Differences in the path to exit the ribosome across the three domains of life.

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As the results of many groups working on translation keep exemplifying, there is no such thing as “the ribosome”. In other words, ribosomes are not all alike, even within the same cell. They all perform the same function (turning a message into a protein sequence), but it’s how they carry it out (rate? regulation? protein folding?) that reveals differences. This article by Dao Duc et al. is original in addressing the differences in the organization of the peptide exit tunnel. They first came up with a procedure to derive the geometry of the tunnel from the structures of several ribosomes from all kingdoms of life. This made them realize that bacterial tunnels (as well as that from ribosomes from organelles!) are about 30% larger than tunnels in eukaryotic ribosomes. The difference mostly lays beyond the constriction site created by protein uL4; in eukaryotes, an extension of uL4 actually leads to a narrowing of the tunnel through a second constriction site, further supported by the presence of eL39. The functional consequence of a narrower tunnel in eukaryotes is that folding of the nascent polypeptide chain is not favored inside the ribosome, as reflected by the presence of chaperones and recognition mechanisms for incorporation of membrane proteins that differ between bacteria and eukaryotes. Overall, this work stresses the meaningful insights about biology that can be gained from thoroughly comparing available structures.

Disclosures

None declared

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