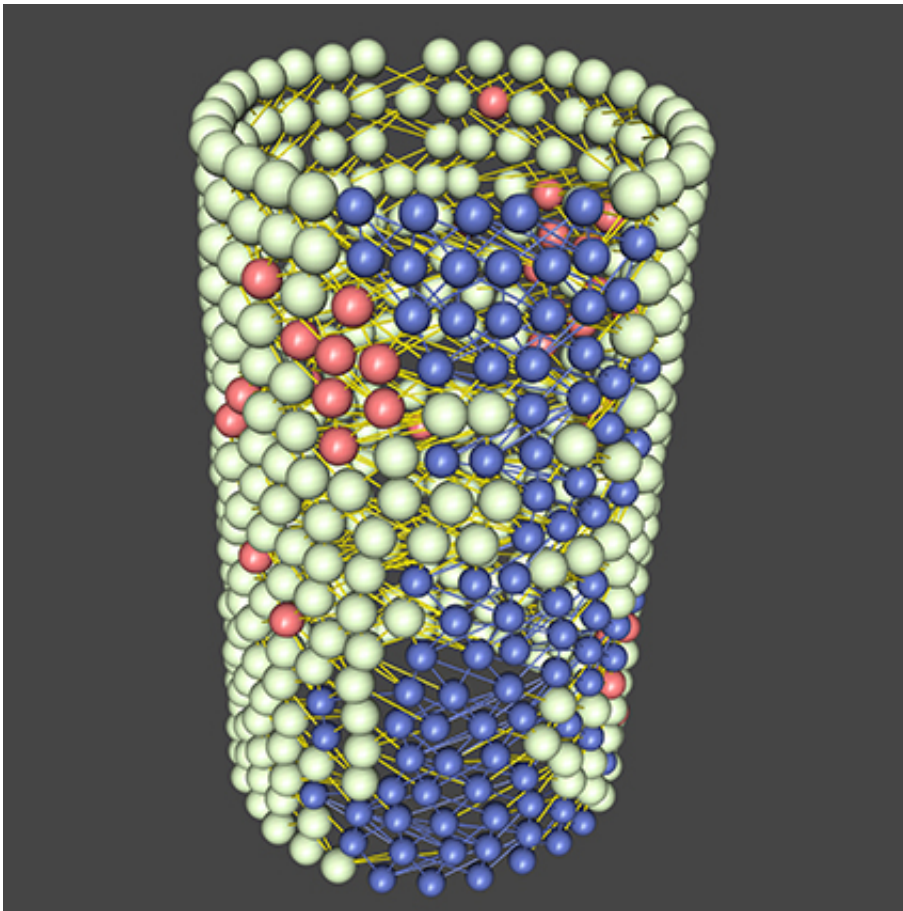


A fresh look inside the protein nano-machines

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The essential nano-mechanic features of proteins can be conveniently studied by a simplified geometry. Taking, for example, a cylinder, and asking for «evolution» to find a fluid channel (shown in blue) a multitude of realistic properties of real proteins appear naturally, and exhibit the advantage of conceptual, rather than detailed models of proteins. Credit: © UNIGE - Jean-Pierre Eckmann

Proteins digest food, and fight infections and cancer, and serve other metabolic functions. They are basically nano-machines, each one designed to perform a specific task. But how did they evolve to match those needs, and how did genes encode the structure and function of proteins? Researchers from the University of Geneva (UNIGE), Switzerland, the Institute for Basic Science, Korea, and the Rockefeller University, U.S., have conducted a study that tackles this question and explains the basic geometry of the gene-to-protein code by connecting proteins to properties of amorphous physical matter.

The full article appears in *Physical Review X*.

A protein is a chain made of 20 different kinds of amino acid with elaborate interactions, and unlike standard physical [matter](#), proteins are selected by evolution. "The blueprint for protein synthesis is written in long DNA [genes](#), but we show that only a small fraction of this huge information space is used to make the functional [protein](#)," explains Jean-Pierre Eckmann, Professor at the Department of Theoretical Physics from the Faculty of Science of UNIGE.

Together with Prof. Tsvi Tlusty from the Center for Soft and Living Matter, Institute for Basic Science (IBS) in Korea and Prof. Albert Libchaber from the Rockefeller University in New York, Prof. Eckmann shows that the only changes in the code that matter are those occurring in the segment of the gene coding the mechanically relevant hinges of the nano-machine. The changes in other regions of this highly redundant code have no impact. "We are now using this new approach to understand the relation between the function and dynamics of several important proteins."

Provided by University of Geneva

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