Structure Watch

TURNING HEADS

Reporting in *Science*, Cate and colleagues now describe two 'head-turning' ribosomal structures. The 3.5-Å-resolution crystal structures are of 70S ribosomes from *Escherichia coli*. Over the past 45 years, a wealth of biochemical data have been obtained for the *E. coli* ribosome, and these data have been interpreted in light of the structures of ribosomes from other species. Now, at last, these data can be interpreted in light of the corresponding structural information.

The crystals contained two independent copies of the ribosome that adopted markedly different conformations. For example, the differences between the two structures indicate that the head of the small 30S subunit rotates in a manner that matches the path taken by tRNAs through ribosomes. During protein synthesis, following peptide-bond formation, tRNAs move from the A and P sites to the P and E sites, and this movement seems to require an 'unlocking' step. Comparing the new structures with previous data indicates that the 'lock' is a steric block between the P and E sites on the small subunit. The authors therefore propose that, together with the ratchet-like motion of the two ribosomal subunits that has been seen previously, the elongation-factor-catalysed opening of this lock and a turn of the head provide a potential mechanism for controlling mRNA and tRNA movements during translocation.

REFERENCE Schuwirth, B. S. *et al.* Structures of the bacterial ribosome at 3.5 Å resolution. *Science* **310**, 827–834 (2005)

CAUGHT CONDUCTING

Membrane proteins and secreted proteins are translocated into or across cell membranes by protein-conducting channels (PCCs), and Frank and colleagues have now obtained a snapshot of the co-translational insertion of a nascent polypeptide into a PCC. Using single-particle cryo-electron microscopy and computational methods, they have reconstructed a structure of the PCC from *Escherichia coli* — the heterotrimeric complex SecYEG — bound to a translating ribosome.

In their reconstruction, mRNA, three tRNAs, the nascent polypeptide chain and the detailed features of two PCCs can be discerned. One of the PCCs is a translocating PCC; it makes three contacts with the ribosome, which leave a large frontal opening through which the translocating polypeptide can be seen. Surprisingly, a second PCC was found bound to the mRNA-exit site and, although this PCC was non-physiologically bound, the authors believe that its structure might reflect that of a non-translocating PCC bound to the polypeptide-exit site. By fitting a related archaeal PCC structure into the electron densities for the two PCCs, the authors showed that each PCC contains two SecYEG complexes. They were also able to differentiate between the two main models for SecYEG monomer arrangement, which has helped to clarify the structural and mechanistic details of co-translational translocation.

REFERENCE Mitra, K. *et al.* Structure of the *E. coli* protein-conducting channel bound to a translating ribosome. *Nature* **438**, 318–324 (2005)