

# SOMD SAMPL5 Predictions

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D3R Workshop  
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# OVERVIEW



## ➤ Host-Guest:

- Methods: how we calculate binding free energy?
- OAH-O1 as a reference study
- Comparison of results for: OAH, OAMe, CBC

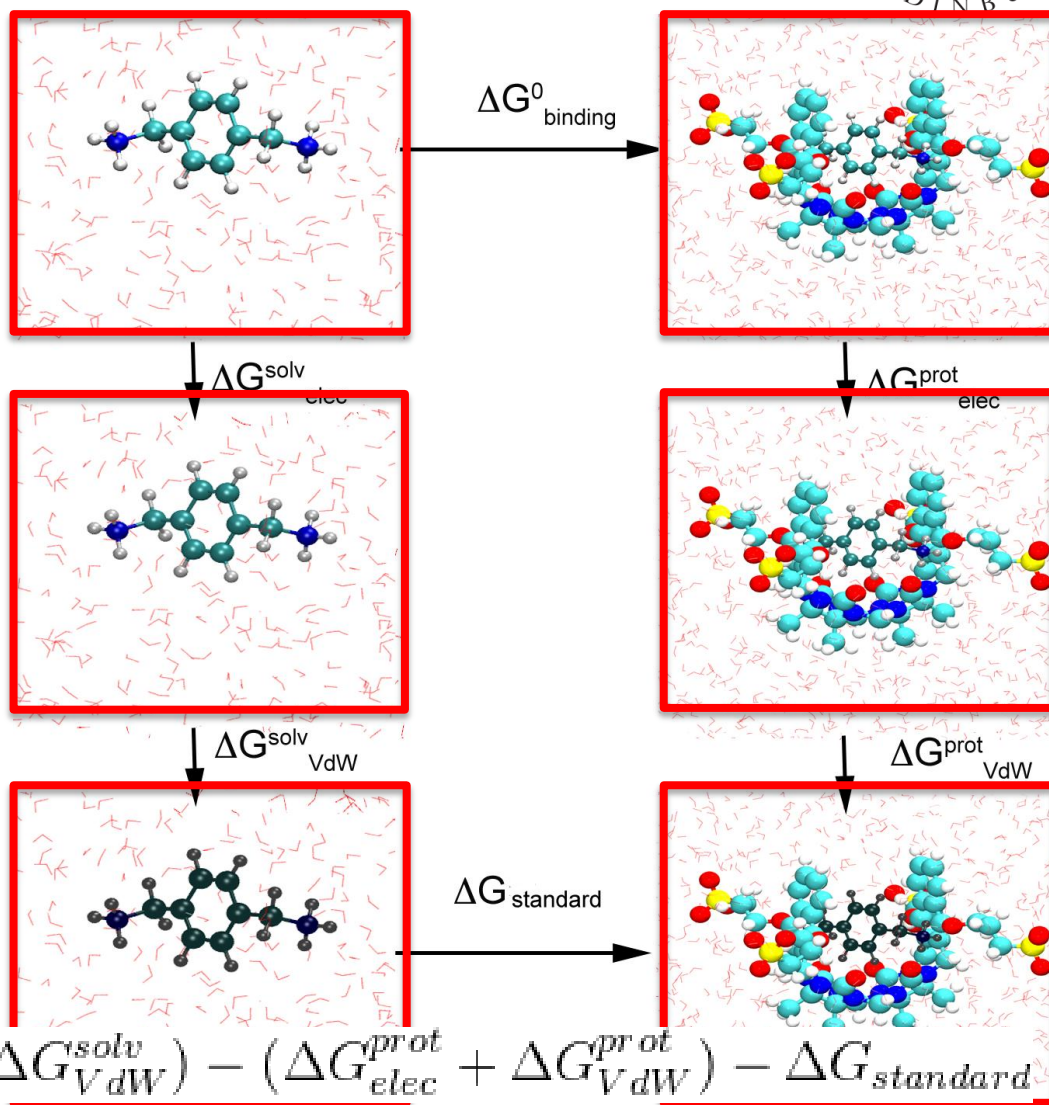
## ➤ Distribution Coefficient:

- Minnesota Database as a reference study
- Comparison with experimental results
- Comparison with free energy estimations
- Correction

# METHODS

## Absolute free energy

- Absolute free energy
- Double decoupling
- Single topology
- GAFF



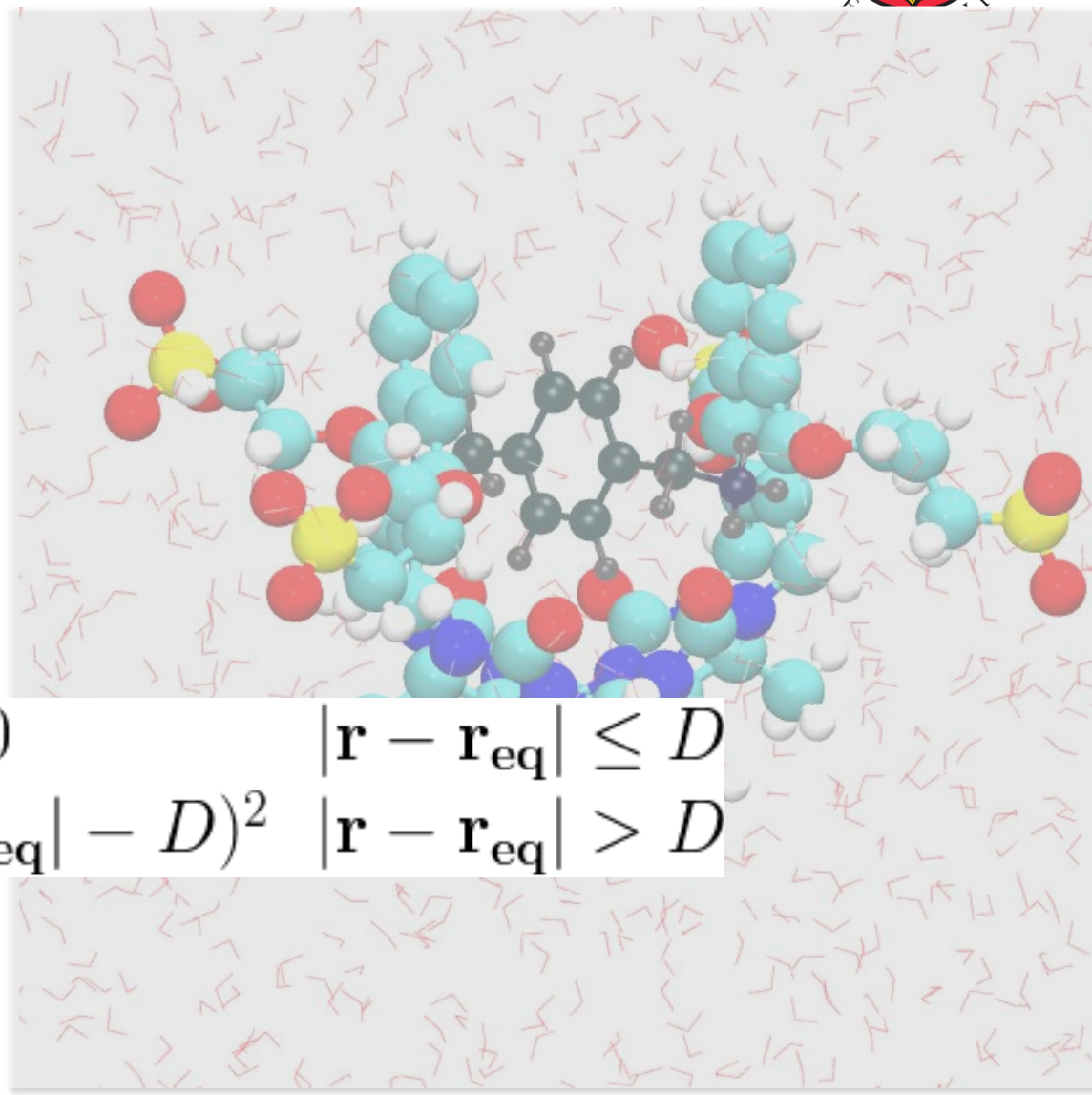
$$\Delta G^0_{\text{binding}} = (\Delta G^{\text{solv}}_{\text{elec}} + \Delta G^{\text{solv}}_{\text{VdW}}) - (\Delta G^{\text{prot}}_{\text{elec}} + \Delta G^{\text{prot}}_{\text{VdW}}) - \Delta G_{\text{standard}}$$

# METHODS

## *Absolute free energy*



- Absolute free energy
- Double decoupling
- Single topology
- GAFF
- Flat bottom restraint:



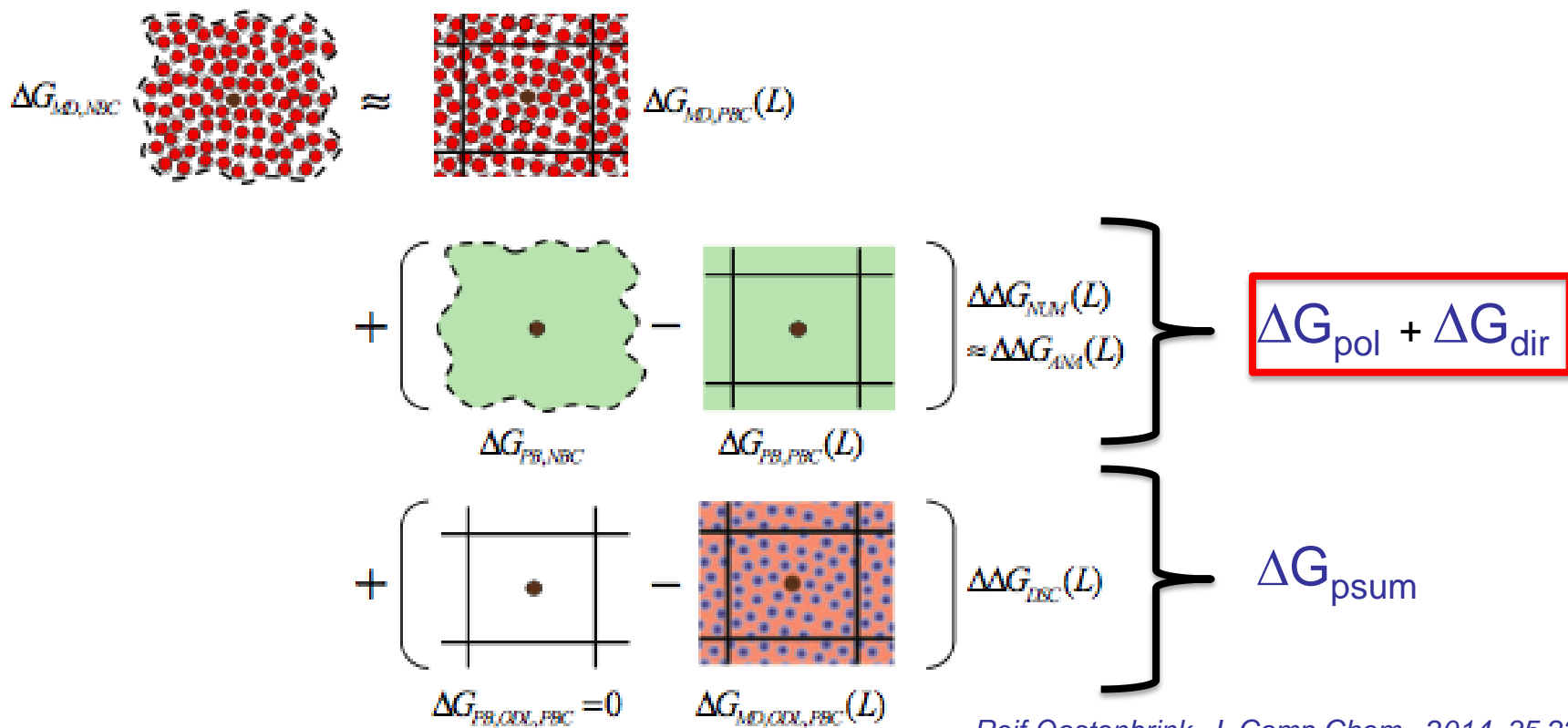
$$U(\mathbf{r}) = \begin{cases} 0 & |\mathbf{r} - \mathbf{r}_{\text{eq}}| \leq D \\ K(|\mathbf{r} - \mathbf{r}_{\text{eq}}| - D)^2 & |\mathbf{r} - \mathbf{r}_{\text{eq}}| > D \end{cases}$$

# METHODS

## Charging free energy



Rocklin et al. *J. Chem. Phys.*, 2013, 139 184103



Reif, Oostenbrink, *J. Comp Chem.*, 2014, 35, 227-243

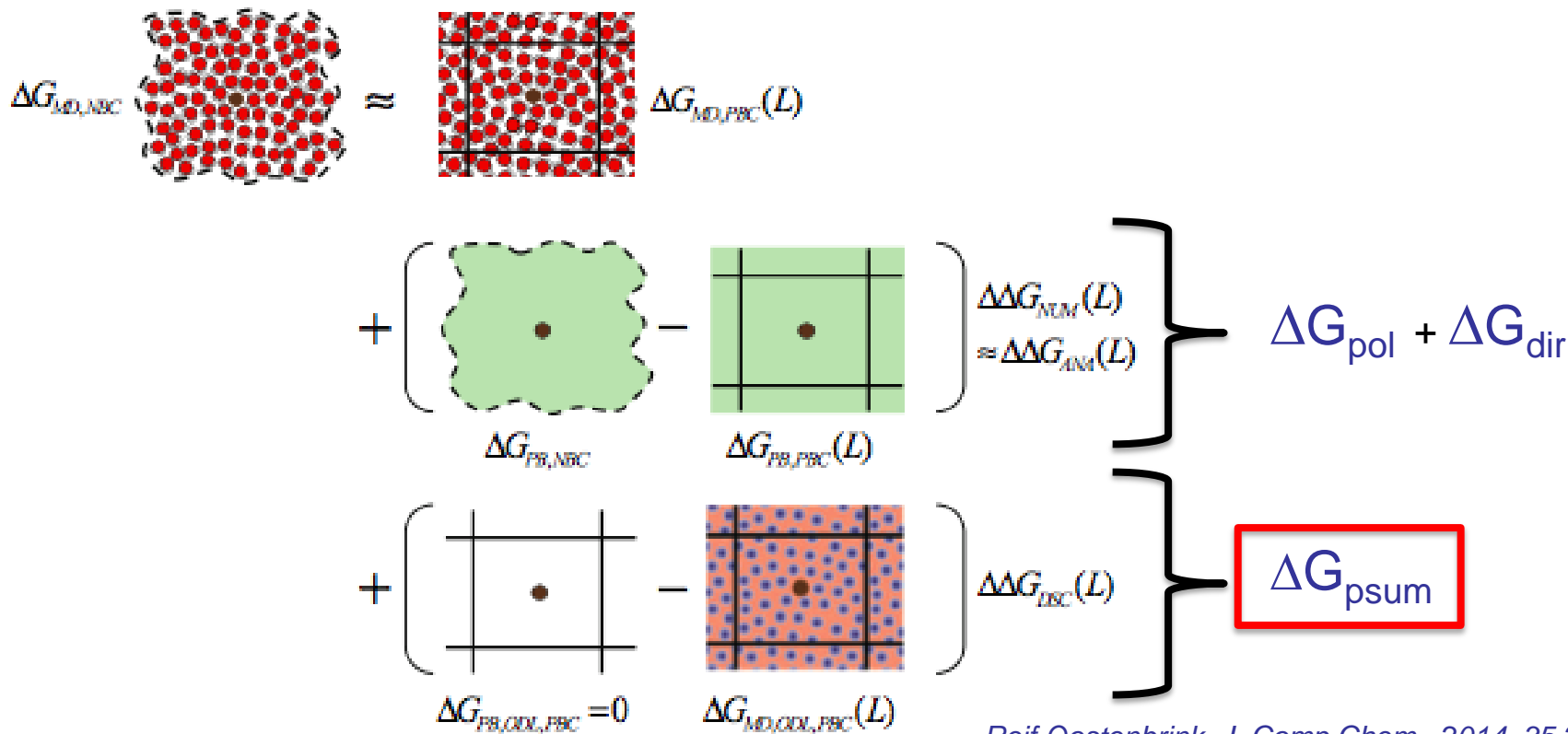
Reaction field Atom Based : APBS PB non periodic conditions  
 Custom Code given by P. Hunenberger

