MBG FOCUS TALK

hosted by Lasse B. Jenner

MBG Focus Talks in Molecular Biology

Wednesday 28th October 14:15 - 15:00

3130-303 SciencePark Auditorium

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Investigation of Protein Synthesis by Cryo Electron Microscopy

Protein synthesis is one of the fundamental processes in the cell. Here we present structural investigations of this process at different levels of complexity using different techniques and methods.

In order to investigate the formation and structural organization of polyribosomes (polyRs) we have used sedimentation and cryo electron tomography techniques. The conformations of eukaryotic polyribosomes formed in a long-term cell-free translation system were analyzed over all the active system lifetime. Three distinct types of the conformations were observed: (i) circular polyribosomes, (ii) linear polyribosomes and (iii) densely packed 3D helices. At the start, during the first two rounds of translation mostly the circular (ring-shaped and double-row) polyribosomes and the linear (free-shaped and zigzag-like) polyribosomes were formed. The progressive loading of the polyribosomes with translating ribosomes induced the opening of the circular polyribosomes and the transformation of a major part of the linear polyribosomes into the dense 3D helices. Functional tests showed a reduced translational activity in the fraction of the 3D helical polyribosomes.

For investigation of the isolated 80S ribosome we have used the single particle method and a new way for image data collection and processing. Thanks to this, we were able to obtain the near-atomic structure of the human ribosome and build an atomic model of it. The structure has an average resolution of 3.6 Å and reaches 2.9 Å resolution in the most stable regions and thus provides unprecedented insights into rRNA entities and amino acid side-chains of the ribosomal proteins.