# Quasi-two-dimensional diffusion of interacting protein monomers and dimers: a MPC simulation study

Zihan Tan<sup>1</sup>\*, Jan K. G. Dhont<sup>1</sup>, Vania Calandrini<sup>2</sup>, and Gerhard Nägele<sup>1</sup>

1. Biomacromolecular Systems and Processes (IBI-4), Institute of Biological Information Processing, Forschungszentrum Jülich, 52428 Jülich, Germany

2. Computational Biomedicine (INM-9/IAS-5), Institute for Advanced Simulation, Forschungszentrum Jülich, 52428 Jülich, Germany z.tan@fz-juelich.de



#### Abstract: Modeling lateral diffusion of proteins at a membrane

- **Diffusion of proteins along a membrane:** e.g., in postsynaptic signal transduction where specific proteins diffuse along a postsynaptic membrane, triggering a cascade of biochemical processes.
- Minimalistic model: Interacting Brownian particles embedded in a three-dimensional (3D) Newtonian bulk fluid but confined to a planar monolayer.
- Onset of large-scale collective diffusion under quasi-two-dimensional (Q2D) confinement
- Hydrodynamic retardation effects in concentrated Q2D protein solutions.
- More detailed model: Non-spherical proteins diffusing at a fluid-fluid interface.
- Effects of membrane-cytosol viscosity difference on diffusion of proteins.



#### 1. Globular protein model



#### Globular proteins $\implies$ Brownian spheres



♦ Proteins confined in-plane are interacting by short-range attraction (SA) and long-range electrostatic repulsion (LR):



### 3. Hydrodynamic retardation in concentrated Q2D protein systems

**Vorticity diffusion:** Long-time tail in (angular) velocity autocorrelation functions  $C_{VV}(t)$  ( $C_{\omega\omega}(t)$ ).



- $\diamond$  Positive  $t^{-3/2}$  ( $t^{-5/2}$ ) long-time tail in (A)VAFs for concentrated Q2D hard-sphere systems at  $t > \tau_h$ .
- $\diamond$  Area fraction ( $\phi_{2D}$ )-dependence of (A)VAFs is roughly captured using  $\eta_{eff} = (1 + 2.5\phi_{2D})\eta$  for singleprotein (A)VAF functions (dashed).
- ♦ Slower long-time decay of Q2D-SALR systems for stronger attraction.

**Role of sound propagation:** Distinct longitudinal current-current correlation function

$$J_d(q,t) = \frac{1}{Nq^2} \left\langle \sum_{i=1}^N \sum_{j=1}^N \mathbf{q} \cdot \mathbf{V}_i(t) \mathbf{V}_j(0) \cdot \mathbf{q} \exp\left[i\mathbf{q} \cdot (\mathbf{R}_i - \mathbf{R}_j)\right] \right\rangle$$

- hardcore + short-range attraction long-range repulsion
- ♦ Fluid motion is described by multiparticle collision dynamics (MPC) [1].

# 2. Anomalous enhancement of H(q)

**Hydrodynamic** function H(q): Characterizes strength of hydrodynamic interactions (HIs).



- ♦ Divergence of H(q) as  $q^{-1}$  for  $qR \leq 1$ :
- ♦ Well captured by theoretical predictions (dashed) for Q2D hard-sphere systems.
- $\diamond$  SALR system: typical  $q^{-1}$  behavior at small q. Stronger attraction gives rise to higher amplitude of  $H(q \approx 0)$ .



- ♦ Anti-correlations (dashed ellipse) in VAFs for Q2D hard-sphere systems at larger  $\phi_{2D}$  due to multiple scattering of sound.
- $\diamond$  Sound damping at small q persists much longer than single-particle sonic time  $\tau_c$ .
- ♦ Small, intermediate, and large wavenumber regions are observed consistent with those of  $H_d(q, t)$ .

# 4. MPC results for lateral protein diffusion near fluid-fluid interface

Coarse-grained protein-membrane-cytosol model using MPC Hydrodynamic effects of fluid viscosity difference (viscosity ratio  $\eta_B/\eta_A = 0.21$ ).





Solid curves are numerical calculations from Ref. [2].

Dumbbell model of a GPCR at fluid-fluid interface  $(\eta_B/\eta_A = 0.21)$ 



- $\diamond$  Onset of HIs at  $t \sim \tau_h$  (single protein vorticity) diffusion time).
- $\diamond H_d(qR \leq 1, t) > 0$ : enhancement of HIs.  $H_d(1 \leq qR \leq \pi, t) < 0$ , backflow-induced anti-correlations.  $H_d(qR \approx \pi, t) > 0$ : protein drags along its neighbours.



 $\diamond$  Mean-squared displacement (MSD) of bead centers  $C_A$  and  $C_B$ , and hydrodynamic center of mobility  $C_{\gamma}$ .  $C_{\gamma}$  has smallest MSD, for  $1 \ll$  $t/t_h^A \ll 10^2$ .

 $\diamond$  For  $t \gg t_h^A$ : MSD enhanced in presence of two interfaces (solid curves, marked by dashed ellipse).

## References & Acknowledgement

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