# METHODS

## Charging free energy



Rocklin et al. *J. Chem. Phys.*, 2013, 139 184103



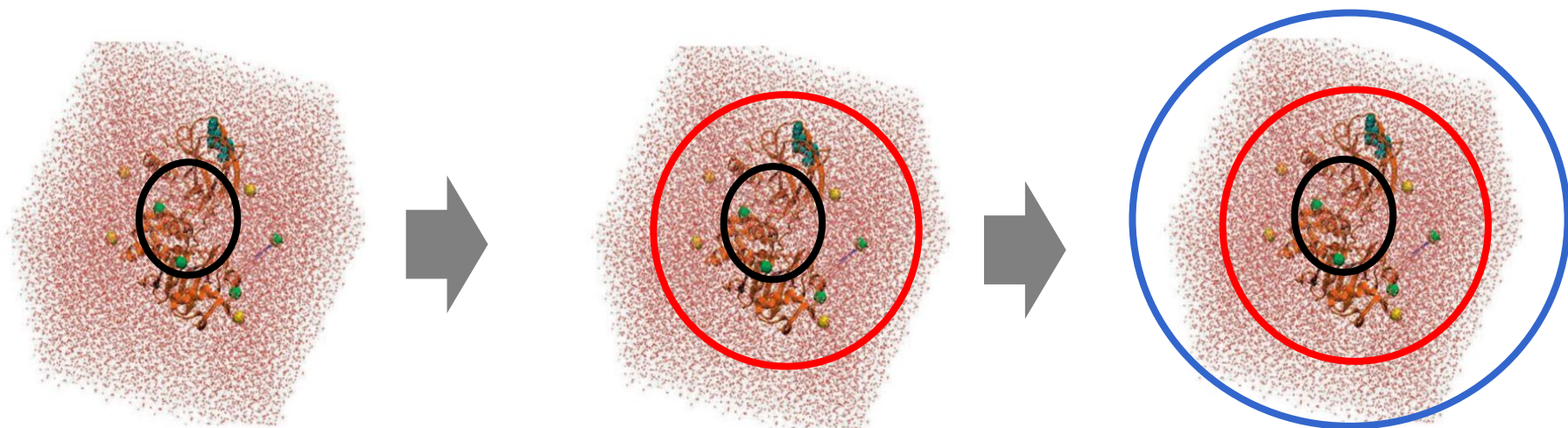
$$\Delta G_{psum} = -N_A(6\epsilon_0)^{-1} \left( \frac{2(\epsilon_{RF}-1)}{2\epsilon_{RF}+1} \right) \gamma_w Q_G \langle N_w(R_c) \rangle \left[ \frac{4}{3} \pi R_c^3 \right]^{-1}$$

# METHODS

## Long-range dispersion correction



Shirts et al. *J. Phys. Chem. B*, Vol. 111, No. 45, 2007



$U_{LJ,sim}$

$U_{LJ,LRC-num}$

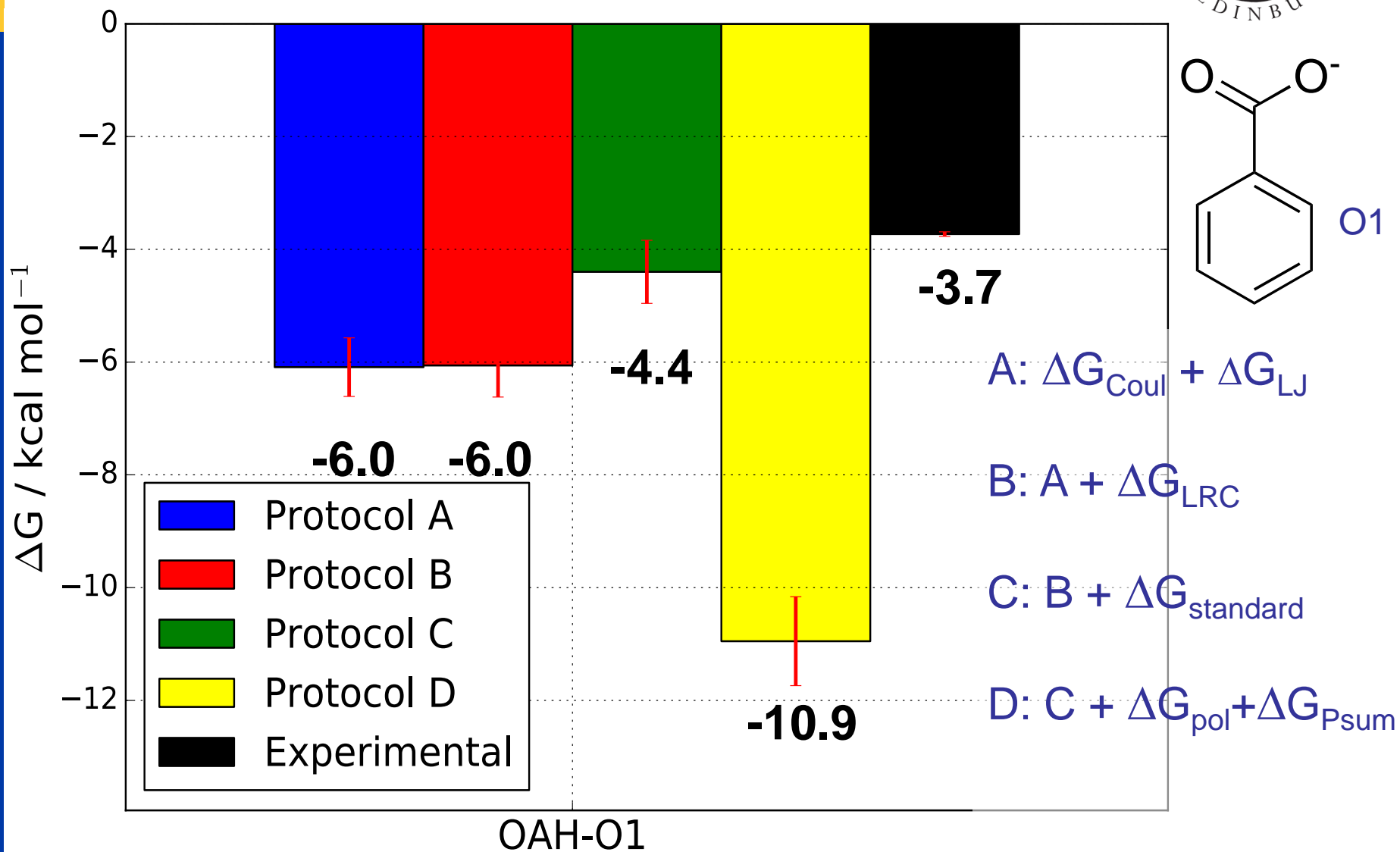
$U_{LJ,LRC-ana}$

$$\Delta G_{LJLRC} = -\beta^{-1} \ln \langle \exp(- (U_{LJ,long}(\mathbf{r}) - U_{LJ,sim}(\mathbf{r}))) \rangle_{sim}$$



# OAH-O1

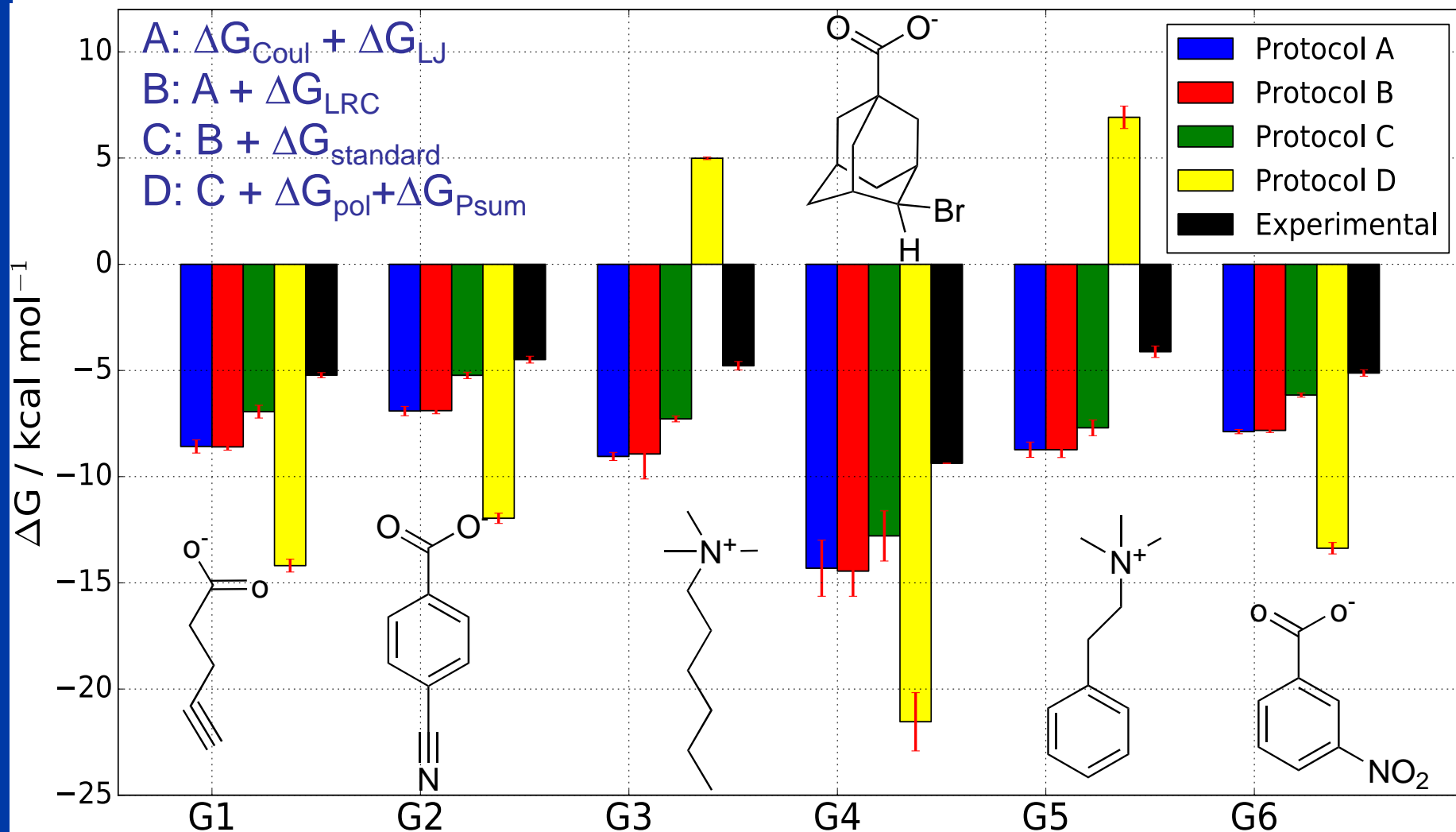
## Reference simulation





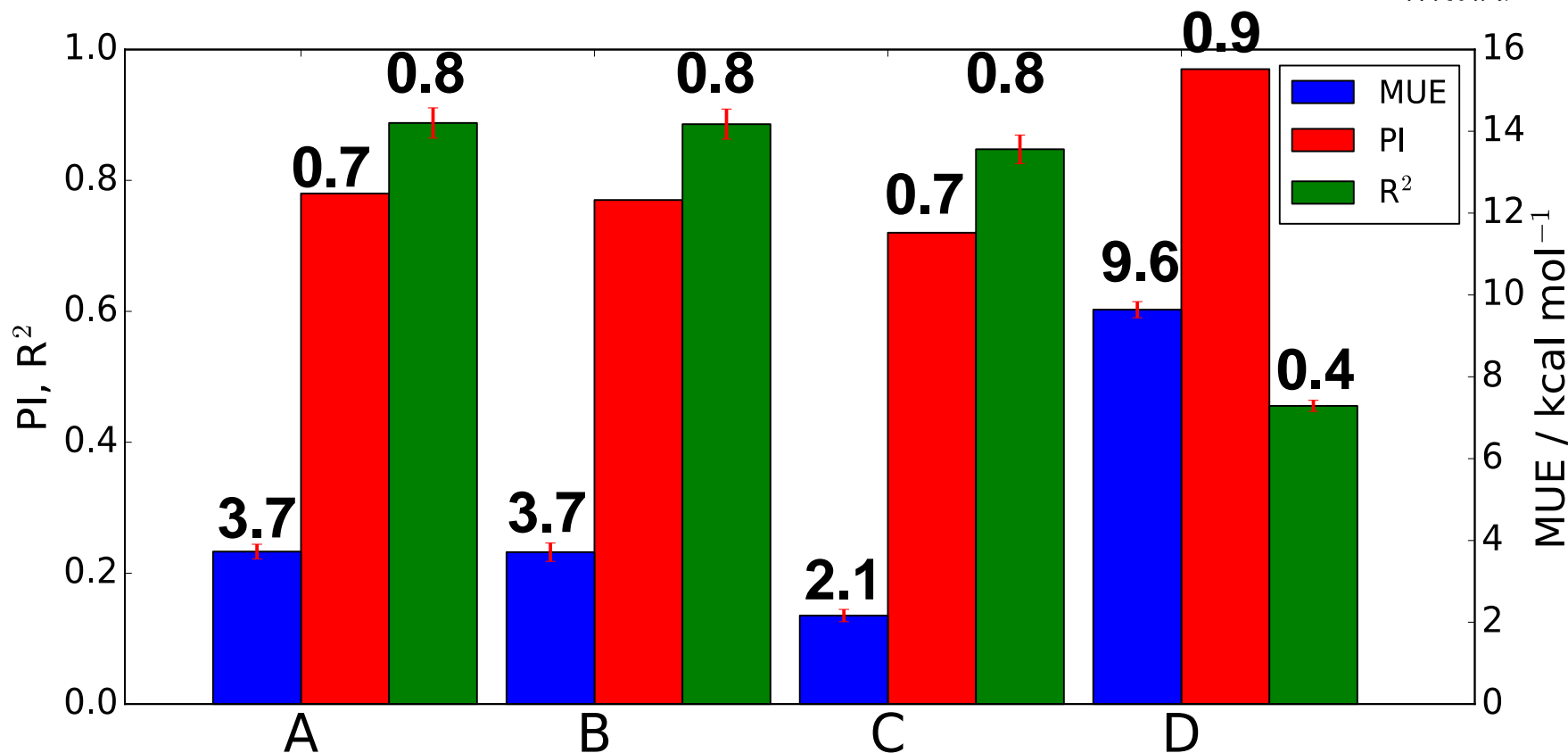
# OAH DATASET

## Prediction vs experiment



# OAH DATASET

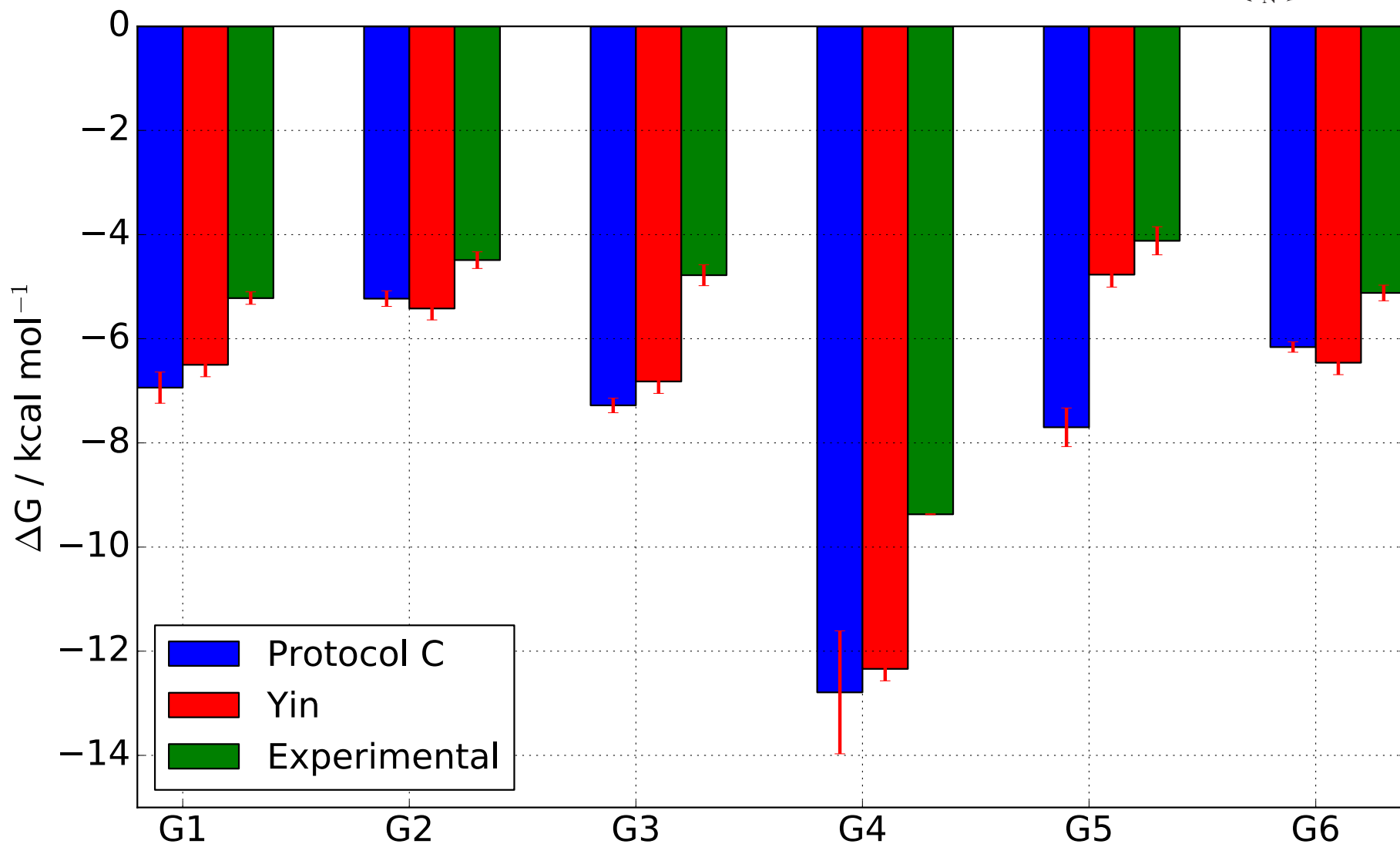
## Statistical analysis



AUE:	$3.7 \pm 0.4$	$3.7 \pm 0.4$	$2.1 \pm 0.5$	$9.6 \pm 0.6$
R:	$0.9 \pm 0.5$	$0.9 \pm 0.5$	$0.9 \pm 0.6$	$0.7 \pm 0.2$
Max Err:	$2.4 \pm 0.3$	$2.4 \pm 0.4$	$0.6 \pm 0.4$	$11 \pm 2$

