

Antifouling mechanism of hydrophilic polymer brushes

Graduate School of Engineering Science,
Osaka University,
Takuma Yagasaki

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Adsorption of organic matter in water

Ship bottoms



Energy loss

Artificial organs



Thrombus (血栓)

Infection (感染症)

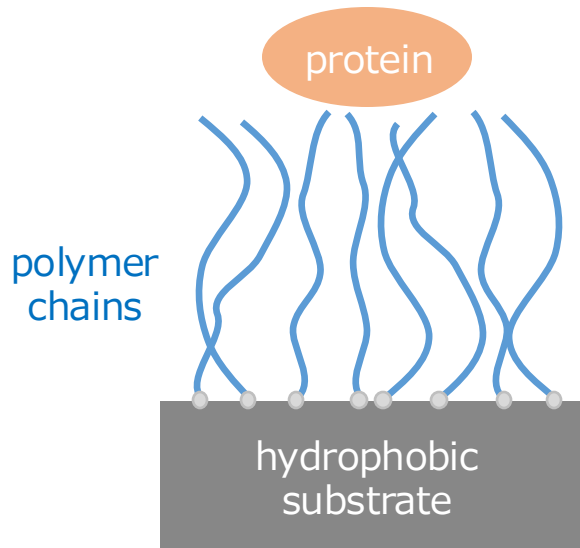
Membranes



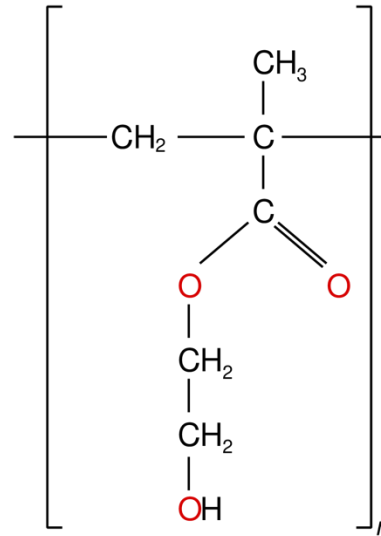
Flow reduction

Antifouling surfaces are desired.

