which specify each of the amino acids and the complementary anticodon sequences of the appropriate aminoacyl-tRNAs at the 30S subunit decoding site; promote catalysis of the peptide bond between the resident peptidyl-tRNA and the incoming aminoacyl-tRNA by an activity located in the 50S subunit; and carry out the coordinated translocation of the mRNA and the newly extended peptidyl-tRNA from the aminoacyl-tRNA site to the peptidyl-tRNA site.

Frank *et al.*[1] have assigned many of these functional sites on their model by analogy with what is known from lower-resolution ribosome models, using characteristic morphological features as guides. These identifications must be regarded with some caution, however, as substantive landmarks on the new structure, such as the locations of specific ribosomal proteins, the positions of defined segments of rRNA or the placement of tRNA, mRNA and protein ligands, have not yet been pinned down. Therefore, it is not possible to make full use of the vast storehouse of information on the relative positions of the ribosomal constituents determined by immune electron microscopy, neutron diffraction and intramolecular crosslinks[2–6]. By the same token, a host of data on the proximity of mRNA, tRNA, antibiotic and protein ligands to these components[6–8] cannot yet be employed to best advantage.

Despite the difficulties in making definitive correlations of the morphological features visualized by cryo-electron microscopy with specific ribosomal components and ligands at this time, some of the former, such as the head and platform of the 30S subunit, and the L1 arm, central protuberance and L7/L12 stalk of the 50S subunit, are so distinctive that there can be little doubt that Frank *et al.*[1] have made the correct assignments in these cases and reasonable proposals in others. Perhaps the most controversial feature of the new model is the bifurcating tunnel through the 50S subunit, which is imagined to serve as the exit route for nascent polypeptide chains. In particular, implication of this tunnel in protein export is problematical because, in contrast to the secretory process in eukaryotes, there is no compelling evidence that the *E. coli* ribosome docks with specific receptors in the cytoplasmic membrane[9].

Interest in the prokaryotic ribosome has remained high, in part because of the tantalizing expectation that sustained and diligent effort will lead to an intimate understanding of the way in which this complex organelle mediates protein synthesis. The *E. coli* prototype clearly has the advantage here as no eukaryotic ribosome has been subjected to the same level of scrutiny. Almost every aspect of the *E. coli* ribosome has been examined, from the protein–rRNA interactions that underlie assembly to the functional role of individual nucleotides in synthesis of the peptide bond, and it is from prokaryotes that inferences about the key role of rRNA in ribosome function have been drawn[10]. More generally, it has become apparent that the basics of ribosome structure and protein biosynthesis have been conserved to a remarkable extent throughout evolution. Thus, there is a strong belief that a detailed understanding of the *E. coli* ribosome should be of wide applicability to ribosomes from all organisms.

Although the path ahead is daunting, the detailed model described by Frank *et al.*[1] offers a promising foundation for future experimentation. The first step might be to determine how the morphological features seen in cryo-electron microscopy reconstructions relate to specific ribosomal proteins and specific domains of the rRNA. A second could be to ascertain the locations of the ligands and the functional sites to which they bind. A third would be to investigate the nature of the multiple intersubunit bridges and of the tunnel(s) that the nascent polypeptides are supposed to traverse while avoiding unfavourable steric contacts with surrounding ribosomal constituents.

When all is said and done, what Frank *et al.*[1] present is not really a model of protein synthesis in a mechanistic sense, but a plausible depiction of the apparatus that carries out protein synthesis. While the new structural insights are important in themselves, they draw attention to the intricacy of the ribosome and the challenge of making sense of this marvellous machine in all its complexity. The structure of the ribosome as derived from cryo-electron microscopy is likely to become the new pattern for modelling the ribosome and ribosome–ligand interactions. □

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DAEDALUS

Star Wars 2

In the early days of radar, there were hopes that it might be a weapon as well as a detector. A strong radar beam, it was thought, might usefully sabotage the electrics of an enemy aircraft. This soon proved unfeasible. Daedalus is now reviving the idea.

A conventional radar beam diverges too fast to be an effective weapon. Even with the biggest steerable dish-aerial, 100 kW of power at the transmitter is diluted to 1 W per square metre or less at the target. But Daedalus recalls the aperture-synthesis technique used by radioastronomers. A network of aerials spread out over a large area, but coupled together as a phase-coherent receiver, has the angular resolution of a single aerial as big as the whole area containing the network. Modern synthetic-aperture systems can locate a radio-source to within a tiny fraction of an arcsecond. So Daedalus plans to run such an array in reverse, as a transmitter — which will, of course, have the same angular resolution. A set of radar transmitters distributed over a few thousand square kilometres, worked as a synthetic-aperture array and aimed to converge at a distant aircraft, could focus on it with awesome precision. An array resolving to 0.1 arcsec could reach out 100 km and still concentrate its power in a circle 10 cm across.

Focused to this intensity, 100 kW of microwave energy would melt a hole in any aircraft. Even a brief or glancing strike would wreck its avionics. The beam could be aimed and steered by instant computer-generated phase-shift commands. An aircraft could be destroyed as soon as sighted, and even a big fleet of them could be knocked out in rapid succession. A really big synthetic-aperture radar could even attack missiles and satellites in space, making a 'Star Wars' defence feasible at last.

As a weapon, this ultimate in phased arrays is fairly benign. It threatens nobody, and can only be used to defend the area over which it is distributed. Terrorists could not steal it or hijack it. Even if they took over one aerial installation they couldn't focus it without the others.

The system might even have peaceful uses. An electric model aircraft has already been powered by a microwave beam aimed at it from below. The technology could easily be scaled up. It should be feasible to fit a light aircraft with microwave-rectifying wings, and use their output to drive electric propellers. The resulting craft would need no fuel and would eject no exhaust. Simple, silent and safe, it could transform short-haul civil aviation. David Jones