Functional Dynamics of Biomolecular Machines Revealed by Theoretical Methods

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Functional dynamics plays an important role when biomolecular machines fulfill their functions. For example, motor proteins walk on the rail or rotate relative to the stator by using ATP hydrolysis energy. Transporter proteins transport their substrates across the membrane by changing their conformation between the inward-open and outward-open states. We aim to clarify molecular mechanism of these precise, yet dynamic nano-machines developed by nature.

Functional dynamics of biomolecular machines involve wide spectrum of intricate motions and reactions. In order to understand such dynamics, we need a multiscale approach to cover full range of these motions and reactions. Conventional atomistic molecular dynamics (MD) simulations alone cannot cover millisecond-long (or even longer) functional dynamics, especially for a large system like typical biomolecular machines. Thus, we use techniques like importance sampling, coarse-graining, and statistical/kinetic modeling to tackle this problem.

We have been working on biomolecular motors such as ATP synthase and chitinase. ATP synthase is a rotary motor that produces most of ATP required in the cell. It is composed of two rotary motors: F_o and F_1. F_o motor is embedded in the membrane driven by proton gradient, while F_1 motor is driven by ATP hydrolysis reaction. We studied how rotation of F_1 is caused by elementary steps such as product release from the catalytic site. Chitinase is a new type of molecular motor that uses hydrolysis energy of single chitin chain, a polysaccharide from exoskeleton of crab *etc.*, for its unidirectional motion. The sliding motion of chitin chain into the catalytic site of chitinase was studied by atomistic simulations. We also developed a novel framework to estimate free energy profiles and diffusion coefficient from single-molecule trajectories.

Transporters are membrane proteins that transport their substrates across the membrane. We have studied Na^+/H^+ antiporter that exchanges sodium ions and protons inside and outside the cell. The ion-transport cycle was simulated in atomic detail with the transition path sampling technique. The simulations predicted the mutation that can speed up the ion transport, which was confirmed by experiments. Another membrane-associated protein, F-BAR protein Pacsin1 that remodels the membrane, is our interest too. The curvature induction and sensing of Pacsin1 on the membrane was studied by multiscale MD simulations using both all-atom and coarse-grained models.

Selected Publications

- K. Okazaki and G. Hummer, "Phosphate Release Coupled to Rotary Motion of F_1-ATPase," *Proc. Natl. Acad. Sci. U.S.A.* **110**, 16468–16473 (2013).
- K. Okazaki and G. Hummer, "Elasticity, Friction, and Pathway of γ-Subunit Rotation in F_oF_1-ATP Synthase," *Proc. Natl. Acad. Sci. U.S.A.* **112**, 10720–10725 (2015).
- A. Nakamura, K. Okazaki, T. Furuta, M. Sakurai and R. Iino, "Processive Chitinase is Brownian Monorail Operated by Fast Catalysis after Peeling Rail from Crystalline Chitin," *Nat. Commun.* **9**, 3814 (2018).
- K. Okazaki, D. Wöhlert, J. Warnau, H. Jung, Ö. Yildiz, W. Kühlbrandt and G. Hummer, "Mechanism of the Electroneutral Sodium/Proton Antiporter PaNhaP from Transition-Path Shooting," *Nat. Commun.* **10**, 1742 (2019).

1. Mechanism of Unidirectional Motions of Chitinase

Processive cellulase and chitinase recently have been cast new light as a different type of biomolecular motors that use hydrolysis energy of polysaccharides for their unidirectional movements. With the high-precision single-molecule experiments, it was shown that chitinase SmChiA showed fast unidirectional movement of ~50 nm s^{-1} with 1-nm forward and backward steps.[1] The rate constants of the hydrolysis reaction and decrystallization of single chitin chain were also clarified. The sliding motion of chitin chain into the catalytic site of chitinase was simulated by atomistic simulations. These results suggested that chitinase works by the burnt-bridge Brownian ratchet mechanism. We have been developing a novel framework to estimate its diffusion model from the single-molecule trajectories behind this mechanism too.