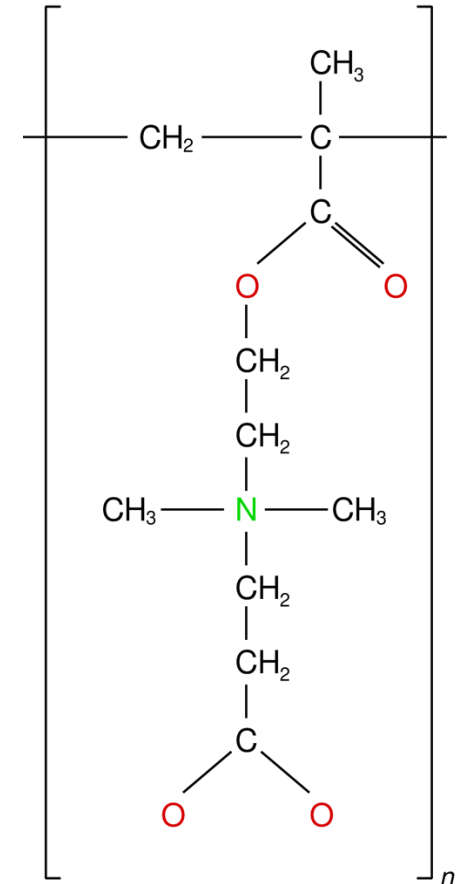
Hydrophilic polymer brushes



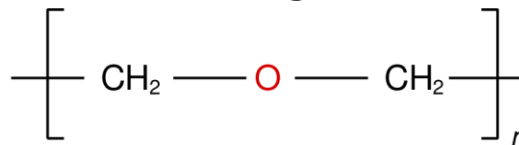
PHEMA



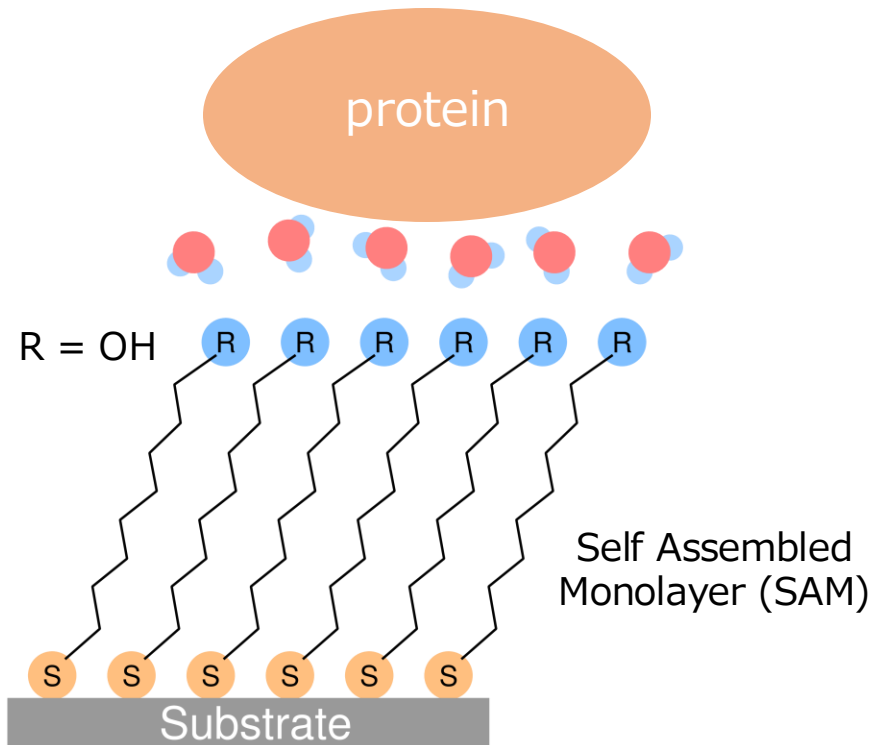
PCBMA



PEG



Antifouling of hydrophilic SAMs



Steric repulsion of bound water molecules

J. Zheng et al., *Biophys. J.* **89**, 158–166 (2005).

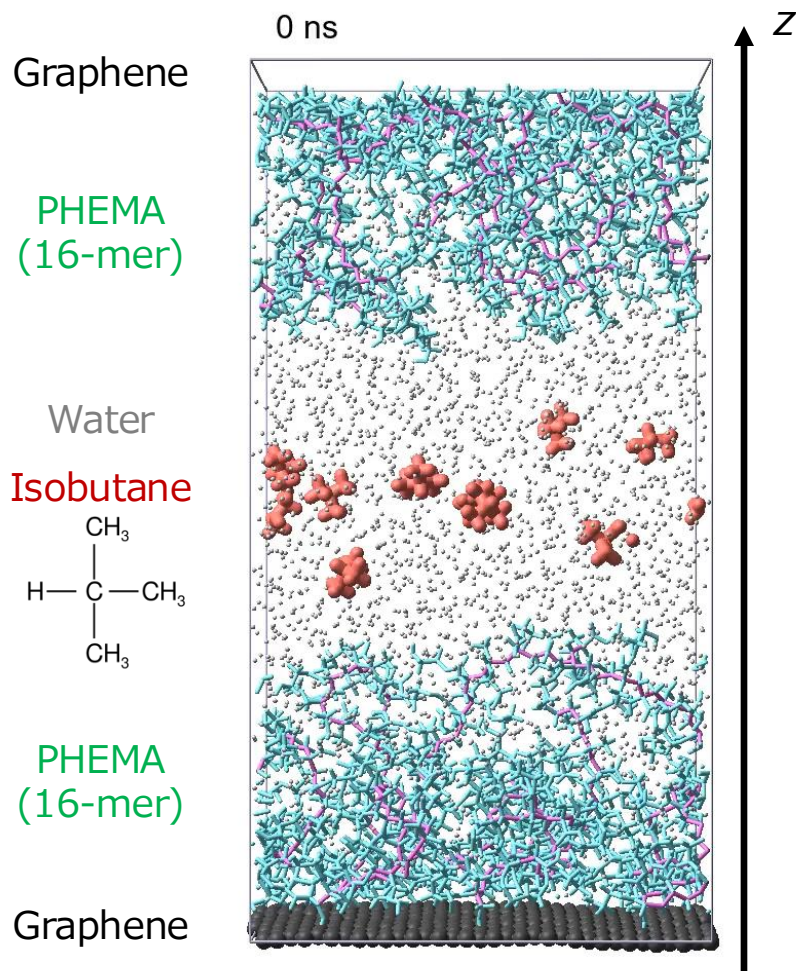
J.I. Monroe et al., *Proc. Natl. Acad. Sci. USA* **118**, e2020205118 (2021).

Water barrier mechanism

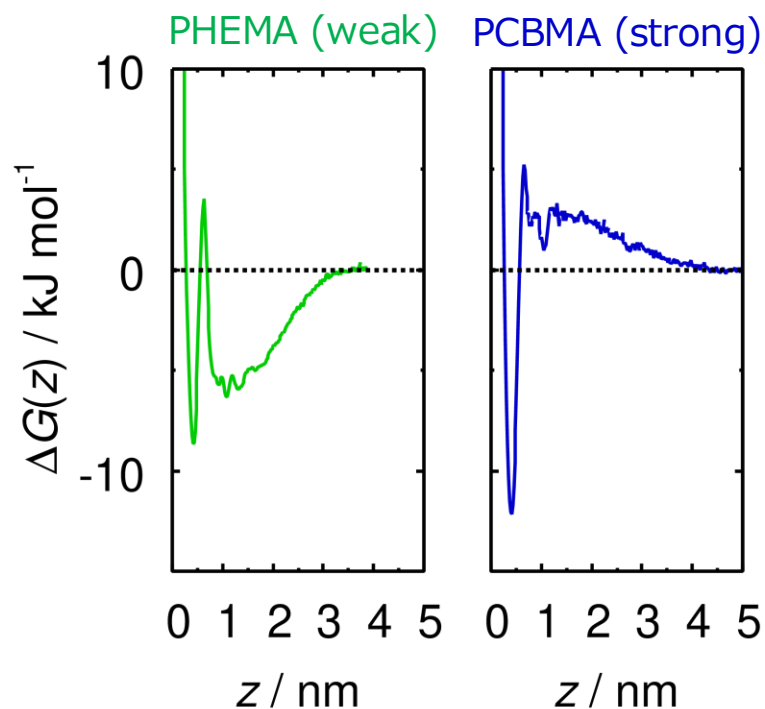
Almost no study for polymer brushes

Is it the only antifouling mechanism?

