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Small-Angle X-ray Scattering Study of Complexes of Individual Components from *E. Coli* Ribosomes*

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As part of a general X-ray scattering study on individual ribosomal components and their specific complexes, this study deals with the proteins S1, S8, S15, S16 and S20, the the S4-binding region of 16-S RNA, S4-RNA, as well as the specific complexes 5-S RNA–L18, 5-S RNA–L18–L25 and S4–RNA–S4; the proteins were prepared under non-denaturing conditions. In agreement with the previous X-ray scattering studies (Österberg, Sjöberg, Liljas & Pettersson, 1976; Österberg, Sjöberg & Garrett,1976*a*; Österberg, Sjöberg, Garrett & Littlechild 1977), involving the proteins L7/L12, L18, L25 and S4, the present data indicate that the proteins are elongated. However, there are individual variations; for instance, S4, L7/L12, and S1 appear to be more elongated than S8, S15 and S16. Most of the curves can be interpreted in the form of the scattering from elongated ellipsoids, but an alternative description of the data recorded for the proteins S4 and L7/L12 takes into consideration not only the well-structured domains of the molecules but also the possibility that there might be some flexible parts. Some of the structured fragments have been prepared in pure form (Liljas & Kurland, 1976; Changchien & Craven, 1976) and that of L7/L12 has been crystallized (Liljas & Kurland, 1976). The X-ray scattering from the L7/L12 fragment is in good agreement with the data previously reported (Österberg, Sjöberg, Liljas & Pettersson, 1976).

X-ray scattering titrations of the 5-S RNA complexes of L18 and of L18 and L25 indicate that the 1:1 and 1:1:1 complexes predominate *in vivo*. There is a slight but defined increase in the radius of gyration at the stepwise binding of first L18 and then L25 to 5-S RNA, indicating that the electron-density centres of the proteins must be relatively far from that of 5-S RNA. If the Y-shaped 5-S RNA structure (Österberg, Sjöberg & Garrett, 1976*b*) is assumed, then, it is possible to explain the data *via* the scattering from models where L18 and L25 interact with both of the minor arms of the Y-model (*cf.* Österberg & Garrett, 1977).

The binding region for protein S4 on 16-S RNA, S4-RNA, yields an X-ray scattering curve that, in its proximal part, can be interpreted as the scattering from an oblate ellipsoid; the best-fitting two-parameter ellipsoid has the dimensions of $132 \times 132 \times 32$ Å (Österberg, Sjöberg, Garrett & Ungewickell, 1977). X-ray scattering titration data indicate that S4-RNA forms a stable S4 complex with $\log K \sim 7$. The X-ray scattering from this 1:1 complex is very similar to that of S4-RNA, indicating that no major conformational change of S4-RNA takes place at the complex formation.

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Neutron Small-Angle Scattering of *E. Coli* Ribosomes. A Contrast Variation Study

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Neutron small-angle scattering with the contrast-variation method has established that for 50S and 70S ribosomal particles the RNA–protein distribution is such that the RNA component is located predominantly towards the interior and the protein towards the exterior of the particle. In contrast, the 30S subunit is much more homogeneous in its RNA–protein distribution. The shape of the 50S subunit has been determined at low resolution.