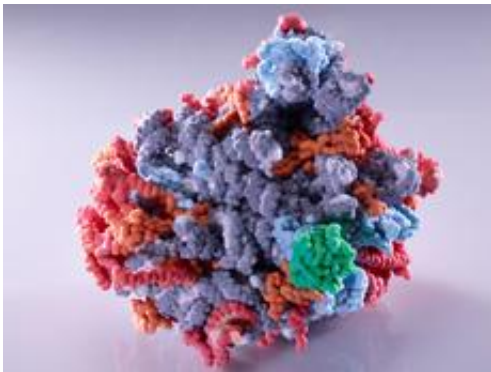


Detailed view of a crucial enzymatic complex revealed

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Model of the large subunit of the ribosome from a higher organism (Photograph: Katharina Bohm, Felix Voigts-Hoffmann / ETH Zürich)

Researchers led by ETH professor Nenad Ban have now completed the three-dimensional structure of the ribosome from a higher organism. This structure will increase the understanding of this cellular “protein factory” and facilitate the development of novel drugs.

The machinery that reads genetic information within a cell and translates it into corresponding proteins, the so-called [ribosome](#), is among the most complex cellular enzymes known in biology. It has been studied for decades. Ten years ago, scientists have solved the first three-dimensional [structure](#) of this complex from prokaryotes (ie. bacteria). They were awarded with the Nobel Prize in Chemistry in 2009.

In higher [organisms](#) such as fungi, plants and animals (so-called eukaryotes), the ribosome is even more complex than in bacteria. Researchers led by Nenad Ban, professor at the Institute for Molecular Biology and Biophysics at ETH Zurich have now solved the three-dimensional structure of the larger of two ribosomal subunits from a higher organism, the single-celled ciliate *Tetrahymena thermophila*. This ribosome is akin to the ones of multi-cellular organisms such as humans. The scientists published their work today in the magazine Science. Researchers of the same group at ETH Zurich had already published the structure of the smaller ribosomal subunit of the ciliate earlier this year.

Towards a better understanding of the ribosomal function

Comparing the ribosomal structures of both, bacteria and higher organisms, will enable scientists to develop novel specific pharmaceutical compounds against pathogens and pests. Among these could be antibiotics and fungicides. Furthermore, the findings could lead to the development of novel antiviral drugs since many viruses need to bind to and manipulate the ribosomes of their host cells in order to replicate.

The newly revealed structure could furthermore help to better understand the initiation of protein synthesis and to gain insights into the evolutionary development of the ribosomes of higher organisms.

Ribosomes of higher organisms have been a major focus at the laboratory of Prof. Ban since 2001. The work of the scientists at ETH Zurich was supported by the National Centre of Excellence in Research (NCCR) in Structural Biology of the Swiss National Science Foundation. Data used for structure determination was collected at the Swiss Light Source.

More information: Klinge S, Voigts-Hoffmann F, Leibundgut M, Arpagaus S, Ban N: Crystal Structure of the Eukaryotic 60S Ribosomal Subunit in Complex with Initiation Factor 6. *Science*.

Provided by ETH Zurich

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