Polymer brush in water



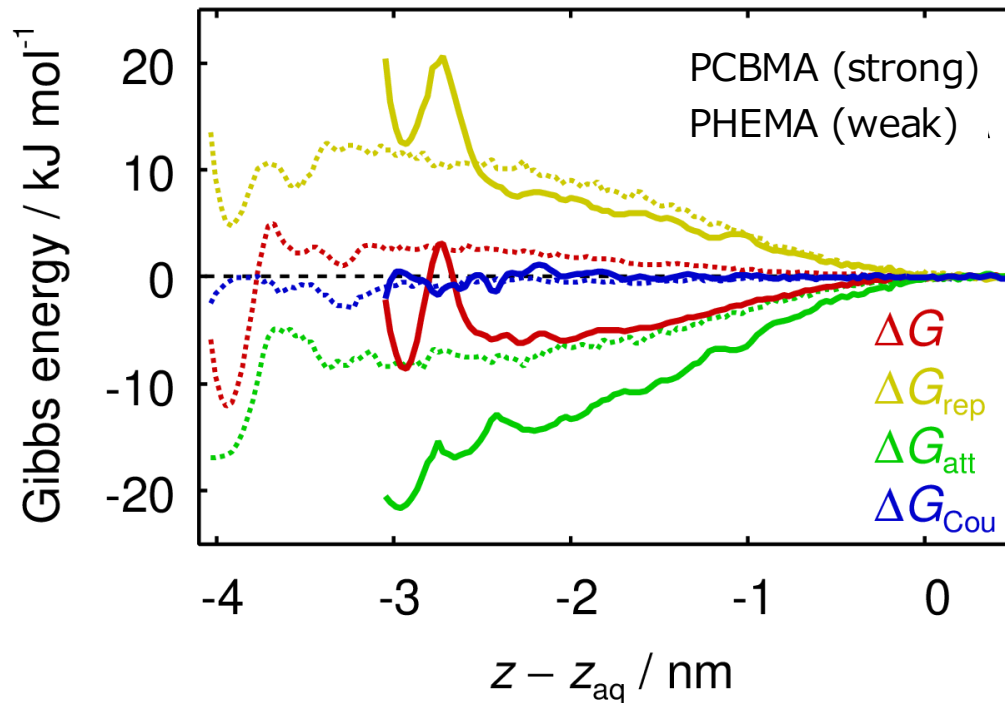
$$\Delta G(z) = -k_B T \ln \rho(z) - k_B T \ln \rho_{\text{bulk}}$$



Isobutane binds to PHEMA,
but not to PCBMA.

Components of Gibbs energy

$$\Delta G(z) = \Delta G_{\text{rep}}(z) + \Delta G_{\text{att}}(z) + \Delta G_{\text{C}}(z)$$



$$\Delta G(z) = \Delta G^{\text{np}}(z) + \Delta G_{\text{C}}(z)$$

↑
G for the hypothetical nonpolar solute

$$\Delta G^{\text{np}}(z) = -T\Delta S_{\text{UV}}^{\text{np}}(z) + \Delta E_{\text{UV}}^{\text{np}}(z)$$

ΔG Total
 ΔG_{rep} Steric repulsion (entropy)
 ΔG_{att} London dispersion (energy)
 ΔG_{Cou} Coulomb (energy)

Steric repulsion is strong (water barrier mechanism)
 Stabilization due to London dispersion is small

} in the PCBMA brush

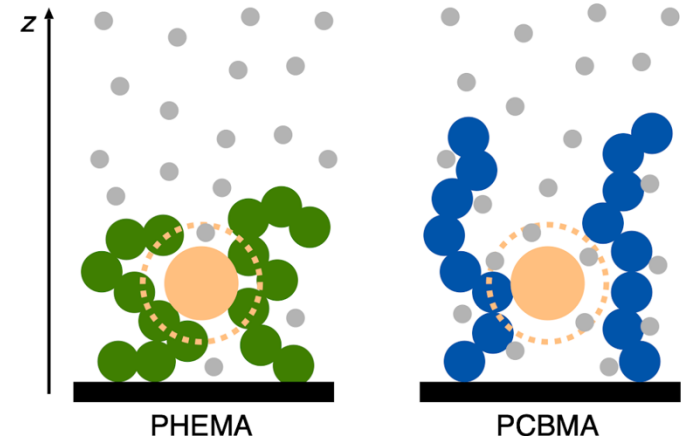
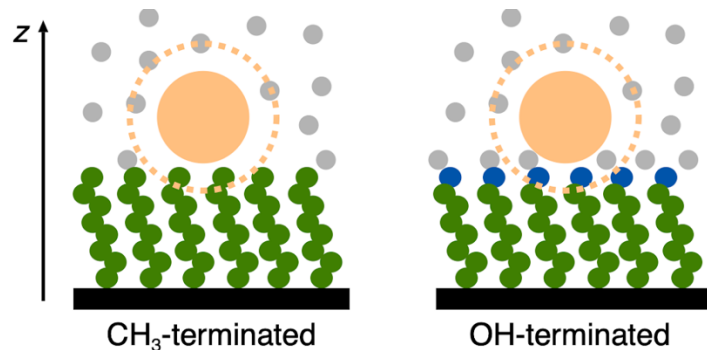
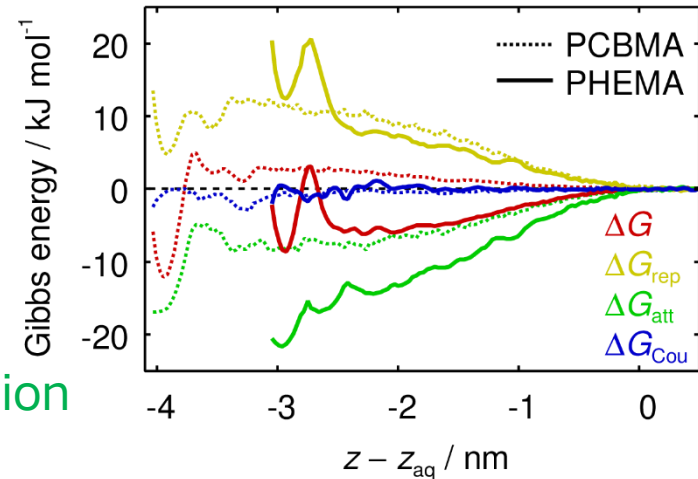
Two roles of water in the brush