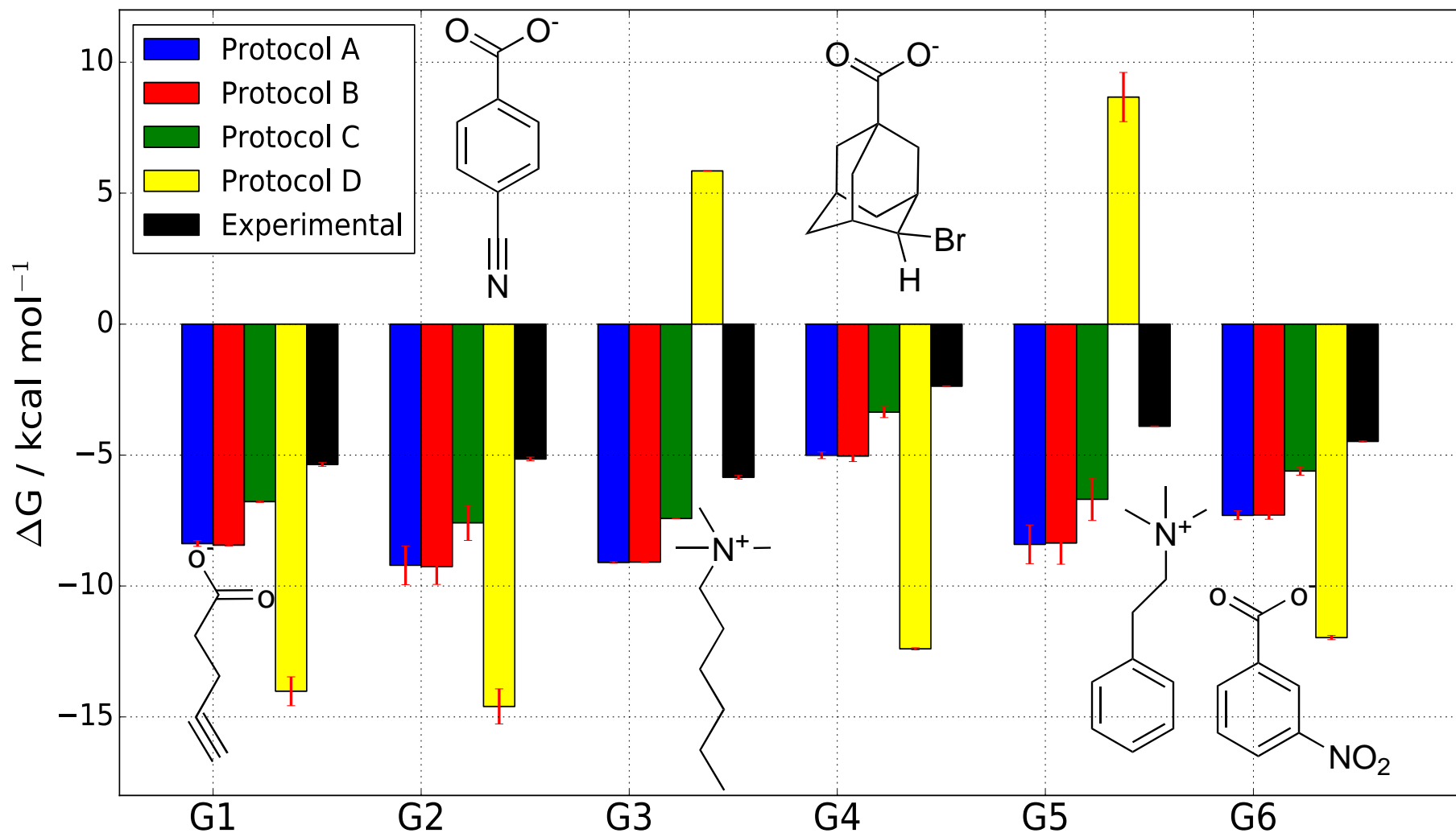
# OAH DATASET

## Comparison with Yin's APR simulations



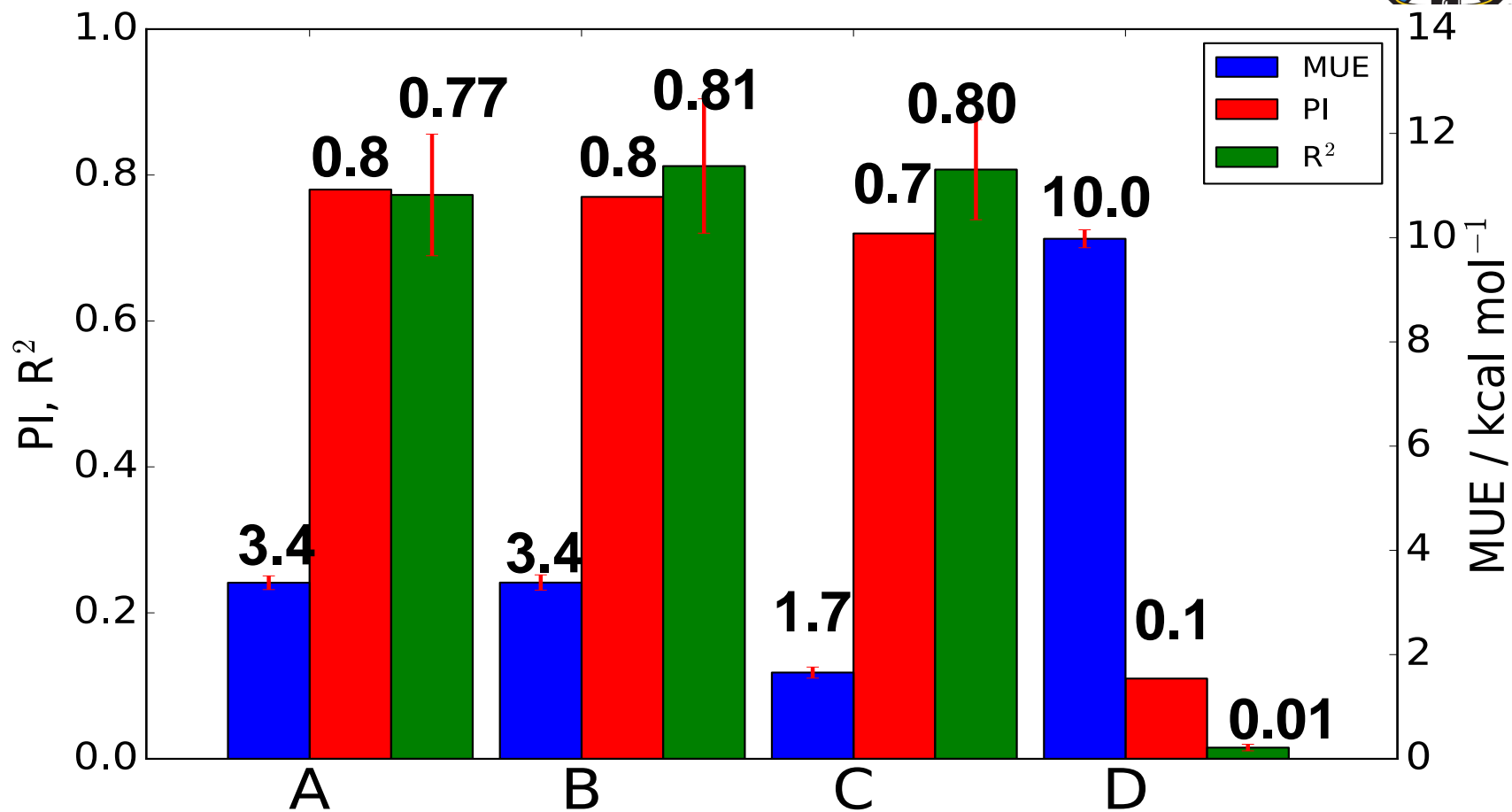
# OAME DATASET

## Prediction and experiment



# OAME DATASET

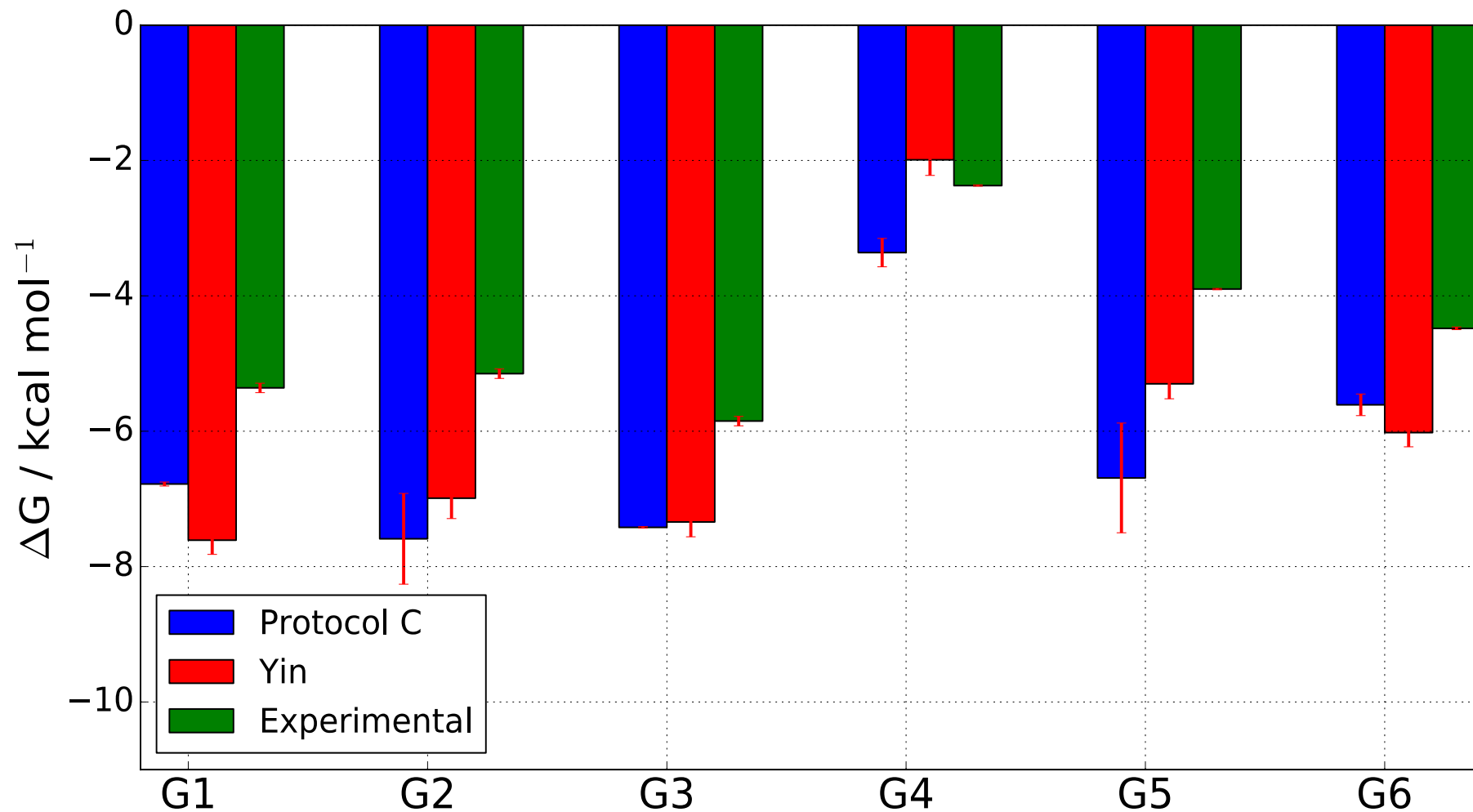
## Statistical analysis



AUE:	$3.4 \pm 0.3$	$3.4 \pm 0.3$	$1.7 \pm 0.3$	$10.0 \pm 0.7$
R:	$0.9 \pm 0.3$	$0.9 \pm 0.3$	$0.9 \pm 0.2$	$-0.1 \pm 0.5$
Max Err:	$2.6 \pm 0.4$	$2.7 \pm 0.4$	$0.1 \pm 0.4$	$12.6 \pm 0.5$