2. Mechanism of Na^+/H^+ Antiporter and Engineering of a Faster Transporter

Na^+/H^+ antiporters control pH and Na^+ concentration in the cell by exchanging sodium ions and protons across lipid membranes. They belong to the cation/proton antiporter (CPA) superfamily, and prevail in all domains of life. The archaeal Na^+/H^+ antiporters PaNhaP from *Pyrococcus abyssi* and MjNhaP1 from *Methanocaldococcus jannaschii* as well as human NHE1, which is linked to a wide spectrum of diseases from heart failure to autism and has no structure solved yet, are electroneutral antiporters of the CPA1 family, exchanging one proton against one sodium ion. As a model system in mechanistic studies of electroneutral Na^+/H^+ exchange, we studied the transport mechanism of PaNhaP.[2]

Na^+/H^+ antiporters use the gradient of either sodium ion or proton to drive the uphill transport of the other ion (Figure 1A). The conformational transition of the transporter makes the ion-binding site accessible from either side of the membrane in the alternating manner. For PaNhaP, the inward-open conformation was obtained by X-ray crystallography, while the outward-open conformation is not known experimentally. We modelled the outward-open conformation by MDFF flexible fitting to the low-resolution outward-open structure of the homologous MjNhaP1 from cryo-EM, followed by the long equilibrium MD simulations. It was shown that the transporter domain moves ~3.5 Å in the direction normal to the membrane to take the outward-open state (Figure 1B).

The inward-open and outward-open conformations described above only provides the end points of the ion-transport. The transition dynamics between the two states is central to the transport mechanism, revealing at once rate-limiting steps, substrate pathways, and the opening and closing of the gate preventing ion leakage. However, with ion exchange occurring on a timescale of seconds at ambient conditions, regular MD simulations are far too slow to resolve transitions. Instead, we can resort to importance sampling of transition dynamics. To sample unbiased transition paths between the inward- and outward-open states, we used techniques from the transition path sampling.

In analysis of the transition paths, we found hydrophobic gates above and below the ion-binding site, which open and close in response to the domain motions (Figure 1C). From the reaction coordinate analysis, it was shown that open-close motion of the outside gate (Ile163-Tyr255) is a rate-limiting step of the alternating-access conformational change. Based on this result, we weakened the outside gate by mutating the residues to both alanine. It was expected that this mutation lowers the barrier and makes the ion transport faster. It was confirmed by experiments that the ion-transport speed of the mutant is indeed twice faster than the wild-type transporter.

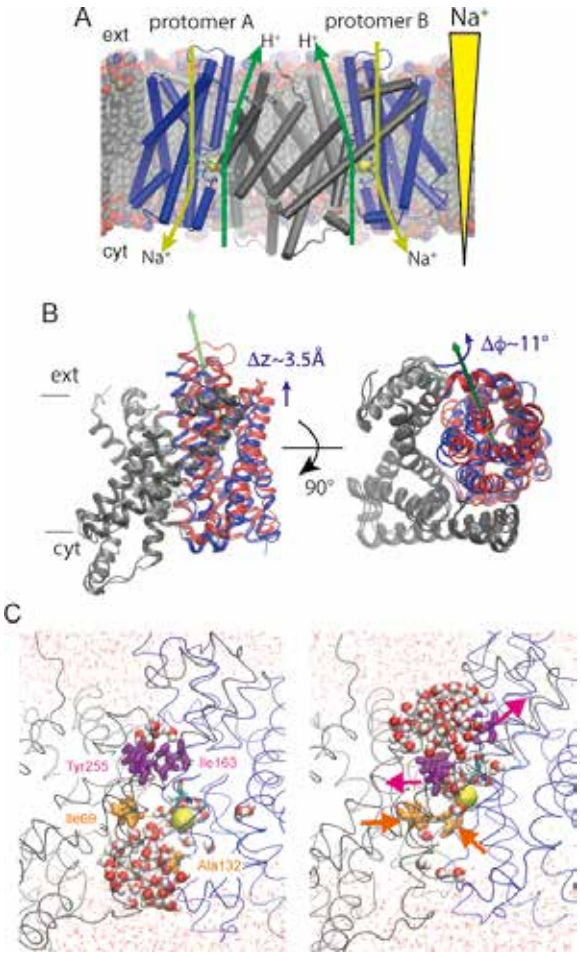

Figure 1. (A) PaNhaP dimer structure. (B) Comparison of the transporter domain between the inward-open (blue) and outward-open (red) states. (C) The outside (purple) and inside (orange) gates found in the transition paths.

References

1) A. Nakamura, K. Okazaki, T. Furuta, M. Sakurai and R. Iino, *Nat. Commun.* **9**, 3814 (2018).
2) K. Okazaki, D. Wöhlert, J. Warnau, H. Jung, Ö. Yildiz, W. Kühlbrandt and G. Hummer, *Nat. Commun.* **10**, 1742 (2019).