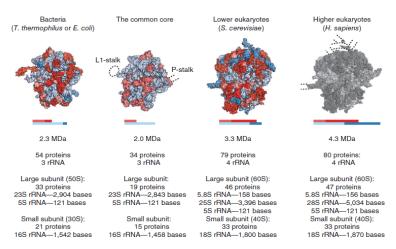
Figure 2 Composition of bacterial and eukaryotic ribosomes and the common core. Bacterial and eukarvotic ribosomes share a conserved core composed of RNA (light blue) and proteins (light red). In addition to the core, ribosomes in each domain of life contain their own set of proteins, extensions and insertions in conserved proteins (both in red). and extension segments in ribosomal RNA (blue), 5.8S and 25S-28S rRNA are both homologous to 23S rRNA in bacteria. Dashed lines around the core indicate positions of flexible stalks of the ribosomes that are usually disordered in X-ray structures. For simplicity these lines are not shown in the other structures. The 80S structure of higher eukarvotes has not vet been determined but is predicted to be highly similar to the structures of yeast and T. thermophila ribosomes, based on genetic analysis and cryo-EM studies. Therefore, instead of the human ribosome structure, the yeast 80S



structure is shown, in gray with dashed lines indicating the positions of human-specific long rRNA expansion segments, the major distinctive feature of ribosomes from higher eukaryotes. The figure is based on X-ray and cryo-EM structures from refs. 15,20,55,82–84.

- Armache, J.P. et al. Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-A resolution. Proc. Natl. Acad. Sci. USA 107, 19748–19753 (2010).
- Ben-Shem, A. et al. The structure of the eukaryotic ribosome at 3.0 A resolution. Science 334, 1524–1529 (2011).
 - X-ray structure of the complete 80S ribosome from *S. cerevisiae* reports the precise location, architecture and registry of all eukaryote-specific proteins and almost all eukaryote-specific rRNA moieties, and describes interactions between ribosomal subunits.
- Jenner, L., Demeshkina, N., Yusupova, G. & Yusupov, M. Structural rearrangements of the ribosome at the tRNA proofreading step. *Nat. Struct. Mol. Biol.* 17, 1072–1078 (2010).
- Dunkle, J.A. et al. Structures of the bacterial ribosome in classical and hybrid states of tRNA binding. Science 332, 981–984 (2011).
- Spahn, C.M. et al. Cryo-EM visualization of a viral internal ribosome entry site bound to human ribosomes: the IRES functions as an RNA-based translation factor. Cell 118, 465–475 (2004).
- Jarasch, A. et al. The DARC site: a database of aligned ribosomal complexes. Nucleic Acids Res. 40, D495–D500 (2012).
 - The paper describes a recently constructed publicly available database of all existing structures of ribosomes; all structures are aligned, and coordinates are available to download in Protein Data Bank (pdb) format.