

Structure of a bacterial energy-coupling factor transporter

With the support by the National Natural Science Foundation of China and the Ministry of Science and Technology (973 Programs 2009CB918801 and 2013CB910602), Prof. Shi Yigong's laboratory in School of Life Sciences, Tsinghua University, reported the crystal structure of a bacterial energy-coupling factor transporter, which is published in *Nature*, **2013**, 497(7448): 272—6.

The energy-coupling factor (ECF) transporters constitute a novel family of conserved membrane transporters in prokaryotes that have a similar domain organization to the ATP-binding cassette transporters. Each ECF transporter comprises a pair of cytosolic ATPases (the A and A' components, or EcfA and EcfA'), a membrane-embedded substrate-binding protein (the S component, or EcfS) and a transmembrane energy-coupling component (the T component, or EcfT) that links the EcfA-EcfA' subcomplex to EcfS. With the crystal structure of a nucleotide-free ECF transporter from *Lactobacillus brevis* at a resolution of 3.5 Å, the molecular mechanism of the ECF transporters is uncovered. The structure revealed that the T component has a horseshoe-shaped open architecture, with five α -helices as transmembrane segments and two cytoplasmic α -helices as coupling modules connecting to the A and A' components. Strikingly, the S component, thought to be specific for hydroxymethyl pyrimidine, lies horizontally along the lipid membrane and is bound exclusively by the five transmembrane segments and the two cytoplasmic helices of the T component. These structural features suggest a plausible working model for the transport cycle of the ECF transporters.

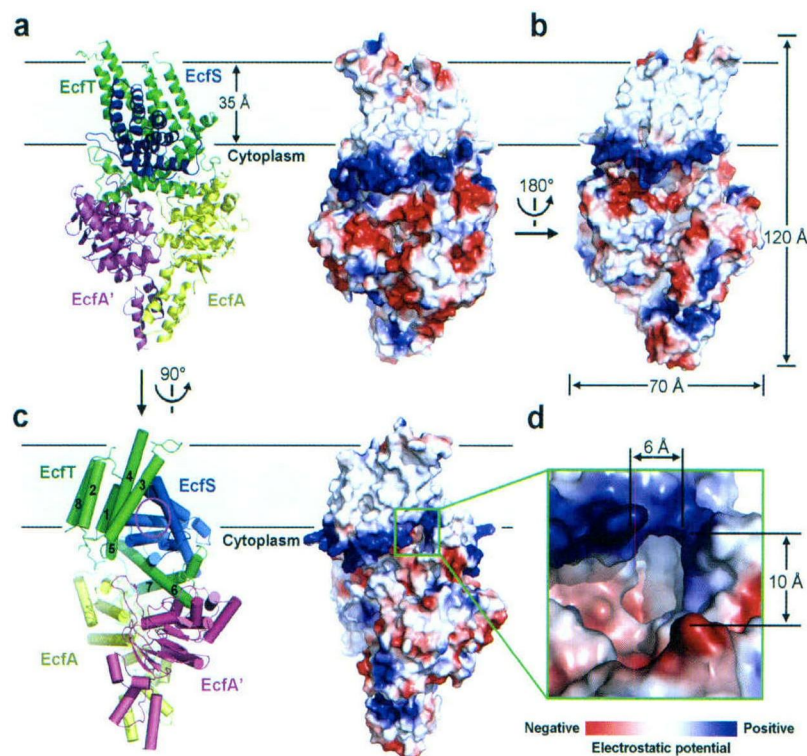


Figure Overall structure of a quaternary ECF transporter. **a**, Structure of a quaternary ECF transporter shown in ribbon representation (left) and in terms of surface potential (right). **b**, The electrostatic surface potential of the ECF transporter is viewed after a 180° rotation relative to that in figure **a**. **c**, The putative substrate-binding pocket in EcfS (indicated by a magenta circle in the left panel and a green box in the right panel) opens just below the lipid membrane on the cytoplasmic side. **d**, A close-up view of the location of the putative substrate binding pocket.