Enhancement of steric repulsion

- Large effective volume due to bound water molecules
- Also observed for SAMs

Reduction of London dispersion interaction

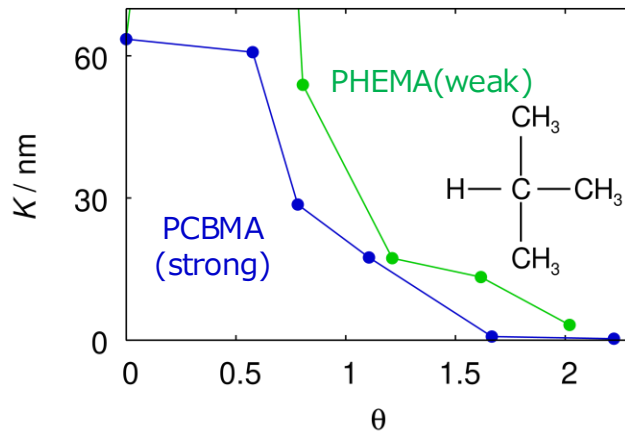
- Not observed for SAMs



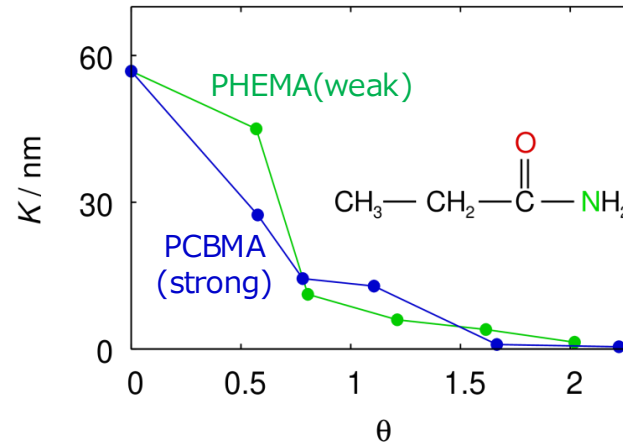
Hydrophilic groups
 increase decrease
 the number of surrounding atoms

Dependence on grafting density

Isobutane (Leu)



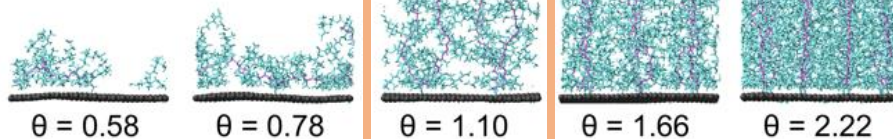
Propionamide (Gln)



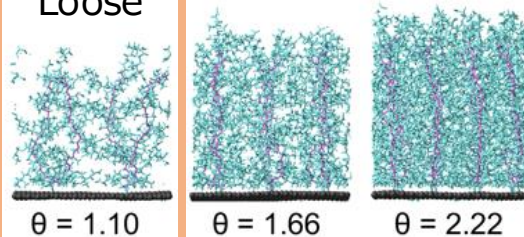
Antifouling performance is **better for PHEMA** around $\theta \sim 1.2$!

$$(\theta = 2R_g/L)$$

PCBMA



Loose



Tight

Adsorbate molecules reach the substrate easily

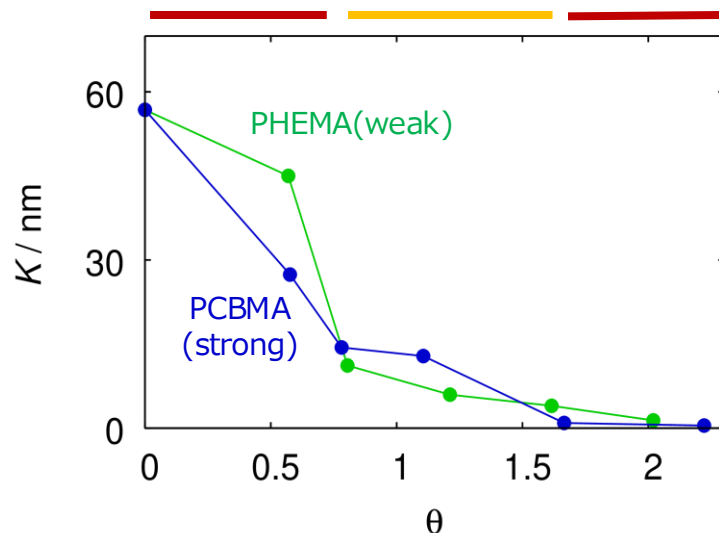
The tight layer blocks the adsorbate molecules

Experimental studies

Better antifouling for more hydrophilic polymers

- C. Zhao et al., *Langmuir* **26**, 17375–17382 (2010).
- W. Zhao et al., *J. Mater. Chem. B* **2**, 5352–5357 (2014).
- B.L. Leigh et al., *Biomacromolecules* **18**, 2389–2401 (2017).
- W. Dai et al., *J. Mater. Chem. B* **7**, 2162–2168 (2019).

