

### **X-ray Crystal Structures of the *E. coli* Ribosome**

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We are using x-ray crystallography to probe the structural basis for the many aspects of protein biosynthesis that require the intact ribosome. Our goal is to make an atomic-resolution “movie” of a ribosome in the process of making a protein. We have obtained crystals of the entire *E. coli* ribosome that diffract x-rays to a resolution of 3.1-3.2 Å. Thus, we now have the means to determine the first atomic-resolution structure of the intact ribosome, the first frame of the movie. Moreover, we are using these crystals to probe in atomic detail the effects of antibiotics on the full ribosome and mutations in the ribosome that lead to antibiotic resistance or perturb key steps in translation. We are presently refining ribosome structural models at a resolution of 3.5 Å, the results of which will be presented.

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