The structure of a bacterial 30S ribosomal subunit

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pl11 **The structure of a bacterial 30S ribosomal subunit**. V. Ramakrishnan, D. Brodersen, A.P. Carter, W.M. Clemons, Jr., R. Morgan-Warren, B.T. Wimberly, *MRC Laboratory of Molecular Biology, Hills Road, Cambridge CB2 2QH, United Kingdom.*
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The 30S ribosomal subunit consists of about 1540 nucleotides of RNA and 21 proteins, with a total mass of nearly 850 kilodaltons. It provides the binding sites for mRNA and the anticodon stem-loop of tRNA during translation. The subunit is responsible for decoding, which involves recognition that the correct codon-anticodon pairing has occurred. The decoding step is a prerequisite for conformational changes that eventually results in peptide bond formation in the 50S. Translocation also involves a movement of the 30S with respect to mRNA by precisely one codon and concommitant movements of tRNA. Finally the 30S subunit is the site of action of many antibiotics. Since none of these phenomena are understood in molecular terms, it is clear that mechanistic studies on translation will greatly benefit from a high resolution structure of the ribosome.

Developments during the last decade in the brightness, stability and tunability of synchrotron sources, the use of anomalous scattering at absorption edges, large CCD area detectors, more powerful computation and improved software for data analysis and phasing have all contributed to making the ribosome a tractable problem despite its large size.

We have crystallized the 30S subunit from *Thermus thermophilus.* These crystals diffract to beyond 3 Å resolution. Over a year ago, we solved the structure of this crystal form to a resolution of 5.5 Å. At this resolution, we could place all proteins of known structure and trace the fold of the central domain of 16S rRNA. We could also identify the penultimate stem-loop of 16S rRNA, part of which is involved in decoding. The structure sheds interesting light on protein-protein interactions as well as a switch involved in translational fidelity.

Currently, we are trying to improve the resolution to a point at which a complete model for the ribosome can be built and refined. Our progress towards this goal will be reported, along with any new structural and functional insights.

Notes