High and low surface coverage regimes



Stronger antifouling of less hydrophilic polymers

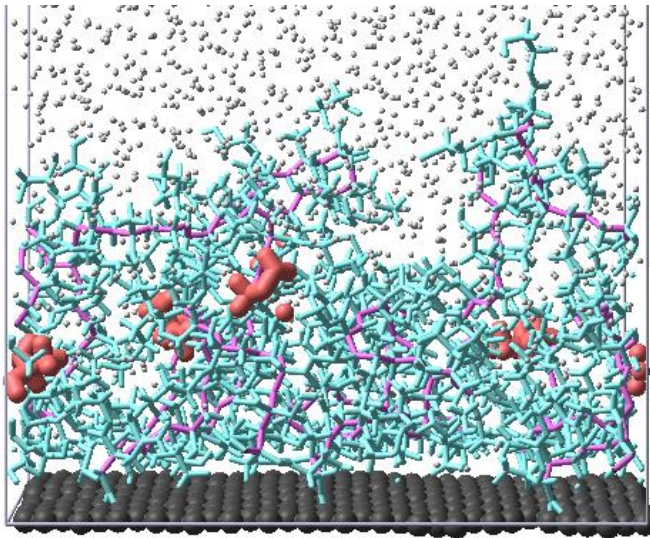
- C. Zhao et al., *Langmuir* **27**, 4906–4913 (2011).
- E. van Andel, et al., *Langmuir* **35**, 1181–1191 (2019).

Medium surface coverage regime

No contradiction between the two types of experimental result

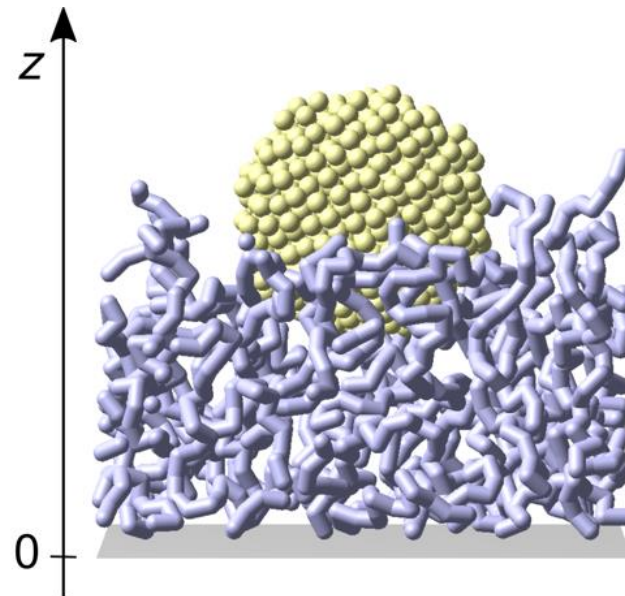
Coarse-grained simulations

All-atom (AA)



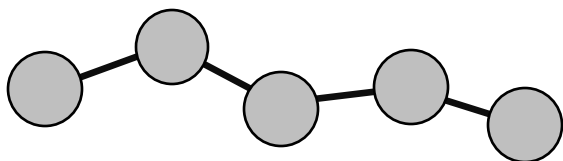
- Small organic molecules
- 16-mer
- Graphene

Coarse-grained (CG)



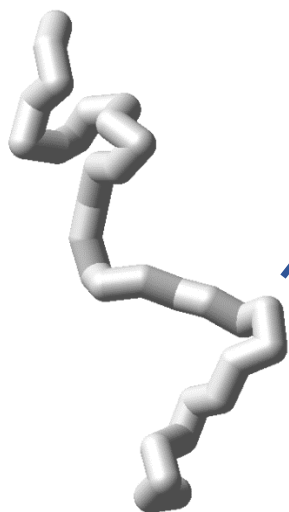
- Proteins
- Long chains
- Various substrates

Kremer-Grest type model

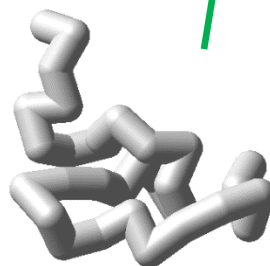


$$V_{\text{FENE}}(r) = -0.5k_{\text{FENE}}R_0^2 \ln \left\{ 1 - \left(\frac{r}{R_0} \right)^2 \right\}$$

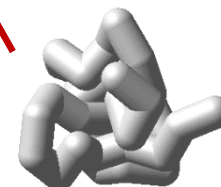
$$V_{\text{LJ}}(r) = 4\epsilon \left\{ \left(\frac{\sigma}{r} \right)^{12} - \left(\frac{\sigma}{r} \right)^6 \right\}$$



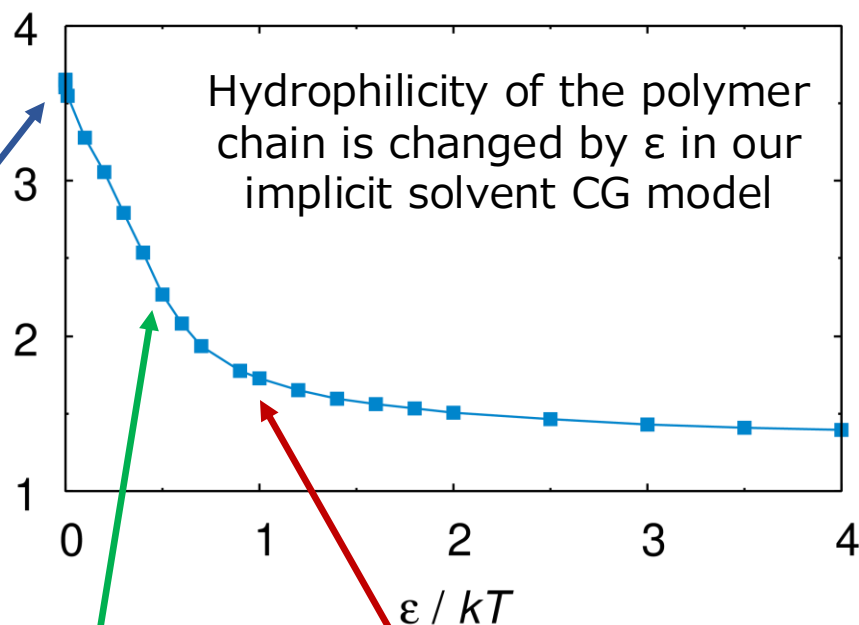
$\epsilon = 10^{-6} kT$
Strongly hydrophilic



