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Visualization of conformational modes of ribosomal complexes by multi-particle cryo-EM.

The ribosome is a dynamic macromolecular machine capable of undergoing large-scale conformational changes. Throughout the four functional phases of translation, i.e. initiation, elongation, termination and recycling the ribosome is controlled and guided by translation factors and binding of such a factor can induce conformational movements within the ribosomal machinery. However, the ribosome appears to be also capable of spontaneous conformational changes that occur in the absence of factor binding. Recent structural work has shown that pre-translocational (PRE) complexes from prokaryotes are conformational heterogeneous and that the ratchet-like subunit rearrangement and tRNA hybrid state formation occurs in a subset of the complexes [1, 2]. This behaviour has been previously proposed by single molecule FRET experiments [3, 4]. By using cryo-EM and multi particle methods we can directly visualize various conformational modes of the ribosome in a variety of other ribosomal complexes as well, including a PRE complex from eukaryotes, a decoding complex [5], a 80S-IRES complex and complexes between the 70S ribosome and EF-G. Thus, the ribosome is even more dynamic than previously anticipated. Our results support the emerging theory of the energy landscape for the ribosome [4].

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