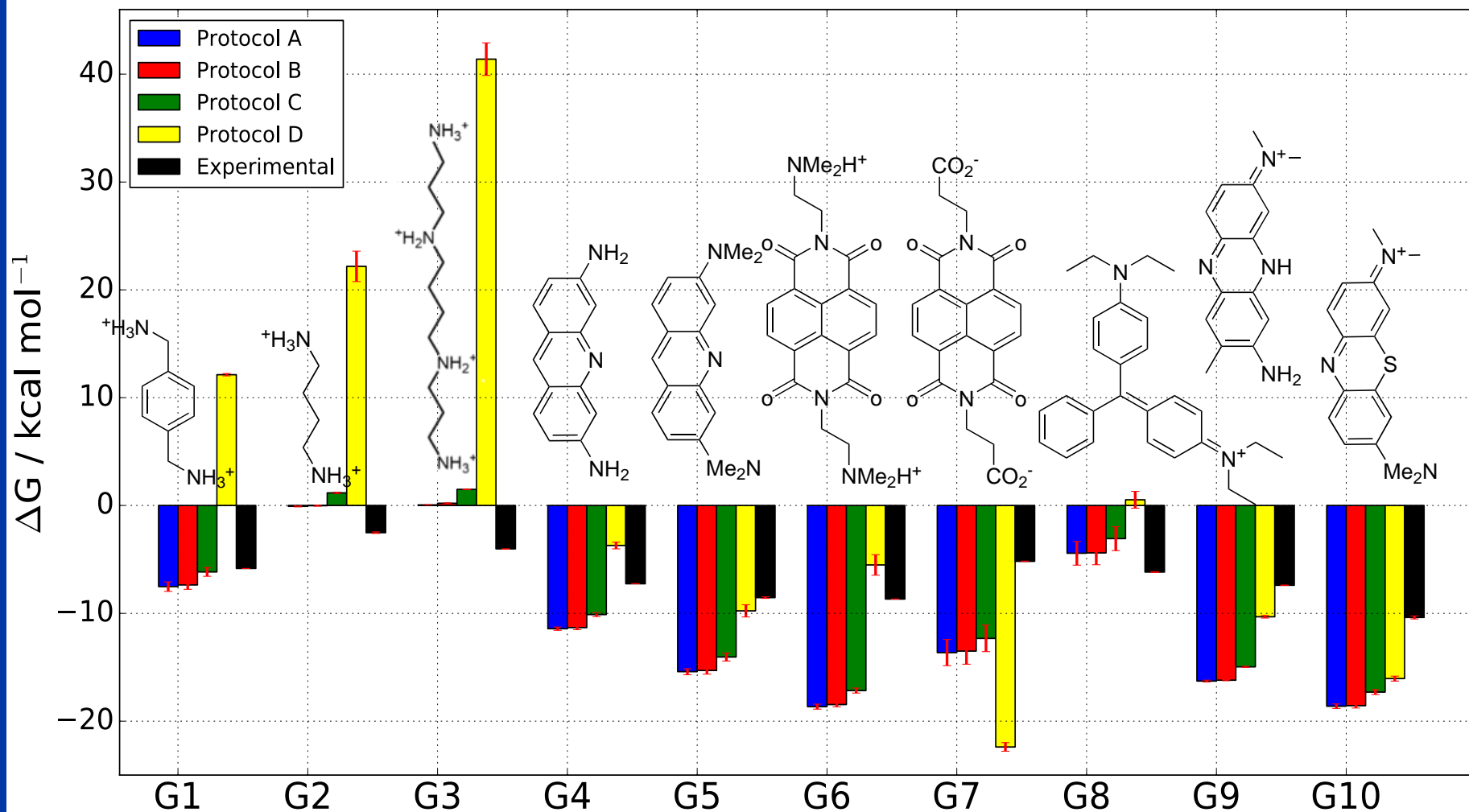
# OAME DATASET

## Comparison with Yin's APR simulations



# CBC DATASET

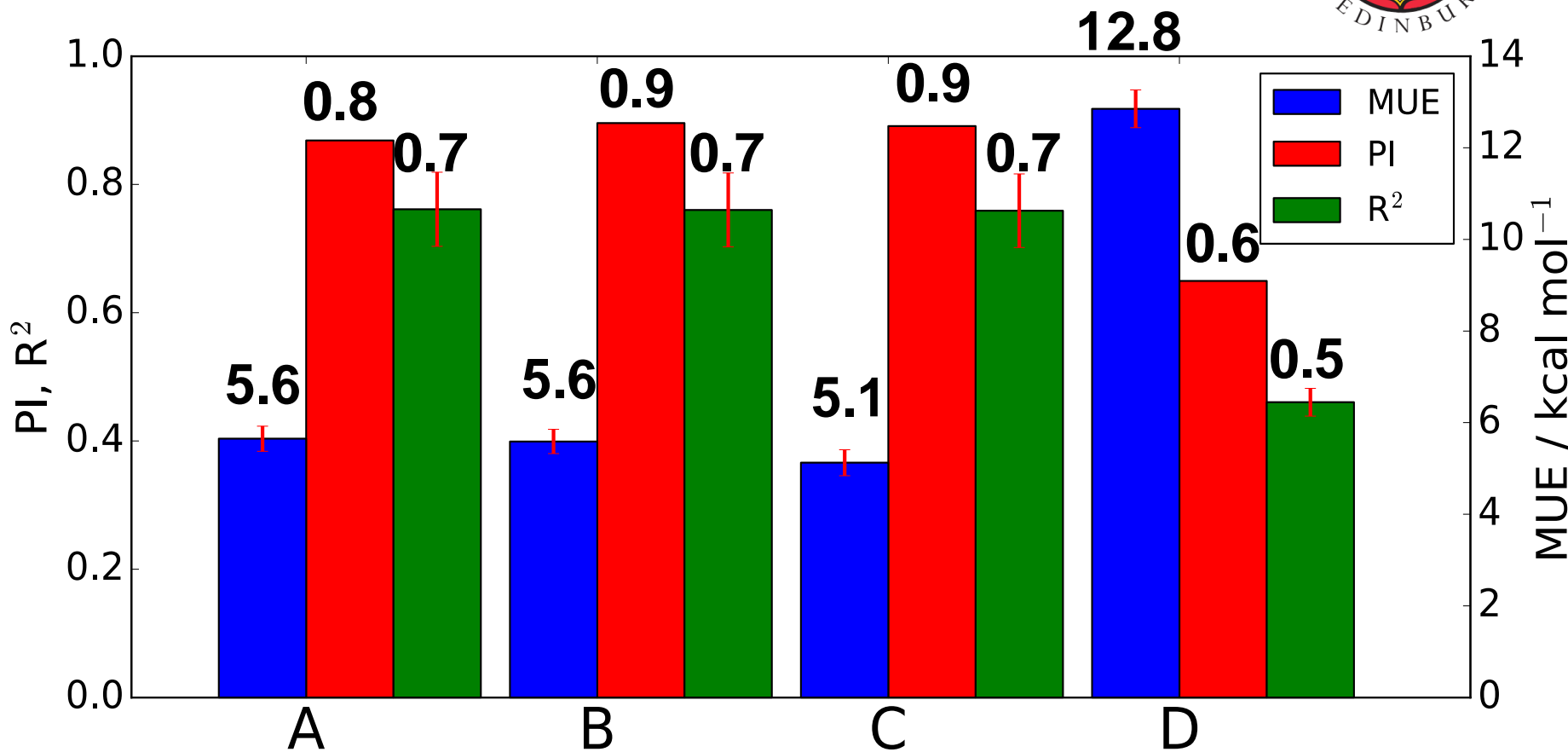
## Prediction and experiment





# CBC DATASET

## Statistical Analysis



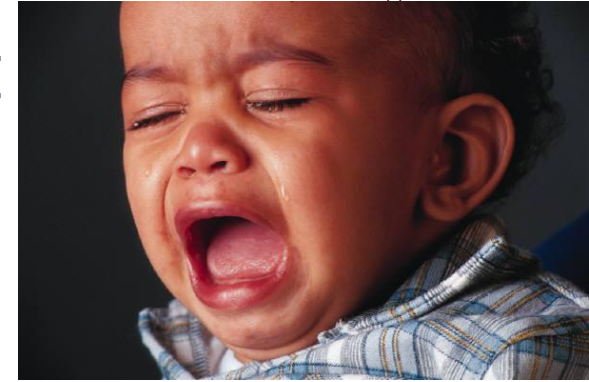
AUE:	$5.7 \pm 0.9$	$6.0 \pm 0.1$	$5.1 \pm 0.8$	$13.0 \pm 4.0$
R:	$0.9 \pm 0.1$	$0.9 \pm 0.1$	$0.9 \pm 0.1$	$0.7 \pm 0.3$
Max Err:	$4.1 \pm 0.6$	$4.2 \pm 0.6$	$5.5 \pm 0.6$	$45.0 \pm 6.0$

# HOST-GUEST

## *What we have learned*



- Charging corrections: CHECK THE CODE
- Long range corrections small contribution
- All protocols, except D, present a good  $R^2$
- Reasonable reproducibility with other methods



# DISTRIBUTION COEFFICIENT

## Minnesota database

- Absolute free energy of solvation

$$\Delta G_{\text{HYD}} \text{ and } \Delta G_{\text{CYC}}$$

- GAFF/AM1BCC

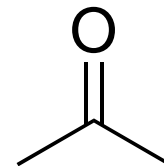
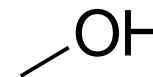
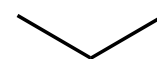
- Protocols:

$$\text{A: } \Delta G_{\text{Coul}} + \Delta G_{\text{LJ}}$$

$$\text{B: } \text{A} + \Delta G_{\text{LJ-LRC}}$$

$$\text{C: } \text{A} + \Delta G_{\text{charge}}$$

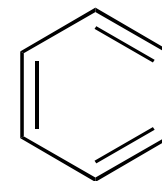
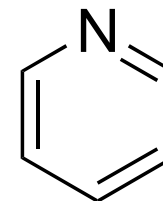
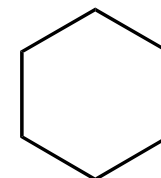
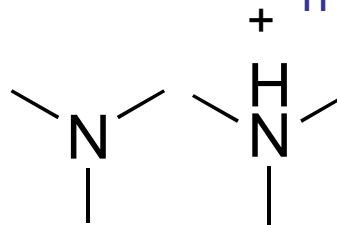
$$\text{D: } \text{B} + \text{C}$$



n-propane

methanol

acetone

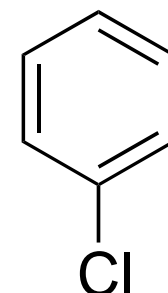
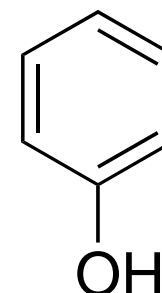
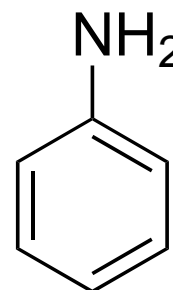
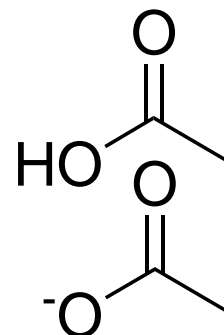


Trimethylamine

Cyclohexane

Pyridine

Benzene



Acetic Acid

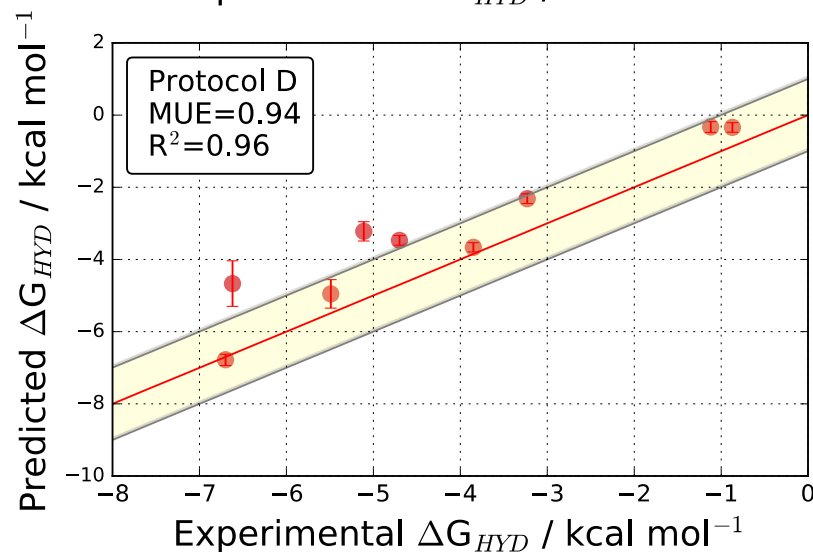
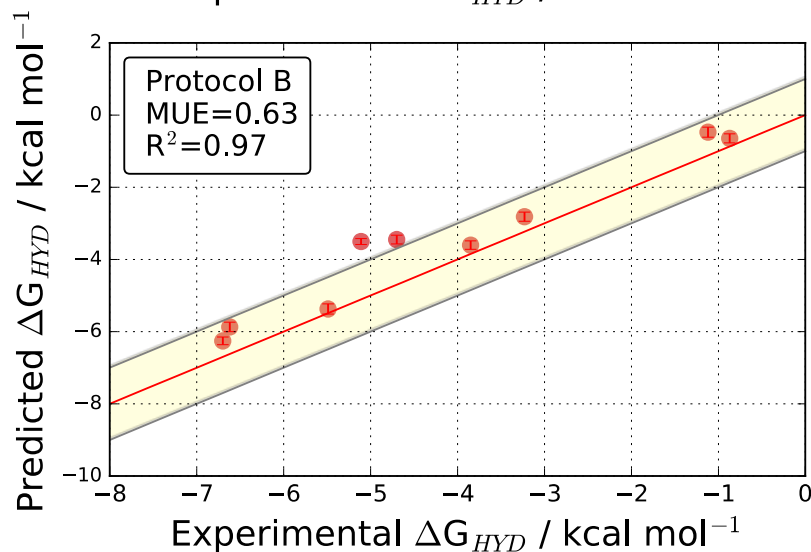
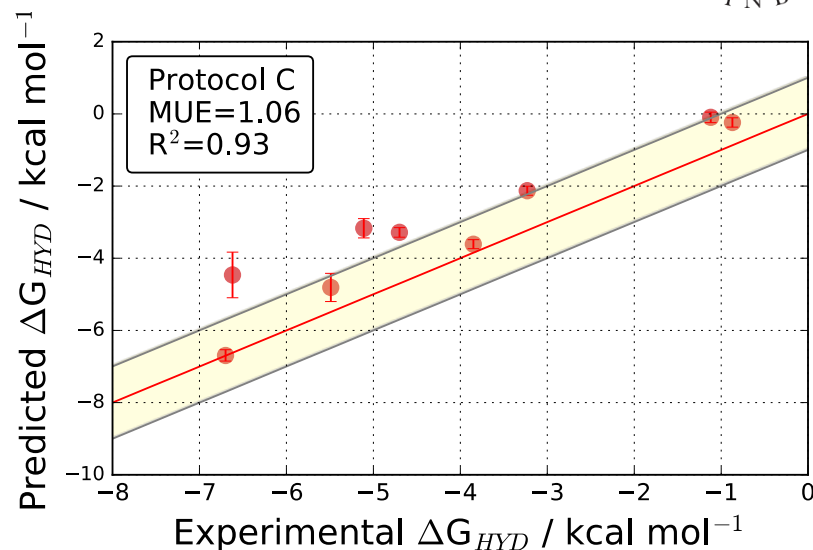
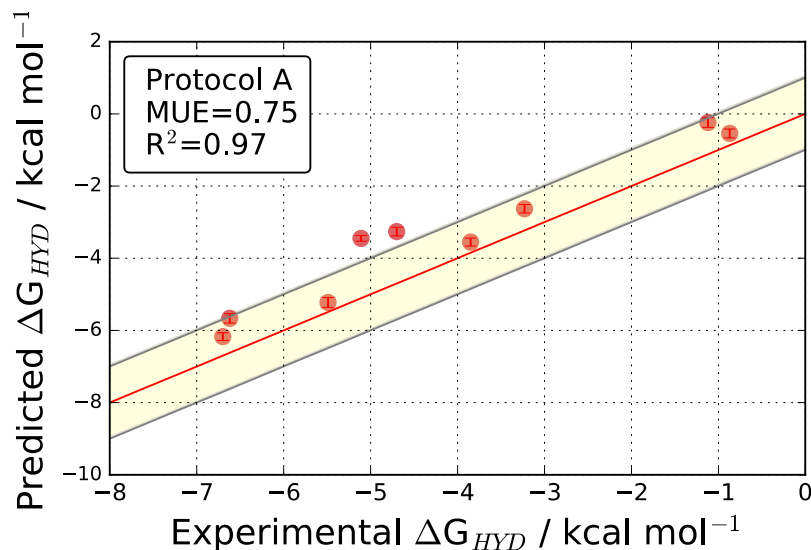
Aniline

Phenol

Cl-Benzene

# DISTRIBUTION COEFFICIENT

## Minnesota database



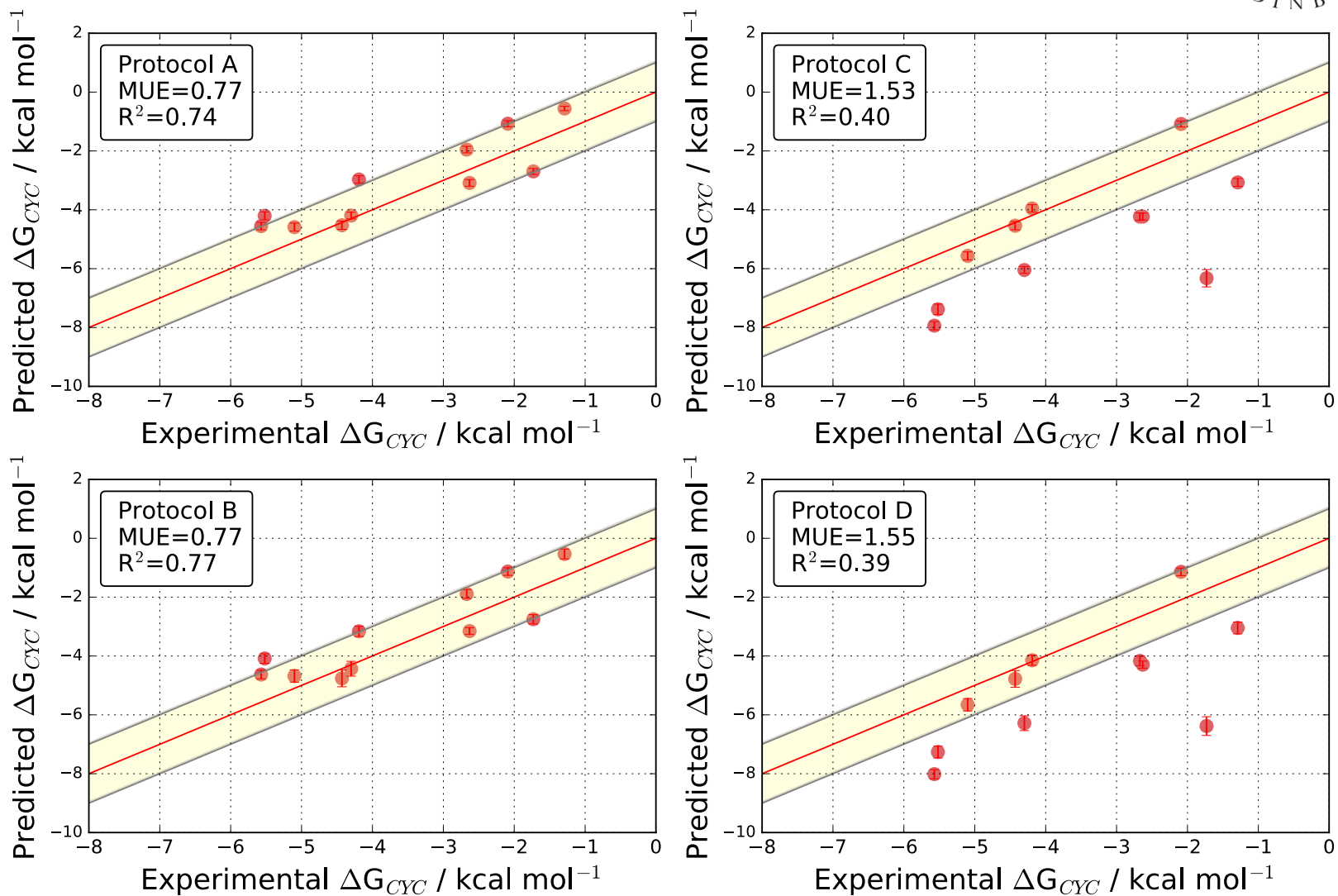
# DISTRIBUTION COEFFICIENT

## Minnesota database

Molecule	$\Delta G_{\text{HYD}} \text{ EXP}$	$\Delta G_{\text{HYD}} \text{ A}$	$\Delta G_{\text{HYD}} \text{ B}$	$\Delta G_{\text{HYD}} \text{ C}$	$\Delta G_{\text{HYD}} \text{ D}$
benzene	-0.9	-0.7	-0.9	-0.5	-0.6
cyclohexane	1.2	1.2	1.1	1.2	1.1
trimethylamine_positive	-61.4	-24.7	-24.8	-61.9	-62.0
acetic_acid_neutral	-6.7	-5.8	-6.0	-5.4	-5.6
trimethylamine_neutral	-3.2	-2.9	-3.0	-2.6	-2.7
chlorobenzene	-1.1	-0.4	-0.6	-0.3	-0.5
methanol	-5.1	-3.3	-3.4	-3.1	-3.2
n-propane	2.0	2.4	2.4	2.5	2.4
pyridine	-4.7	-2.9	-3.1	-2.8	-3.0
phenol	-6.6	-5.2	-5.4	-4.0	-4.1
acetic_acid_negative	-77.6	-74.5	-74.6	-81.0	-81.1
acetone	-3.9	-3.4	-3.6	-3.4	-3.6
aniline	-5.5	-5.2	-5.4	-4.4	-4.6
MUE_all		3.70	3.58	1.20	1.11
MUE_neutral		0.75	0.63	1.06	0.94

