

Microsymposium

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How my Experiences at the MRC-LMB led to the Structure of the Ribosome

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Max Perutz's Dunham Lectures at Harvard in 1963, in which he showed the first atomic structure of a protein (myoglobin) that anyone in the room had ever seen, led to my working on the structure of carboxypeptidase A (CPA) (in the Lipscomb lab) before going to the MRC LMB in Cambridge. "Rapid" data collection on CPA in the mid-1960s was 5,000 reflections in a week, and now obtaining 2.7 Å resolution data on crystals with two 70S ribosomes in the asymmetric unit takes 5 minutes. Importantly, the LMB promoted creative and novel science because of its cooperative, interactive atmosphere where everyone interacted in the hall or over coffee, lunch or tea. This influenced how I have carried out science over the subsequent years. In the canteen, Crick, Brenner, Perutz, etc., would be interacting and talking with postdocs and students about asking important questions and solving scientific problems. It was a great place to learn, develop and use the most advanced methods in protein crystallography and apply them to explore the most interesting and significant questions in molecular biology. The importance of integrating structure and function in our research goals was made clear. My interactions in the Cambridge LMB led me to pursue the structural basis for understanding Crick's Central Dogma of Molecular Biology – DNA makes DNA makes RNA makes proteins. This resulted in our ultimately determining the structures of the ribosome and its various complexes.

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