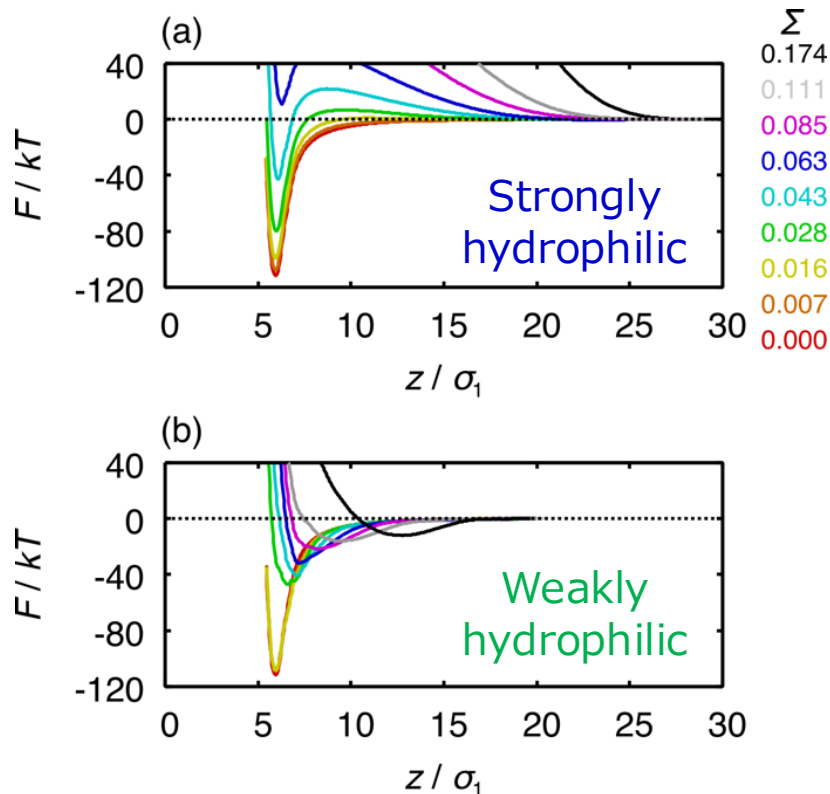
$\epsilon = 0.5 kT$
Weakly hydrophilic



$\epsilon = 1 kT$
Hydrophobic

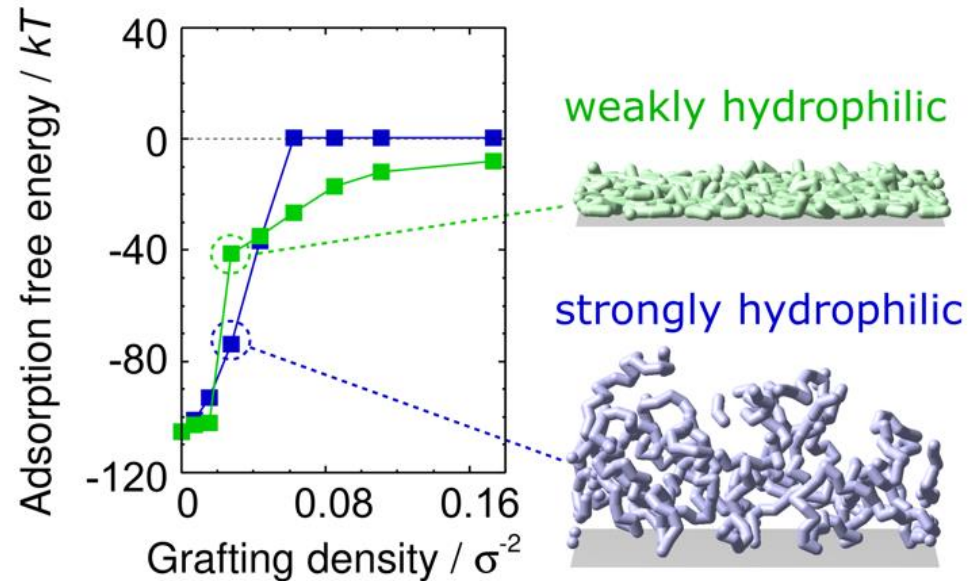


Adsorption free energy



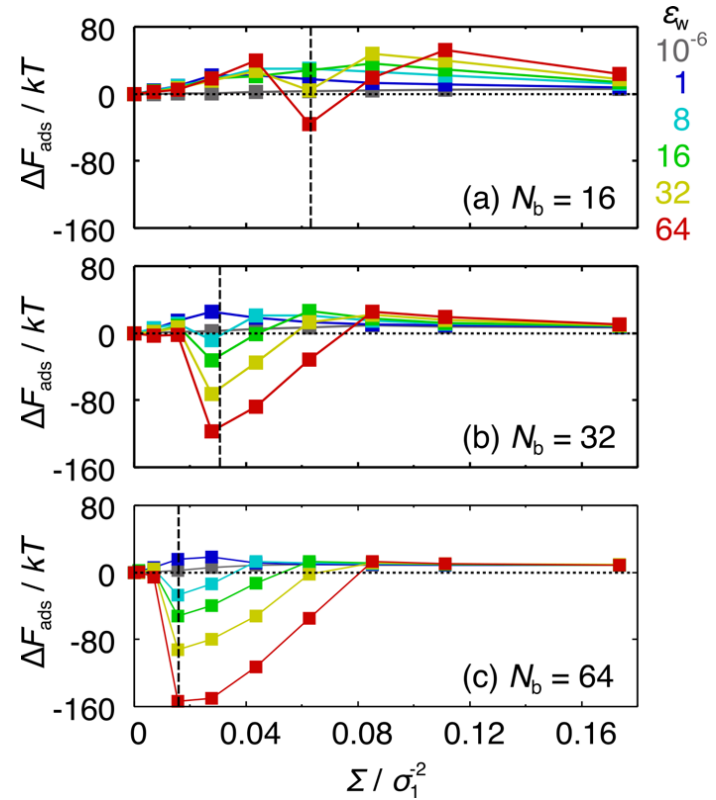
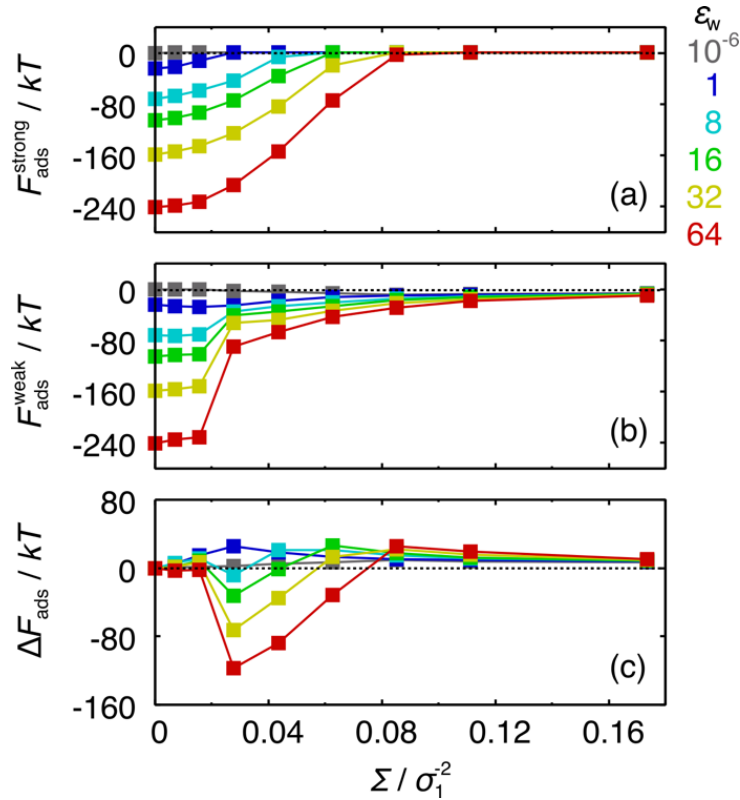
$$F_{\text{ads}} = -kT \ln K$$

$$K = \frac{1}{\delta} \int_0^{\delta} e^{-F(z)/kT} dz$$



Antifouling performance is better for the less hydrophilic polymer brush in a range of grafting density

Anomalous regime



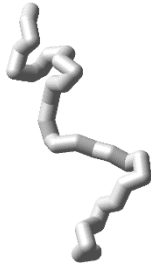
