

Proteins may behave differently in natural environments

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When in an environment similar to that in which they exist naturally, proteins and multiprotein assemblies may demonstrate actions or dynamics different than those they exhibit when in the static form in which they are most often studied, said researchers at Baylor College of Medicine in a report in the current issue of the journal *Structure*.

In a study using electron cryomicroscopy, Dr. Steven Ludtke, assistant professor of biochemistry and molecular biology and co-director of the National Center for Macromolecular Imaging at BCM, and colleagues from BCM and The University of Texas Southwestern Medical Center in Dallas, found such dynamic behavior in a mutant form of a protein called GroEL, which chaperones or helps misfolded protein molecules fold into the shape that allows them to achieve their purpose in the cells. Misfolded proteins have been implicated in a number of neurodegenerative and other diseases.

Electron cryomicroscopy allows scientists to take very detailed two-dimensional images of individual molecules in a native-like environment. Then, using computers and the science of computational biology, they assemble tens of thousands of such images into three-dimensional models that demonstrate the dynamics of the proteins.

When Ludtke and his colleagues followed this procedure with the GroEL mutant with its sister-protein, GroES, they were surprised. Two of the structures were as they expected, but the third was "a strange-looking structure blown up like a balloon," he said.

"This sort of expansion has never been observed before," he said.

In terms of native GroEL, the finding may indicate the need to look at the chaperone itself more closely.

"The expansion was directly related to the function of the assembly. From a more global perspective, this is strong evidence that we need to study how any macromolecule behaves in a solution environment."

Source: Baylor College of Medicine

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