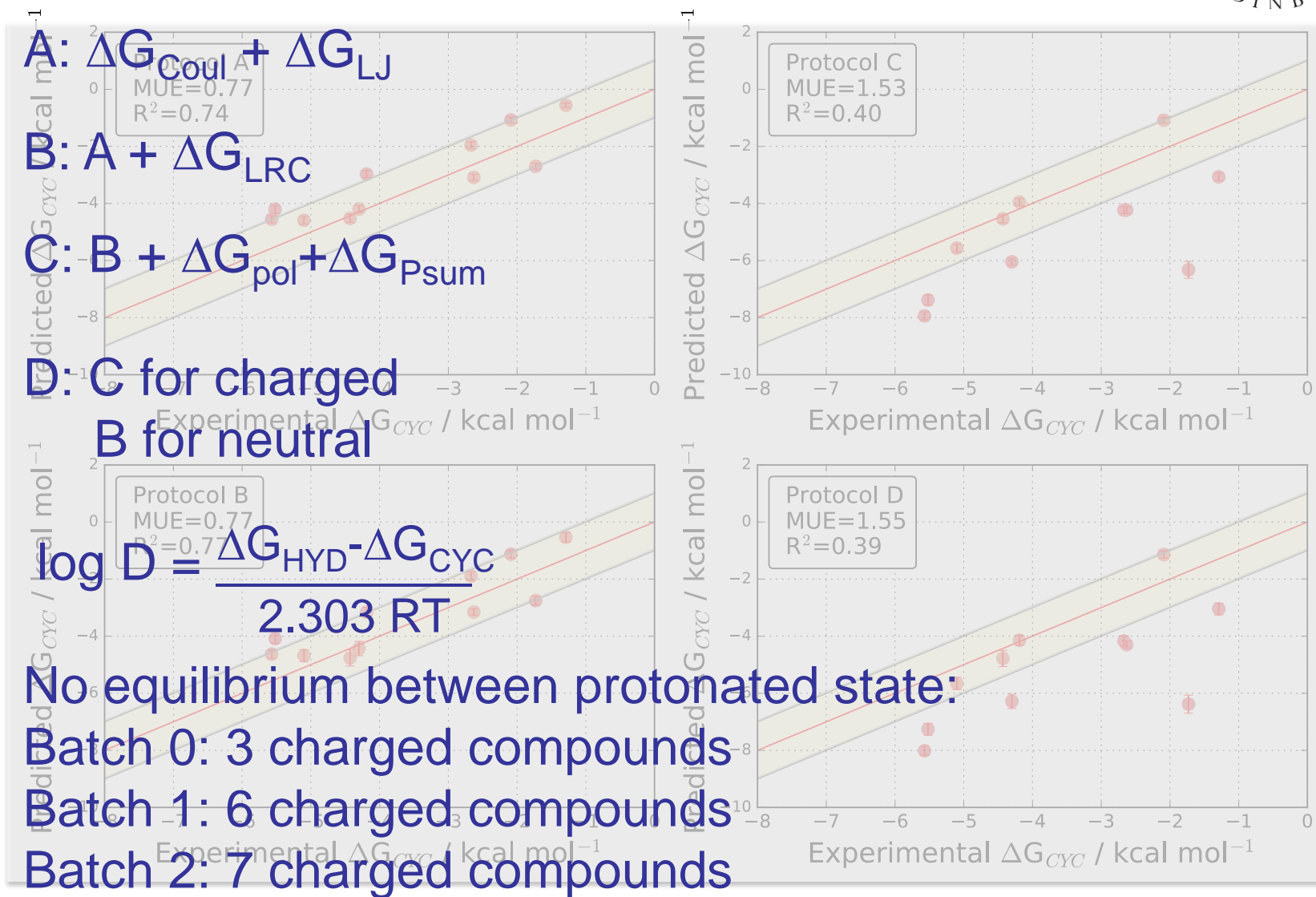
# DISTRIBUTION COEFFICIENT

## *Minnesota database*



# DISTRIBUTION COEFFICIENT

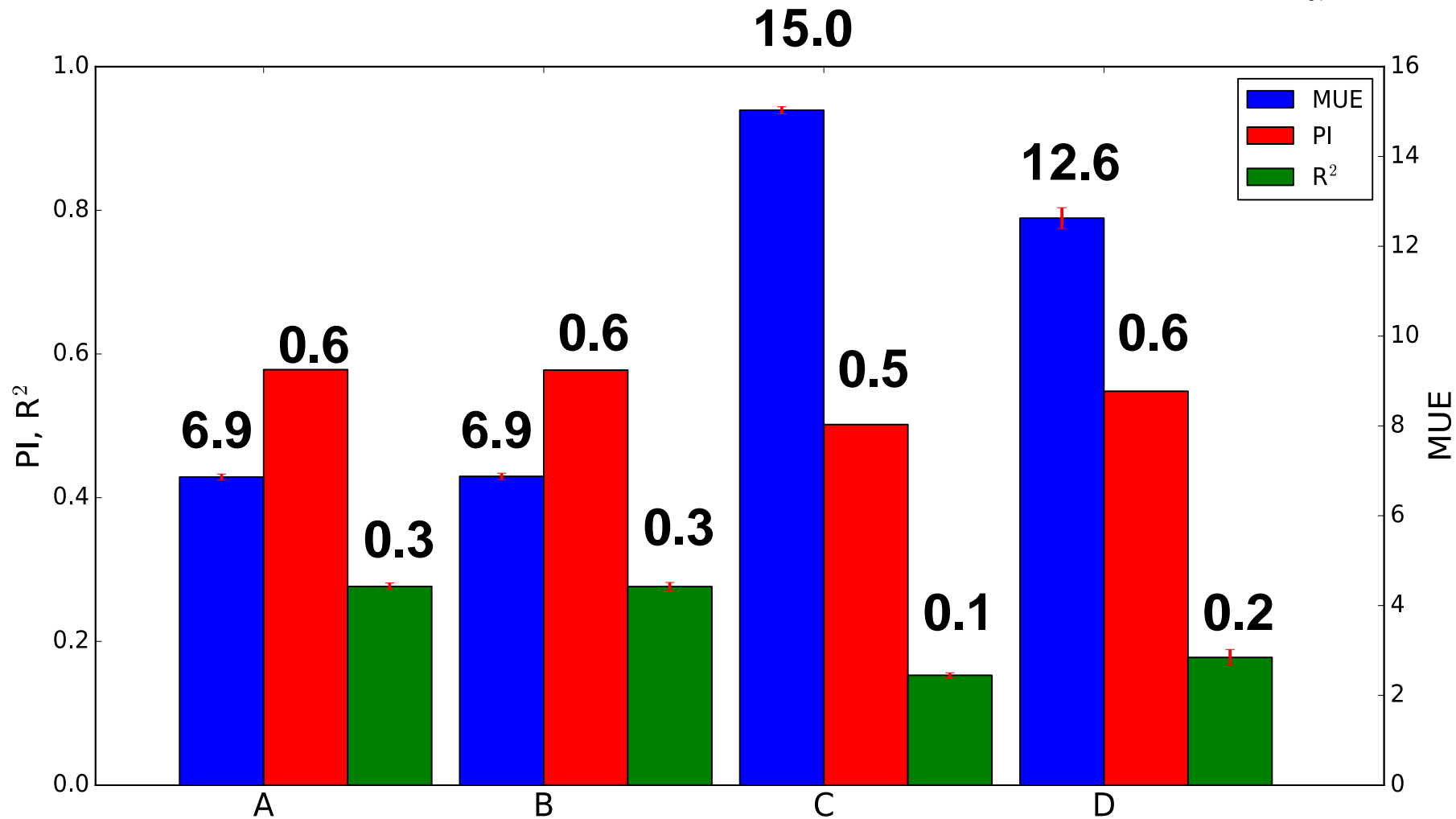
## Protocols setup



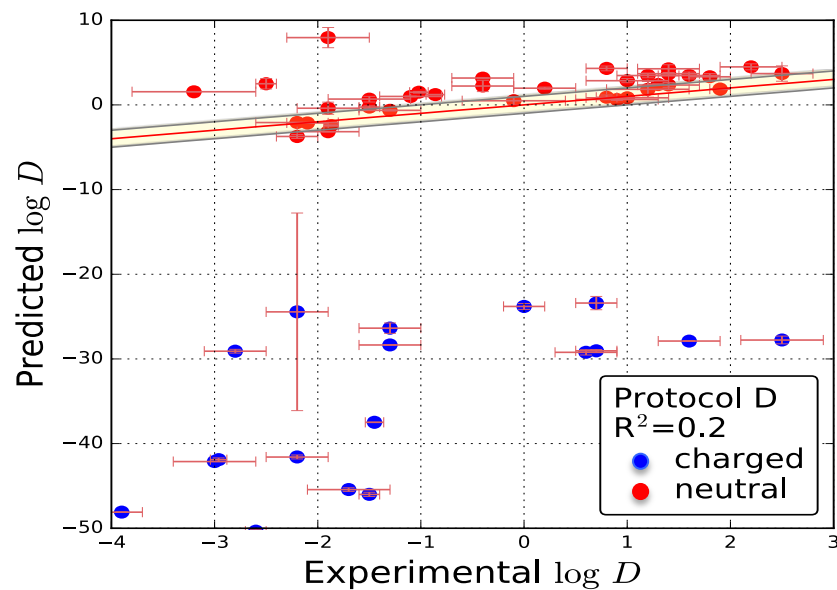
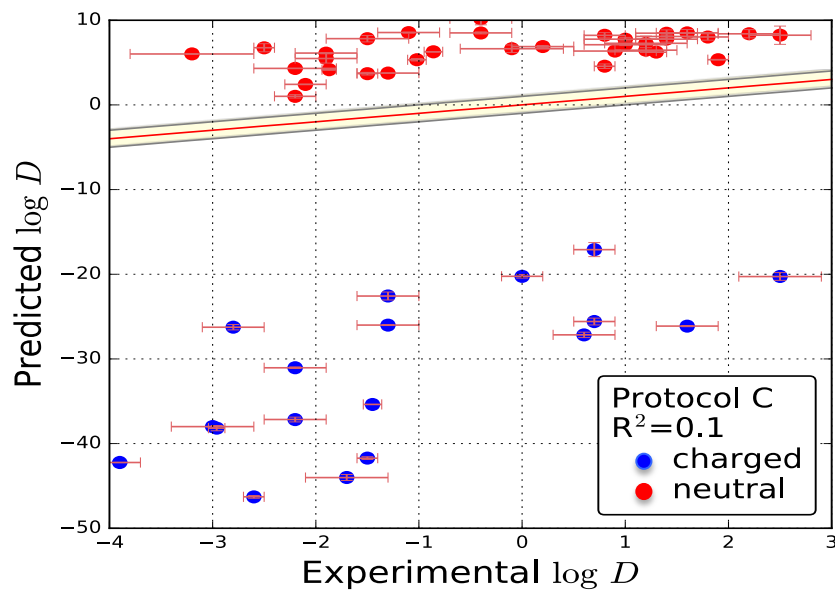
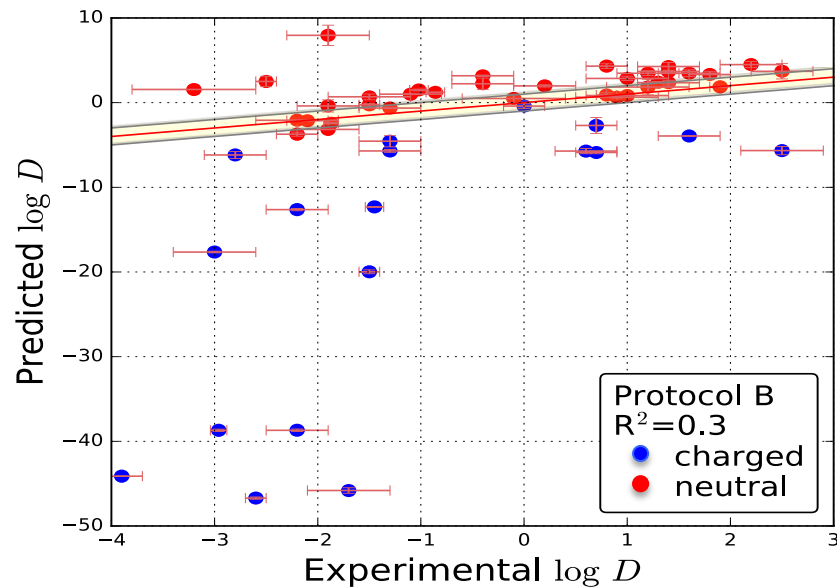
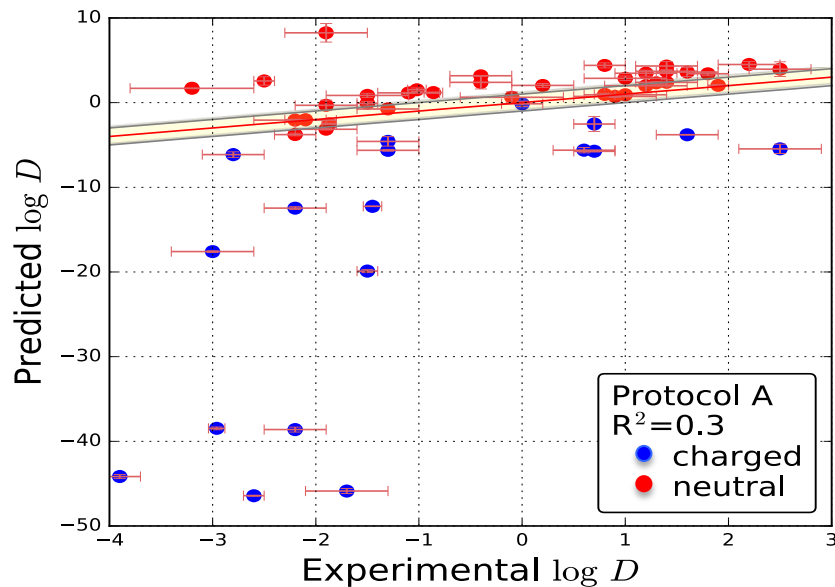


# ALL DATASET

## *MUE – PI – R<sup>2</sup>*

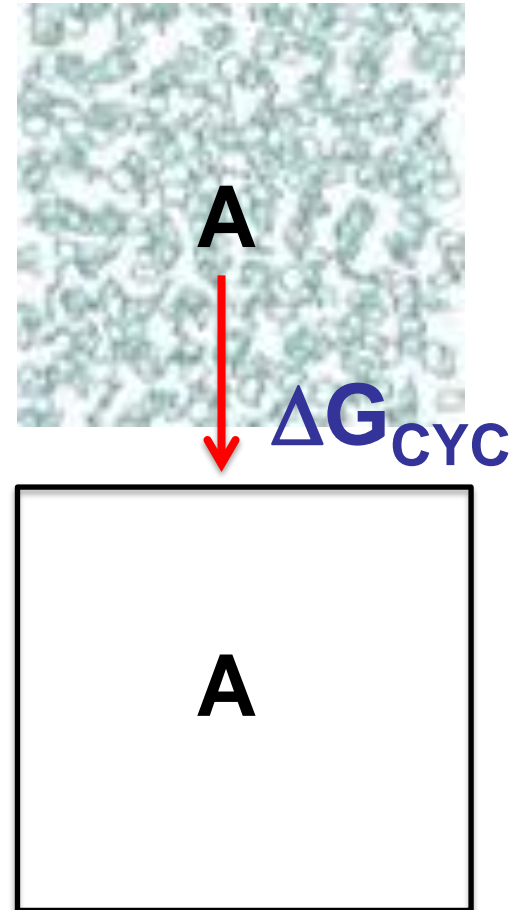
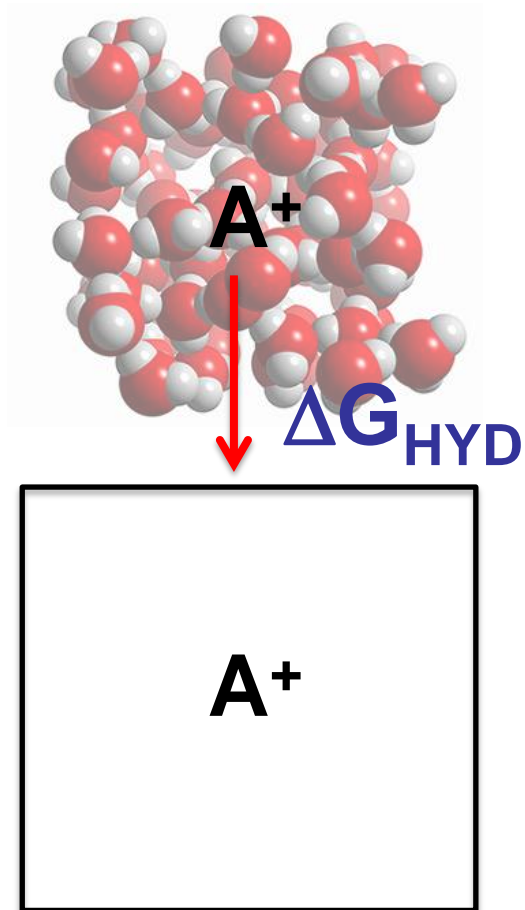