The anomalous behavior is found for

hydrophobic substrates
long chains

Correspondence between CG and AA

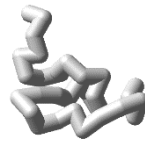
Strongly hydrophilic

$$\varepsilon = 10^{-6} kT$$

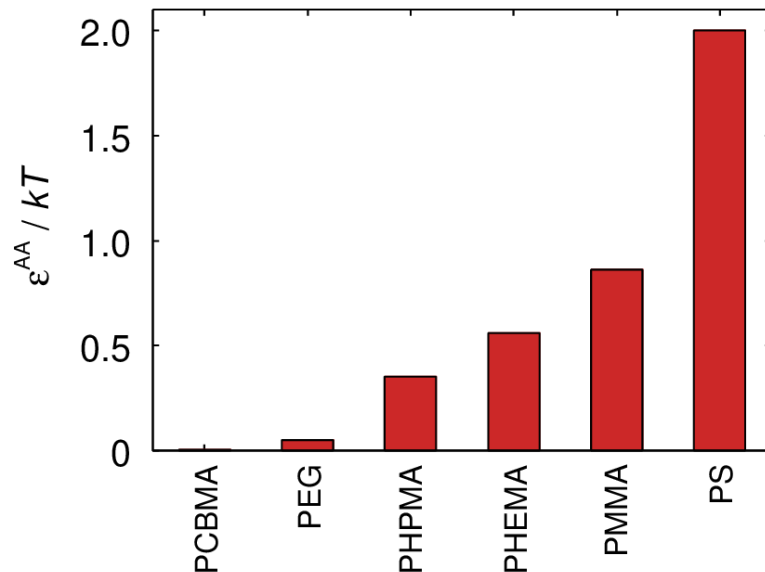


Weakly hydrophilic

$$\varepsilon = 0.5 kT$$



Do these two CG models well represent real polymers?



Two equations for CG model

$$R_g^{gs} = 0.491 N_b^{0.59} \sigma$$

(R_g in good solvent)

$$R_{max} = 0.97 N_b \sigma$$

(maximum chain length)



