas @ 270-550K;  
CHARMM22/CMAP<sup>GBSW</sup>/GBSW;

The population shown are computed from clustering  
the last 10 ns of the lowest temperature ensemble.