# ALL COMPOUNDS



# A FIRST LESSON

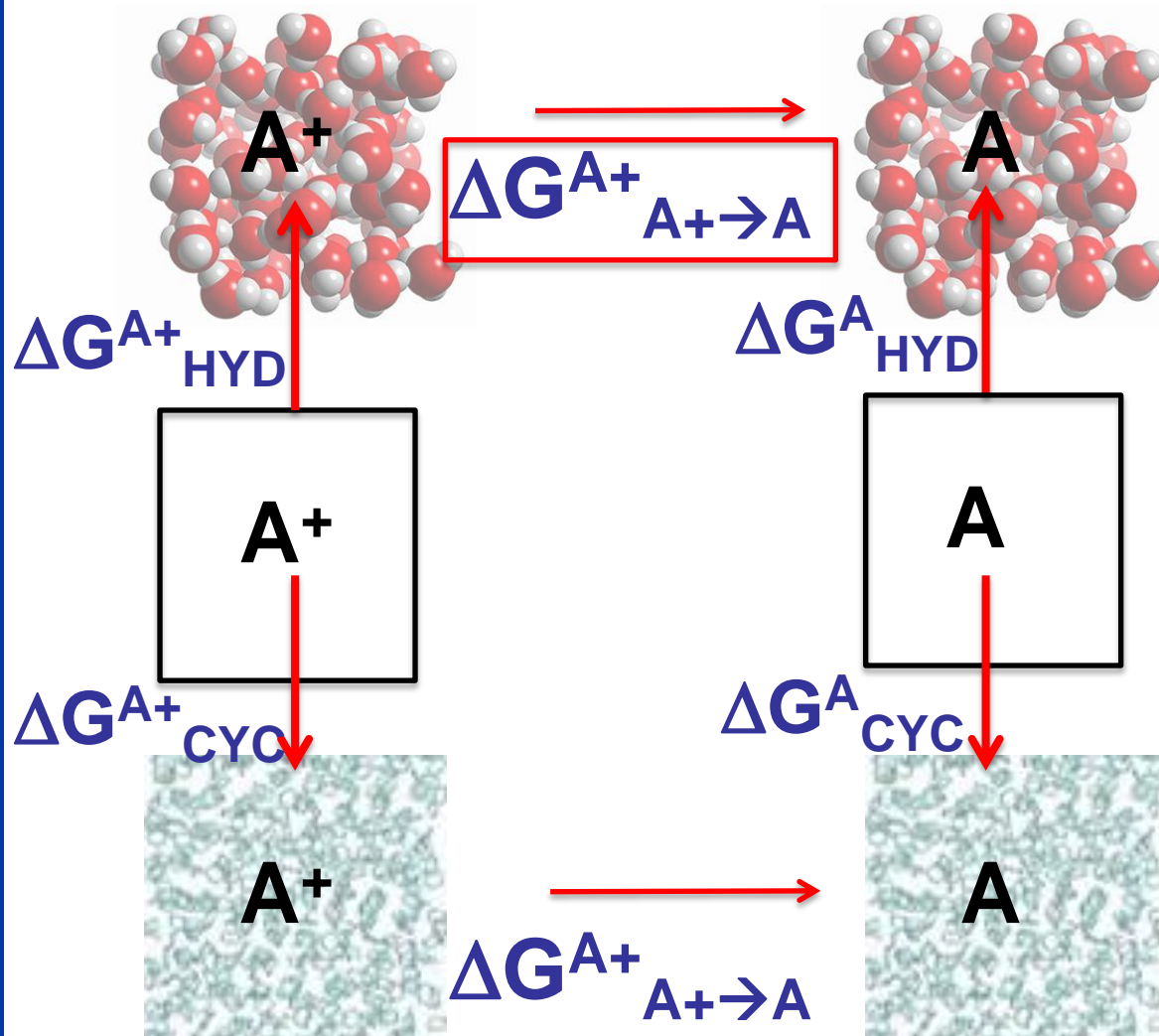
## One-specie equilibrium model



# CORRECTION

## Multi-species equilibrium model

chemicalize.org



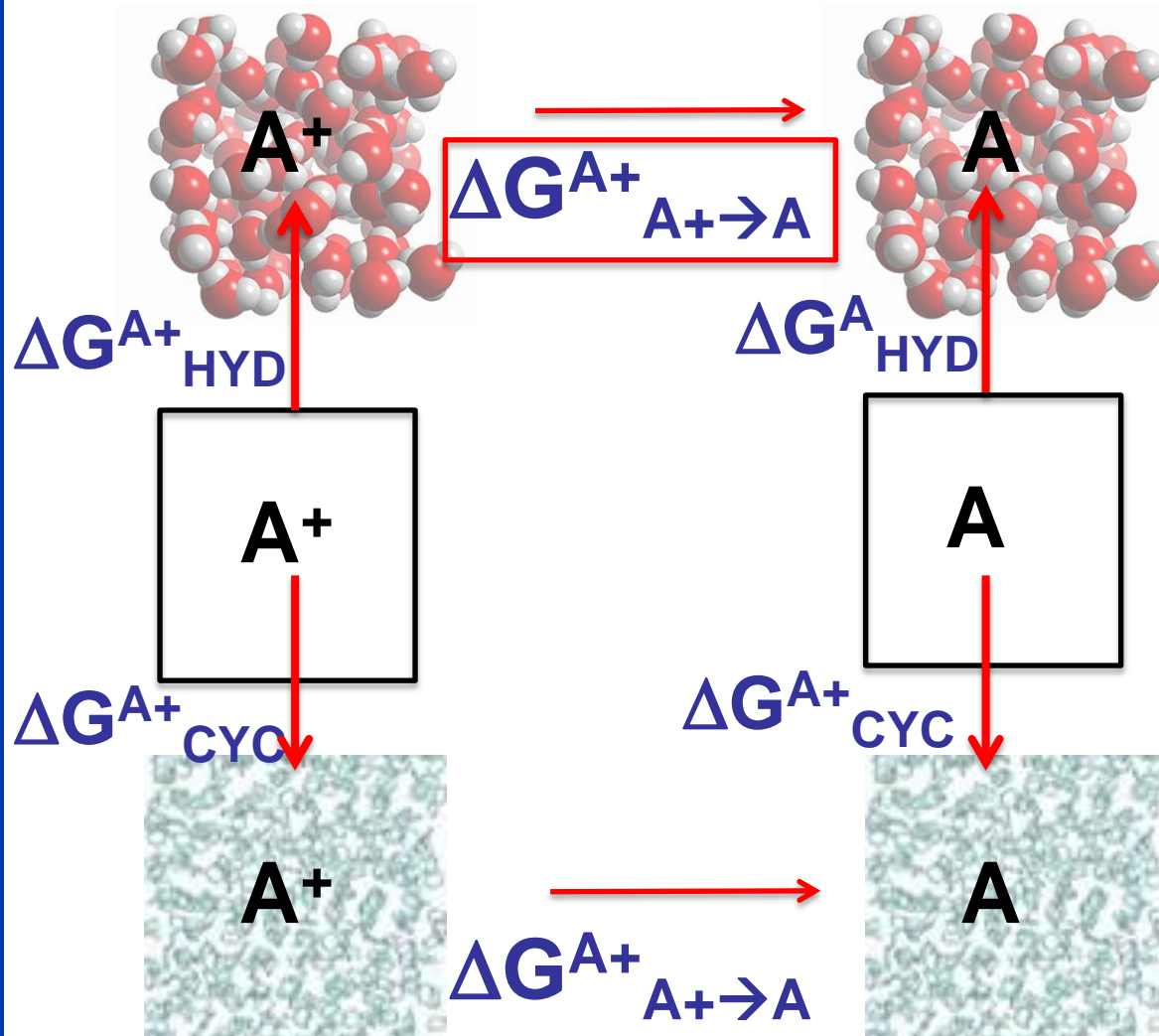
$$[A^w_{tot}] = [A^{w+}] + [A^w]$$

$$1M = 1-x \quad x$$

# CORRECTION

## Multi-species equilibrium model

chemicalize.org



$$[A^w_{tot}] = [A^{w+}] + [A^w]$$

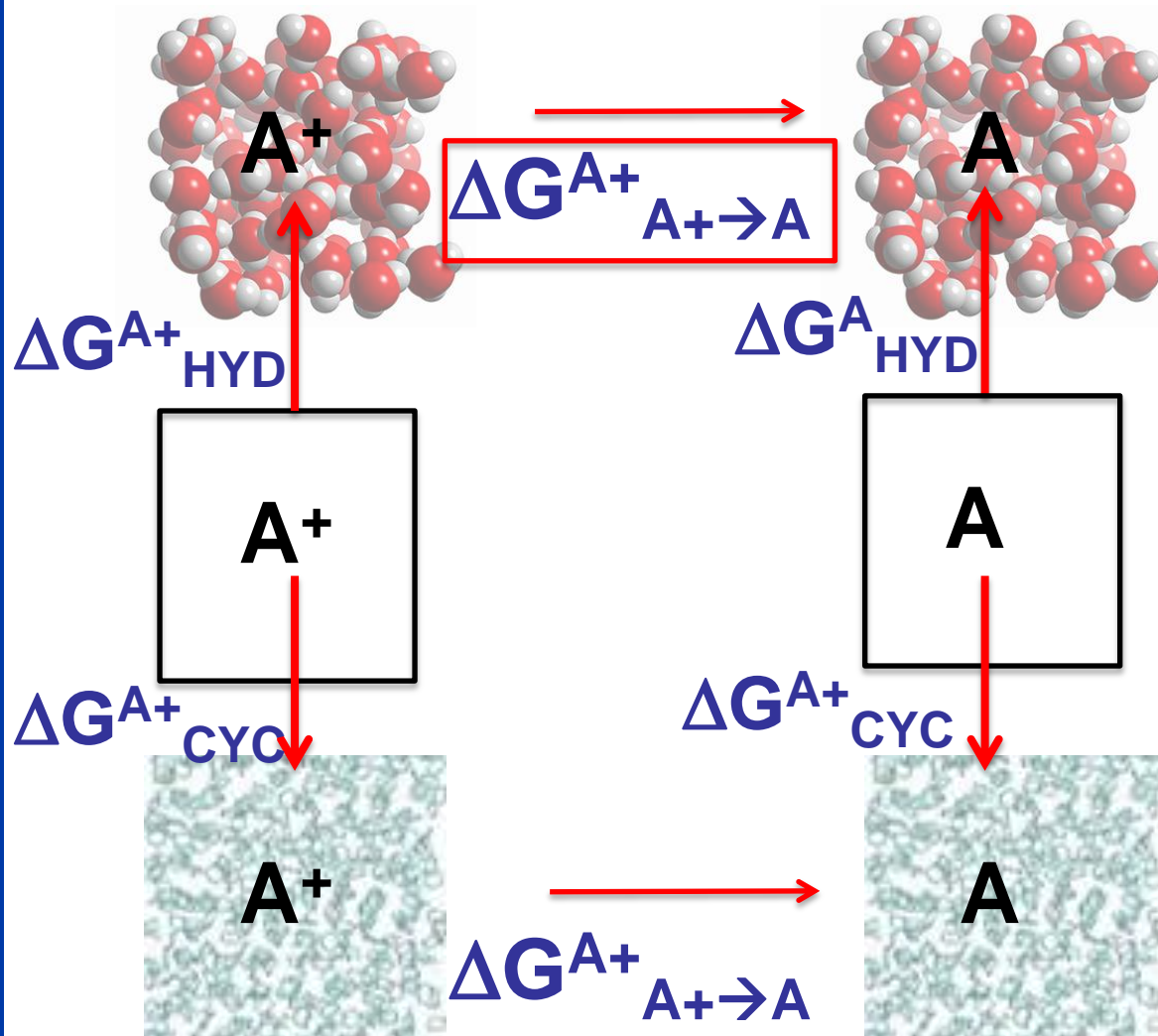
$$1M = 1-x \quad x$$

$$[A^c_{tot}] = [A^{c+}] + [A^c]$$

# CORRECTION

## Multi-species equilibrium model

chemicalize.org



$$[A^w_{tot}] = [A^{w+}] + [A^w]$$

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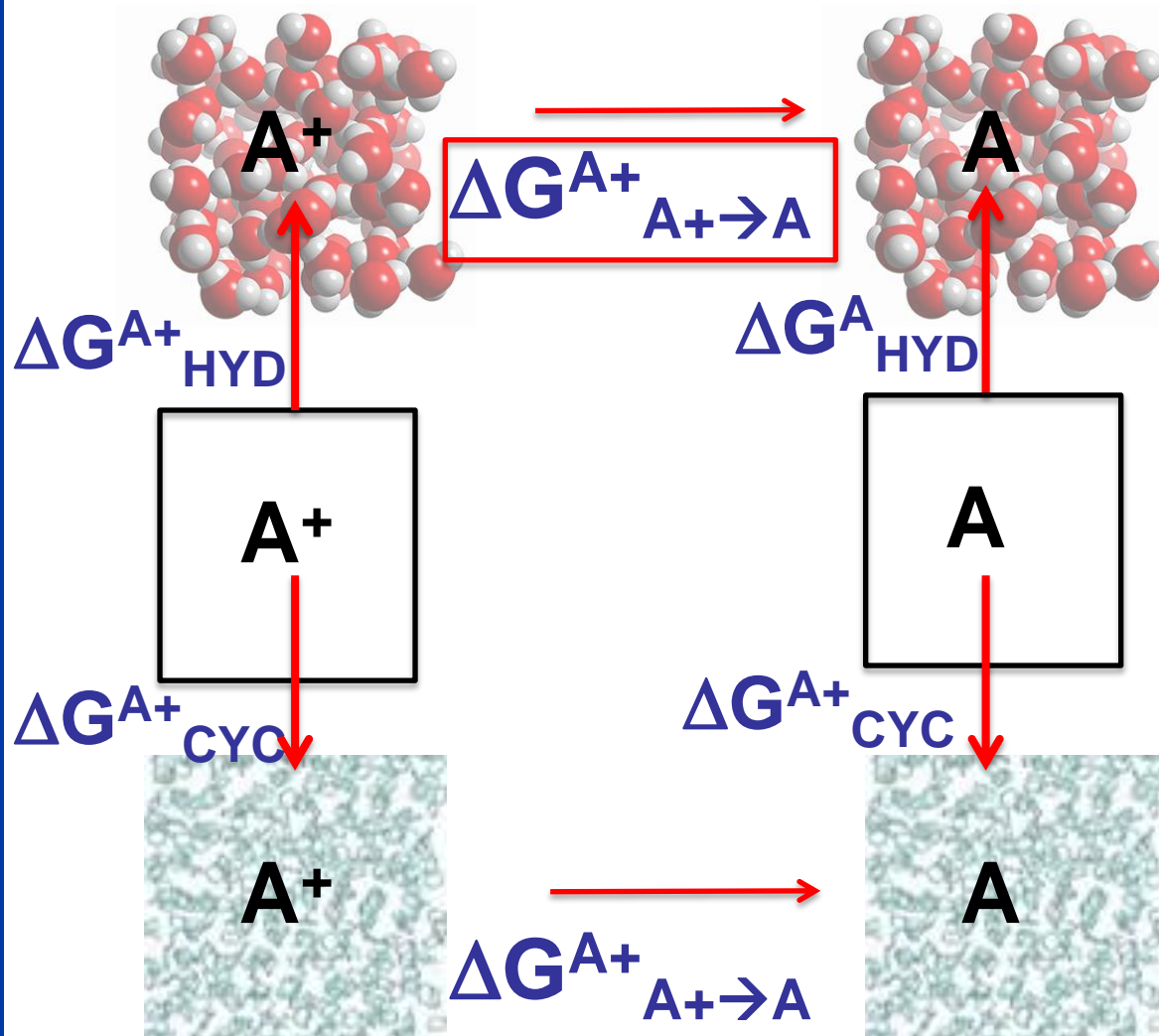
$$[A^c_{tot}] = [A^{c+}] + [A^c]$$

