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Molecular basis for rotational switching in the bacterial flagellar motor

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The bacterial flagellar motor is one of the most efficient rotary motors known to man. It rotates at hundreds of revolutions per second, yet can reverse its direction in less than one millisecond [1], [2]. Both of these attributes facilitate the rapid movement of bacteria towards favourable environments. The motor uses the potential energy from an electrochemical gradient of cations [3] across the cytoplasmic membrane to generate torque. A rapid switch from counterclockwise to clockwise rotation determines whether a bacterium runs smoothly forward or tumbles to change its trajectory [4], [5]. A protein called FliG forms a ring in the rotor of the flagellar motor that is involved in the generation of torque [6], [7] through an interaction with the cation channel forming stator subunit MotA [8]. FliG has been suggested to adopt distinct conformations that induce switching but these structural changes and the molecular mechanism of switching are unknown. We have recently determined the X-ray structure of the full-length FliG protein from *Aquifex aeolicus* [9], identified conformational changes that are involved in rotational switching and uncovered the structural basis for the formation of the FliG torque ring. This allowed us to propose a model of the complete ring (Fig. 1) and switching mechanism in which conformational changes in FliG reverse the electrostatic charges involved in torque generation.

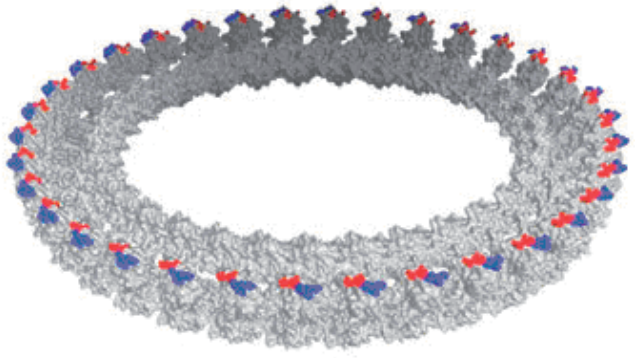

Figure 1: Proposed model of the torque ring of the *A. aeolicus* flagellar motor consisting of 34 FliG proteins. Charges known to be involved in torque generation and switching are located at the outer circumference of the ring [9].

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Structure and function of protein-based metabolic organelles in bacteria

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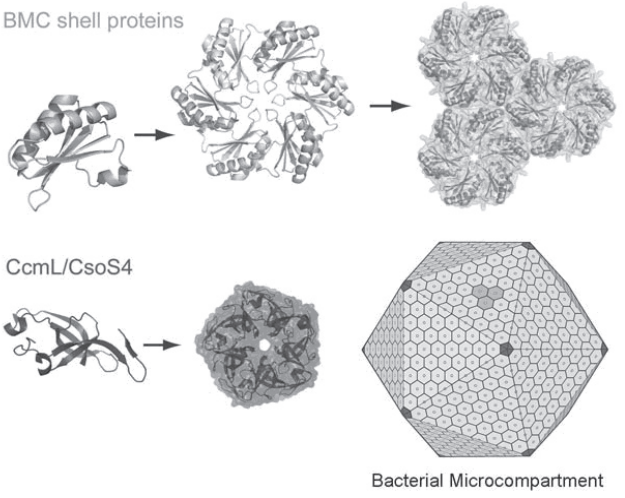
Although it is not widely appreciated, many bacterial cells contain giant protein-based organelles that make it possible to carry out certain metabolic processes in a sequestered environment [1,2]. The simplest and best characterized type of bacterial microcompartment (BMC) is the carboxysome, which in cyanobacterial cells encapsulates the enzymes RuBisCO and carbonic anhydrase within a capsid-like protein shell in order to enhance the rate of CO_2 fixation. Other more complex types of bacterial microcompartments are produced under specific conditions by well-studied bacteria such as *Salmonella* and some strains of *E. coli*. These more complex microcompartments typically encapsulate a larger set of enzymes, which metabolize a small molecule (like ethanolamine) without allowing the escape of a volatile or toxic metabolic intermediate (like acetaldehyde). The main (so-called BMC) shell proteins form hexamers, which further assemble in side-by-side fashion to form a tightly packed molecular layer. Other minor proteins form pentamers that are believed to sit at the vertices of the roughly icosahedral shell. Intact microcompartments are roughly 100 nm in diameter, with an outer shell composed of a few thousand shell proteins and an interior containing a similar numbers of enzyme molecules. Crystal structures of numerous shell proteins from various microcompartments are shedding light on principles of protein assembly and evolution, and mechanisms of molecular transport of substrates and products. Current crystallographic work will be presented.



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Unlikely crystals: poxvirus spheroids in vivo crystallization

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