Insert R_g^{gs} and R_{max} calculated from AA simulations with $N_d = 98$

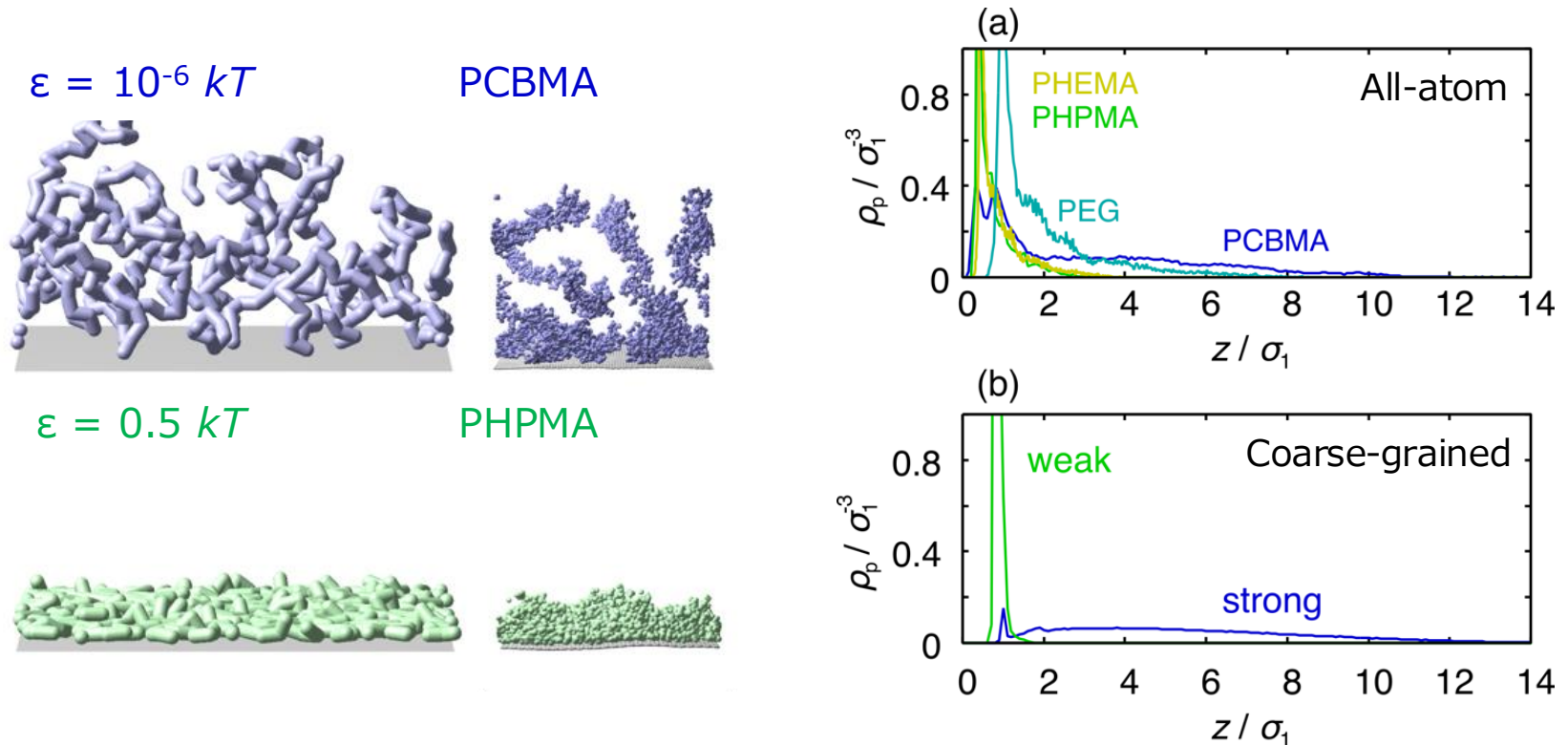


σ and N_b that reproduce the structure of the AA polymer with $N_d = 98$



ε is determined by comparison of **R_g in water** calculated from CG simulations with AA simulations

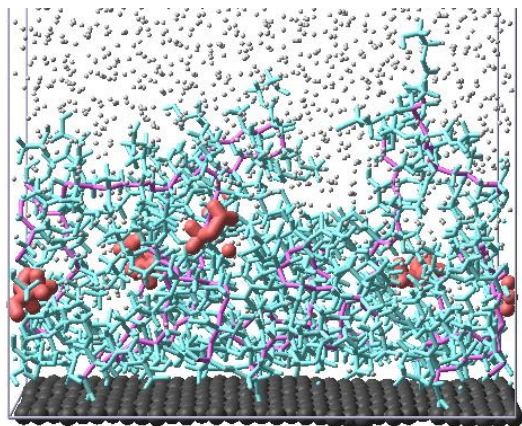
Structures of the CG and AA simulations



The CG models are structurally similar to the AA models.

Conclusions

All-atom (AA)



PCBMA

VS

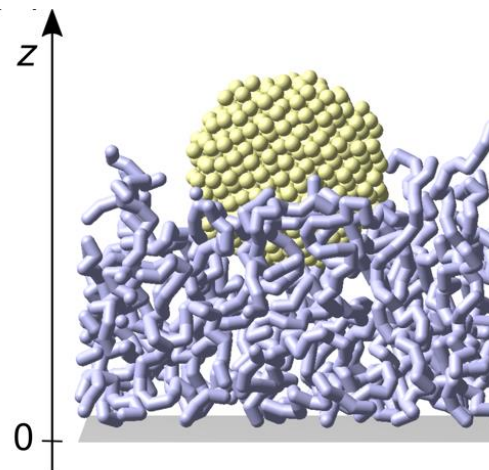
PHEMA

Two roles of bound water

- Enhancement of steric repulsion
- Reduction of London dispersion interactions

Better antifouling performance of the less hydrophilic PHEMA brush

Coarse-grained (CG)



$\epsilon = 10^{-6} kT$

VS

$\epsilon = 0.5 kT$

Better antifouling performance of less hydrophilic brushes

- Hydrophobic substrates
- Long chains

Correspondence between CG and AA models

- T. Yagasaki and N. Matubayasi, *Langmuir* **39**, 13158–13168 (2023).
- T. Yagasaki and N. Matubayasi, *Langmuir* **40**, 15046–15058 (2024).

Acknowledgments

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