$$= \varepsilon \quad y$$

# CORRECTION

## Multi-species equilibrium model

chemicalize.org



$$[A^w_{tot}] = [A^{w+}] + [A^w]$$

$$1M = 1 - x - \varepsilon \quad x - y$$

$$[A^c_{tot}] = [A^{c+}] + [A^c]$$

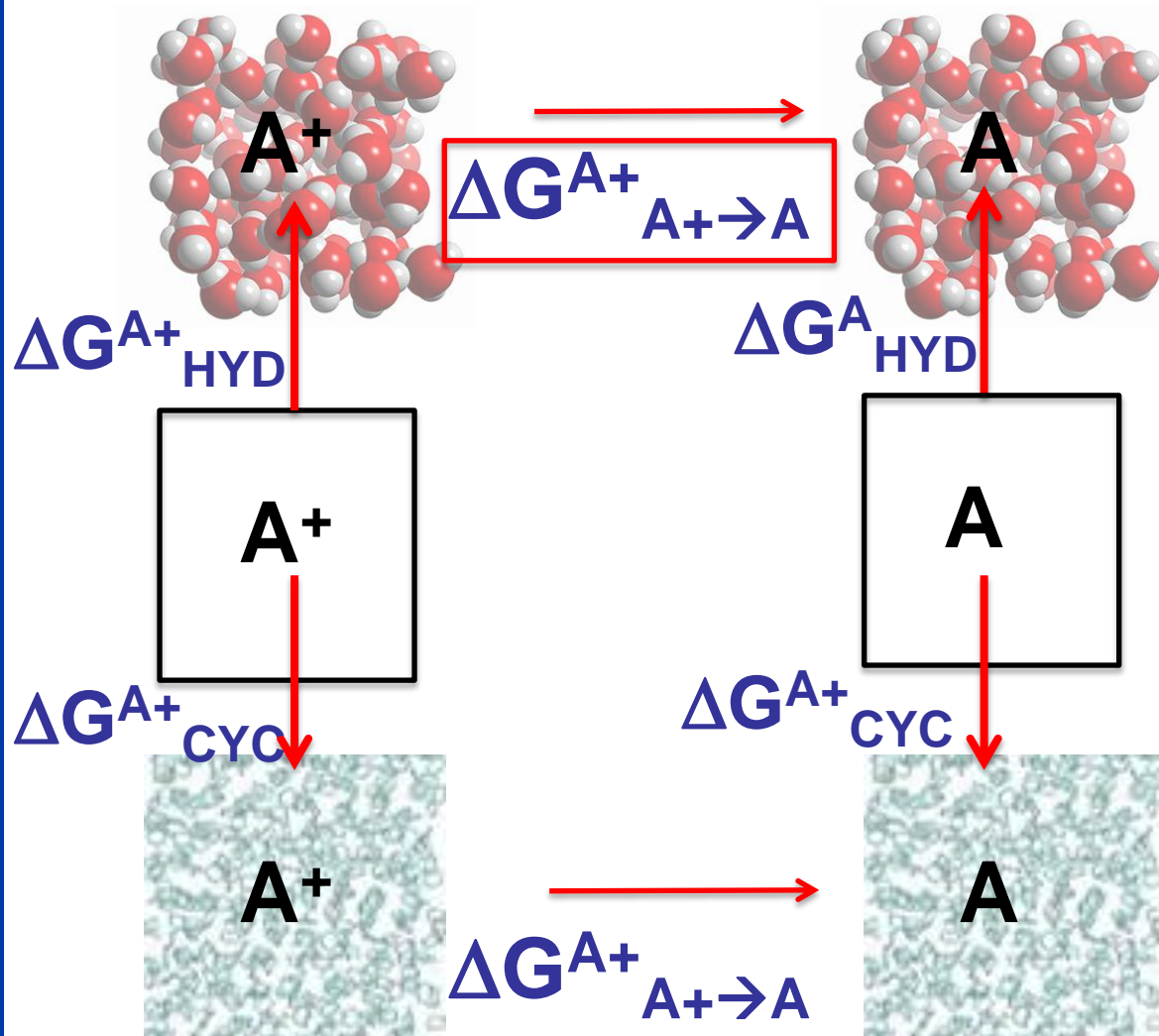
$$= \varepsilon \quad y$$



# CORRECTION

## Multi-species equilibrium model

chemicalize.org



$$[A^w_{tot}] = [A^{w+}] + [A^w]$$

$$1M = 1-x-\varepsilon \quad x-y$$

$$[A^c_{tot}] = [A^{c+}] + [A^c]$$

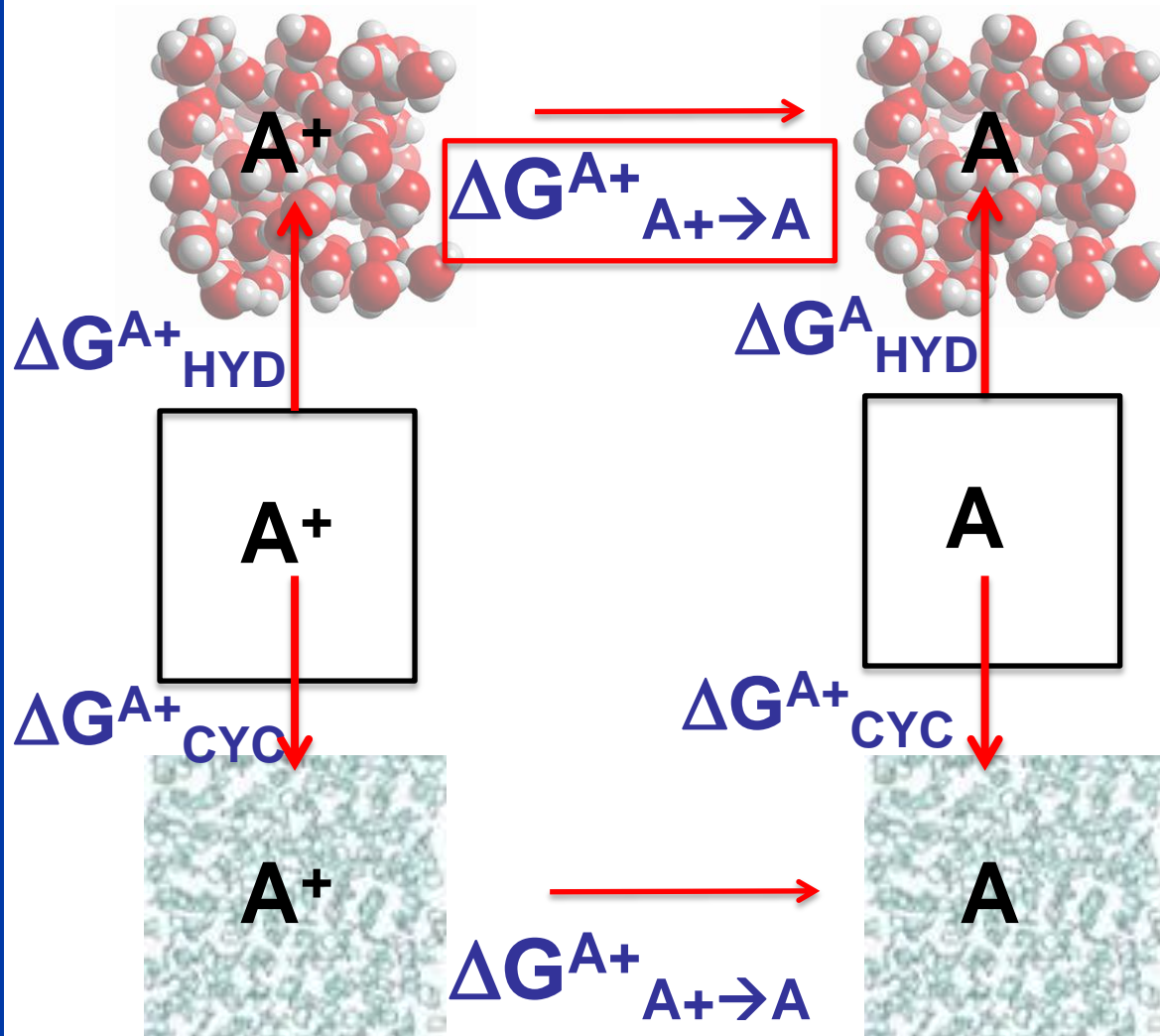
$$= \varepsilon \quad y$$

$$\log D = \log_{10} \frac{[A^{c+}] + [A^c]}{[A^{w+}] + [A^w]}$$

# CORRECTION

## Multi-species equilibrium model

chemicalize.org



$$[A^w_{tot}] = [A^{w+}] + [A^w]$$

$$1M = 1 - x - \epsilon \quad x - y$$

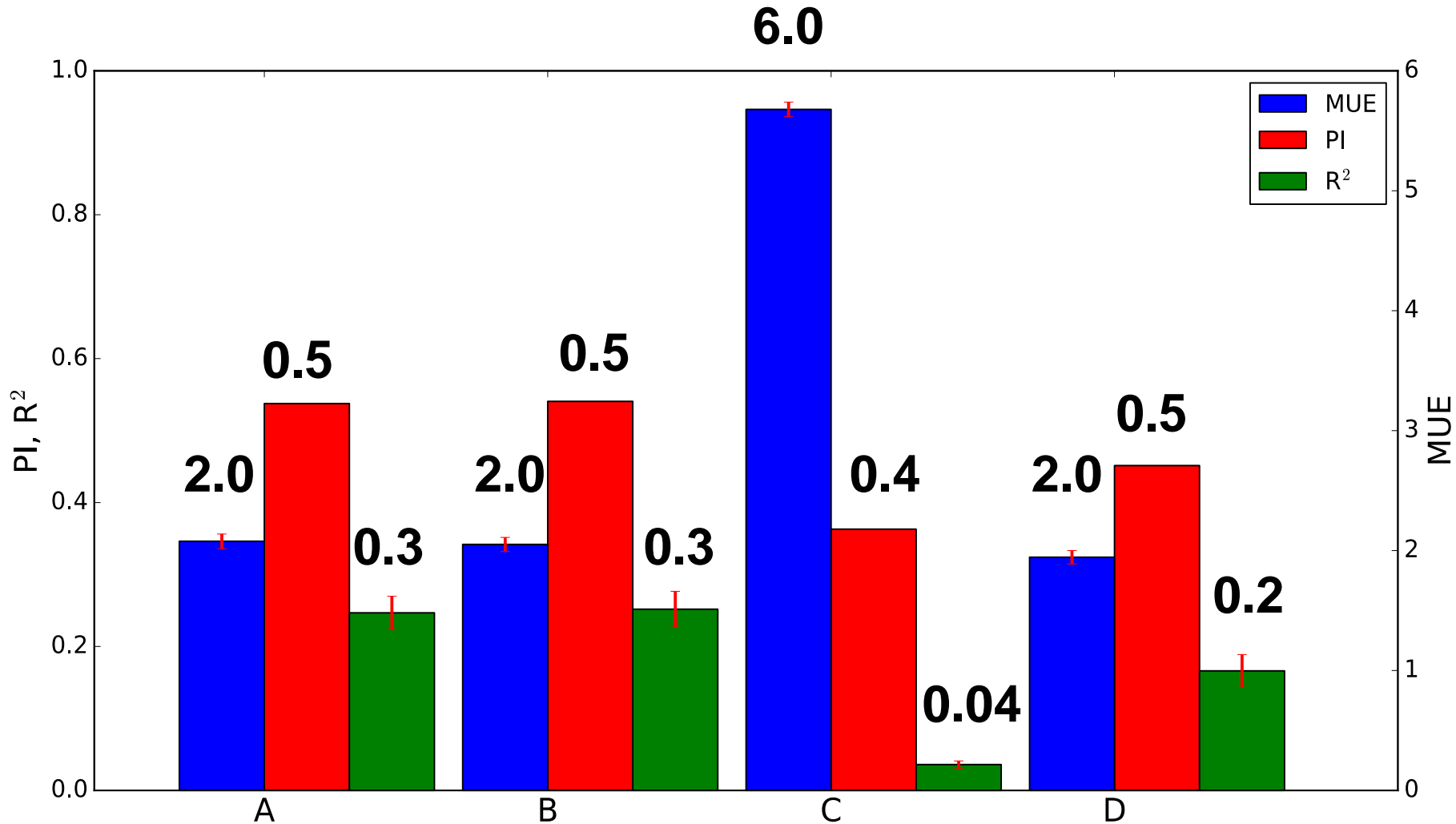
$$[A^c_{tot}] = [A^{c+}] + [A^c]$$

$$= \epsilon \quad y$$

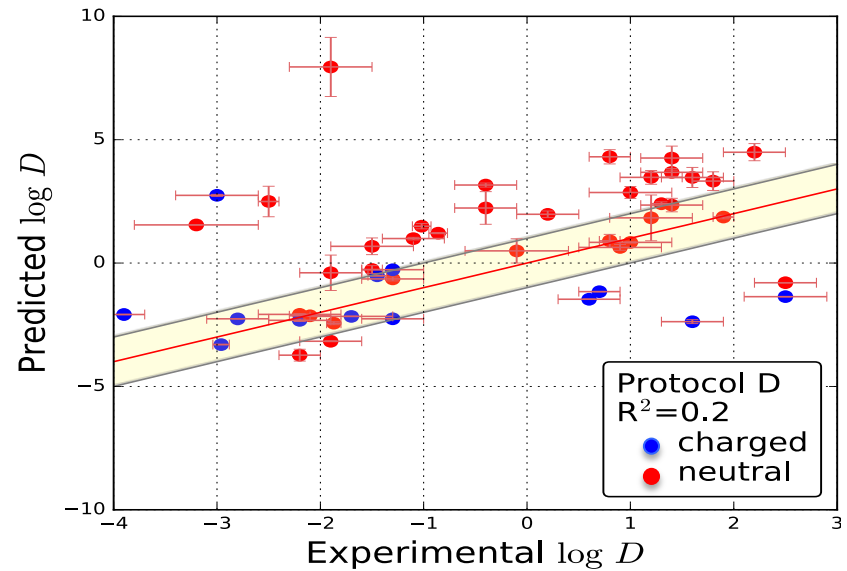
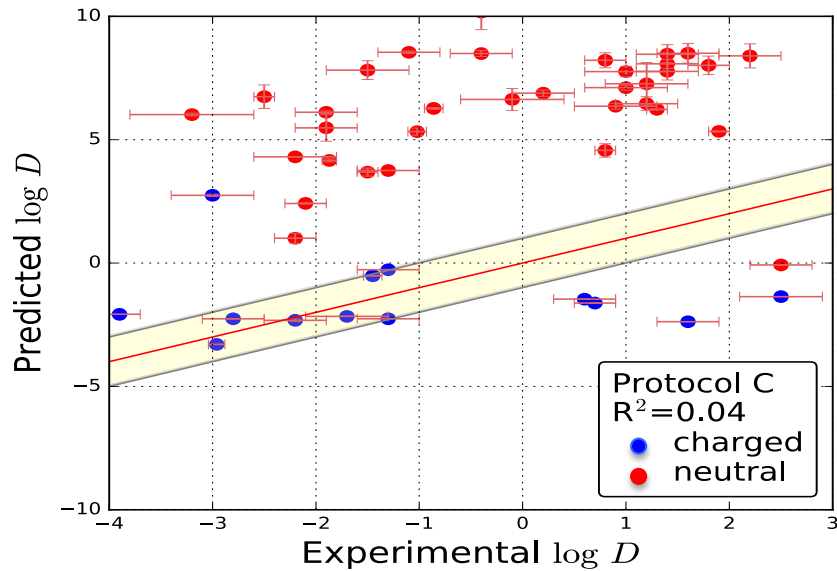
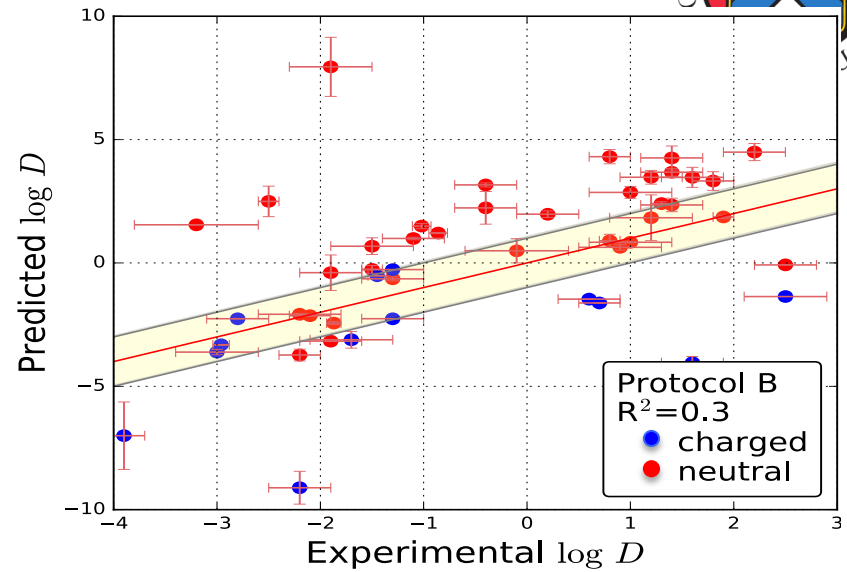
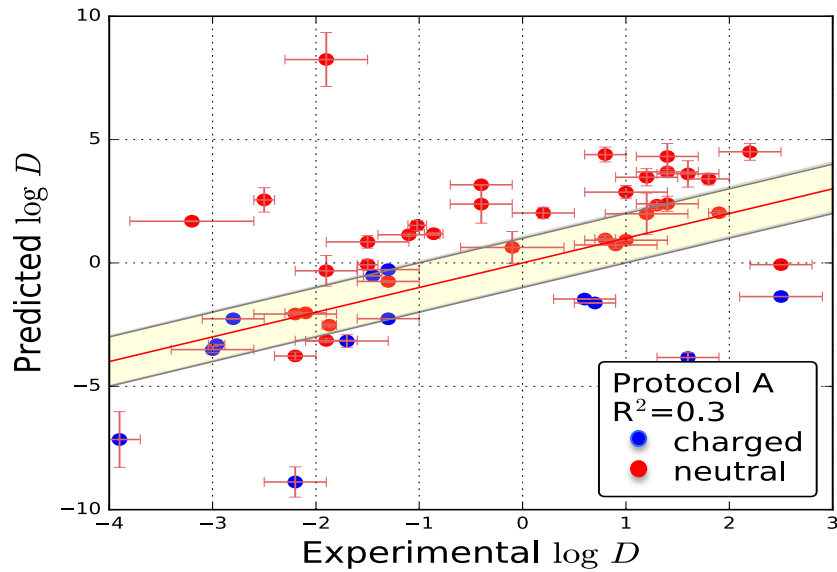
$$\log D = \log_{10} \frac{\epsilon + y}{1 - x - \epsilon \quad x - y}$$

# CORRECTION

## Multispecies statistics

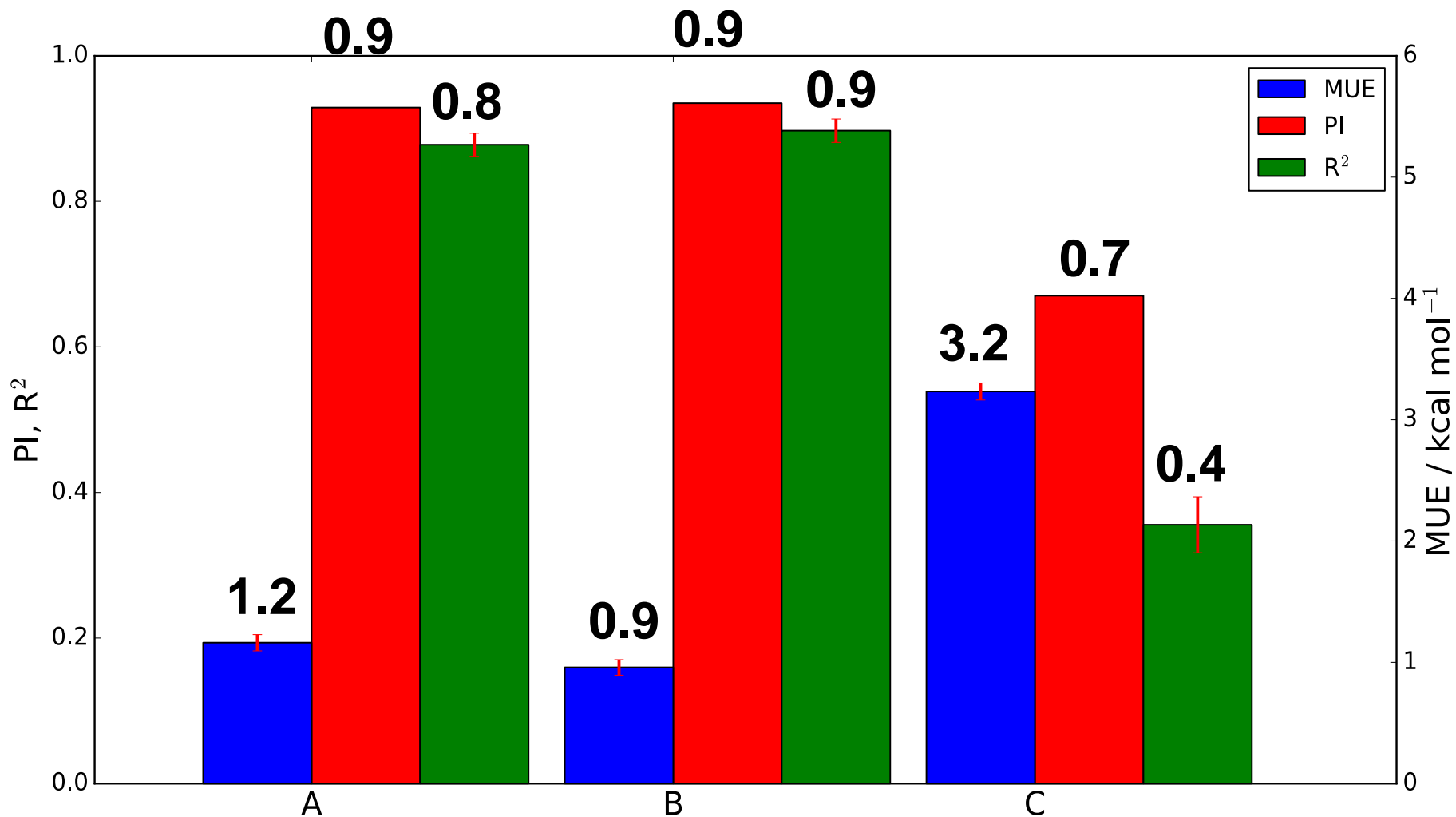


# CORRECTION

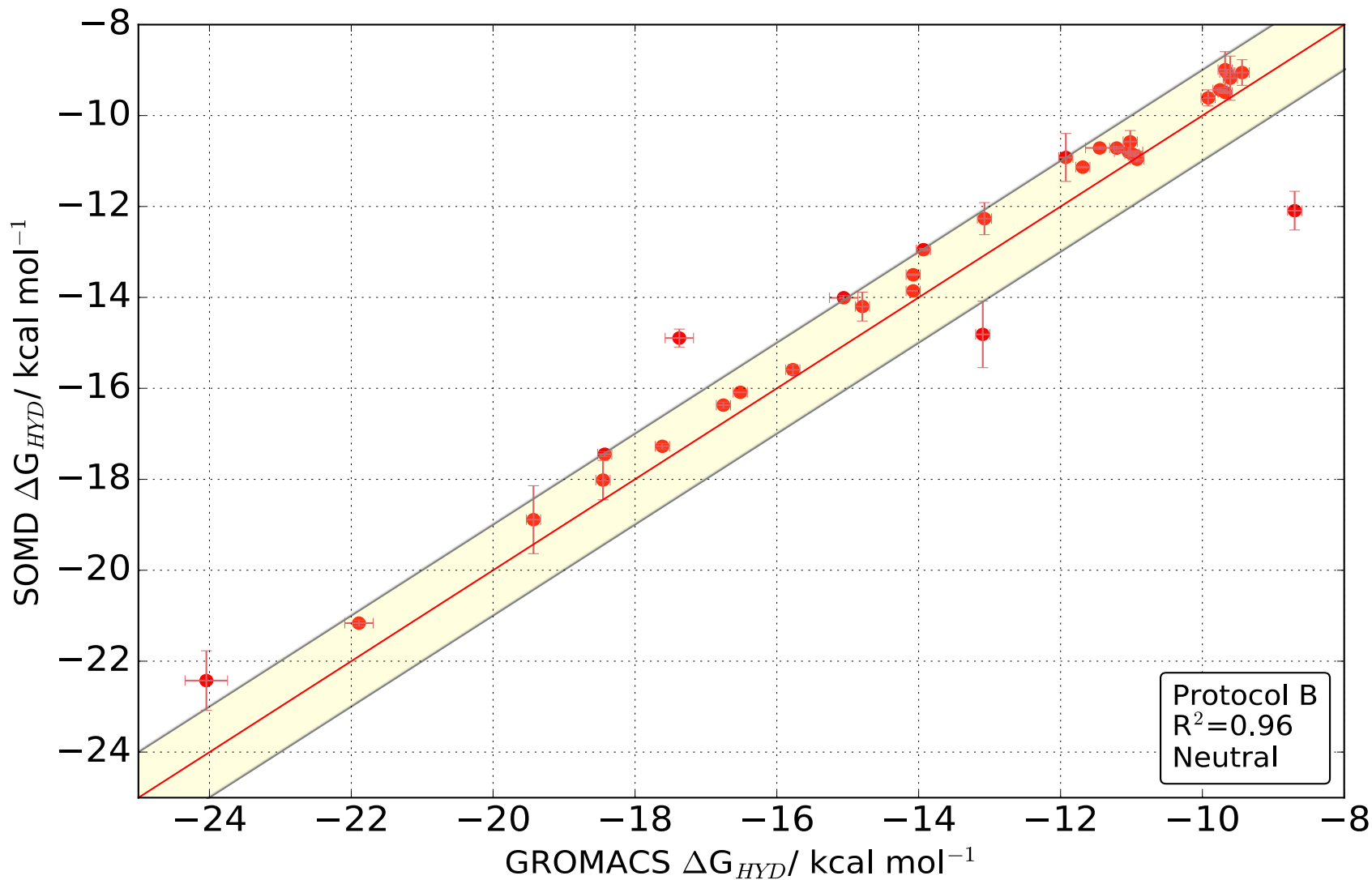


# ALL NEUTRAL?

## A Comparison with GROMACS $\Delta G_{\text{HYD}}$

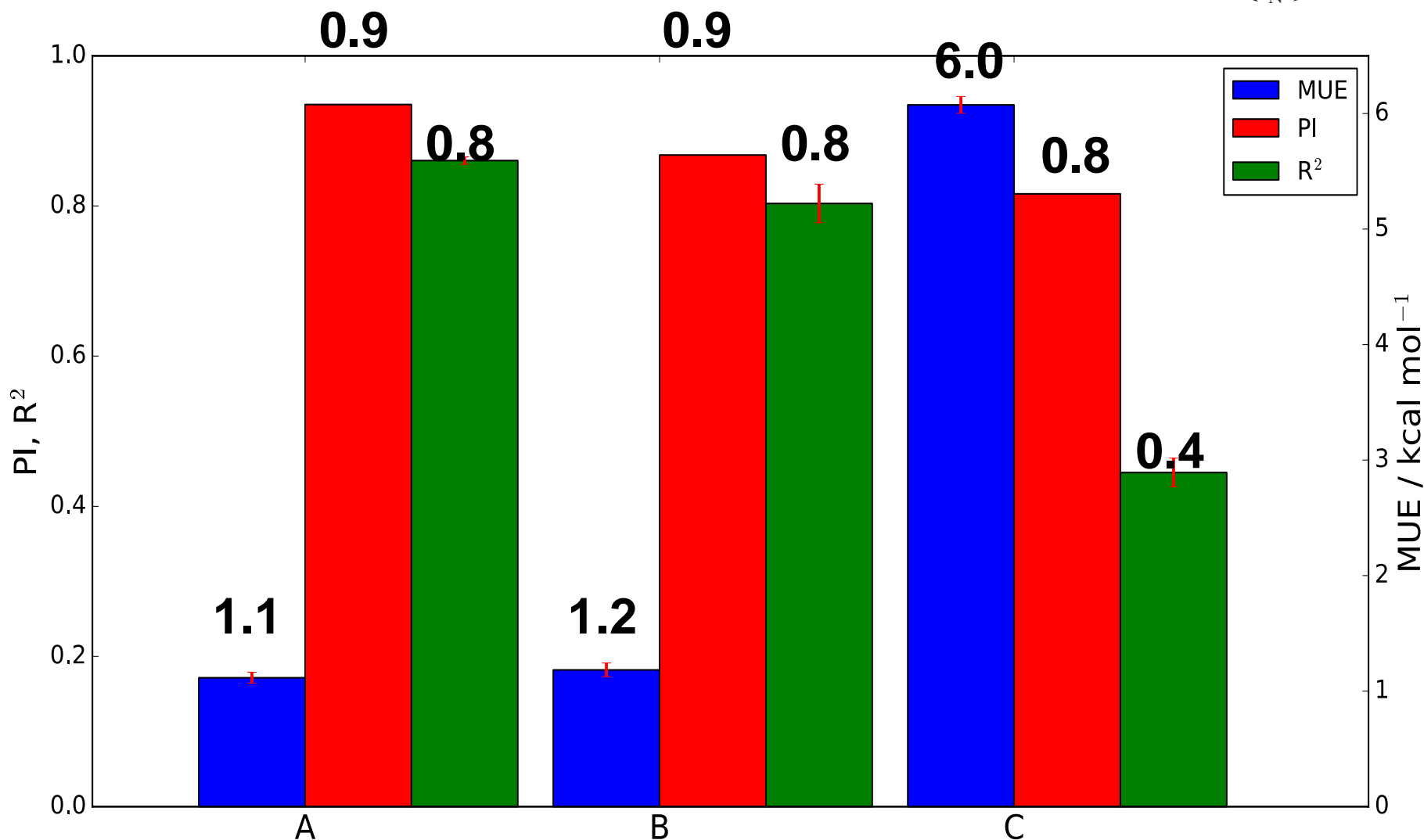


# ALL NEUTRAL? Hydration Free Energies A Comparison with GROMACS



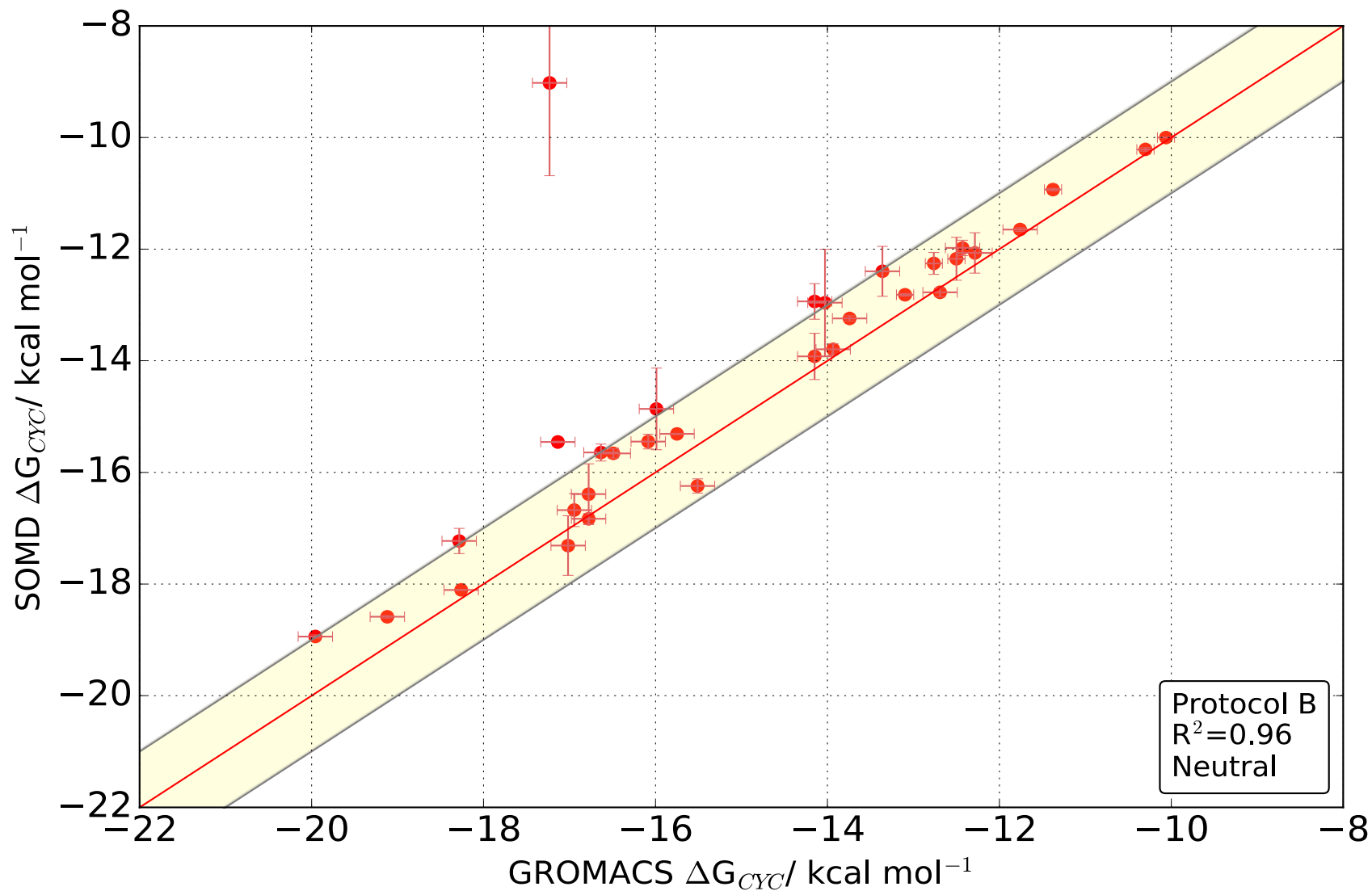
# ALL NEUTRAL?

## A Comparison with GROMACS $\Delta G_{\text{CYC}}$





# All neutral Reproducibility-GROMACS



# CONCLUSIONS



## HOST-GUEST:

- Good  $R^2$  for all protocols, except D
- Very good agreement with other simulations

## DISTRIBUTION COEFFICIENT:

- Protonation state must be considered
- Poor results unless neutral species are considered in water
- GAFF is too hydrophobic, always favorable to cyclohexane

# ACKNOWLEDGMENT



## **Julien Michel Group:**

Dr. Julien Michel

Dr. Antonia Mey

Dr. Jordi Juarez Jimenez

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## **D3R Workshop Organizers**

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Thanks for your attention

QUESTIONS?

